Public Policy Improvements to Norwegian Salmon Aquaculture Operations – A Case Study

by

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Foreword

The model was built in collaboration with Richard Hesleskaug, Md Fazla Rabbi Alam and Osland Havbruk AS. It is a broad model, containing structures explaining the smolt growth process, fish growth process, slaughtering, lice growth and treatment, and economics of the wider fish farming industry. Each of our papers will focus on specific sectors of the model, and it is best to read all three to gain a complete understanding of the working of the model. Additionally, by working in collaboration with an aquaculture producer, this model aims to give back to the industry by being a learning tool for farmers looking to improve their operations.

Abstract

The aquaculture industry is an important food production industry both in Norway and around the world. As a young industry, it is still developing and growing. Industry-wide challenges exist, including but not limited to idle capacity, lice infestations, an inability to reach the maximum allowed fish biomass and long and risky periods of salmon growth in the sea. This paper focuses on public policy solutions which when implements would improve the problematic behaviour in the industry. To study these challenges, a model has been constructed, using the method of system dynamics. The model is a case study, and is built based on the real-life aquaculture operation of Osland Havbruk AS in the Sogn og Fjordane region of Norway. This model first reproduces the normal behaviour of the fish farm, and pinpoints the location of the problems in the operation. Then, the model is tested for validity, compared to real-life data and analyzed to ensure it is recreating the correct behaviour for the correct reasons. Policies are then created and experimented with which help improve the problematic behaviour of idle capacity, not reaching the maximum allowed biomass and long periods of salmon growth in the sea. Though this paper focuses on public policy improvements, it also looks at the effects these would have on the population of lice in the fish farm.

Keywords: Fish Farming, Salmon Farming, Aquaculture, Atlantic salmon (Salmo salar), Norwegian Aquaculture, System Dynamics

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1. Introduction

Aquaculture is a growing industry, not only in Norway but all over the world. In 2014, over 78 million tons of farmed aquaculture products were produced (FAO State of World Fisheries and Aquaculture, 2016). It is projected that by 2030, 62% of fish for human consumption will come from the aquaculture industry (Salmon Farming Industry Handbook, 2017). However, the industry is not without its problems or challenges.

The aim of this project is to find ways in which an aquaculture operation could be improved, to the benefit of all involved parties. Currently, companies in the fish farming industry are faced with problems including but not limited to reaching the maximum allowed biomass, long periods of sea-based salmon growth, idle capacity and lice infestations. To study these problems, a model has been constructed based on the hypotheses of the causes of these problems. Once replicated, the model can explain where the problems come from, and help form a better understanding of them. Through this understanding and by use of the model of the company, ways to improve these problems can be formulated, through experimentation and analysis. The policies discovered during the analysis process can then be implemented to improve the operations of a fish farm. A policy in one sector has implications on the other sectors, and this interaction between sectors is key in deciding which policies are best overall.

Two other studies of Fish Farming using System Dynamics have been of great help during this modeling process and must be acknowledged. The first is A System Dynamics Model of Marine Cage Aquaculture (Château and Chang, 2010). This paper models a fictitious cobia farm in Taiwan, and includes sectors for production, profits, and the effects of natural forces such as dissolved oxygen, nitrogen, algae, and phytoplankton. The structure of this model, with its many sectors, was helpful in planning out the broad structures of this model. There is also the paper by The Economic Sustainability of land-based aquaculture systems: an integrated analysis (Bennich, 2015). This paper looks at a theoretical land-based salmon farm set in Norway. This model too helped the planning of the overarching structure of this model.

This model differs from these two approaches in that it is based not on a fictitious farm, but on a real aquaculture operation, that of Osland Havbruk. The model adheres to as many Norwegian

government regulations surrounding fish farming as possible, in order to make it as accurate as possible.

The focus of this paper will be on the production sector of the model, and the inefficiencies in this sector. These are idle capacity, long sea-based salmon growth and the inability to reach maximum allowed biomass. First, there will be a short background introduction to the process of aquaculture farming in Norway. Then the sectors of the model will be explained, parameters established, and normal behaviour simulated. The model will then be analysed and tested, to ensure it is producing the right behaviour for the right reasons. Then the inefficiencies seen in the normal behaviour of the model will be improved through policy experiments, and there will also be a look at how these policies may influence the lice problem. The paper will end with a brief look at the feasibility of implementing the new policies based on the results of those tests are considered in the implementation sector.

2. The Farming of Salmon: A Brief Overview

The production cycle of salmon is between two and three years. Wild salmon are anadromous; they are born in fresh water, migrate to salt water to live and then return to fresh water to spawn (Salmon Farming Industry Handbook, 2017). The aquaculture operation mimics this natural process. Salmon have three stages of youth – fry, parr and smolt. First, the fry are hatched indoors in temperature controlled freshwater tanks. While indoors, the fish, now called parr, are grown for 10-16 months in freshwater, depending on the desired smolt size. Traditionally, salmon parr were grown to between 50g and 80g before undergoing smoltification and being put out to sea (Stead & Laird, 2002), but the trend has shifted to growing larger and larger parr (Salmon Farming Industry Handbook, 2017). In Norway, producers need permission from the Directorate of Fisheries in order to grow parr to sizes over 250g (Bruland, 2016).

