

Modelling the Impact of Coordinated Policies to Reduce Sea Lice Abundance in Farmed Salmon Populations

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ABSTRACT

Farmed salmon has large potential as a source of food to the worlds growing population. It is also an important source of income, both to local communities and Norway. The introduction of large biomass into the sea by the fish farming industry greatly increases the available hosts for parasites in Norwegian fjords. Due to the great outnumbering of wild populations by farmed salmon, the management of aquaculture has an effect on the environment, as host density increases disease and parasitic development. This salmon lice population growth has resulted in governmental restrictions on industry expansion, as the effect of some treatments is decreasing due to intensive use. The problem is also a large cost to the producers, who estimate that more than 10% of production cost is caused by the lice problem.

The model consists of sub-models of the biomass in several locations within one area, lice populations and reproductive processes, dependent on temperatures, abundance and infection pressure divided between internal and external infection pressure on farm locations. The model aims to clarify the intensity of relationships governing some of these challenges, in order to find leverage points for improving the situation. The model is a framework for studying coordination of risk mitigating actions through scenario simulation. This allow users to test simple policies for lice mitigation, coordinated fallowing and pre-emptive treatment of salmon lice in locations. Further, the model forms a framework for expansion with the large sets of reported data openly available in order to increase its prediction power and thus be used as a tool to aid planning events. By making this framework available and easier to use, the value of data collection to operators in the industry may be made clearer, further improving the basis for model expansion in the future. We demonstrate that recreating the system and simultaneously using policies recommended by research, enhances the impact of parasite mitigating policies.

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1. INTRODUCTION

The industry of salmon farming is becoming increasingly important both as a source of feeding the world's growing population, and as a source of income to Norway and other nations where aquaculture is rapidly becoming a substitute for traditional fisheries. Farmed populations are responsible for the increase in fish harvests the last years, and this is an important contribution when estimates indicate that the world's food production must double to meet the increasing demands in the coming 50 years (Marra, 2005). One of the most significant problems facing the Norwegian salmon farming industry is the salmon louse *Lepeoptheirus salmonis*. It is a parasite that attach to Atlantic salmon, and its abundance grows rapidly with the increase of available hosts in Norwegian fjords. Farmed salmon greatly outnumber wild population of migrating salmon, up to 250 - 700 times (Johansen et al 2011). The larvae released from infected fish spread between farms (Samsing et al 2017), making networks of infectivity between neighboring farm locations. There is clear evidence pointing towards an active host-parasite relationship being the main driver of the exponential lice population growth when great concentrations of salmon biomass are put into fjord ecosystems (Salama & Murray 2011, Jansen et al 2012), making management of biomass an important part of parasite mitigation.

This thesis describes an exploratory simulation model that reproduces production results from a real aquaculture company based in Sognefjorden. The model is built using system dynamics methodology and software¹, which let us input reported datasets and equations in order to experiment with less known variables and policies in a model framework. The method is especially suitable when studying systems that relate in a coupled and non-linear manner, as pointed out by Forseth et. al. (2017): *The impact factors were considered separately, whereas in most cases, several factors impact Atlantic salmon populations simultaneously. The interactive effects of two or more impact factors may be non-linear, unpredictable, and consequently difficult to study.*

The thesis focuses on salmon lice as a problem to aquaculture, and the operator's influence on the biological system through his daily decisions.

While the real locations are relatively close to other companies' locations, and locations holding other species farmed in the sea, the study is isolated to one license holder, and the four salmon-license locations Osland operates in Sognefjorden: *Torvund, Sørevik, Måren and Mjølsvik (Figure 1).*

¹ Stella Architect, ver. 1.6.2, Isee systems



Figure 1: Map of the Osland Locations showing even number year locations in yellow and odd number year locations in red, divided in two zones by the red diagonal line.

The industry and individual farmers have a clear responsibility when regarding the spread of disease and negative impact on the environment, since sea-based aquaculture is exposed to its surrounding biological environment through the commonly used open net cages that let water from the surroundings float freely in and out of cages. Hence, the sea lice problem does not only concern the aquaculture industry.

The model is not an optimization tool first and foremost, but an exploratory framework. This can help operators and other actors establish a testing and validation environment for combining research results and policy recommendations that affect their surroundings. The complexity of these systems and the biological and economic value of the industry creates a problem that is an interesting subject for modelling within the system dynamics method, which forms the scientific approach to this paper.

While prior study suggests that coordination of measures and active area management on a local scale might help reduce the salmon lice problem (Werkman et al, 2011, Samsing et al, 2017), the implementation of such measures are not widely used by operators in the industry, and their effects remain to be verified in a real system. This paper aims to help implementation of such measures by showing effects through system dynamics modelling, and creating a framework that resembles the real system closely enough to be valuable in pre-implementation training and further policy work.

The model seeks to reproduce the growth pattern of farmed salmon biomass in a four location system operated by one licence holder, in order to test:

- That the timing of introduction of fish to sea, and that partial or full coordination of

following gives results in lowering and moving the peaks of lice infestation levels according to research by Werkman et al (2011).

- That timing and varying coordination of treatments used to counter lice is important also beyond farm-level (Hamza et al. 2014), because of the spread of infection between neighbouring locations (Kristoffersen et al 2014, Salama & Murray 2011).

By simulating the systems and introducing isolated policies based on prior research, the model helps study of the enhanced impact of positive developments by coordination and timing of introduction, location selection, coordinating following and timing of treatments more than if treated and managed individually. This is presented in an intuitive way that facilitates learning.

To the farmed biomass model, we add several sub-models that show how even relatively small operators in this industry have an effect on their immediate ecological surroundings. The scope of this thesis is how aquaculture is contributing to increased salmon lice population growth by introducing high host densities throughout the year, and suggesting changes to management and regulations that may be altered to improve on the situation. We add to this a financial model that illustrates to the user how changes in policy may change the problematic behavior and hence the costs or profit of the aquaculture operation².

There are several specified sub-models that focus on key factors and limitations to the industry;

- Government policies like stocking density, maximum allowed biomass (MAB), cage sizes, louse counts and so on.
- A biological lice model dependent on fish biomass, treatments, temperature and reproduction rate.
- A Treatment module describing effects of treatment strategies.

These sectors are connected and simulated in order to capture the non-linear relationships we expect to see when trying to manage a biological system (Ford, 2010, p.24 - 26). We simulate over a five-year period in order to capture long-term effects of any policies we want to propose, especially when these have an impact on environmental issues and wild populations.

The operators of aquaculture have to account for these exogenous variables over relatively long cultivation periods, where decisions taken at early points in time have a delayed effect on growth and quality of the salmon population. This leads to a complicated planning process and management of large quantities of operational data in order to improve and ensure close to optimal responses to changing conditions.

While there is no shortage of research on the problem of parasite behavior and consequences to aquaculture, there are relatively few decision support models available that explore

² The economic sector is treated separately in a thesis due August 2018

relationships beyond cost-benefit analyses (Hamza et al 2014), in direction of the dynamics between biology, ecology of diseases and population dynamics.

The following chapters discuss the literature supporting this thesis, followed by an analysis describing the literature that is used in building the model. The third chapter is an overview of the model framework, with focus on key variables and equations. This structure is then validated, before policy options are tested against the base run, ending with conclusions³.

2. BACKGROUND AND LITERATURE REVIEW

Most of the available research used in this paper is focused on specific aspects and dedicated to testing quite narrow hypotheses, and in some cases a mathematical language barrier, which reduces the availability and application to operators in the real system. While a system dynamics modelling may be applied to conventional mathematical models, the real utility of these models is that of studying several and nonlinear causal relationships under one framework, preferably built on these former research papers and its equations for the best possible response when compared to real systems (Morecroft, 2015, p63).

When building the fish production and population growth model, we were able to look to other production models within the system dynamics framework, such as described by Morecroft (2015, 120) and others. The challenging part of this process is the timing of very limited production slots when moving through different stages and sizes, before being introduced to sea, when fish go from cohorts to locations. In this we rely on several logical functions and built-in statements in order to recreate the operation and population growth in the system. The learning point of this exercise is the great difficulty of planning up to a year in advance how much biomass you want to introduce and how much is needed to stay close to maximum allowed biomass (MAB), even when a model is built to aid in this task. We are not familiar with all aspects of how this planning process accounts for variability in the fish weight growth and other factors in the real system, but it may be assumed that optimal production is difficult to achieve when managing a biological growth system with long delays between decisions being taken and visible results occur (Ford, 2010). Prior work within system dynamics methodology on parts of the problem statement includes a study by Hamza et al (2014), who focused on the development of a lice population in an isolated location, and the effect of pre-emptive treatment to reduce abundance peaks and costs associated with treatment of salmon lice. Natural fisheries with focus on maximum sustainable yield,

³ *The complete model was developed in cooperation with Erica Jane McConnell and Md Rabbi Fazla Alam. The description of the Salmon production sector of the model was written by McConnell, and is tested further in a thesis due June 1st 2018.*

unknown populations and investments are studied by Moxnes (2010) and Ford (2010) among others.

The environmental and operational data in this paper is supplied by Osland Havbruk and cooperating research entities. In addition, much of the data on biomass and lice is available online from Barentswatch and the Norwegian Directory of Fisheries.

The data collected as basis for this paper is therefore considered to be well suited to isolated results and parameters used in the model. This is theoretical based on real world data provided by commercial actors and available reports to be used as a sensitivity analysis of system changes in policy in order to provide better solutions to long term problems.

The dynamic connecting aquaculture biomass and the abundance of planktonic stage lice is well documented in the case of sea lice in Norwegian fjords.

Research suggests that salmon lice may be the main constraint to aquaculture expansion in Norway (St. meld 16, 2014). Specifically, Jansen et al (2012) describe a potential for infectious disease as a potent negative feedback mechanism that limit industry growth.

The model is built on results indicating that farm size (measured in biomass) matters to the infectivity of salmon lice and their reproduction rate. This comes from a parasite – host density relationship that drives their population dynamics, which is described by Salama and Murray (2011), Werkman et al (2011), Jansen et al (2012) and others. Further, there is work in support of there being a significant hydrodynamic transfer of parasites between two or more farms, although these are modelled as being of constant population size by Salama and Murray (2011), arguing for the geographical placement of aquaculture locations as an effective means of limiting lice abundance. The real system has populations that are changing dramatically even on a local scale since biomass in farms is so large compared to the wild population. Also, this study leaves the wild population out of the system of parasite-carrying agents.

In addition to dispersal in the water column, lice transmission through long distance fish movement is possible (Krkosek et al 2009), but probably not as much of a problem as the hydrodynamic transmission between local networks of farms. To wild fish, this is necessarily an important variable in infection, as discussed by Werkman et al (2011), as the mode of transportation determines the potential reach of infectious lice. The effect of coordinated fallowing strategies is discussed by Werkman et al (2011), proposing different levels of synchronized, partially synchronized and unsynchronized strategies for infection pressure, while reporting that isolating locations from other infectious sites minimize infection risk. Lice have reproductive rates and growth dynamics that are temperature dependent (Krkosek et al 2009, Stien et al 2005) which also in part influence the distance planktonic stages of sea lice may be transferred after dispersal from reproductive lice.

Treatments are an important countermeasure to control sea lice abundance, and while different types of treatments and developing technology have an impact on lice mortality rates and fish feeding patterns and welfare, some chemotherapeutic treatments show signs of declining effect with increase in use (Denholm et al 2002), indicating that alternatives to these

substances are important to ensure effective treatments in order to sustain current production levels in Norwegian waters.

In addition to treatments, Kristoffersen et al (2014) and Hamza et al (2014) (one of few studies applying system dynamics as a method) emphasize the importance of keeping infestation low at infected sites, both to decrease the peak infection levels, but also on a local scale to minimize inter-location infection. Hamza et al (2014) study effects of timed treatments in one location only, leaving the effect of external infection pressure (EIP) outside the model boundary.

As for study of internal infection pressure and lice development, Stien et al (2005) and Kristoffersen et al (2014) develop models on predicting the next generation abundance by observing pre-adult and adult males (PAAM). This is the key predictor of next stage infestation, in addition to calculating external infection pressure from nearby aquaculture locations, which is especially influential in the first 16 weeks of a location being stocked with non-infected fish, as well as in periods succeeding treatments. This indicates the importance of reducing EIP either through management policy, timing of treatments, isolation of production areas, or other measures that reduce the EIP. The question of whether or not previously treated salmon cohorts are more readily exposed to later infections of sea lice is not documented, and was subsequently dropped from the problem formulation.

The lice population growth and its sub-models connected to treatments, the wild population and looping back to the farmed salmon population was built based on an aging chain, as this model structure gives a basis for tracking some of the life stages of lice, as its attributes change with development stages. This model was arrayed to create one lice cohort per salmon location. Over this base model, there is a separate structure to capture the force of infection between the different locations, as these are placed with different distances separating each other. The structure itself was inspired by Duggan (2016), who described the application of S-I-R models applied to one population system to model the transmission of tuberculosis between different age cohorts of a population, where the age cohorts interact with differing frequency, and therefore have different transmission parameters between them. This is developed to match the present problem definition, which describes the interaction between a host and a specialist parasite.

A significant difference however, is that sea lice do not necessarily come one per host (susceptible – infected - recovered), but may infect one host more than once. This means that we don't have one constant population that moves through stages of susceptible, infected and recovered and gives the nonlinear infection rate that these models often show. This is important to properly model the reproduction of lice and the consequences of high levels of infestation, and there is therefore made several changes to this structure.

For variables as input to lice population growth and infection, the model relies on published results of other research. While this is a topic widely studied, some have proven especially valuable, on which the model supporting this thesis is built and calibrated against as a part of the validation process.

DATA COLLECTION AND ANALYSIS

The Norwegian salmon industry is well suited for study and model development, as much of the key data for developing the parasite – host population dynamics models is collected continuously. This includes host population data of locations, biomass, and population sizes, as well as data concerning lice counts over several of the later stages of lice development. When analyzed together, these datasets allow estimation of internal and external infection pressure among different locations, and estimations on the parasite abundance dependency on host biomass (Aldrin et al 2017). This data is available through the Barents watch and directorate of fisheries' websites.

Hence, the data used in building the sub-models of this systems are based on different expert opinions and papers, compiled in a dynamic model that lets actors explore the combined consequence of several documented and nuanced effects. When describing the production model, we rely on personal correspondence with Erik Osland and his descriptions of how the process works and on what basis management decisions are made.

Werkman et al 2011 and Kristoffersen et al 2014 discuss similar models for the risk of infection at one location being effective on the infection pressure of another in the same region. It should also be noted that Werkman describes a general model for pathogen transfer between locations, while Kristoffersen specializes on the spread of salmon lice abundance. Data for fish counts, lice counts and much of the production data that we use for this model is published online by governmental bodies like the department of fisheries in Norway (fiskeridir.no). By combining relatively easy access to data and a low threshold for using the model interface, we hope that the model may be adopted as a tool for various decisions taken by the participant to the project, and that it may in that way contribute to an understanding of how the industry operators and governing bodies actually affects its environmental and biological surroundings.

Key parameters with sources are added in the appendix.

3. MODEL AND EXPERIMENTAL DESIGN

Overview of the Model Sectors

The model is put together by several smaller models that interact. At the center of the model, there is a production model that shows how fish biomass grows on land in pre-smolt stages, and how these are distributed into sea-based locations. This production model is used for recreating the operation of the fish farmer, and it is a foundation on which the other sub-models are built. In addition to the farmed fish, we have a variable of wild fish, which varies with seasons to simulate a wild migratory salmon presence. This small model is mostly of interest as an input to the lice model, which consist of three separate sub-structures.

The first is an aging chain showing the most important stages of lice development in order to show how lice reproduce and establish the abundance at different stages, where lice have different effects on their surroundings. Attached to this (the second) is an inter-location infectivity model, that feeds into the most important flow of the lice model, the “attachment rate” in order to show how lice infection pressure originating at one location affects the others. The third part of the louse subset of models is the treatment module, which acts as a policy module on the problem of lice infestation. This directly affects the attached lice mortality in the locations in which a treatment is used, but also shows how that mortality affects the infestation pressure of following generations on own and other locations` infection. This module also feeds into the production sector, affecting growth of fish and their mortality, as well as to a financial sector accounting for costs of treatment.

The financial model keeps track of operation costs, and helps users identify the outcome of policies that are chosen in economic terms, which we believe to be a priority for operators encouraged to implement suggested policies that change long term impacts of multi-location fish farms.

3.1 Model Overview – Production and Growth Sectors⁴

Section 3 describes the production and fish growth sectors of the aquaculture operation run by Osland Havbruk AS. The model is run over a total duration of 5 years (1825 days), and starts on January 1st.

3.1.1 Assumptions and limits of the production and growth sectors

There are a number of assumptions built into the sectors of the model, explained below.

3.1.1.1 Juvenile Growth Sector

Osland Havbruk produces their own fry, and the fry can remain at a small size, under 2g, by being kept at 7°C and fed minimally (Osland, 2018). For this reason, the model assumes that Osland Havbruk always has the capacity and ability to produce as many smolt from their stock of fry as they need, at any given time.

The process of smoltification (transforming the freshwater parr into saltwater smolt) is not included in the model. This process takes place during the last stage of parr growth, and when it takes place is decided by the farmer. As it has no effect on the growth of the parr, it has been omitted from the model.

3.1.1.2 Juvenile Feeding Sector and Fish Feeding Sectors

As Norwegian law states that aquaculture operations should have acceptable water quality, including among other factors levels of water circulation, dissolved oxygen, and algae, (Bruland, 2016) the assumption has been made that these variables are within acceptable limits and are outside of the boundaries of this model.

The feed conversion ratio, (the amount of food needed to produce one unit of growth) changes over a fish's lifetime. Fish appetite is also dependent on many factors, including fish

⁴ The overview of the production and salmon growth sectors (3.1 – 3.1.6.4) was written by Erica McConnell (2018) in a paper discussing public policy changes to the aquaculture industry.

size, time of day the fish are fed, and access to light (Bolliet, Azzaydi, Boujard, 2001). For simplicity's sake, the feed conversion ratio has been set to an average over the fish's lifetime, rather than changing with the size of the fish, and the assumption has been made that the fish eat all the food they are given.

It is also assumed that the fish are all exactly the same weight, where in reality there would be some variation in fish weight within a cohort. There are methods, such as “grading” (separating the larger fish from the smaller ones) which minimize the variation in parr and fish size (Stead and Laird, 2002). The stocks of “parr weight” and “fish weight” can then be thought of as an average weight of one fish in the cohort.

3.1.1.3 Sea and Slaughter Sector

The model assumes that there is always available capacity to slaughter. Osland Havbruk contracts slaughter to an outside company, who provide their own boats and equipment (Osland, 2018). Whether or not boats are available is out of the control of the fish farmer, and outside of the limits of the model. The model assumes a fixed mortality rate in this sector. Usually, there is higher fish mortality in the 1-2 months after the smolt have been introduced to sea (Salmon Farming Industry Handbook, 2017). But with a lack of data on the magnitude of this change, the model uses a fixed mortality rate.

3.1.2 Juvenile Growth Sector

Osland Havbruk does not buy smolt from another company, but instead produces its own smolt from fry. They have three rooms (Figures 2 – 5) in which they grow the fry from parr to smolt in tanks. To reflect this set-up, the juvenile growth sector is built to match the physical facility. The capacity of fry, parr and smolt in the rooms in the model does not exceed the capacity of the facility.



Figure 2 - Salmon fry Figure 3 - Tanks where salmon fry are kept



Figure 4 - Tanks in room Figure 5 - Tanks in room 2

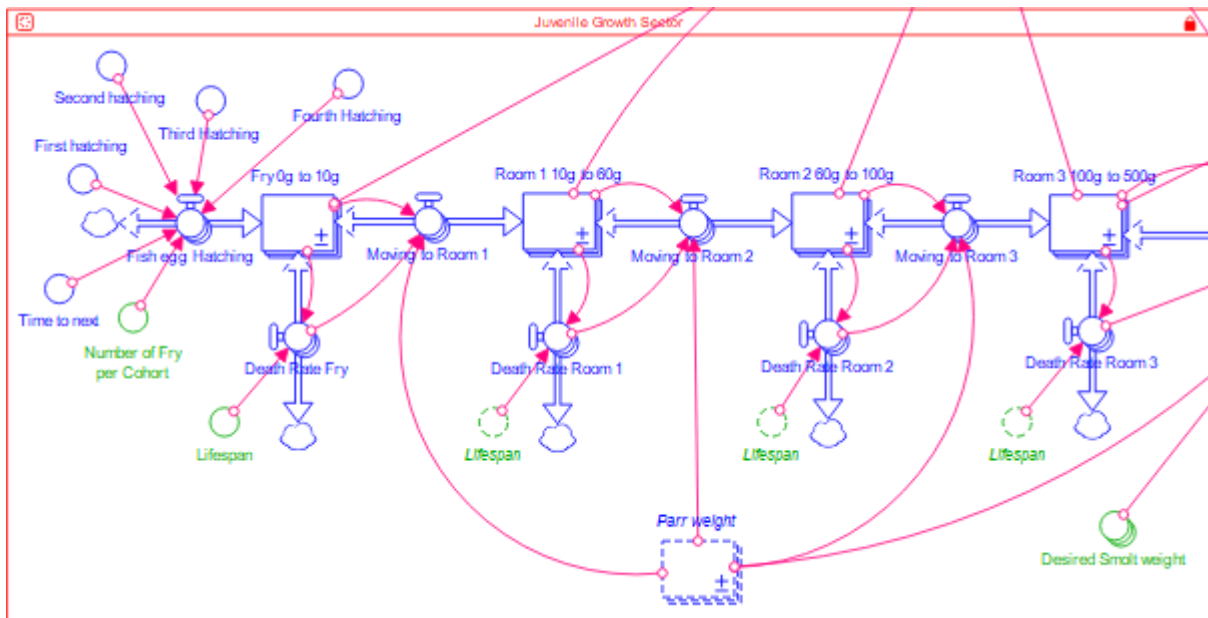


Figure 6 – Juvenile Growth Sector

This sector (Figure 6) is an aging chain, with arrays. There are four cohorts, one for each location Osland Havbruk has in the sea. The “number of fry per cohort” is the maximum

amount allowed at one location at sea with 6 cages – 1 200 000 (Bruland, 2016) – plus the amount expected lost due to the natural death rate – 20 fish per day over approximately 240 days (Osland, 2018) – and is set at 1 205 000.

Fish farmers put their cohorts out to sea at two different times of year: spring and autumn. The fish take around 240 days to grow to the reference mode “desired smolt weight” of 250g. Our introduction dates, therefore, are 240 days before the time when the farmer wants to put the smolt into the sea. The equation for hatching is then a pulse function which transfers the “number of fry per cohort” at the chosen “hatching” time, and repeats based on the value of “time to next hatching”.

Hatching[n] = Pulse (Number of Fry per Cohort, [n]Hatching, Time to next hatching)

The fry then remain in the “Fry 0g to10g” stock until they have reached 10g. Their weight gain is shown in the next sector, Juvenile Feeding Sector. Once this sector indicates that the fry are at the maximum weight for the room, a pulse function moves them to the next room, “Room 1 10g to 60g”. From this room onward, the fry will be called parr.

This pattern continues for rooms two and three; when the maximum weight in the name of the room is reached, the parr are moved to the next room. Each room also has a lifespan of 60000 days, which corresponds to a death rate of 20 fish per day.

3.1.3 Juvenile Feeding Sector

The Juvenile Feeding Sector is based on a reinforcing loop (Figure 7) where the “amount of food fed per day” is a percentage of the “parr weight”, and this amount changes based on the “temperature” of the water and the size of the parr being fed.

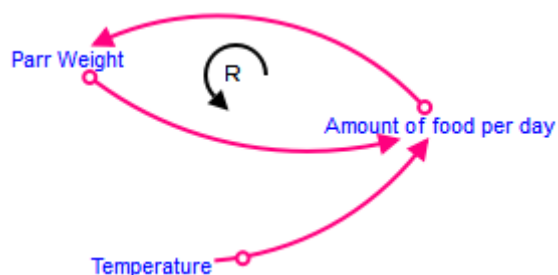


Figure 7 - Juvenile growth re-enforcing loop

The complete sector, with arrays, is seen below.

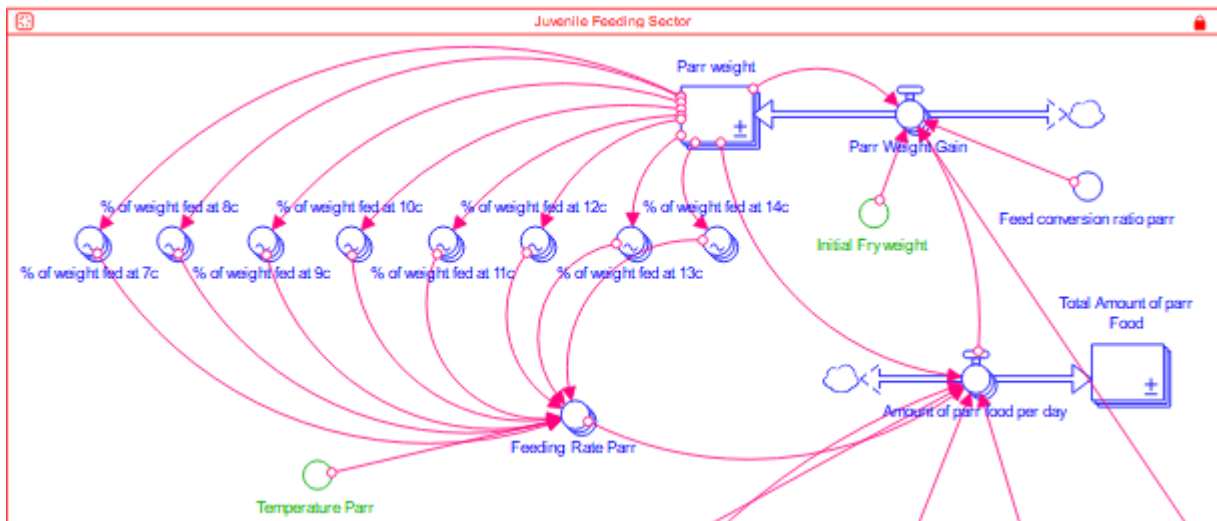


Figure 8 - Juvenile Feeding Sector

Osland Havbruk grows their parr to smolt from fry (when the salmon have just hatched and left the egg sac), so the “parr weight” stock is initialised with an “initial fry weight” of 0.2g. The parr then gain weight based on the “amount of parr food per day”, divided by the “feed conversion ratio parr”.

The feed conversion ratio is the amount of input (food) which produces one unit of output (growth). It is impossible for 100% of the food fed to the parr to go towards growth; some of it is expended through other biological processes. Fish food has become very refined over the years, and Skretting AS, the food producer which Osland Havbruk uses, calculates that based on their best current practices, they have a feed conversion ratio for Atlantic salmon of 1.15 (Skretting.com, 2018) – that is, it takes 1.15 units of food to produce 1 unit of weight.

