Agent-based modeling for environmental management

Case study: virus dynamics affecting Norwegian fish farming in fjords

Saleh Alaliyat

Thesis for the degree of Philosophiae Doctor (PhD)
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Scientific environment

This thesis uses agent-based modeling to simulate fish disease dynamics to analyze and predict risks, and to support design policies for aquaculture systems.

This doctoral work has been performed in collaboration between the Faculty of Engineering and Natural sciences, the Norwegian University of Science and Technology in Aalesund (NTNU), and the Department of Geography, University of Bergen (UiB), under the supervision of Professor. Pål I. Davidsen (UiB) as main supervisor and under the co-supervision of Professor Harald Yndestad (NTNU).

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Preface

This thesis is submitted to the University of Bergen, Bergen, Norway, for partial fulfillment of the requirements for the degree of philosophiae doctor.

The research for this thesis began in 2012 as a part of Virtuelle Møre project (2006 – 2014) at Aalesund Unversity College, Aalesund. The purpose was to develop flexible, self-adaptive agent-based models for simulation of complex systems.

In 2013, I started to develop agent-based models to identify transmission patterns of fish diseases in marine fish farming in Norway as a case study. I found that agent-based modeling is a powerful simulation technique to simulate complex systems. I compared agent-based method with statistical method that has been used by Dr. Anne Stene in her research about transmission of pancreas disease in marina salmon farming in Norway at Aalesund University College.

I started with simple models to test the ideas, and then I added more complexity to develop a model that can be used in analysis, prediction and managements. The results were presented in different international conferences and journals.

Abstract

Background: Norwegian fish-farming industry is an important industry, rapidly growing, and facing significant challenges such as the spread of pathogens[1], trade-off between locations, fish production and health. There is a need for research, i.e. the development of theories (models), methods, techniques and tools for analysis, prediction and management, i.e. strategy development, policy design and decision making, to facilitate a sustainable industry.

Loss due to the disease outbreaks in the aquaculture systems pose a large risk to a sustainable fish industry system, and pose a risk to the coastal and fjord ecosystem systems as a whole. Norwegian marine aquaculture systems are located in open areas (i.e. fjords) where they overlap and interact with other systems (e.g. transport, wild life, tourist, etc.). For instance, shedding viruses from aquaculture sites affect the wild fish in the whole fjord system.

Fish disease spread and pathogen transmission in such complex systems, is process that it is difficult to predict, analyze, and control. There are several time-variant factors such as fish density, environmental conditions and other biological factors that affect the spread process. In this thesis, we developed methods to examine these factors on fish disease spread in fish populations and on pathogen spread in the time-space domain. Then we develop methods to control and manage the aquaculture system by finding optimal system settings in order to have a minimum infection risk and a high production capacity.

Aim: The overall objective of the thesis is to develop agent-based models, methods and tools to facilitate the management of aquaculture production in Norwegian fjords by predicting the pathogen dynamics, distribution, and transmission in marine aquaculture systems. Specifically, the objectives are to assess agent-based modeling as an approach to understanding fish disease spread processes, to develop agent-based models that help us predict, analyze and understand disease dynamics in the context of various scenarios, and to develop a framework to optimize the location and the load of the aquaculture systems so as to minimize the infection risk in a growing fish industry.

Methods: We use agent-based method to build models to simulate disease dynamics in fish populations and to simulate pathogen transmission between several aquaculture sites in a Norwegian fjord. Also, we use particle swarm optimization algorithm to identify agent-based models' parameters so as to optimize the dynamics of the system model. In this context, we present a framework for using a particle swarm optimization algorithm to identify the parameter values of the agent-based model of aquaculture system that are expected to yield the optimal fish densities and farm locations that avoid the risk of spreading disease. The use of particle swarm optimization algorithm helps in identifying optimal agent-based models' input parameters depending on the feedback from the agent-based models' outputs.

Results: As the thesis is built on three main studies, the results of the thesis work can be divided into three components. In the first study, we developed many agent-based models to simulate fish disease spread in stand-alone fish populations. We test the models in different scenarios by varying the agents (i.e. fish and pathogens) parameters, environment parameters (i.e. seawater temperature and currents), and interactions (interaction between agents-agents, and agents-environment) parameters. We use sensitivity analysis method to test different key input parameters such as fish density, fish swimming behavior, seawater temperature, and sea currents to show their effects on the disease spread process. Exploring the sensitivity of fish disease dynamics to these key parameters helps in combatting fish disease spread. In the second study, we build infection risk maps in a space-time domain, by developing agent-based models to identify the pathogen transmission patterns. The agent-

[1] A pathogen is anything that causes a disease.

based method helps us advance our understanding of pathogen transmission and builds risk maps to help us reduce the spread of infectious fish diseases. By using this method, we may study the spatial and dynamic aspects of the spread of infections and address the stochastic nature of the infection process. In the third study, we developed a framework for the optimization of the aquaculture systems. The framework uses particle swarm optimization algorithm to optimize agent-based models' parameters so as to optimize the objective function. The framework was tested by developing a model to find optimal fish densities and farm locations in marine aquaculture system in a Norwegian fjord. Results show so that the rapid convergence of the presented particle swarm optimization algorithm to the optimal solution, - the algorithm requires a maximum of 18 iterations to find the best solution which can increase the fish density to three times while keeping the risk of infection at an accepted level.

Conclusion: There are many contributions of this research work. First, we assessed the agent-based modeling as a method to simulate and analyze fish disease spread dynamics as a foundation for managing aquaculture systems. Results from this study demonstrate how effective the use of agent-based method is in the simulation of infectious diseases. By using this method, we are able to study spatial aspects of the spread of fish diseases and address the stochastic nature of infections process. Agent-based models are flexible, and they can include many external factors that affect fish disease dynamics such as interactions with wild fish and ship traffic. Agent-based models successfully help us to overcome the problem associated with lack of data in fish disease transmission and contribute to our understanding of different cause-effects relationships in the dynamics of fish diseases. Secondly, we developed methods to build infection risk maps in a space-time domain conditioned upon the identification of the pathogen transmission patterns in such a space-time domain, so as to help prevent and, if needed, combat infectious fish diseases by informing the management of the fish industry in Norway. Finally, we developed a method by which we may optimize the fish densities and farm locations of aquaculture systems so as to ensure a sustainable fish industry with a minimum risk of infection and a high production capacity. This PhD study offers new research-based approaches, models and tools for analysis, predictions and management that can be used to facilitate a sustainable development of the marine aquaculture industry with a maximal economic outcome and a minimal environmental impact.

Abbreviations

2D	Two-dimensions
3D	Three-dimensions
3D maps	Three-dimensional maps
ABM	Agent-based modeling
ABMs	Agent-based models
ab_j	Pathogen ability (energy)
ACO	Ant Colony Optimization
A_r	Attack-rate
C	Constant
CA	Cellular automata
C_d	Average sea currents direction
CFU	Colony forming units
C_s	Average sea currents speed
C_{sr}	Relative current speed
DEM	Discrete event modeling
EIA	Extensive Integrated Aquaculture
$FA_i(t)$	The fish agent
FF(t)	Set of fish farms
GA	Genetic Algorithms
GIS	Geographic Information System
H1N1	Influenza A virus
hed	Heading
I_f	Fish density
IIA	Intensive Integrated Aquaculture
IMTA	Integrated Multi-Trophic Aquaculture
IPNV	Infectious pancreas necrosis virus
IPSO	Integer-particle swarm optimization
IR	Infection risk
I_v	Pathogen density
$L(t)$	Landscape
$L(y)$	Water levels of the sea (surface, y=0)
$L_{cu}(t)$	The sea currents landscape
$L_{sa}(t)$	The salinity landscape
$L_{tm}(t)$	The sea temperature landscape

$L_{tr}(t)$	The terrain landscape
MODS	A SINMOD project: Ocean modeling system for mid-Norway
MOM	Monitoring, On growing fish farm - Modeling
MOO	Multi objective optimization
N_{rf}	Noise value
P(t)	Swarm of pathogens
$PA_j(t)$	The pathogen agent
PD	Pancreas disease
PFU	Plaque forming units
pit	Pitch
PSO	Particle swarm optimization
R	Random number in a range of [0,1]
R_0	Stability point
R_n	Normally distributed floating point
RF_i	Fish resistance factor
S(t)	Aquaculture system
SA	Simulated Annealing
SAV	Salmonid alphavirus
SD	System dynamic
SEIR	Susceptible, exposed, infectious, recovered
SI	Swarm Intelligence
SINMOD	SINTEF ocean modeling system
SINTEF	An independent research organization in Trondheim, Norway
SIR	Susceptible, infectious, recovered
T	Threshold
$T(x, y, z, t)$	Water temperature at the position *(x, y, z)* at the time *t*
$TCID_{50}$	The amount of virus required to kill 50% of infected hosts
std	Standard deviation
$\overrightarrow{v(t)}$	Velocity vector
w	Inertia weight

List of publications

Alaliyat, S., Osen, O. L. and Kvile, K. O. (2013), An Agent-Based Model To Simulate Pathogen Transmission Between Aquaculture Sites In The Romsdalsfjord, Proceedings of the 27th European Conference on Modeling and Simulation, Aalesund, Norway, pp. 46–52.

Alaliyat, S., Yndestad, H. and Sanfilippo, F. (2014), Optimization of Boids Swarm Model based on Genetic Algorithms and Particle Swarm Optimization Algorithm (comparative Study), Proceedings of the 28th European Conference on Modeling and Simulation, Brescia, Italy, pp. 643–650.

Alaliyat, S., Yndestad, H. (2015a), An agent-based model to simulate contagious disease dynamics in fish populations. International journal of simulation. Systems, Science and Technology. vol. 16 (3).

Alaliyat, S., Yndestad, H. (2015b), An Aqua Agent-Based Model to Simulate Fish Disease Dynamics with Reference to Norwegian Aquaculture, Proceedings of 11^{th} International Conference on Innovations in Information Technology (IIT'15), Dubai, UAE, 01-03 November 2015, pp 350-355.

Alaliyat, S., Yndestad, H. and Davidsen, P. (in press), An agent-based approach for predicting patterns of pathogen transmission between aquaculture sites in the Norwegian fjords. Aquaculture.

Alaliyat, S., Yndestad, H. and Davidsen, P. (2019), Optimal fish densities and farm locations in Norwegian fjords – A framework to use a PSO algorithm to optimize an agent-based model to simulate fish disease dynamics (submitted).

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1. Introduction

This chapter describes the problem outline. In particular, the motivation for underlying the research work, the fundamental research objectives, and the research themes are being presented. Finally, there is a summary of the included published papers.

1.1 Problem outline

1.1.1 Aquaculture in Norway

Aquaculture in Norway has a long history that dates backs to 1850 when the first brown trout were hatched. The Sunnmøre[2] district made its first attempt at transferring rainbow trout to seawater before World War I. After World War II, the interest in aquaculture increased, and in the early of 1960s the first time rainbow trout was successfully transferred to seawater. Commercial salmon farming started around 1970 with a technological revolution in this sector, and at that time the first fish pen was constructed (Trygve, 1993).

Fish pens (i.e. cage) at sea provide a natural marine environment where fish grow naturally. Fish farming at sea has economic advantages of scale that could be huge compared to inshore farming because the available space at fjords and sea (Nesset & Tunsvik, 2017; Worldfishing.net, 2018). However, many environmental issues of fish farming in seawater have arises, such as threaten wild life, pollution, fish welfare and fish diseases (Holmer, 2010; Olaussen, 2017).

Norway has a long and a sheltered coastline with thousands of islands and fjords with fresh seawater. This environment provides good opportunities for fish farming activities. The Norwegian aquaculture industry has become a major important industry since 1970s. Today, Norway is the world's leading producer of Atlantic salmon and the second largest seafood exporter in the world (Fiskeridir.no, 2018; FAO, 2016).

Fish farming is not just an important industry to the Norwegian economy at large, but is also an industry that provides significant labor opportunities and financial income to areas that are often sparsely populated and where other economic opportunities are sometimes limited. Today, farming of salmon and rainbow trout is taking place in close to 160 municipalities all along the Norwegian coast, approximately 7,850 people are directly employed in aquaculture production, and 21,000 people are employed in aquaculture related activities. In 2017, Norwegian aquaculture production amounted to approximately 1,4 million tons, 99 percent of which was Atlantic salmon and trout. The first-hand value of the annual aquaculture production reached 64 billion NOK in 2017, - an all-time high. Today, fish is the third most important export product after oil/gas and metal, and accounts for 10 percent of the total Norwegian export value (Fiskeridir.no, 2018; SSB, 2018).

Norwegian aquaculture industry is probably the fastest growing food-production sector in the world, providing a significant supplement to, and substitute for, wild aquatic organisms. Only since 2005, the production has doubled. This progress has brought about challenges in the industry such as biomass and economic losses due to diseases, on the one hand, and various kinds of harmful impact on the marine ecosystem on the other. Iversen et al (2005) assessed ten years ago the general cost of disease to the Norwegian fish farming industry to be US$ 150 million annually (Iverson et al., 2005). And, so far, 40 percent of the produced salmon from the western Norwegian coast cannot be exported

[2] Sunnmøre is the southernmost district of the western Norwegian county of Møre og Romsdal.

to China due to the Pancreas disease (PD) (Berge, 2018). Preventing and combatting these diseases is therefore an important research field (Johansen et al., 2011) and a hot topic in public debates (e.g. NTB, 2011; Lie, 2013; Kyst og Fjord, 2018; Nordnorsk Debatt, 2018; Forskning.no, 2018).

Fish disease	**Causative agent**
Viral diseases	Caused by viral agent such as Infectious Pancreatic Necrosis (IPN), Infectious Hematopoietic Necrosis (IHN), Viral Haemorrhagic Septicaemia (VHS), Channel Catfish Virus (CCV), etc.
Bacterial diseases	Caused by bacterial agent such as Furunculosis, Bacterial kidney Disease, Columnaris, etc.
Mycotic diseases	Caused by fungal agent such as Saprolegniosis, Branchiomycosis, etc.
Parasitic diseases	Caused by parasitic agent such as: • Protozoa: such as Ichthyobodoosis. Hexamitosis, Coccidiosis, Whirling diseases, etc. • Trematodes: such as Dactylogyrosis, Gyrodactylosis, etc. • Cestodes: such as Khawiosis, Caryophyllosis, and Ligulosis, etc. • Nematodes: such as philometrosis. • Crustacea: Such as Argulosis, Lerneosis, etc.
Nutritional diseases	They are the diseases, which caused nutritional deficiency, such as protein and amino acids deficiency, vitamins and minerals deficiency.
Diseases caused by toxic substances	Caused by different toxic substances such as: • Toxic metals: such as zinc, copper, mercury, etc. • Toxic Organic compounds: such as oil and phenolic compounds, etc. • Toxic gases: such as ammonia, H2S, Chlorine, etc. • Pesticides: such as, chlorinated hydrocarbon, Organophosphate, etc. • Therapeutic compounds: such as antibiotics and sulfonamides, etc.
Environmental diseases	Caused by environmental conditions such as temperature, Oxygen, pH, CO2, … etc.
Other diseases	Incident diseases whose causes are unknown, but may be associated with poor water quality.

Table 1.1. Fish diseases are classified according to causative agent (Trygve, 1993; Roberts & Shepherd, 1997; Poppe et al., 2002)

Fish are subject to diseases carried by pathogens including viruses that cause the most troublesome diseases in salmon aquaculture (Olsen & Helberg, 2011). Atlantic salmon is by far the most important species in Norwegian aquaculture. Knowledge of pathogens in wild fish stocks is generally poor, and it is therefore difficult to predict which diseases might occur once an aquaculture facility has been established in an area (Bergh, 2007; Stene, 2013). A wide range of pathogens exists, from viruses and bacteria to crustacean parasites (Olsen & Hellberg, 2011). These might be introduced to an aquaculture system through various pathways; movement of infected stocks, equipment or fish products from other areas; or by exposure to wild fish pathogens (Murray & Peeler, 2005). Once introduced, pathogens can benefit from the aquaculture environment and pose a graver risk to farmed fish than wild stocks. This is because of factors such as a non-favorable marine environment, stress and pollution that might reduce resistance against diseases among individual fish (Murray & Peeler, 2005), and also because the artificially high density of fish (i.e. potential hosts for the pathogen) in a fish farm may induce outbreaks (Bergh, 2007; Rimstad, 2011). Diseases may be transmitted along sea currents at distances that depend on the survival time of the pathogen in seawater, - and also through vectors such as wild fish or escaped farmed fish (Murray & Peeler, 2005). We can classify the fish diseases according to causative agents (see Table 1.1). An example of a waterborne virus is the Salmonid alphavirus causing PD, an increasing problem in Norwegian aquaculture (Kristoffersen et al., 2009; Stene, 2013;Stene et al., 2014; Vetinst.no, 2018). All major viruses affecting Norwegian aquaculture are thought to spread between fish through seawater (Johansen et al., 2011), as infected fish shed pathogens to the surrounding waters.

A risk assessment report of Norwegian aquaculture that was issued in February, 2018 shows that there was some success in reducing the mortality of fish in salmon and rainbow trout production in the sea in 2017, and in reducing escapes and genetic interactions. However, the report shows that over 50,000 salmon escapes have already been reported by February 2018. The assessment shows that there is still a risk of salmon louse related mortality on post-smolts, especially in western Norway. There are still some farms exceed the threshold for acceptable environmental impacts. And, viral diseases continue to represent major risks to the Norwegian aquaculture industry (Grefsrud et al., 2018).

1.1.2 Sustainable development

The most common definition of sustainability is suggested by the UN World Commission for the Environment and Development in 1987. There sustainability is defined as a “development which meets the needs of current generations without compromising the ability of future generations to meet their own needs” (World Commission on Environment and Development 1987: chapter 2, point 1). The sustainability of any system can be divided into three main aspects: a social aspect, an economic aspect and an environmental aspect as illustrated in the Venn diagram in Figure 1.1. In the history of the Norwegian aquaculture industry, economic and social sustainability has been challenged on several occasions. Nowadays, however, the main challenges that the industry faces is to ensure environmental sustainability.

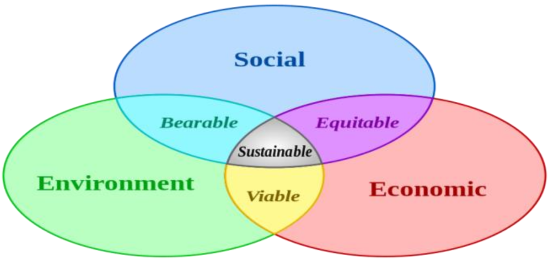

Figure 1.1. Scheme of sustainable development: at the confluence of three constituent parts. Source: Johann Dréo (Wikipedia, 2006)

The rapid growth of Norwegian aquaculture industry has presented it with a range of challenges. Environmental concerns related to infectious diseases, sea louse and escaped farmed fish have remained unresolved (Grefsrud er al., 2018). Even though the statistics show a significant decrease in the total escaped farmed fish recently, it still poses a high risk since the production of biomass has increased massively as well (www.fiskeridir.no). Other challenges related to the scarcity of suitable locations and to the effects of fish density, have appeared in recent years. Aquaculture industry has an environmental impact resulting from e.g.; discharges of waste, reduction of biodiversity, and consumption of non-renewable resources, such as oil for energy production, or renewable resources, such as the raw ingredients in feed. Making sure the aquaculture industry is environmentally sustainable is vital to secure a long-term development in this industry.

The Norwegian government is collaborating with all the stakeholders (including stockholders) to ensure that the Norwegian aquaculture industry is operated in a sustainable and eco-friendly manner (Figure 1.1). The strategy of the Norwegian government identifies five key areas where aquaculture industry may potentially have a negative impact on the environment (FKD, 2009); 1) Escaped fish/genetic interaction; 2) Pollution and discharges; 3) Diseases and parasites; 4) Use of coastal areas; 5) Feed and feed resources. The strategy set goals and explains what needs to be done to achieve them (Table 1.2). In order to achieve the goals in Table 1.2, several strategies, regulations and monitoring processes must be followed. For instance, preventing outbreaks of fish diseases will contribute to an environmentally sustainable aquaculture industry and genetic sterilization is a viable solution to mitigate damage to the ecosystem if fish escape (Aarvig, 2013). Solutions have to be viable for the entire socio-ecological system. There are limits to what the ecosystem can tolerate before it collapses.

There are many questions about financing the Norwegian fish farming industry that is a highly profitable industry. But the dynamics of the global industry work to promote strengthening of the industry into the hands of few large companies against small, local ones. The aquaculture industry brings jobs to small, coastal areas, but it also spreads unevenly and forces changes in local societies and work, - even for those who do not work in the industry. An economic competitive is an advantage, but the requirement to use a developed technology to solve the environmental problems, make the industry viable only for the few (i.e. large companies) who can afford it (Moe, 2017).

The social-economic trade-off rises a question about what solutions are acceptable to both human and natural systems? To answer this question, we need to outline the sources of stress that the fish farming industry pose to natural systems (i.e. fjord systems) at various levels. The difficulty in calculating how much stress a given system can carry (accept) in turn makes it difficult to calculate the risks to natural systems posed by specific industry configurations. The booming salmon business benefits Norway as a country, but not necessarily local Norwegian communities.

Number	Element	Goal
1	Genetic influence and escapes	Aquaculture does not cause irreversible genetic changes of the wild fish populations
2	Pollution and discharges	All aquaculture sites in use keep within an acceptable environmental condition and do not have a higher discharge of nutrients or organic material than the recipient can handle.
3	Disease and parasites	Diseases in aquaculture do not have a population effect on wild fish, and as fish much as possible are produced to harvestable size without the use of therapeutics.
4	Use of area	The aquaculture industry has a layout of sites and area use that minimize the environmental effects and exposure hazard
5	Feed resources	The need for feed ingredients /resources are covered with out over exploiting the wild marine fish stocks

Table 1.2. The five focus elements for a sustainable development of the aquaculture sector set by Norwegian Government (FKD, 2009).

A sustainable aquaculture industry should be operated with a consideration to the environment, and be adapted to the surrounding marine environment and biological diversity. It is important to select optimal production locations and densities for aquaculture so as to maintain a clean marine environment characterized by a minimum risk of infection and a minimum impact from transport emissions and pollution from local sources. Therefore, authorities and industry must cooperate to ensure a profitable, sustainable development of the aquaculture with a maximal social and economic pay-off, less conflict of interests and a minimal environmental impact.

1.1.3 Complex problem

Aquaculture growth invariably involves the expansion of cultivated areas, higher density of aquaculture installations and of farmed individuals, and use of feed resources produced outside of the immediate area. As indicated above, this may produce negative effects unless the sector is allowed to grow only under a strict regulatory regime and under effective management practices. Costal/fjord ecosystems are tightly interwoven by a variety of interdependencies. When fish pens are installed in such a complex environment, additional interdependencies are being established between such an artifact and the surrounding natural environment. That environment includes fresh water input, rich in organic and mineral nutrients derived from erosion, urban, agricultural, aquaculture and industrial effluents, and subject to strong anthropogenic pressures resulting from the fish farming. The interactions between land and sea reveal high physical, chemical and biological complexities, making the management decisions process challenging. Thus it may be very hard to predict the consequences of these decisions.

Fjord systems are embedded and very complex and representing them effectively require sophisticated modeling. Models developed thus far, we would argue, have not addressed the full complexity in the natural context of fish pans. Currently we rely mainly on laboratory data that only partially characterize the system under a very restricted set of circumstances.

Spread of fish infectious diseases in such complex systems (i.e. fjord system) has not been addressed scientifically, - we cannot rely merely on experience and need to assess the future using models based on assumptions and associated risks. Computational models[3] are important to achieve sustainable development,- models can serve a wide variety of roles such as: hypothesis testing, deepening understanding, suggesting and interpreting experiments, doing sensitivity analysis, integrating knowledge, and revealing causes (Brodland, 2015).

1.1.4 Model based management of aquaculture systems

Model based management of aquaculture systems and the associated environmental problems is challenging, the difficulty is in exploring and analyzing aquaculture systems in a holistic way (Valenti et al., 2008). Simulating aquaculture systems requires including and combining different environmental, biological, and physical factors (e.g. sea currents speed, seawater temperature, salinity, fish type, ... etc.). However, model based management is an essential part of any sustainable development strategy to reduce the risk and increase robustness.

The authorities, research communities and industry should work together to make sure the Norwegian aquaculture is managed sustainably. In order to facilitate a sustainable industry, we need research, i.e. the development of theories (models), methods, techniques and tools for analysis, prediction and management, i.e. strategy development, policy design and decision making, to facilitate a sustainable industry.

The developed tools we develop for effective aquaculture management are intended to help us identify the most important processes and components of the aquaculture systems. The tools must include models of disease spreading processes, tools for risk analysis and evaluations, and tools for developing strategies, designing policies and assisting decision making to achieve the sustainability.

The main aim of this study is to develop a tool, based on an agent-based approach, for modeling the dynamics of a fish disease within and between the aquaculture sites in the Norwegian fjords, as a result of individuals' (fish and pathogens) interactions and their interactions with their environment in a space-time context. This will help us to understand the processes underlying the disease dynamics and will contribute to the prevention of the spread of such a disease (Figure 1.2).

[3] A computational model is a mathematical model in computational science that requires extensive computational resources to study the behavior of a complex system by computer simulation.

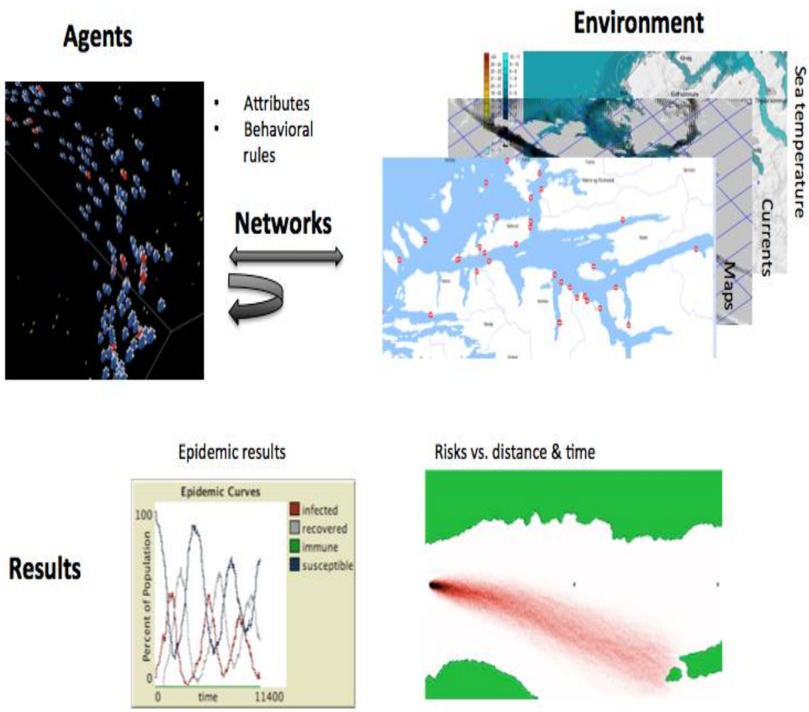

Figure 1.2. Overview of the presented models and tools. The upper-side of the figure shows the main components of the system (agents: fish and pathogens, networks (interactions between the agents-agents and between agents and their environment), and the environment (sea currents, seawater temperature and the terrain)). The lower-side of the figure shows samples of how the results can be: e.g. epidemic curves (left) or infection risk maps (right).

Figure 1.2 summarizes the presented models and tools in this research work. We build Agent-based models (ABMs) to simulate fish disease dynamics in Aquaculture systems. ABMs have two types of agents (fish and pathogens) that each have a number of attributes (e.g. positions, health status, lifespan, …etc.) and behavioral rules to update these attributes in time and space domains. The agents have different relationships (Networks) with each other and with their environment. For example, the fish swim in schools and become infected if they encounter pathogens. Pathogens move by sea currents and their lifespan is influenced by seawater temperature. The results of ABMs are presented in real time and in different ways. For example, epidemic curves are being produced that show the disease dynamics in the aquaculture sites in time domain and by risk maps that show the infection risk in time-space domains.

1.2 Related works

1.2.1 Integrated plans to Norwegian coast managements.

Aquaculture is a vital industry in Norway. It creates jobs and value. Poor management and unregulated aquaculture industry will lead to many negative effects on the whole ecosystem. The Norwegian government is working with all the stakeholders to ensure that the Norwegian aquaculture industry is operated on an eco-friendly sustainable basis (Figure 1.1). The strategy of the Norwegian government identifies five key areas where aquaculture may potentially have a negative impact on the environment (FKD, 2009); 1) Escaped fish/genetic interaction; 2) Pollution and discharges; 3) Diseases and parasites; 4) Use of coastal areas; 5) Feed and feed resources. The strategy set goals and explains what needs to be done to achieve them (Table 1.2).

The Norwegian government has established an integrated management plans that cover all Norwegian Sea areas; the Barents Sea, the sea areas outside the Lofoten[4] Islands, the Norwegian Sea, and the Norwegian part of the North Sea and Skagerrak (see Figure 1.3). The management plans provide an overall framework for both existing and new activities in these waters, and facilitate co-existence of different activities, such as the aquaculture, fisheries, maritime transport and the petroleum activity. The aim is to establish an ecosystem-based management of the activities in the relevant sea area. It is a goal that aquaculture activities do not threaten the natural fluctuations in ecosystems.

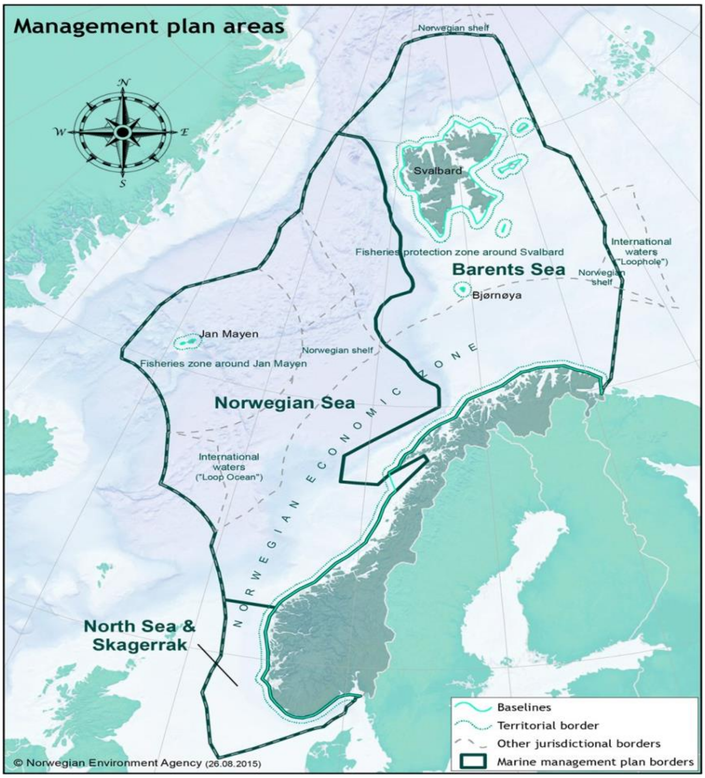

Figure 1.3. Integrated management plan areas: the Barent Sea, The Norwegian Sea and the Norwegian part of the North Sea and Skagerrak. (www.miljodirektoratet.no).

The integrated management plan for the Norwegian part of the Barents Sea and the sea areas off Lofoten was adopted by the Norwegian Parliament in 2006 and revised in 2010. The plan for the Norwegian Sea was adopted in 2009 and plan for the Norwegian part of the North Sea and Skagerrak was adopted in 2013.

[4] Lofoten is a district in the county of Nordland, Norway.

The management plans are large-scale spatial management tools and cover the areas in Norway's exclusive economic zone outside the coastal baseline. An Interministerial Steering Committee coordinates work on the management plan. The scientific basis for the management plans is coordinated by the Management Forum of the Norwegian Sea Areas, in collaboration with an Advisory Forum on Monitoring (www.miljodirektoratet.no).

1.2.2 Methods to simulate fish and pathogen dynamics

Previous studies of infectious disease dynamics in aquaculture systems have mainly employed mathematical models that have all been based on the assumption that the fish population is homogeneous (e.g. Murray, 2009; Green, 2010). Kermack and McKendrick were pioneers in establishing the mathematical modeling of disease epidemics in 1927 (Kermack et al., 1927). They created the ordinary differential equation model template SIR (Susceptible, Infectious, Recovered) . SIR models treat the fish as the unit of analysis, not the pathogens. So they do not treat the pathogens as individuals that may survive without hosts. Moreover, in their simple form, they do not represent the environmental conditions explicitly in the model. Many researchers have used such models to simulate disease dynamics, and some of them have coupled them with simple hydrodynamic models or distance measures of transmission between separate populations (Ogut, 2001; Viljugrein et al., 2009; Aldrin et al., 2010; Werkman et al., 2011; Salama & Murray, 2011).

Hydrodynamic models coupled with particle tracking and statistical analyses have been widely applied in Norway to identify the salmon louse and PD transmission dynamics in Norwegian fjords (MODS, 2012, Stene, 2013). SINTEF has developed SINMOD hydrodynamic model (www.sinmod.no) that combines physical and biological processes in the ocean. Hydrodynamic models typically do not take into consideration the variety among pathogens, and the statistical analyses are based on the assumption that the fish populations are homogeneous.

In this research, I have applied the agent-based method to simulate fish disease dynamics. ABMs may be valuable for analyses that are based on the interactions between individuals (i.e. where the overall dynamic behavior results from the interaction between individual fish and pathogens), and may also allow for the incorporation of the spatial aspect of the system that have not previously been taken into consideration.

1.2.3 Agent-based approach to simulate infectious diseases

Infectious diseases in humans such as Ebola and H1N1 or in fish such as PD can significantly impact their lives and cause large economic damages. Recent epidemic outbreaks have prompted the research on the dynamics of such epidemics. In the past years, Agent-based modeling (ABM) has been applied to an increasing degree in the modeling and simulation of disease dynamics, - partly made possible by the revolutionary development of computational capacity in modern computers. ABMs offer an alternative to classical mathematical models or discrete models in that they allow us to use as a point of departure the dynamic interactions between individuals and their impact on the system under study. Kelly et al. (2013) has found that ABMs are particularly suitable when the purpose of the model is to develop an understanding of the system under investigation based upon assumptions about individual processes and interactions that who's macro dynamics may be explored through simulation. By linking ABMs to GIS we may explore the complexity of disease transmission in space (Persez & Dragicevic, 2009). The landscape and the sharing of resources that exist in the environment have an impact on disease transmission (Nunn et al., 2014). In light of these advantages, the application of ABM in the simulate the epidemics has been growing, and applications range from studying dengue fever (Lourenço & Recker, 2013), the foot-and-mouth disease (Dion et al., 2011), hepatitis (Ajelli & Merler, 2009), influenza (Ciofi et al., 2008; Milne et al., 2008; Rao et al., 2009; Khalil et al., 2010), malaria (Linard et al., 2008), measles (Perez & Dragicevic, 2009), mumps (Simoes, 2012), smallpox (Epstein et al., 2002), swine flu (Epstein, 2009), tuberculosis (Patlolla et al., 2006), cholera (Augustijn-Beckers et al., 2011)) etc.

1.2.4 Methods and tools to facilitate integrated eco-systems management

Ecosystem management processes aim at conserving major ecological services and restore natural resources while meeting the socio-economic, political, and cultural needs of current and future generations. Ecosystem management includes several steps to achieve these goals and to prioritize these actions. The steps are scoping of ecosystem boundaries, defining indicators, setting thresholds, performing risk analysis, and monitoring to obtain feedback and to evaluate the effectiveness of the management strategies.

The Norwegian government follows a strategy aimed at ensuring an environmentally sustainable Norwegian aquaculture industry. Table 1.2 shows the five sustainability elements and summaries the goals of each element (FKD, 2009). In order to achieve these goals, there are several regulations and tools to be used at different scales; farm scale, fjord scale, and global scale (Alaliyat, 2014). In Norway, regulatory authorities require the use of the MOM (Monitoring, On growing fish farm - Modeling) method to monitor the effects of fish farming on the bottom and on the benthic fauna under and near farming facilities. This method describes how effects on the sea-bed are to be monitored and recorded, and which environmental thresholds are to be applied (Ervik et al., 1997) when considering mitigating actions. One research project (Integrate) by SINTEF, focused on Integrated Multi-Trophic Aquaculture (IMTA) (Wang et al., 2013). For small-scale farm system (distance up to 100 m from cages), an Intensive Integrated Aquaculture (IIA) model has been developed, while for large-scale /fjord system (distance in km), an Extensive Integrated Aquaculture (EIA) model has been developed to evaluate IMTA feasibility (www.sintef.no).

In Norway, there are different methods and tools applied to facilitate integrated planning for the Norwegian coast management (www.miljodirektoratet.no). Many tools are aimed at data collection and monitoring the systems (e.g. MOM). For that purpose, statistical methods are used predominantly to build economy-based strategies (e.g. economy-based management for Barents Sea and Lofoten areas (www.npolar.no), or building risk-assessments in the aquaculture systems (Taranger et al., 2011).

ABM is a valuable asset when evaluating multiple-use management strategies for coastal marine ecosystems (McDonald et al., 2008). Using an integrated ABM system to implement multiple-use management strategies evaluation framework, allows for evaluating the response of the system under a range of model characteristics, management strategies and set of scenarios affecting system dynamics.

1.3 Research objectives

The overall objective of the thesis was to develop ABMs, methods and tools to support the management of aquaculture production in Norwegian fjords by facilitating the prediction of pathogen dynamics, distribution, and transmission in marine aquaculture systems. Fish disease dynamics originates from a complex system, and the transmission of pathogen is a process that is hard to keep under control. The first objective of the thesis has been to apply the ABM technique to simulate fish disease dynamics and pathogen transmission in a single marine aquaculture system. The second objective has been to optimize the location and fish density in various aquaculture farms so as to maintain the sustainable aquaculture industry by minimizing the outbreak of fish diseases and the transmission of infectious diseases between fish farms. To achieve these objectives, the following studies have been undertaken:

1. The development of ABMs to simulate fish disease dynamics in fish populations.

In this study; the objective was to investigate the effects of different biological, environmental and physical factors such as seawater temperature, sea current, fish population and fish swimming behavior on the fish disease dynamics in a single aqua fish farm. An agent-based approach was used to build various ABMs to simulate fish disease dynamics. The spread of a disease in fish populations is a dynamic phenomenon; fluctuations in occurrence and impact are dependent on the interactions between fish, pathogen, and the environment. Small changes in the key input parameters in the ABMs that we use to simulate fish disease dynamics, may lead to a change in the model output that ranges from insignificant to essential. In order to achieve the objective of this study, the sensitivity of the ABMs output to the key input parameters values was explored. Subsequently, the dependence of the model's output on the various key input parameters were determined. At the end, the tipping points[5] in the input vector that contains all the input key parameters were identified.

2. The development of ABMs to allow for the simulation of disease transmission between several aquaculture sites in a Norwegian fjord.

   In this study, the objective was to build ABMs to predict patterns of pathogen transmission with the purpose of identifying risks and hazards in the space and time domains, so as to help prevent and, if needed, combat infectious fish diseases by informing the management of the fish industry in Norway. In order to achieve the objective of this study, the ABMs in the previous study were extended to include several aquaculture sites, and then the pathogen transmission pattern in the time-space domain was investigated and infection risk maps were built.

3. The application of particle swarm optimization (PSO) algorithm to automatically optimize ABMs input parameters.

   In this study, the objective was to optimize marine aquaculture system that contains several aquaculture facilities, by determining the optimal fish densities and farm locations, aimed at avoiding the risk of a fish disease epidemic. To simulate fish disease dynamics within and between fish farms ABMs were developed and then made subject to optimization. Then, a framework was developed for using a PSO algorithm to identify the optimal values of the ABMs input parameters that provide the maximum value of the objective function. The objective function was designed to capture the main goal of the model such as minimizing the infection risk.

1.4 Scope of the thesis

The following subjects form the scope of the research presented in this thesis:

1.4.1 Agent-based modeling (ABM) of complex systems

A comprehensive study about ABM of complex systems is performed to achieve the main objective of the thesis. ABM is a powerful modeling and simulation technique that has been applied in a variety of domains during the last few years (e.g. biology, environmental management, etc.), and it is now a well-recognized approach to the modeling and analysis of complex systems.

[5] Tipping Points: places where a small change in an input can dramatically affect the outcome.

ABM is a bottom-up modeling technique, which is different from top-down modeling techniques (e.g. system dynamics), developed to simulate complex systems. There are some advantages and disadvantages of using ABM. ABM is flexible, captures emergent phenomena and provides a convenient description of the system by simulating the actions of and interactions between individual agents. The interactions between the agents in complex systems are typically varied, non-linear, and discontinuous or discrete. Thus, it may be difficult to describe the individual behavior using traditional methods such as differential equations. ABM offers an alternative, algorithmic approach, to deal with the complexities of such systems.

1.4.2 Model-based simulation of infectious fish diseases

The diffusion of infectious diseases in fish populations is a dynamic phenomenon originating from the interactions among fish, pathogen, and environment (Figure 1.4). Fish are stressed in an unfavorable environment such as one characterized by crowding and relatively high seawater temperatures. Pathogens are transmitted by water. Fish shed pathogens, and pathogens infect fish. We implemented a variety of ABMs to simulate disease spreading in fish populations. The objective was to investigate how the ABM method may be applied to simulate fish disease dynamics. The effects of different parameter values, associated with the fish, pathogens and environment on the epidemic were investigated. We conducted a sensitivity analysis of the ABMs outputs to changes in parameter values so as to generate hypotheses about the dynamics of fish epidemics. Both cross-validation and model alignment methods were used to validate the ABMs. The marine fish farming industry in the Romsdalsfjord[6] inspired the data used in the models.

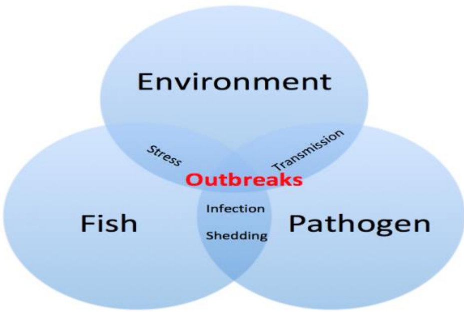

Figure 1.4. Interactions between fish, pathogen, and environment causing disease outbreaks

1.4.3 Simulation based analysis and prediction of pathogen dynamics, distribution and transmission.

With the purpose of identifying the infection risk in space-time domains, different simulation based analysis were performed. The simulations of ABMs of aquaculture systems in parts of the Romsdalsfjord with different settings were performed for the purpose of identifying the pathogens transmission patterns in the fjord. Results of these simulations are used to derive infection-risk maps.

[6] Romsdalsfjord is 88 km Long and located in the Romsdal district of Møre og Romsdal county in mid-Norway.

1.4.4 Particle swarm optimization algorithm developed to facilitate ABMs parameter space optimization

ABMs have many parameters that relate to the individual agents' attributes and their behavior rules, the environment, and the network between the agents or between the agents and the surrounding environment. These parameters determine the global behavior dynamics of the system, and small changes in a single parameter sometimes lead to major modifications of the dynamics of the entire system. Parameter setting for the ABMs may require significant time and resources unless an effective strategy has been developed to explore the parameter space. Swarm Intelligence (SI) algorithms are well-suited to traverse such large solution spaces. We developed a framework for using a particle swarm optimization (PSO) algorithm, so as to automatically identify optimal values for the model parameters.

1.5 Structure of the thesis

This thesis is based on three main studies that are performed for the purpose of achieving the research objectives. The main objective of the thesis has been to develop ABMs, methods and tools to manage aquaculture production in Norwegian fjords and facilitate the prediction of pathogen dynamics, distribution, and transmission in marine aquaculture systems. The thesis synopsis contains seven chapters. In Chapter 2, materials and methods that are used in the studies are summarized. This chapter is divided into three sections: First there is a theory section that presents a comparison of System Dynamic (SD), Discrete Event Modeling (DEM), and the ABM simulation paradigms in the context of aquaculture system modeling. The second section summarizes the methods used in the, simulation and analysis. The third section reviews the used tools and techniques applied.

In Chapter 3, we offer a summary of a complete discussion on ABM applied to complex, dynamic systems. This chapter spans sections on the modeling of complex systems, on the purpose, the principles, the advantages and the limitations of ABM applied in this context and on the verification and validation of ABMs.

Chapter 4 contains first a description of how to build ABMs so as to simulate disease dynamics in a fish population. In the second section, the transmission of pathogens between fish farms in sea aquaculture systems is presented. In the last section, a framework for optimizing the ABMs by using PSO is presented.

In Chapter 5, the results of the different studies and how they relate to the research objectives are presented. Potential, future applications are presented at the end of the chapter.

In the first section of Chapter 6, we present some important advantages of applying ABM to environmental management challenges in Norwegian fjords in general, - and, in particular, to the simulation of fish disease dynamics and pathogens transmission between fish populations. In the second section, some limitations are addressed such as those associated with; model boundary, scaling in the time-space domain, lack of data, the application of standard validation methods, the interpretation of results, and ethical issues.

Finally, the general conclusions of the research project and the possible topics, subject to further investigation are presented in Chapter 7.

1.6 Publications

The material presented in this thesis are based on several conference and journal papers. The papers are categorized into three main studies as listed below.

1.6.1 Study I: Simulation of fish disease dynamics in a fish population

Alaliyat, S., Yndestad, H. (2015a) **"An Agent-Based Model to Simulate Contagious Disease Dynamics in Fish Populations"**. International journal of simulation. Systems, Science and Technology. vol. 16 (3).

In this paper, we present an agent-based model that simulates the spread of contagious disease dynamics in a single aquaculture facility. Unlike previous models that describe the spread of disease based on the assumption that populations are homogeneous and that focus on the population as a whole, in this work we build a heterogeneous model. We simulate both fish and pathogens as individual agents that interact with each other and their environment. This gives the model the capability to overcome the limitations of classical population-based models, permitting us to study specific spatial aspects of the spread of infections and to address the stochastic nature of the infectious process. The implemented model in this work enables us to study the sensitivity to model's input key factors such as fish density, infection radius, shedding rate, etc., in which the infectious disease takes place.

The model is implemented in NetLogo[7], and different simulation experiments are designed to explore the impact of factors such as fish density and infection radius (distance around fish containing pathogens) on the fish disease dynamics in an aquaculture facility. Simulation results show that the fish disease dynamics are more significantly influenced by changing the infection radius parameter than by changing the fish density parameter (thus increasing the pathogen amount released).

Alaliyat, S., Yndestad, H. (2015b), **"An Aqua Agent-Based Model to Simulate Fish Disease Dynamics with Reference to Norwegian Aquaculture"**, Proceedings of 11th International Conference on Innovations in Information Technology (IIT'15), Dubai, UAE, 01-03 November 2015, pp 350-355.

In this paper, we extended the previous model in this study to examine the impact of sea currents and fish swimming behavior on the disease dynamics in fish populations. Fish populations epidemics is a dynamic phenomenon; variations in occurrence and impact are dependent on the interactions between fish (host), pathogen, and the environment. In this work, we build an aqua agent-based model that simulates the contiguous disease transmission in a single aquaculture site. The model combines the most important factors in the fish disease process, environmental factors, fish swimming behavior and infection process parameters.

We design the simulation experiments so as to explore the impact of sea currents and swimming behavior on the disease dynamics. We vary the current speed between a set of boundary values to test its effect on the disease dynamics. Also, we simulate different fish swimming behavior (i.e. swarm, circular and random) in order to investigate the impact of the swimming behavior on the disease spread. The simulation results show that the infection rate increases when the sea current speed decreases, and when the fish swim in a regular pattern (circular or in school).

[7] NetLogo is an agent-based programming language and integrated modeling environment.

1.6.2 Study II: Simulation of pathogen transmission between aquaculture sites

Alaliyat, S., Osen, O. L. and Kvile, K. O. (2013), **“An Agent-Based Model To Simulate Pathogen Transmission Between Aquaculture Sites In The Romsdalsfjord”**, Proceedings of the 27th European Conference on Modeling and Simulation, Aalesund, Norway, pp. 46–52.

In this paper, we build an agent-based model to simulate the emergence of a hypothetical fish pathogen in an aquaculture facility in the Romsdalsfjord and to observe how this pathogen could possibly spread to multiple facilities within the fjord. This model enables us to observe how key parameters such as the water current speed, the current direction, the pathogen life span, the contagiousness and the fish density affect the disease dynamics.

In this work, the fish were stationary in the cages, while the pathogens moved by sea currents in the fjord. The model is implemented in NetLogo, and we have included three fish farms at the Romsdalsfjord in the simulation experiment. The results show that the number of infected fish in each farm is predicted by factors such as current speed and pathogen life span. The results provide a good base for exploring the relationship between these variables and others (infection rate, pathogen release rate current bias etc.), and platform on which more complexity can be added to the model at a later stage.

Alaliyat, S., Yndestad, H. and Davidsen, P. (in press), **“An Agent-Based Approach for Predicting Patterns of Pathogen Transmission Between Aquaculture Sites in the Norwegian Fjords”**. Aquaculture.

In this paper, we build ABMs to predict patterns of pathogens transmission for the purpose of identifying risks/ hazards in space and time domains. This risk assessment will help in combating the infectious fish diseases and in managing the fish industry in Norway. Previous models that predict the spread of a disease within and between the fish populations are mostly based on the assumption that these populations are homogeneous and they focus on the population as a whole. We are assuming that the fish populations and pathogens are heterogeneous. Consequently, we apply an agent-based approach to modeling the dynamics of fish diseases within and between the aquaculture sites in the Norwegian fjords, dynamics resulting from the interaction between individuals (fish and pathogens) and with their environment in a space-time context.

The process of disease transmission is influenced by many factors, including the condition of individuals (fish and pathogen), movement behavior and environmental conditions. The model presented is implemented in NetLogo, and explores the potential effects of these factors on the spread of a simulated fish disease. The simulation results demonstrate how the infection risk increases when the pathogen or fish densities increase. The pathogen density decreases exponentially as a function of an increase in the seawater temperature, and the pathogen density increases with the speed of the current or the fish density at the infected sites. The pathogens are being moved faster by higher current speed, so this will slow down the infection process at the local infected sites. Nevertheless, the current will carry the pathogens to nearby places faster.