Once the parr have reached a desired size, they undergo the process of smoltification, where the fish adapt to living in salt water. This process can be controlled and sped up by the farmer using light manipulation (Salmon Farming Industry Handbook, 2017). The cohort of smolt are then transported to cages in the sea. Salmon are introduced into the sea in either the spring or the fall.

Over the next 14 to 24 months, they grow to be adult salmon between 4kg and 5kg. Once they have reached a desired size, they are slaughtered and frozen, ready to be sold. After the salmon have been harvested, the site must be fallowed for 2 to 6 months, to disperse any parasites (mainly lice) that may be living in the water (Salmon Farming Industry Handbook, 2017).

While indoors, the temperature of the water can be controlled, allowing the producer to slow down or speed up the growth of the salmon. Salmon fry can be kept at the relatively low temperature of 7c to prevent any growth until the farmer decides it is time to grow them (Osland, 2018). It is becoming more and more popular to grow the salmon indoors to larger and larger sizes, as this lessens the amount of time the fish will be at sea, where they are most at risk, though there are higher costs associated with keeping the fish indoors.

Of all the factors that influence the growth and development of salmon, temperature has the greatest effect. (Brown and Gratzek, 1980). Traditionally, temperatures between 13c and 17c have been seen as the ideal temperature for salmon growth (Wallace, 1993), though new research has pointed toward lower temperatures being more viable than previously believed (E M Hevrøy et al., 2013). While higher temperatures do allow for increased growth, there is also an increased risk of disease as parasites, such as fish lice, also prefer the warmer temperatures (Salmon Farming Industry Handbook, 2017).

This industry is very capital intensive. While indoors, one of the largest costs is heating the tanks to 14c for the parr to grow most efficiently. (Osland, 2018) Outdoors, the cost of cages and boats to move or harvest salmon are high. There is also a significant cost of getting a license to open a fish farm. The most recent round of licences issued by the Norwegian Government would cost successful applicants between 50 and 60 billion Norwegian Kroner (Davies, 2016). The cost of fish feed adds up too, and makes up the largest share of total cost – from 40% to 60% of the production cost (Stead and Laird, 2002; Huntingford et al 2012). Attaining a licence can be difficult in Norway, as the Norwegian government limits the number of licences (Salmon Farming Industry Handbook, 2017). Many years, it is not possible to expand production capacity because of high lice levels in the fjords (Burland, 2016). When it is possible, production areas may grow by a maximum amount of 6% every two years (Salmon Farming Industry Handbook, 2017). One licence allows a farmer a maximum total biomass of 780 tons, which can be farmed in up to four saltwater sites (Bruland, 2016).

The riskiest part of the operation for both the farmers and the fish is the time fish spend at sea. Here, the fish are susceptible to wide variances in temperature and diseases such as fish lice, and there is also the possibility of the fish escaping from the net. According to the Norwegian Directory of Fisheries, over 243,000 salmon or trout escaped from cages in 2007 (Strategy for a competitive Norwegian aquaculture industry, 2007). Breakouts of diseases have caused farmers to have to cull large portions of their stocks (Osland, 2018). Because fish farming operations share the same water, often only a few kilometers from each other, diseases can easily spread to other locations. Passing groups of wild salmon can also spread lice from one farm to another.

Fish farmers prefer to harvest throughout the year, though it can be difficult to harvest large fish year-round if the temperatures are too low for ideal growth, which is the case in Norway over the winter. Fish introduced into the sea in the fall grow much slower than those introduced in the spring, due to low winter temperatures. There is often a boom in harvesting at the end of the summer, after the fish have enjoyed the warmest temperatures the Norwegian fjords have to offer (Salmon Farming Industry Handbook, 2017).

3. Collection of data and research methods

This paper uses the methods of system dynamics to create a computer model of an aquaculture farm in Norway. System Dynamics is, in the words of John Sterman, "a perspective and set of conceptual tools that enable us to build formal computer simulations of complex systems and use them to design more effective policies and organizations" (Business Dynamics, pp vii, 2000). This methodology that relies on the interaction, or feedback, between multiple variables in a system. It puts great importance on the idea of change over time, and the interconnectedness of variables in a simulation. System dynamics aims to build models that allow for learning and change, and that exceed the capacity of mental models humans have about the world.

System Dynamics computer modeling uses three main structures: stocks, flows and converters. A stock is an entity that accumulates or depletes, and is a quantity that is measured at a specific point in time. To cause the stock to change, a flow either increases or decreases the stock, and is measured as a unit over a time – like a rate. A converter is an external variable which has a

variety of purposes: it can be used to make calculations, or to set an initial value of a stock, or as an input to a flow. The model is composed of these three structures, and it is important to understand them before reading. The simple model below of fishing hatching and dying shows all three of these structures.