The first part of the “parr weight gain” equation ensures that there are parr to feed in Juvenile Growth Sector and also resets the parr weight once a cohort has left the Juvenile Growth Sector, by going through the “to sea” flow which connects this sector to the Sea and Slaughter Sector. The second part of the equation feeds the parr.

*Parr Weight Gain[Cohorts] = IF To Sea[Cohorts,1] > 0 OR To Sea[Cohorts,2] > 0 OR To Sea[Cohorts,3] > 0 OR To Sea[Cohorts,4] > 0 THEN (-Parr weight + Initial Fry weight)/DT ELSE Feed conversion % parr*Amount of parr food per day*

To decide the flow “amount of parr food per day”, we take the “feeding rate parr”, divide it by 100 and multiply it by “parr weight”, so that the amount of food fed is a percentage of the body weight of the parr. This formula also has a mechanism in the beginning to ensure that

there are parr in the rooms before they are fed:

*Amount of parr food per day[Cohorts] = IF Fry 0g to 10g > 0 OR Room 1 10g to 60g > 0 OR Room 2 60g to 100g > 0 OR Room 3 100g to 500g > 0 THEN (Feeding Rate Parr/100)*Parr weight ELSE 0*

The “feeding rate parr” then depends on the temperature and the “percentage of weight fed at Xc” variables. This structure is based on the growth chart by the feed producer Osland Havbruk uses, Skretting AS (Skretting Fôrkatalog, 2012). This chart gives us the amount of growth, as a percentage of bodyweight, that the parr gain at a given temperature. When we multiply this growth by our above mentioned feed conversion ratio of 1.15, we get the amount of food needed to produce this growth. The original charts can be seen on the next page. In room three, the parr undergo smoltification (the change from living in fresh water to living in seawater) and are now called smolt. Osland grows their smolt to between 150g and 250g, which is larger than the size of smolt grown by traditional producers (between 50g and 80g) (Stead & Laird, 2002). This is to reduce the amount of time the fish spend in the sea, where temperatures are often lower, growth is slower, and the risk of disease or accidents is higher. The growth tables (Figure 9 & 10) provided both for parr and fish (salmon) have been combined to create the graphs used in the model.

Settefisk

Laks

Tilvekst (% per dag) laks settefisk, basert på ClubN 2009

Forventet daglig tilvekst i ulike vekstintervaller

°C	Startf.-1 g	1-5 g	5-15 g	15-30 g	30-60 g	60-100 g
1	0,41	0,35	0,17	0,12	0,07	0,04
2	0,82	0,69	0,38	0,28	0,20	0,12
3	1,23	1,04	0,59	0,44	0,32	0,21
4	1,65	1,38	0,80	0,60	0,44	0,30
5	2,06	1,73	1,01	0,76	0,56	0,39
6	2,47	2,07	1,22	0,92	0,69	0,47
7	2,88	2,42	1,43	1,09	0,81	0,56
8	3,29	2,76	1,64	1,25	0,93	0,65
9	3,70	3,11	1,85	1,41	1,05	0,74
10	4,11	3,45	2,06	1,57	1,17	0,82
11	4,52	3,80	2,27	1,73	1,30	0,91
12	4,94	4,14	2,48	1,89	1,42	1,00
13	5,35	4,49	2,69	2,05	1,54	1,09
14	5,76	4,83	2,90	2,21	1,66	1,17
15	6,17	5,18	3,11	2,38	1,78	1,26

Figure 9 – Parr, Salmon. Growth (% per day) salmon parr, based on ClubN 2009. Expected daily growth for different growth intervals

Atlantisk laks

Tilvekst (% per dag) og biologisk førfaktor for atlantisk laks (basert på resultater fra Skretting R_{max}-databasen)

Temperatur (°C)																						
gram	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	tt ¹	tt ²
30	0,17	0,33	0,51	0,70	0,89	1,09	1,29	1,49	1,69	1,89	2,08	2,26	2,42	2,57	2,68	2,75	2,78	2,74	2,63	2,42	0,81	0,81
100	0,12	0,29	0,48	0,67	0,86	1,06	1,25	1,44	1,62	1,79	1,95	2,09	2,21	2,31	2,38	2,41	2,39	2,32	2,18	1,98	0,81	1,16
200	0,12	0,28	0,45	0,62	0,80	0,98	1,15	1,32	1,49	1,64	1,77	1,89	1,99	2,07	2,12	2,14	2,12	2,05	1,93	1,75	0,82	0,96
300	0,11	0,25	0,41	0,57	0,73	0,90	1,06	1,21	1,36	1,49	1,61	1,72	1,81	1,88	1,92	1,94	1,91	1,85	1,74	1,57	0,83	0,91
400	0,10	0,23	0,37	0,52	0,67	0,83	0,97	1,12	1,25	1,37	1,48	1,58	1,66	1,72	1,76	1,77	1,75	1,69	1,59	1,44	0,84	0,89
500	0,09	0,21	0,34	0,48	0,62	0,77	0,90	1,04	1,16	1,27	1,37	1,46	1,54	1,59	1,63	1,63	1,61	1,56	1,47	1,32	0,84	0,88

Figure 10 - Atlantic Salmon. Growth (% per day) and biological food conversion for Atlantic salmon (based on results from Skretting R database).

Standard industry practice, which Osland Havbruk follows, is to grow parr at 14c (Stead and Laird, 2002), so “temperature parr” is set to 14c. This means that under reference mode conditions, only the converter “% of weight fed at 14c” is used when running the model, however other temperatures were included in order to allow for experimentation with growing the parr to smolt at different temperatures. The graph (Figure 11) showing the feeding percentages at 14c is below.

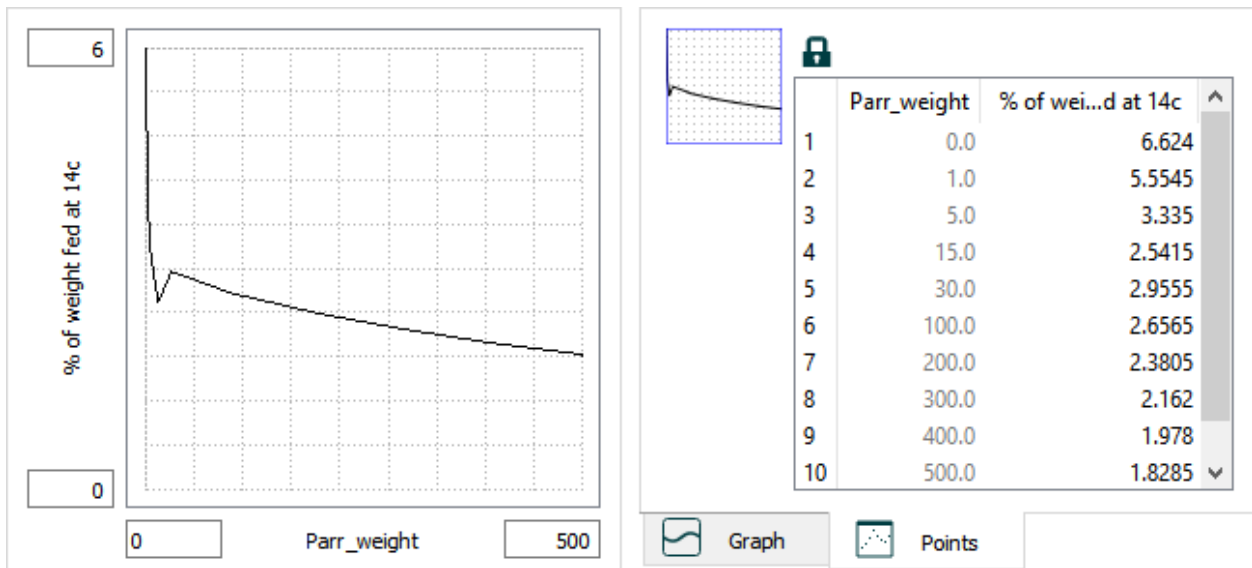


Figure 11 - Graph and values of parr feeding levels at 14c up to parr weight of 500g. Graph is a product of Skretting’s tables multiplied by the food conversion ratio.

3.1.4 Fish Feeding Sector

The fish feeding sector (Figure 12) is similar in structure to the juvenile feeding sector. It too is based on a reinforcing loop where the “amount of food fed per day” is a percentage of the “fish weight”, and this amount changes based on the “temperature” of the water and the weight of the fish.

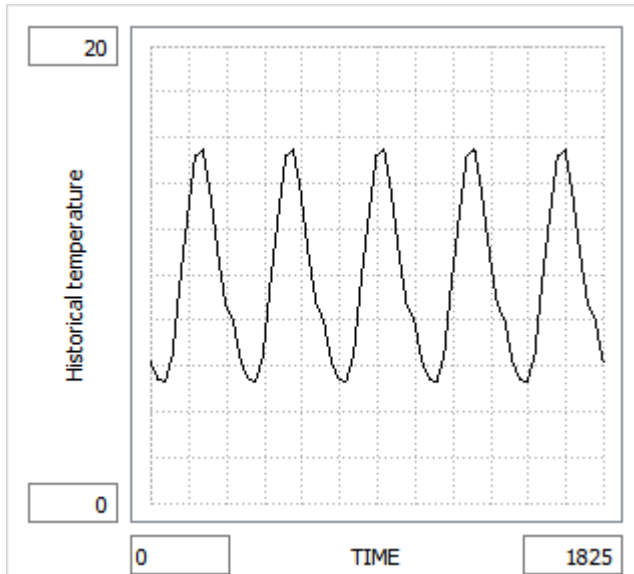


Figure 13 - Historical temperature data for Sognesjøen, Ytre Sogn as programmed in Stella Architect

Temperaturprofiler														
		jan	feb	mar	apr	mai	jun	jul	aug	sep	okt	nov	des	årsmiddel
Middeltemp														
Indre Utsira, Rogaland		7.8	6.3	5.7	5.8	8.9	11.0	12.7	16.2	14.6	13.6	11.4	9.8	10.3
Sognesjøen, Ytre Sogn		6.2	5.4	5.3	6.5	9.7	12.6	15.2	15.5	13.5	10.9	8.7	8.0	9.8
Eggum, Lofoten		5.5	5.5	5.5	5.5	6.0	8.0	10.0	12.0	11.5	10.0	10.0	7.5	8.1
Ingøy, Måsøy, Finnmark		5.7	5.0	5.3	5.4	5.4	7.0	9.0	9.2	9.8	8.9	8.0	7.4	7.2

Figure 14 – Historical temperature data for Sognesjøen, Ytre Sogn in its original form

3.1.5 Sea and Slaughter Sector

Smolt move from room three in the Juvenile Growth Sector into the Sea and Slaughter Sector through the flow “to sea”. Osland Havbruk’s smolt producing facility provides the fish for four locations in the Sognefjord – Torvund, Sørevik, Mjølsvik, and Måren (Figure 15). Two locations are where they put the smolt to sea in the spring, and two where they put the smolt to sea in the autumn.

Osland Havbruk

Lokalitets struktur m/adskilt generasjons utsett i 2 soner

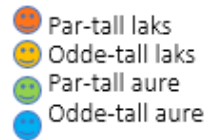


Figure 15 – Osland Aquaculture Location structure with separate generations set in two zones. Red is even-number (years) salmon, yellow is odd-number (years) salmon. Green and blue are trout locations. Image provided by Osland Havbruk.

The smolt from one cohort move all at once to a location. In order to move smolt to a location, conditions must be met:

1. There must be smolt in room 3
2. The smolt must be the desired size
3. The location must be empty, and
4. The locations must have been fallowed (empty) for 60 days.

The equation to move the smolt to the locations through the “to sea” flow ensure these four requirements are met. The equation is below:

To Sea $[n,n]$ = IF Parr weight $[n]$ \geq Desired Smolt weight $[n]$ AND Locations $[n]$ $<$ 100 AND TIME $>$ Next introduction Date $[n]$ THEN PULSE (MAX (0, Room 3 100g to 500g $[n]$ -Death Rate Room 3 $[n]$ *DT),Time when fish are in room 3 $[n]$, 0) ELSE 0

Below is an overview of the Sea and Slaughter Sector (Figure 16), including its connection to

room 3 of the Juvenile Growth Sector via the “to sea” flow:

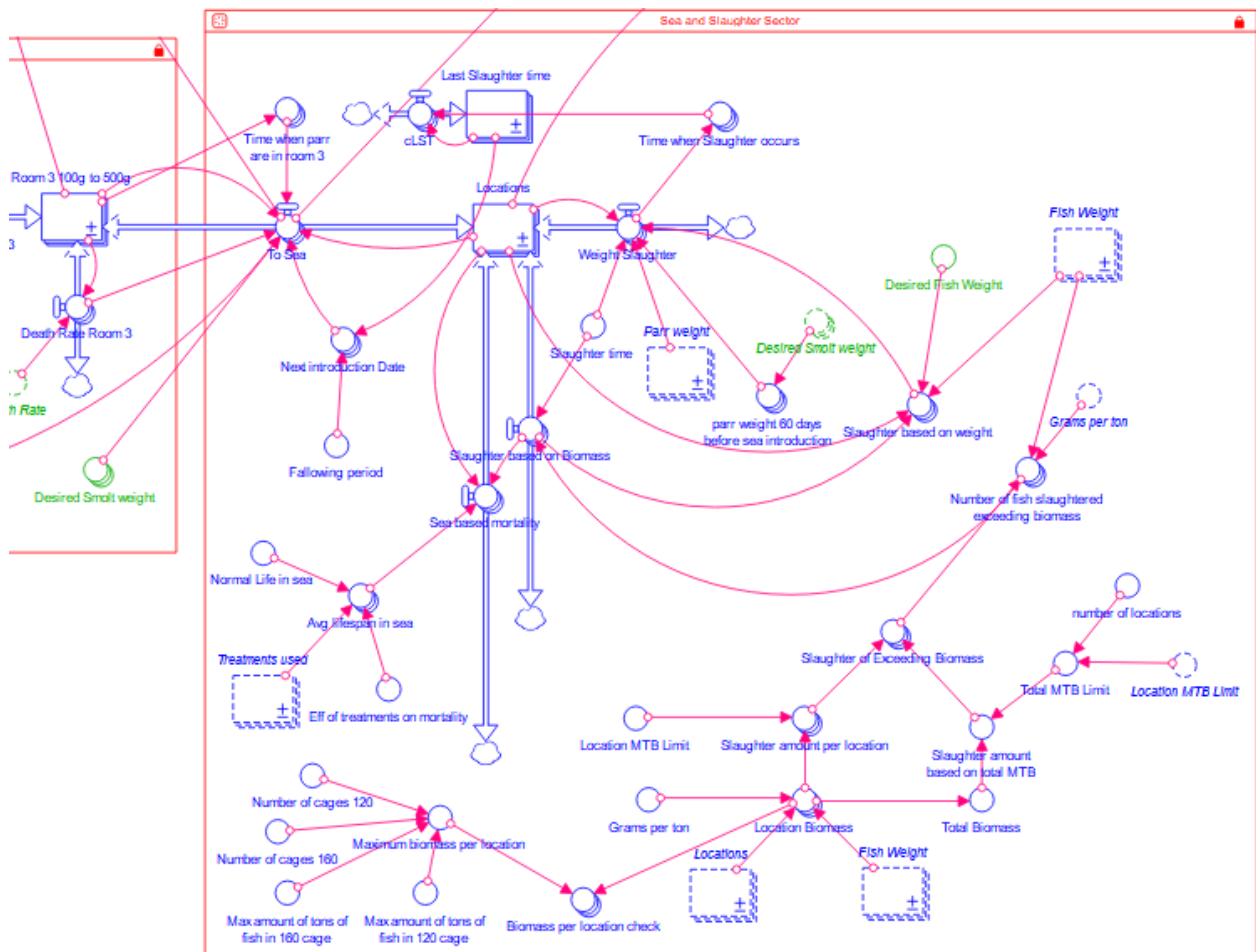


Figure 16 - Sea and Slaughter Sector, with the connection of the Juvenile Growth Sector

Once in the locations stock, the fish grow until they are slaughtered. The ghost variable “fish weight”, taken from the fish growth sector, measures the size of the fish. Slaughter happens if any of these conditions are met:

1. When the fish have reached their “desired fish weight”.
2. When smolt in room 3 are 60 days away from being ready for sea and the location needs to be emptied.
3. When the location reaches a certain biomass.

Each of these policies will be explained individually below.

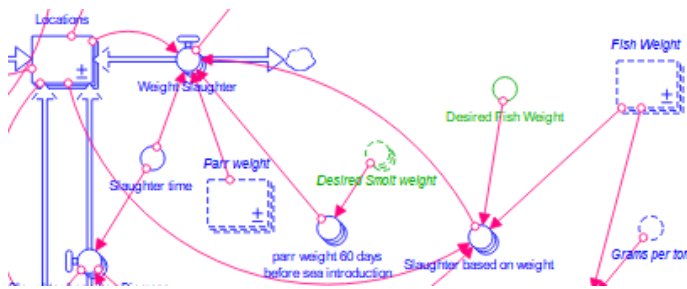


Figure 17 - Section of the Sea and Slaughter Sector focusing on the slaughter mechanisms based on fish, parr and smolt weight

Policy 1: When the fish have reached a desired fish weight

The variable “Slaughter based weight” compares a “desired fish weight” to the current “fish weight”, with a condition that there must be fish in the locations in order to compare these two. If the “fish weight” is equal to or greater than the “desired fish weight”, then the model slaughters everything that is in the location, minus any “slaughter based on biomass” that may have occurred at the same time.

Policy 2: When smolt in room 3 are 60 days away from being ready and the location needs to be emptied.

A location needs to be fallowed (empty) for at least 60 days before a new cohort of smolt can be introduced (Bruland, 2016). As the amount of time it takes to grow smolt to a given size is fixed, it is possible to calculate what size the smolt will be 60 days before they need to be in the sea, and empty the location at that time. This prevents a “backup” of smolt stuck in room 3 if the fish in a location have not reached the desired fish weight by the time the next cohort is ready to use that location.

Policy 1 and 2 are combined in the outflow “weight slaughter”. If either condition is met, the fish from a location are slaughtered. The equation is below:

Weight slaughter[n] = IF Parr weight[n] >= Parr weight 60 days before sea introduction[n] AND Locations[n] > 10 THEN Locations[n]/Slaughter time ELSE Slaughter based on weight[n]/Slaughter time

Policy 3: When the location reaches a certain biomass

The group of converters in the bottom right corner calculate when to slaughter based on exceeding the biomass limit. The converter “location biomass” multiplies the amount of fish in each location of the “locations” stock by the “fish weight” at that location. The “location biomass” is then used to calculate the “total biomass”, which is the sum of the biomasses at all four locations. The “location biomass” also calculates the “slaughter amount per location”, which is each location’s biomass, minus the location MTB limit of 780 tons (Osland, 2018). This is the total number of tons of fish slaughtered per location, which is then added to

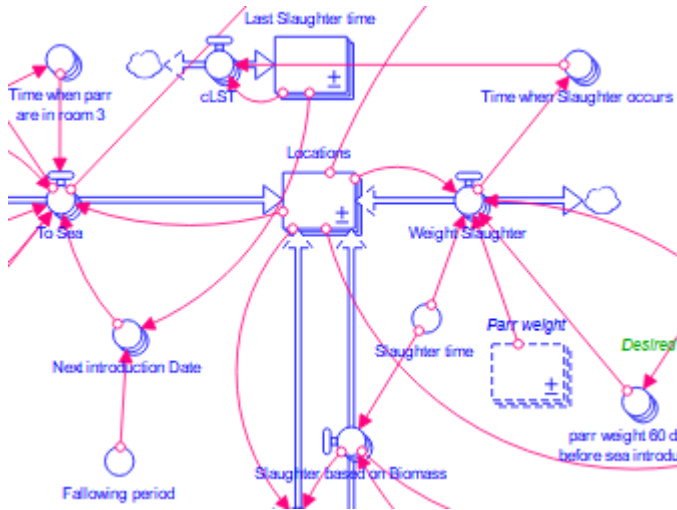


Figure 19 - Section of the sector showing the Last Slaughter time, following period, and next introduction date

Our locations stock also has a death outflow, “sea base mortality” (Figure 20). This is based on the “normal life in sea”, which is the amount of time a salmon spends in the sea (400 days) and the “effect of treatments on mortality”. Treatments for lice can affect the mortality of salmon, and we have added a multiplier based on the amount of treatments.

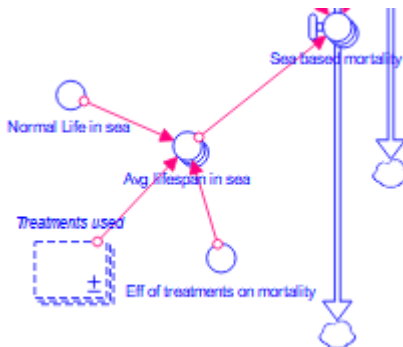


Figure 20 - Sea based mortality outflow from locations stock

There is also a biomass per location check in the lower left corner of the sector (Figure 21). This check ensures that the density of the number of fish in any location does not exceed the maximum number of fish allowed per cubic meter of water in the cages. Osland Havbruk has two sizes of cages, with circumferences of either 120 metres or 160 metres, and a volume of 15278 metres cubed or 27190 metres cubed, respectively. For our reference mode we assume 6 cages with a circumference of 120 metres. The biomass per location check compare our “location biomass” with the “maximum allowed biomass per location”, based on the size and number of cages. The density allowed by the Norwegian government is 25kg of fish per cubed meter of water (Bruland, 2016). If the biomass location check registers 1, then the

locations have exceeded maximum allowed biomass. Using the values from our reference mode, our biomass check never registered that we have exceeded the allowed density limit.

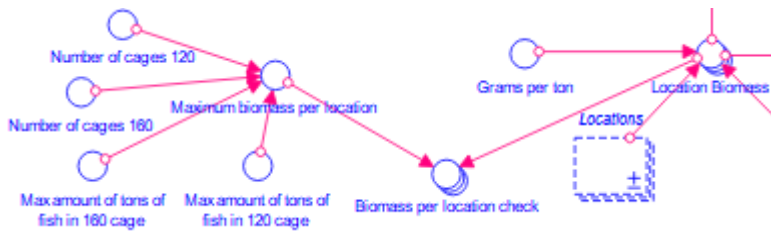


Figure 21 - Section of the sector showing the biomass per location check

3.1.6 Reference mode behavioural results

The tables below list the initial values and units of the fixed parameters in these four sectors of the model under reference mode conditions. All of the stocks in the model are initiated at 0 under reference mode conditions.

Table 1 – Juvenile Growth Sector Parameters

Juvenile Growth Sector		
<u>Parameter Name</u>	<u>Value</u>	<u>Unit</u>
First Hatching	0	Days
Second Hatching	10	Days
Third Hatching	192	Days
Fourth Hatching	200	Days
Time to Next Hatching	470	Days
Lifespan	60000	Days

Table 2 – Juvenile Feeding Sector Parameters

Juvenile Feeding Sector		
<u>Parameter Name</u>	<u>Value</u>	<u>Unit</u>
Initial Fry Weight	0.2	Grams
Temperature Parr	14	Degrees c
Feed Conversion Ratio	1.15	Unitless
Desired Smolt Weight	250	Grams

Table 3 – Fish Feeding Sector Parameters

Fish Feeding Sector		
<u>Parameter Name</u>	<u>Value</u>	<u>Unit</u>
Feed Conversion Ratio Fish	1.15	Unitless

Table 4 – Sea and Slaughter Sector Parameters

Sea and Slaughter Sector		
<u>Parameter Name</u>	<u>Value</u>	<u>Unit</u>
Fallowing Period	60	Days
Slaughter Time	2	Days
Desired Fish Weight	4.5	Kilograms
Normal Life in Sea	400	Days
Number of Cages 120	6	Cages
Number of Cages 160	0	Cages
Maximum Number of Tons of Fish in 120 Cages	381.9719	Tons per cage
Maximum Number of Tons of Fish in 160 Cages	679.750	Tons per cage
Location MTB Limit	780	Tons
Number of Locations	4	Locations

3.1.6.1 Juvenile Feeding Sector

The key stock in the Juvenile Feeding Sector is the “parr weight” (Figure 22).

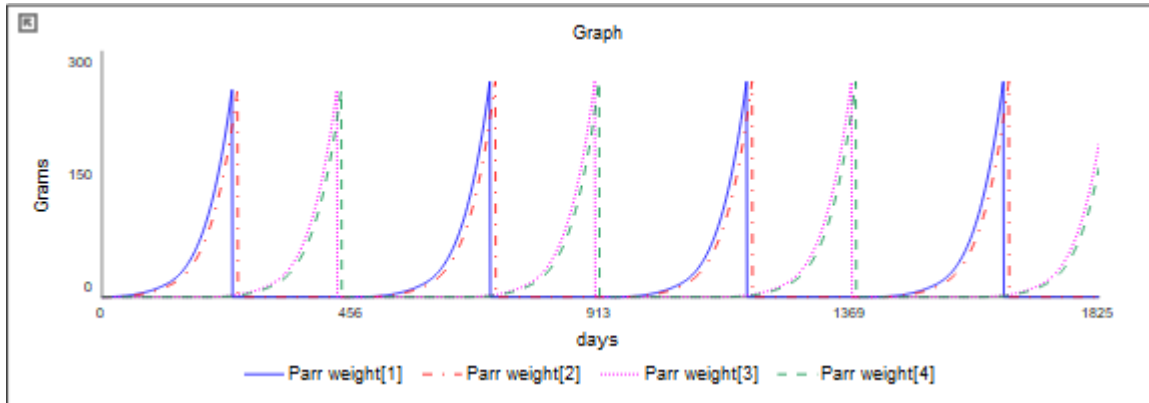


Figure 22 - Reference mode parr weight growth, all four cohorts

The graph (Figure 22) exhibits a regular pattern as temperature is fixed and there are no lice in the Juvenile Growth Sector. Each cohort of parr grows to the “desired smolt weight”, and then the model resets the weight when that cohort has moved out of the Juvenile Growth Sector and gone into the Sea and Slaughter Sector. Cohorts 1 and 2, and cohorts 3 and 4 grow at the same time.