1.6.3 Study III: Optimization of ABMs input parameters

Alaliyat, S., Yndestad, H. and Sanfilippo, F. (2014), **"Optimization of Boids Swarm Model based on Genetic Algorithms and Particle Swarm Optimization Algorithm (comparative Study)"**, Proceedings of the 28th European Conference on Modeling and Simulation, Brescia, Italy, pp. 643–650.

In this paper, we present two optimization methods for a generic boids[8] swarm model that has been derived from the original Reynolds' boids model to simulate the aggregate movement (dynamics) of a fish school. The aggregate motion is the result of the interaction of the relatively simple behaviors of the individual simulated boids. The aggregate movement vector is a linear combination of every simple behavior rule vector. The vector coefficients should be identified and optimized to obtain a realistic flocking behavior. We proposed two methods to optimize these coefficients, by using genetic algorithm (GA) and particle swarm optimization algorithm (PSO). Both GA and PSO are population based heuristic search techniques that may be used to solve the optimization problems. The boids swam model is implemented in Unity3D[9]. The simulation results show that optimisation of boids model by using PSO algorithm is faster and gives better convergence than using GA.

Alaliyat, S., Yndestad, H. and Davidsen, P. (submitted), **"Optimal Fish Densities and Farm Locations in Norwegian Fjords –A Framework to Use a PSO Algorithm to Optimize an Agent-Based Model to Simulate Fish Disease Dynamics"**.

In this paper, we present a novel method to find the optimal fish density and location of each farm in an aquaculture system in a Norwegian fjord, aiming to obtain the optimal aquaculture system with a minimum risk of spreading disease and high fish production. For this purpose, agent-based models (ABMs) are used to simulate and analyze fish disease transmission within and between fish facilities. While a modified particle swarm optimization (PSO) algorithm is used to identify the optimal values of fish densities and farm locations. The objective function is defined as being the weighted sum between the fish density and infection risk. The PSO algorithm with the optimal objective function is validated by demonstrating its capability to drive the system to produce an expected behavior and output in tested known scenarios.

The simulation results of simple aquaculture system in the Romsdalsfjord show the ability of the PSO algorithm to converge rapidly to the optimal solution. In only 18 iterations, it finds an optimal solution that is three times larger than the initial fish density (i.e. before applying the optimization to the system) and in a location that keeps the infection risk at an accepted level. The use of PSO algorithm to identify the parameter values of the model that yield an optimum behavior, will reduce significantly the simulation time required and make the model very useful in planning for a sustainable aquaculture industry. The presented model is implemented in NetLogo.

[8] Boids are bird-like objects that were developed in the 1980s to model flocking behavior.
[9] 3D game engine, www.unity3d.com

2. Materials and methods

2.1 Theory

The starting point in this model-based research project is the identification of a system of study based on a definition of the real world problem. Then a model (i.e. a representation of the system) may be developed, one that represents our understanding of the system and the associated problem. The system characteristics and the problem at hand determine our choice of a modeling method. In this case, we face a dynamic problem, one that develops over time, appropriately addressed using a simulation model that is based on the structural assumptions that reflects our systems and problem understanding (Robinson, 2008).

Infectious fish diseases are caused by pathogens that are transmitted by way of the water currents. In fish populations, diseases spread dynamically (over time) where the fluctuations in occurrence and impact are dependent on the interactions between fish, pathogens, and the environment. Fish disease dynamics in marine fish farming systems may be considered as a high (aggregate) level feature of the system, - a system-level feature. The marine aquaculture system can be formalized as follows (Yndestad, 2010):

$$S(t) = \{A(t), L(t), N(t)\} \quad (2.1)$$

where *S(t)* is the aquaculture system, *A(t)* is a set agents (i.e. fish and pathogens), *L(t)* is the landscape or the environment in which the agents are located, and *N(t)* is the networks between the agents themselves and between the agents and the landscape. The characteristics of the landscape determine how the agents (i.e. fish and pathogens) act and interact. For instance, agents act differently in variant seawater temperature.

The aquaculture system is a complex system and have several features in common with other complex systems. In general, these features can be classified into high-level, or aggregate, features and low-level, or disaggregate features. The features at a high-level of aggregation describe the system behavior (e.g. flocking behavior), while features at the low-level of aggregation describe the structure of the system (i.e. components and relations). Study the dynamics (behavior) of the system and how this may be recreated in a simulation and explained through analysis of the systems structure at disaggregate level is our focus in this thesis.

The following detailed properties are common descriptors of aquaculture systems at a disaggregate level:

- Numerousness: The aquaculture system consists huge number of elements (agents); e.g. fish and pathogens.
- Heterogeneity: Agents differ in their characteristics; fish and pathogens populations are heterogeneous.
- Local interactions: Relationships between the agents (interactions among them) and between agents and their local environment are prominent in aquaculture systems. For instance, fish swim in schools where they socialize.
- Activity: Fish is an active entity that act and re-act (thus interact).
- Mobility: System elements (fish and pathogens) can roam is the aquaculture system space, e.g. within and between fish farms.

The aquaculture systems have generally these aggregate (system-level) features:

- Emergence: The dynamics, i.e. the disease outbreaks, of aquaculture systems emerge from the behavior of individual agents and their interactions.
- Self-organization: The interaction between individual agents, including their feedback, is what ultimately determines the dynamics of the system. The lack of a centralized control is what may possibly cause its self-organization.
- Co-evolution: The characteristics of aquaculture system components (i.e. agents, landscapes, networks) change over time. When the environment (i.e. seawater temperature and currents) change over time, then the agents (i.e. fish and pathogens) adapt to that changing environment by modifying the rules of interaction with other agents and that environment (i.e. there is a dynamic structure).

There is a variety of modeling paradigms that may be applied when addressing complex systems. We may distinguish between "top-down" and "bottom-up" paradigms. "Top-down" modeling paradigms, such as system dynamics (SD), help us focusing on system observables and modeling the system components using state variables at an aggregate level (Heath et. al., 2011). While "bottom-up" modeling paradigms, such as discrete event modeling (DEM) and agent-based modeling (ABM), model the system by focusing on the individual parts of the system and their interactions. The selection of a simulation paradigm constrains our ability to capture system and individual-level features in our models. Table 2.1 summarizes how the SD, DEM and ABM simulation paradigms enable us to capture the specific features of an aquaculture systems for the purpose of simulating the spread of fish diseases.

		SD	DEM	ABM
low-level of aggregation	Numerousness	No distinctive entities	Distinctive entities	Distinctive entities
	Heterogeneity	Homogenous	Heterogeneous entities	Heterogeneous entities
	Local interactions	Average value for interactions	Interactions in technical level	Interaction in social and technical levels
	Activity	No activity	No activity	Activity is an agent property.
	Mobility	No mobility	No mobility, passive entities	Agents move in space-time domain.
High-level of aggregation	Emergence	Debatable	Debatable	Has the capability to capture it.
	Self-organization	Not (lack of individual decision-making)	Not (lack of individual decision-making)	Has the capability to capture it (modeling autonomous agents)
	Co-evolution	Not (the system structure is fixed)	Not (Processes are fixed)	Has the capability to capture it (Network structure is modified by agents' interactions)

Table 2.1. Comparison of SD, DEM and ABM simulation paradigms in aquaculture system modeling

Unlike "bottom-up" simulation approaches, SD typically represents aggregates (of individuals) in stock level and flow rates and is not, typically representing individual-level features. On the contrary, DEM and ABM paradigms work with distinctive entities (individuals). In DEM, the entities are passive without any decision-making capability (i.e. behavior). Therefore, the DEM paradigm has the ability to capture heterogeneity and partially local interaction, but not activity and mobility features. In ABM, the agents are active and social, - they move and interact in the space-time domain. Therefore, using the ABM paradigm, we may capture all the individual-level features of relevance.

Using the ABM paradigm, we model autonomous decision-maker agents that obey rules and can change their way of interactions with other agents and the environment without a centralized control (Heath et. al., 2011), unlike the SD and DEM paradigms. Therefore, ABM may represent the self-organizing feature (e.g. fish swim in schools) that some systems exhibit, while SD and DEM typically do not represent the emergence of self-organization. Co-evolution is a feature at a high-level of aggregation and is not represented in SD and DEM, since the system structure is fixed in SD, and the processes are fixed in DEM. In contrast, ABM captures this feature of structural dynamics because the system and network structure is being modified by the interaction of the agents.

2.2 Methods and analysis

In this thesis, the main method underlying most of the work in the studies is ABM (Agent-Based Modeling). In addition, a particle swarm optimization (PSO) algorithm is used in the third study to optimize the ABMs of aquaculture systems. In this section, a summary of these methods is offered, while Chapter 4 contains a full description of them.

2.2.1 Agent-based modeling

In this thesis, the ABM approach has been applied to build models of marine aquaculture systems. The purpose has been to simulate disease transmission in such systems. In this case, the ABMs contain two types of agents, - fish and pathogen. Fish agents are confined to cages within which they move freely, while pathogens are being transported by the water throughout the entire simulation space. The agents have characteristics that can be modified according to a variety of (behavior) rules. The environment is the seawater, characterized by temperature and velocity (due to currents). The agents interact with one another and with their environment. Fish may become infected if there is high density of pathogens nearby, and when infected, fish shed pathogens.

2.2.2 Particle swarm optimization algorithm

A PSO algorithm was used to optimize the ABMs of aquaculture systems by finding the optimal fish density and farm locations. PSO is a computational method that helps us identify the optimal solution to such a problem by hill-climbing, - i.e. by iteratively searching for an improvement in the solution with respect to a certain set of criteria. The objective function in this case is defined so as to find the optimal mix of densities and locations across large number of possible values, i.e. one that poses a minimum infection risk. The PSO algorithm was selected because it has advantages over other optimization techniques such as Genetic Algorithms (GA) and Ant Colony Optimization (ACO). The PSO is a simple algorithm, easy to modify, has a rapid convergence and need less computationally resources comparing to GA and ACO.

2.2.3 Sensitivity analysis

ABM is a paradigm that we effectively adapt to the modeling and simulation of disease dynamics in fish population in general, and in marine aquaculture systems in particular. In this context, the ABMs applied are characterized by a variety of parameters. There is often a significant uncertainty associated with the values of each of these parameters, - statistically represented by distribution functions. This uncertainty affects the result of the simulations as well as the result of the optimizations performed. In particular, the non-linearity characterizing the underlying structure of such systems causes the uncertainty originating from different sources to synthesize.

Sensitivity analysis is the study of how this uncertainty in ABMs behavior can be apportioned to different sources of uncertainty in key input parameters. There are many approaches to perform a sensitivity analysis such as one-at-a-time, scatter plots, variance-based methods, ...etc. However, most procedures follow these steps:

1. Determine the range for each input parameter.
2. Identify the model output to be analyzed.
3. Run the model a number of times using design of experiments.
4. Calculate the sensitivity measures of interest.

In this study, we used one-at-a-time method to perform sensitivity analysis in NetLogo. One-at-a-time (OAT/OFAT) is the most common approaches and the simplest one, - changing one-factor-at-a-time, to see what effect this produces on the output.

In the first study, where ABM is applied to simulate fish disease dynamics in single fish populations, we have performed an analysis to assess the sensitivity of the model dynamics to various key input parameters. A variety of sensitivity analyses have been undertaken to estimate the attack-rate that determines the rate at which a disease spreads, and its sensitivity to various biological, physical and environmental factors. Some of these factors are individual-level characteristics such as fish swimming behavior and pathogen lifespan. While the other factors are part of the system structure such as fish density, seawater temperature, sea currents, and infection radius.

It is important to perform an extensive sensitivity analysis in order to the identify the effect of parameter value variations on the simulation results (model output), - including variations in values characterizing the modeling method and techniques applied, such as time scale and sample size.

2.3 Techniques and tools

2.3.1 Techniques

The models presented in this thesis are generic and may be applied to a variety of fish and the associated infectious diseases in different geographical areas. The data applied in this case are from Romsdalsfjord[10] and the associated aquaculture industry. The aquaculture data, including the maximum allowed capacity of the fish farms in the area, are available on the webpage of the Norwegian Directorate of Fisheries, www.fiskeridir.no. The oceanographic data include sea currents data (speed and direction) and seawater temperature. In the simulations, I used the monthly average sea currents data from the SINMOD model (MODS, 2012) with a resolution of 800 m x 800 m, and I added noise by benefiting from the distribution functions in NetLogo to achieve natural variety in the data. The data on the monthly average of the seawater temperature is available on the webpage of the Institute of Marine Research, www.imr.no/en/. The values for the infection and shedding parameters and the pathogen life span depend on the types of pathogens and fish involved. I used data that refer to the spread of PD among salmon (Stene, 2014; Alaliyat & Yndestad, 2015a). When simulating the swimming behavior of fish in aquaculture facilities, I refer to the data from the literature.

2.3.2 Simulation

A variety of tools were employed to perform the studies that form the basis for the thesis. These tools are divided into three main categories in the following way:

[10] Romsdalsfjord is 88 km Long and located in the Romsdal district of Møre og Romsdal county in mid-Norway.

- **Tools to prepare the data:** The data used in the ABMs are gathered from different sources and are expressed in a variety of formats, - often not fully compatible with the modeling requirements. For instance, the fish capacity is provided in "tons" by the Norwegian Directorate of Fisheries, while I use individual agents (fish) in the models. Mathematical equations were used to scale the quantitative data, while estimations were used to substitute the qualitative data (i.e. stress in fish agents). The topographical data for Norwegian fjords come in different formats (i.e. raster and shape formats). 3D maps of the Romsdalsfjord were built in GlobalMapper (Bluemarblegeo.com*)* by combining the terrain (i.e. raster) and bathymetry (i.e. vector) data. I removed the noise from the data and rescaled the maps to fit in ABM tool. Global mapper is the geographic information system (GIS) software that I used to facilitate such a process. It handles vector, raster and elevation data, and provides conversion and combining features.
- **Simulation tools:** In order to implement models using agent-based methods, NetLogo 3D was used. The NetLogo software was chosen among a variety of platforms developed to build ABMs such as RePast, Swarm and Mason. In table 2.2 we present a list of most of the NetLogo features that formed the basis for our choice. NetLogo is a multi-agent programmable modeling environment, and offers a set of built-in libraries. The NetLogo toolkit allows for simulations within a GIS environment and allows for the inclusion of physical and environmental data as well. NetLogo also provides a graphical tool for easily constructing interfaces (GUIs) to operate ABMs effectively and to display the simulation results originating from such models (Wilensky, 1999).
  At the start of this research, I implemented sample ABMs in the Unity3D game engine (Unity3d.com). Unity3D is a three-dimensional physics game engine that is used for building 2D and 3D games realistically portrayed in graphics and with dynamics consistent with the laws of physics. I had to give up this line of research because Unity3D is not a multi-agent programmable language, and I need to write the programs to effectively represent the conceptual model from scratch.

- **Analysis tools:** BehaviorSpace was employed to perform the sensitivity analysis. BehaviorSpace is a software tool integrated with NetLogo and developed to perform model experiments. BehaviorSpace runs the model many times, while systematically varying the model's settings and recording the results of each model run. This facilitates the exploration of the input parameters and behavior space of the model. It helps us determine which of the many combinations of settings that causes the behavior patterns of interest / concern. BehaviorSpace has the capacity to run models in parallel as well (Wilensky, 1999).
  MATLAB was used to analyze the simulation results and to create publication-ready figures (MATLAB, 2015). MATLAB is a multi-paradigm numerical computing environment. It allows for matrix manipulations and plotting of data in 2D, 3D and 4D.

System	• Free, open source • Cross-platform: runs on Mac, Windows, Linux, et al International character set support
Programming	• Fully programmable • Approachable syntax • Language is Logo dialect extended to support agents • Mobile agents (turtles) move over a grid of stationary agents (patches) • Link agents connect turtles to make networks, graphs, and aggregates • Large vocabulary of built-in language primitives • Double precision floating point math • First-class function values (aka anonymous procedures, closures, lambda) • Runs are reproducible cross-platform
Environment	• Command center for on-the-fly interaction • Interface builder w/ buttons, sliders, switches, choosers, monitors, text boxes, notes, output area • Info tab for annotating your model with formatted text and images • HubNet: participatory simulations using networked devices • Agent monitors for inspecting and controlling agents • Export and import functions (export data, save and restore state of model, make a movie) • BehaviorSpace, an open source tool used to collect data from multiple parallel runs of a model • System Dynamics Modeler • NetLogo 3D for modeling 3D worlds • Headless mode allows doing batch runs from the command line
Display and visualization:	• Line, bar, and scatter plots • Speed slider lets you fast forward your model or see it in slow motion • View your model in either 2D or 3D • Scalable and rotatable vector shapes • Turtle and patch labels
APIs	• Controlling API allows embedding NetLogo in a script or application • Extensions API allows adding new commands and reporters to the NetLogo language; open source example extensions are included

Table 2.2. NetLogo features (https://ccl.northwestern.edu/netlogo/docs/)

3. Agent-based modeling of complex systems

Agent-based modeling (ABM) approaches have been used extensively to model complex systems and are proving successful in a variety of contexts such as economics, business, technology, social sciences, biology and medicine. More recently these models have also been used within environmental management research (LePage et al., 2013).

The aim of this chapter is to discuss the principles, limits, validation and uses of ABM in the context of complex systems.

3.1 Modelling of complex systems

In the following, I introduce a general definition of a system, and how we characterize a system as complex. People in various scientific disciplines have different perspectives on what a "system" is (Hall, 1962; Kauffman & Draper, 1980; Martin 1997; Hitchins, 1997; Stevens et al., 1998). In general, a system is defined as a set of objects/components/parts/elements, including the relationships between them, i.e. between their attributes. Sometimes a system is considered serving a purpose, in which case an objective to be accomplished (satisfied) is associated with the system. As in the case of "system", scientists from various disciplines have proposed various definitions of the term "complex", - an attribute of many systems (Cariani, 1992; Simon, 1996; Kirschbaum, 1998; Goldenfeld & Kadanoff, 1999; Weng et al., 1999; Whitesides & Iyengar, 1999; Rind, 1999; Arthur, 1999; Rocha, 1999; Yndestad, 2010; Worldscientific.com, 2018). There is no agreed-upon, formal definition of the term "complex system", as there are no precise boundaries between simple and complex systems. The definition of what is a complex system depends on the point of view and on the level of abstraction. But, in general, complex systems have common specific characteristics that challenge us when we try to understand the structure and the dynamics of such systems and the relationship between the two. For that purpose, we represent systems in the form of models that we validate through reality checks and utilize for the purpose of conducting simulation experiments. Complex systems may have the following general characteristics (Cilliers, 1999):

- Complex systems consist of a large number of elements that, in themselves, may be simple (e.g. school of fish, and flock of birds). In such a case, the conventional methods (e.g. differential equations) become impractical when we are to offer a formal description of the behavior of the elements.
- Time variant: A large number of elements are not sufficient and interactions between them need to take place. In order to constitute a complex system, the elements must interact dynamically.
- Nonlinearity: The interactions are non-linear. This means a certain perturbation may cause different effects (e.g. large, medium, small), conditioned upon the current state of the system (e.g. weather systems). In contrast to what is the case in linear systems, where the effects of a perturbation is always proportional to the perturbation (i.e. the cause).
- Feedback: There are many direct and indirect feedback loops. Both negative and positive loops are commonly found in the structure of complex systems.
- Complex systems are open systems: Complex systems interact with their surroundings and it is often difficult to define the border of a complex system (e.g. fjord systems).
- State memory: The history of a complex system is important. Complex systems evolve through time, and their past is co-responsible for their present behavior.
- Presence of emergent behaviors: The behavior of the system is determined by the nature of the interactions, not merely by what is contained within its components. Since the interactions are rich, dynamic, fed back, and nonlinear, the behavior of the system as a whole cannot be predicted from an inspection of its components.

- Complex systems are adaptive: They can re-organize their internal structure without the intervention of an external agent (e.g. school of fish).

Previously, when studying a subject, scientists tended to use a reductionist approach, which endeavored to summarize the processes, dynamics, and change that occurred regarding lowest common denominators and the simplest, still most widely provable and applicable graceful explanations.

This reductionistic approach has been common as a result our limited analytic capability (our ability to solve equations) and what, for a long time, was a limited computational capacity. Nowadays, powerful computers that can perform vast computational tasks over short periods of time. That allows scientists to study the dynamics resulting from the true complexity characterizing the structure of many systems. It is now possible to simulate models bottom-up (in great detail)[11], such as ABMs where the emergent dynamic behavior of systems outcome is a deterministic or stochastic aggregate outcome of the behavior of the individual agents of the system. In one sense, therefore, ABM is a reductionist approach. ABM represents the system behavior at the least aggregate level of the agents. The emergent outcome of the complex system is a product of the interactions between the system components (i.e. the agents), an aggregate outcome that may feed back to the individuals, i.e. the agents.

Challenges in Modeling

A model is a representation of a system. Up to the second half of 20th century, modeling tools (i.e. computer software) did not have the capacity to support computationally intensive modeling methods (e.g. ABM) applied in the simulation of complex systems. In the 1950s came the theory of cellular automata and artificial intelligence, not applicable in practice due to the high computational demand. Later in the 1980s and 1990s, sufficiently powerful computers were made available. Along with this development in hardware, there was a parallel software development where object-oriented modeling tools, such as ABM also became available. Reality, however, in all its complexity defies our modeling tools as well as our computational capacity. Thus, we face challenges when modeling and simulating truly complex natural systems.

The first challenge in the modeling of complex systems (e.g. fjord ecosystems) with a large number of components with many relations between them is to overcome the computational demand of these kind of models by finding methods to reduce the computational time (i.e. use parallel processing and distributed systems).

The behavior[12] of complex systems cannot be easily described (Chu, 2011). Complex systems may exhibit behaviors that are emergent (e.g. traffic jam problem), and are sensitive to initial conditions. The system's behavior is a product of the interactions between the system components (i.e. agents). The presence, absence, or type of the relationships between the components may affect the behavior of the aggregate system, so a description of this behavior must take into account each of these relationships.

The structural characteristics of complex systems pose many challenges to the modeling of the system. First, this constitutes a challenge in the implementation part. How can we represent the system components and the relations? Components (e.g. fish in a school of fish) are closely coupled, governed by feedback, are self-organized and are adaptive. Relations are dynamic and nonlinear. The challenge is in describing the behavior of the components in the model in a way that represents the

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[11] An approach of modeling a system by begins with details and works up to the highest conceptual level.

[12] I mean here the system behavior, dynamics of the system exhibited over time.

components and their interrelations in the real world. This requires us to have sufficient information at our disposal to describe the components and the relations in the model, - including which details to be included and excluded when modeling the individual parts of the system (e.g. details to model fish in aquaculture systems). Even if we have experienced a technological improvement in computers, we still have limited computing power that calls for a careful trade-off between the model complexity on the one hand and the computability of the model on the other.

Reality is continuous in time while as digital computer models operate discretely in time. A model as defined by (Longley & Batty, 2003) is a simplified representation of reality. A model can be constructed as a computer programme that uses (usually to some degree) a simplified digital representation of one or more aspects of the real world (e.g. fish disease dynamics). The challenge is the degree to which we can reduce the amount of information that we have about reality to produce a model of that reality that complies with the purpose of the model. This causes challenges both with respect to the amount and the type of data that we may need and disregard while creating the model. This challenge increases with the complexity of the structure of the system being modeled. The difficulties exist not only because of the amount and kind of data, but also due to the uncertainty of the interaction between the system's elements. And the challenges are more significant if we need to represent autonomous (intelligent) agents that exhibit some kind of ability to learn / adapt. Modeling this ability will result in an additional complexity in the model implementation and analysis.

3.2 Agent-based models

Increasingly ABM is being used for managerial purposes in a variety fields. The efficient and effective use of ABM for such purposes is obstructed by the fact that there is no clear definition of what ABM is or what an agent should be (Hare & Deadman, 2004). At the same time, this allows for a significant degree of freedom in the application of the ABM paradigm. Different models serve different purposes and thus the interpretation of the agents may vary from one application to the next. The aim is to build ABMs that are valid, yet simple enough representations of reality to facilitate our understanding of that reality. As George Box, a statistician, said, "Essentially, all models are wrong, but some are useful" (Box & Draper, 1987). In the following, I will set aside the diversity of ABMs in different fields and focus on common characteristics of agents and ABM. Here I will briefly define agents and ABMs.

As already pointed out, there is no universal agreement on the definition of the term "agent" (Macal & North, 2005). Agent characteristics may not easily be elicited by way of literature studies in a consistent and brief manner because the concept of an agent is applied diversely across disciplines. The concept of an agent is meant to be a tool for analyzing a system, not just an absolute categorization where entities are defined as agents or non-agents (Russel & Norvig, 2003). Some modelers consider any type of independent components in the system (i.e. software, model, individual, etc.), to be an agent. Others require that a component's behavior must be adaptive in order for this component to be considered an agent, i.e. where the term agent is reserved for components that can, to some degree, learn from their environments and modify their behaviors[13]accordingly. Regardless, and from a pragmatic modeling viewpoint, there are several features that are common to most agents (Wooldridge & Jennings, 1995):

- Autonomy: Agents are autonomous and self-directed. They are capable of processing information, to exchange this information with other agents, and to make independent decisions (e.g. organisms, - fish).
- Heterogeneity: Agents permit the creation of autonomous individuals. Sets of agents may

[13] I means here the agent/individual behavior, how the agent reacts to inputs to transform its state.

exist, but they may also create, by spawning, combinations of similar autonomous individuals.

- Activity: Agents are active because they exert independent influence in a simulation. The subsequent active features can be identified, - agents are;
  1. Goal-directed: Agents are often considered goal-directed, having goals to be achieved by way of their behaviors, - individually and collectively.
  2. Perceptive: Agents may have some awareness of their environment (surroundings). Agents may also be equipped with prior knowledge that constitute or affects their "mental map" of their environment, so as to provide them with an awareness of other entities, obstacles, or desired destinations within their environment.
  3. Interactive: Agents communicate effectively with their peers. For example, agents can obtain information about the states of other agents and/or the environment within a neighborhood, via neighborhoods of (potentially) varying size, searching for specific attributes, with the capability to ignore inputs that do not surpass a pre-specified threshold.
  4. Mobile: The mobility of agents is a specifically useful feature. Agents may be characterized by its coordinates and can roam the space defined by a model (e.g. fish in an aquaculture system).
  5. Adaptive and Learning: Agents may also be adaptive so as to make up Complex Adaptive Systems (Holland, 1995).

ABMs are comprised of a multiple of interacting agents that exist within a model or simulation environment. A relationship between these agents is specified, linking agents to one another or other entities (i.e. landscapes) within a system. Relationships may be specified in a variety ways, from simply reactive to goal-directed. The behavior of agents can be programmed to take place synchronously (every agent performs actions at each discrete time step), or asynchronously (agent actions are scheduled by the actions of other agents, or with reference to a clock). Environments define the space in which agents operate, serving to support their interaction with the environment and other agents.

In a modeling perspective, ABMs can be used as an experimental media for running and analyzing agent-based simulations. In such a laboratory, attributes and the behavior of agents, as well as the environment in which they are operating, may be changed and the resulting dynamics may be observed and analyzed. Typically, ABMs incorporate a large number of parameters operating within wide value ranges. The large parameter space in ABMs creates challenges in finding suitable methods by which one may explore that space in a way that realistically relates the model behavior to the purpose of the model (we address this problem in our third study). But the capability to simulate the individual actions of many diverse agents and analyze the resulting system behavior over time implies that ABMs may be useful tools for studying the effects of changing the attributes of agent's and that of their environment on processes that operate at multiple scales and organizational levels (Brown, 2006).

3.2.1 Advantages of Agent-Based Models

Some authors have portrayed ABM as an advantageous approach in many cases for the following reasons: It; 1) captures some emergent phenomena; 2) provides a natural environment for the study of certain systems; 3) is flexible.

Emergence is a characteristic of complex systems, and, by definition, emergent dynamic phenomena cannot be attributed to the dynamics of system's parts, - the whole is more than the sum of the parts. Therefore, emergent phenomena can exhibit properties that may not be easily derived from the properties of the system's parts. For example, a traffic jam may result from the behavior of the all individual car drivers who are following certain traffic rules, and may be triggered by, say, an accident or the fault of a driver driving in the wrong direction. The emergent dynamics (i.e. traffic jam) is an aggregate result of the actions of all the drivers in response to that accident or fault. Studying the behavior of collections of agents focuses attention on relationships between entities (O'Sullivan, 2004). Since ABMs describe the behavior of and interactions between various parts of a system (i.e. bottom-up), ABM is the conventional approach for modeling emergent phenomena.

In many cases, ABM is a convenient method for describing and simulating a system composed of real world entities. In particular, the agent-based approach may be useful when it is more appropriate to describe the component units of a system under some of the following conditions (Bonabeau, 2002): 1) The behavior of individuals cannot clearly be defined through aggregate transition rates, - for example, fish stress when feeling the crowd, or the decision to move; 2) The behavior of individuals is complex. Although hypothetically any process can be explained by an equation, the required number of differential equations increases exponentially as the complexity of behavior increases. Expressing complex individual behavior by a single equation, may, therefore, become intractable; 3) Activities are more convenient way of describing a system than processes; and, 4) Agent's behavior is stochastic. In ABM, sources of randomness may be applied very specifically to represent the stochasticity in the behavior of an agent, - as opposed to adding noise more or less arbitrarily in aggregate equations.

The agent-based approach to modeling is flexible, and, as such, particularly well-suited for geospatial modeling (e.g. virus spreading in a fjord system). Spatial simulations benefit from the mobility that ABMs offer. Agent mobility makes ABM very flexible regarding potential variables and parameters that may be included. Neighborhoods can also be identified using a variety of mechanisms. The implementation of agent interactions can easily be governed by space, networks or a combination of structures. It would be extremely demanding to represent such mobility using differential equations, - see for example (Axtell, 2000). Most importantly, ABMs can regulate behaviors based on interactions at a specific distance and direction. ABMs also supply a robust and flexible framework for tuning the complexity of agents (i.e. their behavior, the ability to learn and evolve, the degree of rationality, and rules of interaction). Additional such flexibility enables us to adjust levels of description and aggregation. It is easy to experiment with aggregate agents, sub-groups of agents, and single agents, where the different levels of description coexist within a model.

3.2.2 Limitations of Agent-Based Models

Some limitations reduce the applicability of the ABM approach in modeling at large. Although this is common to all modeling techniques, one issue relates to the purpose of the model. A model is only as useful as the purpose for which it was built. A model has to be built at the correct level of granularity or aggregation for every phenomenon, wisely selecting the appropriate amount of detail for the model to serve its purpose (Couclelis, 2002). The advancements made in ABM offers a means to increase the utility of simulation models, by closely tailoring the model and the subsequent analysis to the needs of end users (Parker et al., 2003). However, a model's output must be interpreted correctly. Varying degrees of accuracy and completeness in the model inputs determine whether the output should be used purely to gain qualitative insight, or to facilitate accurate quantitative foretelling (Axtell, 2000).

By definition, ABMs represent systems at a relatively disaggregated level (a high resolution or granularity perspective is applied). This level of detail typically implies the description of very many agents, attributes, and behaviors and their interaction with an environment. The way to treat this type of challenge in agent computing is through multiple runs whereby initial conditions and/or parameter values are being systematically varied to assess the robustness of simulation results (Axtell, 2000). There is a practical upper limit to the size of the parameter space that can be explored for robustness, and this computational process can be extremely demanding and time-consuming. Although the computing power available is rapidly increasing, the computational requirement of ABM remains a limitation when modeling large systems.

The main challenge for modelers is to find system boundaries and time limits that retain the required level of precision in the simulation results originating from a particular model designed for a particular purpose. Complex natural systems, such as fjord systems, are radically open and contextual systems. Fjord systems are radically open systems because their extent goes beyond what can be represented endogenously by a model. ABMs have clear boundaries, and they are closed systems where any state changes of the system or parts of it are due to the interactions between the parts within the system. The contextual system may include elements that occur in different systems or is itself is a shared element between many systems. For example, wild fish can be an element (a class of agents) that is included in different systems (i.e. an aquaculture system and fjord ecosystem), and the aquaculture system can be an element in the fjord system. The contextuality is a consequence of dividing the world into system and ambiance. ABMs have only internal contextuality since they don't have ambiance. Still, ABMs may display some contextuality, but they are not radically open and they do operate within well-defined boundaries. Understanding the theories of complexity may be helpful in deciding how to draw the system boundaries to capture the essential elements required to portray emergent phenomena purposefully (Chu et al., 2003).

Critics of complexity theory point out that the wide variety of unexpected dynamics exhibited by mathematical and computational models are rarely found in the real world, particularly because ABMs are very sensitive to initial conditions and small variations in interaction rules (Couclelis, 2002). Consequently, modelers of complex systems are never likely to enjoy the intellectual comfort of laws. Despite this, and the other limitations that have been underlined, ABM is a useful tool for exploring systems that exhibit complex behavior.

3.2.3 The purpose of Agent-Based Models

There is a variety of ways in which a model may be applied, just as there are different types of models that have different characteristic features, and where each one has some advantages and some disadvantages (Casti, 1997). When considering these applications, one may gain a better understanding of what distinguishes an appropriate, valid, and purposeful model from less useful ones. The utility of ABM may be of one of three broad categories: explanatory, predictive and control.

When employing explanatory modeling we attempt at exploring theory and generating hypotheses. Explanatory models usually focus on a specific aspect of a system and placing emphasize on some specific details of a phenomenon. These models are intended to be explanatory by saying how reality should or would be, under ideal conditions, but they do not attempt to reproduce actual systems (Parker et al., 2003). In our first study, we focused on building explanatory models. We built ABMs models to simulate fish disease dynamics in fish populations. In these explanatory models, we programmed plausible agent (i.e. fish and pathogen) behaviors and interactions to produce similar patterns that are observed from the real world systems. Then, we ran different simulations to explore theory and generate hypotheses. For example, we built different models with different fish swimming behaviors (i.e. swimming in schools, follow circular paths, or swimming randomly) to study the effects of the fish swimming patterns on the fish disease dynamics.

In our second study, we focused on building predictive models (i.e. predict a pattern of fish disease dynamics in a Norwegian fjord). Predictive models are commonly used in order to evaluate scenarios, to identify and "extrapolate" dynamic trends, and to predict future state trajectories. Specifically, changes in initial conditions parameter values and exogenous inputs may be used to evaluate the possible effects on the model outcome. Part of the thesis work was to build infection risk maps in the Norwegian fjords to evaluate the future scenarios. Predictive models are proposed to mimic real world systems and are specifically useful for scenario development and policy design.

Control models are providing guidelines and control mechanisms for the intervention and manipulation of systems. In our third study, we developed a framework for using a PSO algorithm to identify optimal aquaculture system characteristics (i.e. fish densities and farm locations).

Whether aiming for an adopting, an explanatory, a predictive, or a control approach to modeling, the choice is not entirely exclusive. This choice is mainly dependent on the required level of precision in the model. This, in turn, is directly related to the type of information and knowledge that is required, i.e. the purpose of the model. For instance, the more the model is aimed for control, the more precise it must be.

3.3 Verification and validation of agent-based models

In the previous sections, I have provided an overall view of ABM as applied to complex systems. Once we have implemented an agent-based model by overcoming the limitations and addressing the purpose of the model, the model must be verified by checking that the model performs to our expectation, i.e. produces the expected simulation results. In general, we must assess the validity of the model, - a process that serves the purpose of strengthening our confidence in the model and the results it produces. For that purpose, we need a robust and a valid model that can we depend on.

3.3.1 Verification and Calibration

When the model has been developed either by using an ABM tool (e.g. NetLogo) or by programming from scratch using low-level programming languages, the model must be verified by checking the model behaves as expected; often referred to as "inner validity" (Axelrod, 2006a; Brown, 2006). To achieve inner validity, I have tested the developed models to simulate fish disease dynamics and disease spread among many aqua facilities, under extreme conditions that should result in some easily predictable dynamics. It is, however, hard for a modeler to know whether unexpected outcomes are a reflection of a mistake in the computer programme (bug error), a logical errors, or a surprising consequence of the model itself (Gilbert & Terna, 2000). This difficulty is composited because complex systems can often produce emergent, unexpected and counterintuitive results. A modeler must still find out whether unexpected results are due to errors in the coding or the model logic (i.e. fish get infected process), or just a feature of the system being modeled. I safeguard against these problems by adopting different tests (i.e. execute the computer programme after each modification of the code to check if there is a bug) while programming the model. The difficulties of verification are increased by the fact that most simulations are dependent on random distribution functions and random number generators to simulate the properties of unmeasured variables and random choices. Therefore, repeated runs can produce very different outcomes (as shown on our simulation results of ABMs to simulate fish disease spread). However, one of the main advantages of ABMs is that they provide an easy method for simulating a real-world system that helps simplify the model logic, which make it easy to program (Batty, 2001). For instance, an individual susceptible fish will get sick if it is exposed to a number of pathogens in its surrounding.

Another way of verifying a model is to re-implement it using a different programming language. For example, I implement the swimming behavior model of fish in cages by starting from scratch in C sharp (i.e. an object-oriented programming language), then I re-implement the model in NetLogo to include it in the fish disease model. This method will not guaranty the inner validity, but I became more confident by following this method.

After a model has been verified, the subsequent stages include the calibration and validation of the model. Calibration comprises setting the model structure and parameter values in ways to reflect a real world system. Calibration takes place in stages until the outcomes of the model fit (within a reasonable tolerance) the real world data gathered. Therefore, calibration is useful for assessing the ability of the model to simulate the real world system (i.e. showing that the model can generate results that match the real-world data). Calibration of ABMs to simulate fish disease spread requires data on the individual rules (i.e. fish and pathogens behavior rules). Several ways are followed to obtain these data (e.g. from literature, reports from aquaculture in Norway, people working in the field, statistical analysis of empirical data, …etc.).

The level of correspondence between the model and the real data is dependent on the purpose of the model, and the modeler must develop confidence in the accuracy of the available data originating from reality (e.g. the data does not represent extreme situations). But calibrating a model may lead to the model being over-fitted, and in this situation, a model is insufficiently general to represent a diverse range of system outcomes or to apply it to other systems. A model with sufficient number of parameters can be tweaked until the real world data is matched (Carley, 1996). But modelers should be aware if the fact that calibration does not guarantee the validity of a model.

3.3.2 Validation of Agent-Based Models

A model is valid to the extent that it sufficiently represents the system being modeled (Casti, 1997). Of course, any model has a certain degree of validity and it cannot be categorized as valid or invalid in a simple form (Law & Kelton, 1991). Validity can be determined by comparing the output of the model with comparable data gathered from a real-world system. For example, in order to understand the output (i.e. behavior) of ABMs to simulate fish disease spread, it is necessary to evaluate deeply the details of the simulation history. The validation procedure is related to the use of the model. Gross and Strand (2000) has listed these approaches to validate ABMs of complex systems:

- Validation through prediction: The modeler is repeating testing events until the accuracy of the model has proven satisfactory. Under normal conditions, this procedure is theoretically unproblematic, but many systems do not allow repeated testing of events (e.g. disease spread) and/or the changes are too slowly (e.g. climate change) to allow for a validation procedure through predictions across a relevant time-space scale. This method of validation is unrealistic in the validation of models developed to simulate disease spread in general, and fish disease spread in particular. It is not allowed to repeat testing events of fish disease outbreaks in aquaculture systems, and the false predictions of the model can cause huge losses and unexpected consequences.
- Validation through retrodiction: The model output (i.e. behavior) is tested against historical data, so the available information in the historical data causes the future behavior of the system. If the model is able to reproduce a historical record correctly, then the model may be trusted to simulate the future. But this assumption is not justified when historical data is limited and uncertain. In fish disease spread processes, the historical data is limited, uncertain and part of the data is qualitative only. Also, there will always be a different model yielding a correct retrodiction of the historical record within some error margins. Therefore, through retrodiction validity alone we may not be not able to assess whether the mechanisms that constitute the model are valid (i.e. structural validity).
- Structural similarity: The modeler strives for structural similarity between the model and the system, as we know it. Complex systems include huge numbers of and a major heterogeneity across parts and causal relations. Thus, a structural similarity approach may seem unrealistic. However, an assessment of the model including its structure on different levels (i.e. micro and macro levels) will truly determine whether the implemented model reflects the way in which the fish disease spread. For instance, do fish agents' behavior match, with satisfactory accuracy, our conception of the aquaculture system?

- Pseudo-validation: If a great number of models all yield the same prediction, then the prediction is somewhat justified. In our case, the simulation of fish disease spread in Norwegian fjords, there are not many available models that has produced results with which we may compare. In this thesis work, we compared the results from simple versions of the implemented models to SIR model's output. Also, we compared the results from all the simulation to the qualitative results from different previous studies (i.e. results from Stene work (Stene, 2013) and from SINMOD (www.sinmod.no).

In general, it is very difficult to validate fish disease spread models due to the lack of reliable field data. In this work, we have applied a variety of validation techniques as follow:

1. Validate simple models, and then add more complexity.
2. Extreme condition tests: We use unlikely combinations of key factors (e.g. fish density, currents speed, seawater temperature, … etc.), usually high or low values of input parameters to test whether the simulation continues to make sense at the margins.
3. Sensitivity analysis: In order to determine the effect of the input parameters and the agents' interactions on the behavior of the model, sensitivity analysis is used. The aim of using sensitivity analysis technique is to;
   - Understand the conditions under which the model behaves as expected;
   - Find the condition that maximizes the correspondence between the model and the system behavior, as we know it; and
   - Identify the conditions to which the model is sensitive, for example, which inputs yield disease outbreak.
4. Cross-validation technique: This may be accomplished by comparing the results of the models with empirical data at a single time period. We accomplished this by running the models for simple scenarios where the results were expected.
5. Compare the model output with other available models: We aligned the models with SIR models for simple scenarios.

It is necessary to evaluate the simulation history in details (in micro and macro levels) to understand the behavior of ABMs. The analysis of individual histories is interesting in general, but they can be misleading; particularly if the model includes random elements. It is necessary to undertake a repeated number of simulations using identical parameters and initial conditions (using different random number seeds) to determine whether the conclusion of a simulation run is typical. Running many simulations will help discriminate whether particular patterns observed in a single illustrative history are unusual or typical. The results from these simulation runs will need to be presented as distributions, and statistical analyses will be required to assess any variation in the model output and to determine whether inferences from the simulation histories are well founded. Gilbert and Troitzsch (2005), and Axelrod (2006b) claim that regression will be required for analyzing quantitative changes in the output of a simulation, and analysis of variance will be required to assess the output of a simulation if the differences are qualitative.

Usually, it is desirable to engage in sensitivity analysis when a model, at least for a specific set of parameter values and initial conditions, appears to be valid. The purpose of sensitivity analysis is to determine to what extent the level of variation in the model's assumptions yield differences in the model output. The principle behind sensitivity analysis is to change the initial conditions and the parameter values of the model by a small amount and observe differences in the model outcomes (Castle & Crooks, 2006). However, a note of caution should be observed since complex systems can exhibit large and sudden dynamic shifts in response to relatively small perturbations in inputs (Manson, 2007).

There are a few cautions that must be considered while validating and analyzing the output of a model (Gilbert & Troitzsch, 2005). Firstly, both the model and the system under analysis are likely to be stochastic. Therefore, the comparison between the model output and data from the real-world system are unlikely to correspond in every case. A second problem relates to the ability of the model to offer valid predictions, since prediction will almost always be conditional (i.e. it is unlikely that all guessed outcomes can be produced). Additionally, there is a possibility that the model is correct, but that the data from the real-world system is not (i.e. inappropriate assumptions or estimates could have been obtained from the data). Finally, many simulations are path dependent: The outcome of a simulation is dependent on a specific initial setup. So different runs of the same model can generate variation in outputs due to changes in initial conditions, parameters, or the stochastic behavior / interaction of agents. Therefore, the history of a simulation is highly significant.

Validation and calibration are the hardest two issues of ABMs. Even though there may be a correspondence between a model's output and a real world system, this is not sufficient condition to conclude that the model is correct (Gilbert, 2004). Similar outcomes can be generated from different processes, and just because a model generates similar outcomes does not prove that the processes included within the model account for the real world outcome. However, a model should be considered as a basic for reducing uncertainty about the future, from a prior state of unawareness, to one of more limited uncertainty (Castle & Crooks, 2006).

4. Agent-based models to simulate fish diseases

In this chapter, we will describe how to build ABMs to simulate fish disease dynamics in a fish population and to simulate transmission of pathogens between fish farms in sea aquaculture systems. In the last section, a framework for using a particle swarm optimization (PSO) algorithm to identify the optimal model parameter values is used.

4.1 Aquaculture system model

The aquaculture system has a set of fish farms, a swarm of pathogens, and a landscape. This system *S(t)* can be formulated as:

$$S(t) = \{FF(t), P(t), L(t), N(t)\} \tag{4.1}$$

where *FF(t)* is a set of fish farms, *P(t)* is a swarm of pathogens, *L(t)* is the landscape or the environment where the previous components are located, and $N(t)$ is the mutual relation between these parts.

The landscape L(t)

The landscape *L(t)* is divided into four sub-landscapes and can be formulated as:

$$L(t) = \{L_{tr}(t), L_{cu}(t), L_{sa}(t), L_{tm}(t)\} \tag{4.2}$$

where $L_{tr}(t)$ represents the terrain, $L_{cu}(t)$ represents the map of the sea currents, $L_{sa}(t)$ represents the map of the seawater salinity, and $L_{tm}(t)$ represents the map of the seawater temperature.

The terrain $L_{tr}(t)$ covers fjord area where the fish farms are located. The terrain is divided into many 3D grids. The sea current landscape, $L_{cu}(t)$, represents the speed and direction of the sea currents. The seawater salinity, $L_{sa}(t)$, and seawater temperature, $L_{tm}(t)$, landscapes are changing in time and space. The user can set the average seawater temperature and salinity at the surface level, and then we add some noise to include the variation that is present in nature. The water temperature also varies in the deep levels, as follows:

$$\vec{T}(x, y, z, t) = \vec{T_0}(x, y, z, t) - C\,\vec{L}(y) \tag{4.3}$$

where $\vec{T}(x, y, z, t)$ is the water temperature at the position (*x, y, z)* at the time *t*, $\vec{T_0}(x, y, z, t)$ is the water temperature at the surface level (*y* = 0, maximum temperature value at the surface), *C* is a constant that represent the decay rate, and $\vec{L}(y)$ is the water levels of the sea.

The fish farm $FF_k(t)$

Each fish farm, $FF_k(t)$, has a swarm of fish agents, *FA(t)*. Each fish farm is represented by number of 3D grids. The swarm of fish agents has some social rules that manage the individual movements in the swarm, consumes pathogens, and produces pathogens. Fish farms can hypothetically be located at any position in the simulated space. Closer distance between the farms (i.e. higher cohesion) increases the infection risk, while higher separation decreases the infection risk.

The pathogens swarm $P(t)$

The pathogens swarm consists of many individual pathogens:

$$P(t) = \{PA_1(t), PA_2(t), \ldots, PA_n(t)\} \tag{4.4}$$

where $PA_j(t)$ is the pathogen agent *j*, and *n* is the total number of pathogens at time *t*.

Pathogens move by sea currents. The swarm of pathogens also has social rules (e.g., move together and align with others), and the swarm networks to the landscapes to manage the pathogen individuals' movements (Reynolds, 1999). We assume that the simulation space is free of pathogens at the beginning.

The relationships N(t)

There are mutual relations between all the system elements (i.e. fish, pathogens and landscape). *N(t)* represents the relationships between fish and pathogens (e.g. infection process), and between them and the landscape (e.g. pathogen transmitter by currents).

4.2 Agent-based model

In this section, I will explain how to apply the ABM approach to simulate fish disease dynamics and pathogen transmission in a fjord aquaculture system. Table 4.1 shows the agent-based model's agents. We have two types of agents, fish and pathogen. Each agent has many attributes and behavioral rules that update these attribute values in the context of time and space.

Agent type	***Attributes***	***Behavioral rules***
Fish	• Position • Health status • Energy • Vaccinated	• Update position • Update health status • Update energy (resistance factor) • Shed pathogens
Pathogen	• Position • Life span • Ability	• Update position • Update life span • Update ability

Table 4.1. Agents in the model

4.2.1 The fish agent

The fish are located in the farms, and each fish farm $FF_k(t)$ has a swarm of fish that is composed of many fish agents, $FA(t)$:

$$FF_k(t) = \{FA_1(t), FA_2(t), \ldots, FA_n(t)\} \tag{4.5}$$

A fish agent $FA_i(t)$ has several attributes and behavioral rules that update these attributes (see Table 4.1). In the following, I will introduce how to set these attributes and update them in space-time domain.

Fish swimming rules: Fish agents swim only within cages. I have developed three different fish movements behavior:

a) Moving randomly: If a large time step (i.e., 10 minutes or one hour) is used in the simulation, the fish's positions are updated randomly at each time step, as:

$$\overrightarrow{FA_i}(x,y,z,t+\Delta t) = \overrightarrow{R_i} * \left(\frac{max_{x,y,z} - min_{x,y,z}}{2}\right) + \overrightarrow{FF_k}(x,y,z,t) \quad (4.6)$$

where $\overrightarrow{FA_i}(x,y,z,t+\Delta t)$ is the fish i position vector, $\overrightarrow{R_i}$ is a unit random vector in 3D, $(max_{x,y,z} - min_{x,y,z})$ is the fish farm dimensions, and $\overrightarrow{FF_k}(x,y,z,t)$ is the farm position in the simulation space. Fish can swim in different patterns, and they can socialize to form a school.

b) Schooling behavior: Fish normally swim in schools to benefit from the flocking behavior such as: enhanced foraging success and defense against predators.
A fish has three simple rules of steering behavior that describe how an individual fish move, based on the positions and velocities of its flock mates (Reynolds, 1987).

- Cohesion (Figure 4.1): Each fish tends to move to the middle position of its neighbors. Cohesion, $\overrightarrow{Coh_i(t)}$, of the fish ($FA_i$) is calculated in two steps. First, the center (c_i) of the flock (f) that has this fish is calculated:

$$\vec{c_i} = \sum_{\forall FA_j = f} \frac{\overrightarrow{FA_j}(x,y,z,t)}{N} \quad (4.7)$$

where, $\overrightarrow{FA_j}(x,y,z,t)$ is the position of fish j and N is the total number of fish in f.