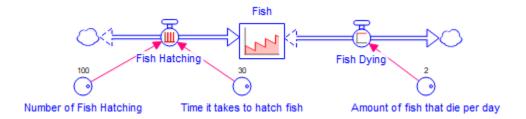


Figure 1 - And example of stocks, flows and converters. The stock "Fish" is in the middle, while the arrow going in to it on the left is an inflow, and the arrow going out of it on the right is an outflow. The three circles at the bottom are converters.

The model built for this paper relies on data from the aquaculture producer Osland Havbruk AS, and is based on their aquaculture operation. This data was collected over the course of several meetings, emails and a trip to their facility in Sogn og Fjordane. Osland Havbruk also provided documents detailing their own research and experiments which were used as a guide for the type of behaviour expected from the model.

The Norwegian government has many regulations concerning fish farming. It is essential that any model created adheres to the current laws concerning fish farming, including but not limited to fish cage densities, farm sizes, disease and antibiotic regulations. For this, publications from the Norwegian Directorate of Fisheries have been consulted, as has the compilation of aquaculture laws *Materialsamling i Havbruksrett* (Bruland, 2016).

4. Model Overview – Production and Growth Sectors

Section 4 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.

4.1 Assumptions and limits of the production and growth sectors

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

4.11 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.

4.12 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 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.

4.13 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 morality 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.

4.2 Juvenile Growth Sector

Osland Havbruk does not buy smolt from another company, but instead produces its own smolt from fry. They have three rooms 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

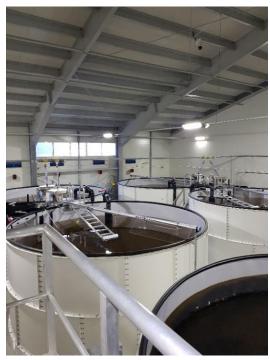


Figure 4 - Tanks in room 1



Figure 5 - Tanks in room 2

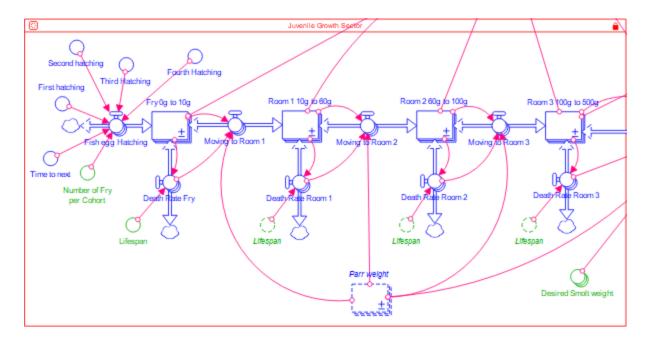


Figure 6 – Juvenile Growth Sector

This sector 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. The 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 to 10g" 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.

4.3 Juvenile Feeding Sector

The Juvenile Feeding Sector is based on a reinforcing loop 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.

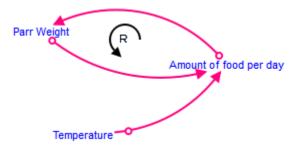


Figure 7 - Juvenile growth re-enforcing loop

The complete sector, with arrays, is seen below.

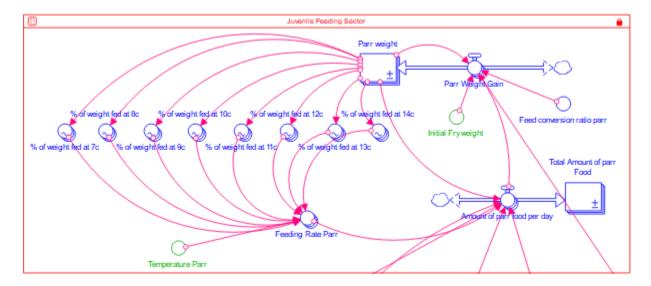


Figure 8 - Juvenile Feeding Sector

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", the "feeding rate parr", is taken, divided 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 the amount of growth, as a percentage of bodyweight, that the parr gain at a given temperature. When this growth is multiplied by the above mentioned feed conversion ratio of 1.15, the amount of food needed to produce this growth is calculated. 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 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	Startf1g	1-5 g	5-15 g	15-30 g	30-60 9	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
16	6,58	5,52	3,32	2,54	1,91	1,35
17	6,99	5,87	3,53	2,70	2,03	1,44

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 förfaktor for atlantisk laks (basert på resultater fra Skretting R -databasen)

	Tomp	Temperatur (°C)																				
gram	1	2	3	4	5	6	7	8	Q	10	Ħ	12	13	14	15	16	17	18	19	20	± ³	첫 발
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	18,0
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	1,80	1,99	2,07	2,12	2,14	2,12	2,05	1,93	1,75	0,82	0,96
300	O;H	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	10,01
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	1,50	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 showing the feeding percentages at 14c is below.