3.1.6.2 Juvenile Growth Sector

The key indicators in the Juvenile Growth Sector are the graphs (Figure 23) of the time spent in each of the four rooms. In the reference mode, the amount of fish and the time spent the four rooms looks as below:

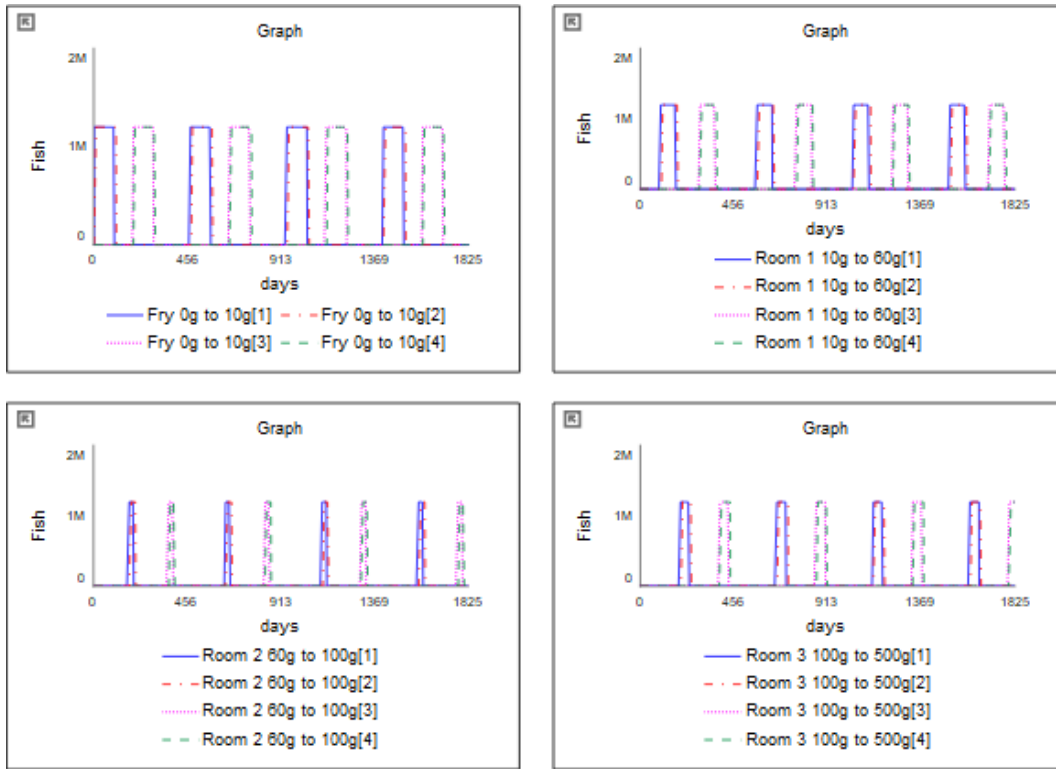


Figure 23 - Graphs, number of fish and time spent in the four rooms in the juvenile production facility

As the amount the parr grow in each room is different, the amount of time spent in each room is different. Though not apparent in the graphs, due to large amount of fish, the number of fish in each room does decline slightly due to the death rate of 20 fish/day. As four different cohorts are introduced at two different times of year, cohorts 1 and 2 (blue and pink) and cohorts 3 and 4 (red and green) are in the rooms at the same time.

3.1.6.3 Fish Feeding Sector

Much like the Juvenile Feeding Sector, the key indicator is “fish weight” growth.

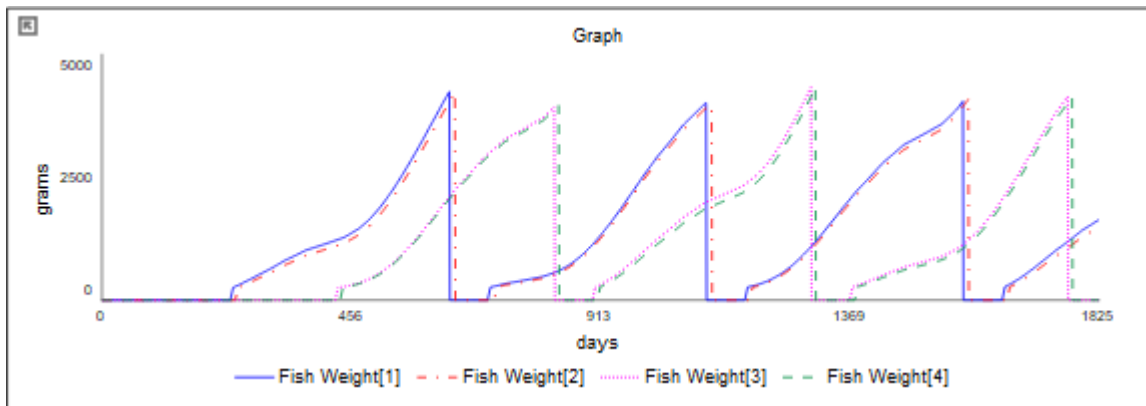


Figure 24 - Fish weight growth, without the effect of lice

This graph is a bit less normal than the graph for “parr weight”, due to the fluctuating sea temperatures slowing and speeding up feeding. The fish weight resets itself to 0 after the

cohort has been slaughtered. In the above graph, the effect of the lice sector has been turned off, to reflect what growth would look like under ideal health conditions.

The fish also do not always reach 4.5kg, as there is a policy where if the next cohort will be ready to use a location 60 days in the future (the minimum following time of a location allowed by law), the fish in the location are then slaughtered in order to free space for the next cohort.

3.1.6.4 Sea and Slaughter Sector

The most important indicator in the Sea and Slaughter Sector is the biomass versus the maximum total biomass (MTB). That is to say, the biomass of the four locations in the fjord versus the maximum amount of biomass in four locations allowed under law. The graph (Figure 25) of biomass vs. MTB is below.

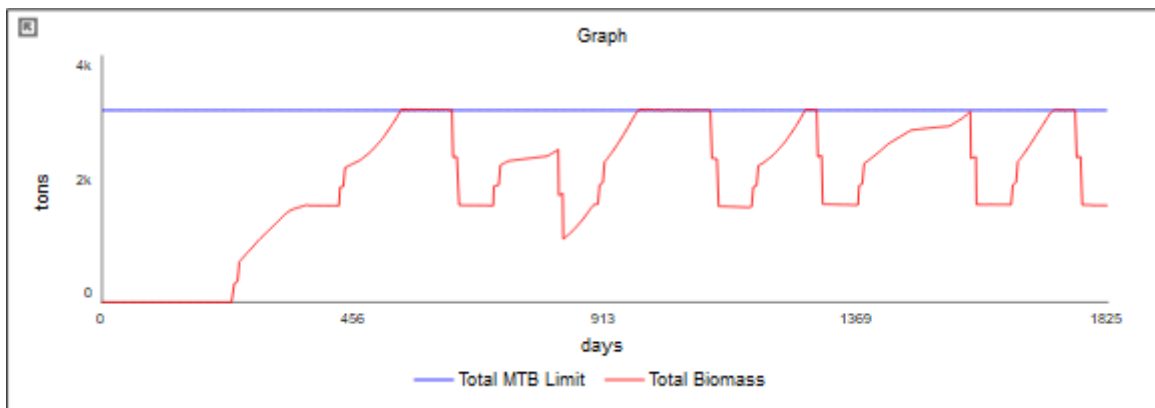


Figure 25 - Maximum total biomass limit vs total biomass

The goal of the fish farmer is to be as close to this maximum as possible at all times. In the reference mode, from the time the first cohort goes into sea until the end of the simulation, the average total biomass is around 71% of the maximum total biomass.

Production and Biomass Model as input to the Lice module

The core of the model we have developed in order to analyze the operations' causal relationship with its biological environment is based on the process of growing fish and processing the biomass to the finished product. By making this the starting point, the model aims to take the view of the producer. This is to clarify and contextualize how management policy within the fish farm have encompassing influence on its environment, both ecological and economical. This is an important aspect of systems thinking in general, and also at the center of how we may want to suggest changes to any policy or practice and how those are contained within existing processes.

There are two products in particular from the production model that give important input to the lice model: The number of fish being grown and processed, as an expression of the collective biomass of the standing population in the sea, as well as the cycles of host availability.

The number of fish is mostly of value as a quantity that helps determine biomass, as well as being of policy and economic importance, as some regulations directly decide how many fish are allowed in one cage, in each location, per cubic meter and so on. These restrictions are set as limitations to the producer, and most of these are simulated in the model based on the *compendium for Aquaculture by Wikborg & Rein* 6th Edition, (Bruland, 2016). The location-specific number of fish is also used to calculate cost and profit in the financial model, and as a variable in the biomass-dependent lice sub-model.

As the total time from fry to market weight salmon is 20 – 23 months, the delay of this production line is challenging to predict, and therefore the model uses several Boolean conditions for the flow of cohorts through the growth process to help users identify where delays occur and make decision rules clear in order to relieve pressure on these points.

Sea based period and outputs concerning the lice model

When cohorts are put into sea-based locations, there is a change in the dimension of the array values from cohorts to locations. Even though these are still separated by cohort in the different locations, it is necessary to monitor the biomass in what is essentially different stages of the same process. If smolt are introduced at different times of year, they should be different weights at the time of introduction in order to continually maintain as close a biomass as possible to the maximum allowed biomass (MAB). This is because fish grow more slowly at lower temperatures, and because of desired weekly slaughter due to starting costs of processing (Osland, 2017)

As an output to the lice model, the structure separates the locations in a matrix with infection pressure as a function of host population and seaway distance as input variables. As these relationships change over time and with seasons, it is likely that the order in which you put fish into the four different locations and the time of introduction to these locations has an impact on how lice will infect these locations and continue reproduction.

The model uses the number of fish in locations along with lice estimates and their dispersed infectivity over seaway distance between locations in order to initiate treatments. This dispersal is a point of own estimations, as this is usually determined by physical counts on sampled fish, and there is not sufficient research that empirically states the population of younger stages of lice based on counts of adult and pre-adult lice. The equations used for estimating the between-location infestation pressure are described in detail in the lice model description. However, such calculations are highly dependent on lice mortality rate, which in this case is both mortality of the attached stages of lice and early stage lice that are unable to find a host within viable time. The estimated attachment rate is therefore based on an approach that can be tested against the production in each location separately, with the estimates of external pressure added. Over time, this generates the effect that as long as one of the locations holds reproductive lice, other locations with hosts will get infected without any larvae originally produced at that location, making external infection pressure especially important at early sea based stages (Aldrin et al 2017).

The policy model connected to the lice sector initiates treatments for high lice counts, and this module has an effect on the feeding of sea based fish. Even though the effects of different kinds of treatments on fish may be specified, and these in reality have different impacts on the feeding and mortality of fish, the model returns the expected negative impact on fish growth in the form of stopping the feeding of fish for some days before treatment, which in turn temporarily stops the weight growth, delaying the growth towards desired weight while mortality remains constant, giving a lower count of fish than without treatment when they reach their target weight.

In addition to chemotherapeutic treatments, the policy model contains a cleaner fish sub-model, that releases cleaner fish into the salmon locations, increasing the mortality rate of pre-adult and adult stage lice through an effect on mortality multiplied with the fraction of cleaner fish of hosts. This stock is refilled when initiated by the user, and is emptied through a constant mortality rate (Aldrin et al 2017).

3.2 Lice Module

3.2.1 Life Cycle

The salmon lice are directly transmitted parasites, which have a planktonic phase and a parasitic phase in their life cycle, without the need for an intermediate host before the latter phase (Krkosek et al 2009). The copepodid is the infectious stage when the louse attaches to a host and develop through chalimus and mobile stages of its life cycle. These latter stages include the louse's reproductive stages from which non-feeding nauplii hatch into the water column. These may drift for several days before developing into infectious copepodites, and the duration of these phases vary with water temperature (Stien et al 2005). An overview of the model structure is shown in Figure 26:

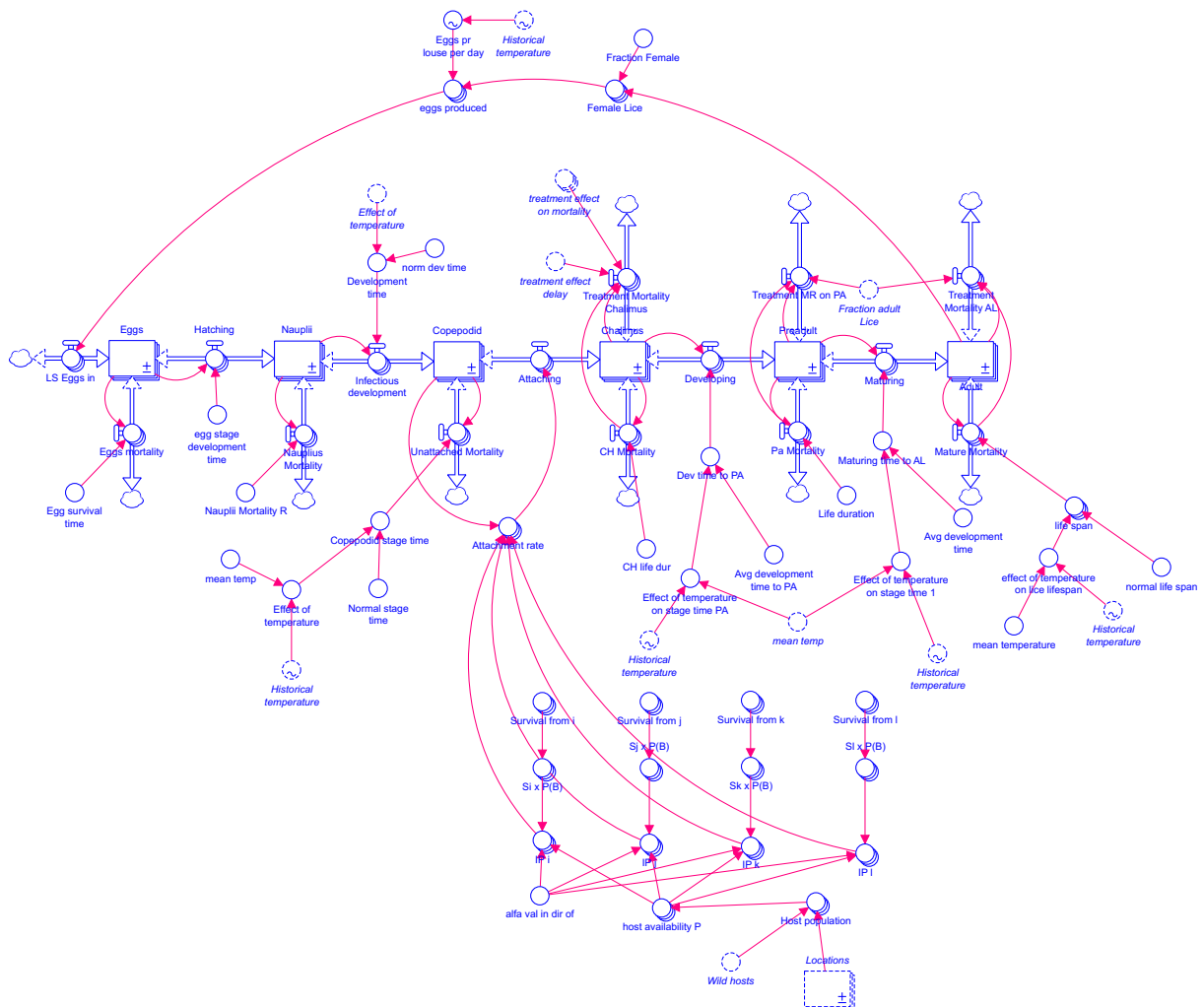


Figure 26: Overview of the lice population growth and infection pressure structure. The aging chain simulates the population in the distinct stages of lice development, while the infection structure in the lower right corner calculates infection pressure between locations.

The change through these phases changes the size and behavior of the lice, as they transition from being sedentary on hosts to being freely mobile on its host and motile among hosts

(Krkosek et al 2009). The abundance of lice and their development is seasonal, affected by temperatures in the duration of development stages.

3.2.1.1 The spread of Lice abundance

Lice infestation is driven endogenously at the farm level by a reproduction process and dependent on the availability of hosts, temperature and salinity (Stien et al 2005). At the regional level the inter-farm dispersal of lice has been shown to depend on seaway distance from neighboring farms hosting infectious lice (Kristoffersen et al 2014). Biomass as an expression for host availability, distance between locations and temperature act as reinforcing factors in this model, while the weighted effects of other factors, such as salinity and daylight hours are less thoroughly documented on farm and regional scale, and are therefore excluded from the model framework. In the model, farmed biomass is treated as an endogenous variable, while temperature is based on historical data, as is the migration pattern and population of wild salmon as an external variable of hosts that would sustain a population of lice even if the farmer in question fallowed all his locations at once. Damage to the wild population from high infestation levels is not studied within the model framework, although such infection is known to harm young stages of wild salmon, and over time contribute to the reduction seen in the total return of wild salmon (Krkosek et al 2009).

Below are the data based (Figure 27) and model generated lice counts (Figure 28) as a reference mode to the problem. (note: the real system operates with treatments and cleaner fish as regulated, making the reference mode generated by the model one where policies are turned on, as opposed to how models are usually initiated. In addition, the lice model is initiated with fish in locations 3 and 4 to utilize the 5-year simulation on lice abundance)

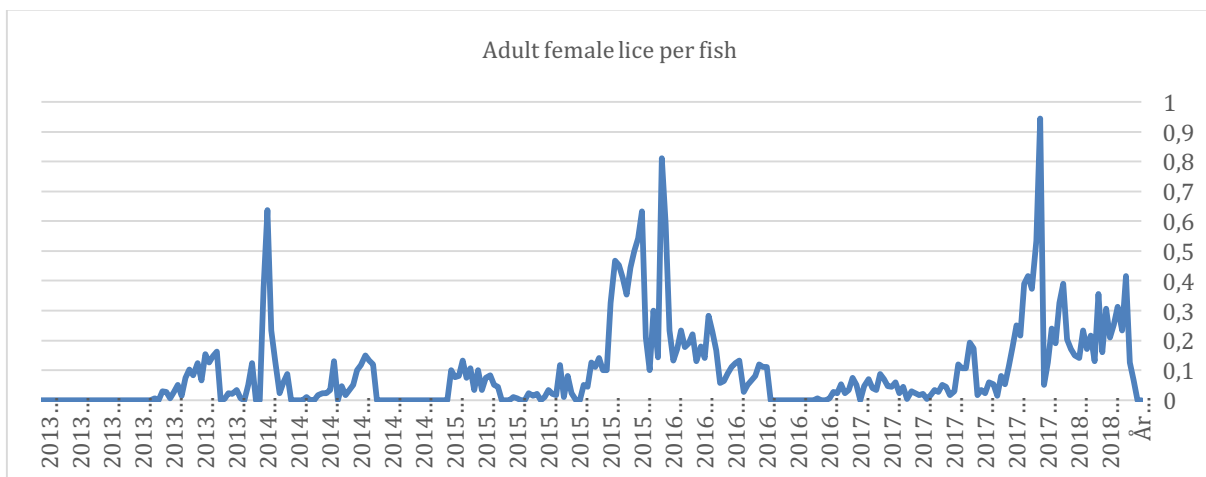


Figure 27: The average count of adult female lice per fish in three locations (Sørevik, Torvund and Måren) 2013 – 2018. Mjølsvik was left out of the dataset due to incomplete data to remove biased results in the graph.

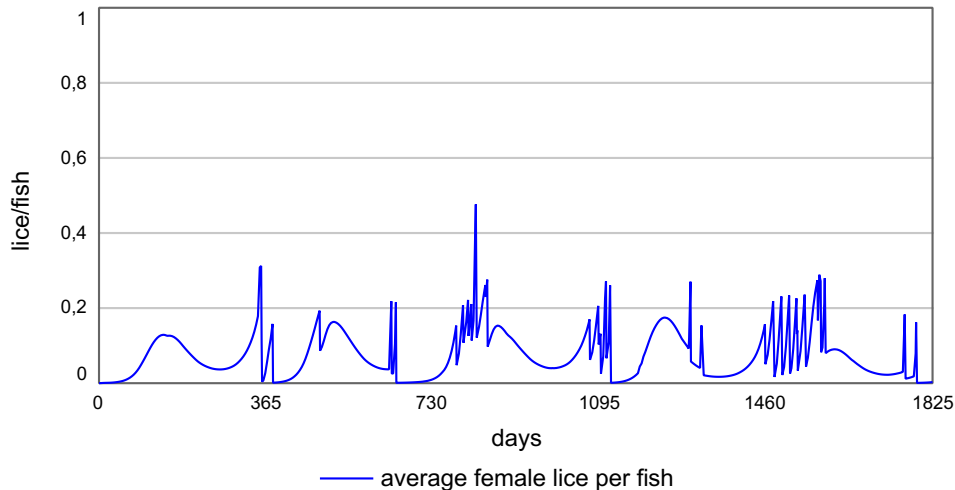


Figure 28: Model generated lice abundance (5yr) of all attached stages of lice on all four modelled locations, showing comparable data to the reference mode (Figure 3)

In the model the focus is on the four locations operated by Osland containing salmon, excluding the locations run by other operators in the area. This is a simplification chosen to focus the model on what the farmer can do to influence his surroundings without having to consult with other producers nearby. This is, however, not difficult to expand in a later version of the model in order to adapt to several operators. The focus on salmon is also a simplification, as the rainbow trout licenses operated by Osland are close by and susceptible to parasite emission to and from its neighbors even if these are different species.

Lepeophtheirus salmonis is a specialist on Salmon species, and will therefore also affect trout populations. While some generalist lice exist, these are not a problem on the same scale as salmon lice on salmon population (*Caligus elongatus*) (Jansen et al, 2012).

Lice infestation may be transferred by two main modes of transportation. Local transmission from hydrodynamic movement from farming and long range transmission caused by wild migrating fish (Werkman et al 2011). In the model, the focus is on transmission through water column dispersal, as the latter mode of parasite transfer mainly affects the migrating wild population of salmon. The sea water temperature affects how far inter-location connections reach, as well as development times between stages and mortality rate.

The model uses survivability of the infectious stage over distance as a proxy for diffusion of planktonic stages of lice. This has been applied to earlier models (Kristoffersen et al 2018). This approximation lets the model calculate generic simulation results that are independent of wind and currents, but that still hold explanatory power in the model.

There are four important inputs to the sub-model: 1: The farmed fish population simulated in the production sector. 2: The wild fish population, varying through seasons. 3: The historical temperature. 4. The slaughter of fish in locations.

I use the assumption made by Kristoffersen et al (2014), that exposure to salmon lice infection depends on the number of infective copepodites, that is, the stage of lice that are able to attach to hosts, in the local environment. Further, the model takes use of some of the same data categories: Numbers of fish, female lice, water temperature. In addition, the model contains a full life cycle model of the lice development, that helps us estimate the production of life stages within locations, as well as those locations' impact on other locations' external infection pressure.

This is matched with data on Pre-Adult and Adult Male (PAAM) counts, which is also mentioned in Kristoffersen et al (2014), because the physical counting of smaller stage lice is difficult, creating biased data that does not fully represent the lice abundance. One can therefore estimate their numbers backwards by applying known mortality rates and development rates determinant in their move through the population growth structure.

3.2.2 Lice population growth and life cycle

At the center of the lice module is the location population stocks (Figure 29), which accumulates the net flow between lice births and lice deaths in each location, shown as one structure with arrayed variables. Each array dimension represents one of the locations in the producer's network. This lets the model simulate internal reproduction of lice in each of those locations. One could theoretically model the total infestation in the area with one aging chain, but that would imply perfect mixing of all lice development stages over the production area. This would make it impossible for our producer to simulate the impact of taking different managerial actions on different locations on the lice abundance.

The sector is therefore divided, following the cohorts of fish released into the sea stage of their development in the production model. This leaves the lice in infective stages that are "in transit" between locations belonging to their original location until they attach to fish in another, even if these physically are somewhere between the two. This helps determine the directional pressure connecting two locations by reducing the number of stocks involved in the structure.

The life cycle of the salmon lice is broken down into the developmental stages that are most important to our abundance calculations: eggs, larvae (nauplii), copepodites, chalimus, pre-adult and mature lice. The last stage is divided between male and female lice at a fraction of 0,5.

Eggs are released from pairs of egg strings on the gravid female lice. Each string contains around 150 eggs on average (Stien et al 2005), increasing from the first set to recorded fifth pair of egg strings produced by a female louse.

Eggs hatch and nauplii are released into the water column, and develop into their next larvae stage depending on water temperature. The inflow of eggs is regulated by one reinforcing and one balancing loop that says that the more available hosts you have, the more lice will be able to find one and reproduce, to increase the number of eggs produced in the next generation.

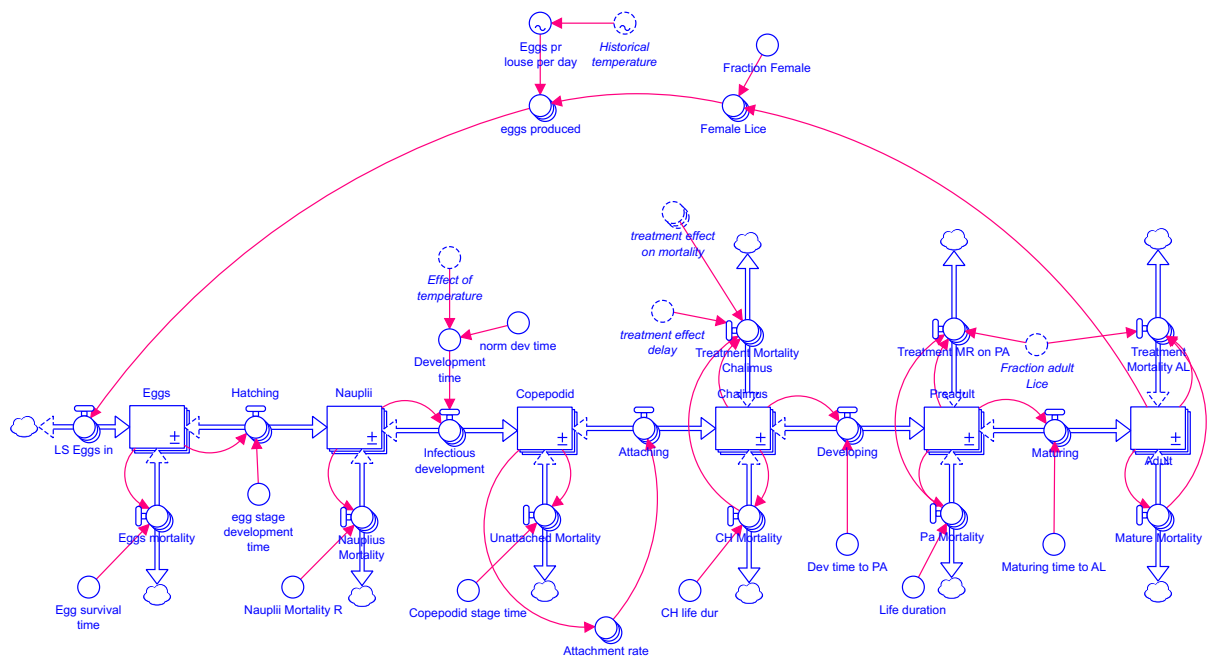


Figure 2: The structure of the lice aging chain and reproduction divided by populations of each stage of the lice life cycle.