Then the tendency of the fish to navigate toward the center of density of the flock is calculated as the cohesion displacement vector:

$$\overrightarrow{Coh_i(t)} = \vec{c_i} - \overrightarrow{FA_i}(x,y,z,t) \quad (4.8)$$

- Alignment (Figure 4.2): each fish match the direction and the speed of its neighbors. This rule causes fish to follow each other. The alignment $(\overrightarrow{Ali_i(t)})$ is calculated in two steps. First, the average velocity vector of the flock mates ($\overrightarrow{v_f(t)}$) is calculated by:

$$\overrightarrow{v_f(t)} = \sum_{\forall FA_j \epsilon f} \frac{\overrightarrow{v_j(t)}}{N} \quad (4.9)$$

Then $\overrightarrow{Ali_i}$, is calculated as the displacement vector between the average velocity of the flock and the velocity of the fish:

$$\overrightarrow{Ali_i(t)} = \overrightarrow{Fv_i(t)} - \overrightarrow{v_i(t)} \quad (4.10)$$

A fish has a limited speed that depends on its weight and length. In general, the weight-length relationship can be described by the following equation (Jones et al., 1999):

$$W = a * (L^b) \quad (4.11)$$

where W is observed fish weight, L is observed fish length, and a and b are computed by:

$$log\ (W) = log\ (a) + b * log\ (L) \quad (4.12)$$

where a is the regression intercept and b is the regression slope.

The fish speed depends on many factors. In this study, I computed it by:

$$Fish\ speed = k * L \quad (4.13)$$

where L is fish length, and k is a constant that depends on the environment condition.

- Separation (Figure 4.3): Each fish keep a distance from other fish nearby to avoid collision and prevent crowding. This rule acts as the complement of the cohesion rule. There are many ways to implement this rule. I calculate the separation ($\overrightarrow{Sep_\iota(t)}$) of fish by:

$$\overrightarrow{Sep_\iota(t)} = -\sum_{\forall FA_j \epsilon f} \left(\overrightarrow{FA_\iota}(x,y,z,t) - \overrightarrow{FA_j}(x,y,z,t)\right) \tag{4.14}$$

Vectors defined by the position of the fish $FA_i(t)$ and each visible fish $FA_j(t)$ are summed, then separation steer $\overrightarrow{Sep_\iota(t)}$ is calculated as the negative sum of these vectors.

Fish has a minimum separated distance to keep between it and other neighboring fish, and the fish has a limited vision distance.

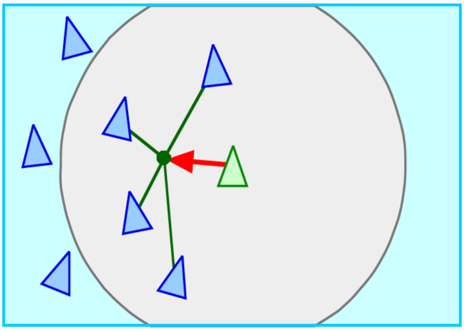

Figure 4.1. Cohesion social rule (http://www.red3d.com/cwr/boids/)

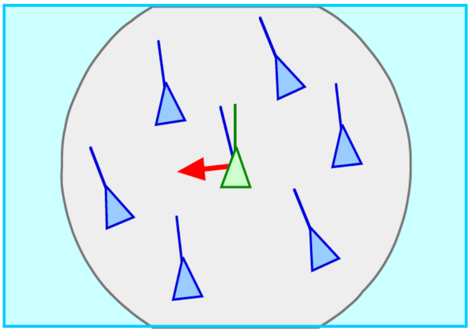

Figure 4.2. Alignment social rule (http://www.red3d.com/cwr/boids/)

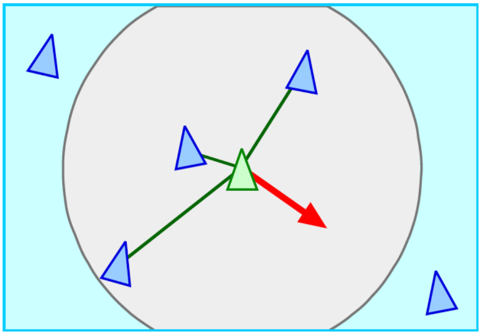

Figure 4.3. Separation social rule (http://www.red3d.com/cwr/boids/)

c) Circular behavior (Figure 4.4): Fish in sea cages prefer to swim in the middle of the cage referencing to the cage depth and follow a circular movement (Folkedal et al., 2012). The fish agent ($FA_i(t)$), follow a horizontal circle path with small disturbance in its orientation (i.e. direction) as seen in Figure 4.4. The fish is using a separation rule to avoid crowding and being hit by other fish. The fish agent is slightly disturbed in its direction in horizontal plane (horizontal direction) by applying:

$$FA_i(t)_{hed} = FA_i(t)_{hed} \pm R_n * (FA_i(t)_{hed}, std) \tag{4.15}$$

where $FA_i(t)_{hed}$ is the heading of fish agent i that is the rotation of it around the z-axis, R_n is a normally distributed random floating point with a mean of current heading and a standard deviation std.

Also, the fish has a small disturbance in its vertical direction in z-direction by applying:

$$FA_i(t)_{pitch} = FA_i(t)_{pitch} \pm R_n * (FA_i(t)_{pitch}, std) \tag{4.16}$$

where $FA_i(t)_{pitch}$ is the angle between the orientation vector of fish agent i and the horizontal plane, R_n is a normally distributed random floating point with a mean of current *pitch* angle and a standard deviation std.

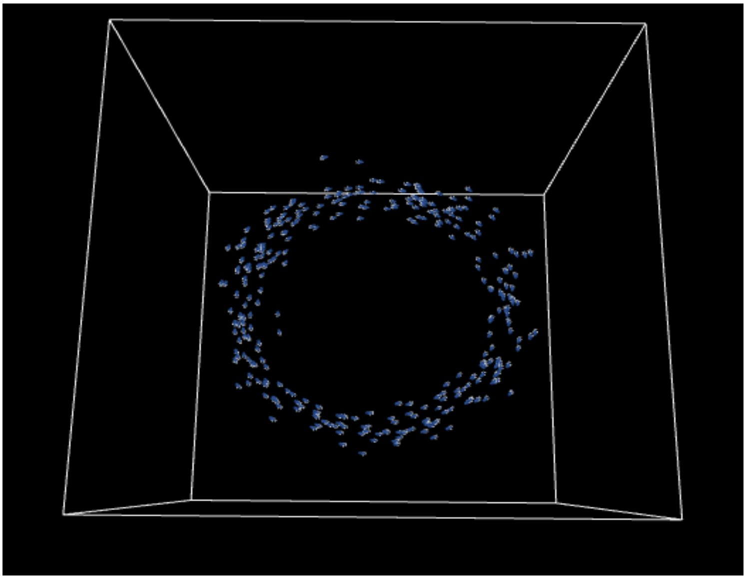

Figure 4.4. Fish swimming in circular path behavior.

Fish energy attribute: Each fish has an epidemic resistance factor that reflects the ability of its immune, which is a value between 0 and 1. We assign reference values of 0.8 with some noise:

$$RF_{\,i} = RF_{\,ref} \pm R * N_{rf} \tag{4.17}$$

where $RF_{\,i}$ is the resistance factor of fish i, $RF_{\,ref}$ is the reference resistance factor value that can be set by the user, R is a random number in the range of [0,1], and N_{rf} is the noise value.

Infection rules: Fish agents are categorized into four main health states as in the SEIR (susceptible, exposed, infected and removed) model (Bjørnstad, 2005). In the following text, I will explain how the fish health state of individuals will be updated over time. A susceptible fish becomes infected if there are many pathogens around it, the pathogens have a good ability to infect, and the fish has a week RF, as determined by the *Algorithm 4.1* procedure.

Algorithm 4.1. *infection rules*

1: **For each** susceptible fish agent i…**then**

2: **If** $(RF_{\,i} * \sum_{p_j\, in\, r}(p_j \;*\; ab_j) \;\geq\; T)$,

Where

$RF_{\,i}$ is a fish i resistance factor, p_j is any pathogen j in r distance from fish i, ab_j is the infection ability of pathogen j, and T is a selected threshold.

3: get infected

4: **End if**

5: **End for each**

Once the fish has been infected, it will leave the susceptible category and enter the exposed category. All fish agents move between these four health states. Therefore, the population of agents is divided into four groups or compartments consisting of individuals that are susceptible, exposed, infected or removed. The fish agents are heterogeneous, and each agent has its own individual discrete SEIR model. The contact rate in the SEIR model is equivalent to the individual fish infection rules in ABMs. The fish agent health state in ABMs is dynamically updated. The number of fish with the same health state provides the number of fish agents in the four groups.

The process of updating the fish health states at each time step is achieved by applying the health-state update method, as shown in *Algorithm 4.2*.

Algorithm 4.2. *Fish health-state updating*

```
For each fish agent…then
        Check health status
    If fish is susceptible then
        If there are a number of pathogens around the fish then
            1. Change fish state to exposed
            2. Die by normal death rate
        Else
            Die by normal death rate
        End If
    End If
    If fish is exposed then
        If fish passed exposed period then
            1. Change fish state to infected
            2. Die by illness death rate
        Else
            Die by normal death rate
        End If
    End If
    If fish is infected then
        Produce a pathogen by a given probability "shedding rate"
        If fish passed infected period then
            1. Change fish state to recovered
            2. Die by normal death rate
        Else
            Die by illness death rate
        End If
    End If
    If fish is recovered then
        If fish passed immune period then
            1. Change fish state to susceptible
            2. Die by normal death rate
        Else
            Die by normal death rate
        End If
    End If
End for each
```

Producing pathogens process: The infected fish i sheds pathogen j at the same place where it is located using a given rate (*shedding rate*) at each time step. Different sources use different units, and values range across $10^{6.5}$ PFU/fish/h (PFU=plaque forming units) (Gregory, 2008), 10^5-10^8 CFU/fish/h (CFU=colony forming units) (Rose et al., 1989) and $6.8*10^3$ $TCID_{50}$ /ml/ kg fish/ h/ (maximum rates) ($TCID_{50}$=the amount of virus required to kill 50% of infected hosts) (Urquhart et al., 2008). The units are not single pathogens, - rather, they are units that are measurable in the lab. Since the numbers are very high and computationally difficult to implement in the model, I set a probability between 0-1 (adjustable) that an infected fish sheds a pathogen, but this model pathogen represents a large number of real pathogens.

4.2.2 The pathogen agent

The pathogens swarm *P(t)* consists of many individual pathogens:

$$P(t) = \{PA_1(t), PA_2(t),\dots, PA_n(t)\} \tag{4.18}$$

where $PA_j(t)$ is the pathogen agent *j*, and *n* is the total number of pathogens at time *t*. The pathogen agent $PA_j(t)$ has three main attributes (see Table 4.1); position in the space, ability to infect fish, and life span.

Rules governing movement: The pathogens are drifted by sea currents. Each pathogen moves based on the current speed and direction, which is based on the location of the pathogen at the start of each time step. Pathogens inherit the current direction of the place they are presently located, and by moving to a new place, they inherit the direction of that new place. When moving, the pathogen might hit dry land. In this case, the pathogen is removed from the model (dies).

The pathogen *j* updates its position as follows:

$$\left\|\overrightarrow{v(t)}\right\| = C_{sr} \,.\, R_n(C_s, std_s) \tag{4.19}$$

$$\overrightarrow{PA_j}(x, y, z, t + \Delta t) = \overrightarrow{PA_j}(x, y, z, t) + \overrightarrow{v(t)} * \Delta t \tag{4.20}$$

where $\left\|\overrightarrow{v(t)}\right\|$ is the magnitude of the velocity, C_{sr} is the relative current speed that is inherited from the grid where the pathogen *j* is, and R_n is a normally distributed random floating point with a mean of C_s (average current speed in this area) and a standard deviation std_s. Then, the new pathogen agent j position, $\overrightarrow{PA_j}(x, y, z, t + \Delta t)$ is the new pathogen agent *j*, position $\overrightarrow{PA_j}(x, y, z, t)$ is the current pathogen agent *j* position, $\vec{v}$ is the pathogen velocity, and Δt is the time step.

The velocity direction is related to the pathogen's orientation. The pathogen's orientation is defined by two variables: heading $PA_j(x, y, z, t)_{hed}$ and pitch $PA_j(x, y, z, t)_{pit}$. Heading is the angle between the forward vector of the pathogen projected onto the horizontal plane and the vector [0 1 0], and pitch is the angle between the forward vector of the pathogen and the horizontal plane. We calculated these variables as follows:

$$PA_j(x, y, z, t)_{hed} = C_d + R_n(C_{bias}, std_d) \tag{4.21}$$

$$PA_j(x, y, z, t)_{pit} = pit_{in} - R * pit_v \tag{4.22}$$

where C_d is the current's direction angle, R_n is a normally distributed random floating point with a mean of C_{bias} (current heading bias variable) and a standard deviation std_d, pit_{in} is the initial pitch value, R is a random number in the range of [0,1], and pit_v is the pitch value.

Life cycle: Pathogen life span is a function of seawater condition (temperature and salinity). Salama estimated the values for infectious salmon anemia virus (ISAV), infectious pancreatic necrosis virus (IPNV) and salmonid alphavirus (SAV) to be between 8.33 and 62.5 hours (Salama & Murray, 2011). The life span's relation to the seawater temperature can be modeled as (Stene et al., 2014):

$$PA_j(x, y, z, t)_{LC} = q * exp\,(- T / h) \tag{4.23}$$

where *T* is the water temperature, *q* is the pathogen life span at a water temperature of 0°C, and *h* is the decay rate.

Ability to infect: Each pathogen has an ability attribute that has values between 0 and 1. I used initial values of 0.8 and added some noise:

$$PA_j(t)_{ab} = PA_j(t)_{ab0} \pm R * N_{ab} \tag{4.24}$$

where $PA_j(t)_{ab}$ is the ability of pathogen j *to infect*, $PA_j(t)_{ab0}$ is the initial value of that ability that can be set by the user, R is a random number in the range of [0,1], and N_{ab} is the noise value.

Once the pathogens arrive at the neighboring sites (i.e., susceptible farms), they will try to infect the susceptible healthy individual fish in that farm. The infection rules described in *Algorithms 4.1 & 4.2* applies.

4.3 Using PSO algorithm to identify automatically agent-based models parameter values

ABMs to simulate fish disease spread are characterized by dozens of parameters that all together determine the general behavior of the system. Finding optimal set of values for input parameters is needed to get optimal solutions in running scenarios. Typically, in ABMs, a small change in a single parameter can lead to a radical change to the system's behavior. In such systems in which small differences in parameter settings produce very different results, the search for a set of desirable parameter values may become a long and tedious process due to the huge number of parameters that characterizes the model and thus the large search space that exists. Therefore, it is crucial to develop an efficient strategy to automatically explore and tune the parameter space of ABMs.

With the purpose of finding the optimal parameter values that characterizes an aquaculture production system with a minimum risk of fish disease spread, we present a methodological framework for finding the optimal values for fish density and location of fish farms by using a PSO algorithm to explore the value space of these parameters.

In this section, I will first provide an overview of PSO algorithm. Then I will introduce a framework for optimizing the selected parameters to achieve a maximization of the proposed objective function.

4.3.1 Particle Swarm Optimization

PSO is a computational method that optimizes the solution to a problem by iteratively trying to improve a candidate solution with regard to a given measure of quality. In 1995, Kennedy and Eberhart (Kennedy, and Eberhart, 1995) introduced PSO originally developed to solve non-linear continuous optimization problems. More recently it has been used to solve many real-life problems. For example, PSO has been successfully applied to track dynamic systems (Eberhart, and Shi, 2001) and estimate weights and structure of neural networks (Zhang et al., 2000).

The PSO methodology operates by placing a group of individual particles into a continuous search space, wherein each particle is initialized with a random position and a random initial velocity in the search space. The position and velocity are updated synchronously in each iteration of the algorithm. Each particle adjusts its velocity according to its own experience and the experience of the other individuals in the swarm in such a way that it accelerates towards positions that have high fitness values in previous iterations. In other words, each particle keeps track of its coordinates in the solution space that are associated with the best solution that it has achieved so far. This value is called personal best (*pbest*). Another best value that is tracked by the PSO is the best value obtained so far by any particle in the neighborhood of that particle. This value is called (*gbest*). So the basic concept of PSO lies in accelerating each particle toward its *pbest* and the *gbest* locations, with a random weighted acceleration at each time step.

Each particle modifies its position by applying the standard continuous PSO algorithm as follows:

$$\vec{v}(k+1) = w\vec{v}(k) + c_1\overrightarrow{R_1}\left(\overrightarrow{pbest} - \vec{s}(k)\right) + c_2\overrightarrow{R_2}\left(\overrightarrow{gbest} - \vec{s}(k)\right) \tag{4.25}$$

$$\vec{s}(k+1) = \vec{s}(k) + \vec{v}(k+1) \tag{4.26}$$

where

$\vec{v}(k)$ is the velocity of a particle at iteration k.
$\vec{s}(k)$ is the position of a particle at iteration k.
$\overrightarrow{R_1}$ and $\overrightarrow{R_2}$ are random numbers in the range of [0,1] with the same size swarm population.
$\overrightarrow{pbest}$ is the particle's personal best solution has achieved so far.
$\overrightarrow{gbest}$ is the best solution achieved among all the particles.
c_1 and c_2 are learning factors, which will be fixed through the whole process.
w is the inertia weight:

$$w = w_{start} - \frac{w_{start} - w_{end}}{M}\, k \tag{4.27}$$

where *M* is the maximum iteration number and k is the current iteration, and we change the real position values to integer values that represent fish density and the indexes of the cells at each iteration.

The pseudo code of PSO is shown in *Algorithm 4.3*.

Algorithm 4.3. *PSO algorithm*

```
For each particle
   Initialize particle
End

Do
  For each particle
     Calculate fitness value
     If the fitness value is better than the best fitness value (pbest) in history
        set current value as the new pbest
     End If
  End

  Choose the particle with the best fitness value of all the particles as the gbest
  For each particle
     Calculate particle velocity according PSO velocity equation
     Update particle position according PSO position equation
  End
While maximum iterations or minimum error criteria is not attained
```

4.3.2 PSO to find optimal fish densities and farm locations

In this section, a framework to apply PSO algorithm to find the optimal combinations of fish densities and farm locations, - the ones that provide minimum risks of infection in the aquaculture system, is presented.

Integer particle swarm optimization (IPSO)

The standard continuous PSO algorithm must be modified to solve this problem. The search space is discrete; it is the cell coordination that contains two integer numbers, and the number of fish in each farm. Therefore, the search space is a three-dimensional space {fish density (I_f), x, y}.

Objective function

The main objective is to increase the production in the aquaculture systems while avoiding the fish disease spread. Disease outbreaks pose a significant loss in the aquaculture systems and pose a threat to the total ecosystem in the fjords. The fish farms have maximum capacities, but to avoid the infection risk, optimal capacities must be identified. The objective function in this case is a multi-objective function that is divided into two functions representing a conflict of interest. The first function is to maximize the fish density, while the second one is to minimize the infection risk (i.e. minimizing the attack-rate). A combined objective function of the two objective functions is a weighted sum between the fish density and the infection risk, - calculated using the following equation:

$$J = \sum_{\forall FF_k(t) \in S(t)} \left[w_0 \, (1 - A_r(k)) + \frac{w_1 \left(I_f\,(x_k, y_k) - I_f\,(x_k, y_k)_{min} \right)}{\left(I_f\,(x_k, y_k)_{max} - I_f\,(x_k, y_k)_{min} \right)} \right] \tag{4.28}$$

where $A_r(k)$ is the attack-rate (proxy for the infection risk) in farm $FF_k(t)$, $I_f\ (x_k, y_k)$ is the fish density of farm $FF_k(t)$, and w_0 , w_1 are selected weights.

5. Main findings

In this chapter, I summarize the results of the studies carried out in this PhD and present how they relate to the research objectives. Further work, in the form of additional applications, are presented at the end of the chapter.

5.1 Fish disease dynamics in fish population sensitivity to different factors

Norwegian marine aquaculture systems are located in open seawater areas such as in the fjords that also receive an annual influx of fresh water from land and provide a range of nutritional, social and economic benefits to humans. Coastal and fjords water are supplemented with a variety of substances resulting from onshore activities, from the offshore oil and gas industry, from fish farming and other offshore activities. Norwegian fjords systems are complex systems that are generally difficult to understand and that exhibit dynamics that one may not easily control for. The fish disease dynamics in such systems depends on many factors such as biological, physical, chemical and environmental factors. The disease transmission process is a complex, non-linear and unstable process. In this section, highlights from the results of the research on the use of ABMs to simulate and analyze contagious disease dynamics in fish populations, will be presented. Specifically, the sensitivity of fish disease dynamics to a variety of factors will be summarized. Sensitivity analyses contribute significantly to the exploration of the dynamics of such complex system models, because there is a high degree of parameter values uncertainty associated with such models.

5.1.1 Effects of fish density

Fish agents constitute the main part of the fish disease dynamics process. Infected fish are hosts of pathogens and shed pathogens to infect other fish. In crowded fish farms, the opportunities for the fish to swim is limited. Moreover, fish are stressed and more susceptible to diseases (Ogut, 2001). *Algorithm 4.1* reflects all these issues. Increasing the fish density, increases the attack-rate that is the measure of the rate at which a disease spreads in a fish population. The individual fish infection process as described in *Algorithm 4.1*, is determined by four factors; the degree of fish resistance to the disease, an infection radius (i.e. the distance from the susceptible fish that determine the area around it to be checked if there are pathogens in the neighborhood), the number of pathogens within the infection radius, and the pathogen's ability to infect fish. These factors depend on simulated fish and pathogen types. An individual fish in the ABMs represents a huge number of fish in real Norwegian aquaculture facility (up to 1000 fish). The sum of pathogens is associated with the fish density because infected fish release (shed) pathogens so that this sum increases with an increased fish density. Subsequently, the attack-rate increases due to the increased probability of combined fish and pathogen presence resulting from a higher fish density in the fish farm.

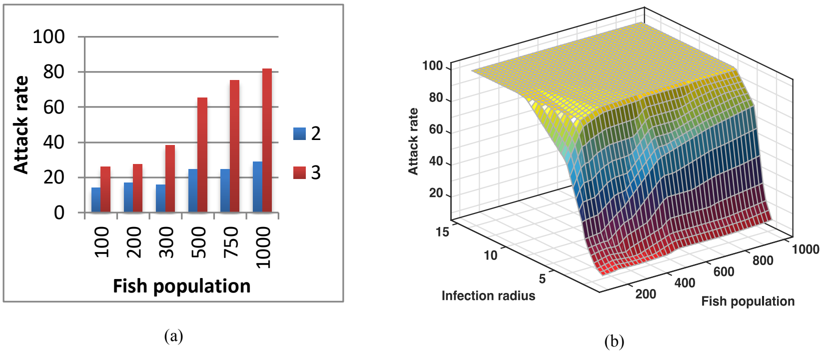

Figure 5.1. (a) Attack-rate after 20 days (y-axis), vs. fish population (x-axis), with infection radius 2 and 3. (b) Attack-rate after 20 days (y-axis), vs. fish population (x-axis) and infection radius (y-axis) varied.

Figure 5.1 shows the attack-rate reported in the infected farm due to resulting from a change in both fish population (proxy for fish density, since the physical size of the fish farm is constant) and infection radius (infection distance). 10% of the fish population is assumed infected initially. Increasing the infection radius and fish population, increases the attack-rate. It will reach 100% if the infection radius increases by more than 5 units regardless of the fish population value due to the increasing probability of pathogen presence (Figure 5.1(b)). The attack-rate shall not exceed its maximum value depending on the fish population (fish density) as shown in Figure 5.1(a). For example, attack-rate will not exceed 65% if the fish population value is equal or less than 500. Therefore, optimal fish densities in fish farms will reduce the disease spread and lead to a sustainable Norwegian aquaculture industry.

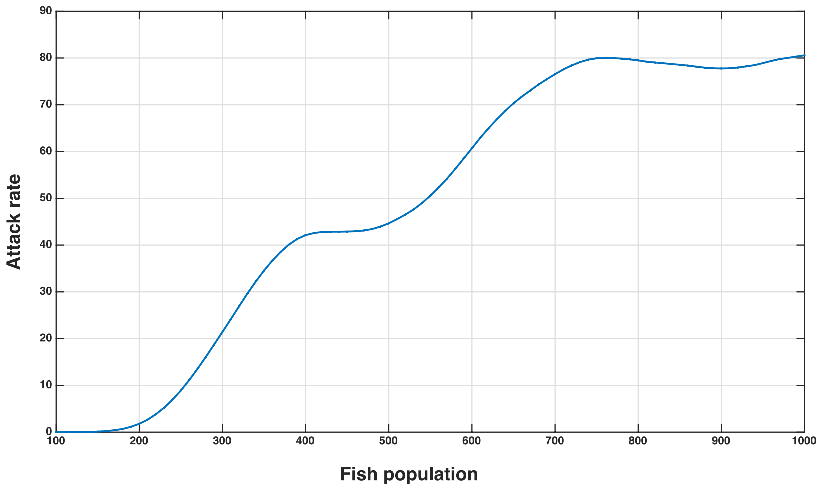

Figure 5.2. Attack-rate (y-axis) vs. fish population (x-axis) in the susceptible farm after 8 days.

Figure 5.2 shows the attack-rate reported in the susceptible farm resulting from a change in the fish population. In this case, the susceptible fish farm is placed near the infected farm (i.e. distance between infected farm and susceptible farm is 9.6 Km), and we run the model with default values as in study three (Alaliyat et. al., 2019). The pathogens drift by the sea currents from the infected farm to the susceptible farm. The number of pathogens released from the infected site depends on the fish density in the infected farm. When the pathogens arrive at the susceptible farm, the infection process in *Algorithm I* is applied. As we see in Figure 5.2, the attack-rate depends on the fish population (i.e. fish density), and the infection is only happening if the fish population passes a certain threshold.

5.1.2 Effects of environmental factors: sea-water temperature and currents

The spread of diseases in fish populations is a dynamic phenomenon; there is the dynamics of occurrence (incidence) and prevalence depending the interactions between fish (host), pathogen, and the environment. The virulence of the pathogen and the conditions of the fish (health, age, stress etc.) will affect the spread of disease (Rimstad, 2011). Both fish and pathogens are directly influenced by the condition of the seawater in which they live. The speed and direction of the water-currents affect the swimming behavior of the fish (Oppedal et al., 2011). Pathogens drift mainly by current (Stene, 2013). Consequently, the current speed and direction are the major factors determining the movements of pathogens. Pathogens move quickly out of the fish farm when the current speed is high. Therefore, the pathogens' density in the farm decreases when the various current speed values in a single infected fish farm: The attack-rate decreases as the current speed increases, see Figure 5.3.

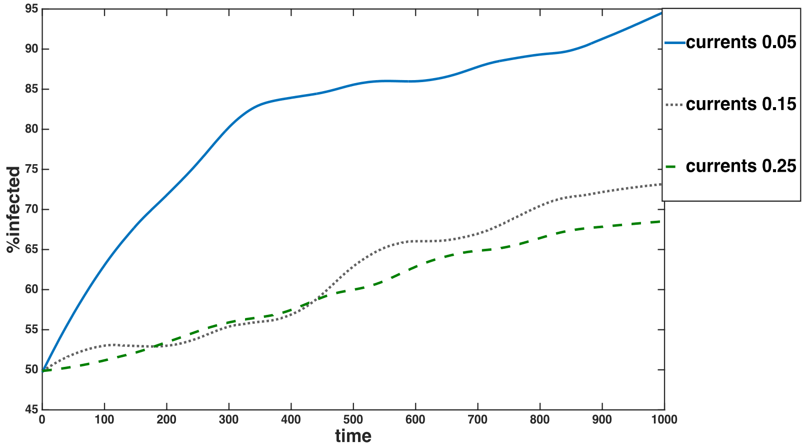

Figure 5.3. Infected percentages (y-axis) dynamics in different current speed values.

Figure 5.4 shows the percentage of the infected fish in the infected farm and in the susceptible farm (the susceptible farm is placed near the infected farm, 9.6 Km) under a variety of current speeds, sea temperatures and fish population parameter values. The infection process inside the farms is faster with low current speed as shown in the left two columns. While the infection at the susceptible site starts only if current speed is high (25 cm/s), - as shown in the third column. Thus the speed of the current plays a major rule in the infection process inside and between the fish populations.

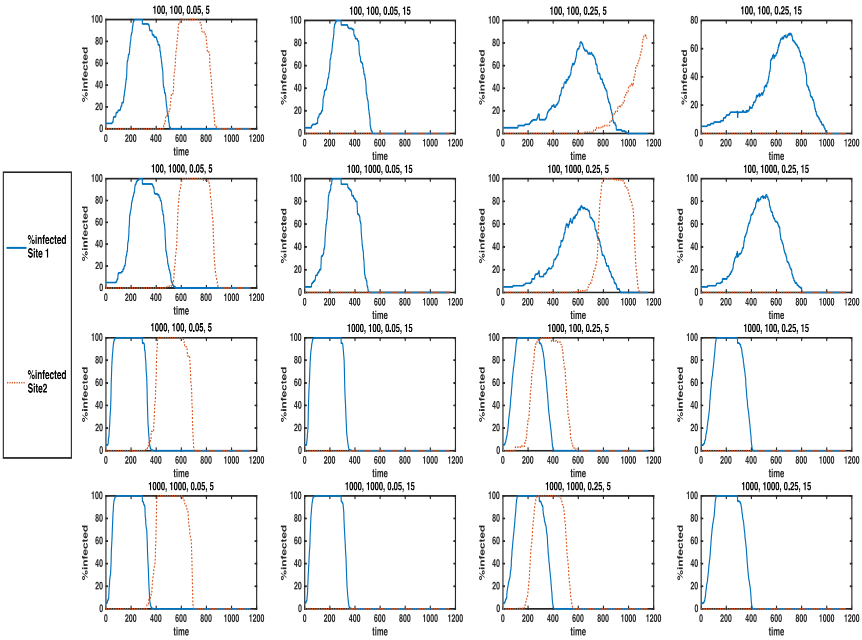

Figure 5.4. Percentage of infected fish at site one, an infected farm (blue), and site two, a susceptible farm (red), as a result of water temperatures, current speeds and fish population values.

Seawater temperature affects both the fish and pathogens. High seawater temperature decreases the fish resistance to infection, and decreases the pathogen lifespan as well (Stene et al., 2014). The shedding pathogen process and the pathogen lifespan are highly dependent on environmental conditions such as seawater temperature, and thus alter with seasonal environmental conditions (Krkosek, 2010). The seawater temperature is a variable associated with the sea depth as well. In short periods during the simulation, the seawater temperature values are assumed constant and one that depends on the depth. The average seawater temperature is not changing over short periods of time; its warming or cooling processes is slow. Therefore, when simulating over a short period of time, such as one day or one week, there will not be a significant difference in the horizontal seawater temperature. Specifically, this is true if this period is within a season and does not include the seasonal changes, from spring to summer or from summer to autumn. The pathogen lifespan is an important factor in the pathogen transmission to near aquaculture facilities, but has less effect on the disease dynamics within the infected aquaculture site since the pathogens residence time will typically be short and the pathogen will move out of the site by way of seawater currents.

Figure 5.4 shows that the susceptible fish farm will become infected only if the seawater temperature is low ($< 5^{\circ}$), column one and three. While, when the water temperature is high ($\geq 15^{\circ}$), column two and four, most of the pathogens die before arriving at the susceptible site, so that the pathogens will not infect that site.

The fish density plays major roles in both the infected and susceptible farms as illustrated in the previous section. Figure 5.4 shows that the disease is spreading faster when the population in a particular farm is larger, - as shown in the lower two rows.

5.1.3 Effects of fish swimming behavior

Fish swimming behavior is a significant factor in the fish disease dynamics, since the fish agents become infected if it swims only in water that contains pathogens above a certain density. Fish prefer to swim in schools (Reynolds, 1987; Alaliyat et al., 2014), but in the sea cages their swimming ability is impaired and affected by a variety of factors (e.g. access to food and light). Previous studies show that fish in sea cages prefer to swim in the middle of the cage depending on the cage-depth and that they follow a circular movement in the normal current speed. But they remain nearly in place at fixed positions in high current speed (Oppedal et al., 2011; Folkedal et al., 2012; Johansson et al., 2014). Fish swimming speed depend on the fish length-weight relationships (Jones et al., 1999). In the first study, three fish swimming behaviors were tested: random, swarming and circular behavior. The tests were conducted under low current speed (i.e. 5 cm/s average). The average fish speed was 40 cm/s. Figure 5.5 shows the attack-rate in the three fish swimming behavior modes. The lowest attack-rate was experienced when the fish swam randomly, while the highest attack-rate occurred when the fish swam in a circular path in the middle of the cage. When the fish swim randomly, they are uniformly distributed in the simulation space, while if they swim in a circular or in a school pattern; their movements are concentrated in a specific area of the available space.

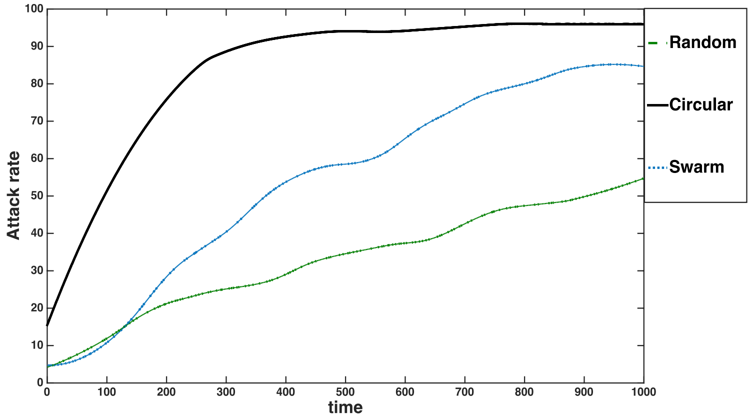

Figure 5.5. Infected percentages (y-axis) dynamics in different fish swimming behavior.

5.2 Infection risk maps

Identifying infection risk in space-time domain is an important process in preventing emerging fish diseases in marine aquaculture systems, and will help us understand how to prevent an existing disease to spread. The infection process of individual fish depends on a variety of factors as described in *Algorithm 4.1.* Infection risk in a specific location at a specific time depends on the densities of fish and pathogens at that location. The environmental condition (i.e. water temperature and current pattern), and the fish densities in infected sites affect the pathogen density in the simulation space. In this study, only pathogens that are relocated by sea currents contribute to the infection risk. In reality, pathogens move by other ways as well; - associated with escaped infected fish, fish boats, sea birds, and wild fish. Figure 5.6 portrays the maximum risk distance that live pathogens can travel based on the seawater temperature and current speed over a duration of 8 days. By identifying the distance (i.e. Risk Distance) that the pathogen can spread, we may identify the infection risk at a particular location. This distance decreases with higher seawater temperatures because the life spans of pathogens are shorter in hot water than in cold water. Moreover, the risk distance increases the stronger the currents are that relocate the pathogen.

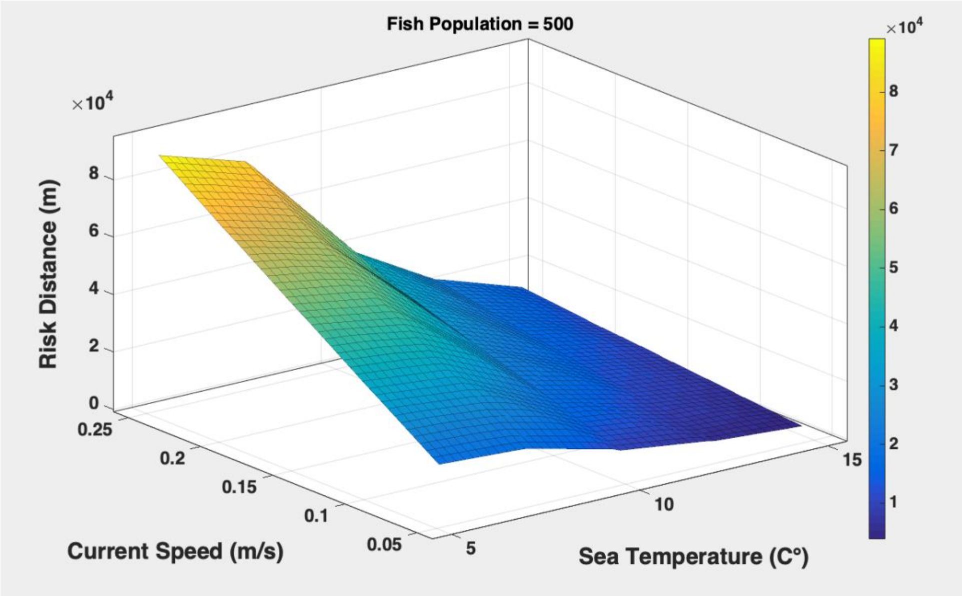

Figure 5.6. Risk distance from the infected site when it contains 500 individuals (risk distance vs. current speed & seawater temperature).

In reality, current speed and direction in Norwegian fjords may change significantly in the time and space domain, and we can expect values to remain steady for short period only (i.e. a few hours or days). The currents in fjords are affected by topographical distinctions and they are driven by many forces such as winds, river runoffs, tides and water exchange due to water density differences. Figure 5.7 shows how the risk patterns resulting from the pathogen density, follow the sea current patters in part of the Romsdalsfjord, - affected by the topography of the fjord. By building infection risk maps in space-time domain around the fish sites under different environmental conditions, one may assist in the management of the Norwegian fish industry, by preventing the emergence of fish diseases that may cause large losses in the Norwegian aquaculture industry.

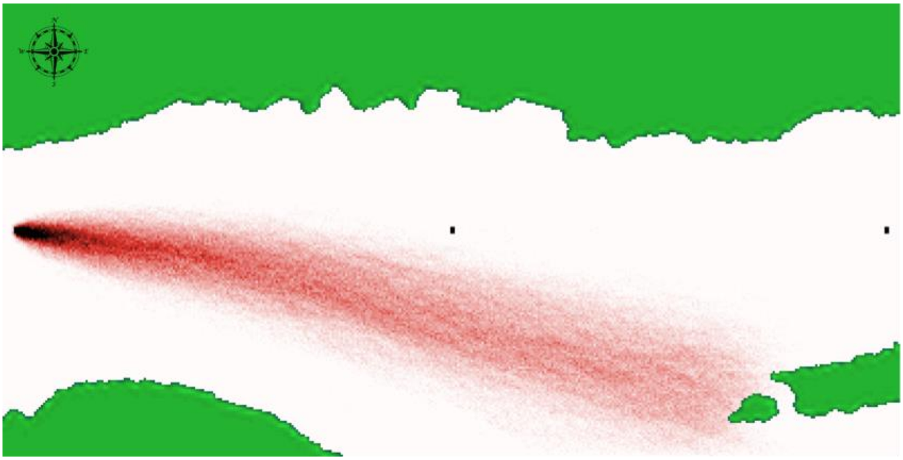

Figure 5.7. Pathogen concentration in two dimensions (2-D) after a period of time. Midsund[14]

5.3 Optimization of aquaculture system

The Norwegian government is promoting an environmentally sustainable aquaculture industry by preventing the fish disease outbreaks that harm the marine ecosystem and destabilizes the biological diversity. Norwegian marine aquaculture systems are complex, dynamic systems in which the emergent outcome of the system is a product of the interactions between the many and diverse parts of the system. In modeling such systems using ABM techniques, we may identify tipping points in the input vector value space, where a small change in one of the parameter values may dramatically affect the model output. Particularly, in fish disease dynamics, such tipping points separate two dynamic modes that a model can exhibit; one where the disease dynamic is stable or is dampened (i.e. attack-rate is constant or decreasing), and another one where the disease dynamics is unstable (i.e. attack-rate is increasing). Such input parameters represent different environmental, physical and biological properties that affect the infection process, such as site fish densities and locations, sea currents and seawater temperature. Some of these factors may not be controlled, such as sea currents and water temperature. Others, such as farm locations and fish densities may be subject to management and optimal values may be found under the current environmental circumstances. Optimizing the fish density and farm locations can reduce the infection risk. Sensitivity analysis is time consuming and are often unrealistic in such cases, as the value space of the parameters is typically huge. In the third study, applying a PSO algorithm to optimize ABMs input parameters, we document the development of an automatic search to effectively and efficiently explore the parameter space so as to find optimal values that give the desired dynamics. By utilizing the PSO algorithm, we present a feedback control mechanism that causes a stable model behavior mode. The stability in the model behavior is measured by an objective function that comprises two conflicting objective functions; minimize the attack-rate in the system and maximize the fish density. Figure 5.8 demonstrates that even a simple PSO algorithm needs only 18 iterations to find an optimal fish density and farm's location. Thus such an optimization supports the management of aquaculture systems aiming towards a sustainable aquaculture industry system.

[14] It covers part of the Romsdalsfjord near Midsund municipality in Møre og Romsdal County, Norway.

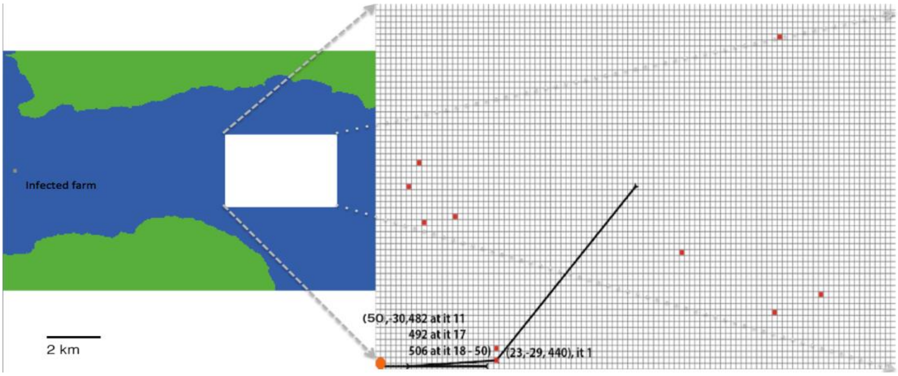

Figure 5.8. Best solution tracking in PSO: the left side shows the part of the Romsdalsfjord where is the simulation took place, and the right side shows the best solution tacking (black line) and the red cells are the initial random particles' positions.

5.4 Potential applications

In the previous sections, we presented the main results from a variety of our studies. In this section, we will discuss potential applications of the models developed. The application of any model is tightly associated with the reason and the need for working with such a model. Skov (2008) has listed some of these reasons; 1) to simplify and idealize so as to focus on issues of interest and, thereby, gain knowledge; 2) to compensate for lack of data; 3) to test possible future situations; and 4) to use the models' idealized image of real world phenomena as a platform for communication including environmental learning situations, participatory planning process, etc. In this PhD research, all of these reasons are applicable.

When applying ABMs to model and simulate fish disease transmission, we focus on a disease outbreak phenomenon. Applying sensitivity analysis, we may assess the sensitivity of model output (i.e. attack-rate) to the various input parameters so as to explore current theory and generate new hypotheses regarding the fish disease dynamics. In the first study, various hypothesis about fish disease dynamics were generated, such as; the attack-rate increases when the fish swim in a circular path in the middle of the cage, conditioned by the cage depth. Also, using ABMs to simulate possible future fish disease transmission scenarios could provide a method to compensate for lack of data regarding fish disease transmission by way of a risk analysis.

In the second study, ABMs are applied to simulate fish disease transmission between several aquaculture sites. Moreover, predictive models are being implemented to evaluate the location of future farms by building infection risk maps in space-time domain. The infection risk maps are built after running the ABMs with specific initial parameter values for a period of time. The results can help in the control or prevention of the fish disease outbreaks by applying proper actions (e.g. removal and vaccination). Building risk maps after running specific scenario will help in fish industry develop management policies that govern their decision-making.

In the third study, optimizing the aquaculture system by finding the optimal fish densities and farm locations, models are implemented to provide guidelines and control mechanisms for the management of Norwegian aquaculture systems. The objective to develop a planning process that ensures a sustainable fish industry, may be translated to an objective function: The model is trying to maximize/ or minimize the objective function value by applying a feedback mechanism process to identify optimal values for the inputs parameters (i.e. fish densities and farm locations), - those that result in the optimal value in the objective function. The objective function aims at minimizing the infection risk in the system and maximizing the fish densities.

Predictive and control models can be used in the management of the fish industry and assist in the policy design, - say, by applying actions (e.g. moving susceptible fish or slaughtering infected fish) depending on the simulation of future scenarios in the predictive models, or by using control models (such as the developed model, in the third study, to find the optimal fish densities and farm locations) to plan sustainable fish industry system and apply policy decisions.

6. Merits and limitations of agent-based modeling

In this chapter, we present some important advantages of applying ABM to environmental management challenges in Norwegian fjords in general, - and, in particular, to the simulation of fish disease dynamics and pathogens transmission between fish populations. Then, we address some limitations that associated with; model boundary, scaling in the time-space domain, lack of data, the application of standard validation methods, the interpretation of results, and ethical issues.

6.1 Advantages of applying Agent-based modeling to the problem at hand

In this section, we address some of the advantages of applying ABM and simulation to the environmental management of Norwegian fjords and its resources in general, and to re-enforce our understanding of fish disease dynamics and pathogens transmission between fish populations in fjords in particular. In chapter 3, advantages of applying ABM to complex systems in general, were summarized. In this section, we discuss these advantages in the context of the problem addressed in this research.

As indicated initially, we need scientific-based models to assist in planning and management processes aimed at achieving sustainability in the Norwegian aquaculture industry by considering the its context. As already established, the process of fish disease transmission in aquaculture systems is influenced by many factors, including individual (fish and pathogen) conditions, movement behavior and environmental conditions. Fish disease dynamics originates from a complex system, and the transmission of pathogen is a process that it is very difficult to predict, analyze or control. Norwegian marine aquaculture systems are complex systems since they have the following features that are characteristics of all complex systems.

System behavior:

- Emergent behavior: Emergence is a phenomenon that cannot be reduced to the system's parts; the whole is more than the sum of the parts (Holland, 2014). This property can only be studied at a higher level. Aquaculture systems on many different scales exhibit emergent behavior as following:
    1. Fish disease outbreaks: Disease outbreaks are common in fish populations. Individual fish are infected by pathogens around, and pathogens drift by sea currents from one site to another. The fish disease process exhibits a phase change from non-spread (i.e. the disease disappears) to spread (i.e. the disease spreads indefinitely) by changing the parameters in the individual infection process.
    2. Fish behavior: Fish swim individually and in schools. Fish swim in a complicated pattern to socialize with others by forming a school or by swimming in a circle, or to re-act to internal and external needs or threats (e.g. foraging and defending). A school of fish behavior is a product of the interactions between the fish and the feedbacks between this emergent behavior and individual decisions. The effects of the group behaviors result on the decisions of the individuals (Reynolds, 1999).

    Emergence is difficult to predict at the macro level (i.e. aggregate level) by knowing the micro level (individual behavior), or by the opposite, finding the micro structure that generate the known emergent behavior. These difficulties result from the system structure that has features such as e.g. path dependency, non-linearity and dynamics.

- Sensitivity to initial conditions: This means that each state in the system is arbitrarily closely located to other states from which significantly different future trajectories may originate. The fish disease process depends on the interactions between fish, pathogen, and the environment (i.e. seawater). Consequently, our models, developed for the purpose of simulating disease spread processes merely consist of these three elements (fish, pathogen, and environment). Small change in the initial condition of the system modeled may cause a large effect (i.e. disease outbreak). For instance, a small change in the seawater temperature can increase the infection rate massively. Norwegian marine aquaculture systems are located in large natural systems (i.e. fjords systems). The environment characteristics (i.e. sea currents and seawater temperature and salinity) are predictable only for short periods of time and are distributed in space domain in complex, dynamic patterns. However, we know the approximate boundaries and the average values in time series and how they are distributed in the space domain also.

System structure:

- Uncertain boundaries: Norwegian marine aquaculture systems are open systems. Their openness goes beyond what can be represented by a model because they are located in open areas with a variety of connections to other systems. Pathogens can be introduced to the system from other fjords and coastal areas, or by methods other than transport by water (e.g. human activities and seabirds). The seawater characteristics (i.e. currents and water temperature) are affected by different factors such as: weather conditions and human activities.
- Nesting: The components of aquaculture systems may, themselves, be complex systems that exhibit dynamics such as current pattern and fish swimming behavior. Currents in the Norwegian fjords are driven by winds, tides, river runoffs and water exchange due to offshore density differences. Fish usually swim in schools, and these schools are complex systems as well.
- Nonlinearity: A small perturbation may cause a large effect, a proportional effect, or even no effect at all. The nonlinear nature of the system, which determines the system behavior, is sensitive to the initial inputs. In a nonlinear structure, fish, pathogens, and environment interact with each other. For instance, pathogen's lifespan is a non-linear function of the local environment (Alaliyat & Yndestad, 2015c). The individuals' outcomes are dependent of one another, and this constitutes a form of structural interaction that cannot be ascertained by using linear methods.
- Feedback loops: Both negative and positive feedbacks are found in aquaculture systems. An aquaculture system is an example of biological systems where the system consists of populations of organisms (i.e. fish and pathogens). A positive feedback loop occurs in the aquaculture system when the reactions to the disease outbreaks increase/ amplify the infection rate. In the aquaculture system, more pathogens are produced by an increased number of infected fish, which, in turn, will cause the infection rate to increase. A negative feedback loop occurs when the reactions to the disease outbreaks decrease the infection rate. For example, susceptible fish will modify their immune system to avoid infectious. Negative feedback loops are responsible for the stabilization of the system.
- Time variant system: Aquaculture system has a large number of parts that are modeled as agents and environment in our models. Agents (fish and pathogens) interact with each other and their local environment. Fish, pathogens and the environment have some properties that change over time. For example, fish immune system, fish and pathogen activity, seawater temperature, currents speed and direction.