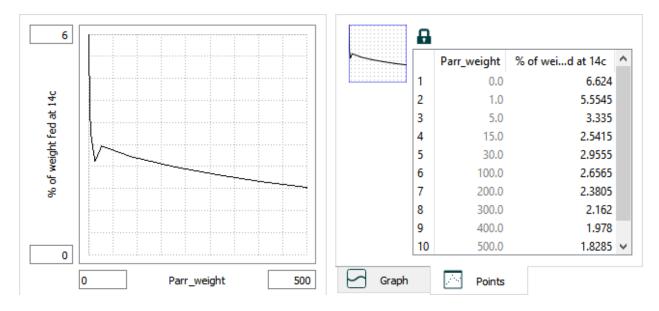


Figure 11 - Graph and values of parr feeding levels at 14c up to parr weight of 500g. Graph is a product of Skretting's tables multiplied by the food conversion ratio.

4.4 Fish Feeding Sector

The fish feeding sector 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.

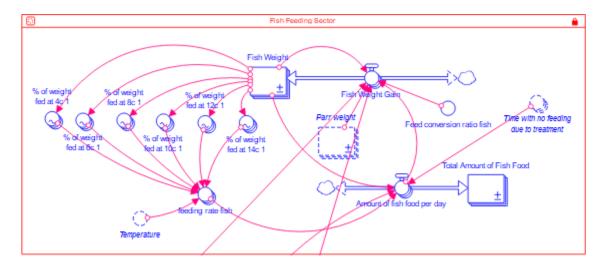


Figure 12 - Fish Feeding Sector

The "fish weight" stock is initialised at 0, and the flow "fish weight gain" is based on the "amount of fish food per day", divided by the "feed conversion ratio". This inflow too has a condition that prevents the model from feeding the fish if there are no fish in the cages at sea, and resets the fish weight to 0 when the fish are slaughtered.

Fish Weight Gain [n] = IF To Sea[n,n] > 0 THEN (Parr weight[n])/DT ELSE IF Weight Slaughter[n] > 0 THEN (-Fish Weight[n]/DT) ELSE Amount of fish food per day/Feed conversion ratio fish

The flow of "fish food per day" is dependent on the "fish weight" and the "feeding rate fish", as long as there are fish in the sea cages, and as long as the fish are not being treated for lice. If the fish are undergoing treatment for lice, then they cannot be fed for 5 days before the treatment has starts (Robb, 2008). The times when they are not being fed are calculated in the lice treatment sector, and "time with no feeding due to treatment" is simply a switch that turns on and off feeding in this circumstance.

Amount of fish food per day[n] = IF Locations[n] >100 AND Time with no feeding due to treatment[n] = 0 THEN feeding rate fish/100*Fish Weight ELSE 0

The "feeding rate fish" is dependent on the temperature. In the sea, temperatures can vary widely depending on the season. Historical temperature data, provided from Osland Havbruk for the Sognesjøen, Ytre Sogn region has been used in this model, and repeated over 5 years.

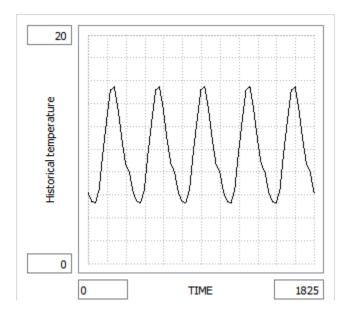


Figure 13 - Historical temperature data for Sognesjøen, Ytre Sogn as programmed in Stella Architect

Tempera	turprofiler													
	Middeltemp	jan	feb	mar	apr	mai	jun	jul	aug	sep	okt	nov	des	årsmiddel
	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

4.5 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. 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] >= 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, including its connection to room 3 of the Juvenile Growth Sector via the "to sea" flow:

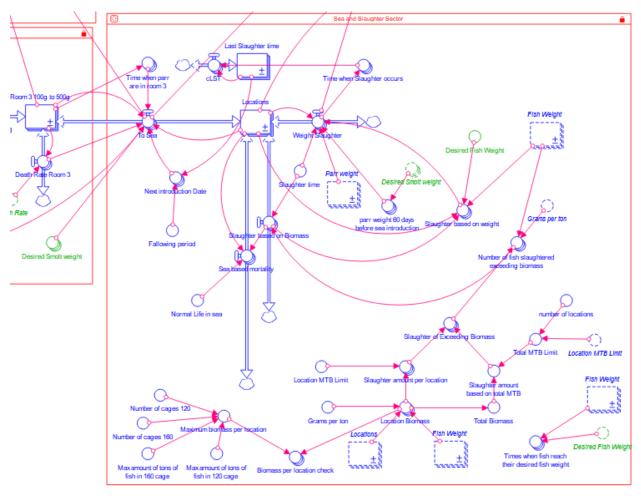


Figure 16 - Sea and Slaughter Sector, with the connection of the Juvenile Growth Sector

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.