Water temperature is an important part of development time in all life stages of the salmon louse, and is therefore built in as a historic variable that recreates five years (2012 – 2017) of temperature data in the region. Research on the differences along the Norwegian coast on this dependency indicates lower lice abundance in northern, colder areas, and higher abundance in southern production areas, but this could also be linked to lower biomass and densities of hosts (Jansen et al 2012). Samsing et al (2017) show strong seasonality in lice abundance and inter farm infection pressure, which is likely connected to temperatures. This gives variable development and mortality rates for some stages, given in Table 5.

Table 5: Initial parameter values for Development and Mortality rates in the lice population growth model

Development	Hatching	days	5
(mean)	Infectious development	degree/days	40
	Attaching	1/days	Equation
	Developing	degree/days	155,00
	Maturing	days	11
	Eggs mortality	days	6
Mortality	Dispersal (Naupli) mortality	1/days	0,17
(mean)	Unattached mortality	degree/days	155
	Ch mortality	1/days	0,05
	Mature mortality	1/days	0,047

The present model has a variable that shows the effect of an increase or decrease in temperature on fish and lice populations, but this is not discussed further with regards to the effect on lice abundance in this paper.

Beginning at the earliest stage of the salmon louse development, the eggs develop from egg strings released by an adult female louse. They then hatch from the egg stage at a rate of

$$\text{Hatching} = \text{Eggs} / \text{Egg stage development time}$$

with a mortality of

$$\text{Eggs mortality} = \text{Eggs} / \text{Egg survival time}$$

The planktonic stages are important mainly in order to calculate the population sizes of the next stages, which later helps calculate the attachment rate of the first infectious stage of lice. There are two outflows from this stock: The development rate flow equation, which is stated as

$$\text{Infectious development} = \text{Nauplius (larvae)} / \text{Development time}$$

with development time being temperature dependent, and the mortality of the larvae stock being continuously subject to its mortality rate,

$$\text{Nauplius mortality} = \text{Nauplius} * \text{NL mortality rate}$$

The next development stage is the copepodid stage, where the population of planktonic lice in the water column become parasitic, and will have to attach to a host in order to continue its development through the stage structure. This stage-representing stock accumulates all the survivors from the Nauplius stage, and is emptied by a mortality rate and an attachment rate,

that is, finding a host, which over time will lead to next stage development. The Copepodid mortality rate is:

$$\text{Unattached mortality} = \text{Copepodites} / \text{Copepodid Stage Time}$$

The attachment rate is calculated with the number of copepodids and time, determined by an infection pressure. This structure is separate from the aging chain model structure.

The next paragraphs describe the co-flow of farmed fish populations and the wild population as available hosts and the growth of the lice population between farms with a delay, before returning to the description of the final stages of lice development.

3.2.3 Parasite transmission between Locations

Transmission of parasites between locations is a key factor in the population dynamics of sea lice (Aldrin et al 2013), and thus an important part of the real system depicted by the model. In system dynamics, there are many former examples of diffusion of disease, like adaptations to SIR-models, but these are generally between humans or within one species, and with the indicating conditions being either infected or not infected. Since the lice transmission is a parasite-host relationship, dependent on the presence of two species as well as being transferrable and reproductive at a larger scale than regular contact rates (infected / not infected) will accurately represent, the model utilizes an array structure to model a four-way diffusion between the locations.

When a single farm lice population was modelled by Hamza et al (2014), the lice population and the farmed fish mixed randomly, in order to recreate the exponential growth of the parasite population and a policy system to handle single farm infestation. In this scenario, when there are four locations in a network, it is necessary to build a disaggregate model that fits better with the distance and temperature-dependent infection between the neighboring locations.

Samsing et al (2017) describe a seasonal model-generated variation on the number of connected locations because of a decreased development rate and therefore longer range of the pre-infective stages in low temperatures. This factor is accounted for by changing development times in the model, however, the network modelled contains locations that are all well within this range all year, meaning there are links between the locations within the normal range of temperatures in the region. This variable is however, an interesting way to expand the framework of further research into regional level and among several producers.

This is an important topic for research as it greatly affects the effectiveness of separation zones and production areas.

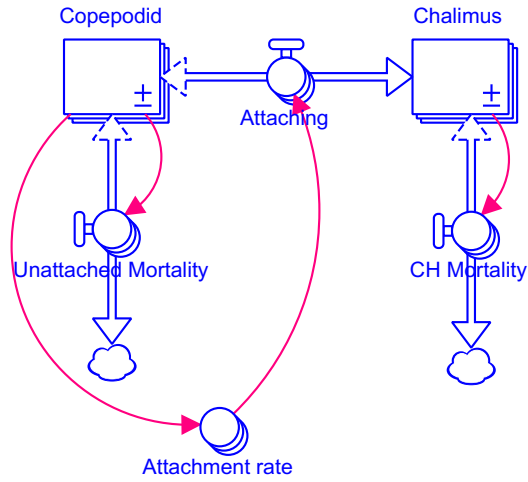


Figure 30: Model section highlighting the flow between stages and the connection of infection pressure, which gives the attachment rate. This variable accounts for step between produced infective lice and lice that find a host and start reproduction.

The internal infection pressure (Figure 30) is defined as the population of infective stages multiplied with transmission rates. As the distance between a location and itself is set to 0, the internal infection pressure is most significant to each location, given that hosts are available, and that there are lice present the previous time step (Aldrin et al, 2013).

The infection rate is a product of the abundance of sea lice, survivability over distance, available hosts and a parameter alpha, given a constant mortality rate. Unattached stages of lice will, at slaughter and fallowing events, still disperse to the surrounding water column, giving a short time where these stages of eggs and lice are present and modelled in the aging chain even if there are no available hosts, but these will not develop past the infective stages in that location. Some of these pre-infective and infective stage lice will, however, contribute to the infection pressure of the other locations where hosts are available, and to wild hosts.

The external infection pressure is the sum of contributions from all external source farms, relative to the distance between source locations (j) and recipient locations (i). The relative contribution S_{ij} from a source farm (j) with seaway distance d_{ij} is defined by the formulation (Aldrin et al (2013):

$$S_{ij} = \frac{e(-1,444-(d_{ij}^{0,57}-1)/0,57)}{e(-1,444-(d_{jj}^{0,57}-1)/0,57)}$$

The distances between locations are fed into a matrix (Figure 31) and calculated for each distance relationship connecting Torvund (i), Måren(j), Mjølsvik (k) and Sørevik (l). The seaway distance is rounded up to its closest whole kilometer (calculations in appendix).

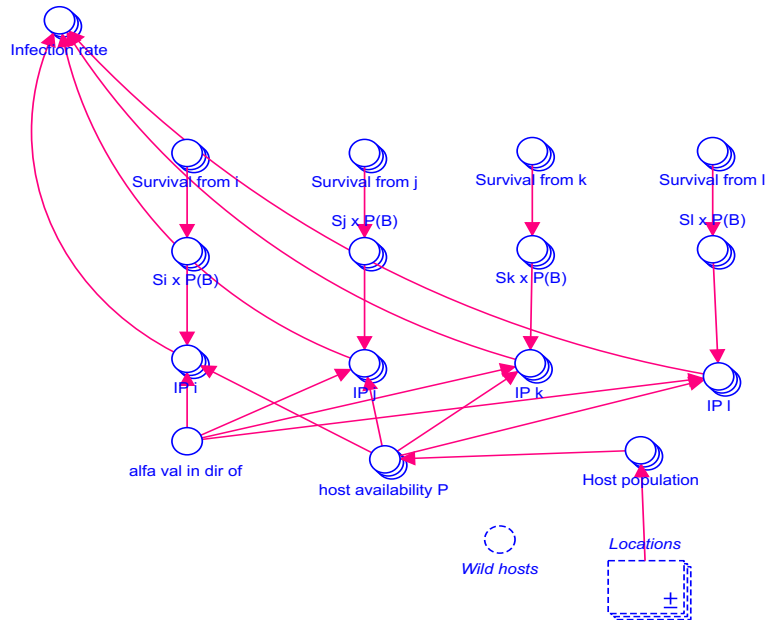


Figure 31: External infection pressure sector, showing the structure used to estimate the infective pressure within and between locations, used for calculating the number of lice that successfully attach to a host from the parasites produced.

When the risk of infection per day is established as parameters in the model, 16 in total, these are multiplied with a parameter α , which is a normalized value between 0 and 1. This represents a power variable to the infection that describes the value of the produced parasites that successfully attach and continue their stage development.

This gives the infectivity at a given distance and between locations to indicate one location's dispersed lice pressure on another location that may be within range and in the direction this dispersal must have in order to reach another location.

This value is multiplied with a probability of there being hosts $P(B)$ in the sector. As actual infection pressure is calculated in the aging structure of the model, this is a binary choice of 0 or 1, dependent on there being fish in the target location at time of dispersal. In Aldrin et al (2013), this condition is stated as fish or no fish. Since it is reasonable that there must be a number of hosts that is significantly different from the wild population for this indicator to be 1, and the model continually calculates the actual number of fish in each location, the number of fish for $P(B) = 1$ is set to 10 000 fish. This value is then multiplied with the number of copepodid stage lice in the location of origin, to give us the attachment rate from one location to another.

$$AR_{i,j} = S_{i,j} * \alpha_{i,j} * P(B_j) * C_i$$

Where C_i is the number of copepodid stage lice in location i at that time step.

The external pressure is added to each location's own production of internal pressure in order to calculate the effect of total infection pressure, meaning that even if only one of the locations were infected in the area, the other three would also become infected given availability of hosts in those locations over time (Duggan 2016).

This gives total infective pressure for one location i :

$$\begin{aligned} & C_{ii} * \alpha_{ii} * S_{ii} * P(B_i) + \\ & C_{ii} * \alpha_{ji} * S_{ji} * P(B_i) + \\ & C_{ii} * \alpha_{ki} * S_{ki} * P(B_i) + \\ & C_{ii} * \alpha_{li} * S_{li} * P(B_i) \end{aligned}$$

Which is calculated separately for each of the four locations i, j, k, l .

When lice attach to a host, they move from being planktonic to the parasitic stages, the first being the Chalimus stock of the model, implying the next stage of development. From this stock, there are two outflows describing mortality, the first being life span, in which life duration is estimated at 20 days, matching a mortality rate of 0,05 (Kristoffersen, 2014).

$$CH \text{ mortality} = Chalimus / CH \text{ Life_duration}$$

The second being the mortality caused by treatments initiated by the farmer:

$$\begin{aligned} & Treatment \text{ mortality } chalimus = Chalimus / \\ & (Chalimus * treatment_effect_on_mortality / treatment_effect_delay) - CH_Mortality \end{aligned}$$

The next outflow is the development time to the pre-adult and reproductive stages, where development time is dependent on temperature by having an average development time of 15,5 days multiplied with the effect of temperature on that development time. The effect of temperature is the deviation of the historical temperature from the average temperature of 10 degrees C, giving the effect of temperature through a graphical function:

$$Effect \text{ of } temperature = Temperature / average \text{ temperature}$$

Which gives the rate of the development into the next stage:

$$Developing = Chalimus / Dev_time_to_PA$$

The outflows from the pre adult and adult stages are the same formulations as for chalimus, with the addition that cleaner fish add to their treatment mortality. This is due to the cleaner fish effect on mortality, which is dependent on size of the parasite.

From pre adult, the lice mature into their reproductive stage through an inflow from the pre adult stage:

$$\text{Maturing} = \text{Preadult} / \text{Maturing_time_to_AL}$$

In the last stage of development, sea lice reproduce. There is a loop back to the inflow of eggs that starts the development structure. This inflow is calculated by multiplying the mature lice population with the fraction female lice, and multiplying with the average number of eggs produced. The birth rate of lice is given through temperature and the normal reproductive rate of lice at some probability of finding a host. This is simplified in the model; there are male and female lice, at 50% of each. Female lice produce about 300 eggs released from two strings, which in turn become infective stage copepodid that are brought with currents away from the original location.

From the last stock, there is an outflow of mortality, similar to that of the previous stage, also dependent on temperature. In addition, there is an outflow that separate natural mortality from treatment induced mortality, which is connected to the treatment structure and gives increased mortality from the attached lice stages when treatments are initiated. This outflow is similar to the one in the two preceding stage stocks.

Next, the treatment structure is described. This structure contains variables for calculating the abundance of lice in different stages. Most important is the adult female lice per fish, which is used to initiate treatments. Further, there are switches that let the user choose between policies for reducing the lice abundance.

3.2.4 The treatment structure

Treatments are an important way to limit the growth of lice abundance by removing attached stages of lice from the fish population. The treatment structure calculates the effect of different treatment policies and adds these to the mortality of parasitic lice stages in the lice population growth segment.

The key indicator for initiating treatments is counts of attached stage lice per fish. This is used to take a decision of whether or not to start a treatment, which feeds into a counter of

treatments and a policy option of how treatments are to be coordinated. The model structure of the treatment sector is shown in Figure 32.

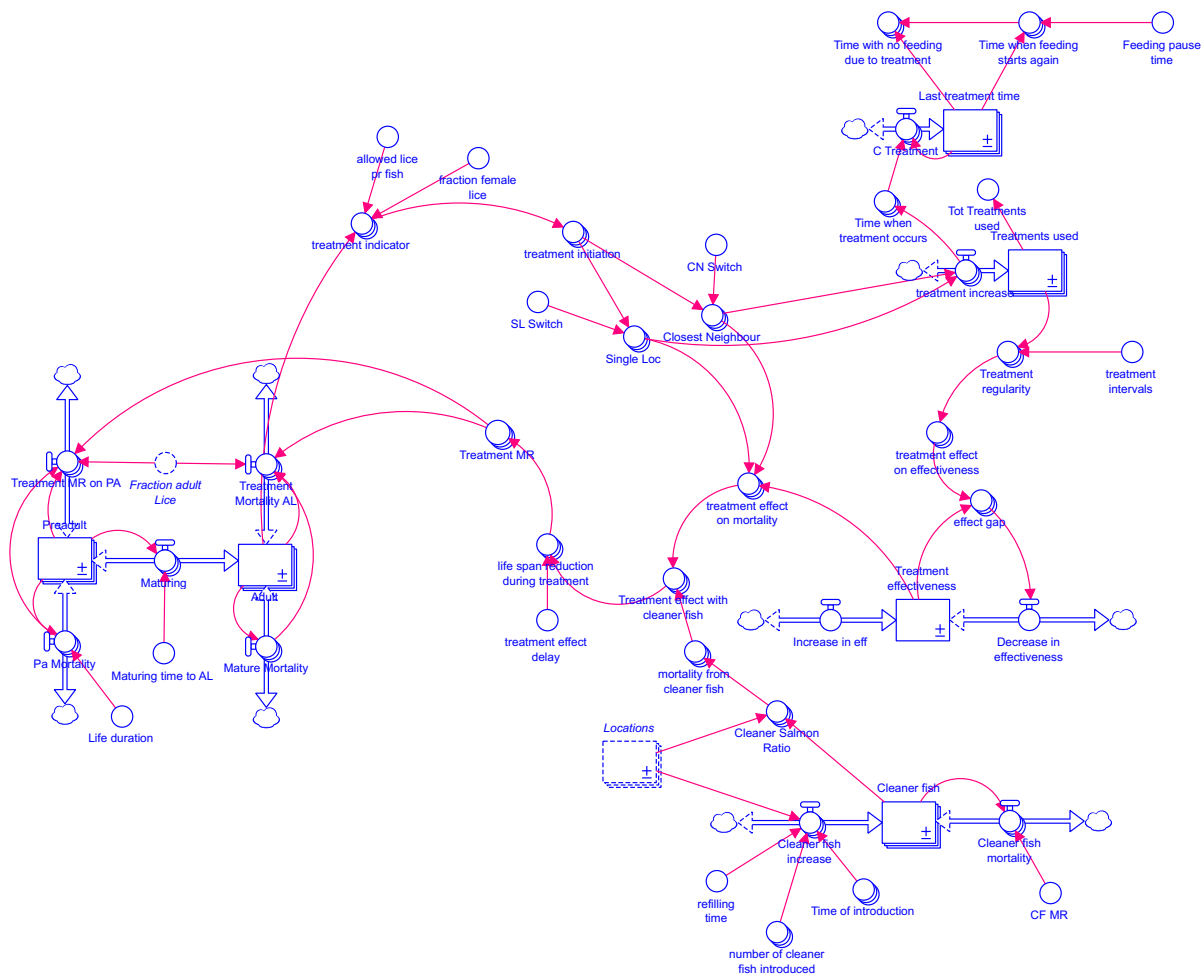


Figure 32: Overview of the treatment model connected to attached stages of lice

Treatments have a negative impact on the average lifetime of lice, meaning that the number of lice that pass through the outflow of lice death increases per DT when treatments are initiated at an endogenously generated “lice per fish” fraction. As infestation falls rapidly, so does the next generation’s reproduction, as it is dependent on the population of mature lice. Lice mortality is also influenced by slaughtering fish, as this physically removes attached stages of lice from the locations.

The treatment sub-model is important to the management of the fish farm as one of the main ways of reducing infestation levels once they occur in sea-based salmon populations (the other includes culling of an entire cohort, which is rarely beneficial to the farmer unless it occurs close to the end of production or at especially beneficial salmon prices (Osland, 2017). This is more relevant as a countermeasure to infectious salmon anemia or other viral diseases that form an immediate epidemic threat to other locations and the wild salmon population.

Treatments are also costly, can be damaging to the fish, and is one of the most important decision points for farmers along with feeding rates when fish are in the sea. The model allows for automated treatments or user-initiated treatments through a testing interface, such as introducing cleaner fish to locations at early stages of lice infection.

As an initial setting the model is run with treatments turned off in order to see the effects of unrestricted lice population growth until it reaches a preset carrying capacity per fish. This returns s-shaped growth, but varying with the amount of biomass in the sea, as its level stabilizes close to the maximum lice allowed by all fish in all locations. This would in turn start to increase the mortality of fish, and these would not reach their weight goal within the production time of the model.

When treatments are turned on, the model uses the maximum allowed threshold for female lice per fish (0,5) as the indicator for when to initiate a treatment. This decision starts a treatment cycle that increase the mortality of attached stage lice, hence reducing the reproduction of coming cohorts of lice and eventually the infection pressure of that location on other locations. The automated treatments are programmed in such a way as to initiate treatments in the location that experiences the high counts of adult female lice, without regarding policies of other locations' treatments with growing abundance or locations within the peak area of infection pressure (Samsing et al 2017), and this must therefore be specified if the user wants to initiate coordinated treatments at one or several neighboring locations if there are high counts of reproductive stage lice in one location.

When behavior testing coordinated treatments, there are two different policies built in:

- Synchronized treatments in all locations containing fish if one location approaches the threshold value of female lice
- Treatment of the closest location to the starting location (The modelled locations are paired together east and west of Osland in the fjord, making two sets of neighbors about 6 km from the other. Between the pairs there is an estimated 21km)

The treatment strategy options could be expanded in order to find combinations of treatment events that minimize the number of treatments while achieving the desired effects, as well as combinations that reduce the diminishing effect of repeated use of certain chemotherapeutic treatments.

There is also a counting structure that follows the number of treatments used in each location. This has two functions:

1. The more chemical treatments are used, the less effective they become, leading to a balancing loop that over time could limit their effect and ultimately slow the industry growth
2. That have a way of showing how costs are related to treatment measures.

The cleaner fish structure (Figure 33) is added to the mortality of attached stage lice in the same way as other treatments, but with a somewhat different behavior. With 10% cleaner fish to salmon ratio, the MR of lice increases to 0,079/days, reducing life from 8,2 to 5,2 days at 10c (especially PA stage lice) (Aldrin et al 2017). Cleaner fish inhabit a stock that is physically in the locations along with salmon. These are introduced as a number chosen by the operator, calculated by the desired fraction of salmon in the location, as this fraction influences the effect of the cleaners. The outflow from the cleaner fish stock is a set mortality rate, meaning that the fraction of cleaner fish to salmon is not constant, giving a variable that changes over time with regards to its effect on lice mortality. The introduction of cleaner fish is controlled by introduction times and the availability of fish in that location, to avoid introducing a lice countermeasure into a location where there is no biomass for parasites to attach to (Aldrin et al 2017).

Inflow:

*IF(Locations[1]>1000) THEN PULSE(number_of_cleaner_fish_introduced[1];
Time_of_introduction; refilling_time) ELSE 0*

The amount of cleaner fish and salmon from “locations” are used to calculate the cleaner fish ratio, which determines the mortality on lice from cleaner fish (Aldrin et al 2017):

*1-EXP(-0,0823*Cleaner_Salmon_Ratio[1])*

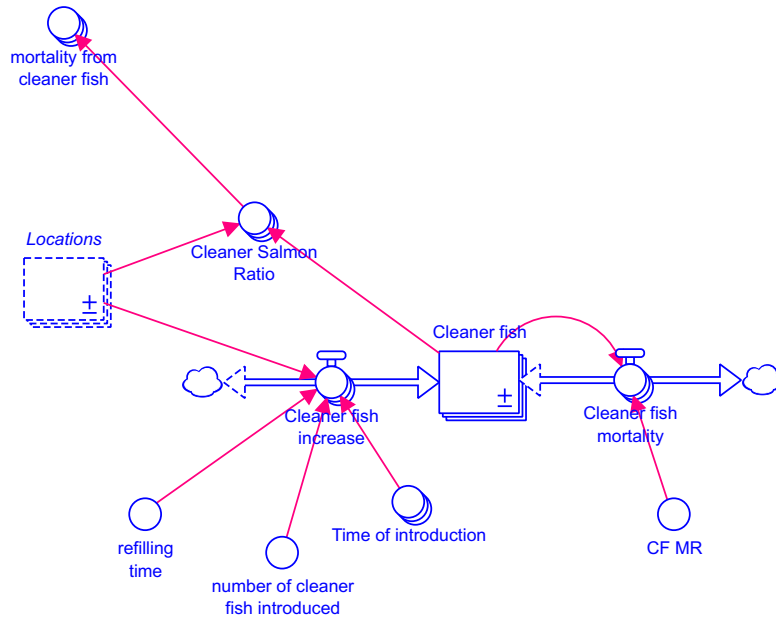


Figure 33: The structure of the cleaner fish model, showing the stock of cleaner fish. the inflow is initiated by the fish farmer, and the outflow has a constant mortality rate of 0,028 (Aldrin et al 2017)

The initial values for the cleaner fish sector are given in Table 6.

Table 6: Initial inputs to the cleaner fish model used with an automatic replenishment of cleaner fish when the population runs low.

Cleaner fish (Stock)	fish	0
Refilling time	days	50
Number of cleaner fish introduced	fish	10000
Time of introduction	days	250
Cleaner Fish MR	Fish/days	0,028

4. MODEL VALIDITY

The model described above includes the key processes governing the population growth and dispersal of salmon lice between salmon farms in a defined region of marine life.

As a simplified representation of a real system, focus should be on reproducing behavior rather than making point predictions (Barlas, 1996). The model recreates reference behavior when run with base values, but this is tested further to validate and build confidence in the model framework.

The validity of a model relies heavily on its purpose, since this is what determines confidence in the model as a tool for system analysis and implementation of policies. This cannot be stated clearly as a result of a formal procedure (Barlas, 1996), but must be continuously performed through the conceptualization and building of the model. Forrester and Senge (1979) present some guidelines of model validation. Among these are real system comparison to reference mode, parameter verification and extreme condition tests.

Extreme values

By testing extreme values, we ensure that the model generates results matching the physically possible behavior of the real system, also when the inputs to the model are well outside of the normal values. We also get an indication of whether or not we have accounted for and closed all important feedback loops in the system. In some cases, best estimates are chosen in order to move the modelling process forward. These variables are formerly discussed in their respective sub-models.

In the production part of the model, it would be unexpected to see negative fish or negative weight values. Even if feeding is zero or mortality is extremely high, these values would only go to zero, because physical stocks make no sense with zero values (Sterman, 2000).

In the lice module, we test extreme values by initiating the lice population with zero value (Figure 33), meaning no lice are present in the region, hence there can be no reproduction, even if there are hosts available. Opposite, high initial values to the lice stocks can be inserted, and still we expect to see an adjustment to the carrying capacity of the total amount of fish biomass in the sea, and the effect of treatments and cleaner fish that break lice reproduction cycles and thus export of infectious stage lice.

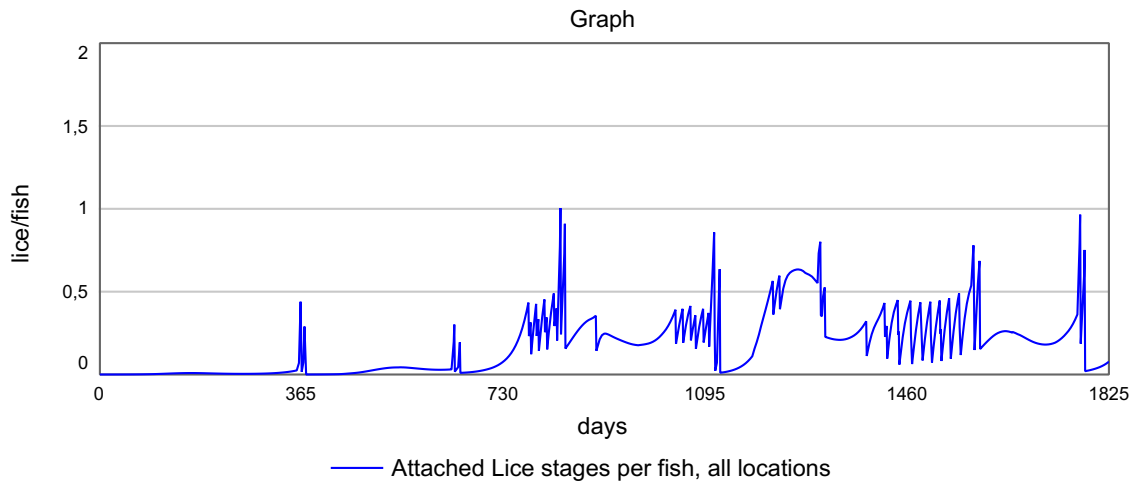


Figure 33: Average Adult lice per fish base run.

Parameter tests

Value testing on the lice aging chain growth model reveals that the abundance of lice is very sensitive to the attachment rate, that is the rate at which the copepodid stage actually finds and attach to a host. There is currently no good parameter estimate for this in research, and the model relies on best estimates of the other stages to recreate the behavior that can be recreated and verified with experiments (Kristoffersen et al 2018, Stien et al 2005, Aldrin et al 2017). This is then multiplied with the α parameter as an expression of the gap between the produced parasites and the actual attachment rate.