ABM is the known approach for modeling emergent phenomena because it describes the behavior and interactions of the system's components bottom-up. By applying ABMs to simulate fish disease spread, we were able to study the dynamics of this phenomenon at an aggregate level, - from the realization of how individuals act and interact to cause the emergent dynamics at the systems level. ABMs are useful in the simulation of disease spread in marine aquaculture systems for the following reasons:

- Complex interactions: The interactions between the agents (fish and pathogens), and between the agents and the environment, are typically non-linear feedback processes characterized by delays.
- Heterogeneous populations: In ABMs, agents (fish and pathogens) may be described individually in a heterogeneous population, - as opposed to what many other modeling methods (e.g. SIR) allows for. The heterogeneity allows for specification of agents with varying degrees of purposefulness and rationality. Also, the topology of agent integrations may be heterogeneous.
- Flexibility: The flexibility of ABM to simulate fish disease spread can be observed along several dimensions. For example, we can easily add more agents (e.g. fish) to the model. Also ABMs provide a flexible framework for describing and adjusting the complexity of agents, -their behavior (e.g. fish swimming behavior). In addition, we can change levels of description and aggregation by using subgroups of agents (e.g. fish farm).
- Spatial mobility: In ABMs, we can dynamically assign a location in space to each individual agent (fish and pathogen) so as to allow for roaming is the simulation space. This mobility makes ABM very flexible in terms of potential variables and parameters that can be specified.
- Stochasticity: In ABMs we may represent processes as stochastic by way of Monte-Carlo simulation. Due to the ambiguity and the lack of data, there is uncertainty associated with individual agent behavior in fish disease spread processes. Consequently, this feature significantly contributes to realistic model descriptions of the reality of aqua-systems in Norwegian fjords.
- Visualization: In ABMs, we can obtain a good visualization of the simulation process in real-time. Moreover, we can visualize the outputs in various methods (e.g. epidemic curves, plots, text, ..., etc.). Many ABM tools (e.g. NetLogo) provide a 3D visualization option as well.
- User-friendly: Many of ABM tools (e.g. NetLogo) allow for the creation of a good graphical user interfaces (GUIs). This adds flexibility to the implementation and simulation processes by allowing the user to interact effectively (even during the simulation) with the model. The GUI allows for different users to create and test various scenarios by setting values of key parameter in the model without need of modeling understanding. ABM tools generally provide the users by statistics and analysis tools to understand the model's behavior.
- Evaluation future scenarios: The use of ABMs to simulate possible future fish disease transmission scenarios could provide a method to compensate for lack of data regarding fish disease transmission.
- Control mechanism: By using ABMs to simulate future scenarios, and applying feedback control theory to adjust the input parameters of the model so as to achieve model stability, we can develop a managerial control mechanism of fish disease spread in Norwegian fjords.
- Appropriate model framework: The behavior of fish agents cannot clearly be defined through aggregate transition rates (e.g. stress under crowding, or swimming behavior under variable currents). Fish and pathogen exhibit complex individual behavior that aggregate into systems behavior. It is typically challenging to describe the aggregate dynamics using differential equations without reference to the behavior of the individual agents. In ABM one meets that challenge by modeling how agents behave individually in interaction with each other. As a consequence, the resulting aggregate dynamics emerges from the behavior playing out at the disaggregate level.

6.2 Limitations

6.2.1 Model boundary

Norwegian marine aquaculture systems are radically open and contextual systems because they are parts of larger complex natural systems (i.e. fjord systems). ABMs have clear boundaries, and they are closed systems where any state changes of the system or parts of it are due to a defined input function (Chu et al., 2003). Therefore, the modeler has to draw the system boundaries so as to capture all essential feedback relevant to the time interval under investigation to achieve the purpose of the model.

The general scope of this thesis was to use ABM to build models and simulate fish disease spread in marine aquaculture systems. The studies were limited to the horizontal disease transmission that takes place by water contact only (e.g. PD). The fish are assumed only to move inside the farm cages, while the pathogens move by currents also between the aquaculture sites. The transmission of pathogens such as IPN[15], VHS[16] and SVC[17] that may take place by way of infected escaped fish, wild fish, seabirds, well boats, multi-site operations including equipment, are excluded from this study (Peters & Neukirch, 1986).

6.2.2 Scaling in time and space

The model is a discrete representation of a continuous reality. The challenge is how we may accomplish a valid data reduction (i.e. reduce the time granularity) and still retain the model validity (effectively represent reality). The models we use to simulate fish disease spread include data that are related to the agents (i.e. fish and pathogens) and the environment, originating from various sources (e.g. Norwegian Mapping Authority, SINMOD, Statistics Norway, ..., etc.). These data are provided in different time and space scales. Therefore, the modeler is challenged to combine all these data to represent the various component of the model in space, - including the agents' interactions in time-steps.

Due to the computational effort required, we may not take into consideration the entire fish population of the aquaculture facility and not the real number of pathogens in such a facility. The Norwegian real salmon sea fish farm typically hosts around a million fish (www.fiskeridir.no), and the pathogens are practically uncountable. The Norwegian Sea fish farms do, however, have different sizes and different shapes. A real sea fish farm could have a size of around 10,000 square meters, and depth of 40 meters. The farms in our models are in a cube shape of cages of 40 x 40 x 40 meters. The fish farm model contains a maximum population with 1000 fish while in reality you would expect to see about 1000 times more fish in an actual fish farm of this size. This simplification was made in order to save computer resources while running the model. A tick is the time step in the model and it represents a second, a minute, 10 minutes, an hour or one-day, (it can be selected by the user). When simulating disease spread in only one fish farm, a high resolution was used: 1 meter is represented by 26 pixels, and a tick represents one second. When simulating marine aquaculture systems with more than one farm, 1 meter is represented by 0.65 pixels in the farms' sites and by 0.065 pixels outside

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[15] Infectious pancreatic necrosis (IPN) virus, causes a severe viral disease of salmonid fish.

[16] Viral hemorrhagic septicemia (VHS) virus, causes a deadly infectious fish disease.

[17] Spring viraemia of carp (SVC) virus has been shown to infect a wide variety of fish species.

the farms. The tick size was set to 10 minutes. Each pathogen in the model actually represents a batch of pathogens (i.e. uncountable number of pathogens). The infection process depends on the infectiousness and shedding dose that are very difficult to quantify. In our models, we used estimated probability functions to approximate them.

Scaling the model in time and space may affect the number of contacts between the agents and the infection process. For instance, increasing the time step in the simulations causes a less frequent position-updating of agents and consequent loss of detail on system behavior.

6.2.3 Lack of data

An important limitation in our studies is the lack of data related to the behavior of the individual agents in the time-space domain, and the lack of data characterizing the infection process. In general, this is a limitation in most disease transmission models, - so also here. Data related to fish behavior in cages are rare, and mostly qualitative. In reality, fish behave differently under different conditions depending on light, current, water temperature, food sources, crowds, stress, infection, etc., - a fact we have ignored in our models.

Truly empirical data characterizing the infection process is unavailable. The existing data related to the infection dose and shedding rates are taken in the labs under unrealistic conditions. Also these data are difficult to interpret quantitatively for our use in models like ours.

There is uncertainty regarding the relationships between the agents (i.e. infection process and shedding pathogen process), and between the agents and their environment (i.e. fish swimming behavior and pathogen behavior, - life span and spreading).

6.2.4 Limitations to apply standard validation methods

The usefulness of the model depends on the validity of the model that is closely associated with the purpose of the model. Standard validation methods such as validation through prediction or behavior replicability tests are unrealistic in a case of complex systems such as Norwegian marine aquaculture systems. Replicative validation is not a choice when the historical data is uncertain and limited as in fish disease transmission process. Predictive validation (i.e. repeating testing event) is impossible to apply on a relevant time-space scale.

Validating the implemented model's output by comparing them with validated outputs from some other models developed using the same or other methods is unrealistic also in the case of simulation of the diffusion of fish diseases in marine aquaculture systems. The available outputs from other models are mostly qualitative output since these models are explanatory models, or the output is derived from uncertain historical data (e.g. SINMOD).

The last option is striving for structural similarity between agent's behavior in simple models and the real system, as we know it, and validates the models' outputs through retrodiction method. Then, extend the validated simple models by adding complexity to them. Applying structural similarity between the model and the system, as we know it, makes the model structural valid. But in the case of complex systems that include a massive number of components and dynamic interactions between them, it is unrealistic to apply structural similarity on all levels (i.e. individual and aggregate levels). The model's output of the simple cases can also be compared with the output of other models (e.g. SIR). This technique has been applied in the first study in the PhD work (Alaliyat & Yndestad, 2015c). However, adding complexity to the validated simple model is challenging and requires deep verification process. The output of the model is sensitive to the initial conditions and can be an emerging behavior, which is difficult to relate to the model's structure.

6.2.5 Interpretation of results

The results of these studies are limited to the objectives of the whole PhD study. The main objectives have been to examine the spread of a fish disease using ABM and simulation, and to build a strategy for optimizing the location and fish density of aquaculture production systems.

The aquaculture industry data used in the studies reflects the aquaculture systems in the Romsdalsfjord, and the models developed either used the data or were inspired by these data. The data are biological, physical and environmental in nature. Even if there are some similarities across the Norwegian fjords, other fjords could be very different in terms of geographical structure, water temperature, sea currents, etc. Consequently, one should be careful when generalizing the results from our study that are directly addressing the case of Romsdalsfjord.

When using ABMs to simulate complex systems such as marine aquaculture systems, the resulting, emergent dynamics (effects) may not easily be attributed to the underlying structure causing such dynamic effects due to the complex, non-linear feedback nature of that structure causing e.g. sensitivity to initial conditions. This limits the process of interpreting the results, - especially when the purpose is to develop effective policy recommendations.

6.2.6 Ethical issues

The uses of the model may create some ethical issues. These issues can arise when the results of modeling and simulation affects the services and the benefits for some stakeholders. For example, the directorate of fisheries may justify their decision of granting or denying a new fish farm license or ordering the shut-down of a fish farm, using models as the one we have developed. Therefore, one needs to very carefully validate any such model before its output is put to use in a management process. The validity needs to be assessed in terms of its impact to avoid that management processes are being misguided by invalid models, say, due to errors or uncertainty in the empirical data.

This is also true because ABMs constitute closed representations of systems that, in reality, are open and contextual. This context may be economic, social, and environmental. If this context is not realistically represented or carefully considered in the implementation of the model-based policy recommendations, then stockholders, other stakeholders, such as the fish industry employees and their dependents, as well as the environment, may suffer. From time to time the economic, social and environmental interests may be in conflict with each other. In those cases, a model may, when carefully developed, validated and applied, effectively portray the true nature of such conflicts and contribute to their resolution.

7. Conclusions and future studies

7.1 General conclusions

Background: The Norwegian fish farming industry has increased rapidly in terms of volume and value production in recent years and is expected to continue this expansion in the near future. Emerging diseases continue, however, to pose a serious challenge to the industry and limit its expansion. It is necessary to structure and manage a growing, environmentally sustainable aquaculture industry in a way that minimizes risks to the marine environment and to biological diversity, - including the transmission of fish diseases. Fish disease transmission processes in marine aquaculture systems are complex, and dynamic and defies analysis and prediction. This process originates from a complex system, i.e. an infected fish farm, and is influenced by many factors, - individual biological conditions of fish and pathogens, their geographical dynamics (movement and relocation) and related environmental conditions (e.g. currents and seawater temperature). Norwegian aquaculture systems exist in open areas (i.e. fjords) and they are exposed to several time variant external factors that threaten the sustainability of the industrial aquaculture production and threaten the marine ecosystem in general. Therefore, it is very important to build properly validated models to enhance our understanding of how sustainability may be ensured and how threats may be mitigated. That will form the basis for effective strategy development, policy design, and decision-making.

Objective: The objective of the study behind this thesis is two-fold:

- To examine the dynamics of fish diseases spreading within and between marine aquaculture sites by means of ABM-based simulations. More specifically, a bottom-up method is applied to simulate the fish horizontal disease dynamics that originates from interactions between agents (fish and pathogen) themselves and their environment.
- To optimize the fish densities and farm locations of marine aquaculture systems based on minimizing the infection risk, and maximizing the opportunity to obtain a sustainable system. This objective is two-fold as well. The first one is to build ABMs to predict the pathogen transmission pattern in a Norwegian fjord and to create infection risk maps to identify the risk areas associated with a particular fish farm location. The second objective is to develop a method by which we may optimize the production volume of aquaculture systems based on minimizing the infection risk.

Methods: The ABM and PSO algorithm were used to implement the models so to accomplish the objectives in the studies. The ABM approach is the principle method that was employed in building all the models of the fish disease transmission process presented in this thesis. The PSO algorithm has been applied in the third study to optimize the aquaculture system production by finding the best farms distribution and optimal fish density in each of them, i.e. the combination that minimizes the infection risk (i.e. that maximizes the production by maximizing the number of healthy fish). Sensitivity analysis was applied to explore the effects of variations and uncertainty in the input parameter values of the ABMs on the results of our study.

Results: The results can be divided into three main categories, corresponding to the three studies undertaken:

In the first study, we conducted an analysis of the sensitivity of the fish disease dynamics to different key input parameter values:

1. Sensitivity to fish density: The attack-rate (i.e. the measure of the rate at which a disease spread in a fish population) increases generally when the fish density increases. Our results show that attack-rate follow a logistic curve as the fish density increases.
2. Sensitivity to the fish swimming behavior: The attack-rate is higher when the fish swimming in schools (maximal when they swim in a circular pattern), than when the fish swim randomly.
3. Sensitivity to the environmental factors (i.e. seawater temperature and currents): The attack-rate in a single site decreases with strong currents, while strong currents move pathogens quickly to near sites to start new infections. As pathogens live longer in the cold water, they can infect new sites located further away. The temperature though will not have a significant impact on the spread of a disease within a single fish farm.

In the second study, the aim was to identify pathogen transmission patterns and build risk maps. Results show how the pathogen transmission pattern matches the current patterns, and how the infection risk in a space-time domain is influenced by the seawater temperature that determines the pathogen lifespan, and by the fish density in farms fish being infected. In this study, the emerging/ dynamic infection rate is characterized by an equation that is derived by theory supplemented by the result of the simulations. The infection risk at any point around the infected site is dependent on both the pathogen and the fish density at that point, and the infection risk increases when the pathogen or fish densities increase. The pathogen density decreases exponentially related to the increase in the seawater temperature, and the pathogen density increases with the speed of the current or the fish density at the infected site. The pathogens are being moved faster by higher current speed, so this will slow the infection process at the local infected site. Nevertheless, the current will carry the pathogens to nearby places faster. The direction of the current is very important since the pathogens are predominantly moved by the currents.

In the third study, a framework to find optimal fish densities and farm locations in marine aquaculture systems was developed. Risk of pathogen transmission in Norwegian fjords is related to the fish density and location of farms. A framework to use a PSO algorithm to optimize ABMs to simulate fish disease dynamics within and between fish farms in Norwegian fjords was introduced. The results show the capability of our modeling framework to control the production system so as to maintain the objective function that was to increase the productivity while to minimize the infection risk (the objective function is a weighted sum of the fish density and the infection risk). The simulation results show how the proposed PSO algorithm converge rapidly to the optimal solution, - results show that PSO algorithm in only 18 iterations finds an optimal solution that results in an increase in the fish density up to three times its original value while keeping the risk of infection at an accepted level (i.e. same level before being exposed for optimization process). The use of the PSO algorithm to identify optimal parameter values of ABMs is significantly reducing the simulation time and producing a useful model to use in planning for sustainable aquaculture industry.

Conclusion: The contribution of this research is the application of agent based modeling (ABM) for the purpose of developing a strategy to maintain sustainable development in the Norwegian fish farming industry. ABM is flexible and well suited for simulating complex systems (i.e. virus spreading in a fjord system). Agents (i.e. fish and pathogens) mobility make ABM very flexible regarding potential variables and parameters that may be included. ABM allows for adjusting the complexity of agents (i.e. their behavior and rules of interaction). In addition, we can change levels of description and aggregation by using subgroups of agents. The simulation results demonstrate how the models may be useful, in part by overcoming the problem associated with the lack of data on fish disease transmission. The ABM allows us to simulate the disease dynamics process even with lack of data regarding the process by using random numbers to compensate the lack of data. Also, by using ABMs, we simulate possible future scenarios. Using PSO algorithm to find optimal parameter values of ABMs will open new applications for the models in management of aquaculture industry. The models can be used to generate hypotheses, simulate future scenarios, or for the basis for general planning strategies.

7.2 Future studies

The research documented in this thesis was designed so as to identify and test a method by which one may develop strategies for optimal location and capacities of fish farms in Norwegian fjords. In particular, we documented that agent based modeling (ABM) potentially could serve as such a method and it was demonstrated how ABM could successfully be applied in three cases of increasing complexity. But, there are still a variety of investigations that ABM opens up for so as to add value to these kinds of studies:

- Include more factors that could affect the contact rate between fish and pathogens:
  1. Escaped fish: Although transmission by way of water currents is the most important route for marine pathogens, a further step could be to incorporate the movement of escaped farmed fish that could be infected or not. Fish escapees can, in fact, pose a risk of infection of both to other farms and the wild population (Naylor et al., 2005), - a risk that increases when farmed fish are in the vicinity of other farms or wild populations of the same species and when the farmed population contributes with a large quantity compared to the wild fish.
  2. Wild fish: Another step is to incorporate wild fish agents in the fjords. A study on the distribution of saithe within a fjord with salmon aquaculture showed aggregations around aquaculture sites and a high proportion of fish moving between different farms, indicating that the wild fish might constitute an important potential path of infection between fish farms (Uglem et al., 2009).
  3. Sea-birds: Pathogens can also be carried by sea-birds, from one fish farm to another. Some types of pathogens may also be shed from infected dead fish.
  4. Well-boats and other working operations: When there is a shared ownership between infected farms, the relocation of fish, well-boats, people and equipment are factors that may potentially increase the contact rate.
  5. Effect of environmental conditions on fish swimming behavior: Fish may respond to different environmental conditions such as light, temperature, salinity, water currents and dissolved oxygen (Oppedal et al., 2011). Results from the study show the significance of the swimming behavior of the fish on the spread of the disease. Consequently, it would be important to relate swimming behavior to environmental conditions.
  6. Effect of other factors on fish swimming behavior such as stress, sickness and weight: Fish behave differently under stress and sickness (Ogut, 2001). Also the fish maximum speed depends on its weight (Jones et al., 1999). So it could potentially be important to include additional characteristics of the individuals of the fish population.
  7. Dynamic water temperature: Water temperature is an important factor because its affect the behavior of fish and pathogens. Fish feel stress in high temperatures, making them less resistance to diseases. Also, pathogens are more aggressive in high temperatures and more capable of infecting stressed fish. The fast change in water temperature affect dramatically the degree of activity in pathogens and fish. Therefore, it will be valuable to include fast changes in water temperature (e.g. between days and nights, over the year).
  8. Higher resolution: Higher resolution in space and time in our model will probably affect the simulated contact frequency between the agents. The simulation space is divided into many cells (i.e. patches) that have different characteristics even if they are neighbors, since we use random numbers in building the characteristics of water environment (i.e. seawater temperature and currents). Then, a higher resolution in space provides a new simulation space. Agents (fish and pathogens) interact and update their properties (e.g. positions, fish health status) in discrete time. So a higher resolution will affect

the infection process.

- Self-adaptation: Develop models of self-adaptive individuals in which the model parameters may be adjusted by an adaptive learning process. By introducing feedback processes in the agents, such a model can cause a local adaptation to specific environmental conditions, - including the fjord geography.
- Validation: The purpose of the model determines how the validation of the model takes place. Validation infuses trust in the model, - that the model may be used for a specific purpose. Therefore, it is important to find ways to validate the model and its output. In addition to intimate knowledge of the mechanisms that govern the dynamics of the fish, pathogens and diseases, more accurate data (parameter values and time series) associated with the spread of fish diseases must be made available. The model may guide us in the search for the most significant (informative) data to be identified and collected.
- Optimization: When conducting numerical optimization, results may diverge significantly. We would therefore suggest that a variety of optimization algorithms be employed, such as Genetic Algorithms (GA), Simulated Annealing (SA), Ant Colony Optimization (ACO) and a comparison be made across the result of the different algorithms.
- Methods to overcome the computational demands of ABMs: In this study, distributed processing was employed using regular desktop/laptop computers. This imposes limitations in our study, - in particular limiting the number of agents to be included and the time granularity (the tick size) to be employed. Considerably more accurate simulations (with higher resolution) may be conducted if the models are transferred to more powerful computers (i.e. super computers / massive parallel computers).
- Visualization: Good visualization allows for a better interpretation of the simulation results. Consequently, it would be important to develop separate simulation from visualization and to develop advanced methods of process visualization.
- Multi-objective optimization (MOO): In optimization of the model, one may use several objective functions so as to illustrate the challenge of negotiating between potentially conflicting goals. Likewise, a more complex set of constraints may be considered.

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Studies

Study
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An Agent-Based Model to Simulate Contagious Disease Dynamics in Fish Populations

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Abstract — **Aquaculture industry is about to revolutionize the way we consume fish and other marine food products as agriculture has already done on land. However, emerging diseases continue to be a serious challenge to the aquaculture industry and limit its expansion. Most models that describe the spread of disease are based on the assumption that populations are homogeneous and focus on the population as a whole. In this paper, we present an agent-based model that simulates the spread of contagious disease dynamics in an aquaculture facility. We simulate both fish and pathogens as individual agents that interact with each other and their environment. This gives the model the capability to overcome the limitations of classical population-based models, permitting to study specific spatial aspects of the spread of infections and addressing naturally stochastic nature of the infectious process. The model enables us to study the sensitivity to key factors such as fish density, infection radius, shedding rate, etc., in which the infectious disease takes place. The model experiment is designed to explore the impact of fish density and infection radius (distance around fish to check the existence of pathogens) factors on the fish disease dynamics in an aquaculture facility. Simulation results show that the fish disease dynamics are more influenced by changing the infection radius parameter than the fish density parameter, while the released pathogens amount is mainly connected to the fish density parameter. Exploring the sensitivity of fish disease dynamics to these factors helps in combatting these diseases. The model and its results are presented in this paper.**

Keywords* — *Agent-based modeling, fish diseases, aquaculture, infection simulation, Netlogo.

I. INTRODUCTION

Aquaculture, probably is the fastest growing food-producing sector, now accounts for nearly 50 percent of the world's food fish [1]. In Norway, the development of commercial aquaculture began around 1970 and since that time it has developed into a major industry. Nowadays, Norway is the largest exporter of aquaculture products in Europe, and the second largest seafood exporter in the world [2]. However, emerging diseases continue to be a serious challenge for the aquaculture industry and limit its expansion [3]. Diseases both induce large economic costs to the industry [4] and might threaten wild populations [3]. A major problem in many areas is the uncontrolled use of antibiotics leading to resistant bacteria strains [5]. Combatting diseases is therefore an important research field [6] and a hot topic in public debates [7].

The objective of this study is to develop an agent-based model (ABM) to simulate the dynamics of contagious fish diseases in an aquaculture facility, as a result of individuals' (fish and pathogens) interactions in a time-space context. Fish disease dynamics are affected by many factors, and this creates the complexity in modelling this non-linear process. The main benefits of using agent-based approaches over traditional disease transmission modelling techniques (top-down techniques of non-linear dynamical systems in which related state variables are aggregated) for fish disease simulation are summarized as: (*i*) flexibility in modelling, and the capability to add more complexity through simulations; (*ii*) provides a realistic representation of the system due to the interactions of the individuals, while classical computational modelling techniques describe systems in equilibrium or as moving between equilibrium; (*iii*) overcoming the lacking of empirical data regarding fish disease dynamics: in classical disease transmission models, it is difficult to predict a threshold for density-dependent outbreaks of diseases while in ABMs, the parameters regarding disease transmission can easily be varied within a range.

The model presented aims to simulate infectious disease dynamics in an aquaculture facility and observe how different factors affect disease dynamics. This model uses many parameters such as fish density, infection radius, infection rate, shedding rate, infection period, immune period and pathogen life span. Before describing the model in detail; a more complete background on the dynamics of fish disease transmission and previous studies on this issue will be given in the next section.

This paper is an extension of work originally reported in Proceedings of UKSIM-AMSS 17th International Conference on Modelling and Simulation [37].

A. Dynamics of fish diseases

The dynamics of the occurrence, severity and spread of diseases within and between fish populations are similar to those associated with diseases in human and terrestrial animal populations [8][9]. However, one additional component in fish populations is the water environment which may facilitate the spread of disease-causing agents (pathogen). Diseases are generally transmitted from one individual to another in one of two ways: vertical transmission or horizontal transmission. In vertical transmission, pathogens are transmitted from one or both parents to offspring. Horizontal transmission involves the spread of the pathogens from one individual to another through direct contact, air, or water [10].

The development and severity of a disease following exposure to a pathogen involves a complex web of variables such as: the virulence (ability to cause disease) of the pathogen; the immune, genetic and physiological condition have the host; stress; and population density [11][12]. Different strains of the same pathogen may vary considerably in their ability to cause disease. That is, some strains can infect a host without causing a clinical disease. Also, individual animals differ in susceptibility to disease. Some individuals may be more resistant to the disease because of their genetic composition or as a result of previous exposure and development of immunity. Conversely, individuals may be more susceptible to a disease because of poor nutritional status, stress or any of a number of other factors [13]. The actual development of a disease and the relevant severity of that disease within a fish population are influenced by a complex interaction of these variables associated with the pathogen, the host and the environment.

B. Diseases in aquaculture

Infectious diseases pose one of the most significant threats to the aquaculture industry [3]. The maintenance of large numbers of fish crowded together in a small area provides an environment conducive for the development and spread of infectious diseases. In this crowded, relatively unnatural environment, fish are stressed and more susceptible to disease. Moreover, the water environment facilitates the spread of pathogens within fish populations.

Knowledge of pathogens in wild fish stocks is generally poor, and it is therefore difficult to predict which diseases might occur once an aquaculture facility is established in an area [15]. A wide range of pathogens exists, from viruses and bacteria to crustacean parasites [14]. These might be introduced to an aquaculture system through various pathways: movement of infected stocks, equipment or fish products from other areas; or by exposing to wild fish pathogens. Once introduced, pathogens can benefit from the aquaculture environment and pose a graver risk to farmed fish. This is both because of factors such as poor environment, stress and pollution that might reduce individual fish resistance [3], but moreover because the artificial high density of fish, and thus potential hosts for the pathogen, in a fish farm can induce outbreaks [15][16]. Pathogens that benefit from higher host densities follow so-called density-dependent transmission [8]. The rate of transmission is the product of the densities of susceptible and infected individuals.

$$t = \beta SI \tag{1}$$

Where t is the rate of transmission, β is the contact rate, S is the number of susceptible individuals and I is the number of infected individuals.

Several pathogens affecting aquatic organisms fit to a density-dependent model, e.g. the bacterium Aeromonas salmonicida, causing the furunculosis disease in wild and farmed salmonids [17]. Another famous example is the salmon lice (Lepeophtheirus salmonis). Although this parasite existed in Norwegian waters before the arrival of the aquaculture industry, today it has a much larger pool of hosts and thus higher potential to spread, both between farmed and back to the wild populations.

C. Previous simulation methods

Fish disease dynamics are affected by many elements, and this creates the complexity in modelling this process. Fish disease dynamics within an aqua site or between many aqua sites is a complex system.

Previous modelling studies on the infectious disease dynamics in the aquaculture system have focused on the disease transmission between aquaculture sites, and they have either used classical SIR disease transmission models (Susceptible, Infected, Recovered) that focused on the population as a whole [8][9], or such population models coupled with simple hydrodynamic models or distance measures of transmission between separate populations [4][21][22][23].

In SIR models, the population is grouped into categories and equations are derived that express the rates at which different events (infection, recovered, death, etc.) occur. The models describe how the individuals in the population move from one category to another. Basically, the SIR model involves three groups: susceptible, infected and recovered (or removed). A susceptible (S) becomes infected (I), and infected that recover are immune (R). The models that result from this kind of analysis involve a series of partial differential equations [31].

Cellular automata (CA) theory has been used for modelling dynamics of contagious disease spread [24][25], but the representation of individual's movements and interactions over the space was no presented. This is an important factor to consider in highly contagious diseases and therefore this methodology gave way to a new approach (agent-based modelling).

D. Using agent-based method

To our knowledge no previous studies have applied agent or individual-based methods to assess the transmission of diseases within and/or between aquaculture fish populations. On the other hand, agent-based methods have been applied to simulate transmission of human viral diseases such as influenza [18][19][20].

The agent-based method is a bottom-up approach, similar to CA models, but has the advanced capability to track the movement of a disease and the contacts between each individual in a group located in a geographic area [32].

Agent-based models (ABMs) can be valuable for the analyses focused on individual interactions, and also to incorporate the spatial aspect of the system. Classical SIR-models, on the other hand, like those used in disease transmission modelling, represent total populations. In this study, an ABM is applied to simulate the infection process of an individual fish, and the way that pathogens spread spatially by representing these as agents.

Agent-based methods can address research questions common to many disciplines and facilitate interdisciplinary collaboration. By applying an ABM, more complexity can be added and analysed through simulations. Another reason for applying an ABM is the lacking of empirical data regarding fish pathogens. Therefore it is difficult to predict a threshold for density-dependent outbreaks of diseases in classical disease transmission models [17]. In an ABM, the parameters regarding disease transmission can easily be varied.

II. THE MODEL

Disease in fish populations is a dynamic phenomenon; fluctuations in prevalence and impact are dependent on the interactions among fish (host), pathogen, and environment. In our model, we aim to simulate the horizontal transmission that involves the spread of the pathogen from one individual to another through water. The presented model is a generic model, which can be adjusted to various pathogens and environmental scenarios.

We used the general system theory to define our multi-agent system [33]. The general multi-agent system can be formulized as

$$S(t) = \{A(t), L(t), N(t)\} \quad (2)$$

Where, S(t) is the system, A(t) is the agents, L(t) is the environment and N(t) is the network.

The system S(t) is composed of agents, A(t) and landscapes, L(t) or environment, and the interaction between the agents themselves and between them and the landscapes, called networks N(t), as shown in figure 1.

The model has two types of agents, fish and pathogen. The environment is the seawater. The fish has three main states, as SIR model (Susceptible, Infected, Recovered). If the fish is in an infected state, then will shed pathogens at a given rate (shedding rate). The pathogens are moving by sea currents, and their life span is a function of sea temperature. The susceptible fish will get infected if there is a pathogen near by (infection radius). In the following, we will explain the model agents' attributes and behavioural rules, scaling the model and infection process.

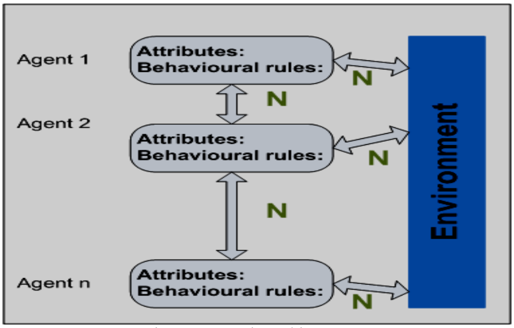

Figure 1. Generic Multi-agent System

A. *Fish agent*

The fish are created during the setup procedure of the model and they are distributed across the farm's area. Figure 2 shows the fish agent's attributes and behavioural rules.

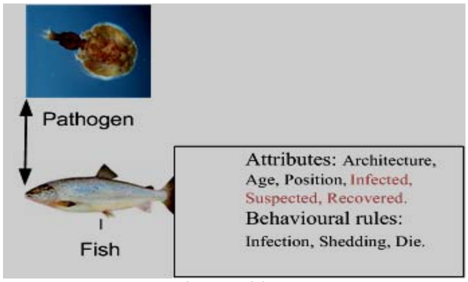

Figure 2. Fish agent

As in SIRS model, the fish will update its health status at every time step depending on the infection process (Figure 3). The heath status is altering between a three main statuses (susceptible, infected and recovered), the agent will die by mortality rate if it's in the infected state. If the fish agent is alive, then the agent's health status must be one of the three statuses. As in SIRS models (figure 4), we can categorize the agents into three groups depending on their health status (Susceptible, Infected, Recovered). Then the fish's number dynamics in each category can be formulated by the following differential equations:

$$\begin{aligned} ds/dt &= -\beta s(t)i(t)/n(t) + fr(t) \\ di/dt &= \beta s(t)i(t)/n(t) - Ri(t) - ui(t) \quad (3) \\ dr/dt &= Ri(t) - fr(t) \end{aligned}$$

Where s(t) is the number of fish in the Susceptible category at time t, i(t) is the number of fish in the Infected category at time t, r(t) is the number of fish in the Recovered category at time t, β is the contact rate, u is the mortality rate, 1/R is the average infectious period, 1/f is the average immune period and n(t) is total population at time t.

We will give a thorough explanation of how fish's agent updates its health status in the infection process section.

In the setup procedure, a number of fish set by the *fish-number* slider are randomly placed in the farm. A percentage of these fish are made infected (set by the slider *initial-infected*), and a percentage of them are made prior immunity (set by slider *prior-immunity*). If the vaccinated switch is on, then all the fish are prior immunity.

The fish agent moves randomly in the space (farm), and updates its position at every time step by moving one space unit.

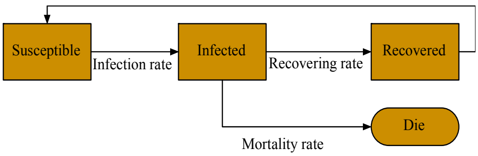

Figure 3. Fish agent states

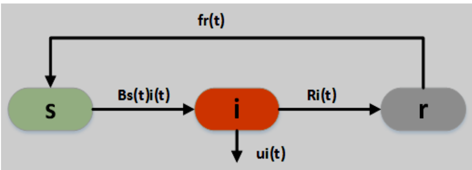

Figure 4. The diagram of SIRS models

B. *Pathogen agent*

Pathogens are also represented as agents. Figure 4 shows the pathogen agent's attributes and behavioural rules. It is important to note that one pathogen agent does not represent one pathogen, but a batch of high number of pathogens. Each pathogen is moved by the currents (current speed and direction) given by the place the pathogen is at the start of every time step.

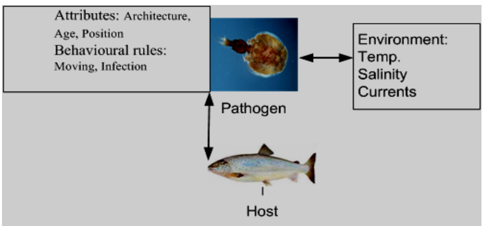

Figure 4. Pathogen Agent

The pathogen lifespan depends on the environment, sea temperature and salinity. Figure 5 shows the changes in Pancreas Disease (PD) virus lifespan according to the changes in sea temperature [13]. In the model, we use pathogen age function as an exponential decay function in equation 4, which is inspired by data from Figure 5.

$$\text{Pathogen life span} = a * \exp(- x / b) \qquad (4)$$

Where x is the sea temperature, a is the pathogen life span at 0° sea temperature, and b is the decay rate.

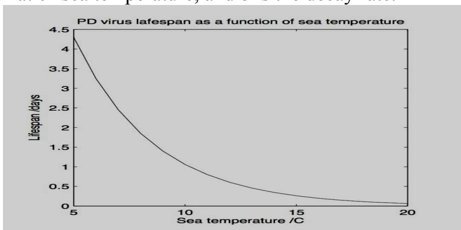

Figure 5. Pathogen lifespan vs sea temperature

C. *Scaling the model in time and space*

The real sea fish farms have a size of around 10,000 square meters, depth of 15 meters and host around a million fish each [26]. We constructed the model in a cube space of 40 x 40 x 40 patches (Patches represent the grids in the landscape in NetLogo [28]); and the patch size is 8 x 8 x 8 pixels. Our model represents one fish farm cage. This means that each meter is represented by 24 pixels or 0.375 patches in the model. The fish farm has a maximum population of 1000 fish, while in reality you would expect to see about 1000 times more fish in an actual fish farm at this size. This simplification was made in order to save computer resources while running the model. According to SINMOD [27], the average current speed in the Norwegian fjords is typically 0.2 m/s. This equals 12 m/min (720 m/hour). Tick is the time step in the model and it's representing one-hour or one-day, (it can be selected by the user, *time-step*).

Each fish moves one space unit randomly inside the fish facility at the start of each time step. While each pathogen is moved by the sea currents, with the current speed and direction given by the place the pathogen is at by the start of each time step. In order to create a model that incorporates some of the variation presents in nature we used normally distributed random numbers for both the current speed and current direction. By introducing this randomness we avoid a very specific case scenario to some extent that would be less valuable for generalizations. The user can select these variables by the sliders, *current_speed, current_speed_std_dev, current_direction,* and *current_direction_std_dev.*

The sea temperature is variable among the sea depth (see Figure 6). In the simulations only one aquaculture site where the depth is around 15 meters only, then the temperature is almost the same, except small changes around the surface that we ignored. The slider *sea-temperature-deep-1*, can set the temperature. The sea temperature is variable with time as well. Figure 7 shows

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the average monthly sea temperature at 1m sea depth at Bud station in the Norwegian sea. The sea temperature is not changing soon; it needs time to get warm or cold (with surface temperature exception). So to simulate a short period as one day, one week or even a month; will not be a big difference in the sea temperature from 1m depth to 15m depth, specifically if this period is inside one season and not including the seasonal changes, from spring to summer or from summer to autumn as shown in figure 7. To simulate long periods we should create functions to represent the sea temperature changes among the time as well.

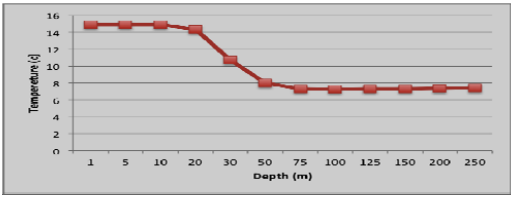

Figure 6. Average temperature from 1 m to 250 m depth during August 2014 from Bud station. (www.imr.no).

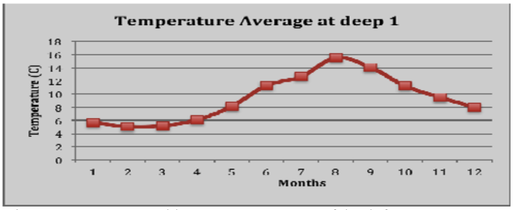

Figure 7. Average monthly temperature at 1 m of depth from 2008 to 2014 from Bud station. (www.imr.no).

D. Infection process

The fish agent moves randomly in the space and updates its status at each time step. The fish has three main health statuses, susceptible, infected and recovered. The fish agent updates its status by following the infection rules described in the flow chart (Figure 9).

The fish that is healthy (susceptible) will look around within an infection radius, if there any pathogen in the sphere where is the fish agent is in the centre of, and the radius is infection radius. If there is a pathogen, then the fish will get infected with a certain probability. Figure 8 shows the agent vision and the space which will be checked around by equation 5.

$$V = (4/3)\,\pi r^3 \tag{5}$$

Where, V is the sphere volume, and r is the infection radius.

The contact rate (β) is decided by infection radius and infection rate. There is no contact rate if the sphere in figure 8 contains no pathogens, but if there any pathogens within the radius r, the contact rate depends on the infection probability factor.

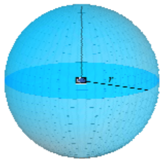

Figure 8. Sphere representing the space which will be checked by the susceptible fish (blue fish in the centre), r-infection radius

When the fish get infected, it has to pass an infectious period before it can get recovered or die. The user can set the infectious period by the slider *infectious-period*. The infected fish shed pathogens by a shedding rate which can be set by the user with slider *shedding-rate*. The fish shed pathogens at the same location where they are. The infected fish can be recovered or die by the rates recovering rate and mortality rate that they can set by sliders *recovering-rate* and *mortality* consequently. The fish agents after passing an immune period, they will enter the susceptible status again. We have added some noise to the infectious and immune periods in our implemented model.

III. Simulation

A. Agent-based Simulation Toolkit

In order to implement the designed agent-based model, NetLogo 3D [28], was used. NetLogo is a multi-agent programmable modelling environment. It is used by tens of thousands of students, teachers and researchers worldwide. NetLogo toolkit allows simulations within a geographic information system environment and it's easy to include physical and environmental data also.

B. Implementation

The entire fish population of the aquaculture facility and the real number of pathogens cannot be taken in consideration due to computational reasons. Implemented model has several parameters such as: simulation parameters, disease model parameters and agents' attributes (see Table I).

The graphical user interface (GUI) (Figure 10) was developed to add flexibilty to the implemation and model output scenarios visualization capabilty. The GUI allows different users to create and test various scenarios by changing all or some of the parameters in Table 1.

The model has a 3D vitalization view, which is updated at each time step, so the users can see the interaction between the agents during the simulation and how fish update their health status. Blue fish are susceptible, red fish are infected and grey fish are recovered. The users can see some statistics and analysis from the model output and the epidemic curves also.

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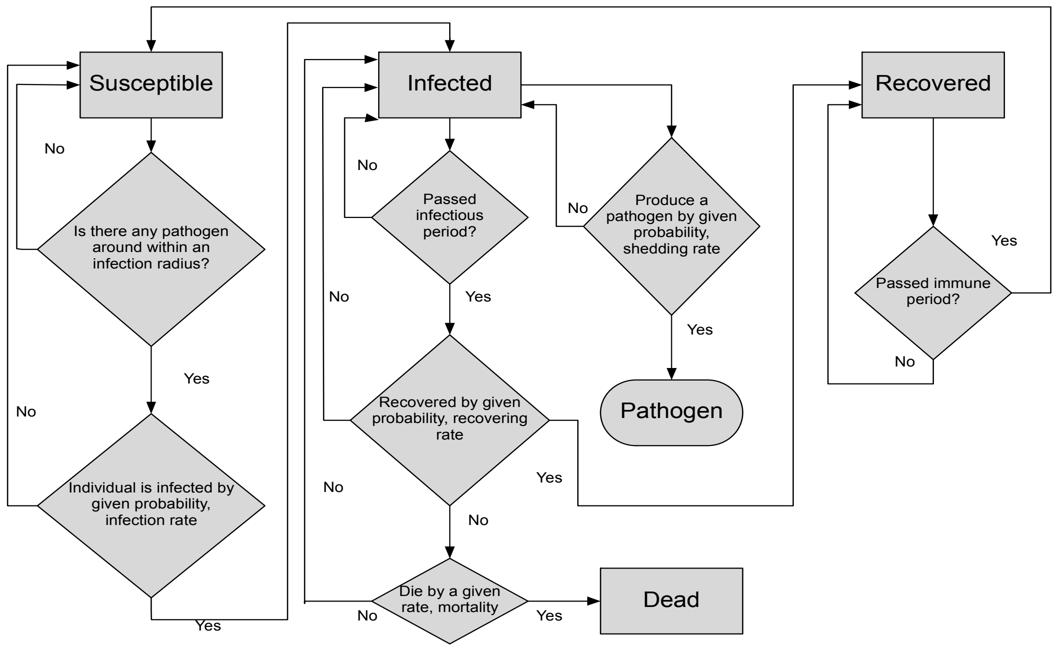


Figure 9. Flow chart for the fish individual infection rules

TABLE I: MODEL PARAMETERS

Parameter	Min value	Max value	Default value
Fish number	*1*	*1000*	*500*
Infection rate (%)	*0*	*100*	*50*
Recovering rate (%)	*0*	*100*	*50*
Shedding rate (%/	*0*	*100*	*50*
Infection period (days)	*0*	*100*	*5*
Immune period (days)	*0*	*100*	*10*
Infection radius (patches)	*0*	*20*	*5*
Initial infected (%)	*0*	*100*	*10*
Prior immunity (%)	*0*	*100*	*0*
Mortality (%)	*0*	*100*	*10*
Current speed (m/s)	*0*	*1*	*0.05*
Current speed std.	*0*	*0.1*	*0.01*
Current heading bias (degree)	*-5*	*5*	*0*
Current heading std	*0*	*90*	*30*
Temperature (c)	*0*	*20*	*10*
Vaccinated			*Off**
Time step			*Hour**

*Parameters that can assume two values or (on/off)

C. *Model Validation*

In general, it is often very difficult to validate epidemiological simulation models due to the lack of reliable field data, and in aquaculture industry case is more difficult. The logical choice of validation techniques in such situation is to use cross-validation (i.e. to run a validated model for some simplified scenarios where the result is known or obvious) or to compare the model output with other available models that have been validated (so called model alignment [34]).

We have to validate the proposed model against other available models that have been validated such as SIR(S) model [35]. Our proposed model should be aligned with the SIR(S) model at least for some simplified scenarios. In order to align our model to SIRS model, we used Matlab [36] to evaluate SIRS models for given parameters for simple scenarios in our proposed model. Table II shows the parameters that we used for both models. The contact rate is measured differently in both models.

TABLE II: PROPOSED AND SIRS PARAMETERS

Parameter	SIRS	ABM
Fish number	*500*	*500*
Infection radius		*5*
Contact rate	*1/6*	
Initially infected	*50 (10%)*	*50*
Infection period (days)	*10*	*10*
Immune period (days)	*20*	*20*

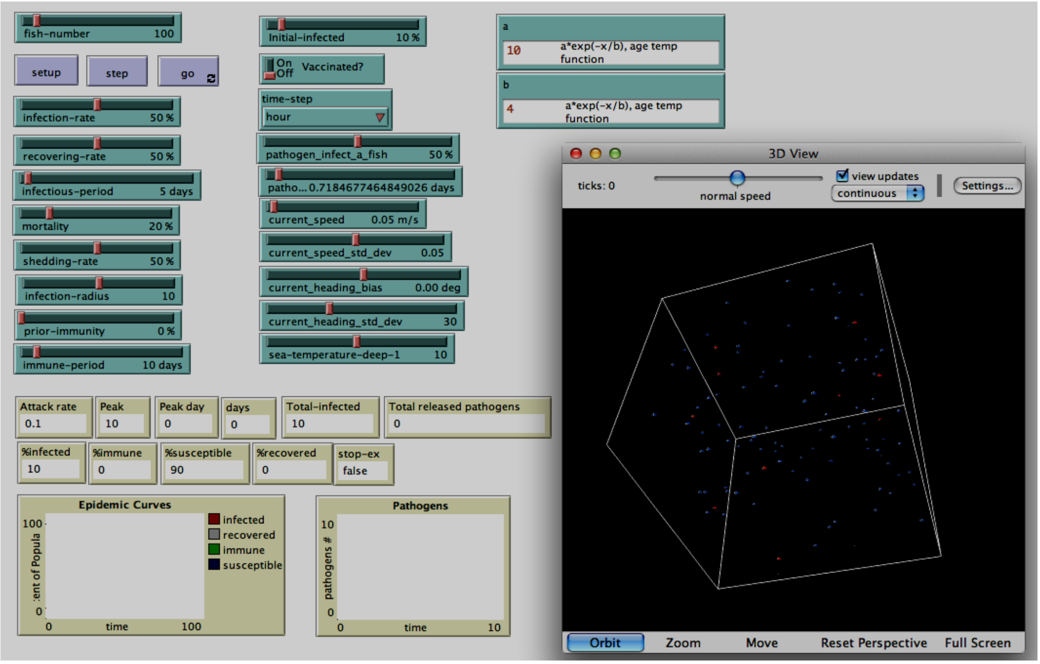
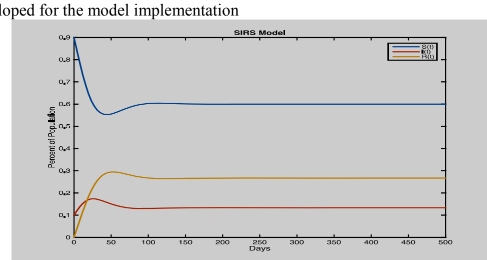


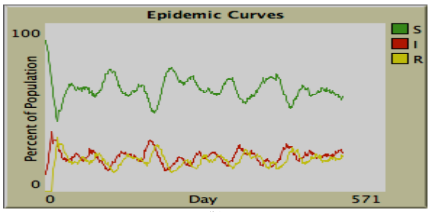
Figure 10. Graphical user interface (GUI) developed for the model implementation

Figure 11. shows the epidemic curves (the dynamics of Susceptible, Infected and Recovered groups in 500 days). Two graphs are not a perfect match, but the ABM graph match the general behaviour of SIRS model graph. Two graphs differ by the magnitude and the smoothness of the curves. The difference in the behaviour of the curves is limited thanks to the following factors: the heterogeneous structure of the population and the use of randomness instead of deterministic values in SIRS model. While the contact rate is determines simply in SIRS model, ABM uses many parameters that changing from individual to another and depending on agent locations and other parameters (such as environmental parameters).

In this study, we build a model to examine the effect of key parameters such as infection radius and fish density to the model output and make relative comparisons through sensitivity analysis. We use hypothetical parameters values even if we refer to some real data from different resources to set the parameters ranges, but we didn't set the parameters for specific disease. Validation of the model parameters values that are related to the fish disease progress and transmission is a very complex process due to the lack of real data. The available data is provided by some lab experiments [38].



(a)



(b)

Figure 11. (a) Epidemic curve from SIRS model, (b) Epidemic curve from the Agent-Based Model

D. *Simulation experiment*

In order to explore how each of the parameters we put into the model affects the outcome, we should vary this parameter in the simulation while we keep the others constant.

We built a generic model, which can be used for many fish disease types and in different environmental conditions. Some of the model parameters are connected to the type of disease, and realistic data are not always available or trusted.

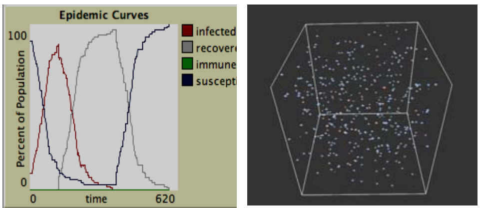
In order to explore the importance of fish density and infection radius parameters on the fish disease dynamics, we ran our experiment for 20 days, by varying the fish density and infection radius (see Table III), while we kept the other parameters at default values. The simulation experiment output was the percentage of infected/ susceptible/ recovered/ immune fish at each time step, the maximum number of infected fish (peak), day when the peak happened and total released pathogens.

TABLE III: EXPERIMENT PARAMETERS

Parameter	Values
Fish number	*100, 200,300,500,750,1000*
Infection radius	*1,2,3,5,10,15*

IV. Results and Discussion

The model is a generic model, and all the parameters can be set easily in the GUI. We need to run the model with different scenarios to explore how each of the parameters we have put into the model affects the outcome. This is one of the most powerful capabilities of a model, the ability to explore dynamically the relationships between the variables used to define the model. The users can see the interaction between the agents during the simulation, and the epidemic curves also (see figure 12).



(a) (b)

Figure 12. (a) Epidemic curve, (b) simulation world

A. Sensitivity Analysis

Sensitivity analyses are important to explore the behaviour of complex system models, because the model is coupled with a high degree of uncertainty in estimating the input parameters' values [29].

The simulation experiment was designed to explore the sensitivity of the model outcome to the fish density and the infection radius. The model outcome includes individual fish health status, total pathogens number in the facility and some analysis to show the fish disease progress and dynamics. Figure 13 shows the attack rate reported due to the change in both fish density and infection radius. The attack rate is increased by increasing the infection radius and fish density. It will reach 100% if the infection radius increases by more than 5 units regardless of the fish density value. Figure 14 shows the sensitivity of attack rate to fish density and infection radius change.