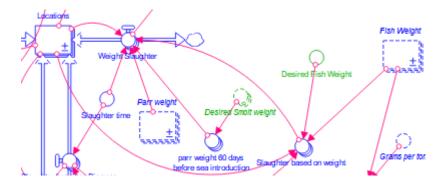


Figure 17 - Section of the Sea and Slaughter Sector focusing on the slaughter mechanisms based on fish, parr and smolt weight

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.

<u>Policy 2</u>: 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 amount of tons of fish slaughtered per location, which is then added to "slaughter amount based on total MTB" in the converter "slaughter of exceeding biomass". To convert "slaughter of exceeding biomass" to a number of fish, it is divided by the "fish weight" stock. This number is then put into the outflow "slaughtered based on biomass", which takes this number of fish out of the respective locations in the locations stock. This biomass slaughtering mechanism keeps the biomass below the maximum total biomass allowed by law, and provides a more constant flow of slaughtered fish for the farmer to sell.

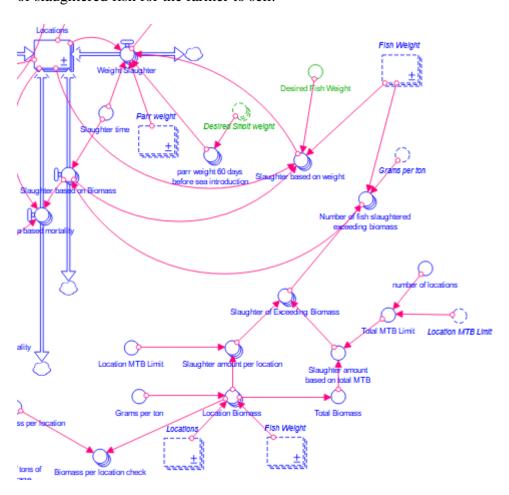


Figure 18 - Section of the Sea and Slaughter Sector focusing on the slaughter mechanisms based on biomass

Once the fish have been slaughtered, the location needs to be fallowed for a minimum of two months (60 days) before a new cohort of smolt can be introduced (Bruland, 2016). The converter "time when slaughter occurs" records the slaughter time, and the flow "cLST" (cumulation last slaughter time) accumulates the slaughter time in the stock "Last Slaughter time". The fallowing period of 60 days is then added to the converter "next introduction date" and is part of the pulse function which allows the smolt from the "to sea" stock to move into the locations stock.

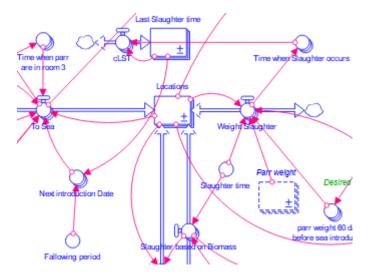


Figure 19 - Section of the sector showing the Last Slaughter time, fallowing period, and next introduction date

Our locations stock also has a death outflow, "sea base mortality". 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".

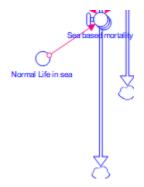


Figure 20 - Sea based mortality outflow from locations stock

There is also a biomass per location check in the lower left corner of the sector. 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. The reference mode uses 6 cages with a circumference of 120 metres. The biomass per location check compares the "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 the reference mode, the biomass check never registers that the model have exceeded the allowed density limit.

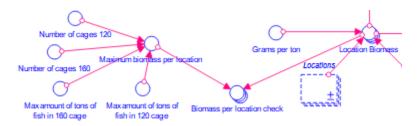


Figure 21 - Section of the sector showing the biomass per location check

4.6 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						
Parameter Name	<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							
Parameter Name	<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							
Parameter Name	<u>Value</u>	<u>Unit</u>					
Feed Conversion Ratio Fish	1.15	Unitless					

Table 4 – Sea and Slaughter Sector Parameters

Sea and Slaughter Sector							
Parameter Name	<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					

4.61 Juvenile Feeding Sector

The key stock in the Juvenile Feeding Sector is the "parr weight".

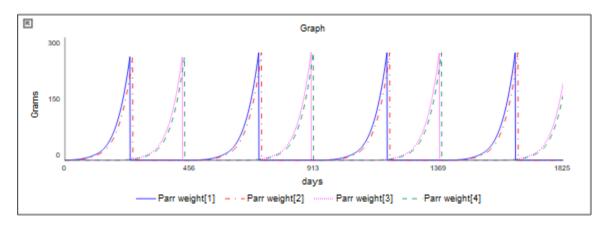


Figure 22 - Reference mode parr weight growth, all four cohorts

Within each cohort the graph 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.