Each gravid female produces about 300 eggs, which develop into Nauplius and next to the copepodid stage, at which they can attach to a host. This process is dependent on mortality at an average of 0,17 (Stien et al 2005). The time all these pre-infective lice float with currents that may or may not take them into contact with a host, and that may happen at a time when they are able to attach, and this varies with temperature, making an estimate or parameterization of the actual attachment rate extremely difficult to determine without testing with in-field samples. The part of the model that simulates the infection between farms is simplified in that it does not account for all the farms within the real boundary of infestation pressure, but only the farm locations that are controlled by our license holder. The effect of this is likely lower abundances than in reality, although that will have to be tested if relevant to use of the model. The variables relied on for calculating risk of infection pressure being contributive to other farms` infection is utilized both by Kristoffersen et al (2014) and Werkman et al (2011) although with varying model DT (time step values) and different estimations of the influence of external infestation pressure. It should also be noted that Werkman describes a general model for pathogen transfer between locations, while Kristoffersen specializes on the dispersal of salmon lice.

However, estimates based on the life cycle and reproductive rates have their merit, and the focus of this thesis is behavior to proposed policy, not exact lice counts. It is possible to determine reasonable estimates of the infection pressure by ensuring the model acts according to the known parameters and a viable coefficient of such pressure as such makes up the unknown, and serves as input to the model. It is important that this estimation would have to be tested before being used in other studies with different sets of variables and other model structure.

Since lice population growth through reproduction is temperature dependent and correlates with host density, we expect to see exponential increases in lice density with linear increases in local host density (Kristoffersen et al 2018). This may be tested by increasing the smolt numbers for some cohorts in the production model and running comparative graphs of mature females, which is an important indicator of the produced lice in the next generation given comparable numbers of hosts.

We run the model at different settings using the high leverage variables in the structure, and check key variables in the lice module itself, as well as other key indicators in the model, like biomass and decision variables for the production management. These are values that would have great impact on the resulting values of other parts of the model, and these keeping viable values is an indication of reasonable behavior as a part of robustness testing.

Comparison to reference mode

Since much of the behavior (Figure 33) of both the host and parasite sectors is endogenously generated, some key variables are dependent on changes in others, and this creates the possibility that several parameter values may return the same overall behavior. The lice model is sensitive to changes in temperature, which influence development times, mortality and the attachment rate from planktonic stages. In addition, the estimated effects of treatments are important to the behavior of the reproductive rates, as low efficiency will increase the numbers of treatments, lowering their effect further, and too powerful effects will eradicate lice infection, which is an unlikely scenario in the real system due to the presence of hosts that are not treated directly.

Further comparisons to reference mode data and model generated behavior is discussed in the following behavior testing segment.

5. BEHAVIOR TESTING

The model is run with base values (Table 6) to determine response when compared to reference mode data. The validity of the model must be based on several parameters. Ability to reproduce historic behavior is one, but even if the model matches, testing is required to find out if it reproduces the observed behavior for the correct reasons. Within behavior analysis we may apply extreme value testing, to see if we are able to produce irrational or improbable results within the model boundary. We start validation by structure testing as a part of the modeling process and as an ongoing process while adding or removing structure from the model. This stepwise approach reduces the risk of hidden mistakes, and helps isolate problems to clarify their purpose.

Table 6: Initial values for base run of the lice model with parameter name and units.

Initial Values			
Lice model	Parameter	Unit	Value
Stocks	Eggs	Lice	1000
	Nauplii	Lice	1000
	Copepodite	Lice	1000
	Chalimus / preadult	Lice	1000
	Adult	Lice	1000
Fish Stocks	Locations (3&4)	Fish	1200000
	Fish weight (3&4)	Grams	350
	Desired Fish weight	Grams	4500
Development (mean)	Hatching	days	5
	Infectious development	days	4
	Attaching	1/days	Equation
	Developing	degree/days	15,5
	Maturing	days	11
Mortality (mean)	Eggs mortality	days	6
	Dispersal (Naupli) mortality	1/days	0,17
	Unattached mortality	degree/days	155
	Ch mortality	1/days	0,05
	Mature mortality	1/days	0,047
	Treatment MR on CH and PA	1/days	equation
	Treatment Mortality AL	1/days	equation
Treatment Sector	Allowed lice per fish	lice/fish	0,5
	Fraction female lice	dmnl	0,5
	Treatment Switch	dmnl	1
	SL switch	dmnl	1
	CN Switch	dmnl	0
	Treatment effect delay	days	2
Cleaner fish Sector	Cleaner fish (stock)	fish	0
	Refilling time	days	50
	Number of cleaner fish introduced	fish	10000
	Time of introduction	days	250
	Cleaner Fish MR	Fish/days	0,028
Infection Pressure Sector	Alpha value	dmnl	0,0972
	Self recruitment (IIP) mean	dmnl	equation
	Median Migration weight	dmnl	equation

For model testing, we assume policies in the other sub-models are set to their initial values (Table 6), so that the model displays changes in response to parameter changes in the lice model. This means that there are initially no fish in locations, as we wait for the first cohort of salmon to be introduced. At this time, there will be no increased biomass other than the wild population to drive lice reproduction, keeping lice counts at the start of the simulation period close to zero (Figure 34).

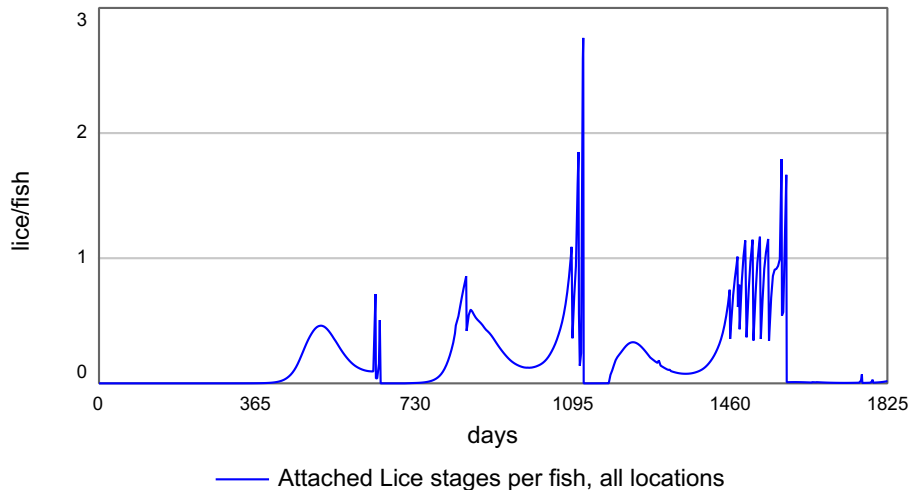


Figure 34: Model results with fish initiated at 0. This delays the growth of the lice population due to lack of hosts until the first cohorts are introduced to sea based locations

If initiated at zero lice in the locations, there will be no reproduction. Initiating with high abundance in this case, there will be most flow through mortality outflow, as there are no fish to drive infestation pressure between locations or on each site.

6.1 Test of the infection pressure

At normal values (Table 6), we initiate with lice in only one location, which stays close to zero until fish are introduced in that location. This drives lice population growth up in that location, and generates external infection pressure towards the other locations. If there are no fish in those locations, there are no hosts for the parasites, and mortality will become abundant on dispersed lice. As soon as a second location is filled with fish, lice abundance and reproduction will start growing in that location as well as adding external infestation pressure to the first location's attachment rate (Figure 35). As we have modelled the infection pressure between different locations, one viable experiment is to see if any of the locations transfer more infection than the others, such that the net infestation pressure of all farms is not the same, and that some are exporters and some are importers of infestation (Werkman et al, 2011, Salama and Murray 2011)

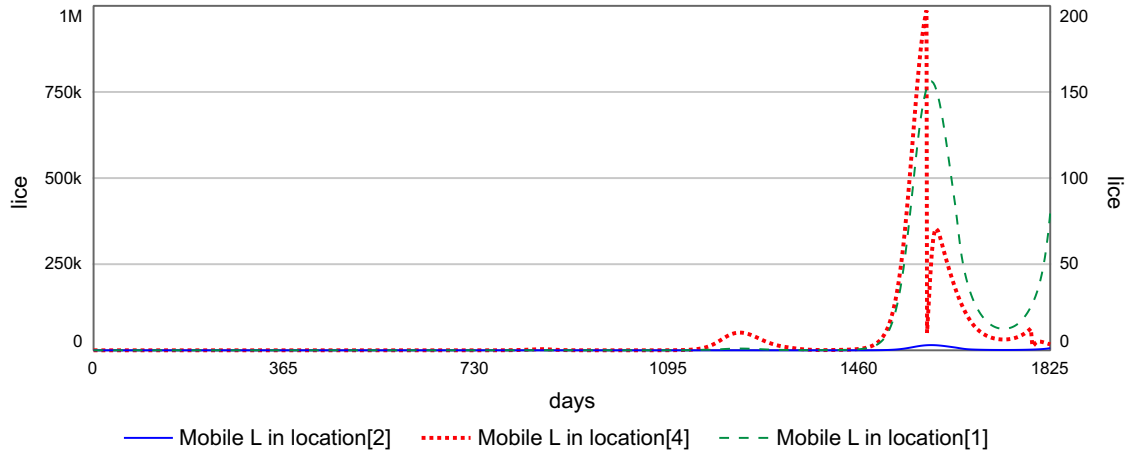


Figure 35: Infection spread between locations. The model is initiated with lice only in location 3, and over time infect others. This is most effective on location 4 (red, dotted), the closest location. Locations 1 (green, dash) and 2 (blue, solid) are measured on the right axis, and show increasing infection towards the end of the simulation.

The reference mode (Figure 37) shows cycles of increased lice abundance that roughly follow seasonal temperatures, biomass, and treatments in addition to the regular reproduction of sea lice. It is therefore difficult to pinpoint all the endogenous drivers of this behavior in the model, and we therefore reproduce this behavior with initial values according to operating procedures of the farmer, and responses derived from literature cited above. On the farm level, there may be several peaks of infestation in one season, although the highest levels are usually expected in the autumn (Hamza et al 2014), and at normal values the model recreates such behavior. This is given that normal behavior is based on an operating pattern where treatments against lice are used. Otherwise, such structure as used in the model gives S-shaped growth, reflecting exponential growth with following generations. This would be limited by the biological carrying capacity of the hosts, which is not specified for our current model. This is partly for exogenous values available: The reference mode is from data that are collected during normal management of fish farms, meaning that treatments and introduction of fish biomass have large effects on its behavior.

The model behavior is driven by a reinforcing loop between the lice population and lice births as long as hosts are available. This is balanced by lice mortality, which is increased by introducing treatment events. These treatments are driven by a parasite/host ratio (Figure 36), which is the reason for the occasional sharp reduction in the lice population.

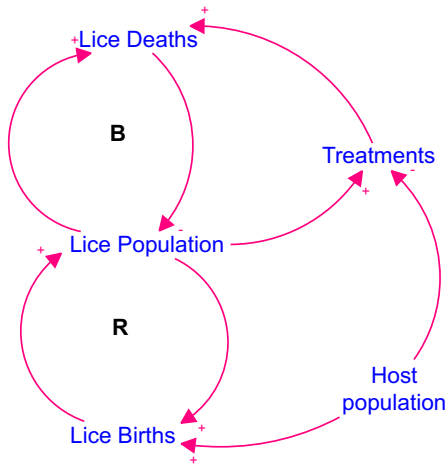


Figure 36: Causal loop diagram showing the drivers of lice population growth. The lice reproduction is a reinforcing loop dependent on host availability, which is balanced by a mortality loop which is strengthened by treatments

The model is then run with fish in locations 3 and 4, and other values as stated in Table 3 to compare model behavior with the reference mode (figures 37 & 38)

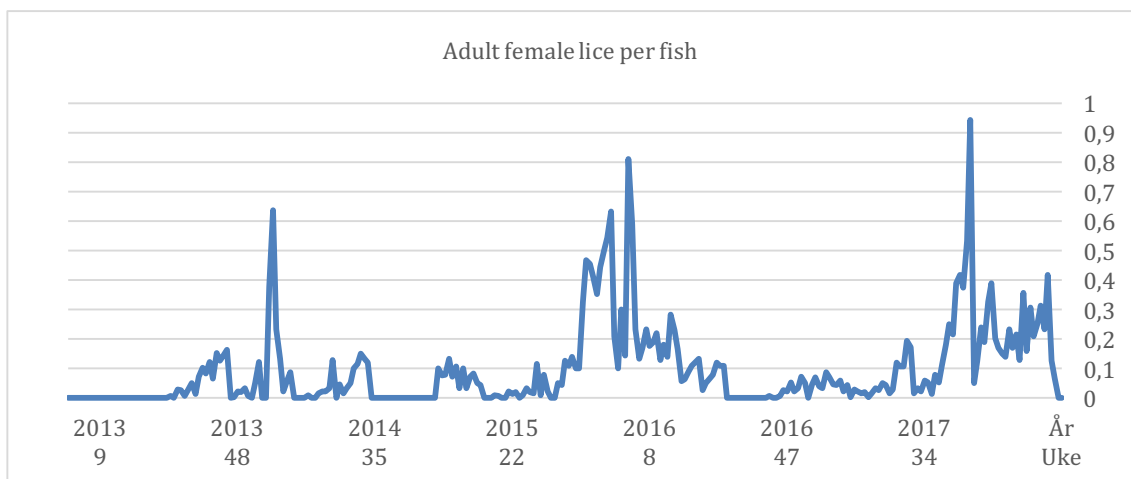


Figure 37: Reference mode based on lice counts from Osland (2018) from three locations. The fourth is left out because the data was incomplete, giving biased results

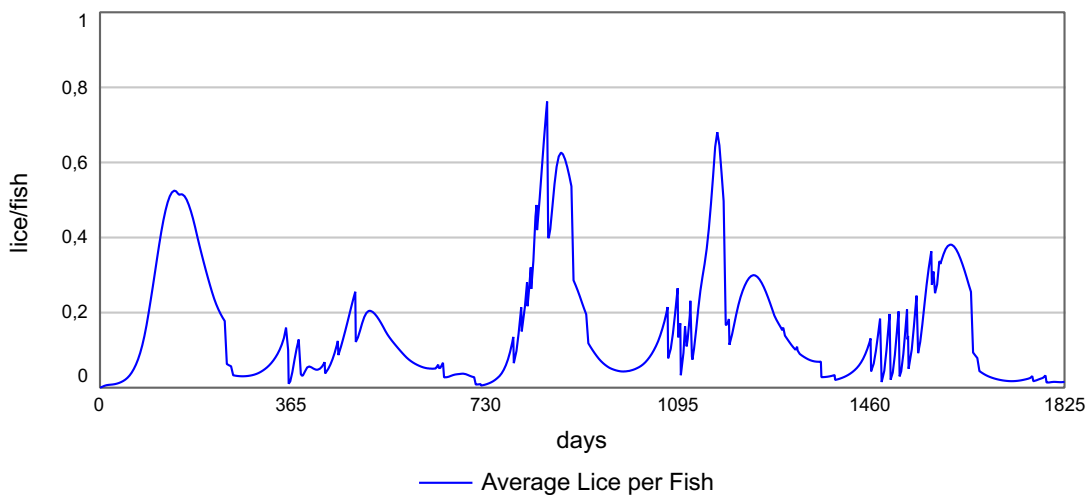


Figure 38: Model generated average of female adult lice per fish

This gives a high number of conducted treatment events (Figure 39), which gives an indication of the costs of high sea lice abundance to the producer.

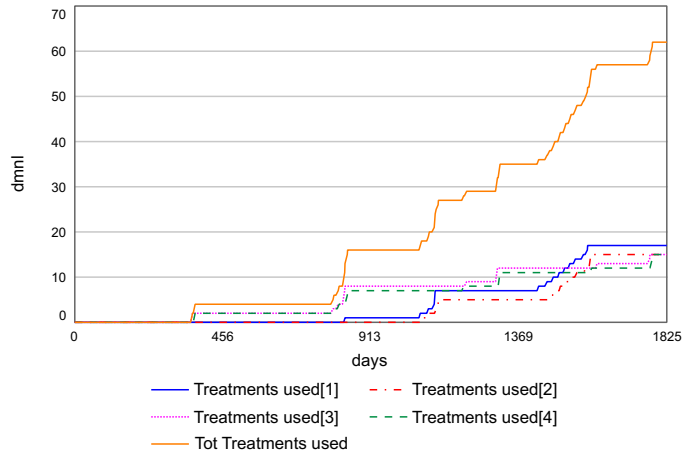


Figure 39: Number of treatments initiated over five years. Locations separated in blue, red, pink and green. Total treatment events for all four locations in orange

Next, policy options for mitigating salmon lice are discussed. These are tested separately against base run results before they are combined and run in a coordinated scenario, giving further effect on the reduction of the salmon lice population.

6. POLICY TESTING

6.1 Coordinated fallowing

The current model framework simulates one company's operation between different sites, and we therefore expect little organizational resistance in implementing coordinated treatments or fallowing. However, we may suspect that if this was enforced on several operators in the same production area, it would be hard to agree upon a time for the actual action, as the value and potential of each operator's stocks are so dependent on time and temperature. This would indicate that coordinated fallowing or treatment should start with coordination at the earliest stages of sea-based production of a cohort.

The model initially runs with the variable time to next set to 470, which gives the time for the next cohort to be hatched in the fish sector. By prolonging this to 490, we increase the time available for the other cohorts to grow while extending the fallowing period of empty locations, indicating that the farmer does not immediately fill up locations that have room. This reduces the external infection pressure because fallowed locations do not contribute to the lice population. This gives fewer treatments performed by the farmer as shown in Figure 40:

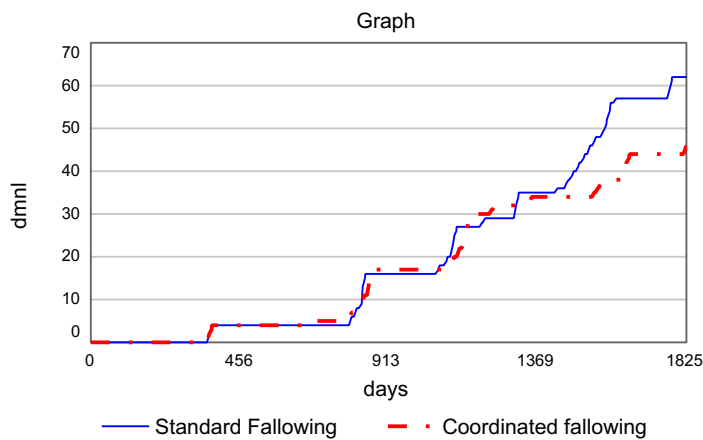


Figure 40: Comparative graphs between standard fallowing policy (blue) and coordinated fallowing (red)

This in turn comes from the reduced lice abundance in the locations (Figure 41)

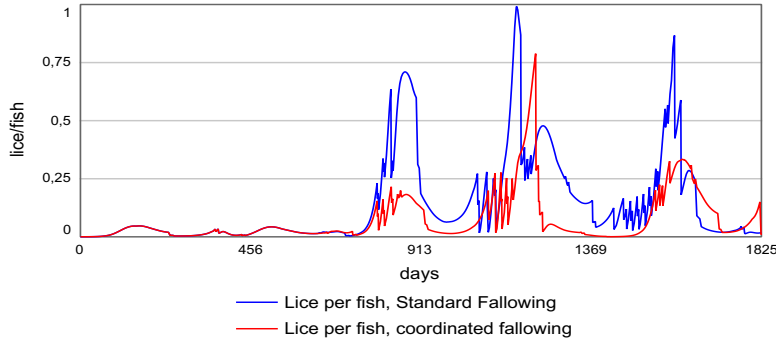


Figure 41: Comparative graph between Standard (blue) and coordinated (red) following

In addition, we compare the total biomass through the period (Figure 42). The producer wants to be as close as possible to MAB through all periods.

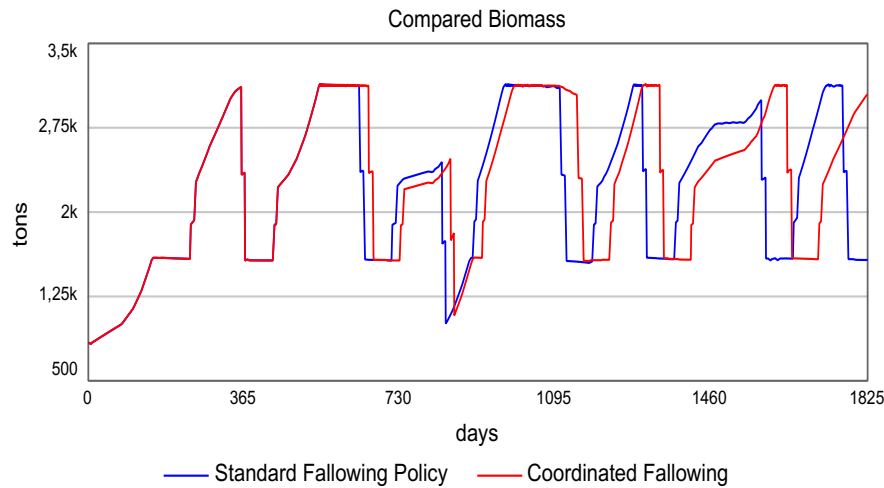


Figure 42: Comparative graph of total biomass. The standard following (blue) and the Coordinated following (red)

The introduction time is reset for the next behavior tests.

6.2 Preventive treatment

Treatment before outbreaks has been tested within the system dynamics framework by Hamza et al (2014) with promising results. This has also been reported by (Kristoffersen 2014, Salama and Murray, 2011). We can test this in the model by setting the value of the variable “allowed lice per fish” lower than the threshold legal value of 0,5 female lice per fish. This gives somewhat lower peak values for the infections, but have little effect on the total number of treatments (Figure 43). This may be partly caused by the model structure, as we in a more sophisticated policy model could make the functionality of occasional preemptive treatments in combination with regular thresholds, which would reduce the total number of treatments through production periods.

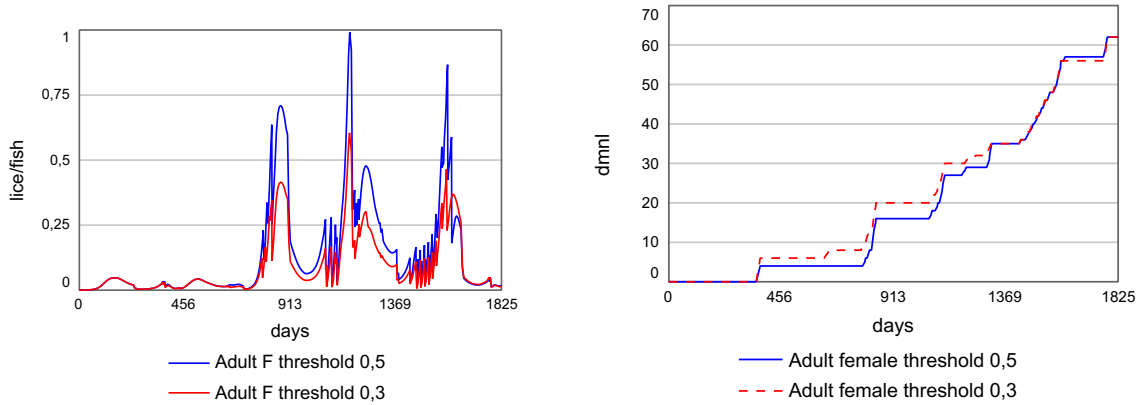


Figure 43: Lice per fish on average when lice treatment threshold is reduced from 0,5 (Blue) to 0,3 (red) giving earlier treatments. This gives lower lice abundance (left), but does not reduce the total number of treatments used at the end of the simulation (right graph)

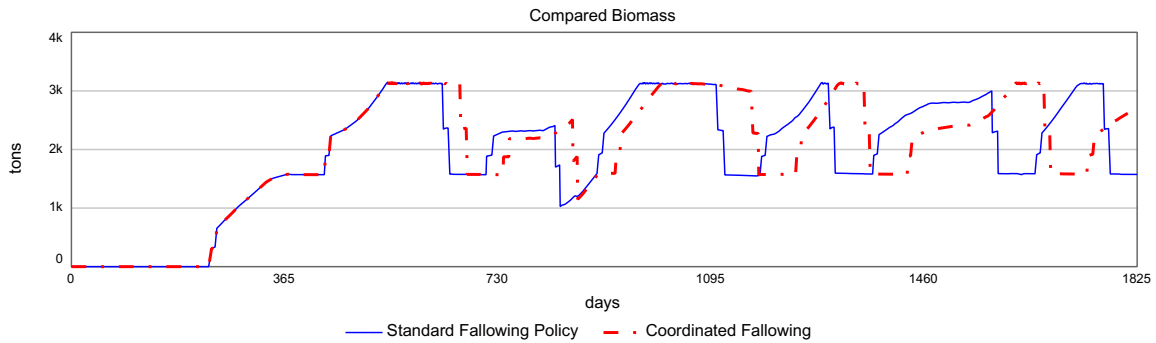


Figure 44: Compared total biomass in locations with different following policies. Normal following blue line, coordinated following in red, dotted. The graphs have a slight offset in time, due to prolonged following periods for some locations at certain times. The coordinated following shows higher biomass at some points compared to standard following policy.

6.3 Coordinated treatments and cleaner fish

The introduction of cleaner fish at a ratio of 10% to the host numbers give a visible effect on lice abundance (Figure 45), which is expected as stated by Aldrin et al (2017). Cyclical behavior due to temperature changes and production cycles (availability of hosts) continue.

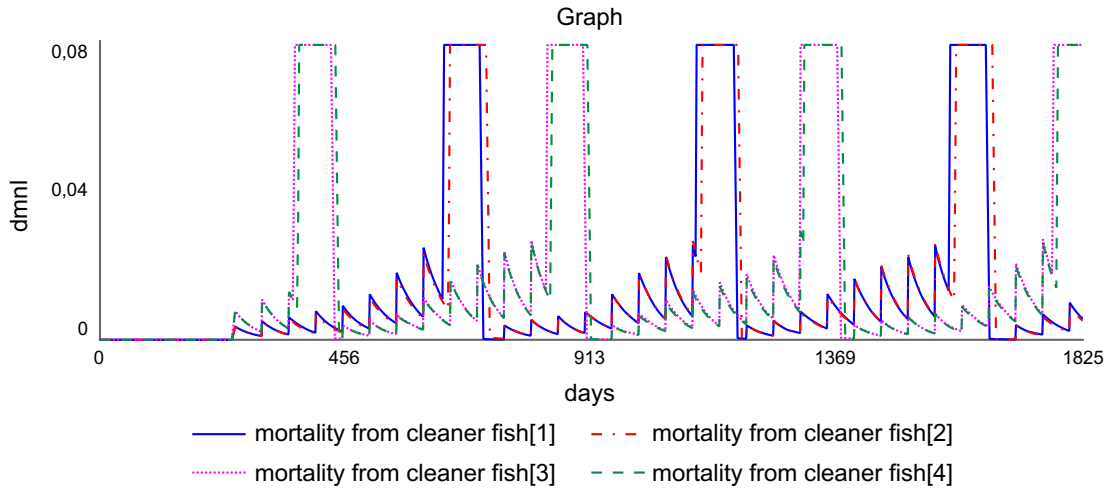


Figure 45: Mortality increase with 10% cleaner fish to host ratio

As expected, cleaner fish add to the mortality of attached lice. This effect is limited to the pre-adult and adult stages, as parasite size is an indicator on mortality from cleaner fish.