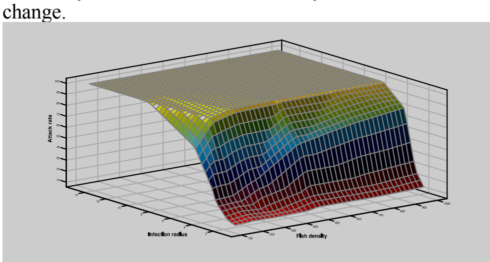
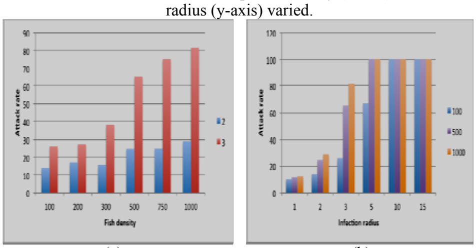


Figure 13. Percentage of infected fish after 20 days (z-axis), with all parameters set at default values except fish density (x-axis) and infection radius (y-axis) varied.



(a) (b)

Figure 14. (a) Attack rate after 20 days (y-axis), vs fish density (x-axis), with infection radius 2 and 3. (b) Attack rate after 20 days (y-axis), vs infection radius (x-axis), with fish density 100, 500 and 1000.

We also analysed the epidemic peak sensitivity to the changes in fish density and infection radius. We have seen that epidemic peak is more affected by infection radius also, and the peak day is getting smaller by increasing the infection radius (see Figure 15).

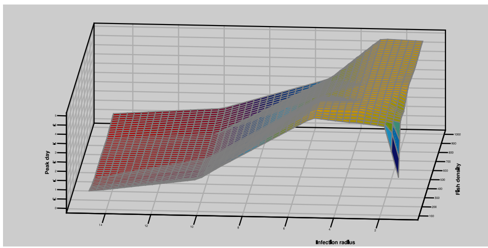


Figure 15. Peak day after 20 days (z-axis), with all parameters set at default values except fish density (x-axis) and infection radius (y-axis) varied.

The total released pathogens are more connected to the fish density as shown in Figure 16. The infection radius has a small influence if it's greater than 5 units. For small infection radius values, there is a big influence because the attack rate is still small.

Figure 16 shows that the total released pathogens increases linearly versus fish density.

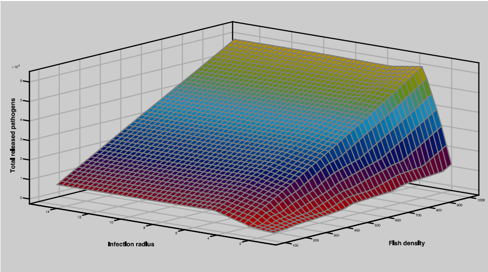


Figure 16. Total released pathogen after 20 days (z-axis), with all parameters set at default values except fish density (x-axis) and infection radius (y-axis) varied.

V. CONCLUSION AND FUTURE WORK

The aquaculture industry is increasingly important for both the producers' economy and marine food availability worldwide. A major challenge for aquaculture development is the infectious disease, which can be due to a large variety of pathogens. It is therefore highly needed to study the fish disease dynamics in the aquaculture sites.

The presented model is a generic model which can be used for different types of infectious fish disease. The model has many parameters that can be varied. In our simulation experiment, we have changed the fish density and the infection radius parameters to explore the output sensitivity to them. The results show that the attack rate is more affected by the infection radius, while the total number of released pathogens is affected mostly by fish density. The infection radius is representing the pathogen density while the released pathogens affect the disease spread to other facilities. The results show that all fish get infected at some point if the infection radius is more than 5 units regardless of the fish density.

To our knowledge, ABMs have never been employed in this type of study before. By using an ABM we were able to simulate both fish and pathogens as individual agents that interact with each other and their surrounding environment. This give the model the capability to overcome the limitations of classical population-based models, permitting to study specific spatial aspects of the spread of infectious and addressing naturally stochastic nature of the infectious process.

Some limitations of this model are with respect to model validation. The lack of reliable fish disease transmission data is making the model partly theoretical. Also computational limitations are an issue because not all the population (fish and pathogens) can be considered given the limited computer memory capacity. This consequently affects the number of contacts between the individuals.

The model enables us to simulate a specific case. So referring to this case, we can set all the model parameters that include agents' attributes, simulation parameters, infection process and environmental parameters.

We can do more sensitivity analysis by running more scenarios, and vary more parameters to see their effects as well. To include so many scenarios, there is a need to run the experiment on a special machine due to the computational need.

The model can be extended by adding more complexity to fish agent movements. There are some studies about the fish movements in the cages that can be used to control fish movements [30]. Also we can add more key parameters related to the fish industry process (i.e. stocking and harvesting process), or related to the interaction with the outside environment, including other factors related to escaped fish, wild fish and workers.

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Study
I-2

An Aqua Agent-Based Model to Simulate Fish Disease Dynamics with Reference to Norwegian Aquaculture

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Abstract — **Disease in fish populations is a dynamic phenomenon; oscillations in occurrence and impact are dependent on the interactions among fish (host), pathogen, and environment. While most of the previous models to simulate disease dynamics are based on the assumption that populations are homogeneous, we build an aqua agent-based model that simulate the contiguous disease transmission as a result of interactions between fish, pathogens and their environment in time-space context. This heterogeneous model gives a realistic representation of the system and tackle naturally stochastic nature of the infectious process. The model combines most important factors in the fish disease process, environmental factors, fish swimming behavior and infection process parameters. The simulation experiments are designed to explore the impact of sea currents and swimming behavior on the disease dynamics. The results show that the attack rate increases when the sea current speed decreases, and when the fish swim in a regular pattern (circular or in school). The model can be applied to different applications due to its ability to show the disease progression based on the individuals' interactions. This can help in understanding of disease-spread dynamics and yield to take better steps towards the prevention and control of a disease outbreak.**

Keywords — Agent-based modeling, fish diseases, aquaculture, infection simulation, fish movements, fish school, Netlogo.

I. Introduction

Emerging infectious diseases are a serious fish health threat, and pose a big challenge for the aquaculture industry and set constraints to its expansion [1]. Fish diseases both induce large economic costs to the industry [2] and might threaten wild populations [1]. Therefore combatting fish diseases is an important research field [3].

Norway has a very long coastline with fresh cold seawater and more than a thousand of fjords that having rich sea life. This environment provides excellent conditions for aquaculture activities and made Norway the second largest seafood exporter in the world [4]. Atlantic salmon is by far the most important species in Norwegian aquaculture, and the most troublesome diseases for the salmon aquaculture are caused by viruses [5]. All major viruses affecting Norwegian aquaculture are thought to spread between fish through seawater [3], as infected fish shed pathogens to the surrounding waters.

In this study, we developed an agent-based model (ABM) to simulate fish disease dynamics in a fish population as a result of interactions between fish, pathogen, and their environment. The process of disease transmission is influenced by many factors, including individuals (fish and pathogen) conditions, movement behavior and environmental conditions. The presented model explores the potential effects of these factors on the spread of a simulated fish disease.

The agent-based method provides a realistic representation of the system due to the interactions of the individuals, gives more flexibility in modeling and more complexity can be added and analyzed through simulations. Another reason for applying an ABM is the lacking of empirical data regarding fish diseases transmission. In an ABM, the parameters regarding disease transmission can easily be varied.

Before describing the model in details; a complete background on the dynamics of fish disease transmission and related works on this issue will be given in the next section.

A. Dynamics of fish diseases

The dynamics of the occurrence, severity and spread of diseases within and between fish populations are similar to those associated with diseases in human and terrestrial animal populations [6][7]. Only one additional component in fish populations is the water environment which may facilitate the spread of disease-causing agents (pathogens). Diseases are transmitted generally from one individual to another in one of many ways: oral, external, direct exposure, vertical or horizontal transmission. In this study, we model the horizontal transmission. Horizontal transmission involves the spread of the pathogen from one individual to another through direct contact, air, or water [8].

The development and severity of a disease following exposure to a pathogen involves a complex web of variables such as: the virulence (ability to cause disease) of the pathogen; the immune, genetic and physiological condition have the host; stress; population density and environmental conditions [9][10]. Different strains of the same pathogen may vary considerably in their ability to cause disease. That is, some strains can infect a host without causing a clinical disease. In addition, individual animals differ in susceptibility to disease. Some individuals may be more

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resistant to the disease because of their genetic composition or because of previous exposure and development of immunity. Conversely, individuals may be more susceptible to a disease because of poor environment status, stress or any of a number of other factors [11]. The actual development of a disease and the relevant severity of that disease within a fish population are influenced by a complex interaction of these variables associated with the pathogen, the host, and the environment.

B. *Related works*

Previous studies on the infectious disease dynamics in the aquaculture system have mainly used mathematical models that focused on the population as a whole [6]-[10]. Kermack and McKendrick were pioneers in establishing the mathematical modeling of disease epidemics in 1927 [11]. Kermack and McKendrick created a mathematical model named SIR (Susceptible, Infectious, Recovered) based on ordinary differential equations. They started with the assumption that all members are initially equally susceptible to the disease and that a complete immunity is conferred after the infection. Many researchers have used mathematical models after that to simulate disease dynamics.

Cellular automata (CA) theory has also been used for modeling dynamics of infectious disease spread [12][13], but the representation of individual's movements and interactions over space was no presented.

Agent-based methods have been applied to simulate transmission of human viral diseases such as influenza [14]-16]. We have applied the agent-based method to simulate fish disease dynamics in a fish population [17], but we didn't focus either on the fish swimming behavior or on the environmental conditions. Agent-based model (ABM) can be valuable for the analyses focused on individual interactions, and also to incorporate the spatial aspect of the system. Whereas classical SIR-models used in disease transmission modeling represent total populations, in this study, an ABM is applied to simulate infection process of an individual fish, fish movement in the cages, and the way that pathogens spread spatially by representing these as agents.

II. THE MODEL

The presented model simulates the spread of diseases in a fish population as a result of the interactions between the agents themselves and between the agents and their living environment. The model has two types of agents, fish, and pathogens. The fish are categorized in four groups (Susceptible, Infected, Recovered and Dead). The healthy susceptible fish will get infected if there are number of pathogens nearby and its resistance factor to diseases is low, and then the sick fish will shed pathogens to the surrounding water, and will die because the sickness or will get recovered. The fish swimming in the cage while the pathogens move by sea currents and leave the cage. In the following, we will explain the agents' attributes and behavioral rules in details.

A. *Agents' attributes*

The model is individual-based, and each agent (fish or pathogen) has different biological, physical and spatial position status. Figure 1 shows the model agents' attributes and behavioral rules.

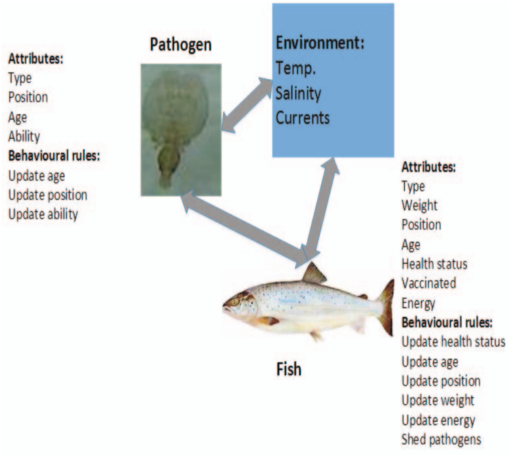

Figure 1. Model agents (fish and pathogen)

Fish has different biological and physical attributes that affect its health status and its resistance to get sickness. The fish's health status is altering between susceptible, infected and recovered statuses (figure 2). The fish agent's attributes that we include in the model are health status, position, weight, age, energy, and vaccinated (figure 1). If the fish is vaccinated, then the fish is prior immunity and will not get infected. Weight affects the fish swimming speed. We will explain fish health status updating process and fish swimming behavior later in this section.

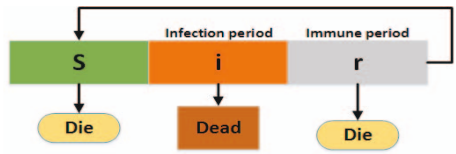

Figure 2. Fish agent health status

In the model, pathogens are agents also. Of course, one pathogen agent represents a batch of a high number of pathogens. Figure 1 shows pathogen's attributes and behavioral rules. Pathogen's lifespan is depending on the environment status (sea temperature and salinity), and the pathogens are moving by sea currents.

B. Fish's health status updating

In the setup procedure, a number of fish set by the *fish-number* slider are randomly placed in the farm. A percentage of these fish are made infected (set by the slider *initial-infected*), and a percentage of them are made prior immunity (set by slider *prior-immunity*). If the vaccinated switch is on, then all the fish are prior immunity. Fish agent swims in the cage and updates its health status at each time step. Figure 3 shows the fish updating health status process.

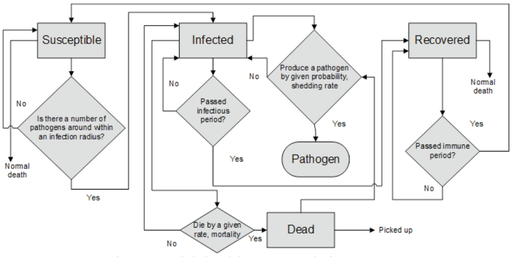

Figure 3. Fish health status updating process

The susceptible fish will look around within an infection radius, if there is a number of pathogens in the sphere where is the fish agent is in the center of, and the radius is infection radius, will get infected. Figure 4 shows the agent vision and the space that will be checked around by equation 1.

$$V = (4/3)\,\pi r^3 \quad (1)$$

Where, V is the sphere volume, and r is the infection radius.

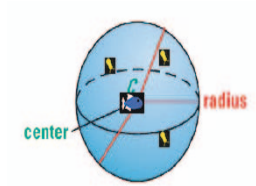

Figure 4. Sphere representing the space which will be checked by the susceptible fish (blue fish in the center) for the pathogens existence, radius-infection radius

Each susceptible fish has its own resistance factor (RF) and each pathogen has its own ability to cause disease, so the infection will happen only if there are a number of pathogens with good ability in the surrounding area and fish has low RF as the following equation:

$$RF * \Sigma\,(\text{pathogen} * \text{ability}) \geq \text{threshold; get infected} \quad (2)$$

When the fish get infected, it will be in the infected category, and it has to pass an infection period before it can get recovered. The user can set the infection period by the slider *infection-period*. The infected fish shed pathogens by a shedding rate which can be set by the user with slider *shedding-rate*. The fish shed pathogens at the same location where they are. The infected fish can be die because the sickness by the mortality rate that can be set *mortality* slider. The recovered fish after passing an immune period that can be set by slider *immune-period*, they will enter the susceptible status again. The un-infected fish can die normally by normal mortality rate (*mortality_noraml*). We have added some noise to the infectious and immune periods in our implemented model. The ability and RF attached to each fish and pathogen when is created. We used normally distributed random numbers for both the RF and ability. The standard deviation is 15 percent of the mean values that entered by the user in input variables: *RF* and *ability*.

The dead fish shed pathogens also until the farmer picks them up.

C. Fish swimming behavior

Fish swimming behavior inside the cages is a significant issue in the disease spreading process, because the fish will get infected if its only swims in the water that has pathogens. If the fish swims in the water which is free from the pathogens, the fish will not get infected.

Fish normally swim in schools to get benefits from schooling motion (defence against predators, enhanced foraging success, and higher success in finding a mate). But the fish swimming in the sea cages are limited and affected by other factors. Fish in sea cages prefer to swim in the middle of the cage referencing to the cage-depth and follow a circular movement in the normal current speed, but keep stations at fixed positions in the high current speed [18][19].

In the model, the fish swim randomly by default, but we have developed two other swimming behaviors, circular movements and schooling in a spiral path. For the schooling behavior, we have used the same model in [20], which is depend on three main rules [21]: Separation (each fish keep a distance from other fish nearby to avoid collision and prevent crowding), Alignment (each fish match the direction and the speed of its neighbours) and Cohesion (each fish tends to move to the average position of its neighbours).

D. Pathogen age and position updating

The pathogen lifespan is depending on the environment, sea temperature and salinity. In the model, we use pathogen age function as an exponential decay function in equation 3, which is inspired by data that related to Pancreas Disease (PD) virus lifespan.

$$\text{Pathogen life span} = a * \exp(-x / b) \quad (3)$$

Where x is the sea temperature, a is the pathogen life span at 0° sea temperature, and b is the decay rate.

The pathogens are moving by sea currents. When the pathogen is moved out of the cage (simulation space), it will be removed from all the simulation.

E. Model sacling in time and space

The Norwegian sea fish farms have different sizes and different shapes. The real sea fish farm could has a size of around 10,000 square meters, depth of 40 meters and host around a million fish [22]. The farms can be formed from circular or square cages. Some of the farms have rectangular shapes while the others have the cages beside each other shaping a line facing the currents. We designed our model in a cube space of 80 x 80 x 80 patches (Patches represent the grids in the landscape in NetLogo) to represent one fish farm cage. The patch size is 8 x 8 x 8 pixels. This means 16 pixels or 0.5 patches in the model represent each meter. The fish farm has a maximum population with 1000 fish while in reality you would expect to see about 1000 times more fish in an actual fish farm at this size. This simplification was made in order to save computer resources while running the model. Tick is the time step in the model and it's representing a second, a minute, an hour or one-day, (it can be selected by the user, *time-step*). The environment's condition parameters (current speed and direction, sea temperature) are selected by the user. In order to create a model that incorporates some of the variation presents in nature we used normally distributed random numbers for current speed, current direction and sea temperature. By introducing this randomness we avoid to some extent to end up with a very specific case scenario that would be less valuable for generalizations.

Pathogens in the model represent a batch of pathogens. The infection process depends on infectious dose and shedding capacity. These parameters are very difficult to quantify. According to [23], infectious dose for Infectious Hematopoietic Necrosis Virus (IHNV) in Atlantic Salmon is ranging from 10 to 10^4 plaque forming units (pfu) per ml, and shedding rate is ranging from 8.8 * 10^6 to 4.8*10^7 pfu per fish per hour. In our model, these parameters are selected by the user (shedding rate and infection radius).

Fish speed is depending on its weight and length [24]. In general, the weight-length relationship can be described by

$$W = a*L^b \tag{4}$$

Where W is observed fish weight, L is observed fish length, and a and b are estimated by:

$$\log (W) = \log (a) + \log (L) \tag{5}$$

Where a is the regression intercept and b is the regression slope.

The fish speed depends on many factors [25], in our model we estimate it by

$$\text{Fish speed} = k * L \tag{6}$$

Where L is fish length, and k is a constant that depends on the environment condition [25].

III. SIMULATION

A. Agent-based Simulation Toolkit

In order to implement the designed aqua agent-based model, NetLogo 3D [26], was used. NetLogo is a multi-agent programmable modeling environment that is used by tens of thousands of students, teachers and researchers worldwide. NetLogo toolkit allows simulations within a geographic information system environment and it's easy to include physical and environmental data also.

B. Implementation

Implemented model has several parameters such as simulation parameters, disease model parameters, and agents' attributes (see Table I). All the model parameters can be adjusted by the user, and the model has a 3D visualisation view and epedimics curves that updated at each time step.

TABLE I: MODEL PARAMETERS

Parameter	Min value	Max value	Default value
Fish number	*1*	*1000*	*100*
Shedding rate (%)	*0*	*100*	*50*
Infection period (days)	*0*	*100*	*4*
Immune period (days)	*0*	*100*	*10*
Infectious radius (patches)	*0*	*20*	*1*
Initial infected (%)	*0*	*100*	*5*
Prior immunity (%)	*0*	*100*	*0*
Mortality (%)	*0*	*100*	*1*
Mortality normal (%)	*0*	*100*	*0.00001*
Pathogen-ability	*0*	*1*	*0.8*
RF	*0*	*1*	*0.8*
Weight (kg)	*0*	*10*	*4*
Current speed (m/s)	*0*	*1*	*0.05*
Current speed std.	*0*	*0.1*	*0.01*
Current heading bias (degree)	*-5*	*5*	*0*
Current heading std	*0*	*90*	*30*
Temperature (c)	*0*	*20*	*10*
Vaccinated			*Off**
Time step			*Sec**

*Parameters that select between many values or on/off.

The fish shooling parameters are summerized in Table II.

TABLE II: FISH SCHOOLING PARAMETERS

Parameter	Min value	Max value	Default value
Vision	*1*	*40*	*10*
Max-velocity	*0*	*20*	*5*
Max-acceleration	*0*	*10*	*3*
Cruise-distance	*0*	*20*	*3*
Spacing-constant	*0*	*20*	*10*
Center-constant	*0*	*20*	*6*
Velocity-constant	*0*	*20*	*6*
Wander-constant	*0*	*20*	*3*
World-center-constant	*0*	*20*	*0*
Follow-leader-constant	*0*	*100*	*0*
Avoidance-constant	*0*	*100*	*50*

C. Scenarios

We have built a generic model, which can be used for many fish disease types and in different environmental conditions. In order to explore the importance of current speed and direction on the fish disease dynamics, we have developed the first scenario where the current speed changes (0.05, 0.1, 0.15, 0.2, 0.25 and 0.3 cm/s) while all other parameters are constants and the fish swim randomly.

In order to explore the effects of fish swimming behavior, we have built another scenario to test this. In this simulation, the fish swim randomly, in a circular path and in a school (figure 5.). In the circular experiment, the fish swim in a regular horizontal circular path with small changes in the vertical positions (figure 5b.). In the fish schooling behavior experiment, the fish swarm follows a leader who moves in a spiral path (figure 5c.) or move randomly in the cage (figure 5d.).

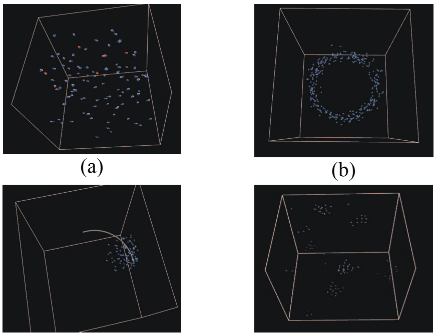

Figure 5. The fish swim (a) randomly. (b) in circular path (c) in school follow a leader (d) in school move randomly.

The simulation output is the percentage of infected/susceptible/recovered/immune fish at each time step (figure 6.), and the total number of pathogens.

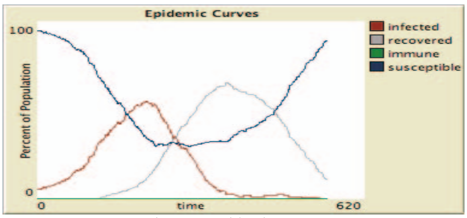

Figure 6. Epidemic curves

IV. Results and Discussion

The presented model is a generic model, and all the model parameters can be set easily in the GUI or by changing few lines in the code. These parameters represent the most important factors that affect the fish disease dynamics in the aquaculture sites. The model can explore dynamically the relationships between these parameters by running different scenarios.

A. Effects of current speed and direction, and other enviromental factors.

The sea current is a significant factor in the fish disease transmission in the aquaculture. The pathogens are moving by currents, so with a high current speed, the pathogens will leave the cage rapidly. Figure 7. shows the pathogens' density in the cage for different current speed values. The pathogens' density decreases when the current speed increases, and of curse increases when the number of infected fish increases.

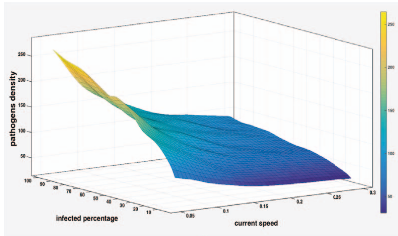

Figure 7. Pathogens' density (z-axis)vs. current speed (x-axis) and infected percentages (y-axis).

Figure 8. shows the attack rate in low and high current speed values. The attack rate decreases as current speed increases, and in low currents the attack rate is very high. Active currents are good also for waste disposal, so to get benefits from active sea currents, it is better to put the cages beside each other shaping a line facing the currents.

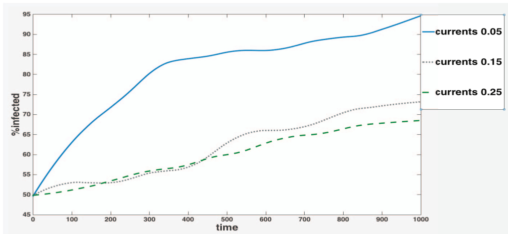

Figure 8. Infected percentages (y-axis) dynamics in different current speed values.

Other environmental factors (sea temperature and salinity) affect both the fish and pathogens. Higher sea temperature and salinity decrease the fish RF to get infected, but decrease the pathogen lifespan also.

B. Effects of fish swimming behavior

Fish movement is another significant factor in the fish disease dynamics. If the fish swim in water that has a percentage of pathogens' density, will get infected, otherwise, the fish will not get infected. There are many studies about fish swimming behavior in the cages and the fish speed as well [24][25]. In our model, we have tested swimming behavior (random, circular, in school) with 40 cm/s average speed. Figure 9. shows the attack rate in different fish swimming behavior. The highest attack rate when the fish move in a circular path, because the fish movements are concentrated in a specific area, while the lowest attack rate when the fish swim randomly because they occupy all the simulation space.

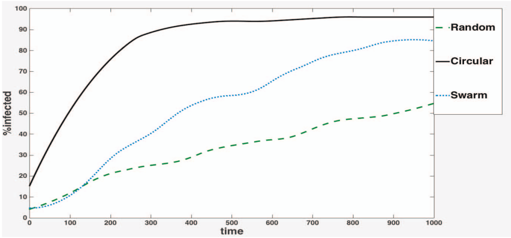

Figure 9. Infected percentages (y-axis) dynamics in different fish swimming behavior.

V. CONCLUSION AND FUTURE WORK

The presented model is designed to simulate the horizontal fish disease transmission that involves the spread of the pathogen from one individual to another through water, and combines most important factors in this process (Table I and II). The model parameters can easily be varied to simulate a specific scenario. In our simulation, we have focused on the effects of sea currents and fish swimming behavior factors on the disease transmission. The results show that the attack rate increases when the sea current speed decreases, and when the sea current's speed is very high, there is less effect on the attack rate. The fish swimming behavior is a significant factor as well. The attack rate increases when the fish swim in a regular pattern (circular or in school).

Some limitations of this model are with respect to the model scaling. Because the computer resources, not all the population (fish and pathogens) can be considered. This consequently affects the number of contacts between the individuals

The model can be extended by adding more key parameters related to the fish industry process (i.e. stocking and harvesting process), or related to the interaction with the outside environment, including other factors related to escaped fish, wild fish and workers.

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Study
II-1

AN AGENT-BASED MODEL TO SIMULATE PATHOGEN TRANSMISSION BETWEEN AQUACULTURE SITES IN THE ROMSDALSFJORD

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KEYWORDS
Agent-based modeling, aqua farms, NetLogo, pathogen transmission, diseases in aquaculture.

ABSTRACT

Fish farming is an important industry along the Norwegian west coast. This industry provides labor opportunities and financial income in areas that are often thinly populated. Fish are subject to diseases carried by pathogens. The value of the fish that are lost due to disease is worrisome, and emergent diseases continue to pose a severe challenge to the aquaculture industry. We have built an agent-based model to simulate the emergence of a hypothetical fish pathogen in an aquaculture facility in the Romsdalsfjord[1] to observe how this pathogen possibly spreads to multiple facilities within the fjord. This model enables us to observe how key parameters such as current speed, current direction, pathogen life span, contagiousness and fish density affect the disease dynamics. The model is implemented in NetLogo, and we have included three aquafarms at the Romsdalsfjord in the experiment.

INTRODUCTION

Aquaculture is about to revolutionize the way we consume fish and other marine food products as agriculture already did on land. During the past few decades world capture fisheries have stabilized or decreased, whereas aquaculture production has increased massively (FAO 2012). In 2010, aquaculture stood for 47% of global food fish production, and in Norway the export value of farmed seafood now exceeds that of wild caught species (FKD 2013). Today, fish is the third most important export product after oil/gas and metal, and accounts for 5.7 per cent of the total Norwegian export value according to Statistics Norway (SSB 2013). Norway is the largest exporter of aquaculture products in Europe, and number six globally, after Asian nations such as China, India and Indonesia (FAO 2012). It is thus clearly of high importance for Norwegian economy to ensure a sustainable aquaculture industry.

However, emergent diseases continue to be a serious challenge to the aquaculture industry and set constraints to its expansion (Murray & Peeler 2005). Diseases both induce large economic costs to the industry (Werkman *et al.* 2011) and might threaten wild populations (Murray & Peeler, 2005). A major problem in many areas has been the uncontrolled use of antibiotics leading to resistant bacteria strains (Defoirdt et al. 2011). Although the antibiotics use in Norway today is restricted, and some important pathogens have been reduced through vaccination programs, new and/or resistant pathogens still emerge (Olsen & Hellberg 2011). Combatting these diseases is therefore an important research field (Johansen *et al.* 2011) and a hot topic in public debates (e.g. NTB 2011).

Atlantic salmon is by far the most important species in Norwegian aquaculture. The most troublesome diseases for the salmon aquaculture are caused by viruses (Olsen & Hellberg 2011). All major viruses affecting Norwegian aquaculture are thought to spread between fish through sea water (Johansen *et al.* 2011), as infected fish shed pathogens to the surrounding waters. To keep fish farms at appropriate distances is therefore a potential measure to combat this horizontal transmission.

This model aims to simulate the pathogen transmission between aquaculture sites in a Norwegian fjord and observe how this pathogen possibly spreads to multiple facilities within the fjord. This model uses many key parameters such as current speed, direction, pathogen life span, contagiousness and fish density to find possible pathogen transmission patterns. Before describing the model in detail; a more complete background on the dynamics of fish disease transmission and previous studies on this issue will be given in the next section.

Diseases in aquaculture

Knowledge of pathogens in wild fish stocks is generally poor, and it is therefore difficult to predict which diseases might occur once an aquaculture facility is established in an area (Bergh 2007). A wide range of pathogens exists, from viruses and bacteria to crustacean parasites (Olsen & Hellberg 2011). These might be introduced to an aquaculture system through various pathways: movement of infected stocks, equipment or fish products from other areas; or by exposition to wild fish pathogens (Murray & Peeler 2005). Once introduced, pathogens can benefit from the aquaculture environment and pose a graver risk to farmed fish than wild stocks. This is both because of factors such as poor environment, stress and pollution that might reduce individual fish resistance (Murray &

[1] Romsdalsfjorden is 88 km Long and located in the Romsdal district of Møre og Romsdal county.

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Peeler 2005), but moreover because the artificial high density of fish, and thus potential hosts for the pathogen, in a fish farm can induce outbreaks (Bergh 2007; Rimstad 2011). Pathogens that benefit from higher host densities follow so-called *density-dependent transmission* (Murray 2009). The rate of transmission is the product of the densities of susceptible and infected individuals.

As previously mentioned, disease transmission can happen with currents, depending on the survival time of the pathogen in water masses, but also through vectors such as wild fish or escaped farmed fish (Murray & Peeler 2005). Hydrodynamic spreading will usually be a local-scale problem, whereas wild fish can become infected nearby a farm and transmit the pathogen over larger distances (Werkman *et al.* 2011). An example of a waterborne virus is the Salmonid alphavirus causing Pancreas disease (PD), an increasing problem in Norwegian aquaculture (Kristoffersen *et al.* 2009). Stochastic models have emphasized the importance of the distance between farms for disease transmission of both this and other diseases affecting farmed salmon, such as heart and skeletal muscle inflammation (HSMI) and infectious salmon anaemia (ISA) (Aldrin *et al.* 2010).

Using an Agent-based model (ABM) to simulate disease transmission in aquaculture

Previous modeling studies on the transmission of pathogens within and between farmed fish populations have either used classical SIR disease transmission models (Susceptible, Infected, Recovered) that focus on the population as a whole (e.g. Murray 2009; Green 2010), or such population models coupled with simple hydrodynamic models or distance measures of transmission between separate populations (Viljugrein *et al.* 2009; Aldrin *et al.* 2010; Werkman *et al.* 2011; Salama & Murray 2011). To our knowledge no studies have previous applied ABMs to assess the transmission of diseases within and/or between aquaculture fish populations. On the other hand, ABMs have been applied to simulate transmission of human viral diseases such as influenza (e.g. Ciofi degli Atti *et al.* 2008; Milne *et al.* 2008). ABMs can be valuable for analyses focusing on individual interactions, and also to incorporate the spatial aspect of the system. Whereas classical SIR-models used in disease transmission modeling represent total populations, we here apply an ABM to simulate individual fish becoming infected, and how pathogens spreads spatially by also representing these as agents. By applying an ABM instead of e.g. differential equations more complexity can be added and analysed through simulations. Another reason for applying an ABM is that empirical data regarding fish pathogens are often lacking. It is therefore difficult to predict the threshold for density-dependent outbreaks of diseases in classical disease transmission models (Krkosek 2010). In an ABM, the parameters regarding disease transmission can easily be varied.

Modelling a real system

Since there are presently research activities regarding aqua farms in the Romsdalsfjord, we decided to look for both inspiration for research problems and potential parameter values that have emerged from these studies. From these studies we pursued the effect of the fact that pathogens may survive in water for days without a host. Furthermore, since there are many aqua farms in the Romsdalsfjord (DF 2013), about 35 (*see figure 1*), the close proximity between the farms becomes an important factor in disease transmission. It is a relevant issue in current research efforts to study under which conditions one infected aqua farm may spread disease to other farms by pathogens "jumping" from one aqua farm to the next, creating a domino effect.

Figure 1: Map, which shows the aqua farms in Romsdalsfjorden.

THE MODEL

This section describes how our model works. The model is implemented in NetLogo (*Figure 2*).The idea behind the model is to simulate three aquafarms which reside in the same fjord area, and that we can suspect are subject to cross contamination between each other. All parameters used in the model are listed in *Table 1*.

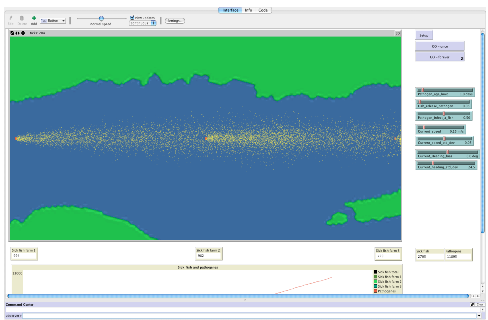

Figure 2: NetLogo model

We do not specifically model the background of introduction of a disease, and assume that the pathogen is a new variant for which no vaccination is yet in place. The model presented is a general model, which can be adjusted to various pathogens and environmental scenarios. Salmon aquaculture is the most common form of aquaculture in Norway, and since the most important mode of transmission of salmon disease is by water currents we chose to model this process.

Table 1: Parameters used in the model

Parameter	*Description*	*Estimate*	*Source*
Current speed	Current speed in m/s	0.02 – 0.2	4,6,7
Current direction	Current direction in degrees		6,7
Transmission parameter +	Probability that a fish is infected by a pathogen in its surrounding water	5.416×10^{-4} – 8.912×10^{-4}/hour (minimum values)	3
Shedding parameter +	Number of pathogens shed by infected fish	High*	1,2,5
Pathogen lifespan +	Lifespan of pathogen in seawater in days	8.33 – 62.5 hours Depends on pathogen and environment	3

+Pathogen values for Infectious salmon anaemia virus (ISAV), Infectious pancreatic necrosis virus (IPNV) and Salmonid alphavirus (SAV).

* Different sources use different units and values are ranging from $10^{6.5}$ PFU/fish/h (PFU= plaque forming units) (1), 10^5—10^8 CFU/fish/h (CFU=colony forming units) (2) and 6.8 $*10^3$ $TCID_{50}$ /ml/ kg fish/ h/ (maximum rates) ($TCID_{50}$ =the amount of virus required to kill 50% of infected hosts) (5). The units are not single pathogens but units that are measureable in the lab. Since the numbers are very high, and computationally difficult to implement in the model we set a probability between 0-1 (adjustable) that an infected fish sheds a pathogen, but this pathogen represents a large number. The probability value is likely to be high (close to 1) as observed shedding rates are on these ranges.

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Scaling the model in space and time

As a real-world basis for our model we use the aqua farms at Midsund (*Figure 3*), in the Romsdalsfjord. This part of the fjord currently hosts three aqua farms, with a distance of about 8 km between each site. The farms have a size of around 10,000 square meters and host around a million fish each (DF 2013). The total area of interest is about 16 km wide. We constructed the model in a rectangular space of 16 x 8 km. In our model all three aqua farms have the same size, 80 m x 120 m. The farm sizes are thus close to some of the real fish farms in the Romsdalsfjord (DF 2013). Each fish farm is populated with 1000 fish, while in reality you would expect to see about 1000 times more fish in an actual fish farm at this size. This simplification was made in order to save computer resources while running the model.

Figure 3: Midsund

According to MODS (2012) the average current speed in the Romsdalsfjord is typically 0.2 m/s. This equals 12 m/min or 120 m/tick. Tick is the time step in the model and its representing 10 minutes. The model enables the current speed to be varied around the default value of 0.2 m/s, and in order to move the pathogens at the correct speed in the simulations the conversion factor was incorporated.

The fish agents

The fish are created during the setup procedure of the model. In each of the three farms; 1000 fish are distributed across the farm's area. When the simulation starts all fish are healthy, i.e. belonging to the susceptible group. The exception is one infected fish in Farm 1. Healthy fish may become infected if there is a pathogen present at the same place as the fish. Once a fish is infected they start to produce pathogens at a rate given by a certain parameter (*Fish_release_pathogen*). This parameter represents the probability that one fish produces one pathogen in one time step. The probability that a healthy fish gets infected while being on same place as a pathogen during one time step is given by the parameter *pathogen_infect_a_fish*. The two probabilities for pathogen production and infection are flexible (between 0 and 1).

Pathogen agents and current simulations

Pathogens are also represented as agents. It is important to note that one pathogen agent does not represent one pathogen, but a batch of a high number of pathogens. Each pathogen is moved by the currents, with the current speed and direction given by the place the pathogen is at by the start of the time step.

In order to create a model that incorporates some of the variation present in nature we used normally distributed random numbers for both the current speed and current direction. By introducing this randomness we avoid to some extent to end up with a very specific case scenario that would be less valuable for generalizations. In theory, the model can be built with very complex current patterns (*see Figure 4*): pathogens inherit the current direction of the place they are presently on, and by moving to a new place they change the direction to the direction inherited from that place. In our Nelogo model, current angle was set directly inwards in the fjord. During each time step a random deviance is added to this current angle. This randomness is given by two parameters: A current standard deviation (*Current_heading_std_dev*) which can be set from 0 to 90 degrees and a bias term (*Current_heading_bias*) used to offset the direction given by the patch[2], which can be set between -5 and 5 degrees. When moving the pathogen might hit dry land. In this case the pathogen is removed from the model (dies).

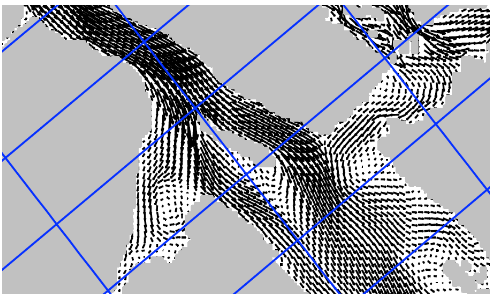


Figure 4: Currents direction in Romsdalsfjorden, MODS (2012).

The current speed is decided by the parameter *Current_speed*, and can be set from 0 to 2 m/s, with a default of 0.2 m/s. The current speed it is also accompanied by a random variation term, given by the parameter *Current_std_dev,* which can be set between 0 - 0.1 m/s. As we expect that current speed is not constant through time and space, this random term is used to make the model more realistic. Likewise the current speed can also depend on the individual patch. This is useful in order to model how current speed varies with the geometry of the fjord (e.g. changes in the width of the fjord, the presence of islands and peninsulas etc.). This aspect is incorporated by adding a constant to each patch, *the relative speed*. Relative speed is a number by which the global current speed is multiplied for each patch. Hence, a relative speed below one indicates a speed below the average in that particular patch. Likewise, a relative speed greater than one indicates a speed higher than the average.

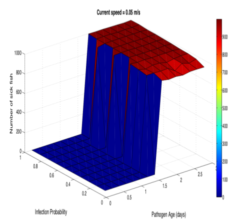
The pathogens are given a fixed life span in the range of the values we found in literature. In the model this parameter can be set between one and ten days, with a resolution of 0.1 day. At each tick all individual pathogens' ages are updated by adding 10 minutes (corresponding to 10/24/ 6 = 0.069 days) to their cumulative age. When a pathogen's age exceeds the value given by the age limit it dies.

RESULTS OF THE EXPERIMENT

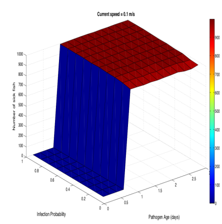
A simulation experiment was set up for the model. The model was run for 400 time steps, and three of the model parameters were varied in the following manner:

- Current speed: 0.05 to 0.25 m/s, at steps of 0.5 (5 values)
- Infection rate (Pathogen infect a fish): 0.1 – 1, at steps of 0.1 (10 values)
- Pathogen age: 0.2 – 3, at steps of 0.2 (15 values)

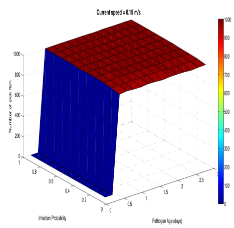
The simulation experiment output was the number of infected fish in each of the three fish farms (Farm 1, Farm 2 and Farm 3) at each time step. Running the experiment by using normal machine took around 15 hours, but to run it by using super-computer with 6 processers took around 5 hours. *Figure 5* (a,b,c,d and e) shows the number of infected fish in Farm 2 after 400 time steps. The interpretations of the figures follow in the next section.



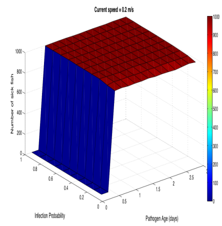
(a)



(b)

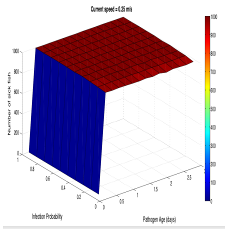


(c)



(d)

[2] Patchs represent the grids in the landscape in NetLogo.



(e)

Figure 5: Number of sick fish (z-axis) in Farm 2 after 400 time steps, with current speed set at five different values (0.05, 0.1, 0.15, 0.2 and 0.25 m/s), and infection probability (x-axis) and pathogen (y-axis) varied.

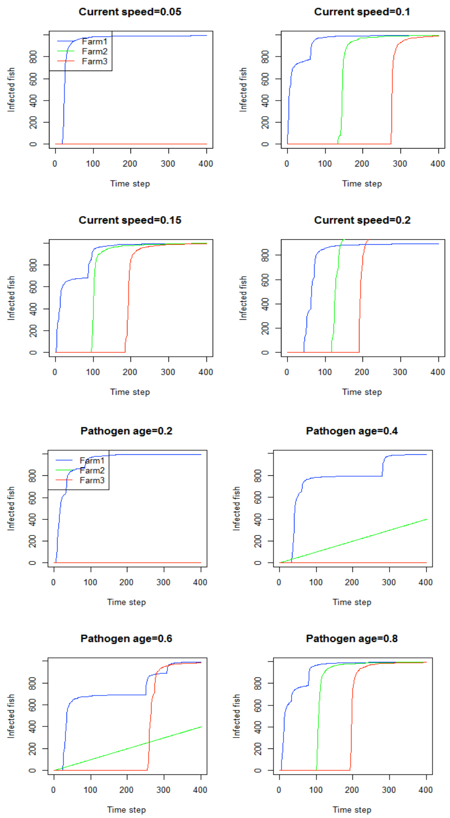


Figure 6: Number of infected fish per time step in the three fish farms (blue line=Farm 1, green line=Farm 2, red line= Farm 3). For the four graphs on the top infection rate and pathogen life span were held constant at 0.5 and 2, respectively and current speed was varied at four different levels. For the four graphs down pathogen age was varied, while infection rate was set at 0.5 and current speed=0.15 m/s.

DISCUSSION

As described above, the aquaculture industry is increasingly important for both the Norwegian economy and people's marine food availability worldwide. A major challenge for aquaculture development is the emergence of diseases, which can be due to a large variety of pathogens. It is therefore highly relevant to study how pathogen transmission between aquaculture sites can vary due to factors such as currents and pathogen virulence. Using an ABM we were able to simulate both fish and pathogens as individual agents and specifically study the movement of pathogens in a simplified fjord system. ABMs have to our knowledge never been employed in this type of study before. Although the model is simplified, we believe that it provides some insight into the transmission of pathogens between fish farm sites.

The simulation output

Current speed was the most important parameter controlling the number of infected fish in the aquaculture sites. The age limit of the pathogens was also important for the number of sick fish in Farm 2 and Farm 3. In fact, as long as the pathogen age was above a certain threshold, all fish in the fish farms would ultimately become infected. When current speed was held constant, the infection rate also had a significant impact on the number of sick fish in Farm 2 and 3, and for Farm 1 for low current speeds (<0.2).

The minimum pathogen age required to get infection in Farm 2 within 400 time steps, and at the lowest current speed we tested (0.05 m/s), was from 1.4 to 1.6 days, depending on infection probability. For Farm 3, the minimum current speed needed in order to get infection within 400 time steps was 0.1 m/s. At this current speed, the minimum pathogen age limit was 0.8 days. With this combination of current speed and pathogen life span the infection process occurs in Farm 2, which is subsequently sending new pathogens to Farm 3. If the current speed maximized to 0.25 m/s, only a lifespan of 0.2 days is needed in order to get infection in Farm 2, and subsequently in Farm 3. I.e., at current speeds above 0.1 m/s the dynamics of Farm 2 and 3 are similar, as Farm 2 acts as a new source of pathogens for Farm 3, and the distances are the same.

Scaling the model

If we were going to represent a realistic number of agents (fish and pathogens) the model simulation would be very computationally demanding. In Norway today, aqua farms can host fish in the order of millions (DF 2013) and for pathogens the numbers would be uncountable, in the order of trillions or higher, depending if we are studying bacteria or virus. In order to be able to run the model we therefore had to scale it down significantly. Even so, the relative magnitude between the number of fish and pathogens is likely incorrect, with the number of pathogens underestimated. To compensate for this, the probabilities of infection and pathogen release should be adjusted accordingly, meaning that they should be set higher than what might be expected. A challenge in this approach is that these parameters are largely unknown. Another issue arising from scaling down the model is that the pathogens might less easily "hit" the aqua farms, since there are likely fewer pathogens in the system than what would be realistic. It is harder to compensate for this issue by adjusting the probability of infection, since infection requires the actual presence of the pathogen. Increasing the probability of pathogen release would, on the other hand, compensate for this issue by creating more pathogens in the system. Another solution could be to make the aqua farms bigger (scaling up their size) in order to increase the probability of an encounter between the pathogens and the sites.

The matter of scaling thus leads to many challenges for creating a model that represents the real world. We still lack good solutions to many of these challenges, but we are aware of their existence and the results of the model simulations should accordingly be interpreted with this in mind. In essence, our simplified model of the Romsdalsfjord is aimed at studying effects that may occur, but it is not appropriate to make any numerical predictions.

Simulating pathogen transmission and infection

The most challenging part of the modeling process was to simulate the pathogen transmission process, due to lacking empirical data on these issues in the literature. There are several uncertain factors regarding the process of transferring illness between fishes. To create a realistic model for the infection process is therefore difficult, and our approach was to model a simplified scenario that can later be tuned to reproduce results observed in fish farms. Moreover, the few studies that have quantified the rates by which pathogens are shed by infected fish use different units which are not single pathogens, but units that are measureable in the lab or practical for disease monitoring (Salama & Murray, 2011). It was not straightforward to convert these values into probabilities, and we therefore had to experiment to find appropriate values. The probability of pathogen infection was varied during the simulations, while the shedding rate (Fish release pathogen probability) was kept constant (0.05). This was done in order to facilitate the interpretation of the results, and because we lacked any references as to what would be realistic values for the latter parameter.

CONCLUSIONS AND FUTURE WORK

In this ABM, we have simulated three fish farms in the Romsdalsfjord. The number of infected fish in each farm is predicted by factors such as current speed and pathogen life span. The results provide a good base for exploring the relationship between these variables and others (infection rate, pathogen release rate current bias etc.), and platform on which more complexity can be added to the model at a later stage. Such possible complexities are described hereunder.

Pathogen transmission

In reality, the proliferation of a pathogen can be highly dependent on environmental conditions such as temperature, and thus vary with seasonal and inter-annual environmental changes (Krkosek 2010). Also, the virulence of the pathogen and the conditions of the host (health, age, stress etc.) will affect the likelihood of an outbreak (Rimstad 2011). At this stage, we have only modeled a short disease proliferation period, and therefore assumed temperature to be constant. A next step could be to incorporate a dynamic temperature variable in our modeled fjord which would affect infection probability and pathogen release.

In this model, we focused on the distance between aquaculture sites, but not their individual sizes. But water-transmitted pathogens can also benefit from the size of the aquaculture site. A next step for our model could be to vary both distances and sizes of the fish farms. This could be interesting for managers deciding upon which areas would be appropriate in order to avoid disease transmission between fish farms.

Currents modeling

In our model, we have assumed the currents speed and direction act according to MODS (2012), and depend on what is written in the literature. We have assumed that current direction is inwards in the fjord and changes between 0.05 to 0.25 m/s in our experiment (at Midsund, *see figure 3*). We have selected these values by analyzing the geographic of the fjord (at Midsund) and results from MODS (2012). But in the reality, the current speed and direction are more variable and depend on many other factors, as season, snow melting rate, and the geographic of the fjord. The model would become more realistic if it was connected to a current model of the fjord.

Fish movement

Although the transmission through water is the most important route for marine pathogens, a further step could be to incorporate the movement of the farmed fish, with a certain probability of escaping (and which could be infected or not). Fish escapees can in fact pose a risk to the wild population through spreading of diseases (Naylor *et al.* 2005), a risk that increases when farmed fish are in the vicinity of wild populations of the same species and the farmed population contributes a large quantity compared to the wild fish.