4.62 Juvenile Growth Sector

The key indicators in the Juvenile Growth Sector are the graphs 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:

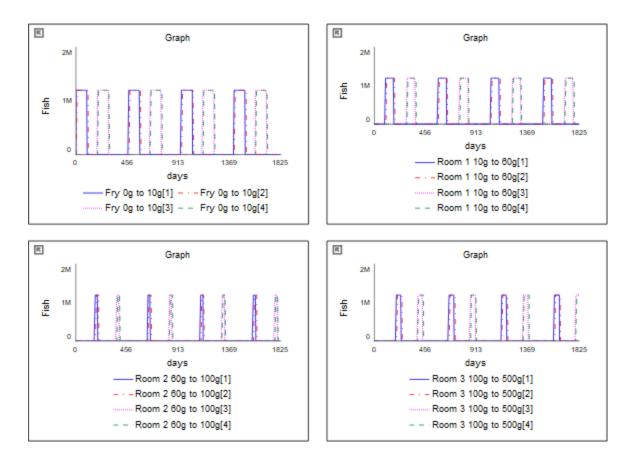


Figure 23 - Graphs, number of fish and time spent in the four rooms in the juvenile production facility

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.

4.63 Fish Feeding Sector

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

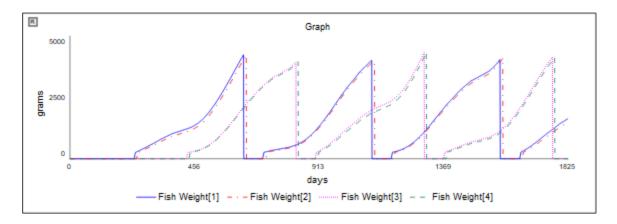


Figure 24 - Fish weight growth, without the effect of lice

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 fallowing time of a location allowed by law), the fish in the location are then slaughtered in order to free space for the next cohort.

4.64 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 of biomass vs. MTB is below.

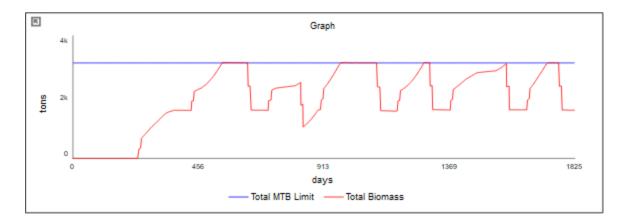


Figure 25 - Maximum total biomass limit vs total biomass

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.

5. Lice Sector

The following chapter is taken from the paper [TITLE] by Richard Hesleskaug and has been formatted for inclusion in this paper.

5.1 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).

5.2 Lice Module

5.21 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:

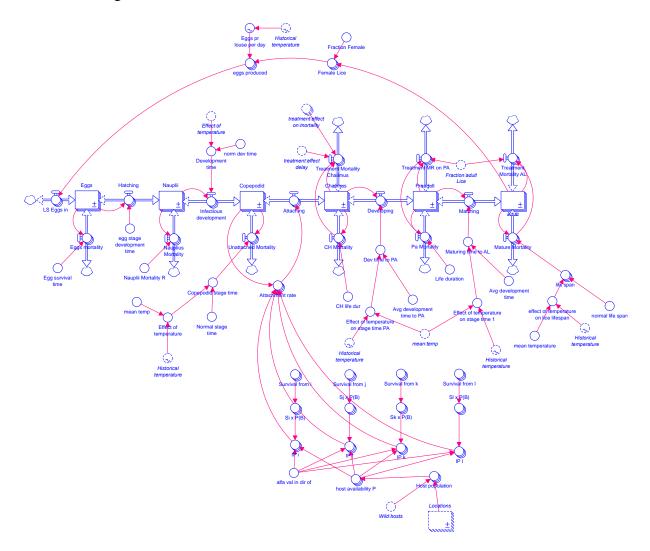


Figure 26 - Overview of the lice population growth and infection pressure structure. The aging chain simulates the population in the distinct stages of lice development, while the infection structure in the lower right corner calculates infection pressure between locations.

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 during the duration of development stages.

5.22 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. The real-life 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.

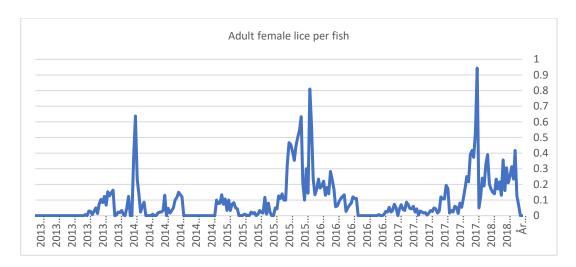


Figure 27 - The average count of adult female lice per fish in three locations (Sørevik, Torvund and Måren) 2013 – 2018. Mjølsvik was left out of the dataset due to incomplete data to remove biased results in the graph.

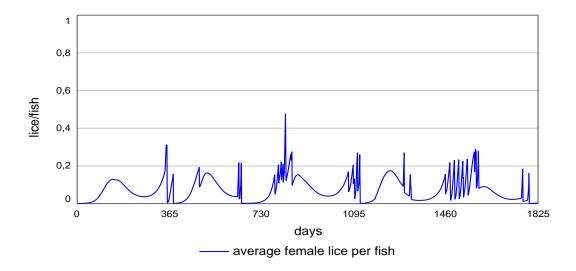


Figure 28 - Model generated lice abundance (5 yrs) of all attached stages of lice on all four modelled locations, showing comparable data to the reference mode (Figure 3)

In the model the focus is on the four locations operated by Osland containing salmon; Torvund, Mjølsvik, Sørevik and Måren, excluding 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. *Lepeophteirus 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.