Establishing that the three policy changes have a separate positive effect on reducing the lice abundance, we may now combine the three to see the effect of combining policies for lice abundance reduction. The model is initiated with fish in locations 3 and 4, and with the single location treatment (SL) switch turned on. The threshold for lice to start a treatment is set to 0,4. The next introduction time is set to 490. The number of cleaner fish is set to 100 000 per location to give a ratio to farmed salmon of 10 (10%) at introduction time 250. This gives the results shown in figures (46 - 49)

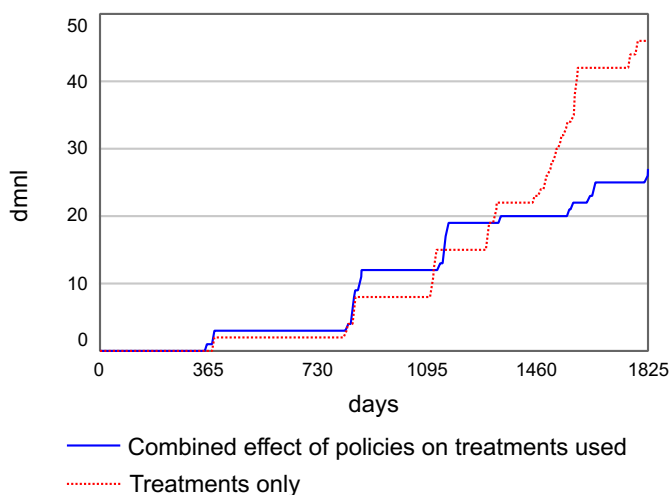


Figure 46: Comparative graph of treatments used when combining lice mitigation policies (blue) and treatments used in the base run, where treatments is the only measure against lice abundance (red, dotted)

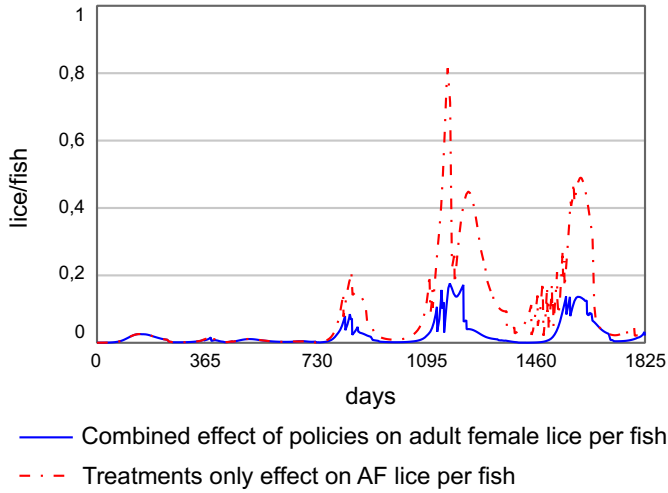


Figure 47: Comparative graph of the adult female lice abundance when combining policies (blue) and when treatments on infected locations is the only measure (red, dotted)

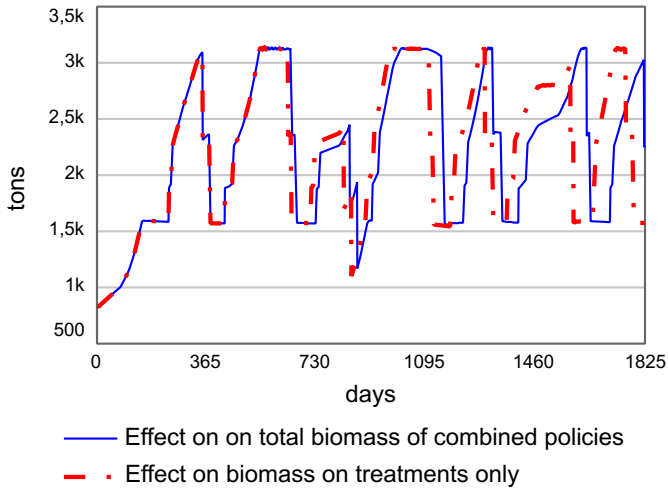


Figure 48: Comparative graph of the effect of combined lice measures on total biomass (blue) and biomass when treatments are the only measure against lice (red, dotted)

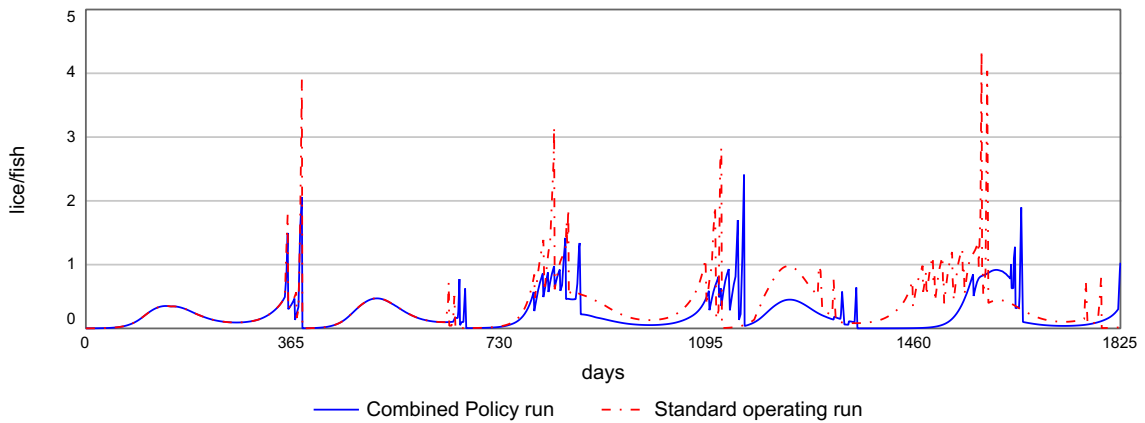


Figure 49: Combination of treatments, Cleaner fish & Following as an average of all attached stage lice per fish on all locations. The combined policy run (blue, solid) shows lower general levels of infestation, as well as lower peak values than the standard setting run (red, dotted)

The last run (Figure 49) incorporates all the policies discussed above into one run. The combined effect on lice abundance is shown to be higher than in previous runs, and according to expected behavior, the change to total farmed biomass is not radically changed from earlier runs. This indicate little consequence to the production, although costs may be significant.

The tests discussed above are subject to many variations and combinations, and the user of the model may vary the amount of cleaner fish, treatment threshold and introduction time to find an optimal result within the model framework.

It is likely that the robustness of the model is dependent on continuing testing and research. There are also likely to be factors left out of the model that have an impact on the simulation results, and one should therefore not expect to be able to translate model generated results fully to a real system. It shows, however, that building a model with various policy choices, may clarify that interventions have non-linear effects and sometimes unexpected outcomes in some other part of the model.

7. CONCLUSIONS

The aim of this paper is building and describing a model framework that describes the relationship between farmed biomass and lice abundance, as well as how coordinating treatments and other policies have an effect on that abundance. This is a part of helping operators in the industry access and use the large amount of data available, and help encourage and incentivize further data collection to improve models such as the present. This is also a part of studying the optimizing a production process with complex interrelationships and material delays.

We demonstrate how coordinating fallowing and treatments at several locations under one license holder have positive effects on reducing lice abundance. Modelling the operation of a single license holder is believed to be an advantage to removing implementing challenges that would normally have to be strictly enforced by the government. The model helps with this by showing that one producer at a local scale can reduce lice abundance with simple management policies.

We observe that the model framework we have built on well-founded data is comparable to reference mode data. However, the lice infection process is excessively responsive to changes in lice the attachment rate, which indicates the knowledge gap between lice produced and actual attachment to a host. The visual difference from the reference mode comes in part from the time step of datasets, which are monthly or weekly, while our model return results at a DT of one day.

By prolonging the land based salmon growth period we also see a postponement of heavy infestation levels. The model shows some improvement on the problematic behaviour by using pre-emptive treatments and cleaner fish when lice counts are high in other locations, to prevent the spread of those parasite stages to locations with low abundance.

The model is capable of reproducing the most important patterns of the relationship between parasite and host population dynamics, the effect of coordinated treatments and the internal and external infection spread, and may as such be used for simulating different mitigation strategies. The results suggest that there is benefit to coordinating and combining different measures towards salmon lice in salmon farms.

On further research, the core model can be expanded to focus on regulation policy, management practice, biomass effects, treatments or other variables in isolation, to explore causal relationships between such factors.

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APPENDIX

A.1 Input for the louse model

Initial values for running the model as described in behavior and policy testing chapters (Table 7).

Table 7: The parameter values used for running the lice model as discussed in the model and policy testing segments of the paper

Initial Values				Citation		
Lice model	Parameter	Unit	Value		Value	Unit
Stocks	Eggs	Lice	1000			
	Nauplii	Lice	1000			
	Copepodite	Lice	1000			
	Chalimus / preadult	Lice	1000			
	Adult	Lice	1000			
Fish Stocks	Locations (3&4)	Fish	1200000	When testing continuous operation, otherwise 0		
	Fish weight (3&4)	Grams	350	When testing continuous operation, otherwise 0		
	Desired Fish weight	Grams	4500			
Development (mean)	Hatching	days	5	Stien et al 2005	41.98	degree/days
	Infectious development	days	4	Samsing et al 2017,	40	degree/days
	Attaching	1/days	Equation	Samsing et al 2017,	150	Degree/days
	Developing	degree/days	15,5	Kristoffersen et al 2014		
	Maturing	days	11	Stien et al 2005	10,4 - 15,4	degree/days
Mortality (mean)	Eggs mortality	days	6			
	Dispersal (Naupli) mortality	1/days	0,17	Samsing et al 2017	17 %	lice/days
	Unattached mortality	degree/days	155			
	Ch mortality	1/days	0,05	Stien et al 2005	0,005 - 0,01	1/days
	Mature mortality	1/days	0,047	Stien et al 2005	0,035 - 0,056	0,056
	Treatment MR on CH and PA	1/days	equation		0-1	1/days
	Treatment Mortality AL	1/days	equation		0-1	1/days
Treatment Sector	Allowed lice per fish	lice/fish	0,5	Lowdata		
	Fraction female lice	dmnl	0,5	Stien et al 2005		
	Treatment Switch	dmnl	1			
	SL switch	dmnl	1			
	CN Switch	dmnl	0			
	Treatment effect delay	days	2	Aldrin et al 2017	2	
Cleaner fish Sector	Cleaner fish (stock)	fish	0			
	Refilling time	days	50			
	Number of cleaner fish introduced	fish	10000			
	Time of introduction	days	250			
	Cleaner Fish MR	Fish/days	0,028	Aldrin et al 2017	$1-EXP(-0,0823*Cleaner_Salmon_Ratio[1])$	
Infection Pressure Sector	Alpha value	dmnl	0,0972	35/360		
	Self recruitment (IIP) mean	dmnl	equation	Samsing et al. 2017	0,29 - 0,19	
	Median Migration weight	dmnl	equation	Samsing et al. 2017	0,042 - 0,017	dmnl

A.2 Equations for the infection pressure sub-model

Table 8: The calculations behind parameter values in the infection pressure model. The declining risk of infection with distance (top), distances between locations (middle) and beta values (bottom)

Risk of contributing infection		Inf over seaway distance				
Distanse ij	Distanse jj					Rrij
6	0	-4,5612	0,3104	-14,6953		4,149E-07
19	0	-9,0872	0,3104	-29,2770		1,928E-13
21	0	-9,6389	0,3104	-31,0544		3,260E-14
22	0	-9,9062	0,3104	-31,9158		1,378E-14
24	0	-10,4257	0,3104	-33,5894		2,584E-15
0	0	0,3104	0,3104	1,0000		2,718E+00
S values						
Aldrin et al 2013						
Distance (km)	Torvund (Tv)	Sørevik (Sø)	Måren (Må)	Mjølsvik (Mj)		
Torvund	0	6	24	21		
Sørevik	6	0	22	19		
Måren	24	22	0	6		
Mjølsvik	21	19	6	0		
R of Inf	Torvund (Tv) i	Sørevik (Sø) j	Måren (Må) k	Mjølsvik (Mj) l		
Torvund i	0,3104	4,14875E-07	1,92827E-13	3,26011E-14		
Sørevik j	4,14875E-07	0,3104	1,37771E-14	1,92827E-13		
Måren k	2,58401E-15	1,37771E-14	0,3104	4,14875E-07		
Mjølsvik l	3,26011E-14	1,92827E-13	4,14875E-07	0,3104		
Werkman et al 2011						
Ro Reproductiv Beta * d * no of cont						
Beta (transmission rate)	production time	no of cont	reproductive rate R	beta per day	R per day	
0,1	12	2	2,4	0,0033	0,08	
0,25	12	2	6	0,0083	0,2	
0,5	12	2	12	0,0167	0,4	
0,028	12	3	1,008	0,0009	0,0336	

A.3 Equation overview of the lice population model, Infection pressure, cleaner fish and treatments sub-models

Cleaner Fish Sector

Cleaner Fish MR = 0,028	1/days
Cleaner_fish[Location](t) = Cleaner_fish[Location](t - dt) + (Cleaner_fish_increase[Location] - Cleaner_fish_mortality[Location]) * dt	fish
INIT Cleaner_fish[Location] = 0	fish
INFLOWS: Cleaner_fish_increase[1] = IF(Locations[1]>1000) THEN PULSE(number_of_cleaner_fish_introduced[1]; Time_of_introduction; refilling_time) ELSE 0 Cleaner_fish_increase[2] = IF(Locations[2]>1000) THEN PULSE(number_of_cleaner_fish_introduced[2]; Time_of_introduction; refilling_time) ELSE 0 Cleaner_fish_increase[3] = IF(Locations[3]>1000) THEN PULSE(number_of_cleaner_fish_introduced[3]; Time_of_introduction; refilling_time) ELSE 0 Cleaner_fish_increase[4] = IF(Locations[4]>1000) THEN PULSE(number_of_cleaner_fish_introduced[4]; Time_of_introduction; refilling_time) ELSE 0	fish/day
OUTFLOWS: Cleaner_fish_mortality[1] = Cleaner_fish[1]*CF_MR Cleaner_fish_mortality[2] = Cleaner_fish[2]*CF_MR Cleaner_fish_mortality[3] = Cleaner_fish[3]*CF_MR Cleaner_fish_mortality[4] = Cleaner_fish[4]*CF_MR	fish/day
Cleaner_Salmon_Ratio[1] = MIN(MAX(0; Cleaner_fish/(Locations[1]+0,0001)); 1) Cleaner_Salmon_Ratio[2] = MIN(MAX(0; Cleaner_fish/(Locations[2]+0,0001)); 1) Cleaner_Salmon_Ratio[3] = MIN(MAX(0; Cleaner_fish/(Locations[3]+0,0001)); 1) Cleaner_Salmon_Ratio[4] = MIN(MAX(0; Cleaner_fish/(Locations[4]+0,0001)); 1)	dmnl
mortality_from_cleaner_fish[1] = 1-EXP(-0,0823*Cleaner_Salmon_Ratio[1]) mortality_from_cleaner_fish[2] = 1-EXP(-0,0823*Cleaner_Salmon_Ratio[2]) mortality_from_cleaner_fish[3] = 1-EXP(-0,0823*Cleaner_Salmon_Ratio[3]) mortality_from_cleaner_fish[4] = 1-EXP(-0,0823*Cleaner_Salmon_Ratio[4])	dmnl
number_of_cleaner_fish_introduced[1] = 10000 number_of_cleaner_fish_introduced[2] = 10000 number_of_cleaner_fish_introduced[3] = 10000 number_of_cleaner_fish_introduced[4] = 10000	fish
refilling_time = 50	days

Time_of_introduction[1] = 250 Time_of_introduction[2] = 250 Time_of_introduction[3] = 250 Time_of_introduction[4] = 250	days
--	------

Infection Pressure Sector

alfa_test = 1/360*20	dmnl
alfa_val_in_dir_of = 0,0556 <i>direction of pressure, as a sector of a 360 degree dispersal that is 1. 1/360 is 0,002 so 20 degrees is 0,056</i>	dmnl
Attachment_rate[1] = (IP_i[1]*Copepodid[1]+IP_j[1]*Copepodid[2]+IP_k[1]*Copepodid[3]+IP_l[1]*Copepodid[4]) Attachment_rate[2] = (IP_i[2]*Copepodid[1]+IP_j[2]*Copepodid[2]+IP_k[2]*Copepodid[3]+IP_l[2]*Copepodid[4]) Attachment_rate[3] = (IP_i[3]*Copepodid[1]+IP_j[3]*Copepodid[2]+IP_k[3]*Copepodid[3]+IP_l[3]*Copepodid[4]) Attachment_rate[4] = (IP_i[4]*Copepodid[1]+IP_j[4]*Copepodid[2]+IP_k[4]*Copepodid[3]+IP_l[4]*Copepodid[4]) <i>The rate at which infectious stage lice are able to develop, find a host and attach to a fish.</i>	lice/days
host_availability_P[1] = IF(Host_population[1]>1000) THEN 1 ELSE 0 host_availability_P[2] = IF(Host_population[2]>1000) THEN 1 ELSE 0 host_availability_P[3] = IF(Host_population[3]>1000) THEN 1 ELSE 0 host_availability_P[4] = IF(Host_population[4]>1000) THEN 1 ELSE 0	dmnl
Host_population[1] = Locations[1]+Wild_hosts/4 Host_population[2] = Locations[2]+Wild_hosts/4 Host_population[3] = Locations[3]+Wild_hosts/4 Host_population[4] = Locations[4]+Wild_hosts/4	fish
IP_i[1] = "Si_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[1] IP_i[2] = "Si_x_P(B)"[2]*alfa_val_in_dir_of*host_availability_P[1] IP_i[3] = "Si_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[1] IP_i[4] = "Si_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[1] <i>The force of infection between locations. "This feedback dynamic can be confirmed by calculating the loop polarity in the SIR model. As the number of infected cases increase, so too does lambda. An increase in lambda leads to an increased in the infection rate (IR), which in turn leads to higher numbers of infected. This is a reinforcing process, and the positive feedback loop can quickly dominate</i>	Dmnl/days

<p><i>the model behavior and so drive the exponential growth processes associated with the outbreak of a contagious disease.”</i></p> <p><i>Duggan (2016)</i></p> <p><i>Kristoffersen et al 2014 estimates the internal infection pressure as 0 most of the first 16 weeks, while EIP is significant correlated with louse counts.</i></p>	
<p>IP_j[1] = "S_j x P(B)"[1]*alfa_val_in_dir_of*host_availability_P[2]</p> <p>IP_j[2] = "S_j x P(B)"[2]*alfa_val_in_dir_of*host_availability_P[2]</p> <p>IP_j[3] = "S_j x P(B)"[3]*alfa_val_in_dir_of*host_availability_P[2]</p> <p>IP_j[4] = "S_j x P(B)"[4]*alfa_val_in_dir_of*host_availability_P[2]</p>	Dmnl/days
<p>IP_k[1] = "Sk_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[3]</p> <p>IP_k[2] = "Sk_x_P(B)"[2]*alfa_val_in_dir_of*host_availability_P[3]</p> <p>IP_k[3] = "Sk_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[3]</p> <p>IP_k[4] = "Sk_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[3]</p>	Dmnl/days
<p>IP_l[1] = "Sl_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[4]</p> <p>IP_l[2] = "Sl_x_P(B)"[2]*alfa_val_in_dir_of*host_availability_P[4]</p> <p>IP_l[3] = "Sl_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[4]</p> <p>IP_l[4] = "Sl_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[4]</p>	Dmnl/days
<p>"Si_x_P(B)"[1] = Survival_from_i[1]</p> <p>"Si_x_P(B)"[2] = Survival_from_i[2]</p> <p>"Si_x_P(B)"[3] = Survival_from_i[3]</p> <p>"Si_x_P(B)"[4] = Survival_from_i[4]</p> <p><i>Kristoffersen et al 2017: To Model Spatial Infestation Pressure, the farm specific estimates of infestation pressure are interpolated in coastal waters from the farm origin, using an empirical kernel density function (Aldrin et al 2013). Infestation pressure at any point is thus expressed as the distance-adjusted sum of cotnributions from all farms within 100 km seaway distance.</i></p> <p><i>RR_{i,j}=</i></p> $e^{(-1.444-0,351(D_{i,j}^{(0,57)}-1/0,57))}$ $e^{(-1,444-0,351(0-1)/0,57)}$ <p><i>where D_{i,j} is the seaway distance from farm i to location j along the coast. Infestation pressure from farms more distant than 100km was set to 0.</i></p>	Dmnl/days
<p>"Sj_x_P(B)"[1] = Survival_from_j[1]</p> <p>"Sj_x_P(B)"[2] = Survival_from_j[2]</p> <p>"Sj_x_P(B)"[3] = Survival_from_j[3]</p> <p>"Sj_x_P(B)"[4] = Survival_from_j[4]</p>	Dmnl/days
<p>"Sk_x_P(B)"[1] = Survival_from_k[1]</p>	Dmnl/days

"Sk_x_P(B)"[2] = Survival_from_k[2] "Sk_x_P(B)"[3] = Survival_from_k[3] "Sk_x_P(B)"[4] = Survival_from_k[4]	
"Sl_x_P(B)"[1] = Survival_from_l[1] "Sl_x_P(B)"[2] = Survival_from_l[2] "Sl_x_P(B)"[3] = Survival_from_l[3] "Sl_x_P(B)"[4] = Survival_from_l[4]	Dmnl/days
Survival_from_i[1] = 0,3104 Survival_from_i[2] = 4,148E-07 Survival_from_i[3] = 2,584E-13 Survival_from_i[4] = 3,260E-14 <i>This is known as the basic reproduction number R0, which is the average number of secondary infectious persons resulting from one infectious person being introduced to a totally susceptible population (Anderson and May 1992). Effective contact rate *total population gives the real transmission parameter</i>	Dmnl/days
Survival_from_j[1] = 4,148E-07 Survival_from_j[2] = 0,3104 Survival_from_j[3] = 1,377E-14 Survival_from_j[4] = 1,928E-13	Dmnl/days
Survival_from_k[1] = 1,928E-13 Survival_from_k[2] = 1,377E-14 Survival_from_k[3] = 0,3104 Survival_from_k[4] = 4,148E-07	Dmnl/days
Survival_from_l[1] = 3,260E-14 Survival_from_l[2] = 1,928E-13 Survival_from_l[3] = 4,145E-07 Survival_from_l[4] = 0,3104	Dmnl/days

Lice Sector

Adult[1](t) = Adult[1](t - dt) + (Maturing[1] - Mature_Mortality[1] - Treatment_Mortality_AL[1]) * dt INIT Adult[1] = 100 Adult[2](t) = Adult[2](t - dt) + (Maturing[2] - Mature_Mortality[2] - Treatment_Mortality_AL[2]) * dt INIT Adult[2] = 100	Lice
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<p>Adult[3](t) = Adult[3](t - dt) + (Maturing[3] - Mature_Mortality[3] - Treatment_Mortality_AL[3]) * dt INIT Adult[3] = 100</p> <p>Adult[4](t) = Adult[4](t - dt) + (Maturing[4] - Mature_Mortality[4] - Treatment_Mortality_AL[4]) * dt INIT Adult[4] = 100</p>	
<p>INFLOWS: Maturing[Location] = MAX(0; Chalimus_and Preadult/Maturing_time_PAAM)</p>	Lice/days
<p>OUTFLOWS: Mature_Mortality[Location] = Adult/life_span Treatment_Mortality_AL[Location] = MAX(0; (Adult*Treatment_MR)-Mature_Mortality-(Lice removed with slaughtered fish*Ad fraction))</p>	Lice/days
<p>"Attached_Lice_stages_per_fish_all_locations" = (lice pr fish[1]+lice pr fish[2]+lice pr fish[3]+lice pr fish[4])/4</p>	Lice/fish
<p>Avg_development_time = 17</p>	days
<p>Preadult[Location](t) = Preadult[Location](t - dt) + (Developing[Location] - Maturing[Location] - Pa_Mortality[Location] - Treatment_MR_on_PA[Location]) * dt INIT Preadult[Location] = 150</p>	lice
<p>INFLOWS: Developing[Location] = Chalimus/Dev_time_to_PA</p> <p>OUTFLOWS: Maturing[Location] = MAX(0; Preadult/Maturing_time_to_AL) Pa_Mortality[Location] = Preadult/Life_duration Treatment_MR_on_PA[Location] = MAX(0; (Preadult*Treatment_MR)-Pa_Mortality-(Lice removed with slaughtered fish*(1-Fraction adult Lice)))</p>	Lice/days
<p>Chalimus[Location](t) = Chalimus[Location](t - dt) + (Attaching[Location] - Developing[Location] - CH_Mortality[Location] - Treatment_Mortality_Chalimus[Location]) * dt INIT Chalimus[Location] = 100</p>	Lice
<p>INFLOWS: Attaching[1] = MAX(0; Attachment_rate[1]) Attaching[2] = Attachment_rate[2] Attaching[3] = Attachment_rate[3] Attaching[4] = Attachment_rate[4]</p> <p>UNITS: lice/days</p> <p>OUTFLOWS: Developing[Location] = Chalimus/Dev_time_to_PA CH_Mortality[Location] = Chalimus/CH life dur</p>	Lice/days