Another interesting, but challenging, possibility would be to include wild fish agents. A study on the distribution of saithe within a fjord with salmon aquaculture showed aggregations around aquaculture facilities and a high proportion of fish moving between different farms, indicating that the wild fish might constitute an important connection between fish farms (Uglem et al. 2009). The fish might aggregate around the farms to feed on waste pellets under or around the nets. A range of pathogens is thought to be common to salmon and saithe, but the likelihood of transmission between caged and wild fish is unknown.

Altogether, the model presented here offers an interesting first step towards more complex models of disease transmission between aquaculture sites, an important research issue for the aquaculture industry.

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Study
II-2

An agent-based approach for predicting patterns of pathogen transmission between aquaculture sites in the Norwegian fjords

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Abstract

The aquaculture industry is a main industry in Norway, and it must be sustainable, i.e. experience long-term growth and development: It is necessary to build an environmentally sustainable aquaculture industry that minimizes risks to the marine environment and biological diversity, - including the transmission of fish diseases. The process of fish disease transmission in aquaculture systems is influenced by many factors, including individual (fish and pathogen) conditions, movement behavior and environmental conditions. Fish disease dynamics originates from a complex system, and the transmission of viruses is an unstable process, making it difficult to predict and analyze.

In preparation for this paper, we built an agent-based model to predict patterns of pathogen transmission with the purpose of identifying risks and hazards in the space and time domains. This risk assessment will help combat infectious fish diseases and help inform the management of the fish industry in Norway. Previous models that predicted the spread of diseases within and between fish populations were mostly based on the assumption that these populations were homogeneous, and focused on the population as a whole. In contrast, we are assuming that the fish populations and pathogens are heterogeneous. Consequently, we developed an agent-based approach for modeling the dynamics of a fish disease within and between the aquaculture sites of the Norwegian fjords; this type of model considers interactions among individuals (fish and pathogens) and the interactions between individuals and their environment in a space-time context. The model presented explores the potential effects of different factors, such as the conditions of individuals, movement behavior and environmental conditions, on the simulated spread of a fish disease.

We applied the model developed to different case studies in the Norwegian fjords. The results demonstrated how the infection risk at any point around the infected site is dependent on both the pathogen and the fish density at that point, and the infection risk increases when the pathogen or fish densities increase. The pathogen density decreases exponentially as a function of an increase in the water temperature, and the pathogen density increases with the velocity of the current or the fish density at the infected site. The pathogens are moved faster by higher current velocity, so this will slow the infection process at the local infected site. Nevertheless, the current will carry the pathogens to nearby places faster. The direction of the current is very important since the pathogens are predominantly moved by the currents.

The agent-based method helps us advance our understanding of pathogen transmission and builds risk maps to help us reduce the spread of infectious fish diseases. By using this method, we may study the spatial and dynamic aspects of the spread of infections and address the stochastic nature of the infection process.

Keywords - *Agent-based method, aquaculture, fish disease dynamics, pathogen transmission, Netlogo.*

1 Introduction

Fish farming in Norway has increased steadily in recent years and is expected to continue to increase for years to come (www.ssb.no). The continued growth of Norwegian aquaculture production has presented the industry with a range of challenges. One of the main challenges is to understand fish disease dynamics within and between the aquaculture sites in the Norwegian fjords, characterized by a rich marine life and considerable human activities. Fish are subjected to diseases carried by different types of pathogens[1]. Pathogens are transported in space and time by sea currents at an irregular velocity (speed and direction). The sea currents in the Norwegian fjords exhibit a complex pattern of behavior, as shown in *figure 2*. Pathogen transmission is dependent on many different biological, environmental, and physical factors. Due to the complex relationships that exist between these different factors and the way they change in time and space, (e.g. fluctuating sea-water temperature alter pathogen's lifespan and its ability to cause a disease), other approaches previously applied to study this issue, that are not including active parts (agents) to model this complex dynamics relationships, they have not successfully reduced the ambiguity in our understanding of how pathogens spread in the Norwegian aquaculture system. Therefore, we need a method that allows us to address this ambiguity so as to limit the risk of fish disease spreading. In this study, we will use an agent-based approach in building models that predict patterns of pathogen transmission for the purpose of identifying the risks and hazards in the space and time domains. It is expected that this risk assessment will inform the fish industry management in Norway in their fight against infectious fish diseases.

1.1 Aquaculture in Norway

In recent decades, the aquaculture industry has probably been the fastest growing food-production sector in the world, and it provides a significant supplement to, and substitute for, the catch of wild aquatic organisms. Norway has a long and jagged coastline that is bordered by cold, fresh seawater endowed with a rich marine life. This environment provides excellent conditions for aquaculture activities. Today, Norway is the second largest seafood exporter in the world and the world's leading producer of Atlantic salmon (Fiskeridir.no, 2018). Since the advent of commercial salmon farming in Norway around 1970, the aquaculture industry has grown to become an industry of major importance. Not only is aquaculture important to the Norwegian economy as a whole, it is also very important to the many local communities along the coast where other economic opportunities are sometimes limited. Today, farming of salmon and rainbow trout takes place in nearly 160 municipalities along the Norwegian coast. Approximately 5,900 people are directly employed in aquaculture production, and 21,000 people are employed in aquaculture-related activities (Fiskeridir.no, 2018; SSB, 2018).

Emerging diseases pose a serious challenge to the aquaculture industry, and the value of the fish that are lost due to disease is worrisome. Ten years ago, Iversen et al 2005 assessed the general cost of such diseases imposed on the Norwegian fish farming industry to be US$ 150 million annually (Iversen *et al.* 2005). Fish are subjected to diseases carried by pathogens, including viruses, and these pose particular challenges to the salmon aquaculture (Olsen and Hellberg 2011). Our knowledge of pathogens and their effect on wild fish stocks is generally poor, and it

[1] A pathogen is anything that causes a disease.

is, consequently, difficult to predict which diseases might occur once an aquaculture facility is established in an area (Bergh 2007). A wide range of pathogens exist, from viruses and bacteria to crustacean parasites (Olsen and Hellberg 2011). These pathogens might be introduced to an aquaculture system through various pathways, e.g.; through the relocation of infected stocks, by the use of equipment or fish products from other areas, or by exposure to wild fish pathogens (Murray and Peeler 2005). Once introduced, pathogens may benefit from the aquaculture environment and pose a graver risk to farmed fish than they do to wild stocks. This is partially because of factors such as unfavorable environmental conditions, stress and pollution, which might reduce the resistance of individual fish (Murray and Peeler 2005). Moreover, pathogens may benefit from the artificially high density of fish, and thus, the numerous potential hosts of the pathogen that are present in a fish farm and thus cause frequent and massive disease outbreaks (Bergh 2007; Rimstad 2011). Pathogens that benefit from higher host densities cause a so-called *density-dependent transmission* (Murray 2009). The rate of transmission is the product of the densities of susceptible and infected individuals. Disease transmission may also occur with currents as carriers, - depending on the survival time of the pathogen in the water masses, and also through vectors such as wild fish or escaped farmed fish (Murray and Peeler 2005). Hydrodynamic spreading will usually be a local-scale problem, whereas wild fish can become infected near a single farm and transmit the pathogen over larger distances to other farms (Werkman *et al.* 2011). An example of a waterborne virus is the salmonid alphavirus that causes salmon pancreas disease (PD), that has turned out to be an increasing problem in Norwegian aquaculture (Kristoffersen *et al.* 2009).

All major viruses affecting Norwegian aquaculture are thought to spread between fish through seawater (Johansen *et al.* 2011), as a result of infected fish shedding pathogens into the surrounding waters. To retain a sustainable fish industry in Norway, we need tools for effective risk analyses and consequence assessments. In this paper, we aim at developing models to help identify the pathogen transmission patterns between fish populations so as to support such analyses and assessment in the combat against fish diseases.

Previous Norwegian studies on fish diseases in aquaculture have used classical SIR (susceptible, infected, recovered) disease transmission models that have focused on the population as a whole (Reno 1998; Ogut 2001; Murray 2009; Green 2010) or such population models coupled with either simple hydrodynamic models or distance measures of transmission between separate populations (Stene *et al.* 2014). These models are inherently limited in their ability to predict the dynamics of diseases because they are based on structural assumptions and historical data that do not offer a valid description of the system at hand. They, consequently, do not offer an adequate explanation for the complex dynamics observed. In particular, they do not capture the phenomenon of emerging diseases, i.e. the onset of a disease in an aquaculture farm.

Fish disease dynamics are affected by many variables that modeling techniques, applied so far, cannot address; however, the agent-based modeling (ABM) technique can include all necessary variables to build a valid model even if there is a lack of available empirical data. By using ABM, we move to the individual's level and how the individuals' characteristics and their behavior are connected to the overall system behavior.

1.2 Related Work

Fish disease dynamics are affected by many different biological, environmental and physical characteristics, such as fish density and stress, water temperature and salinity, as well as current speed and direction. This constitutes some of the complexity to be addressed when modeling these processes. Fish disease dynamics within an aquatic site or between many such sites is itself a part of such a complex environment in which it evolves. Earlier modeling studies on the transmission of pathogens within and between aquaculture farms have mainly been based on mathematical models that focused on the population as a whole (e.g., Murray 2009; Green 2010). Kermack and McKendrick were pioneers in establishing the mathematical modeling of disease epidemics in 1927 (Kermack *et al.* 1927). They created the mathematical SIR (susceptible, infectious, recovered) model, based on ordinary differential equations. That model includes the assumptions that all fish are homogeneous, initially equally susceptible to the disease, and completely immune after having been infected. The SIR models do not treat the pathogens as separate individuals who may survive without a host, and they do not include the environmental conditions that may change over time. SIR models are simple and, typically, deterministic and do not validly represent some important aspects of disease spread, including the variety in properties across in the individuals, the spatial aspect of the spread of disease and the characteristics, including causes of delays, of the environment in which this spread takes place. Many researchers have, over the years, applied a variety of such mathematical models to simulate disease dynamics. Some studies have coupled such models to simple hydrodynamic models and to distance measures of transmission between separate populations (Viljugrein *et al.* 2009; Aldrin *et al.* 2010; Werkman *et al.* 2011; Salama and Murray 2011).

Hydrodynamic models, combined with particle tracking and statistical analyses, have been widely used in Norway to identify the salmon louse and pancreas disease (PD) transmission dynamics in Norwegian fjords (MODS 2012; Stene *et al.* 2014). SINMOD is the most famous hydrodynamic model in Norway (www.sinmod.no), and it couples physical and biological processes in the ocean. Hydrodynamic models are based on the assumption that the pathogen agents drift passively with the sea currents. Hydrodynamic models do not incorporate the effects of the surrounding nature (e.g. sea-water temperature change) on the pathogens, and the heterogeneity among the pathogens is being ignored. Also, the statistical analyses are based on the assumption that the fish populations are homogeneous.

Cellular automata (CA) theory has also been used for modeling the dynamics of infectious disease spread (Sirakoulis *et al*. 2000; Zhen *et al*. 2006), but the individuals movements and interactions across space over time have not been represented in such models.

Agent-based methods have been applied to simulate the transmission of human viral diseases such as influenza (Ciofi *et al.* 2008; Milne *et al*. 2008; Khalil *et al.* 2010). In this project, we have applied the agent-based method to simulate disease dynamics in a fish population (Alaliyat and Yndestad 2015b), but we did not extend the model to simulate how pathogens spread between aquaculture sites in the fjord. Agent-based models (ABMs) can be valuable in analyses focusing on the effects of individual interactions, and they may incorporate the spatial aspect of a system. Whereas the classical SIR models, used in classical disease transmission modeling, represent total populations, in this study, an ABM approach is applied to simulate the infection process of the individual fish, the movement of fish in the cages, and the way that pathogens spread spatially, in the form of individuals, by representing fish and pathogens as agents. ABMs are computationally costly compared to other models, and the costs increase exponentially with the number of individuals included in the model.

1.3 The modeling approach

The main aim of this study was to develop an agent-based modeling approach for studying the dynamics of fish diseases within and across aquaculture sites in the Norwegian fjords. This approach considers the interactions between individuals' (fish and pathogens) and with their environment in a space-time context and is expected to advance our understanding of the disease dynamics process and help combat such a development. The process of disease transmission is influenced by many factors, including the conditions of the individuals (fish and pathogen), movement behavior and environmental conditions. The model presented explores the potential effects of these factors on the spread of a simulated fish disease.

ABM provides a realistic representation of the system by including the interactions of individuals. In addition, ABM offers more flexibility in the modeling and allows for more complexity to be added and analyzed by way of simulation. Another reason for applying ABM is to compensate for the lack of empirical data regarding fish disease transmission. By using ABM for predicting pathogen transmission, a simulation of future disease transmission scenarios could provide a means to compensate for this lack of empirical data. In ABMs, the values of the parameters governing the disease transmission may easily be varied (Build on previous models. Alaliyat *et al.* 2013; Alaliyat and Yndestad 2015a, Alaliyat and Yndestad 2015b).

ABM has been suggested in different fields as one of the most appropriate approaches to modeling and simulation when addressing complex, dynamic system. ABM captures the complex network of interactions and interconnections that comprise real systems and makes it possible to derive emerging dynamic patterns, unexpected changes in those patterns and events characterizing such patterns. This makes such a bottom-up approach advantageous in simulating the spread of pathogens in aquaculture systems. ABM provides insights into the structural origin of emerging phenomena that are caused by the interactions among individuals (pathogens and fish). Using ABM, one may describe how fish and pathogens behave rather than develop equations that we believe govern the overall dynamics of the densities and infection rates of system entities. Reality is transparet in the model by using ABM. ABM is flexible in that it allows for the addition (and elimination) of agents and for adjustments in the agent behavior. ABM provides a framework for analysis and testing of the emergent dynamics. ABM provides a flexible framework for answering questions, such as what is happening, what will occur next, or identifying what the best/worst outcome might be. Thus ABM may serve well as modeling technique with the purpose to predict pathogen transmission between aquaculture sites.

In this study, we focus on the Romsdalsfjord[2]. This fjord has been selected because of the extensive empirical research that has been undertaken at this site, Thus, we had access to the data we needed for our model building, validation and simulation. The Romsdalsfjord is a semi-closed fjord in mid-Norway that has a massive fish industry with more than 35 aquaculture sites throughout the fjord (*figure 1*). The aquaculture industry data, including biological, physical and environmental data, reflects the aquaculture system in the Romsdalsfjord, and our proposed model either used this data or was inspired by this data.

[2] Romsdalsfjord is 88 km long and located in the Romsdal district of Møre og Romsdal county in mid-Norway.

Figure 1: Map of the aquaculture farms in the Romsdalsfjord.

The close proximity between aquaculture sites in the Romsdalsfjord is an important factor in disease transmission. Consequently, it becomes very important to study the environmental, biological and physical conditions of an infected aquaculture site because from that site pathogens may spread to other aquaculture sites by sea currents, - creating a domino effect. The sea currents in the Romsdalsfjord exhibit a very complex pattern (*figure 2*). The currents in fjords are the strongest and most varying in the upper 20 m (closest to the surface), i.e. where the aquaculture farms are located. The currents are driven by topographical distinctions, river runoffs, winds, tides and water exchanges caused by offshore density differences (Urke *et al.* 2011; Stene *et al.* 2009). In this work, we built models to predict the patterns of the spread of pathogens from infected sites. This has enabled us to build risk maps that depicted the hazardous areas around infected sites in which diseases may be transmitted to neighboring sites.

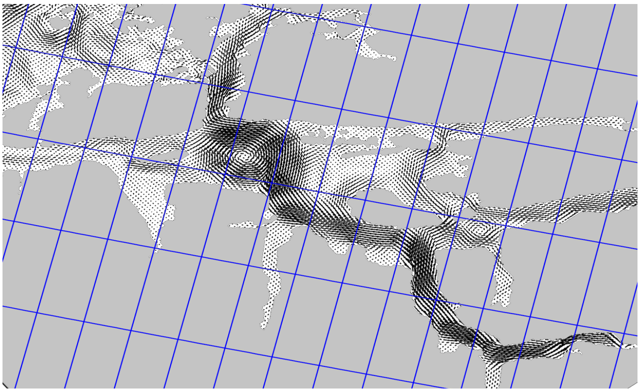


Figure 2: Current speeds and directions in the Romsdalsfjord, MODS (2016).

We have built three different simulation scenarios to explore the potential effects of fish, pathogen and environmental factors on the spread of a simulated fish disease in the Romsdalsfjord. The first simulation experiment had only one hypothetical infected fish farm in an open area, and the sea current moved from the west to the east (i.e., left to right). In this scenario, we ignored the topography of the fjord, but we focused our investigation on the risk-values and -maps that resulted from the pathogen's density in space, over time, and on the largest distance that pathogens could spread. In the second scenario, we added a second hypothetical fish farm to the previous simulation map and tested the effects of various parameters (e.g., sea temperature, current speed, current direction, biomass) on the spread of the infectious disease from the source to the destination. Moreover, we simulated the on-site disease dynamics in this scenario. In the third scenario, we simulated real aquaculture systems with three sites, one of them is assumed infected site. We included the topography of the Romsdalsfjord and the aquaculture industry data in the simulations. The purpose of this scenario was to test the effects of various parameters on the spread of an infectious disease from a source to several destinations, to simulate the disease dynamics in the destinations and identify how the destination sites will become source sites as well (nested).

2 Materials and methods

2.1 Materials

The data used in this study can be categorized into four main types: aquaculture, geospatial, oceanographic and disease data. The aquaculture data included the aquaculture site name, location, operator, maximum allowed capacity, type of production and the farm's current production state.

The aquaculture data are available online on the Norwegian Directorate of Fisheries' webpage, http://www.fiskeridir.no/. The geospatial data utilized consists of three-dimensional (3D) maps of the Romsdalsfjord. We obtained 3D maps that included terrain and bathymetry data from the Norwegian Mapping Authority (NMA 2016). The terrain had a resolution of 10 m x 10 m, while the bathymetry had a resolution of 50 m x 50 m. The oceanographic data included data on the sea currents (i.e., speed and direction), sea temperature and salinity. In our simulations, we used the monthly average sea current data from the SINMOD model (MODS 2012) with 800 m resolutions, and we added some noise to emulate the natural variability. The seawater temperature and salinity data are available online on the Institute of Marine Research webpage, http://www.imr.no/en/. Similar to the data on currents, we used the monthly average data and adding some noise. The water temperature was varied in the water column as well (Alaliyat and Yndestad 2015b).

The fish disease data utilized includes fish health, pathogen biology data and disease transmission factors. Wide ranges of pathogens exist, from viruses and bacteria to crustacean parasites. The infection and shedding parameters and the pathogen life span are dependent on the type of pathogen and the type of host. These data are characterized by uncertainty and have, for the most, been derived from laboratory experiments (Salama and Murray 2011; Stene *et al.* 2014). In our simulations, these values varied between different values.

To implement the models using agent-based methods, NetLogo 3D was used. NetLogo is a multi-agent programmable modeling environment. The NetLogo toolkit allows for simulations within a geographic information system environment, and it is easy to include physical and environmental data (Wilensky 1999). We used MATLAB to analyze the simulation results and create figures that were easy to interrupt (MATLAB 2015). We used GlobalMapper (*Bluemarblegeo.com)* to build 3D maps of the Romsdalsfjord by combining the terrain and bathymetry data, and we removed the noise from the data and rescaled the maps to fit in NetLogo.

2.2 Methods

2.2.1 The system model

In this study, we simulated fish disease dynamics and pathogen transmissions in a Norwegian fjord aquaculture system. The aquaculture system has a set of fish farms, a swarm of pathogens and the landscape. This system *S(t)* can be formalized as shown in *equation 1*.

$$S(t) = \{FF(t), P(t), L(t)\} \quad (1)$$

where *FF(t)* is a set of fish farms, *P(t)* is a swarm of pathogens, and *L(t)* is the landscape or the environment where the previous components are located (Yndestad 2010). The purpose of this study has been to investigate how a swarm of pathogen *P(t)* that was produced by a hypothetical, infected fish farm (initial producer farm) will flow with the current and spread in a given landscape *L(t)*. The fish are producer-consumer agents; they produce pathogens, and at the same time they consume pathogens in the fish disease process (Yndestad 2010).

The landscape L(t)

The landscape *L(t)* is divided into four overlaying sub-landscapes and can be formalized as shown in *equation 2*.

$$L(t) = \{L_{tr}(t), L_{cu}(t), L_{sa}(t), L_{tm}(t)\} \quad (2)$$

where $L_{tr}(t)$ represents the terrain, $L_{cu}(t)$ represents the map of the sea currents, $L_{sa}(t)$ represents the map of the sea salinity, and $L_{tm}(t)$ represents the map of the sea temperature.

In this study, the terrain $L_{tr}(t)$ covers part of the Romsdalsfjord area. The terrain is divided into many 3D grids with pixels of 13 × 13 × 13 points. The sea current landscape, $L_{cu}(t)$, represents the speed and direction of the sea currents. The Romsdalsfjord has very complex current patterns (*see figure 2*). The sea currents are driven by a variety of factors that are changing massively in time and space. Therefore, in order to create a model that incorporates some of the variation present in nature, we use normally distributed random numbers for both the current speed and the current direction. The user can set the average current angle and speed at the beginning of the simulation, and then, at each time step, a random deviance is added to these values for current angle and speed. For the current angle, this randomness is characterized by two parameters: a current direction standard deviation, which can be set from 0 to 90 degrees, and a bias term used to offset the direction given by the grid, which can be set between -5 and 5 degrees. For the current speed, this randomness is also characterized by two parameters; a current speed standard deviation, which can be set between 0-0.1 m/s, and a relative speed, which is associated with each grid and depends on the geometry of the fjord (e.g., changes in the width of the fjord, the presence of islands, and peninsulas). The relative speed is the number by which the global current speed is multiplied to obtain the speed for each grid.

The sea salinity, $L_{sa}(t)$, and sea temperature, $L_{tm}(t)$, landscapes are changing in time and space. The chosen temperature profile from January to December at the surface level is $L_{tm}(t)$ = {5.7, 5, 5.1, 6.1, 8.1, 11.3, 12.7, 15.5, 14.0, 11.2, 9.5, 8.0 (°C)} (www.imr.no). The user can set the average water temperature and salinity at the surface level, and then we add some noise to include the variation that is present in nature. The water temperature also varies in the deep levels, as shown in *equation 3*.

$$\mathrm{temp}(\mathrm{x,y,z}) = \mathrm{temp}_0(\mathrm{x,y,z}) - \mathrm{C} * \mathrm{dy}_\mathrm{l} * \mathrm{temp}_0(\mathrm{x,y,z}) \qquad (3)$$

where $temp(x, y, z)$ is the water temperature at *x,y,z* grid; $temp_0(x, y, z)$ is the water temperature at the surface level (*y = 0*); C is a constant; and dy_l is the water depth level.

The fish farm $FF_k(t)$

Each fish farm, $FF_k(t)$, has a swarm of fish agents, *FA(t)*, and is represented by 3 × 3 × 3 grids that are all assumed equal to 3*20 m × 3*20 m × 3*20 m. Additionally, the grid outside the aquaculture sites measures 200 m × 200 m × 200 m. In this study, the farms' positions are set hypothetically in the first two simulation scenarios, while they are based on real aquaculture data in the third scenario. The swarm of fish agents has some social rules that manage the individual movements in the swarm, consumes pathogens and produces pathogens.

The pathogens swarm $P(t)$

The pathogens swarm consists of many individual pathogens, as shown in *equation 4*.

$$P(t) = \{PA_1(t), PA_2(t), \ldots, PA_n(t)\} \qquad (4)$$

where $PA_j(t)$ is the pathogen agent *j*, and *n* is the total number of pathogens at time *t*.

In reality, the swarm of pathogens also has social rules (e.g., move together and align with one another), and the swarm relates to the landscapes to facilitate the individual pathogens' movements (Reynolds 1999). In this study, however, we have ignored the social rules, while, as we will see in the next section, the pathogens' dependence on the landscape steer the movements of individuals.

2.2.2 Agent-based model

The agent-based approach is applied to simulate fish disease dynamics and pathogen transmission in a fjord aquaculture system. *Table I* shows the agent-based model's agents. We have two types of agents; fish and pathogen. Each agent has many attributes and behavioral rules that update the values of these attributes in the context of time and space.

TABLE I: AGENTS IN THE MODEL

Agent type	*Attributes*	*Behavioral rules*
Fish	• Position • Health status • Energy • Vaccinated	• Update position • Update health status • Update energy (resistance factor) • Shed pathogens
Pathogen	• Position • Life span • Ability	• Update position • Update life span • Update ability

We designed our model in a rectangular shape with 501 × 201 × 3 patches (a patch is a grid in NetLogo). Each fish farm has a maximum population of 1000 fish; however, you would expect to see approximately 1000 times more fish in an actual fish farm of this size. This simplification was made to save computer resources while running the model. A tick is the time step in the model, and it can represent 10 minutes, one hour, or one day (it can be selected by the user, *time-step*).

The fish agent FA(t)

The fish are located in the farms, and each fish farm $FF_k(t)$ has a swarm of fish that is composed of many fish agents, *FA(t)*, as is shown in *equation 5*.

$$FF_k(t) = \{FA_1(t), FA_2(t),\ldots, FA_n(t)\} \quad (5)$$

Fish agent $FA_i(t)$ has several attributes and behavioral rules that update these attributes (see *Table I*). In this context, we are interested in the position, energy, and health status attributes, as well as the behavioral rules that governs the values taken by these attributes and that produce pathogens.

Fish swimming rules: Fish agents swim within cages, and since we use a large time step in our simulations in this study (i.e., 10 minutes or one hour), the fish's positions are updated randomly at each time step, as shown in *equation 6*.

$$\overrightarrow{FA_\iota.p(t)} = \overrightarrow{R_\iota} * \left(\frac{max_{x,y,z} - min_{x,y,z}}{2}\right) + \overrightarrow{FF_k(t)} \quad (6)$$

where $\overrightarrow{FA_\iota.p(t)}$ is the fish position vector, $\overrightarrow{R_\iota}$ is a unit random vector in 3D, $(max_{x,y,z} - min_{x,y,z})$ is the fish farm dimensions, and $\overrightarrow{FF_k(t)}$ is the farm position vector in the simulation space. Fish can swim in different formations, and they can socialize to form a school. We have previously investigated the effects of different swimming behaviors on infectious fish diseases (Alaliyat and Yndestad 2015b). Since, in this study, we used a large time step, we have chosen to ignore the social rules, and assumes that the fish is distributed randomly in the fish farm.

Fish energy attribute: Each fish has an epidemic resistance factor, which is a value between 0 and 1. We assign reference values of 0.8 with some noise, as shown in *equation 7.*

$$RF_{\ i} = RF_{\ ref} \pm R_i * N_{rf} \quad (7)$$

where $RF_{\ i}$ is the resistance factor of fish i, $RF_{\ ref}$ is the reference resistance factor value that can be set by the user, R is a random number in the range of [0,1], and N_{rf} is the noise value.

Infection rules: Fish agents are categorized into four main health states as in the SEIR (susceptible, exposed, infected and removed) model (Bjørnstad 2005). In the following text, we will explain how the fish health state of individuals will be updated over time. A susceptible fish becomes infected if there are many pathogens around it, the pathogens have a good ability to infect, and the fish has a week RF, as determined by the *Algorithm I* procedure. Salama tried to quantify the infection probability, but his results depended on laboratory data (Salama and Murray 2011). In our model, this probability can vary between different values, and it is also related to the densities of fish and pathogens.

Algorithm I: *infection rules*

1: **For each** susceptible fish agent i…**then**
2: **If** $(RF_{\ i} * \sum_{p_j\, in\, r}(p_j * ab_j) \geq T_0)$,
Where
$RF_{\ i}$ is a fish i resistance factor, p_j is any pathogen j in r distance from fish i, ab_j is the infection ability of pathogen j, and T_0 is a selected threshold.
3: get infected
4: **End if**

```
End for each
```

Once the fish has been infected, it will leave the susceptible category and enter the exposed category. All fish agents transfer between the four health states. Therefore, the population of agents is divided into four groups or compartments consisting of individuals that are susceptible, exposed, infected and removed. The fish agents are heterogeneous, and each agent has it´s own individual discrete SEIR model. The contact rate in the SEIR model is equivalent to the individual fish infection rules in ABM. The fish agent health state in ABM is dynamically updated. The number of fish with the same health state provides the number of fish agents in the four groups.

The process for updating the fish health states at each time step is achieved by applying the health-state update method, shown in *Algorithm II*.

Algorithm II: *Fish health-state updating*

```
For each fish agent…then
  Check health status
  If fish is susceptible then
    If there are a number of pathogens around the fish then
      1. Change fish state to exposed
      2. Die by normal death rate
    Else
      Die by normal death rate
    End If
  End If
  If fish is exposed then
    If fish passed exposed period then
      1. Change fish state to infected
      2. Die by illness death rate
    Else
      Die by normal death rate
    End If
  End If
  If fish is infected then
    Produce a pathogen by a given probability "shedding rate"
    If fish passed infected period then
      1. Change fish state to recovered
      2. Die by normal death rate
    Else
      Die by illness death rate
    End If
  End If
  If fish is recovered then
    If fish passed immune period then
      1. Change fish state to susceptible
      2. Die by normal death rate
    Else
      Die by normal death rate
    End If
  End If
End for each
```

Pathogens production process: Each time step the infected fish, i, may shed a pathogen, j, at a certain probability where that fish is located. Different sources refer to different units, and values range from $10^{6.5}$ PFU/fish/h (PFU=plaque forming units) (Gregory 2008), 10^5-10^8 CFU/fish/h (CFU=colony forming units) (Rose *et al.* 1989) and $6.8*10^3$ $TCID_{50}$ /ml/ kg fish/ h/ (maximum rates) ($TCID_{50}$=the amount of virus required to kill 50% of infected hosts) (Urquhart *et al.* 2008). The units are not single pathogens; rather, they are units that are measurable in the lab. Since the numbers are very high and computationally difficult to implement in the model, we set a probability between 0-1 (adjustable) that an infected fish sheds a pathogen, but this pathogen represents a large number of pathogens, i.e. effectively a rate of pathogens per time unit.

The pathogen agent PA(t)

The pathogens swarm *P(t)* consists of many individual pathogens, as shown in *equation 8*.

$$P(t) = \{PA_1(t), PA_2(t),\ldots, PA_n(t)\} \tag{8}$$

where $PA_j(t)$ is the pathogen agent *j*, and *n* is the total number of pathogens at time *t*.

The pathogen agent $PA_j(t)$ has three main attributes (see *Table I*): position in the space, ability to infect fish, and life span.

Moving rules: The pathogens are moved by sea currents. Each pathogen moves based on the current speed and direction, which is based on the location of the pathogen at the start of each time step. Pathogens inherit the current direction of the place they are presently located, and by moving to a new place, they inherit the direction of that new place. When moving, the pathogen might hit dry land. In that case, the pathogen is removed from the model (dies).

The pathogen *j* updates its position, as shown in *equations 9 & 10*.

$$\overrightarrow{PA_j.p(t+\Delta t)} = \overrightarrow{PA_j.p(t)} + \overrightarrow{v(t+\Delta t)} \tag{9}$$

$$\left\|\overrightarrow{v(t+\Delta t)}\right\| = C_{sr} * R_n(C_s, std) \tag{10}$$

where $\overrightarrow{PA_j.p(t+\Delta t)}$ is the new pathogen agent *j* position, $\overrightarrow{PA_j.p(t)}$ is the current pathogen agent *j* position, $\vec{v}$ is the pathogen velocity, *t* is the time step, $\left\|\overrightarrow{v(t+\Delta t)}\right\|$ is the magnitude of the velocity, C_{sr} is the relative current speed that is inherited from the grid where the pathogen j is, and R_n is a normally distributed random floating point with a mean of C_s (average current speed in this area) and a standard deviation std.

The velocity direction is related to the pathogen's orientation. The pathogen's orientation is defined by two variables: heading ($PA_j(t)_{hed}$) and pitch ($PA_j(t)_{pit}$). Heading is the angle between the forward vector of the pathogen projected onto the horizontal plane and the vector [0 1 0], and pitch is the angle between the forward vector of the pathogen and the horizontal plane. We calculated these variables using *equations 11 & 12*.

$$PA_j(t)_{hed} = C_d + R_n(C_{bias}, std) \tag{11}$$

$$PA_j(t)_{pit} = pit_{in} - R_j * pit_v \tag{12}$$

where C_d is the currents' direction angle, R_n is a normally distributed random floating point with a mean of C_{bias} (current heading bias variable) and a standard deviation std, pit_{in} is the initial pitch value, R_j is a random number in the range of [0,1], and pit_v is the pitch value.

Life cycle: Pathogen life span is a function of seawater condition (temperature and salinity). Salama estimated the life span for infectious salmon anemia virus (ISAV), infectious pancreatic necrosis virus (IPNV) and salmonid alphavirus (SAV) to be between 8.33 and 62.5 hours (Salama and Murray 2011). The life span's relation to the sea temperature can be modeled using the following equation (Stene *et al.* 2014).

$$PA_j(t)_{LC} = a * \exp(-x / b) \quad (13)$$

where x is the water temperature, a is the pathogen life span at a water temperature of 0°C, and b is the decay rate.

Ability to infect: Each pathogen has an attribute that represents the ability to infect, that takes values between 0 and 1. We use 0.8 as the initial value and added some noise, as is shown in *equation 14*.

$$PA_j(t)_{ab} = PA_j(t)_{ab0} \pm R_j * N_{ab} \quad (14)$$

where $PA_j(t)_{ab}$ is the ability of pathogen j to infect, $PA_j(t)_{ab0}$ is the initial ability value that can be set by the user, R_j is a random number in the range of [0,1], and N_{ab} is the noise value.

Once the pathogens arrive at the neighboring sites (i.e., susceptible farms), they will try to infect the susceptible healthy individual fish in that farm. We apply the same infection rules as in *Algorithms I & II*.

The density of pathogens is directly related to the risk value in both space and time. A disease outbreak occurs only if there is a high density of pathogens and a high density of fish, as indicated by the following equation:

$$Risk\ (t,s) = C * I_v(t,s) * I_f(t,s) \quad (15)$$

where *Risk (t,s)* is the infection risk value in time and space, $I_v(t,s)$ is the pathogen density at time t and in space s, $I_f(t,s)$ is fish density at time t and space s, and C is a constant.

2.2.3 Investigations

Fish disease dynamics and pathogen transmission depend on many different factors, such as fish density, farm location, fish and pathogen conditions and environmental conditions. In this study, we have built an agent-based model and simulated a variety of scenarios to investigate the effects of different combinations of parameter values on the fish disease dynamics. First, we investigated the minimum safe distance from the infected site under a variety of environmental conditions. Then, we investigated the effects of fish density, sea currents and temperature on the spread of an infectious disease from a source (producer) facility to a destination (consumer) facility, and we simulated the disease dynamics across time. Finally, we built scenarios based on empirical data to test the effects of the fjord's topography and the domino effect (producer-consumer facilities) on the spread of the infectious disease. *Table II* shows the model parameters that the user of our model may change.

TABLE II: MODEL PARAMETERS

Parameter	Min value	Max value	Default value
Fish number	*1*	*1000*	*100*
Shedding rate (%)	*0*	*100*	*50*
Infection period (days)	*0*	*100*	*2*
Immune period (days)	*0*	*100*	*5*
Infectious radius (patches)	*0*	*20*	*0.5*
Initial infected (%)	*0*	*100*	*5*
Prior immunity (%)	*0*	*100*	*0*
Mortality (%)	*0*	*100*	*3*
Mortality_normal (%)	*0*	*100*	*0.00001*
Pathogen-ability	*0*	*1*	*0.8*

RF	*0*	*1*	*0.8*
Weight (kg)	*0*	*10*	*4*
Current speed (m/s)	*0*	*1*	*0.15*
Current speed std.	*0*	*0.1*	*0.03*
Current heading (degree)	*0*	*360*	*90*
Current heading bias (degree)	*-5*	*5*	*0*
Current heading std.	*0*	*90*	*30*
Sea temperature (ºC)	*0*	*20*	*10*
Vaccinated			*Off**
Time step			*10 min**

*Parameters that can select between many values or be turned on/off.

2.2.4 Verification and validation

In general, and in aquaculture industry specifically, it is often very difficult to validate epidemiological simulation models due to the lack of reliable field data. The logical choice of validation techniques in such situations is to use cross-validation (i.e. to run a validated model for some simplified scenarios where the results are known or obvious) or to compare the model output with other available models that have been validated (so-called model alignment) (Chen *et al.* 2004).

We have done both (Alaliyat and Yndestad 2015c): We ran our model for a simple scenario where the results were as expected, and we aligned it with well-known models, such as the SIR model (Skvortsov *et al.* 2007). Internal validation or verification is very important also in ABMs. When the model is implemented by using NetLogo tool, the model must be verified by investigating whether the model behaves as expected. The purpose of the verification process is to build confidence in the behavioral characteristics that we assign to the agents and their interactions. We have tested the model under extreme conditions where the outcome is easily predictable to assess the validity of the agent descriptions used to ensure model consistency (avoid logical errors) as well as model coherence.

3 Results

3.1 Infection risk in an open area

In this experiment we designed a simulation space to identify the risk of becoming infected in the vicinity of an infected aquaculture site: We assumed that the risk of a fish becoming infected is related to the concentration of pathogens in the space. The individual fish becomes infected by the procedure described in *Algorithm I*, so that the risk of any aquaculture site becoming infected in the area in the vicinity of the infected farm depends on the densities of the fish and pathogens at this site, as shown in *equation 15*. *Table III* shows the selected parameters from *table II* to which we assigned the values listed during the simulation experiment.

TABLE III: INFECTION RISK IN AN OPEN AREA EXPERIMENT

Parameters of Susceptible farm	**Values**
Fish number	*100, 250,500,750,1000*
Current speed (m/s)	*0.05, 0.1, 0.15, 0.2, 0.25*
Sea temperature (ºC)	*5, 7.5, 10, 12.5, 15*

Figure 3 shows the farthest distance that live pathogens can reach alive (i.e. Risk Distance) based on the sea currents and water temperature during a simulation time of 8 days (cold water favors survival). The infection risk, which results from the presence of pathogens in a space unit (I_v), is a function of current speed and water temperature. This risk decreases as the distance increases from the infected site.

Figure 3 allows us to estimate the threshold (D_T) (between blue and other colors) of the farthest distance (Far_d $(temp, Cs)$) that the pathogens can spread; under normal sea-water and currents conditions. This threshold can change significantly depending on the current speed and the sea-water temperature. In this case, the threshold is determined by a current speed of $15\ cm/s$ and a sea-water temperature of 10°.

$$Far_d(temp, Cs) > D_T \quad \text{if} \quad temp < 10^{\circ} \quad \text{and} \quad Cs > 15\ cm/s \tag{16}$$

where $Far_d(temp, Cs)$ is the maximum distance where pathogens can travel alive, D_T is a derived threshold from *figure 3*, $temp$ is a sea-water temperature, and Cs is the current speed.

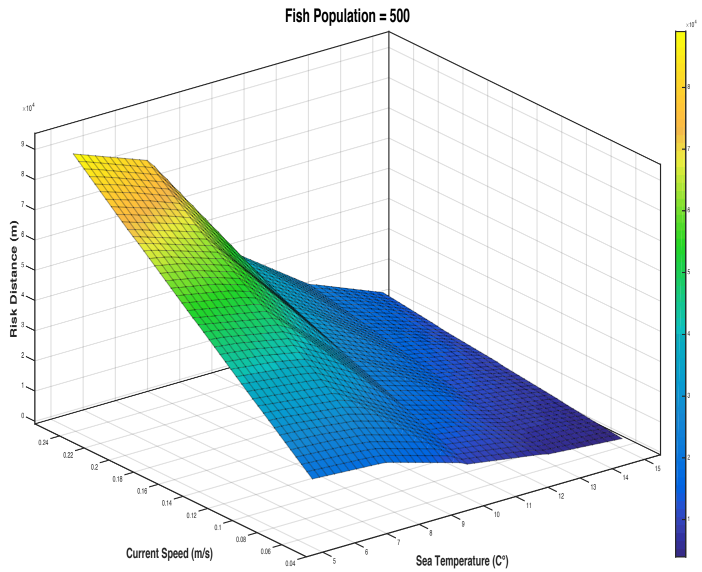


Figure 3: Risk distance from the infected site.

The results (see *figure 3*) show that the farthest distance that the pathogens spread to does not exceed 12 km (D_T) given the current speed and water temperature threshold. This distance could be considerably larger, however, if the current speed was higher and/or if the water was colder.

Using ABM, we are able to track the pathogens in time and space. That enables us to identify the spatial characteristics of the spread of a disease. *Figure 4* shows the pathogen concentration (density) in each spatial cell resulting from running the simulation for a period of time. Thus, if the susceptible fish farm is located in the more risky (more red) area, then the greater is the probability that a fish in the farm becomes infected.

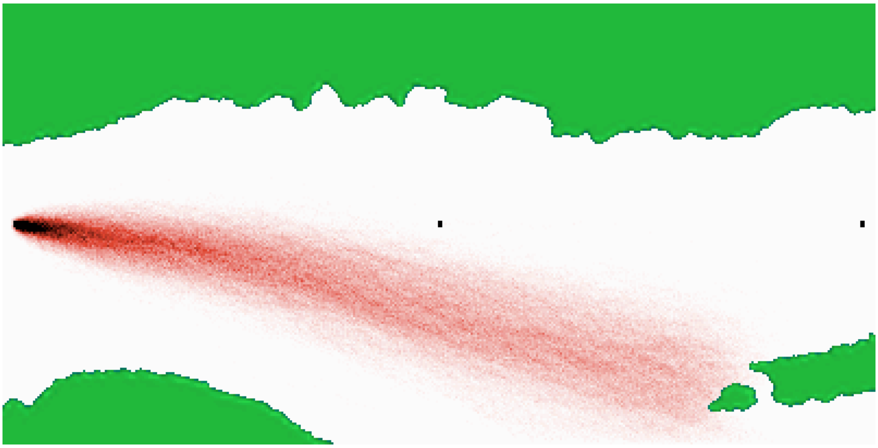


Figure 4: Pathogen concentration in two dimensions (2-D) after a period of time.

The pathogen density as described in *equation 15* is dependent on four main variables: water temperature, current speed, distance from the infected site, and fish density at the infected site. From our simulation results, the pathogen density I_v in cell (x, y, z) after the period of time *t* can be modeled using the following exponential decay equation:

$$I_v(x, y, z, t) = \mathrm{a_0} * \exp\left(-\frac{(\mathrm{temp(x,y,z,t)})}{\mathrm{b_0}}\right) * \mathrm{Cs(x, y, z, t)} * I_f / \, dis(\mathrm{x, y, z, t}) \qquad (17)$$

where $\mathrm{temp(x, y, z, t)}$ is the water temperature, $\mathrm{Cs(x, y, z, t)}$ is the current speed, $dis(\mathrm{x, y, z, t})$ is the distance from the infected site, $\mathrm{a_0}$ is the pathogen density at the infected site, $\mathrm{b_0}$ is the decay rate, and I_f is the fish density at the infected site. We have derived the previous equation by estimating the relation between each input variable (i.e. water temperature) and the simulating results (pathogen density), then we combined these relations in one equation and validated this equation.

3.2 Infection risk between two fish farms in fjord area

In the next scenario, we extended the previous scenario by locating a susceptible fish farm at the edge of the risk area associated with the infected farm, i.e. at a distance, $dis = 9.6\ km < D_T$ from that farm. We simulated the fish disease dynamics in the infected farm that constituted the source of the pathogens to be transferred to the susceptible farm. We designed the simulation space so as to test the effects of changes in parameter values on the spread of the infectious disease from the source to the destination, and then we simulated the disease dynamics in the susceptible farm as well. We used the same scaling for time and space as in the previous scenario, and we used the default values shown in *Table II* for this model. *Table IV* shows the parameter values in *Table II* that we varied in this simulation experiment.

TABLE IV: INFECTION RISK BETWEEN TWO FISH FARMS

Parameter	Values
Fish producer-farm number	*100, 1000*
Fish consumer-farm number	*100,1000*
Current speed (m/s)	*0.05, 0.25*
Sea temperature (ºC)	*5,15*

Figure 5 shows the percentage of the infected individuals (prevalence) in the two fish farms (infected and susceptible) under a variety of current speeds, sea temperatures and fish population parameter values.

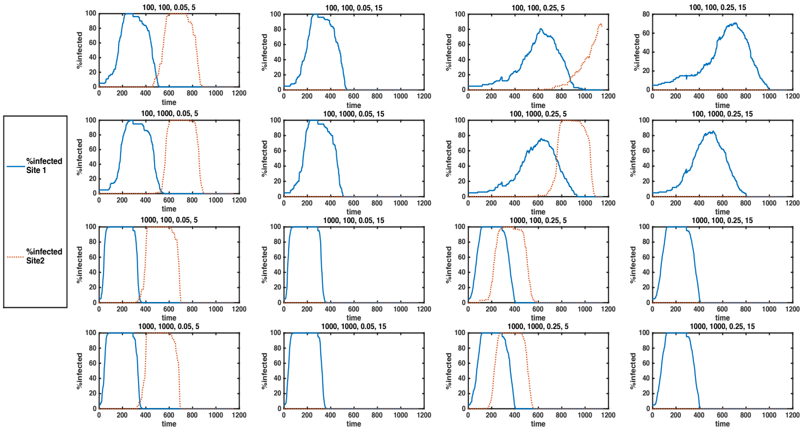


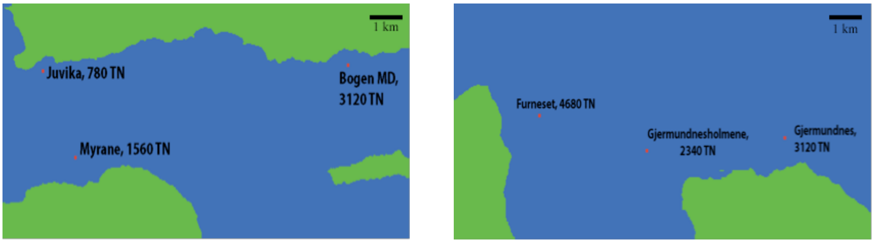
Figure 5: Percentage of infected fish at site one, an infected farm (blue), and site two, a susceptible farm (red), as a result of water temperatures, current speeds and fish population values.

With regard to the infection risk equation (*15*), the infection risk at cell (*x,y,z*) must be greater than a risk threshold R_0 that can be derived from the simulation results, in order for an infection to occur in this cell. The $I_v(x,y,z,t)$ in *equation 17* is dependent only on sea-water temperature, current speed and producer farm pathogen density, since the distance is fixed at 9.6 km. The results show that the susceptible fish farm, located at (9.6 km, 0, 0), will become infected only if the sea-water temperature is low ($< 5^{\circ}$); if this is the case, then all fish become infected at the site. In the case when the water temperature is 15°, most of the pathogens die before arriving at the susceptible fish farm, so the pathogens will not infect that site. The fish densities in both the infected and susceptible farms play major roles, as described in *equations 15 and 17*, and shown in *figure 5*. The disease is spreading faster when the population is higher as shown in the lower two rows in *figure 5*.

The spread of a disease inside a facility is faster when the current speed is low, as we see illustrated by the infected farm in the left two columns of *figure 5*. The infection at the susceptible fish farm starts only after the arrival of a sufficient number of pathogens at the site (*equation 17*); our results show that this happens after an average of two days across the simulation experiments in cases of higher fish density (e.g. 1000 individuals) in the susceptible farm, and the disease will spread to most of the individuals in the susceptible farm in approximately the same amount of time. In a case of lower fish density (e.g. 100 individuals), this time is approximately doubled.

3.3 Infection risk in a multi-farm system in fjord area (domino-effect)

In this scenario, we designed the simulation space so as to test the effects of a number of parameter values on the spread of the infectious disease across many fish farms, including the disease dynamics in each of them. In this scenario, the farms may, in principle, take the role as infected and susceptible and do so simultaneously; any farm can simultaneously shed pathogens to the others and receive pathogens from the others. We used the same scaling for time and space as in the previous scenarios, and we used the default values shown in *Table II* in the model. *Figure 6* shows the experimental setup of the simulation. We have run two different scenarios in the Romsdalsfjord. We have selected these areas because they are different in terms of their geospatial and aquaculture nature.



(a) (b)

Figure 6: Aquaculture system in part of the Romsdalsfjord (TN = tons): (a) Midsund area. (b) Vestness area.

Scenario A (Midsund):

In this scenario, we included three farms (see *figure 6(a)*), and we used the average current speed and direction recorded in May 2008. We scaled the fish population, so that each fish in reality represents 15 tons of fish. In *Table V* we summarize the parameter values applied. These facilities are located within D_T, - less than 12 km apart. We assume that 5% of the fish population in the Bogen facility is initially infected. *Figure 7(left hand side) s*hows the disease dynamics in each site at Midsund.

TABLE V: SCENARIO A PARAMETERS: MIDSUND AREA

Parameter	**Bogen MD**	**Juvika**	**Myrane**
Fish number	*400*	*100*	*200*
Current speed (m)	*0.15*	*0.15*	*0.15*
Sea temperature (°C)	*8*	*8*	*8*
Current direction (degree)	*270*	*270*	*270*

Scenario B (Vestness):

In this scenario, we included three farms (see *figure 6(b)*), and we used the average current speed and direction recorded in April 2008. Again, each fish represents 15 tons of fish in reality. In *Table VI* we summarize the parameter values applied. These facilities are also located within D_T, less than 12 km apart. We assume that 5% of the fish population in Gjermundnes facility is initially infected. *Figure 7(right hand side)* shows the disease dynamics in each site at Vestness.

TABLE VI: SCENARIO B PARAMETERS: VESTNESS AREA

Parameter	**Gjermundnes**	**Gjermundnesholmene**	**Furneset**
Fish number	*150*	*100*	*200*
Current speed (m)	*0.15*	*0.15*	*0.15*
Sea temperature (°C)	*7*	*7*	*7*
Current direction (degree)	*270*	*270*	*270*

The simulation results from both scenarios, presented in figure 7, show the effects of current patterns and the geometry of the fjord on the spread of fish disease in parts of Romsdalsfjord, Midsund and Vestnes. In scenario A, the Myrane facility did not get infected because it was not located along the path of the sea currents that passed the infected sites during this period, - even though it was located within the risk distance (D_T). As a result, the $I_v(x,y,z,t)$ is very low, so the infection risk (*equation 15*) for Myrane is less than R_0. While Juvika got infected after almost three days. However, in scenario B, the Gjermundnesholmene facility became infected and produced pathogens that infected the Furneset facility, which is located along the path of the currents that pass Gjermundnesholmene. Consequently, the $I_v(x,y,z,t)$ is sufficiently high to cause an infection risk (*equation 15*) above the threshold R_0. Thus the infection took place.