The assumption made by Kristoffersen et al (2014) is used in the model. He assumes 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 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.

5.3 Lice population growth and life cycle

At the center of the lice module are the location population stocks (Figure 29), which accumulate 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 the 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 the 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 there are, the more lice will be able to find one and reproduce, to increase the number of eggs produced in the next generation.

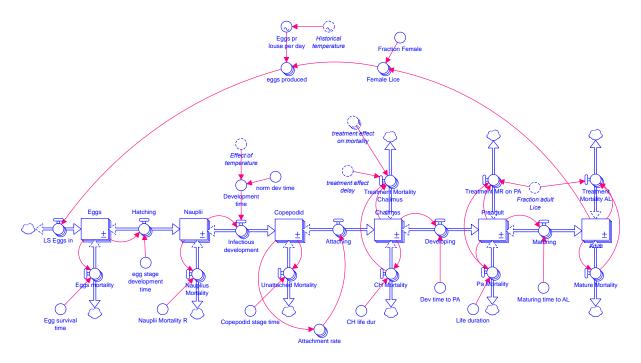


Figure 29: The structure of the lice aging chain and reproduction divided by populations of each stage of the lice life cycle.

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 1.

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

Hatching = Eggs / Egg stage development time

with a mortality of

 $Eggs\ mortality = Eggs / Egg\ survival\ time$

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

Infectious development = Nauplius (larvae) / Development time

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

*Nauplius mortality = Nauplius * 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 their 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:

Unattached mortality = Copepodites / 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.

5.4 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-life system depicted by the model. In system dynamics, there are many former examples of diffusion of disease, like adaptions 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.

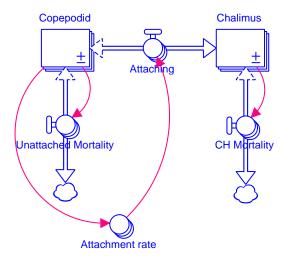


Figure 30 - Model section highlighting the flow between stages and the connection of infection pressure, which gives the attachment rate. This is variable accounts for the step between produced infective lice and lice that find a host and start reproduction.

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 Sij from a source farm (j) with seaway distance dij is defined by the formulation (Aldrin et al (2013):

$$Sij = \frac{e(-1,444 - (dij^0,57 - 1)/0,57)}{e(-1,444 - (djj^0,57 - 1)/0,57)}$$

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).

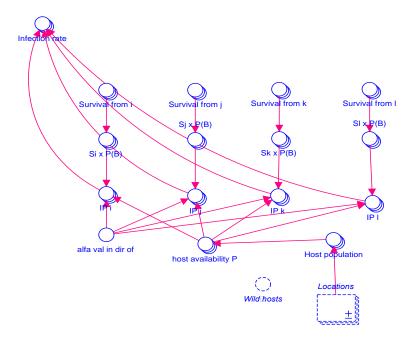


Figure 31 - External infection pressure sector, showing the structure used to estimate the infective pressure within and between locations, used for calculating the number of lice that successfully attach to a host from the parasites produced.

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 to assume 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 calculate the attachment rate from one location to another.

```
ARi,j = Si,j * \alpha i,j * P(Bj) * Ci
```

Where Ci is the number of copepod 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*:

```
Cii * \alpha ii * Sii * P(Bi) +
Cii * \alpha ji * Sji * P(Bi) +
Cii * \alpha ki * Ski * P(Bi) +
Cii * \alpha ki * Sli * P(Bi)
```

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 mortality = Chalimus / CH Life duration
```

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