Treatment_Mortality_Chalimus[Location] = MAX(0; (Chalimus* treatment effect on mortality/treatment effect delay)-CH Mortality)	Lice/days
Copepodid[1](t) = Copepodid[1](t - dt) + (Infectious_development[1] - Attaching[1] - Unattached_Mortality[1]) * dt INIT Copepodid[1] = 100 Copepodid[2](t) = Copepodid[2](t - dt) + (Infectious_development[2] - Attaching[2] - Unattached_Mortality[2]) * dt INIT Copepodid[2] = 100 Copepodid[3](t) = Copepodid[3](t - dt) + (Infectious_development[3] - Attaching[3] - Unattached_Mortality[3]) * dt INIT Copepodid[3] = 100 Copepodid[4](t) = Copepodid[4](t - dt) + (Infectious_development[4] - Attaching[4] - Unattached_Mortality[4]) * dt INIT Copepodid[4] = 100	lice
INFLOWS: Infectious_development[Location] = "Nauplii (larvae)"/Development_time	Lice/days
OUTFLOWS: Attaching[1] = MAX(0; Attachment_rate[1]) Attaching[2] = Attachment_rate[2] Attaching[3] = Attachment_rate[3] Attaching[4] = Attachment_rate[4] Unattached_Mortality[Location] = Copepodid/Copepodid_stage_time	Lice/days
Copepodid_stage_time = Normal_stage_time/(1/Effect_of_temperature_on_stage_time) <i>During the period of development through to chalimus stages we assumed a daily mortality of 0,05 per individual (Stien et al 2005), where delta Tch is the number of days required to accumulate 155 degree-days with the given temperatures.</i>	days
Development_time = norm_dev_time/(1/Effect_of_temperature_on_stage_time)	days
Effect_of_season_on_wild_hosts = GRAPH(season) (0, 0,200), (96,0526315789, 0,800), (192,105263158, 0,700), (288,157894737, 0,300), (384,210526316, 0,400), (480,263157895, 0,200), (576,315789474, 0,800), (672,368421053, 0,700), (768,421052632, 0,300), (864,473684211, 0,400), (960,526315789, 0,200), (1056,57894737, 0,800), (1152,63157895, 0,700), (1248,68421053, 0,300), (1344,73684211, 0,400), (1440,78947368, 0,200), (1536,84210526, 0,800), (1632,89473684, 0,700), (1728,94736842, 0,300), (1825, 0,400) <i>wild stocks migrate into the fjord and up rivers for nesting late winter and early spring. migration out of the fjord occurs during summer and autumn.</i>	dmnl

<i>There are no lice in fresh water (rivers) and in the sea their reproduction rate is low due to the spread of hosts over much larger areas than when in the fjord.</i>	
Effect_of_temperature_on_egg_development_time = GRAPH(Historical_temperature) (0,00, 0,00), (1,00, 0,00), (2,00, 0,00), (3,00, 0,00), (4,00, 26,28), (5,00, 20,87), (6,00, 16,97), (7,00, 14,08), (8,00, 11,86), (9,00, 10,13), (10,00, 8,75), (11,00, 7,64), (12,00, 6,72), (13,00, 5,96), (14,00, 5,33), (15,00, 4,79), (16,00, 4,32), (17,00, 3,93)	dmnl
effect of temperature on lice lifespan = Historical temperature/mean temperature	dmnl
Effect of temperature on stage time = mean temp/Historical temperature	dmnl
Effect of temperature on stage time 1 = Historical temperature/mean temp 1	dmnl
egg_stage_development_time = Effect of temperature on egg development time	days
Egg survival time = 6	days
Eggs[Location](t) = Eggs[Location](t - dt) + (LS_Eggs_in[Location] - Hatching[Location] - Eggs_mortality[Location]) * dt INIT Eggs[Location] = 100	lice
INFLOWS: LS_Eggs_in[Location] = eggs_produced	Lice/days
OUTFLOWS: Hatching[Location] = Eggs/Hatching_time Eggs_mortality[Location] = Eggs/Egg_survival_time	Lice/days
Eggs_pr_louse_per_day = GRAPH(Historical_temperature) (0,00, 0,00), (1,00, 0,00), (2,00, 0,00), (3,00, 0,00), (4,00, 26,28), (5,00, 20,87), (6,00, 16,97), (7,00, 14,08), (8,00, 11,86), (9,00, 10,13), (10,00, 8,75), (11,00, 7,64), (12,00, 6,72), (13,00, 5,96), (14,00, 5,33), (15,00, 4,79), (16,00, 4,32), (17,00, 3,93)	Dmnl/days
eggs_produced[Location] = MAX(0; Female_Lice*Eggs_pr_louse_per_day)	Lice/days
Event_switch = 0	dmnl
Female_Lice[Location] = Adult*Fraction_Female	Lice
Fraction_Female = 0,50	dmnl
Hatching_time = egg_stage_development_time	days
Historical_temperature = GRAPH(TIME)	Degrees C

(0, 6,20), (31, 5,40), (59, 5,30), (90, 6,50), (120, 9,70), (151, 12,60), (181, 15,20), (212, 15,50), (243, 13,50), (273, 10,90), (304, 8,70), (334, 8,00), (365, 6,20), (396, 5,40), (424, 5,30), (455, 6,50), (485, 9,70), (516, 12,60), (546, 15,20), (577, 15,50), (608, 13,50), (638, 10,90), (669, 8,70), (699, 8,00), (730, 6,20), (761, 5,40), (789, 5,30), (820, 6,50), (850, 9,70), (881, 12,60), (911, 15,20), (942, 15,50), (973, 13,50), (1003, 10,90), (1034, 8,70), (1064, 8,00), (1095, 6,20), (1126, 5,40), (1154, 5,30), (1185, 6,50), (1215, 9,70), (1246, 12,60), (1276, 15,20), (1307, 15,50), (1338, 13,50), (1368, 10,90), (1399, 8,70), (1429, 8,00), (1460, 6,20), (1491, 5,40), (1519, 5,30), (1550, 6,50), (1580, 9,70), (1611, 12,60), (1641, 15,20), (1672, 15,50), (1703, 13,50), (1733, 10,90), (1764, 8,70), (1794, 8,00), (1825, 6,20)	
lice_pr_fish[1] = IF Locations[1]>5000 THEN "Mob / _Mot_lice_in_locations"[1]/(Locations[1]+Wild_hosts) ELSE 0 lice_pr_fish[2] = IF Locations[2]>5000 THEN "Mob / _Mot_lice_in_locations"[2]/(Locations[2]+Wild_hosts) ELSE 0 lice_pr_fish[3] = IF Locations[3]>5000 THEN "Mob / _Mot_lice_in_locations"[3]/(Locations[3]+Wild_hosts) ELSE 0 lice_pr_fish[4] = IF Locations[4]>5000 THEN "Mob / _Mot_lice_in_locations"[4]/(Locations[4]+Wild_hosts) ELSE 0	Lice/fish
Lice_removed_with_slaughtered_fish[Location] = MAX(0; MIN(("Mob / Mot lice in locations"/Slaughter time); lice pr fish*Weight Slaughter))	Lice/days
Life duration = 20	days
life_span[Location] = normal_life_span*(1/effect_of_temperature_on_lice_lifespan)	days
Maturing_time_PAAM = Avg_development_time*Effect_of_temperature_on_stage_time_1	days
mean_temp = 10	Degrees C
mean_wild_stock = 6000	fish
"Mob / _Mot_lice_in_locations"[1] = MAX(0; (Chalimus_and_Preadult[1]+Adult[1])) "Mob / _Mot_lice_in_locations"[2] = MAX(0; (Chalimus_and_Preadult[2]+Adult[2])) "Mob / _Mot_lice_in_locations"[3] = MAX(0; (Chalimus_and_Preadult[3]+Adult[3])) "Mob / Mot lice in locations"[4] = MAX(0; (Chalimus and Preadult[4]+Adult[4]))	lice
"Nauplii_(larvae)"[1](t) = "Nauplii_(larvae)"[1](t - dt) + (Hatching[1] - Nauplius_Mortality[1] - Infectious_development[1]) * dt INIT "Nauplii_(larvae)"[1] = 100 "Nauplii_(larvae)"[2](t) = "Nauplii_(larvae)"[2](t - dt) + (Hatching[2] - Nauplius_Mortality[2] - Infectious_development[2]) * dt INIT "Nauplii_(larvae)"[2] = 100 "Nauplii_(larvae)"[3](t) = "Nauplii_(larvae)"[3](t - dt) + (Hatching[3] - Nauplius_Mortality[3] - Infectious_development[3]) * dt INIT "Nauplii_(larvae)"[3] = 100	lice

"Nauplii_(larvae)"[4](t) = "Nauplii_(larvae)"[4](t - dt) + (Hatching[4] - Nauplius_Mortality[4] - Infectious_development[4]) * dt INIT "Nauplii_(larvae)"[4] = 100	
INFLOWS: Hatching[Location] = Eggs/Hatching_time	Lice/days
OUTFLOWS: Nauplius_Mortality[Location] = "Nauplii_(larvae)"*Nauplii_Mortality_R Infectious_development[Location] = "Nauplii_(larvae)"/Development_time	Lice/days
Nauplii_Mortality_R = 0,17	1/days
norm_dev_time = 4,5	days
normal_life_span = 15,5	days
Normal_stage_time = 15,5	days
Percentage_of_normal = 0,8	dmnl
season = TIME	days
Summer_event = IF Historical_temperature > 9,6 THEN Percentage_of_normal ELSE 1	dmnl
Temperature = IF Event_switch = 1 THEN Historical_temperature*Summer_event ELSE Historical_temperature+Temperature_change <i>Same as Historical Temperature. Variable exists incase we want to test the effect of temperatures other than the historical temperature</i>	Degrees C
Temperature_change = 0	Degrees C
Times_when_fish_reach_their_desired_fish_weight[1] = IF Fish_Weight[1] >= Desired_Fish_Weight THEN 1 ELSE 0 Times_when_fish_reach_their_desired_fish_weight[2] = IF Fish_Weight[2] >= Desired_Fish_Weight THEN 1 ELSE 0 Times_when_fish_reach_their_desired_fish_weight[3] = IF Fish_Weight[3] >= Desired_Fish_Weight THEN 1 ELSE 0 Times_when_fish_reach_their_desired_fish_weight[4] = IF Fish_Weight[4] >= Desired_Fish_Weight THEN 1 ELSE 0	Grams
Treatment_MR[Location] = life_span_reduction_during_treatment	1/days
Wild_hosts = Effect_of_season_on_wild_hosts*mean_wild_stock	Fish

Treatments Sector

Ad_fraction = Adult[1]/(Chalimus_and_Preadult[1]+Adult[1])	dmnl
allowed_lice_pr_fish = 0,5	Lice/fish
Closest_Neighbour[1] = CN_Switch*((treatment_initiation[1]+treatment_initiation[2])) Closest_Neighbour[2] = CN_Switch*((treatment_initiation[2]+treatment_initiation[1])) Closest_Neighbour[3] = CN_Switch*((treatment_initiation[3]+treatment_initiation[4]))	dmnl

$\text{Closest_Neighbour}[4] = \text{CN_Switch} * ((\text{treatment_initiation}[4] + \text{treatment_initiation}[3]))$ <p><i>Cooperative treatment of the original location with high lice abundance, and its closest neighbor. Distance being the main determinant of external infection pressure, this takes some of the external pressure off, and could be an alternative between treating all (full coordination) and treating only one.</i></p>	
CN_Switch = 0	dmnl
$\text{effect_gap}[\text{Location}] = \text{Treatment_effectiveness} * \text{treatment_effect_on_effectiveness}$	Dmnl/days
Feeding_pause_time = 5	days
$\text{fraction_female_lice} = 0,5$	dmnl
$\text{Last_treatment_time}[\text{Cohorts}](t) = \text{Last_treatment_time}[\text{Cohorts}](t - dt) + (\text{C_Treatment}[\text{Cohorts}]) * dt$ <p>INIT Last_treatment_time[Cohorts] = 0</p>	days
<p>INFLOWS:</p> $\text{C_Treatment}[\text{Cohorts}] = \text{IF Time_when_treatment_occurs} > 0 \text{ THEN } (\text{Time when treatment occurs} - \text{Last treatment time}) / \text{DT ELSE } 0$	dmnl
$\text{life_span_reduction_during_treatment}[\text{Location}] = \text{PULSE } ((\text{treatment_effect_on_mortality}); \text{treatment_effect_delay})$	1/days
$\begin{aligned} \text{Single_Loc}[1] &= \text{SL_Switch} * \text{treatment_initiation}[1] \\ \text{Single_Loc}[2] &= \text{SL_Switch} * \text{treatment_initiation}[2] \\ \text{Single_Loc}[3] &= \text{SL_Switch} * \text{treatment_initiation}[3] \\ \text{Single_Loc}[4] &= \text{SL_Switch} * \text{treatment_initiation}[4] \end{aligned}$ <p><i>The single location policy only treats the location that have high lice counts. Other locations go untreated until they reach the threshold themselves. This is equivalent to no coordination</i></p>	dmnl
SL_Switch = 1	dmnl
$\begin{aligned} \text{Time_when_feeding_starts_again}[1] &= \text{IF Last_treatment_time}[1] > 0 \text{ THEN } \text{Last_treatment_time}[1] + \text{Feeding_pause_time} \text{ ELSE } 0 \\ \text{Time_when_feeding_starts_again}[2] &= \text{Last_treatment_time}[2] + \text{Feeding_pause_time} \\ \text{Time_when_feeding_starts_again}[3] &= \text{Last_treatment_time}[3] + \text{Feeding_pause_time} \\ \text{Time_when_feeding_starts_again}[4] &= \text{Last_treatment_time}[4] + \text{Feeding_pause_time} \end{aligned}$	days
$\begin{aligned} \text{Time_when_treatment_occurs}[1] &= \text{IF treatment_increase}[1] > 0 \text{ THEN TIME ELSE } 0 \\ \text{Time_when_treatment_occurs}[2] &= \text{IF treatment_increase}[2] > 0 \text{ THEN TIME ELSE } 0 \\ \text{Time_when_treatment_occurs}[3] &= \text{IF treatment_increase}[3] > 0 \text{ THEN TIME ELSE } 0 \\ \text{Time_when_treatment_occurs}[4] &= \text{IF treatment_increase}[4] > 0 \text{ THEN TIME ELSE } 0 \end{aligned}$	days
$\text{Time_with_no_feeding_due_to_treatment}[1] = \text{IF TIME} \geq \text{Last_treatment_time}[1] \text{ AND TIME} \leq \text{Time when feeding starts again}[1] \text{ THEN } 1 \text{ ELSE } 0$	days

<p>Time_with_no_feeding_due_to_treatment[2] = IF TIME >= Last_treatment_time[2] AND TIME <= Time_when_feeding_starts_again[2] THEN 1 ELSE 0</p> <p>Time_with_no_feeding_due_to_treatment[3] = IF TIME >= Last_treatment_time[3] AND TIME <= Time_when_feeding_starts_again[3] THEN 1 ELSE 0</p> <p>Time_with_no_feeding_due_to_treatment[4] = IF TIME >= Last_treatment_time[4] AND TIME <= Time_when_feeding_starts_again[4] THEN 1 ELSE 0</p>	
<p>Tot_Treatments_used =</p> <p>Treatments_used[1]+Treatments_used[2]+Treatments_used[3]+Treatments_used[4]</p>	dmnl
<p>treatment_effect_delay = 2</p>	days
<p>treatment_effect_on_effectiveness[Location] = Treatment_regularity*0,00000001</p> <p><i>Diminishing effect from high chemical use. More data is needed for the correct weight of this phenomenon.</i></p>	Dmnl/days
<p>treatment_effect_on_mortality[1] =</p> <p>Single_Loc[1]+All_delayed[1]+Closest_Neighbour[1]*Treatment_effectiveness+mortality_from_cleaner_fish[1]</p> <p>treatment_effect_on_mortality[2] =</p> <p>Single_Loc[2]+All_delayed[2]+Closest_Neighbour[2]*Treatment_effectiveness+mortality_from_cleaner_fish[2]</p> <p>treatment_effect_on_mortality[3] =</p> <p>Single_Loc[3]+All_delayed[3]+Closest_Neighbour[3]*Treatment_effectiveness+mortality_from_cleaner_fish[3]</p> <p>treatment_effect_on_mortality[4] =</p> <p>Single_Loc[4]+All_delayed[4]+Closest_Neighbour[4]*Treatment_effectiveness+mortality_from_cleaner_fish[4]</p>	dmnl
<p>Treatment_effectiveness(t) = Treatment_effectiveness(t - dt) + (Increase_in_eff - Decrease_in_effectiveness) * dt</p> <p>INIT Treatment_effectiveness = 1</p>	dmnl
<p>INFLOWS</p> <p>Increase_in_eff = 0</p> <p>OUTFLOWS</p> <p>Decrease_in_effectiveness = effect_gap[1]+effect_gap[2]+effect_gap[3]+effect_gap[4]</p>	Dmnl/days
<p>treatment_indicator[Location] = MAX(0;</p> <p>lice_pr_fish*fraction_female_lice/allowed_lice_pr_fish)</p>	dmnl
<p>treatment_initiation[1] = treatment_switch* (IF(treatment_indicator[1]>0,9) THEN PULSE (1; 1,) ELSE 0)</p> <p>treatment_initiation[2] = treatment_switch* (IF(treatment_indicator[2]>0,9) THEN PULSE (1; 1,) ELSE 0)</p>	dmnl

treatment_initiation[3] = treatment_switch* (IF(treatment_indicator[3]>0,9) THEN PULSE (1; 1,) ELSE 0) treatment_initiation[4] = treatment_switch* (IF(treatment_indicator[4]>0,9) THEN PULSE (1; 1,) ELSE 0)	
treatment_intervals = DT	Days
Treatment_regularity[1] = Treatments_used[1]/treatment_intervals Treatment_regularity[2] = Treatments_used[2]/treatment_intervals Treatment_regularity[3] = Treatments_used[3]/treatment_intervals Treatment_regularity[4] = Treatments_used[4]/treatment_intervals	Dmnl/days
treatment_switch = 1	Dmnl
Treatments_used[1](t) = Treatments_used[1](t - dt) + (treatment_increase[1]) * dt INIT Treatments_used[1] = 0 Treatments_used[2](t) = Treatments_used[2](t - dt) + (treatment_increase[2]) * dt INIT Treatments_used[2] = 0 Treatments_used[3](t) = Treatments_used[3](t - dt) + (treatment_increase[3]) * dt INIT Treatments_used[3] = 0 Treatments_used[4](t) = Treatments_used[4](t - dt) + (treatment_increase[4]) * dt INIT Treatments_used[4] = 0	Dmnl
INFLOWS: treatment_increase[1] = (Single_Loc[1]+All_delayed[1]+Closest_Neighbour[1])/DT treatment_increase[2] = (Single_Loc[2]+All_delayed[2]+Closest_Neighbour[2])/DT treatment_increase[3] = (Single_Loc[3]+All_delayed[3]+Closest_Neighbour[3])/DT treatment_increase[4] = (Single_Loc[4]+All_delayed[4]+Closest_Neighbour[4])/DT	Dmnl/days

A.4 Equations for the fish production model

Equations – Production Sectors

Juvenile Growth Sector

Equations and Comments	Unit
Death_Rate = 20	Fish per day
Desired_Smolt_weight[1] = 250 Desired_Smolt_weight[2] = 250 Desired_Smolt_weight[3] = 250	Grams

Desired_Smolt_weight[4] = 250	
First_hatching = 0	Days
Second_hatching = 10	Days
Third_Hatching = 192	Days
Fourth_Hatching = 200	Days
Time_to_next = 470	Days
<p>Fry_0g_to_10g[1](t) = Fry_0g_to_10g[1](t - dt) + (Fish_egg_Hatching[1] - Moving_to_Room_1[1] - Death_Rate_Fry[1]) * dt INIT Fry_0g_to_10g[1] = 0</p> <p>Fry_0g_to_10g[2](t) = Fry_0g_to_10g[2](t - dt) + (Fish_egg_Hatching[2] - Moving_to_Room_1[2] - Death_Rate_Fry[2]) * dt INIT Fry_0g_to_10g[2] = 0</p> <p>Fry_0g_to_10g[3](t) = Fry_0g_to_10g[3](t - dt) + (Fish_egg_Hatching[3] - Moving_to_Room_1[3] - Death_Rate_Fry[3]) * dt INIT Fry_0g_to_10g[3] = 0</p> <p>Fry_0g_to_10g[4](t) = Fry_0g_to_10g[4](t - dt) + (Fish_egg_Hatching[4] - Moving_to_Room_1[4] - Death_Rate_Fry[4]) * dt INIT Fry_0g_to_10g[4] = 0</p>	Fish
<p>Fish_egg_Hatching[1] = PULSE (Number_of_Fry_per_Cohort, First_hatching, Time_to_next)</p> <p>Fish_egg_Hatching[2] = PULSE (Number_of_Fry_per_Cohort, Second_hatching, Time_to_next)</p> <p>Fish_egg_Hatching[3] = PULSE (Number_of_Fry_per_Cohort, Third_Hatching, Time_to_next)</p> <p>Fish_egg_Hatching[4] = PULSE (Number_of_Fry_per_Cohort, Fourth_Hatching, Time_to_next)</p>	Fish per day
Moving_to_Room_1[Cohorts] = IF Parr_weight >= 10 THEN PULSE (Fry_0g_to_10g-Death_Rate_Fry*DT) ELSE 0	Fish per day
Death_Rate_Fry[Cohorts] = IF Fry_0g_to_10g > 0 THEN Death_Rate ELSE 0	Fish per day
Number_of_Fry_per_Cohort = 1200000	Fish

$\text{Room_1_10g_to_60g}[\text{Cohorts}](t) = \text{Room_1_10g_to_60g}[\text{Cohorts}](t - dt) + (\text{Moving_to_Room_1}[\text{Cohorts}] - \text{Moving_to_Room_2}[\text{Cohorts}] - \text{Death_Rate_Room_1}[\text{Cohorts}]) * dt$ $\text{INIT Room_1_10g_to_60g}[\text{Cohorts}] = 0$	Fish
$\text{Moving_to_Room_1}[\text{Cohorts}] = \text{IF Parr_weight} \geq 10 \text{ THEN PULSE } (\text{Fry_0g_to_10g} - \text{Death_Rate_Fry} * \text{DT}) \text{ ELSE } 0$	Fish per day
$\text{Moving_to_Room_2}[\text{Cohorts}] = \text{IF Parr_weight} \geq 60 \text{ THEN PULSE } (\text{Room_1_10g_to_60g} - \text{Death_Rate_Room_1} * \text{DT}) \text{ ELSE } 0$	Fish per day
$\text{Death_Rate_Room_1}[\text{Cohorts}] = \text{IF Room_1_10g_to_60g} > 0 \text{ THEN Death_Rate} \text{ ELSE } 0$	Fish per day
$\text{Room_2_60g_to_100g}[\text{Cohorts}](t) = \text{Room_2_60g_to_100g}[\text{Cohorts}](t - dt) + (\text{Moving_to_Room_2}[\text{Cohorts}] - \text{Moving_to_Room_3}[\text{Cohorts}] - \text{Death_Rate_Room_2}[\text{Cohorts}]) * dt$ $\text{INIT Room_2_60g_to_100g}[\text{Cohorts}] = 0$	Fish
$\text{Moving_to_Room_2}[\text{Cohorts}] = \text{IF Parr_weight} \geq 60 \text{ THEN PULSE } (\text{Room_1_10g_to_60g} - \text{Death_Rate_Room_1} * \text{DT}) \text{ ELSE } 0$	Fish per day
$\text{Moving_to_Room_3}[\text{Cohorts}] = \text{IF Parr_weight} \geq 100 \text{ THEN PULSE } (\text{Room_2_60g_to_100g} - \text{Death_Rate_Room_2} * \text{DT}) \text{ ELSE } 0$	Fish per day
$\text{Death_Rate_Room_2}[\text{Cohorts}] = \text{IF Room_2_60g_to_100g} > 0 \text{ THEN Death_Rate} \text{ ELSE } 0$	Fish per day
$\text{Room_3_100g_to_500g}[\text{Cohorts}](t) = \text{Room_3_100g_to_500g}[\text{Cohorts}](t - dt) + (\text{Moving_to_Room_3}[\text{Cohorts}] - \text{To_Sea}[\text{Cohorts}, \text{Location}] - \text{Death_Rate_Room_3}[\text{Cohorts}]) * dt$ $\text{INIT Room_3_100g_to_500g}[\text{Cohorts}] = 0$	Fish
$\text{Moving_to_Room_3}[\text{Cohorts}] = \text{IF Parr_weight} \geq 100 \text{ THEN PULSE } (\text{Room_2_60g_to_100g} - \text{Death_Rate_Room_2} * \text{DT}) \text{ ELSE } 0$	Fish per day
$\text{To_Sea}[\text{Cohorts}, \text{Location}] \rightarrow \text{Sea_and_Slaughter_Sector:}$ $\text{Death_Rate_Room_3}[\text{Cohorts}] = \text{IF Room_3_100g_to_500g} > 0 \text{ THEN Death_Rate} \text{ ELSE } 0$	Fish per day

Juvenile Feeding Sector

Equations and Comments	Unit
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<p>"%_of_weight_fed_at_7c"[Cohorts] = GRAPH(Parr_weight) (0.0, 3.312), (1.0, 2.783), (5.0, 1.16445), (15.0, 1.2535), (30.0, 1.4835), (100.0, 1.4375), (200.0, 1.3225), (300.0, 1.219), (400.0, 1.1155), (500.0, 1.035)</p> <p><i>Graphs for all of the “% of weight fed at Xc” converters created using tables from Skretting AS, document provided by Osland Havbruk</i></p>	Per day
<p>"%_of_weight_fed_at_8c"[Cohorts] = GRAPH(Parr_weight) (0.0, 3.7835), (1.0, 3.174), (5.0, 1.886), (15.0, 1.4375), (30.0, 1.7135), (100.0, 1.656), (200.0, 1.518), (300.0, 1.3915), (400.0, 1.288), (500.0, 1.196)</p>	Per day
<p>"%_of_weight_fed_at_9c"[Cohorts] = GRAPH(Parr_weight) (0.0, 4.255), (1.0, 3.5765), (5.0, 2.1275), (15.0, 1.6215), (30.0, 1.9435), (100.0, 1.863), (200.0, 1.7135), (300.0, 1.564), (400.0, 1.4375), (500.0, 1.334)</p>	Per day
<p>"%_of_weight_fed_at_10c"[Cohorts] = GRAPH(Parr_weight) (0.0, 4.7265), (1.0, 3.9675), (5.0, 2.369), (15.0, 1.8055), (30.0, 2.1735), (100.0, 2.585), (200.0, 1.886), (300.0, 1.7135), (400.0, 1.5755), (500.0, 1.4605)</p>	Per day
<p>"%_of_weight_fed_at_11c"[Cohorts] = GRAPH(Parr_weight) (0.0, 5.198), (1.0, 4.370), (5.0, 2.6105), (15.0, 1.9895), (30.0, 2.392), (100.0, 2.2425), (200.0, 2.0355), (300.0, 1.8515), (400.0, 1.702), (500.0, 1.5755)</p>	Per day
<p>"%_of_weight_fed_at_12c"[Cohorts] = GRAPH(Parr_weight) (0.0, 5.681), (1.0, 4.761), (5.0, 2.852), (15.0, 2.1735), (30.0, 2.599), (100.0, 2.4035), (200.0, 2.1735), (300.0, 1.978), (400.0, 1.817), (500.0, 1.679)</p>	Per day
<p>"%_of_weight_fed_at_13c"[Cohorts] = GRAPH(Parr_weight) (0.0, 6.1525), (1.0, 5.1635), (5.0, 2.37935), (15.0, 2.3575), (30.0, 2.783), (100.0, 2.5415), (200.0, 2.885), (300.0, 2.0815), (400.0, 1.909), (500.0, 1.771)</p>	Per day
<p>"%_of_weight_fed_at_14c"[Cohorts] = GRAPH(Parr_weight) (0.0, 6.624), (1.0, 5.5545), (5.0, 3.335), (15.0, 2.5415), (30.0, 2.9555), (100.0, 2.6565), (200.0, 2.3805), (300.0, 2.162), (400.0, 1.978), (500.0, 1.8285)</p>	Per day
Feed_conversion_ratio_parr = 1.15	Dimensionless
<p>Feeding_Rate_Parr[Cohorts] = IF Temperature_Parr >= 7 AND Temperature_Parr <= 7.99 THEN "%_of_weight_fed_at_7c" ELSE IF Temperature_Parr >= 8 AND Temperature_Parr <= 8.99 THEN "%_of_weight_fed_at_8c" ELSE IF Temperature_Parr >= 9 AND Temperature_Parr <= 9.99 THEN "%_of_weight_fed_at_9c" ELSE IF Temperature_Parr >= 10 AND Temperature_Parr <= 10.99 THEN</p>	Dimensionless per day