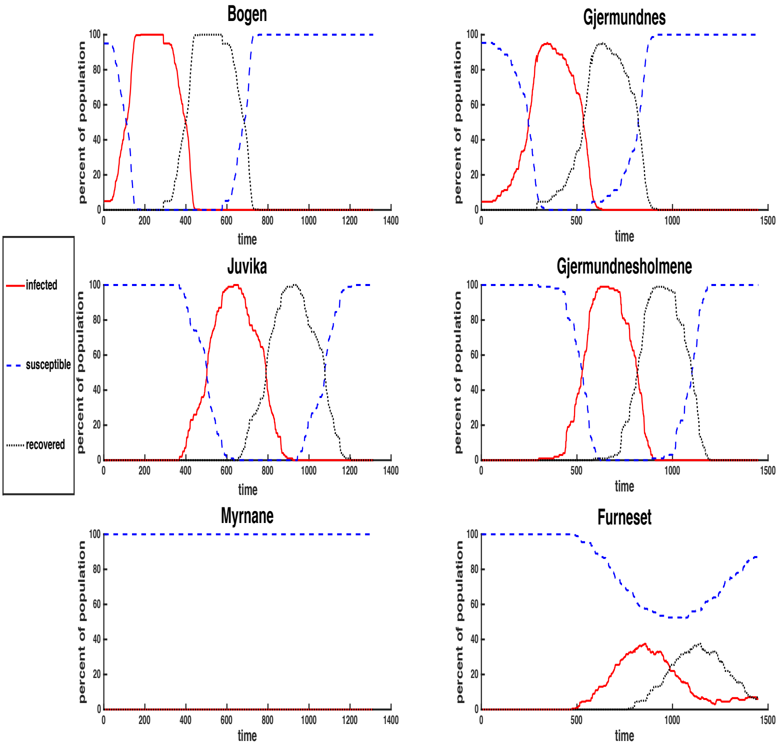


Figure 7: Epidemic curves (results after 10 days).

The infection of the Juvika and Gjermundnesholmene farms started after a sufficient amount of pathogens had arrived at each location. This took place after an average of four days. The Furneset facility was infected after 6 days because the distances from the two infected source sites were longer (see *equation 17*).

The simulation results show that the sea current patterns play major roles in the spread of fish disease in Norwegian fjords. The pathogens are moved by sea currents, so if the fish farms are not in the path of the sea currents carrying pathogens from the infected sites, or they are located sufficiently far apart (beyond D_T), then the chance of infection is very low (as in the Myrnane case).

4 Discussion

4.1 Infection risk in an open area

It is very important to evaluate the infection risk in space and time when we want to assess the probability that a fish farm could act as the origin of an epidemic or as an intermediator.. This evaluation is particularly important when we want to build and locate a new fish farm (Taranger *et al.* 2015) so as to prevent the spread of fish diseases in an aquaculture system. E.g. how will the surrounding area be affected if the fish in this new farm become infected? The first simulation scenario helps answer this question by exhibiting the risk values in space and time in the vicinity of such a new, hypothetically infected farm.

In this scenario, we studied the risk resulting from the pathogens that are predominently relocated by sea currents (Murray and Peeler 2005). The pathogens could, however, also move by way of fish boats or any other ships, or by way of escaped, infected fish. In our simulations, we focused on movement caused by the sea currents and sink effect. It is, however, easy to adjust our model to include other such factors.

Sea current speed and direction may vary significantly in the time and space domain considered, and we can expect values to remain steady for only a few days -or even less (MODS 2012). In reality, we utilized empirical material reflecting average values, limited value ranges under which our model ran, and simulated the worst-case scenarios when the infection pressures are at most. The results demonstrate how the risk patterns are determined by the sea current patterns, - affected by the geometry of the fjord (see *figure 4*).

The pathogen's life span is associated with the sea temperature and salinity (Groner *et al.* 2016) and is influenced by significant changes in these values (Stene *et al.* 2014). In our model, it is easy to include such changes by way of modifications in parameter values.

The sea currents and sea-water temperature impact the distance that the pathogens can travel (spread) and thus the associated risk. A high water temperature decreases the distance since the pathogen's life span is shorter in hot than in cold water, while strong currents can move the pathogens farther away from its point of origin. The results demonstrate the current speed and water temperature thresholds (15 m/s and 10 degrees, respectively) at which the risk distance increased considerably ($> D_T = 12\,k$).

As shown in *equation 15*, the infection risk in space and time is dependent on the densities of the pathogens and fish. In this scenario, we investigated the factors that affect the pathogen density in each space cell in the vicinity of the infected site over a period of time. We derived from our theory and discussion *equation 17*, which shows the effects of water temperature, current speed, distance from the infected site, and fish density at the infected site on the pathogen's density. The pathogen's density exponentially decreases near the infected site as the water temperature increases. Moreover, the pathogen's density decreases as the distance from the infected site increases. The pathogen life span exponentially decreases as the water temperature increases. Conversely, if the water gets colder, then the pathogens spread to a larger area . The pathogens spread more with high current speeds. The pathogen density at a fixed position in the vicinity of the infected site $I_v(x, y, z, t)$ is dependent only on water temperature, current speed and fish density at the infected site.

Building risk maps around the fish farm facilities in different environmental conditions helps inform management of the fish industry and helps prevent the spread of fish diseases that cause serious losses in Norwegian aquaculture.

4.2 Infection risk between two fish farms in a fjord area

If we assume there is a disease outbreak in an aquaculture facility and there is another aquaculture facility located within the infection risk of the infected fish farm (<12 km), then what will happen to the susceptible fish farm that is located in the risk area in the course of time? To answer this question, we simulated the fish disease dynamics in an aquaculture system that consisted of two fish farms located within a risk distance (9.6 km). We simulated the disease dynamics in the infected farm, the pathogen transmission time from the source to the destination, and the disease dynamics in susceptible farm.

The fish disease dynamics in fish populations are affected by many key factors, such as fish density, fish swimming behavior, water temperature, sea currents and other environmental factors (Alaliyat and Yndestad 2015b). The infection process occurs only when there is a sufficient number of pathogens in the vicinity of the susceptible fish (see *Algorithm I*). The fish disease dynamics in a single fish population is faster with higher fish densities and lower sea current speeds (Alaliyat and Yndestad 2015a). The pathogens are moved by sea currents, so with high-speed sea currents, the pathogens spread across larger distances and move faster to nearby sites. The number of pathogens released from the infected site increases as the fish population increases (Alaliyat and Yndestad 2015a).

Once the pathogens arrive at a susceptible farm, the infection process will start as soon as a sufficient number of pathogens arrive the susceptible fish (*see Algorithm I*). The rules of disease transmission that applies to an infected farm, also applies to the susceptible farm.

The results demonstrate that a susceptible fish farm, located 9.6 km from the infected farm, will become infected after two to four days, depending on the fish density, provided the average sea-water temperature is 5°. The pathogens need less than 12 hours to cross the 9.6 km distance from the infected site when the current speed is 0.25 m/s. Yet, based on the diffusion factor that spread the pathogens to a wider area, the probability of reaching the susceptible site is considerably reduced in only 12 hours. In addition, even if the pathogens arrive at the susceptible farm, the pathogen density and the fish density in that farm will have to be sufficiently high to initiate an infection (*equation 15*).

4.3 Infection risk in a multi-farm system in fjord area (domino-effect)

It is important to test our agent-based model on real case studies with more than two fish sites, to simulate cases where the fish farms are infected and susceptible sites, and to include the effects of the topography of the fjord on the simulated fish disease dynamics. In these scenarios, we hypothetically assume that there is an infection in the Romsdalsfjord during the particular period of the year. The Romsdalsfjord is an area that hosts many fish farms that are located close to each other (*Figure 1*), and the dynamics of the sea currents in the fjord exhibit a very complex pattern (*Figure 2*).

Our results show the effects of the topography of the Romsdalsfjord on the spread of fish disease. In scenario A, the Myrane facility was not infected even though it was close to the infected site Bogen (the distance between them is 8.4 km, which is less than 12 km). This is because it was not located along the path of the sea currents that passed the infected sites during this period. However, in scenario B, the Gjermundnesholmene facility was infected and produced pathogens that, subsequently, infected the Furneset facility, located along the path of the sea currents that passed Gjermundnesholmene. In this scenario, the Gjermundnesholmene facility was initially a susciptble site, and then an infected site that shed pathogens.These simulation experiments support the idea that vicinity is a not a sufficient cause for infection; in fact, the current patterns are just as important (Stene *et al.* 2014). The pathogens need a transport vehicle to bring them from the infected site to the susceptible farm.

We used monthly average sea current speed and direction in the Romsdalsfjord. Note that the currents in the fjords change significantly due to wind and other factors. E.g. the current direction in the Romsdalsfjord changes in the spring as a result of the melting snow causing fresh water to be transported along the fjord towards the sea. Tides can cause the water to move back and forth within a range of a few kilometers, and this supports the results from other studies that have demonstrated the impact of the close sea distance between the farms (Aldrin *et al.* 2010; Tavornpanich *et al.* 2012).

There are some limitations in applying the model to real cases in order to analyze the risk and provide advice to the fish industry. Scaling the model in space and time is one of these limitations. We introduced a portion of the individuals (fish and pathogens) in our simulation, since representing a huge number of agents is computationally very demanding. This, however, limits the contact between agents. In addition, there are several factors of uncertainty pertaining to the process of transmitting illness between fish. We are not in the possession of data on this process, and the available data are based on the lab experiments that have limited relevance in empirical settings (Salama and Murray 2011).

4.4 Using agent-based methods

Pathogen transmission within and between aquaculture farms is dependent on a variety of interrelated biological, physical and environmental factors, such as fish density, shedding rate, infection radius, current speed, current direction, pathogen life span, seawater temperature, and seawater salinity. ABM simulates the overall dynamics based on how individuals (fish and pathogens) interact and adapt to such factors. ABM provides insights into the underlying structural causes of emerging dynamic phenomena resulting from the interactions between individuals. Models developed previously have predominantly been relying on differential equations in describing the overall population dynamics of fish diseases (e.g., Murray 2009; Green 2010) or they have been hydrodynamic models combined with particle tracking and statistical analyses (MODS 2012, Stene *et al.* 2014). Mathematical models, such as the SIR model, do not cover the individual variety of the biological and physical characteristics of fish as well as other animals; fish vary in their resistance to pathogens, and the pathogens themselves vary in their ability to infect fish. In non-ABM models this variability in fish and pathogens is being ignored. The analysis is based on the assumption that the populations are homogenous. By using ABM, we are able to address specific spatial aspects of the spread of infections and address the stochastic nature of the infection process of fish diseases.

ABM provides flexibility in modeling, implying that additional complexity may be introduced to form the basis for simulation-based analyzes. Agents may be added to or removed from the model, and the attributes and behavioral rules can be modified as well. For an example, the swimming rules have been included in previous model to create new ones (Alaliyat and Yndestad 2015b).

Another reason for applying ABM is the lack of empirical data we experience regarding fish disease transmission. In ABMs, the parameters characterizing disease transmission, such as fish infection rules and the shedding rates, may easily be varied, to assess how sensitive the results are to the assumptions we introduce in the models. We may assess sensitivities at a high level of resolution rather than merely address the sensitivity aggregate characteristics such as the contact rate in an SIR model.

There are limitations in an ABM approach to the modeling and simulation of fish disease dynamics. Typically the magnitude of the population (fish and pathogens) is too large for a full-scale simulation, even on massive computers. By scaling down, the contact frequency may be affected and suffer from not being sufficiently representative. Moreover, as reliable data on pathogen are hard to come by, the pathogen model component is based on a theoretical foundation. The validation of dynamic fish disease models is inherently challenging, not the least because of the lack of reliable empirical data.

Previous models have typically focused on the analysis of historical data to support future predictions in similar cases (Stene 2013). The pathogen transmission and fish disease dynamics vary significantly, depending on a variety of factors such as sea currents and water temperature. In a model such variations may be included as a basis for sensitivity analyses. The results are generally applicable, but may not be used for point prediction due to the uncertainties characterizing the underlying structural assumptions. The results of the sensitivity analyses will guide us in our evaluation of the validity of any prediction made based on the model, - i.e. tell us whether we can trust the predictions produced by such a model.

ABMs are stochastic models that can capture the randomness in natural systems. Therefore, it may well be advantageous to apply ABM in the modeling and simulation of fish infectious disease dynamics compared to the application of simple deterministic models (such as the SIR model), often characterized by static estimates of parameters that, in reality, vary across the populations and are sensitive to the varying, environmental conditions.

5 Conclusions and future work

The aquaculture industry is one of the main industries in Norway. Emergent diseases continue to pose a serious challenge to the industry and constrains its development. Predicting fish disease dynamics is important when preventing and combating fish diseases. The results of such predictions may facilitate the management process and inform the aquaculture industry, and it also helps combat the spread of diseases by applying actions to stop the spread of the disease, such as through vaccinations or removal of the pathogens. Fish diseases typically cause large economic losses to the aquaculture industry and might threaten wild populations of species as well. To manage our natural resources, such as fish, in a sustainable way, we rely on analyses based on validated models in which we have confidence.

Models, such as the SIR model, predict the spread of fish diseases based on the assumption that the fish population is homogeneous, and focus on the population as a whole. In this paper, we assume that the fish and pathogens are heterogeneous. To do so, we applied an agent-based approach in our modeling of the dynamics of fish diseases within and between aquaculture facilities in a Norwegian fjord. Using this approach, we consider the interaction of each individual with others and with the natural environment in the context of space and time. The agents in our model are fish and pathogens.

We predict the dynamics of the pathogen transmission patterns so to identify the infection risk in a space-time domain. Our results show (see *figure 4*) that the pathogen density decreases as the distance from the infected site increases. Pathogen density at a fixed position around the infected site decreases exponentially by increasing sea-water temperature, while pathogen density increases when current speed and fish density at the infected site increase. Because the pathogens are predominantly relocated by sea currents, such currents play a major rule in the pathogen transmission process, The infection risk is a function of fish and pathogen density, and that risk increases when these densities increase.

Adding fish swimming behavior or additional social behavior rules to the swarm of pathogens constitutes a potential extension of the model. Also, we may include additional key parameters associated with the fish industry process (i.e., stocking and harvesting process) or its interaction with the outside environment, including escaped fish, wild fish, feed, and the working environment.

ABMs are inherently flexible and represent the systems structure at the level of individuals (high resolution). The interaction unfolding between individuals may be analyzed in the context of a wide variety of scenarios, in particular pertaining to the environment in which the interaction takes place. Fish infectious disease dynamics is a complex process that results from the extensive network of interactions existing between large variety of characteristics of fish, pathogens and seawater. The high resolution facilitated by an agent-based approach offers an opportunity to describe the system in relatively realistic terms, - provided we know the processes taking place at that detailed level and the variety in the parameter values governing these processes.

NetLogo is the software applied in this work. It offers a simple user interface that facilitates changes in parameter values and immediate responses to such changes. This way, the models developed may easily be shared among a variety of stakeholders that may benefit from experimentation, simulation and analysis of the results.

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Study III-1

Optimisation of Boids Swarm Model Based on Genetic Algorithm and Particle Swarm Optimisation Algorithm (Comparative Study)

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Flocking behaviour, genetic algorithms, and particle swarm optimisation.

ABSTRACT

In this paper, we present two optimisation methods for a generic boids swarm model which is derived from the original Reynolds' boids model to simulate the aggregate moving of a fish school. The aggregate motion is the result of the interaction of the relatively simple behaviours of the individual simulated boids[1]. The aggregate moving vector is a linear combination of every simple behaviour rule vector. The moving vector coefficients should be identified and optimised to have a realistic flocking moving behaviour. We proposed two methods to optimise these coefficients, by using genetic algorithm (GA) and particle swarm optimisation algorithm (PSO). Both GA and PSO are population based heuristic search techniques which can be used to solve the optimisation problems. The experimental results show that optimisation of boids model by using PSO is faster and gives better convergence than using GA.

INTRODUCTION

Many animals in the nature move in groups: fish swim in schools, birds fly in flocks, sheep move in herds, insects move in swarm and ants distribute to find a food source and then all ants follow path to the food. Simulating the aggregate motion is an important issue in the areas of artificial life and computer animation and in a lot of their applications such as games and movies. Reynolds (1987) proposed a first computer model of group animal motion such as fish schools and bird flocks. He called his model as "boids model", where boids refer to the generic flocking simulated creatures. The aggregate moving of the simulated boids is the result of the interaction of the relatively simple behaviours of the individual simulated boid. An interesting look at boids can be taken from the perspective of artificial life where is the holistic emergent phenomena is the result of interactions of independent entities (Anthony 2002). The boids model has three simple rules applied to the boids. The rules are: each boid move to avoid crowding with its neighbours, match and coordinate its movements with its neighbours, and move to gather with the others. Other rules such as avoiding obstacles and goal seeking have been included in steering behaviour model (Reynolds, 1999) and in many simulations based on boids model later on. For instance, Delgado (2007) extended the basic boids model to include the effects of fear. Olfaction was used to transmit emotion between animals, through pheromones modelled as particles in a free expansion gas. Hartman and Benes (2006) added a complementary force to the alignment (steer towards the average heading of neighbours) that they call the change of leadership. This steer defines the chance of the boid to become a leader and try to escape.

After 1987, the boids model is often used in computer graphics to provide realistic life-look representations of the aggregate motion of groups. For instance, in the 1998 Valve Video Game Company has used boids model in Half-Life video game for the flying bird-like creatures (Valvesoftware.com 2014). The boids model represented an enormous step forward compared to the traditional techniques used in computer animation for motion pictures. The first animation created with the boids model was in the computer animation shot film called Stanley and Stella in: Breaking the Ice in 1987 (Ice' and Malone, 2014). After that, the boids model was used in a feature film introduction of Batman Returns in 1992 (Returns and Burton et al., 2014). Then the boids model has been used in many games and films and in many other interesting applications.

In the boids swarm model, each rule is represented by a vector. The vector by its two components (magnitude and direction) is adaptive to the environment. The boid moving vector is a linear combination of every behaviour rule vector. The setting of the moving vector coefficients becomes more difficult by increasing more behaviour rules. These coefficients should be determined and optimised to have a realistic moving behaviour. In this context, we use two optimisation algorithms to optimise the boids model by finding the best coefficients values and combination in order to minimise the objective function. Firstly, we propose a GA to optimise the coefficients in a generic boids model. Secondly we substitute the GA by PSO to optimise the coefficients in the same generic boids model and use PSO to find food sources. Then we do a comparison of these two models by focusing on the advantages and disadvantages of each algorithm.

[1] Boids are bird-like objects that were developed in the 1980s to model flocking behaviour.

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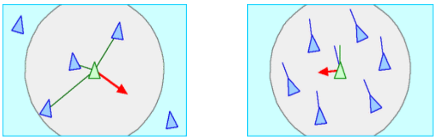
THE BOIDS MODEL

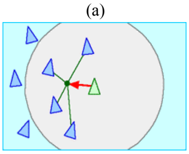
In 1986, Reynolds has developed the boids model. His published paper about the boids model (Reynolds 1987) was cited so many times and extended in so many different ways. Many of the extensions present additional rules to the boids, some describe constrained solution, some tend to easy solutions usable in computer games, some extend the previous work in spite of computational complexity, etc.

Reynolds (1987) describes the flock behaviour[2] as a result of the motion and the interaction of boids. Each boid has three simple rules of steering behaviours that describe how an individual boid move based on the positions and velocities of its flock mates (social reaction).

- Separation (*figure 1(a)*): each boid keep a distance from other boids nearby to avoid collision and prevent crowding.
- Alignment (*figure 1(b)*): each boid match the direction and the speed of its neighbours. This rule causes boids to follow each other.
- Cohesion (*figure 1(c)*): each boid tends to move to the average position of its neighbours.



(a) (b)



(a) Separation rule
(b) Alignment rule
(c) Cohesion rule

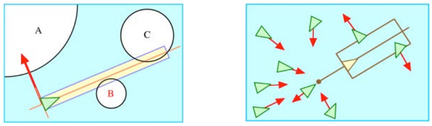
(c)

Figure 1: The boids social rules (Reynolds 1987).

Reynolds (1999) has extended the boids model to include more individual-based rules of the steering behaviours, to have more advanced individuals which are capable to finish specific task or adapt to complex environments. Some of these behaviours are:

- Obstacle avoidance (*figure 2(a)*): The obstacle avoidance behaviour allows the boids move in cluttered environment by dodging around obstacles.
- Leader following (*figure 2(b)*): this behaviour causes one or more boids to follow another moving boid selected as a leader.

[2] We mean by *Flock behaviour* in this paper as behaviour of flock, school, herd and swarm.



(a) (b)

Figure 2: Steering behaviours rules (a) Obstacle avoidance (b) leader following(Reynolds 1999).

Based on Reynolds model, we have implemented a generic boids swarm model in Unity3D (Unity3d.com 2014), the program is written in MonoDevelop Unity-C# (Docs.unity3d.com 2014). The aim is to develop a generic model that can be used in simulating the aggregate motion for flocks of birds, schools of fish or herds of animals. The model has five rules:

- Cohesion: steer to move toward the average position of local flock mates (as in the original Reynolds' model). By applying cohesion rule keeps the boids together. This rule acts as the complement of the separation. If only cohesion rule is applied, all the boids in the flock will merge into one single position. Cohesion (Coh_i) of the boid (b_i) is calculated in two steps. First, the center ($\overrightarrow{Fc_i}$) of the flock (f) that has this boid is calculated as in *equation 1*. Then the tendency of the boid to navigate toward the center of density of the flock is calculated as the cohesion displacement vector as in *equation 2*.

$$\overrightarrow{Fc_i} = \sum_{\forall b_j \epsilon f} \frac{\overrightarrow{p_j}}{N} \quad (1)$$

Where, p_j is the position of boid j and N is the total number of boids in f

$$\overrightarrow{Coh_i}_{=}\overrightarrow{Fc_i} - \overrightarrow{p_i} \quad (2)$$

- Alignment: steer to match the heading and the speed of its neighbours. This rule tries to make the boids mimic each other's course and speed. Boids tend to align with the velocity of their flock mates. The alignment (Ali_i) is calculated in two steps. First, the average velocity vector of the flock mates ($\overrightarrow{Fv_i}$) is calculated by *equation 3*. Then Ali_i is calculated as the displacement vector in *equation 4*.

$$\overrightarrow{Fv_i} = \sum_{\forall b_j \epsilon f} \frac{\overrightarrow{v_j}}{N} \quad (3)$$

$$\overrightarrow{Ali_i}_{=}\overrightarrow{Fv_i} - \overrightarrow{v_i} \quad (4)$$

Where $\overrightarrow{v_i}$ is the velocity vector of boid i
If this rule was not used, the boids would bounce around a lot and not form the beautiful flocking behaviour that can be seen in the nature.

- Separation: steer to avoid collection and overcrowding with other flock mates. There are many ways to implement this rule. An efficient solution to calculate the separation (Sep_i) is by applying *equation 5*. Vectors defined by the position of the boid b_i and each visible boid b_j are summed, then separation steer ($\overrightarrow{Sep_i}$) is calculated as the negative sum of these vectors.

$$\overrightarrow{Sep_i} = -\sum_{\forall b_j \in f}(\overrightarrow{p_i} - \overrightarrow{p_j}) \quad (5)$$

If only the separation rule is applied, the flock will dissipate.

- Leader following: steer to follow another moving boid selected as a leader (p_l). The leader following (Led_i) is calculated by *equation 6*.

$$\overrightarrow{Led_i} = L * (\overrightarrow{p_i} - \overrightarrow{p_l}) \quad (6)$$

Where L is a leader strength factor. (Note: the moving vector (velocity) has limits, minimum and maximum).

- Random movement: this rule is added to have more realistic flock behaviour. This rule is depending on the random number generator inside the game engine (*Unity3D*). The random movement ($Rand_i$) is calculated as in *equation 7*.

$$\overrightarrow{Rand_i} = -ffactor * \vec{r} \quad (7)$$

Where r is a unit sphere random vector and $ffactor$ is a flock random strength factor.

Then the moving vector (V_i) is for boid (b_i) is calculated by combining all the steering behaviour vectors as in *equation 8*.

$$\vec{V_i} = w_1\,\overrightarrow{Coh_i} + w_2\,\overrightarrow{Ali_i} + w_3\overrightarrow{Sep_i} + w_4\overrightarrow{Led_i} + w_5\overrightarrow{Rand_i} \quad (8)$$

Where w_i are the coefficients describing influences of each steering rule and used to balance the five rules.

We have used the Unity3D to implement the boids model to get the benefits of using a game engine. The first benefit is the amazing visualisation that we get in Unity3D. So we skip wasting time to model and program the boid's shape and its geometry. In Unity3D, it is easy to build a boid such as a bird, a fish or a sheep and attach some life-look animation to it, or import the 3D model of the boid from other programs and attach a built in animation to it or program the animation from the scratch. In this model we exploit the collision detection component in Unity3D game engine to avoid the obstacles. Each obstacle has a physic's collision component that doesn't let other objects to move through the collision bounds (obstacle's space). In another words, the obstacles will be excluded from the boids flocking space. We will show the results in the experimental results section.

GENETIC ALGORITHMS FOR OPTIMISATION OF BOIDS MODEL

In this section, we will give an overview of GA in general and some examples of its applications. Then we present our proposed model (GA for optimisation of boids model).

Genetic Algorithm:

Genetic algorithm (GA) is an optimisation and search technique based on the principles of genetic and natural selection (Haupt, 2003). A GA allows a population composed of many individuals to evolve under specified selection rules to a state that maximise the fitness (i.e., minimizes the cost function). Genetic algorithms (GAs) were invented by John Holland in 1960s and were developed by him and his students in 1960s and 1970s. Holland (1975) presented the GA as an abstraction of biological evolution and gave a theoretical framework for adaptation under GA.

GA belong to the larger class of evolutionary algorithms, which generate solutions to optimization problems using techniques inspired by natural evolution such as selection (reproduction), crossover (recombination) and mutation. The evolution process starts from a population of individuals generated randomly within the search space and continues for generations. In each generation, fitness of every individual is evaluated, and multiple individuals are randomly selected from the current population based on their fitness and modified by recombination and mutation operation to form a new population. Then this new population will be used for the next generation of the evolution. In general, the search process ends when either a maximum number of generations have been produced or a fitness level has been reached for the population. The flowchart of GA is shown in (*figure 3)*.

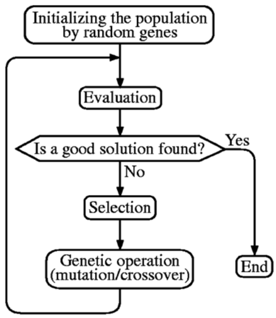


Figure 3: Flowchart of GA

In a GA, it's necessary to be able to evaluate how good a potential solution is relative to other potential solutions. The fitness function is responsible for performing this evaluation and returning a fitness value (positive integer number) that reflects how optimal the solution is. The fitness function is associated with the objective function of the problem. The fitness value of the individual is used to determine the probability with which the individual is selected into the new population. A common metaphor for the selection process is a roulette wheel selection (Fogel, 2000).

Traditional methods of search and optimization are too slow in finding a solution in a very complex search space. GA is a robust search method requiring little information to search effectively in a large or poorly understood search space. In particular a genetic search progress through a population of points in contrast to the single point of focus of most search algorithms. Moreover, it is useful in the very tricky area of nonlinear problems. GAs have been used to solve optimisation problems in different fields such as automotive design, engineering design, robotics, optimised routing, games, etc. Chen (2006) has applied GAs to optimise the behaviour of a school of fish.

GA for optimisation of moving vector in the boids model:

The moving vector (V_i) in *equation 8* for each boid (b_i) is a combination of all the five steering behaviour vectors. And the movements are balanced by the w_i weight coefficients, so these coefficients should be optimized to have realistic and life-look behaviour. We have removed the random steering behaviour in the moving vector to exclude the random movements for the boids. The new moving vector is:

$$\vec{V_i} = w_1 \overrightarrow{Coh_i} + w_2 \overrightarrow{Ali_i} + w_3 \overrightarrow{Sep_i} + w_4 \overrightarrow{Led_i} \tag{9}$$

We have used GA to optimise these coefficients and getting the benefit from using GA for parameters optimisation and finding a global optimum solution. The goal is to find the optimal solutions in terms of the variables (coefficients). Thus we should define mathematically what is the optimal solution. We begin the GA by defining the chromosome. The chromosome is an array of the coefficients values that will be optimised. In this case the chromosome has four variables and is written as a four-element row vector.

$$chromosome = [w_1, w_2, w_3, w_4] \tag{10}$$

Then we should formulate the cost function that gives a cost for each chromosome.

$$cost = f(chromosome) = f(w_1, w_2, w_3, w_4) \tag{11}$$

In our case, the optimal solution is to have life-look flock behaviour. Measuring the flock behaviour can be very complicated process, expensive computationally and then time consuming. Since the purpose of this paper is to build a generic boids model and optimise it by different optimisation methods, we suggest a simple cost function. In the flowing, we explain the proposed cost function which is divided into five parts.

- Related to the alignment rule: The divergence between the direction of the boid and the average direction of the flock should be minimised. The divergence is the angle θ between the boid velocity vector $\vec{v_i}$ and the average flock velocity vector.

$$cost_1 = \theta \tag{12}$$

- Related to the leader following rule: The divergence between the direction and the distance of the boid and the direction and the distance of the leader should be minimised.

$$cost_2 = d \tag{13}$$

  Where d is the distance between p_l and p_i

$$cost_3 = \alpha \tag{14}$$

  Where α is the angle between the boid velocity vector $\vec{v_i}$ and the leader velocity vector.

- Related to the separation and cohesion rules: The boids distribution should be optimised to avoid crowding or losing contact and having nice flocking. To do this; we calculate the distance between the boid and the flock center first d_c. Then we check all the boids, if they are nearby (<*keepd*) or far enough (>*keepd*).

  If $(|(\vec{p_i} - \vec{p_j})| \le keepd)$,

$$cost_4 = \sum\nolimits_{\forall b_j \epsilon f} d_c * \frac{(|(\vec{p_i}-\vec{p_j})| - keepd)^2}{keepd^2} \tag{15}$$

  But for the far boids,

  If $(|(\vec{p_i} - \vec{p_j})| > keepd)$

$$cost_5 = \sum\nolimits_{\forall b_j \epsilon f} d_c * \frac{(|(\vec{p_i}-\vec{p_j})| - keepd)^2}{(d_c - keepd)^2} \tag{16}$$

Then the cost is:

$$cost = cost_1 + cost_2 + cost_3 + cost_4 + cost_5 \tag{17}$$

We have used the continuous GA as explained in (Haupt, 2003). We used the parameters in (*Table 1*). We will analyse the results in experiment results section.

Number of optimisation variables	4
Upper limit on optimisation variables	1
Lower limit on optimisation variables	0
Maximum iteration	100
Minimum cost	0
Population size	20
Mutation rate	0.2
Selection rate	0.5

Table 1: GA parameters

PARTICLE SWARM OPTIMISATION OF BOIDS MODEL

In this section, we will give an overview of PSO algorithm in general and some examples of its applications. Then we present our proposed model (PSO for optimisation of boids model).

Particle Swarm Optimisation:

PSO is a computational method that optimises a problem by iteratively trying to improve a candidate solution with regard to a given measure of quality. Kennedy and Eberhart introduced PSO in 1995 (Kennedy, 1995). PSO was originally used to solve non-linear continuous optimization problems, but more recently it has been used in many practical, real-life application problems. For example, PSO has been successfully applied to track dynamic systems (Eberhart, 2001) and evolve weights and structure of neural networks (Zhang, 2000). PSO draws inspiration from the sociological behaviour associated with bird flocking. It is a natural observation that birds can fly in large groups with no collision for extended long distances, making use of their effort to maintain an optimum distance between themselves and their neighbours.

Cui (2009) has developed a hypried PSO and boids model (Boids-PSO), where cohesion rule and alignment rule are both employed to improve the PSO algorithm for boids simulation and to overcome the weekness of biological background of PSO. But in our case we use PSO as an optimisation technique to optimise the coefficients in the moving vector.

The PSO methodology operates by placing a group of individual particles into a continues search space, wherein each particle is initialised with a random position and a random initial velocity in the search space. The position and velocity are updated synchronously in each iteration of the algorithm. Each particle adjust its velocity according to its own flight experience and the other's experience in the swarm in such a way that it accelerates towards positions that have high fitness values in previous iterations. In other words, each particle keeps track of its coordinates in the solution space that are associated with the best solution that has achieved so far by its self. This value is called personal best (*pbest*), Another best value that is tracked by the PSO is the best value obtained so far by any particle in the neighbourhood of that particle. This value is called (*best*). So the basic concept of PSO lies in accelerating each particle toward its *pbest* and the *gbest* locations, with a random weighted acceleration at each time step as shown in (*figure 4*).

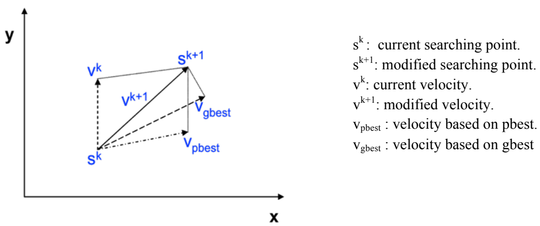


Figure 4: Concept of particle position modification by PSO

The modification of the particle's position can be mathematically modelled according to *equation 18*.

$$\vec{v}(k+1) = \vec{v}(k) + c_1\overrightarrow{R_1}\left(\overrightarrow{pbest} - \vec{s_i}(k)\right) + c_2\overrightarrow{R_2}\left(\overrightarrow{gbest} - \vec{s_i}(k)\right) \quad (18)$$

Where,

$\vec{v}(k)$ is the velocity of a particle at iteration k.

$\overrightarrow{R_1}$ and $\overrightarrow{R_2}$ are random numbers in the range of $[0,1]$ with the same size of the swarm population.

c_1 and c_2 are learning factors which will be fixed through whole the process.

In order to improve the local search precision, Eberhart (2001) added the inertia weight w to *equation 18* to be as following equation.

$$\vec{v}(k+1) = w\vec{v}(k) + c_1\overrightarrow{R_1}\left(\overrightarrow{pbest} - \vec{s_i}(k)\right) + c_2\overrightarrow{R_2}\left(\overrightarrow{gbest} - \vec{s_i}(k)\right) \quad (19)$$

The inertia weight controls the momentum of the particle by weighing the contribution of the previous velocity.

Chatterjee (2006) suggested a dynamic change of inertia weight in his work.

Clerc (1999) indicates that the use of a constriction factor K may also be necessary to ensure convergence of the particle swarm algorithm, defined as when all particles have stopped moving. Then the velocity is calculated by the equation:

$$\vec{v}(k+1) = K[\vec{v}(k) + c_1\overrightarrow{R_1}\left(\overrightarrow{pbest} - \vec{s_i}(k)\right) + c_2\overrightarrow{R_2}\left(\overrightarrow{gbest} - \vec{s_i}(k)\right)] \quad (20)$$

$$K = \frac{2}{\left|2-\varphi-\sqrt{\varphi^2-4\varphi}\right|} \quad (21)$$

Where $\varphi = c_1 + c_2$ and $\varphi > 4$.

Then the new position for the particles is the addition of the position at k iteration and the distance that the particles will fly with the new velocity $\vec{v}(k+1)$. The position is updated by *equation 22*.

$$\vec{s_i}(k+1) = \vec{s_i}(k) + \vec{v}(k+1) \quad (22)$$

The flow chart of a general PSO algorithm is shown in (*figure 5*).

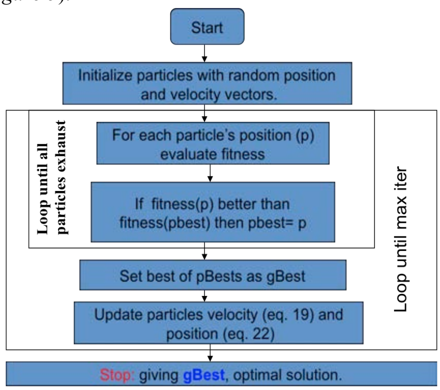


Figure 5: flow chart of general PSO algorithm

Path Planning using PSO:

One of the main applications of PSO is the path planning. PSO has been applied massively for path planning intensely in robots (Chen X 2006 and Nasrollahy 2009).

In the boids model, PSO can be applied to the flock leader, to plan and smooth his path. For this purpose; we have used PSO algorithm to plan the path to the target (i.e. food source). We have used the Euclidian distance between the particle and the target as a fitness function in the PSO.

In PSO for path planning, the inertia weight w is calculated according to the next equation.

$$w = w_{start} - \frac{w_{start} - w_{end}}{K}\,k \quad (23)$$

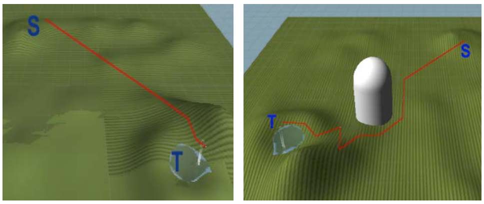
Where, K is the iteration maximum number and k is the current iteration. By linearly decreasing the inertia weight from a relatively large value to a small value, the PSO tends to have more global search ability at the beginning of the run while having more local search ability near the end of the run.

As in robot's applications, PSO gives advantages to the path planning particularly in the dynamics environment containing stationary and moving obstacles.

We have used the parameters in (*Table 2*) for the PSO. In case of facing obstacles; the leader is looking to his target, if there is an obstacle whose obscures the target and the distance to this obstacle is less than a threshold, the leader will change his direction randomly to his right or his left by 45-degrees angle.

Swarm size	20
Dimension of the problem	2
Maximum iteration	100
c1 (cognitive parameter)	2
c2 (social parameter)	2
C (constriction factor)	1
Inertia start	0.9
Inertia end	0.4
Upper limit on optimisation variables	100
Lower limit on optimisation variables	-100

Table 2: PSO parameters for path planning



(a) (b)

Figure 6: PSO for path planning without obstacles (a) and with an obstacle (b).

PSO for optimisation of moving vector in boids model:

As in GA for optimisation of the moving vector in the boids model, we have applied PSO to find the optimum coefficients for the moving vector (V_i) in *equation 9* for each boid (b_i). We have used the same cost function as in equations from 12 to 17. We have used the PSO as explained in (Kennedy, 1995).

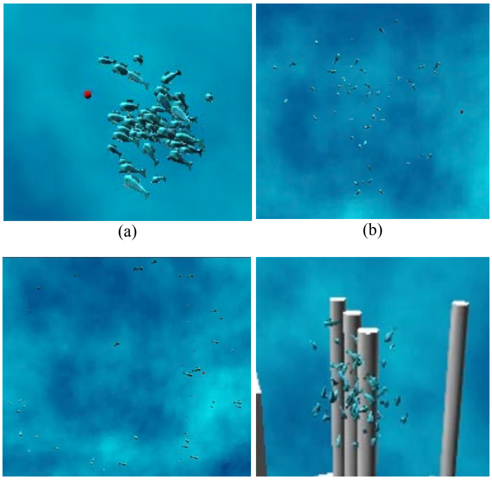
Population size	20
Dimension of the problem	4
Maximum iteration	100
c1 (cognitive parameter)	2
c2 (social parameter)	2
C (constriction factor)	1
Inertia start	0.9
Inertia end	0.4
Upper limit on optimisation variables	1
Lower limit on optimisation variables	0

Table 3: PSO parameters

We have used the parameters in (*Table 3*) and we have used *equation 23* to calculate the Inertia. We will analyse the results in next section.

THE EXPERIMENT RESULTS

For testing the boids model without/with the GA and PSO, we have made a fish school in Unity3D. we have used a ready fish boid from unity website to have a nice fish shape with some animations such as moving the fish tail. The fish school has 50 fish (*figure 7a*). Firstly we have implemented the boids model as in *equation 8* with excluding the random steering, and then we added the random steering and the leader factor. *Figure 7(b,c,d)* shows the simulation from different efforts. It was observed that the model need time to have a nice flocking shape with/without random movement. And the random movement was important to avoid obstacles since we didn't have a separate steering behaviour for avoiding the obstacles. The simulation of a fish school depends on the boids model as in *equation 8* with equal weight coefficients gives a good flocking shape but the model was slow to get the nice flocking shape.



(a) (b) (c) (d)

Figure 7: (a) Fish school system (b) the boids simulation without random movement after few frames from the start (c) the boids simulation with random movement (d) the boids simulation with random movement and adding leader factor and some obstacles.

Using the GA for optimisation the moving vector by finding the optimal coefficients, made the school of fish getting the nice flock shape sooner, but its very computational costly. The frame rate went down from more than 30 frames per second to almost 3 frames per second (this depends on the parameters of GA). And it is noticeable that after passing the start time and having the flock shape, there is no noticeable difference between the original boids model and the boids model with GA. *Figure 8(a)* shows a screen shot from the simulation with GA.

(a) (b)

Figure 8: The boids simulation with (a) GA, and (b) PSO

PSO was faster than GA, and gave more noticeable results as shown in (*figure 8(b)*). It is observed that the boids get the flock shape faster and even the flock behaviour is look nicer than before.

We depend on our observation of the simulation results to do the comparison between the different models, because each simulation/run is different from other simulations/runs and it depends on the starting positions and the random numbers. We have selected the same population size and the number of iterations for both GA and PSO algorithms. The other parameters in GA, were selected by running the GA on many standard optimisation problems and from the literature (Haupt, 2003). The other parameters in PSO algorithm, were selected from the literature and the path planning algorithm. These parameters are selected to have a good convergence. The cost function or the objective fuction in general should be connected to the type of simulation. In our experiment, the objective function is to have nice fish school behaviour.

CONCLUSIONS AND FUTURE WORK

The boids model is often used in computer graphics to provide realistic life-look representations of the aggregate motion. For instance, many animations require natural-looking behaviour from a large number of characters (boids). The aggregate motion of the group is the result of the interaction of the individuals, so let each individual generate its own motion, this is easier and produces natural and unscripted motion. The individual's moving is calculated by combining all the steering behaviour vectors. To have a natural behaviour in different environments, the boid's movements should be optimised and adapted. GA and PSO algorithm are used to optimise a generic boids model by optimising the coefficients of the moving vector to minimise the cost function.

The challenge is to write rules to define natural behaviours. In the boids model, we have defined the cost function which is divided into five parts. These parts are related to the steering behaviours in the model. Thus the cost function reflects how the fish school should look in the nature. Our cost function is not computationally costly and measures simply the boids behaviour. The cost function (objective function) should be connected to type-of-problem we want to solve, and reflects how we want the flock/swarm to behave. The setting of moving vector coefficients is determined by the cost function. We use GA and PSO to find the best coefficients values (waights of the behaviours rules) to minimise the cost function which reflects the wanted behaviour.

GA and PSO have many similarities and both of them use population-based approaches. GA is known as a good algorithm to find the global optimal solution where is PSO could stuck in the local optimum. But PSO has advantage over GA concerning the time. In the boids model, where we have adaptive boids in a dynamic environment, we are interested in a nice flocking behaviour (convergence) as in nature, and in time consuming. From the experiments for both GA and PSO, we observed that PSO is much faster than GA, and gives a faster convergence, and because the PSO is computationally less costly than GA, we could notice the convergence more in PSO than GA.

The challenge is to balance between the convergence (nice flocking behaviour and the adaptively) and the time consuming. Having more advanced cost function probably will give better results, but it will be very expansive and lead to a very slow model. Applying the optimisation algorithm not continuously such as applying the optimisation algorithms for only some parts of the simulation such as at beginning of the simulation until the boids get a nice flock shape which is wanted, or when the boids facing obstacles or enemies, will accelerate the model.

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Study
III-2

Optimal fish densities and farm locations in Norwegian fjords

A framework to use a PSO algorithm to optimize an agent-based model to simulate fish disease dynamics

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Abstract

Risk of pathogen transmission in Norwegian fjords depends on two main factors: location of farms and the density of fish in each farm. This paper presents a novel method to find the optimal values of these two variables that yield the optimal aquaculture system with a minimum risk of spreading disease and high fish production. For this purpose, agent-based models (ABMs) are used to simulate and analyze fish disease dynamics within and between fish farms in Norwegian fjords. Moreover, a modified particle swarm optimization (PSO) algorithm is used to identify the optimal values of fish density and farm's location for each farm. The objective function is defined as being the weighted sum between the fish density and the infection risk. We validated the PSO algorithm with the optimal objective function by demonstrating the capability of the algorithm to drive the system to produce an expected behavior and output in tested, known scenarios.

The simulation results demonstrate the ability of the PSO algorithm to converge rapidly to the optimal solution. In only 18 iterations, it finds an optimal solution that is three times larger than the initial fish farm density and in a location that keeps the risk of infection at an accepted level. The use of the PSO algorithm in finding optimal parameter values of ABMs, will open for new applications of the model in aquaculture industry management, such as planning for a sustainable aquaculture industry.

Keywords: Risk of infection, Particle swarm optimization (PSO), Agent-based modeling, Fish farming.

1 Introduction

Over the past couple of years, the Norwegian aquaculture industry has experienced a period of rapid growth. This progress has resulted in challenges for the industry such as losses due to diseases and various kinds of harmful impacts on the marine ecosystem (Olaussen, 2018). The Norwegian government aims at promoting an environmentally sustainable aquaculture industry by minimizing the risks of disease and harm to the marine environment and thus retaining biological diversity. Infectious diseases and parasites make up one of the five key areas of concern to the Norwegian government in terms of where aquaculture may potentially have a negative impact on the environment (FKD, 2009; Fiskeridirektoratet, 2018).

In this context, it is necessary to develop, assess and apply validated methods and models that can help us effectively analyze and facilitate the management of the aquaculture industry. The Norwegian Directorate of Fisheries applies strict rules to licenses for building and operating aquaculture facilities (The Norwegian Aquaculture Act, 2005), and they use systems to control the operations of the fish industry. For example, based on regulations, the application of the MOM (Monitoring – On growing fish farms - Modeling) method is mandatory as a way to monitor the effects of fish farming on the seabed and on the benthic fauna under and near the farming facilities. This method describes how effects on the seabed are to be monitored and which environmental thresholds are to be applied (Ervik et al., 1997). SINTEF has developed systems for monitoring and decision support in sea-based aquaculture (www.sintef.no). These systems are based on statistical analyses and particle tracking in hydrodynamic models.

Marine aquaculture systems consist of several facilities, located in a dynamic environment and influenced by a variety of factors (e.g. seawater temperature and sea currents). These factors are fluctuating in the space and time domains. For instance, the sea currents in the fjords exhibit a complex pattern of behavior that is predictable only over a short time period (Institute of Marine Research, 2018). A disease emerging from the system is a product of the interactions between the parts of the system (i.e. fish and pathogens). The system exhibits a complex behavior, and there are, typically tipping points[1] where a small change in one or more of the parameters (e.g. fish density) that characterize the system can dramatically affect the behavior of the whole system. These tipping points separate two modes of behavior; the first mode of behavior is when the fish disease prevalence is decreasing or is under control, while the second one is when the disease dynamics is unstable and the disease is out of control (i.e. disease prevalence is increasing). Thus, finding the optimal fish density and location for each facility in the system can stabilize fish disease dynamics in the aquaculture system and subsequently, limiting the negative impact on the environment

The main aim of this study is to develop a management tool and methods that determine the optimal production size in a defined marine aquaculture system with many facilities of variable fish density and locations (we assume that all farms have equal physical size[2]). This optimal production is based on a minimization of the infection risk within and between the aquaculture sites. This optimal production is ensured by increasing the number of fish and minimizing the infection risk (i.e. increase the harvest of farms) by changing the locations of fish farms. The infection risk is identified based on local conditions such as fish density, sea temperature, sea currents, and distances between aqua sites (Alaliyat et. al., in press).

Previous studies on infectious disease dynamics in aquaculture systems have predominantly used mathematical models that were based on the assumption that a fish population is homogeneous (e.g., Murray, 2009; Green, 2010; Stene, 2013). The previous mathematical models treat fish as the unit of analysis, not the pathogens, i.e., they do not treat the pathogens as individuals who may survive without hosts, and, in their simplest form, they do not represent environmental conditions explicitly in the model. Many researchers have used such models to simulate disease dynamics, and some of them have coupled these models with simple hydrodynamic models or distance measures of transmission between separate populations (Ogut, 2001; Viljugrein et al., 2009; Aldrin et al., 2010; Werkman et al., 2011; Salama & Murray, 2011).

In Norway, hydrodynamic models, coupled with particle tracking and statistical analyses, have been widely applied to identify the salmon louse and pancreas disease (PD) transmission dynamics in Norwegian fjords (MODS, 2012, Stene et al., 2014). SINTEF has developed the SINMOD hydrodynamic model (www.sinmod.no) that combines physical and biological processes in the ocean. These models typically do not

[1] Tipping Points: places where a small change in an input can dramatically affect the outcome.
[2] We assume equal size (volume) of all modeled farms in this study, and subsequently, the number of fish (fish population) is a proxy for fish density.

include a variety of pathogens. Moreover, statistical analyses are based on the assumption that fish populations are homogeneous.

Agent-based methods have been applied to simulate the transmission of human viral diseases such as influenza (Ciofi et al., 2008; Milne et al., 2008; Khalil et al., 2010). We have previously applied the agent-based method to simulate fish disease dynamics (Aalaliyat et al., 2013; Alaliyat & Yndestad 2015a; Alaliyat & Yndestad 2015b; Alaliyat & Yndestad 2015c; Alaliyat et al., in press). Agent-based models (ABMs) may be valuable for analyses focusing on individual interactions (i.e., where the overall dynamic behavior depends upon the interaction between individual fish and pathogens) and may also allow for the incorporation of the spatial aspect of the system that has not previously been utilized.

Previous studies that used mathematical models to simulate fish diseases focused on providing qualitative assessments of various infectious diseases using statistical analysis methods (Murray & Peeler, 2005; Gregory, 2008; Viljugrein et al., 2009; Kristoffersen et al., 2009; Tavornpanich et al., 2012; Taranger et al., 2015). These models were predominantly based on historical data and were applied to the study of various factors governing fish disease outbreaks. In Norway, Tavornpanich built risk maps and spatial determinants of the pancreas disease (PD) in Norwegian Atlantic salmon farming sites (Tavornpanich et al., 2012), while Stene studied factors that trigger PD outbreaks (Stene, 2013).

Norwegian aquaculture growth invariably involves the expansion of cultivated areas and increased fish densities in aquaculture installations. In terms of farmed individuals, many negative effects have been identified as a consequence of poorly regulated sector growth and poor management practices. As a result, there is a need for models that help us predict fish disease dynamics, that allow for integration with other sectors, and that are not based only on statistical analyses of historical data. Using agent-based methods, we study specific spatial aspects of the spread of infections and address the stochastic nature of the infection process in fish diseases (Alaliyat & Yndestad, 2015b). ABMs can also include all external factors that affect fish disease outbreaks such as the interaction with wild fish, ship traffic and other marine activities.

ABMs have been widely used in decision support for management in a variety of fields (Skov-Petersen, 2008). ABMs have been extensively used in biology, including the analysis of the spread of epidemics (Hunter et al., 2017). Several methods have already been proposed to automate exploration in the parameter space of ABMs. For example, the tool “BehaviorSpace” in NetLogo allows us to automatically investigate the parameter space (Wilesnsky, 2009). This space is a Cartesian product of possible values that each parameter can take. When the model is coupled with a high degree of uncertainty associated with the values of these parameters, sensitivity analysis becomes a significant contribution to the analysis of the model behavior (Kocabas & Dragivevica, 2006). When, however, we have a large number of parameters where each can take a wide range of values, the parameter space becomes large, and the systematic exploration of that space surpasses our computational capabilities. Brueckner proposed a method that differentially explores the whole parameter space focusing on the most interesting areas (Brueckner & Parunak, 2003). He used a search agent to travel in the parameter space to look for values that provide the highest values in the fitness function between the desired model behavior and the simulation.

If a particular model behavior is desired, then one must identify the model parameter values that will provide that behavior. The solution space can contain many potential solutions that leave a brute-force approach inefficient. Genetic algorithms

(GA) have been applied to properly tune ABM parameters in the exploration of such large solution spaces (Joyce et al., 2012).

We previously developed an aquaculture agent-based system model (AABSM) to simulate fish disease dynamics and predict pathogen transmission patterns in aquaculture systems (Alaliyat et. al., in press). The AABSM has many parameters that relate to the individual attributes and their behavior rules, the environment, and the network between the agents or between the agents and the surrounding environment. These parameters determine the global behavior dynamics of the system, and small changes in a single parameter sometimes lead to major modifications of the dynamics of the entire system. Parameter setting in preparation for a model simulation of the AABSM can be a very tedious process unless we have a strategy for exploring the parameter space.

The AABSM is a bottom-up model that has been built on simple individual and environmental dynamics rules. For instance, individual fish become infected if it is exposed to pathogens that move along with the sea currents. The generic model is, however, complex. The model has many non-linear and dynamic relations (e.g. relationship between pathogen lifespan and seawater temperature). Therefore, the model output (i.e. behavior) is sensitive to the initial conditions. The infection risk depends on many input parameters such as seawater temperature, current speed and direction, farm locations, and the fish density (Alaliyat et al., in press).

With the purpose of finding an optimal aquaculture system that results in lower infection rates and maximum fish production, we need to find an optimal fish density and location (in *x, y* coordinates) of each facility in the system. We need to vary the location and the fish density across all possible values and conduct a follow-up analysis to find the best combination of parameter values. For instance, even if we have an aquaculture system of merely three facilities, each characterized by three parameters (location in *x* and *y*, and fish density), and we have as few as *100* possible values for each parameter, then the possible combinations of these nine parameters are 100^9. Consequently, it is impossible to go through all the combinations of parameter values. Swarm Intelligence (SI) algorithms are well-suited to handle such large solution spaces. We define a cost function that measures the performance of the AABSM, and then the particle swarm optimization (PSO) algorithm automatically searches for the model parameter values that maximize the objective function value (Alaliyat et al., 2014).

We have defined a number of simulation scenarios to test our algorithms. In the first scenario, we defined a simple aquaculture system with only two fixed positioned facilities; - where one facility is infected, while the other one is a susceptible farm. We aim at exploring the impact of the fish density in the susceptible farm (defined as a parameter) on the infection rate in that farm. In subsequent scenarios, we defined an objective function as a weighted sum between the fish density and the infection risk to facilitate the optimization. First, we applied a PSO algorithm to identify which combination of fish density in and location of the susceptible farm within a well-defined area, that will provide the highest values of the objective function (i.e. lower infection rate under a maximum fish production). Therefore, instead of running the model for all the possible parameter values of fish density and location, which could take very long time, and then conducting follow-up sensitivity analyses, the PSO algorithm automatically searches for the parameter values that provide the highest objective function value. We need to improve the normal PSO algorithm to fit this optimization problem, since the AABSM is a stochastic model, and a standard PSO can easily become stuck in local minima. Finally, we have extended this scenario in order to find optimal fish density and locations for all the three facilities in the aquaculture system; - only one of which is initially infected.

2. Materials and methods

2.1 Materials

We present a generic model that uses an ABM and a PSO algorithm. The model can be used for different fish infectious diseases in different areas, but the data used in our simulations are inspired by the aquaculture industry in the Romsdalsfjord[3]. The aquaculture data, including the maximum allowed capacity, are available online on the Norwegian directorate of fisheries webpage, www.fiskeridir.no/. The oceanographic data include sea currents data (speed and direction) and seawater temperature. In our simulations, we used the monthly average sea currents data from the SINMOD model (MODS, 2012) with a resolution of 800 m x 800 m, and we added noise to achieve natural variety. Seawater temperature monthly average data are available online on the Institute of Marine Research webpage, www.imr.no/en/. The water temperature varies in water column as well (Alaliyat & Yndestad, 2015b). Infection, and shedding parameters and pathogen life span depend on the type of pathogen and fish. In this study, we use data references for PD (Stene et al., 2014; Alaliyat & Yndestad, 2015b).

To implement models using agent-based methods, NetLogo 3D was used. NetLogo is a multi-agent programmable modeling environment. The NetLogo toolkit allows for simulations within a geographic information system environment, and it is easy to include physical and environmental data as well (Wilensky, 1999). NetLogo was used also to implement the PSO algorithm to optimize the ABMs. We used also MATLAB to analyze the simulation results and to create figures that are easy to interpret (MATLAB, 2015).

2.2 Methods

2.2.1 Aquaculture system model

The aquaculture system generally consists of a set of fish farms in a semi-closed area (i.e. fjord), a swarm of pathogens and the landscape. This system *S(t)* can be formulized as:

$$S(t) = \{(FF(t), P(t), L(t)), N(t)\} \quad (1)$$

where $FF(t)$ represents a set of fish farms, *P(t)* a swarm of pathogens, *L(t)* the landscape or the environment in which the fish farms and pathogens are located, and *N(t)* is the relationships between the system parts (Yndestad, 2010).

The Fish farms FF(t)

In this study, the modeled aquaculture systems represent parts of the Romsdalsfjord. The choice of this area is due to the data availability and abundance of research activity in it. Fish farms can hypothetically be located at any position in the simulated space. Fish farms shed pathogens if they are infected and consume pathogens if they are susceptible sites. Closer distance between the farms (i.e. higher cohesion) increases the infection risk, while higher separation decreases the infection risk.

Fish farms have these parameters at the beginning of the simulation: fish population, location in the landscape and number of initially infected fish (see Table I).

[3] Romsdalsfjord is 88 km long and located in the Romsdal district of Møre og Romsdal County in mid-Norway.

We assume that all the fish farms have equal physical size. Fish individuals are only located in the fish farms' sites, while the pathogens move in the whole landscape. In this study, fish individuals (i.e. agents) move randomly inside the farms. Therefore, swarm properties (i.e. cohesion, separation, and alignment forces) are ignored. The fish population and farm location parameters take values that are limited within value ranges shown in Table I. Within these ranges, we identify the optimal combinations of values of these parameters that provide us with an optimal aquaculture system (maximum production with minimum infection risk).

TABLE I: FISH FARM PARAMETERS

Parameter		Min value	Max value
Fish population		*100*	*1000*
Location	*X*	*-248.5*	*248.5*
	Y	*-148.5*	*148.5*
	Z	*0*	*0*
Number of initial infected		*0*	*Max (fish population)*

The pathogen swarm $P(t)$

The pathogens swarm consists of many individual pathogens, as the following:

$$P(t) = \{PA_1(t), PA_2(t), \ldots, PA_n(t)\} \quad (2)$$

where $PA_j(t)$ is the pathogen agent j, and n is the total number of pathogens at time t. Pathogens move by sea currents and their social characteristics (i.e. cohesion, separation, and alignment forces) are ignored. Our model assumes that the simulation space is free of pathogens at the beginning.

The landscape L(t)

The landscape, $L(t)$, in this study is limited to the terrain, the sea currents and the water temperature that represent parts of the Romsdalsfjord.

1. The terrain is divided into many 3D grids (i.e. cells) with 13 x 13 x 13 points (pixels). Each fish farm is represented by 3 x 3 x 3 grids, equal to 3*20 m x 3*20 m x 3*20 m.
2. The sea currents model is built on the average current speed and angle in the Romsdalsfjord. The user can set the average current angle and current speed in the beginning of the simulation; then, during each time step, a random deviance is added to these current angles and speeds.
3. The sea temperature changes in time and space. The user can set the average water temperature at the surface level, and then, some noise to account for the variation present in nature is added. The water temperature varies at the lower levels of the sea as well as in the following:

$$\vec{T}(x, y, z, t) = \overrightarrow{T_0}(x, y, z, t) - C\,\vec{L}(y) \quad (3)$$

where $\vec{T}(x, y, z, t)$ is the water temperature at the position (*x, y, z*) at the time *t*, $\overrightarrow{T_0}(x, y, z, t)$ is the water temperature at the surface level (*y = 0*, maximum temperature value at the surface), C is a constant that represents the decay rate, and $\vec{L}(y)$ is the water levels of the sea.

The relationships N(t)

There are mutual relations between all the system elements (i.e. fish, pathogens and landscape). *N(t)* represents the relationships between fish and pathogens (e.g. infection process), and between them and the landscape (e.g. pathogen transmitter by sea currents). As described above, the aim of this study is to identify the optimal fish density and location for each farm in the aquaculture system, at a minimum infection risk and high production. In order to model the infection risk, methods of pathogen dynamics are introduced.

The pathogen dynamics

Infected fish produce pathogens in the aquaculture system. Pathogens may have the following dynamic properties:

Transport in seawater

The pathogens are moving by sea currents. Each pathogen moves according to the current speed and direction by the position of the pathogen at the beginning of the time step. The pathogen $PA_j(t)$ updates its position as:

$$\left\|\overrightarrow{v(t)}\right\| = C_{sr} \,.\, R_n(C_s, std\_s) \tag{4}$$

$$\overrightarrow{PA_j}(x, y, z, t + \Delta t) = \overrightarrow{PA_j}(x, y, z, t) + \overrightarrow{v(t)} * \Delta t \tag{5}$$

where $\left\|\overrightarrow{v(t)}\right\|$ is the magnitude of the velocity, C_{sr} is the relative current speed, which is inherited from the grid where the pathogen is and depends on the geometry of the fjord (e.g., changes in the width of the fjord, the presence of islands and peninsulas, etc.), R_n is a normally distributed random floating point with a mean of C_s (average current speed in this area), std_s is a current speed standard deviation. In the next equation, $\overrightarrow{PA_j}(x, y, z, t + \Delta t)$ is the new pathogen agent j position, $\overrightarrow{PA_j}(x, y, z, t)$ is the current pathogen agent j position, $\overrightarrow{v(t)}$ is the pathogen velocity, and Δt is the time step.

The velocity direction is connected to the orientation of the pathogen that is defined by two variables: heading $PA_j(t)_{hed}$ and pitch $PA_j(t)_{pit}$. Heading is the angle between the forward vector of the pathogen projected onto the horizontal plane and the vector [0 1 0], and pitch is the angle between the forward vector of the pathogen and the horizontal plane. We calculate these variables as:

$$PA_j(x, y, z, t)_{hed} = C_d + R_n(C_{bias}, std\_d) \tag{6}$$

$$PA_j(x, y, z, t)_{pit} = -\, R_j \,.\, pit_v \tag{7}$$

where C_d is the sea current direction angle, R_n is a normally distributed random floating point with a mean of C_{bias} (current heading bias variable used to offset the direction given by the grid) and a current direction standard deviation std_d, R_j is a random float number in the range of [0,1], and pit_v is the pitch value that represents the sinking effect on the pathogens.

Mortality in seawater

The pathogen lifespan is a function of seawater temperature and salinity (Stene, 2013). For example, salmon pancreas disease virus (SPDV) can live more than 4 days in the cold water, but this value is decreased exponentially in the hot water (Alaliyat & Yndestad, 2015c). The life span related to the seawater temperature can be modeled as in the following equation (Stene et al., 2014, Alaliyat & Yndestad, 2015b).

$$PA_j(x, y, z, t)_{LS} = a * exp\,(-\,T/\,b) \tag{8}$$

where T is the water temperature, a is the pathogen lifespan at 0° water temperature, and b is the decay rate.

Pathogen density in infected fish farms

The total number of pathogens at fish farm $FF_k(x, y, z, t)$ is calculated as:

$$\sum \overrightarrow{PA_j}(x, y, z, t) \;\; if \begin{cases} x_{min} \leq x \leq x_{max} \\ y_{min} \leq y \leq y_{max} \\ z_{min} \leq z \leq z_{max} \end{cases} \tag{9}$$

where, $x_{min}, y_{min}, z_{min}, x_{max}, y_{max}, z_{max}$ are the surfaces of the cube that represents the fish farm in the 3D simulation space. Pathogen density depends on different factors such as: fish population, sea currents, distance between fish farms and seawater temperature (Alaliyat et. al., in press).

Pathogen-fish interaction

The infection is happening when the susceptible fish exposed to pathogens. The individuals are heterogeneous: fish resist differently to the pathogens. Also, individual pathogens have different abilities to cause a disease. *Algorithm I* summarizes the procedures of pathogen-fish infection process.

Algorithm I: infection rules (Alaliyat et. al., in press)

1: **For each** susceptible fish agent i **then**
2: **If** $(RF_i * \sum_{p_j \, in \, r}(p_j \, . \, ab_j) \;\geq\; T_0)$,
where
RF_i is a fish i resistance factor
p_j is any pathogen j in r distance from fish i, ab_j is the ability of pathogen j to infect, and T_0 is a selected threshold.
3: **Get infected**
4: **End If**
5: **End For each**

The infection risk

Disease dynamics in the system depends mainly on the infection process (see *Algorithm I*) and fish health recovery process (illustrated in the following section), and these processes depend on many parameters, while in normal compartmental models such as SIR model, there are only two rates that measure disease dynamics: infection rate or contact rate and recovering/removing rate (Bjørnstad, 2005). The fish will get infected if there are enough pathogens in the surrounding area. The number of pathogens in any cell in the simulation space at any time depends on many parameters such as 1) position of fish farms, 2) number of infected fish in the all facilities, 3) water temperature and 4) sea current speeds and directions. Pathogen density is directly connected to the risk value in the space and time. Disease outbreak occurs only if there is a high density of pathogens and high density of fish, as in the following (Alaliyat et. al., in press):

$$IR\,(x, y, z, t) = K * I_v(x, y, z, t) * I_f(x, y, z, t) \tag{10}$$

where *IR (x, y, z, t)* is the infection risk value in position *(x, y, z)* at time *t*, $I_v(x, y, x, t)$ is pathogen density at time *t* at *(x, y, z)*, $I_f(x, y, z, t)$ is fish density at time *t* at *(x, y, z)*, and K is a constant. This equation, with two variables, that we will convert it to an objective function, in order to optimize by using PSO algorithm.

Optimal fish density and farm location

In such complex systems as marine aquaculture systems, it is difficult to change the environment (i.e. seawater) but the fish farm parameters (i.e. location and fish density) can be adjusted, specifically before issuing the farming licenses. As indicated earlier, we can minimize the infection risk (see equation 10) by control fish density and farm's location.

In this case, we have multi-objective optimization (MOO) problem (i.e. multiple criteria decision-making). We aim to maximize the aquaculture system production (i.e. increase number of fish) while minimizing the infection risk. In MOO, there is no single existing solution that simultaneously optimizes all the objectives because the objective functions are conflicting, and there exist a number of Pareto optimal solutions[4]. One way to solve MOO problems is to combine the objective functions in one single objective function by weighting each of them. Therefore, we define our single objective function[5] as it has these control variables: farm location in (x and y), and fish density $I_f\ (x, y)$. Our objective function is a combined of two objective functions: 1) maximize fish population (i.e. maximize the production) and 2) minimize the infection rate. We can write this combined objective function that we aim to maximize as:

$$J = w_0\ (1 - A_r) + w_1 \,.\, I_f\ (x, y) \qquad (11)$$

where A_r is the attack-rate (i.e. the percentage of the new infected fish over the number of susceptible fish in the beginning of the simulation period), $I_f\ (x, y)$ is the fish density, and w_0 and w_1 are selected weights that determine the influence of the attack-rate (proxy for infection risk) and fish density on the objective function value[6]. In order to achieve the goal of this study, we apply PSO algorithm to search for optimal sites distribution and optimal fish density in each farm.

PSO search space

Search space is the domain of the objective function (see equation 11) to be optimized. PSO will search in fish farm location (*x,y*), and fish density I_f to find best values that maximize the value of the objective function. PSO will try to increase fish population and farms' separation to increase the value of the objective function. The search space is three-dimension (*x,y*, I_f) multiplied by the number of fish farms to be optimized.

The accepted risk

As indicated earlier, we can't minimize the infection risk without regarding the fish density, and vice versa. In this study, each farm has limited values of fish density (i.e. minimum and maximum values). Therefore, we search for the optimal solution within a defined range of constrained values. The termination condition of PSO algorithm is whether a number of a defined maximum iterations or after a defined number of interactions without finding better solution.

[4] A solution is called Pareto optimal, - if none of the objective functions can be improved without degrading some of the other objective values.

[5] Objective function is a function of state and control variables, and when it is to maximum the objective function, it is called a fitness function.

[6] We have to normalize I_f and A_r before we use the equation.

Particle Swarm Optimization

In this study, we apply the particle swarm optimization (PSO) algorithm to search for the values of the control variables (i.e. fish density and farm's location) to maximize the objective function (equation 11). We modify the continuous PSO algorithm to solve this problem. The search space is discrete; it is the cell coordinate that contains two integer numbers (x, y) and the number of fish in each farm, I_f. Each particle represents a solution (i.e. vector of values of (x,y) and I_f) and modifies its position by applying the standard continuous PSO algorithm as the following:

$$\vec{v}(k+1) = w\vec{v}(k) + c_1\overrightarrow{R_1}\left(\overrightarrow{pbest} - \vec{s}(k)\right) + c_2\overrightarrow{R_2}\left(\overrightarrow{gbest} - \vec{s}(k)\right) \tag{12}$$

$$\vec{s}(k+1) = \vec{s}(k) + \vec{v}(k+1) \tag{13}$$

where

$\vec{v}(k)$ is the velocity of a particle at iteration k.
$\vec{s}(k)$ is the position of a particle at iteration k.
$\overrightarrow{R_1}$ and $\overrightarrow{R_2}$ are random numbers in the range of [0,1] with the same size of swarm population.
$\overrightarrow{pbest}$ is the particle's personal best solution has achieved so far.
$\overrightarrow{gbest}$ is the best solution achieved among all the particles.
c_1 and c_2 are learning factors, which will be fixed through the whole process.
w is the inertia weight:

$$w = w_{start} - \left(\frac{w_{start} - w_{end}}{M}\right) k \tag{14}$$

where M is the iteration maximum number and k is the current iteration, and we change the real position values to integer values that represent fish population and the indexes of the cells at each iteration.

2.2.2 Agent-based model

Fish disease spread in aquaculture systems can be modeled by ABM technique. In the following, we will describe the agent-based model (see Figure 1). The model contains two types of agents: fish and pathogen. The agents and the landscape have attributes whose values are updated in time-space domain depending on the relationships in the model.

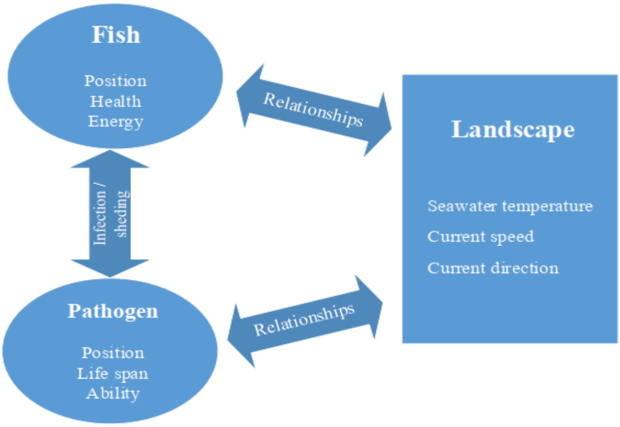

Figure 1: Agent-based model of fish disease spread

The fish agent model

Each individual fish $FA_i(t)$ has a resistance factor RF_i that the user can set between 0 and 1 for all individuals at the beginning, and then some noise is added to each individual value by using normal distribution functions to obtain some variation.

Health status update

Fish agents are categorized into three main health states as in the SIR model (susceptible, infected and recovered) (Bjørnstad, 2005). The fish health status is modified as shown in Figure 2. The susceptible fish $FA_i(t)$ gets infected if there are many pathogens around it with good abilities to infect and the fish has a weak resistance factor (RF) as the procedure in *Algorithm I*. Once the fish become infected, there will be a delay for a short period (latency period LP) before the fish get sick. In the sickness period, the infected fish are shedding pathogens and they have more mortality rate. We suppose that after the infection period the infected fish will enter the recovery/removed category (see Figure 2).

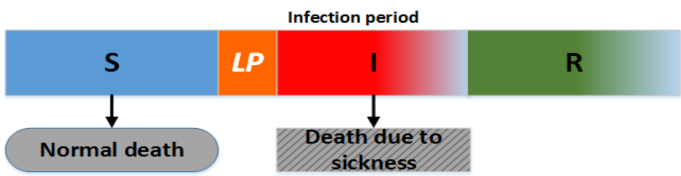

Figure 2: Fish health status update

Shedding of pathogen

The infected fish $FA_i(t)$ sheds pathogen $PA_j(t)$ at the same position where it is at each time step by a given probability. Different sources use different measure units and values (Rose et al., 1989; Gregory, 2008; Urquhart et al., 2008). The units are not single pathogens but are units that are measurable in the lab. Since the numbers are very high and computationally difficult to implement in the model, we set the probability to between 0-1 (adjustable) that an infected fish sheds a pathogen, but this pathogen represents a large number of pathogens.

Fish agent movements

Fish are swimming in the cages, and since we use a substantial time step in our simulations in this study (10 minutes), the positions of the fish are updating randomly at each time step as:

$$\overrightarrow{FA_i}(x, y, z, t + \Delta t) = \overrightarrow{R_i}\left(\frac{max_{x,y,z} - min_{x,y,z}}{2}\right) + \overrightarrow{FF_k}(x, y, z, t) \quad (15)$$

where $\overrightarrow{FA_i}(x, y, z, t + \Delta t)$ is the fish i position vector, $\overrightarrow{R_i}$ is a unit random vector in 3D, $(max_{x,y,z} - min_{x,y,z})$ is the fish farm dimensions, and $\overrightarrow{FF_k}(x, y, z, t)$ is the farm position in the simulation space.

Pathogen agents model

The pathogen agent $PA_j(t)$ has three main attributes (see Figure 1), position, ability to infect fish, and life span. Each pathogen has an ability attribute that the user can set between 0 and 1 for all individuals at the beginning, and then, some noise is added to the value of each individual to get some variation. Pathogen agents move by sea currents, and spread through fjord following normal distribution functions to have some diffusion as in equations 4,5,6 and 7. Pathogen life span is depending on the seawater temperature (see equation 8).

3 Simulation results

The model has 19 parameters that directly affect the behavior of an individual and thus the behavior of the whole system. Since the physical size of the fish farms was constant, the number of fish is proxy for fish density. The maximum number of fish in the farm is 1000 while you would expect to see about 1000 times more fish in an actual fish farm in the Romsdalsfjord (www.fiskeridir.no), then we use an approximate scale 1 fish in the model is equal 1000 fish. Table II provides an overview of the model parameters.

TABLE II: MODEL PARAMETERS

Parameter	Min value	Max value	Default value
Farm (i) location	*(-248.5,-148.5, 0)*	*(248.5,148.5, 0)*	
Fish number in Farm (i)	*1*	*1000*	*100*
Initial infected in Farm (i) (%)	*0*	*100*	*10*
Shedding probability (%)	*0*	*100*	*50*
Infection period (days)	*0*	*100*	*4*
Infectious radius (patches)	*0*	*20*	*1*
Prior immunity (%)	*0*	*100*	*0*
Mortality (%)	*0*	*100*	*1*
Mortality_normal (%)	*0*	*100*	*0.00001*
Pathogen-ability	*0*	*1*	*0.8*
RF	*0*	*1*	*0.8*
Weight (kg)	*0*	*10*	*4*
Current speed (m/s)	*0*	*1*	*0.20*
Current speed std.	*0*	*0.1*	*0.01*
Current heading bias (degree)	*-5*	*5*	*0*
Current heading std.	*0*	*90*	*45*
Temperature (°C)	*0*	*20*	*8*
Vaccinated			*Off**
Time step			*10 min**

*Parameters that select between many values or on/off.

3.1 Scenario 1: Sensitivity analyses of fish density

In this scenario, we built an AABSM that contains two fish farms located close to each other (i.e. distance between them is *9.6 km*) in the Romsdalsfjord, near the Midsund[7] municipality. One farm is *10%* initially infected and is shedding pathogens that spread to the second farm that was initially a susceptible (non-infected) farm. The aim is to investigate the effects of fish density on the attack-rate (A_r) (the attack rate is a proxy for infection risk).

The model was run with the default values in Table II for both facilities. We varied the number of fish in the susceptible farm across many different values, starting with 100 and ending at 1000 individuals, adding 10 individuals at each run. We measure the A_r in every run as the model output.

By conducting a sensitivity analysis of the susceptible fish population parameter, we were able to identify a threshold where the A_r is acceptable, and the fish population is maximum with this accepted risk.

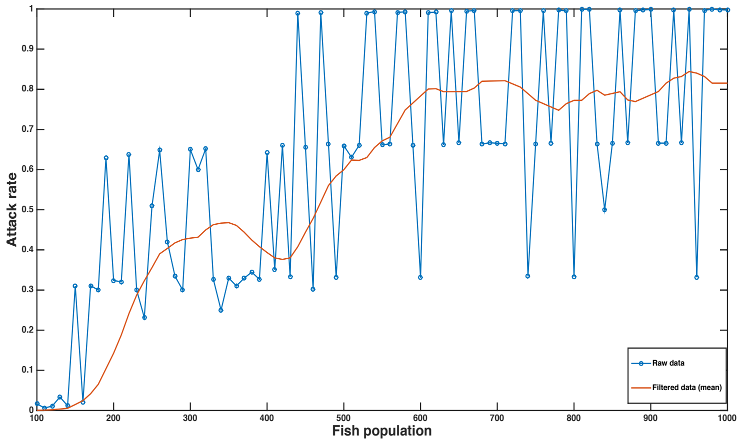

Figure 3: Attack-rate *vs.* fish population

Figure 3 shows the A_r for different fish population values, and shows that A_r is increasing as the fish population increases. The AABSM is a stochastic model, this may yield a variety of results when exposed to Monte-Carlo simulations using the same input parameter values. Figure 3 shows large variations of A_r values (blue line) because of the stochasticity introduced by the model and simulator. That is why we applied a mean filter to remove the noise (red line). By exploring the A_r response of the model to the fish density, we can derive A_r thresholds that are acceptable. The result shows that A_r will not exceed 50% when the average size of the fish population is less than 450 individuals. According to this result, we can hold the infectious under control in a case of disease spread by setting a threshold of the fish density (fish population = 450).

7 Midsund is a municipality in Møre og Romsdal County, Norway. It is part of the Romsdal region.

3.2 Scenario 2: A PSO algorithm to find the optimal fish densities and farm locations

Case A: Find the optimal fish density and location for a new fish facility that we want to locate near to the infected site.

In this scenario, we extended the AABSM from scenario 1, to vary the location of the susceptible farm in the (*x, y*) space domain with the purpose of reaching a lower A_r and a maximum fish density. We used the objective function that is derived from equation 11:

$$J = w_0 \, (1 - A_r) + \frac{w_1 \left(I_f \, (x,y) - I_f \, (x,y)_{min} \right)}{I_f \, (x,y)_{max} - I_f \, (x,y)_{min}} \tag{16}$$

where $w_0 = w_1 = 0.5$ (the desire to fish population is equal to the desire of the A_r on the objective value), $I_f \; (x, y)_{min} = 100$ and $I_f \; (x, y)_{max} = 600$.

We applied the default model parameter values described in Table II for both farms except for the *fish number* (i.e. amount of fish that corresponding to the fish density) in the susceptible farm that is being varied. The PSO algorithm was applied to automatically identify the model parameters in Table III that yield a highest value for the objective function, calculated as in equation 16.

TABLE III: PARAMETERS TO TUNE

Parameter	Min value	Max value
Fish population	*100*	*600*
X	*50*	*150*
Y	*-30*	*30*

Each particle in PSO represents a solution (i.e. vector of x,y,I_f). That is why we need to run the model for each particle at each iteration to evaluate this solution. In addition, because of the stochasticity in ABMs (i.e. random processes are represented by way of Monte-Carlo simulation), one simulation is not enough to evaluate the objective function in equation 16. This compels us to run it three times for the same parameter values to obtain a more reliable result. This is very costly in terms of computation, and the problem, therefore, lends itself better to parallel processing.

TABLE IV: PSO PARAMETERS

Population size	***10***
Dimension of the problem	*3*
Maximum iteration	*50*
c1 (cognitive parameter)	*2*
c2 (social parameter)	*2*
Inertia start	*0.9*
Inertia end	*0.4*
Upper limit on optimization variables	*x = 150, y = 30, f = 600*
Lower limit on optimization variables	*x = 50, y = -30, f = 100*

The PSO algorithm uses the parameters in Table IV to find the optimal solution. Figure 4 shows the simulation space; the red cells show the initial particle positions (i.e. points represent fish farm locations) at the beginning of the running PSO algorithm. The black line traces the best farm location that has been found by PSO. The PSO found the best solution in equation 16 (0.84, see Figure 4) which is the optimal farm location (50,-30) within the white rectangle (see Figure 4), and the associated optimal fish density (fish population = 506) at iteration 18.

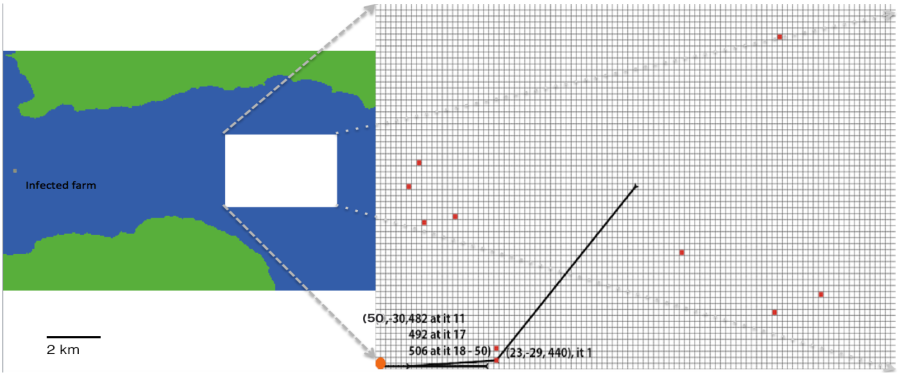

Figure 4: The left side shows the part of the Romsdalsfjord where is the simulation took place, and the right side shows the best solution tracking in PSO, red cells are the initial random particles' positions.

Figure 5 shows the PSO convergence when the model is running three times for each particle. The PSO needs only 18 iterations to identify the optimal values for the selected input parameters of the AABSM. Comparing to the previous scenario, PSO found optimal fish density in the white area (i.e. area around the location of fish farm proposed in scenario 1) that gives minimum infection risk ($A_r = 0$ in this case), while in the previous scenario $A_r=0$ is only achieved if the fish population is ≤150. PSO convergence depends on the algorithm parameters that balance the exploration and exploitation abilities of the PSO algorithm (Qian & Li, 2017).

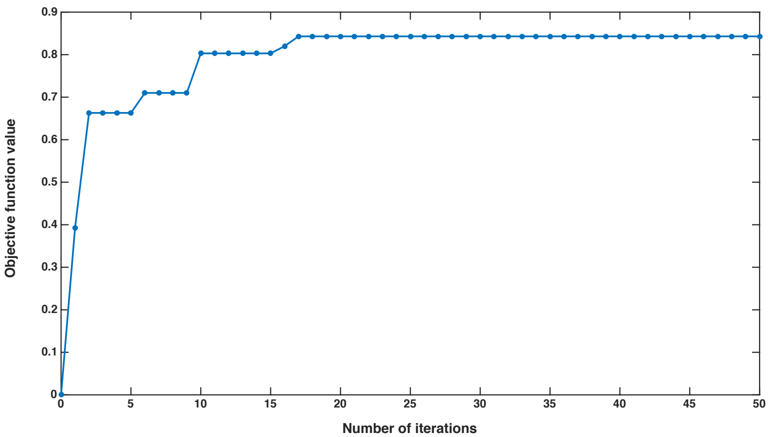

Figure 5: PSO convergence when the model is run three times for each particle, x-axis is the number of iterations vs. y-axis is the objective function value.

Case B: Find the optimal fish density and location for all facilities in an aquaculture system of three sites.

We extended the AABSM in case A, to include three farms instead of only two, and we vary the locations and fish densities for all farms, with the purpose of having a lower A_r and a maximum fish density. We extended the objective function in equation 16 to include the A_r and fish density to all facilities that form the system:

$$J = 1/3 \sum_{i=0}^{2} \left[w_0 \left(1 - A_r(i)\right) + \frac{w_1 \left(I_f\,(x_i,y_i) - I_f\,(x_i,y_i)_{min}\right)}{\left(I_f\,(x_i,y_i)_{max} - I_f\,(x_i,y_i)_{min}\right)} \right] \tag{17}$$

where $A_r(i)$ is the attack-rate in farm i, $I_f\ (x_i, y_i)$ is the fish density of the farm i, and w_0 , w_1 are selected weights (0.5 in this scenario).

The farms are located in the Romsdalsfjord, near the Vestness[8] municipality. In farm 1, *5%* of the fish is initially infected and is producing pathogens that spread to other, initially susceptible, farms *(*see Figure 6*)*.

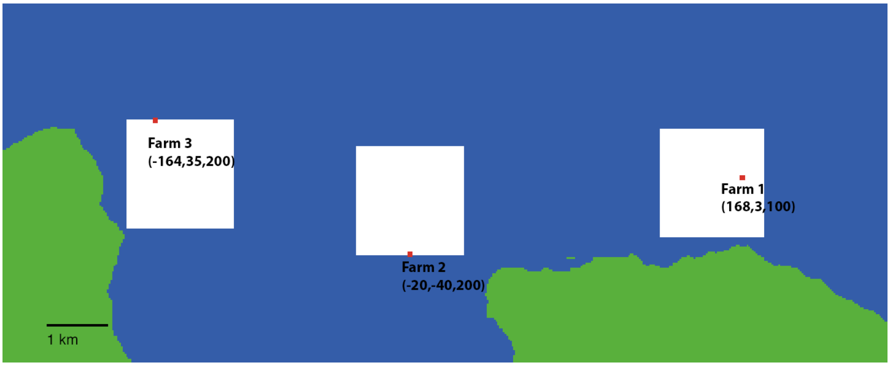

Figure 6: The map shows the part of the Romsdalsfjord where is the simulation took place and the best solution which the PSO algorithm found after 15 iterations (The red points show the farm locations in reference to the center of the system).

We run the PSO algorithm with the parameter values listed in Table V. Figure 6 portrays the simulation space. The white areas show the allowed locations for each farm, and the red cells show that the optimal solution (i.e. optimal fish density and location) has been found by PSO at iteration 15. Figure 7 shows the PSO convergence.

TABLE V: PSO PARAMETERS FOR CASE B

Population size	***10***
Dimension of the problem	*9*
Maximum iteration	*50*
c1 (cognitive parameter)	*2*
c2 (social parameter)	*2*
Inertia start	*0.9*
Inertia end	*0.4*
Upper limit on optimization variables	*x = x0 + 30, y = y0 + 30, f = 200*
Lower limit on optimization variables	*x = x0 - 30, y = y0 - 30, f = 100*
Farm 1 (x0 = 150, y0 = 0), Farm 2 (x0 = -20, y0 = -10), Farm 3 (x0 = -150, y0 = 5)	

The PSO algorithm started with a random set of parameter values that are limited according to Table V, and found optimal values for farm locations and fish densities that give the maximum value (0.55, see Figure 7) in the objective function. Figure 6 shows the optimal values that are found by PSO algorithm. For Farm 1, the optimal location is (168,3) and the fish population is 100. For Farm 2, the optimal location is (-

[8] Vestnes is a municipality in Møre og Romsdal County, Norway. Vestnes is part of the traditional district of Romsdal.

20,-40) and the fish population is 200. And for Farm 3, the optimal location is (-164,35) and the fish population is 200. We validated the PSO algorithm results by running the AABSM with the optimal solution several times to test the behavior and output of the system.

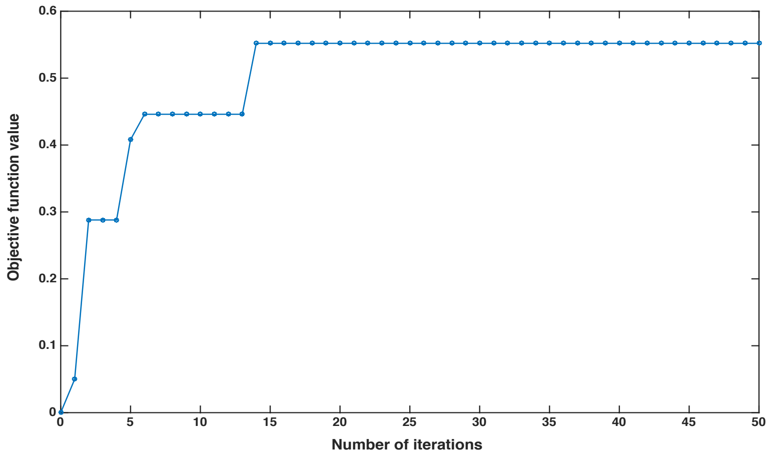

Figure 7: PSO convergence for aquaculture system in *Figure 6*, , x-axis is the number of iterations vs. y-axis is the objective function value.

4 Discussion

The infection rate in the aquaculture system depends on a variety of environmental, physical, and biological factors such as sea currents, water temperature, and fish densities and farm locations. The infection process at any location at a specific point in time (t) depends on fish and pathogen densities (see equation 10). Thus, by optimizing the fish density and location of facilities, we can reduce the infection risk and subsequently the outbreaks of diseases. We developed a method by which we explore the alternative values for these variables in order to find the optimal combination of values, i.e. the optimal solution that minimizes infection in the system and that would cause the system to keep the infection under control. We tested the method, presented in this paper, using different simulation scenarios as described in section 3. The results demonstrate how the method may help us identify the optimal values for facilities with fish densities and locations that reduce the risk of disease spread and thus increase the production.

4.1 Simulation results

4.1.1 Sensitivity analyses of fish density

A large number of fish crowded together in a small area provides an environment conducive to the development and spread of infectious diseases. In a crowded environment, fish are stressed and more susceptible to disease (Ogut, 2001). Pathogens can reproduce faster in a crowded aquaculture system, and they can easily find fish to infect. A higher density of fish results in a high contact ratio and, consequently, a high infection rate (calculated in *Algorithm I)*, leading to disease outbreaks.

Larger fish populations will affect fish swimming behavior and limit their access to food (Alaliyat et al., 2014; Alaliyat & Yndestad, 2015). However, more fish usually means a larger fish production. Therefore, we need to find the optimal fish density for a fish farm that results in the highest production while considering the hazard of infectious diseases and keeping them under control.

By applying sensitivity analysis of the attack-rate to the fish population (Figure 3), we can derive a threshold of fish population (proxy for fish density) that gives an acceptable increase in the attack-rate (an acceptable infection risk). The threshold for the fish population is 450 if we require that the attack-rate must be under 50%. Deriving such thresholds helps us develop strategies to combat and control infectious diseases.

The infectious fish disease outbreak occurs only if the attack-rate passes the threshold (R_0). This is equivalent to the reproduction number in the compartmental models that determine the equilibrium of the model (Diekmann et al., 1990). The infection risk in the susceptible farm depends on the densities of the pathogens and fish (see equation 10). Pathogen density generally depends on many parameters such as the fish density of the infected farms in the aquaculture system, the distance between the farms, the seawater temperature, and the speed and direction of the sea currents (Alaliyat et. al., in press). The fish density in the susceptible farm is the second main factor that affects the infection rate. Therefore, finding the optimal value of fish density which will not allow the attack-rate to exceed a certain value (e.g. 50%), will reduce the risk of disease outbreaks and lead to a sustainable fish industry.

4.1.2 A PSO algorithm to find the optimal fish densities and farm locations

The AABSM presented has many parameters that affect the dynamics of the model. In scenario 1, we tested the sensitivity of its dynamic behavior to a single parameter (*fish density*) by running the model across several different values of that parameter and by conducting a follow-up analysis. This process is very time consuming, and it becomes more difficult when varying several parameter values simultaneously (Calvez & Hutzler, 2006). Therefore, the parameter setting process of the AABSM can become very extensive, tedious and time consuming, provided we have no automatic strategy for quickly exploring the parameter space to find the optimal values (maximizing the objective function).

The choice of strategies for exploring the parameter space depends on the motivation for building and using the model. When using the AABSM for fish industry management, we need to find the AABSM parameters values that may support the sustainability of the fish farm industry (Alaliyat, 2014). Therefore, we applied the PSO algorithm to find the optimal combination of values for the fish density and the location of the farms, i.e. the one that give highest value in equations 16 and 17. We started with the simplest scenario (Figure 4) to demonstrate the ability of the PSO to find the optimal solution (farm location = (50,-30) and fish population = 506) and thus to validate our results. Figure 5 shows that the PSO needs only 18 iterations to search through the parameter space (search domain) (Table III) in the pursuit of the optimal solution. The use of the PSO algorithm provides an opportunity to explore the effects of changing the value for more than one parameter at the same time (e.g. fish population and farm's location). Thus, we found an optimal farm location (50,-30) that gives the opportunity of operating a fish farm at a fish population of 506 with minimum risk of infection (attack-rate = 0 in this case). Without the use of the PSO algorithm, this attack-rate = 0 is only achieved when the fish population is less than 150 (see Figure 3). This result shows the possibility to increase the fish density to three times its initial value (increase fish population from 150 to 506) by changing the location of the farm to the optimal place, while we keep the risk at minimum value.

In the scenario of the three aquatic sites (Figure 6), we extended the objective function to include all the sites (equation 17). We exposed the model to 50 iterative simulations to demonstrate its ability to identify a better solution (see Figure 7). Our results show the ability of the PSO to find the optimal combination of values of the fish density and locations of the farms that yield the highest value in equations 17. The PSO found the optimal values in iteration 15. In this scenario, the PSO algorithm found the best solution in fewer number of iterations than the previous scenario, although the number of exposed variables for the optimization process is larger (9 variables), because the best solution is clearly separated in this case (farm 2 and farm 3 are not infected). The PSO algorithm is a stochastic optimization technique and it is convergence depends on the initialization process and the solution space (Qian & Li, 2017). The PSO searches through a large number of parameter values to find the optimal values of fish density and farm locations that also stabilize the system and keep the infection under control (find the maximum value of the objective function).

4.2 Using the PSO algorithm

If we use the "NetLogo behaviorspace" to explore the three input parameters in Table III within their suggested domains, then we have to run the AABSM 100*60*500 times. On the average, each run requires approximately 10 minutes, which means the simulation of this scenario must run for $3 * 10^7$ minutes. Therefore, we need to develop a strategy to explore the model's input parameter values in an efficient way. Using SI algorithms such as PSO, help us adjust the input parameters of the model depending on the feedback from the model output. The PSO algorithm explores the possible parameters values in an efficient way to find the optimal values in few steps.

The global computation time required to run the PSO algorithm is *(n*N) * T,* where *n* is the number of particles, *N* is the number of iterations, and *T* is the time to compute the objective function. The PSO with the parameters in Table IV needs 10*50*10 minutes only, and *n* is 10, *N* is 50, and *T* is 10 min on average. The PSO substantially reduces the time requirement, but still needs very long time to complete the calculations. Based on the previous cases, it takes approximately three and a half days to complete each simulation. There are two ways to reduce the PSO simulation time; by reducing the particle number or by distributed computations. Reducing the particle number affects the ability of the PSO to find the global maxima. This makes the use of distributed computations the best choice, - enabled by the fact that the simulated models are independent of each other.

Stochasticity

Due to the stochasticity of the agent-based model and the simulator, repeated agent-based simulations may yield slightly different results, - even if the underlying model is exactly the same. Therefore, one simulation is not sufficient to evaluate the objective function. We studied the stochasticity of the AABSM and NetLogo simulator by running the model with same settings several times. Then, we analyzed the output of the model (i.e. objective function value in equation 17) by assessing its variance. The variance is $\cong 0.14$ when the number of simulations is 5, while it is $\cong 0.1$ when the number of simulations is 10 or 20. To avoid obtaining unexpected values (abnormal) in which the PSO is stuck, we run the model three times to evaluate the objective function.

Validation

We follow the PSO trajectory to identify the optimal solution. Thus, we prove that the PSO is exploring the input domains and is converging to the highest value of the objective function. Then, we validate the PSO algorithm with the optimal values by running the model several times under the optimal parameter values so as to demonstrate the capability of the PSO to drive the system to produce the optimal solutions.

GAs vs PSO

The PSO algorithm converges faster than GAs, but it is more likely to get stuck at a local minimum (Alaliyat et al., 2014). However, by modifying the PSO and adding evolution to it, it can avoid becoming stuck at a local minimum.

4.3 Agent-based method to simulate fish infectious diseases

ABMs have been widely used for decision support in different fields (Skov-Petersen, 2008). By using agent-based methods, we are able to study specific spatial aspects of the spread of infectious diseases and address the stochastic nature of the infection process in fish diseases. Agents (fish and pathogens) are described individually in a heterogeneous population, and ABMs can also include all external factors that affect fish disease outbreaks such as the interaction with the wild fish, ship traffic, and other marine activities. Moreover, ABMs provide a flexible framework for analysis and testing. For example, adding more agents to the model, adjusting the complexity of agents by changing their behavior and changing the environment and its dynamics.

Agent-based method is the appropriate method for simulating the spread of infectious diseases in fish to identify the infection risk. In this complex system (spread of fish infectious diseases); it is difficult to describe the aggregate dynamics using differential equations without reference to the behavior of the individual agents that cannot clearly be defined through aggregate transition rates, - for example, fish stress and swimming behavior. While, by modeling how agents behave individually, the aggregate dynamics emerges from the behavior of all the agents (fish and pathogens).

ABMs typically operate with many parameters, and we must develop a method to automatically explore the parameter space effectively since systematic exploration is impossible when the parameter space is huge. Using PSOs to explore the parameter space saves a great deal of time and makes the ABMs more accurate for use in management processes.

ABMs have some limitations in terms of their application to simulate fish diseases. We cannot consider the entire population of fish and pathogens, respectively, and we must scale down the system in the space and time domains in order to reduce the computational complexity.

5 Conclusions and future work

To ensure an environmentally sustainable aquaculture industry, it is essential to use reliable methods and models for its analysis and management. In this study, we developed an agent-based model to simulate fish disease dynamics within and between many fish farms in Norwegian fjords. Then, we presented a framework that uses a PSO algorithm to find the optimal combination of values for farms locations and fish densities, i.e. the combination that yields an optimal aquaculture system with the highest possible production. For this reason, we used an objective function that is a weighted average between the fish density and the infection risk, in order to select the best optimal system among those generated by PSO. Since the physical size of the fish farms was constant, the number of fish was a proxy for fish density in the farm and the attack rate was a proxy for infection risk. The optimal aquaculture system is obtained by finding the best farms distribution and optimal fish density in each of them, i.e. the combination that minimizes the infection risk (i.e. that maximizes the production by maximizing the number of healthy fish).

In this paper, it has been demonstrated how effective the use of an agent-based approach is in the simulation of infectious diseases. In fact, ABMs can include specific spatial aspects of the infection spread and address the stochastic nature of the infection process for fish diseases. ABMs can also include all external factors that affect fish disease outbreaks such as interactions with the wild fish, ship traffic, and other marine activities. On the other hand, ABMs have many input parameters that altogether determine the global behavior of the system. Each of these parameters can take a wide range of values. This makes the identification of optimal values a complex and time-consuming process. Thus, we used a PSO algorithm in order to explore the parameter space of the ABM in a search for the optimal combination of input values (i.e. fish density and farm's location), so as to, eventually, attain the desired behavior. The use of the PSO algorithm helps in identifying optimal ABMs input parameter values based on the feedback from the ABMs outputs (i.e. objective function values).

The method developed is validated by running the model repeatedly with optimal parameter values; this proves also its capability to drive the system so as to produce predefined behaviors and outputs. Our simulation results show how the PSO algorithm presented finds the optimal values of fish densities and farm locations that keep the disease prevalence under control. In addition, the algorithm convergence is rapid and guaranteed; in only 18 iterations, it finds the best solution (fish density and farm location) that results in an increase in the fish density up to three times its original value while keeping the risk of infection at the same level.

As the next step, the plan is to apply the method, presented in this paper, to other scenarios that include more fish farms and more complex contexts. Using other optimization algorithms, such as genetic algorithms, to conduct a comparative study with the PSO is also a part of the future work. Moreover, improving the objective function is an important task. However, simulating more complex scenarios requires the use of distributed computations since the simulation time on a single computer will take a very long time. Thus, we are aiming for the application of parallel computing. This will allow us to simulate larger areas including many fish farms, include more agents (fish and pathogens), simulate more realistically sea currents with tides and include seasonal variation in seawater temperature.

Conflict of Interest

The authors declare that they have no conflict of interest.

Ethical statement

This article does not contain any studies with animals performed by any of the authors

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