<pre> "%_of_weight_fed_at_10c" ELSE IF Temperature_Parr >= 11 AND Temperature_Parr <= 11.99 THEN "%_of_weight_fed_at_11c" ELSE IF Temperature_Parr >= 12 AND Temperature_Parr <= 12.99 THEN "%_of_weight_fed_at_12c" ELSE IF Temperature_Parr >= 13 AND Temperature_Parr <= 13.99 THEN "%_of_weight_fed_at_13c" ELSE IF Temperature_Parr >= 14 AND Temperature_Parr <= 14.99 THEN "%_of_weight_fed_at_14c" ELSE 1 </pre> <p><i>Feeding rate chooses the percentage of body weight fed to the fish per day based on the temperature and the size of the fish.</i></p>	
Initial_Fry_weight = 0.2	Grams
<pre> Parr_weight[Cohorts](t) = Parr_weight[Cohorts](t - dt) + (Parr_Weight_Gain[Cohorts]) * dt INIT Parr_weight[Cohorts] = Initial_Fry_weight </pre>	Grams
<pre> Parr_Weight_Gain[Cohorts] = IF To_Sea[Cohorts,1]> 0 OR To_Sea[Cohorts,2]> 0 OR To_Sea[Cohorts,3]> 0 OR To_Sea[Cohorts,4]> 0 THEN (-Parr_weight+Initial_Fry_weight)/DT ELSE Amount_of_parr_food_per_day/Feed_conversion_ratio_parr </pre> <p><i>This formula includes a condition to reset the parr weight gain when the cohort has left the juvenile growth sector</i></p>	Grams/Day
Temperature_Parr = 14	Degrees C
<pre> Total_Amount_of_parr_Food[Cohorts](t) = Total_Amount_of_parr_Food[Cohorts](t - dt) + (Amount_of_parr_food_per_day[Cohorts]) * dt INIT Total_Amount_of_parr_Food[Cohorts] = 0 </pre>	Grams
<pre> Amount_of_parr_food_per_day[Cohorts] = IF Fry_0g_to_10g > 0 OR Room_1_10g_to_60g > 0 OR Room_2_60g_to_100g > 0 OR Room_3_100g_to_500g > 0 THEN (Feeding_Rate_Parr/100)*Parr_weight ELSE 0 </pre> <p><i>This formula includes a condition that there must be parr in the rooms in order for them to be fed</i></p>	Grams per day

Fish Feeding Sector

Equations and Comments	Units
<pre> "%_of_weight_fed_at_4c_1"[Cohorts] = GRAPH(Fish_Weight) (30, 0.805), (100, 0.7705), (200, 0.713), (300, 0.6555), (400, 0.598), (500, 0.552), (600, 0.5175), (700, 0.483), (800, 0.4485), (900, 0.4255), (1000, 0.4025), (1100, 0.3795), (1200, 0.368), (1300, 0.345), (1400, 0.3335), </pre>	Per day

<p>(1500, 0.322), (1600, 0.3105), (1700, 0.299), (1800, 0.2875), (1900, 0.276), (2000, 0.276), (2250, 0.253), (2500, 0.2415), (2750, 0.230), (3000, 0.2185), (3250, 0.207), (3500, 0.207), (3750, 0.1955), (4000, 0.1955), (4250, 0.184), (4500, 0.184), (4750, 0.1725), (5000, 0.1725), (7000, 0.1725)</p> <p><i>Graphs for all of the “% of weight fed at Xc” converters created using tables from Skretting AS, document provided by Osland Havbruk</i></p>	
<p>"%_of_weight_fed_at_6c_1"[Cohorts] = GRAPH(Fish_Weight) (30, 1.2535), (100, 1.219), (200, 1.127), (300, 1.035), (400, 0.9545), (500, 0.8855), (600, 0.8165), (700, 0.7705), (800, 0.7245), (900, 0.690), (1000, 0.6555), (1100, 0.621), (1200, 0.598), (1300, 0.575), (1400, 0.552), (1500, 0.529), (1600, 0.5175), (1700, 0.4945), (1800, 0.483), (1900, 0.4715), (2000, 0.460), (2250, 0.4255), (2500, 0.4025), (2750, 0.3795), (3000, 0.368), (3250, 0.3565), (3500, 0.345), (3750, 0.3335), (4000, 0.322), (4250, 0.3105), (4500, 0.3105), (4750, 0.299), (5000, 0.299), (7000, 0.2875)</p>	Per day
<p>"%_of_weight_fed_at_8c_1"[Cohorts] = GRAPH(Fish_Weight) (30, 1.7135), (100, 1.656), (200, 1.518), (300, 1.3915), (400, 1.288), (500, 1.196), (600, 1.1155), (700, 1.0465), (800, 0.989), (900, 0.9315), (1000, 0.8855), (1100, 0.851), (1200, 0.8165), (1300, 0.782), (1400, 0.7475), (1500, 0.7245), (1600, 0.7015), (1700, 0.6785), (1800, 0.6555), (1900, 0.644), (2000, 0.621), (2250, 0.5865), (2500, 0.552), (2750, 0.529), (3000, 0.506), (3250, 0.483), (3500, 0.4715), (3750, 0.460), (4000, 0.437), (4250, 0.4255), (4500, 0.4255), (4750, 0.414), (5000, 0.4025), (7000, 0.391)</p>	Per day
<p>"%_of_weight_fed_at_10c_1"[Cohorts] = GRAPH(Fish_Weight) (30, 2.1735), (100, 2.0585), (200, 1.886), (300, 1.7135), (400, 1.5755), (500, 1.4605), (600, 1.3685), (700, 1.288), (800, 1.2075), (900, 1.150), (1000, 1.0925), (1100, 1.0465), (1200, 1.0005), (1300, 0.966), (1400, 0.920), (1500, 0.897), (1600, 0.8625), (1700, 0.8395), (1800, 0.8165), (1900, 0.7935), (2000, 0.7705), (2250, 0.7245), (2500, 0.6785), (2750, 0.644), (3000, 0.621), (3250, 0.598), (3500, 0.575), (3750, 0.552), (4000, 0.5405), (4250, 0.5175), (4500, 0.506), (4750, 0.4945), (5000, 0.483), (7000, 0.483)</p>	Per day
<p>"%_of_weight_fed_at_12c_1"[Cohorts] = GRAPH(Fish_Weight) (30, 2.599), (100, 2.4035), (200, 2.1735), (300, 1.978), (400, 1.817), (500, 1.679), (600, 1.564), (700, 1.472), (800, 1.3915), (900, 1.311), (1000, 1.2535), (1100, 1.196), (1200, 1.150), (1300, 1.104), (1400, 1.058), (1500, 1.0235), (1600, 0.989), (1700, 0.9545), (1800, 0.920), (1900, 0.897), (2000, 0.874), (2250, 0.8165), (2500, 0.7705), (2750, 0.736), (3000, 0.7015), (3250, 0.667), (3500, 0.644), (3750, 0.621), (4000, 0.598), (4250, 0.5865), (4500, 0.5635), (4750, 0.552), (5000, 0.5405), (7000, 0.529)</p>	Per day
<p>"%_of_weight_fed_at_14c_1"[Cohorts] = GRAPH(Fish_Weight) (30, 2.9555), (100, 2.6565), (200, 2.3805), (300, 2.162), (400, 1.978), (500, 1.8285), (600, 1.702), (700, 1.5985), (800, 1.5065), (900, 1.426),</p>	Per day

(1000, 1.357), (1100, 1.288), (1200, 1.2305), (1300, 1.1845), (1400, 1.1385), (1500, 1.0925), (1600, 1.058), (1700, 1.0235), (1800, 0.989), (1900, 0.966), (2000, 0.9315), (2250, 0.874), (2500, 0.828), (2750, 0.782), (3000, 0.736), (3250, 0.713), (3500, 0.6785), (3750, 0.6555), (4000, 0.6325), (4250, 0.6095), (4500, 0.598), (4750, 0.575), (5000, 0.5635), (7000, 0.552)	
Feed_conversion_ratio_fish = 1.15	Dimensionless
<p>feeding_rate_fish[Cohorts] = IF Temperature >= 4 AND Temperature <= 6 THEN "%_of_weight_fed_at_4c_1" ELSE IF Temperature >= 6 AND Temperature <= 8 THEN "%_of_weight_fed_at_6c_1" ELSE IF Temperature >= 8 AND Temperature <= 10 THEN "%_of_weight_fed_at_8c_1" ELSE IF Temperature >= 10 AND Temperature <= 12 THEN "%_of_weight_fed_at_10c_1" ELSE IF Temperature >= 12 AND Temperature <= 14 THEN "%_of_weight_fed_at_12c_1" ELSE IF Temperature >= 14 AND Temperature <= 16 THEN "%_of_weight_fed_at_14c_1" ELSE 1</p> <p><i>The feeding rate chooses the percentage of body weight fed to the fish per day based on the temperature and the size of the fish.</i></p>	Per day
<p>Historical_temperature = GRAPH(TIME)</p> <p>(0, 6.20), (31, 5.40), (59, 5.30), (90, 6.50), (120, 9.70), (151, 12.60), (181, 15.20), (212, 15.50), (243, 13.50), (273, 10.90), (304, 8.70), (334, 8.00), (365, 6.20), (396, 5.40), (424, 5.30), (455, 6.50), (485, 9.70), (516, 12.60), (546, 15.20), (577, 15.50), (608, 13.50), (638, 10.90), (669, 8.70), (699, 8.00), (730, 6.20), (761, 5.40), (789, 5.30), (820, 6.50), (850, 9.70), (881, 12.60), (911, 15.20), (942, 15.50), (973, 13.50), (1003, 10.90), (1034, 8.70), (1064, 8.00), (1095, 6.20), (1126, 5.40), (1154, 5.30), (1185, 6.50), (1215, 9.70), (1246, 12.60), (1276, 15.20), (1307, 15.50), (1338, 13.50), (1368, 10.90), (1399, 8.70), (1429, 8.00), (1460, 6.20), (1491, 5.40), (1519, 5.30), (1550, 6.50), (1580, 9.70), (1611, 12.60), (1641, 15.20), (1672, 15.50), (1703, 13.50), (1733, 10.90), (1764, 8.70), (1794, 8.00), (1825, 6.20)</p> <p><i>The ghost variable "temperature" in the fish feeding sector is the same as the historical temperature above</i></p>	Degrees C
<p>Fish_Weight[Cohorts](t) = Fish_Weight[Cohorts](t - dt) + (Fish_Weight_Gain[Cohorts]) * dt</p> <p>Fish_Weight[Cohorts] = 0</p>	Grams
Fish_Weight_Gain[1] = IF To_Sea[1,1] > 0 THEN (Parr_weight[1])/DT ELSE IF Weight_Slaughter[1] > 0 THEN (-Fish_Weight[1])/DT ELSE Amount_of_fish_food_per_day/Feed_conversion_ratio_fish	Grams per day

<p>Fish_Weight_Gain[2] = IF To_Sea[2,2] > 0 THEN Parr_weight[2]/DT ELSE IF Weight_Slaughter[2] > 0 THEN (-Fish_Weight[2]/DT) ELSE Amount_of_fish_food_per_day/Feed_conversion_ratio_fish</p> <p>Fish_Weight_Gain[3] = IF To_Sea[3,3] > 0 THEN Parr_weight[3]/DT ELSE IF Weight_Slaughter[3] > 0 THEN (-Fish_Weight[3]/DT) ELSE Amount_of_fish_food_per_day/Feed_conversion_ratio_fish</p> <p>Fish_Weight_Gain[4] = IF To_Sea[4,4] > 0 THEN Parr_weight[4]/DT ELSE IF Weight_Slaughter[4] > 0 THEN (-Fish_Weight[4]/DT) ELSE Amount_of_fish_food_per_day/Feed_conversion_ratio_fish</p> <p><i>These formulas include a condition that there must be fish in the locations in order to be fed, and also resets the fish weight once the fish have left the location</i></p>	
<p>Total_Amount_of_Fish_Food[Cohorts](t) = Total_Amount_of_Fish_Food[Cohorts](t - dt) + (Amount_of_fish_food_per_day[Cohorts]) * dt</p> <p>INIT Total_Amount_of_Fish_Food[Cohorts] = 0</p>	Grams
<p>Amount_of_fish_food_per_day[1] = IF Locations[1] > 100 AND Time_with_no_feeding_due_to_treatment[1] = 0 THEN feeding_rate_fish/100*Fish_Weight ELSE 0</p> <p>Amount_of_fish_food_per_day[2] = IF Locations[2] > 100 AND Time_with_no_feeding_due_to_treatment[2] = 0 THEN feeding_rate_fish/100*Fish_Weight ELSE 0</p> <p>Amount_of_fish_food_per_day[3] = IF Locations[3] > 100 AND Time_with_no_feeding_due_to_treatment[3] = 0 THEN feeding_rate_fish/100*Fish_Weight ELSE 0</p> <p>Amount_of_fish_food_per_day[4] = IF Locations[4] > 100 AND Time_with_no_feeding_due_to_treatment[4] = 0 THEN feeding_rate_fish/100*Fish_Weight ELSE 0</p> <p><i>This equation includes a condition that fish must be in the location in order to be fed, and must not be undergoing treatment for lice.</i></p>	Grams per day

Sea and Slaughter Sector

Equations and Comments	Units
Avg_lifespan_in_sea[1] = Normal_Life_in_sea - (Treatments_used[1]*Eff_of_treatments_on_mortality)	Days

<p>Avg_lifespan_in_sea[2] = Normal_Life_in_sea- (Treatments_used[2]*Eff_of_treatments_on_mortality)</p> <p>Avg_lifespan_in_sea[3] = Normal_Life_in_sea- (Treatments_used[3]*Eff_of_treatments_on_mortality)</p> <p>Avg_lifespan_in_sea[4] = Normal_Life_in_sea- (Treatments_used[4]*Eff_of_treatments_on_mortality)</p>	
<p>Biomass_per_location_check[1] = IF Location_Biomass[1] > Maximum_biomass_per_location THEN 1 ELSE 0</p> <p>Biomass_per_location_check[2] = IF Location_Biomass[2] > Maximum_biomass_per_location THEN 1 ELSE 0</p> <p>Biomass_per_location_check[3] = IF Location_Biomass[3] > Maximum_biomass_per_location THEN 1 ELSE 0</p> <p>Biomass_per_location_check[4] = IF Location_Biomass[4] > Maximum_biomass_per_location THEN 1 ELSE 0</p>	Tons
Desired_Fish_Weight = 5000	Grams
Eff_of_treatments_on_mortality = 0.01	Days
Following_period = 60	Days
Grams_per_ton = 1000000	Grams/tons*fish
<p>Last_Slaughter_time[Location](t) = Last_Slaughter_time[Location](t - dt) + (cLST[Location]) * dt</p> <p>INIT Last_Slaughter_time[Location] = 0</p> <p><i>This stock is an imagined stock as opposed to a physical one, and accumulates the last slaughter time for use in calculating when the location has been fallowed.</i></p>	Days
cLST[Location] = IF Time_when_Slaughter_occurs>0 THEN (Time_when_Slaughter_occurs-Last_Slaughter_time)/DT ELSE 0	Dimensionless
<p>Location_Biomass[1] = Locations[1]*Fish_Weight[1]/Grams_per_ton</p> <p>Location_Biomass[2] = Locations[2]*Fish_Weight[2]/Grams_per_ton</p> <p>Location_Biomass[3] = Locations[3]*Fish_Weight[3]/Grams_per_ton</p> <p>Location_Biomass[4] = Locations[4]*Fish_Weight[4]/Grams_per_ton</p>	Tons

Location_MTB_Limit = 780	Tons
<p>Locations[1](t) = Locations[1](t - dt) + (To_Sea[1, 1] + To_Sea[2, 1] + To_Sea[3, 1] + To_Sea[4, 1] - Weight_Slaughter[1] - Slaughter_based_on_Biomass[1] - Sea_based_mortality[1]) * dt INIT Locations[1] = 0</p> <p>Locations[2](t) = Locations[2](t - dt) + (To_Sea[1, 2] + To_Sea[2, 2] + To_Sea[3, 2] + To_Sea[4, 2] - Weight_Slaughter[2] - Slaughter_based_on_Biomass[2] - Sea_based_mortality[2]) * dt INIT Locations[2] = 0</p> <p>Locations[3](t) = Locations[3](t - dt) + (To_Sea[1, 3] + To_Sea[2, 3] + To_Sea[3, 3] + To_Sea[4, 3] - Weight_Slaughter[3] - Slaughter_based_on_Biomass[3] - Sea_based_mortality[3]) * dt INIT Locations[3] = 0</p> <p>Locations[4](t) = Locations[4](t - dt) + (To_Sea[1, 4] + To_Sea[2, 4] + To_Sea[3, 4] + To_Sea[4, 4] - Weight_Slaughter[4] - Slaughter_based_on_Biomass[4] - Sea_based_mortality[4]) * dt INIT Locations[4] = 0</p>	Fish
<p>To_Sea[1, 1] = IF Parr_weight[1] >= Desired_Smolt_weight[1] AND Locations[1] < 100 AND TIME >= Next_introduction_Date[1] THEN PULSE (MAX (0, Room_3_100g_to_500g[1]-Death_Rate_Room_3[1]*DT),Time_when_parr_are_in_room_3[1], 20000) ELSE 0</p> <p>To_Sea[2, 2] = IF Parr_weight[2] >= Desired_Smolt_weight[2] AND Locations[2] < 100 AND TIME >= Next_introduction_Date[2] THEN PULSE (MAX (0, Room_3_100g_to_500g[2]-Death_Rate_Room_3[2]*DT),Time_when_parr_are_in_room_3[2], 20000) ELSE 0</p> <p>To_Sea[3, 3] = IF Parr_weight[3] >= Desired_Smolt_weight[3] AND Locations[3] < 100 AND TIME >= Next_introduction_Date[3] THEN PULSE (MAX (0, Room_3_100g_to_500g[3]-Death_Rate_Room_3[3]*DT), Time_when_parr_are_in_room_3[3], 20000) ELSE 0</p> <p>To_Sea[4, 4] = IF Parr_weight[4] >= Desired_Smolt_weight[4] AND Locations[4] < 100 AND TIME >= Next_introduction_Date[4] THEN PULSE (MAX (0, Room_3_100g_to_500g[4]-Death_Rate_Room_3[4]*DT),Time_when_parr_are_in_room_3[4], 20000) ELSE 0</p> <p><i>These equations contain structures which ensure that all the necessary parameters are in place before fish can enter a location</i></p>	Fish per day

<p>Weight_Slaughter[1] = IF Parr_weight[1] >= parr_weight_60_days_before_sea_introduction[1] AND Locations[1] > 10 THEN Locations[1]/Slaughter_time ELSE Slaughter_based_on_weight[1]/Slaughter_time</p> <p>Weight_Slaughter[2] = IF Parr_weight[2] >= parr_weight_60_days_before_sea_introduction[2] AND Locations[2] > 10 THEN Locations[2]/Slaughter_time ELSE Slaughter_based_on_weight[2]/Slaughter_time</p> <p>Weight_Slaughter[3] = IF Parr_weight[3] >= parr_weight_60_days_before_sea_introduction[3] AND Locations[3] > 10 THEN Locations[3]/Slaughter_time ELSE Slaughter_based_on_weight[3]/Slaughter_time</p> <p>Weight_Slaughter[4] = IF Parr_weight[4] >= parr_weight_60_days_before_sea_introduction[4] AND Locations[4] > 10 THEN Locations[4]/Slaughter_time ELSE Slaughter_based_on_weight[4]/Slaughter_time</p>	Fish per day
Slaughter_based_on_Biomass[Location] = Number_of_fish_slaughtered_exceeding_biomass/Slaughter_time	Fish per day
<p>Sea_based_mortality[1] = MAX(0, (Locations[1]/Avg_lifespan_in_sea[1])-Slaughter_based_on_Biomass[1])</p> <p>Sea_based_mortality[2] = MAX(0, (Locations[2]/Avg_lifespan_in_sea[2])-Slaughter_based_on_Biomass[2])</p> <p>Sea_based_mortality[3] = MAX(0, (Locations[3]/Avg_lifespan_in_sea[3])-Slaughter_based_on_Biomass[3])</p> <p>Sea_based_mortality[4] = MAX(0, (Locations[4]/Avg_lifespan_in_sea[4])-Slaughter_based_on_Biomass[4])</p>	Fish per day
Max_amount_of_tons_of_fish_in_120_cage = 381.9719	Tons per cage
Max_amount_of_tons_of_fish_in_160_cage = 679.750	Tons per cage
Maximum_biomass_per_location = Max_amount_of_tons_of_fish_in_120_cage*Number_of_cages_120+Max_amount_of_tons_of_fish_in_160_cage*Number_of_cages_160	Tons
Next_introduction_Date[Location] = IF Last_Slaughter_time > 0 THEN Last_Slaughter_time+ Following_period ELSE 0	Days
Normal_Life_in_sea = 400	Days
Number_of_cages_120 = 8	Cages

Number_of_cages_160 = 0	Cages
<p>Number_of_fish_slaughtered_exceeding_biomass[1] = IF Fish_Weight[1]> 0 THEN Slaughter_of_Exceeding_Biomass/Fish_Weight[1]*Grams_per_ton ELSE 0</p> <p>Number_of_fish_slaughtered_exceeding_biomass[2] = IF Fish_Weight[2] > 0 THEN Slaughter_of_Exceeding_Biomass/Fish_Weight[2]*Grams_per_ton ELSE 0</p> <p>Number_of_fish_slaughtered_exceeding_biomass[3] = IF Fish_Weight[3] > 0 THEN Slaughter_of_Exceeding_Biomass/Fish_Weight[3]*Grams_per_ton ELSE 0</p> <p>Number_of_fish_slaughtered_exceeding_biomass[4] = IF Fish_Weight[4] > 0 THEN Slaughter_of_Exceeding_Biomass/Fish_Weight[4]*Grams_per_ton ELSE 0</p>	Fish
number_of_locations = 4	Dimensi onless
<p>parr_weight_60_days_before_sea_introduction[1] = 0.2*Desired_Smolt_weight[1]</p> <p>parr_weight_60_days_before_sea_introduction[2] = 0.2*Desired_Smolt_weight[2]</p> <p>parr_weight_60_days_before_sea_introduction[3] = 0.2*Desired_Smolt_weight[3]</p> <p>parr_weight_60_days_before_sea_introduction[4] = 0.2*Desired_Smolt_weight[4]</p>	Grams
Slaughter_amount_based_on_total_MTB = MAX((Total_Biomass-Total_MTB_Limit), 0)	Tons
<p>Slaughter_amount_per_location[1] = MAX((Location_Biomass[1]-Location_MTB_Limit), 0)</p> <p>Slaughter_amount_per_location[2] = MAX((Location_Biomass[2]-Location_MTB_Limit), 0)</p> <p>Slaughter_amount_per_location[3] = MAX((Location_Biomass[3]-Location_MTB_Limit), 0)</p> <p>Slaughter_amount_per_location[4] = MAX((Location_Biomass[4]-Location_MTB_Limit), 0)</p>	Tons
Slaughter_based_on_weight[1] = IF Fish_Weight[1] >= Desired_Fish_Weight AND Locations[1] > 10 THEN Locations[1]-(Slaughter_based_on_Biomass[1]*DT) ELSE 0	Fish

<p>Slaughter_based_on_weight[2] = IF Fish_Weight[2] >= Desired_Fish_Weight AND Locations[2] > 10 THEN Locations[2]- (Slaughter_based_on_Biomass[2]*DT) ELSE 0</p> <p>Slaughter_based_on_weight[3] = IF Fish_Weight[3] >= Desired_Fish_Weight AND Locations[3] > 10 THEN Locations[3]- (Slaughter_based_on_Biomass[3]*DT) ELSE 0</p> <p>Slaughter_based_on_weight[4] = IF Fish_Weight[4] >= Desired_Fish_Weight AND Locations[4] > 10 THEN Locations[4]- (Slaughter_based_on_Biomass[4]*DT) ELSE 0</p> <p><i>These equations contain a condition to make sure there are fish in the location before slaughter.</i></p>	
<p>Slaughter_of_Exceeding_Biomass[Location] = (Slaughter_amount_based_on_total_MTB+Slaughter_amount_per_location)</p>	Tons
<p>Slaughter_time = 2</p>	Days
<p>Time_when_parr_are_in_room_3[1] = IF Room_3_100g_to_500g[1] > 194000 THEN TIME ELSE 0</p> <p>Time_when_parr_are_in_room_3[2] = IF Room_3_100g_to_500g[2] > 194000 THEN TIME ELSE 0</p> <p>Time_when_parr_are_in_room_3[3] = IF Room_3_100g_to_500g[3] > 194000 THEN TIME ELSE 0</p> <p>Time_when_parr_are_in_room_3[4] = IF Room_3_100g_to_500g[4] > 194000 THEN TIME ELSE 0</p>	Days
<p>Time_when_Slaughter_occurs[1] = IF Weight_Slaughter[1] > 0 THEN TIME ELSE 0</p> <p>Time_when_Slaughter_occurs[2] = IF Weight_Slaughter[2] > 0 THEN TIME ELSE 0</p> <p>Time_when_Slaughter_occurs[3] = IF Weight_Slaughter[3] > 0 THEN TIME ELSE 0</p> <p>Time_when_Slaughter_occurs[4] = IF Weight_Slaughter[4] > 0 THEN TIME ELSE 0</p>	Days
<p>Total_Biomass = Location_Biomass[1]+Location_Biomass[2]+Location_Biomass[3]+Location_Biomass[4]</p>	Tons
<p>Total_MTB_Limit = Location_MTB_Limit*number_of_locations</p>	Tons

A.5 Picture of the Lice model