```
Treatment mortality chalimus = Chalimus /
(Chalimus*treatment_effect_on_mortality/treatment_effect_delay)-CH_Mortality)
```

The next outflow is the development time to the preadult 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 of temperature = Temperature / average 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:

Maturing = Preadult/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.

5.5 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 make 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.

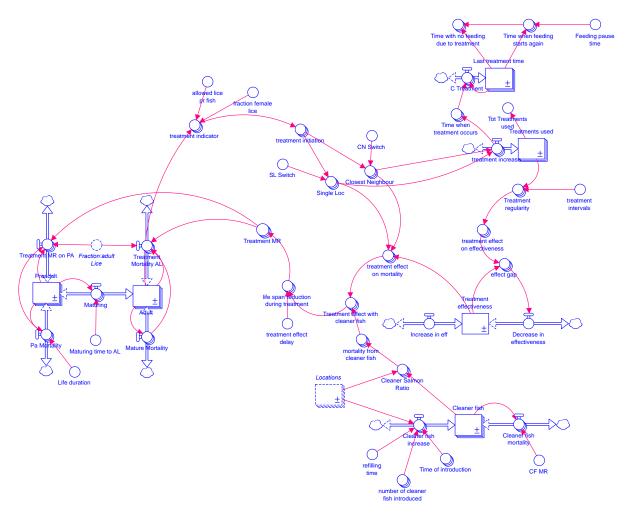


Figure 32 - Overview of the treatment model connected to attached stages of lice

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 are 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 pre-set 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: It is 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):

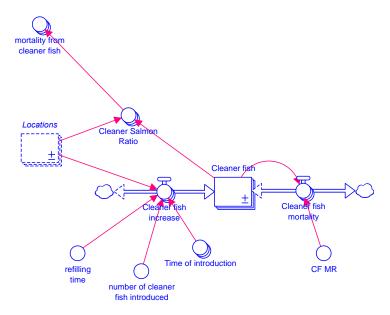


Figure 33 - The structure of the cleaner fish model, showing the stock of cleaner fish. the inflow is initiated by the fish farmer, and the outflow has a constant mortality rate of 0,028 (Aldrin et al 2017)

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

6. Model Analysis and Testing

6.1 Model Validation

6.11 Fish Growth Sector

As the purpose of the production model is to replicate the workings of a real-life aquaculture operation, the most important behaviour that the model must replicate is that of growing the fish.

There are some guidelines to how long the process of growing adult salmon should take. Smolt that start at 100g take between 14 to 24 months in the sea to grow to between 4 and 5kg (Salmon Farming Industry Handbook, 2017). The growth of the fish in this model is a bit faster, with the fish taking 12 months to grow from smolt to adult fish. However, the model has very ideal conditions – in the reference mode there is no effect of lice, and the model assumes no problems with water quality or other diseases.

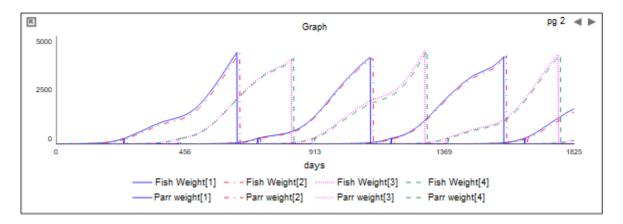


Figure 34 - Combined parr and fish weight graph. The fish take around 640 days from birth to slaughter.

Osland Havbruk has also done its own experiments on the growth of salmon from different sizes of smolt, and provided a graph with the results of these experiments. The shape of their growth curves are similar in shape to the ones produced by the model. When compared to the fish growth both with and without the effect of lice, there is a very similar pattern.

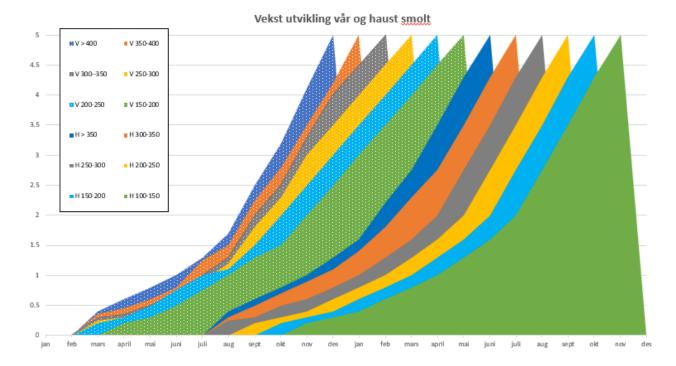


Figure 35 - Table from Osland Havbruk, weight gain, spring and fall smolt.

In the graph above, the left light blue section is the spring introduction of 200-250g smolt, the closest value to the model's reference mode "smolt weight" value of 250g. The right yellow section is the fall introduction of 200-250g smolt.

In both the model results and Osland Havbruk's results, there are steeper levels of growth in the summer - indicated though the steeper slope of the growth line - during warm temperatures, and slower more gradual levels of growth – a flatter slope - in the winter, during cold temperatures. Causes of the discrepancies between the data from Osland Havbruk and the model's reference mode can be attributed to:

- 1. Temperature: the seasonal temperatures during Osland Havbruk's experiments may not have been the same as the seasonal temperatures in the model.
- 2. Feeding rate: the model is based on recommended feeding rates but it is possible in these experiments Osland deviated from the recommended feeding rates, or that the fish had less appetite due to external factors.
- 3. A non-constant feed conversion ratio the model is very sensitive to the feed conversion ratio, and it is a number that is only an average over the fish's lifetime. Different feed

- conversion ratios could exist at different sizes and different water temperatures and qualities, leading to minor differences in actual growth of fish versus the model.
- 4. Water quality and light conditions The model assumes these are ideal, but in real life they may not have been, and may have slowed down the growth of the fish in the experiment.

6.2 Model Testing

To ensure that the model produces the reference mode behaviour for the right reasons, the model will now be subjected to testing, and compared to real fish growth data.

6.21 Sensitivity analysis: feed conversion ratio (FCR)

After sensitivity testing, the growth of the fish is quite dependant on the feed conversion ratio. Raising or lowering this number has a noticeable affect on the speed in which the fish grow. A feed conversion ratio closer to 1 will produce faster growth, as the fish are putting most of their energy towards growing, while higher ratios will produce lower growth, when the fish are expending more energy surviving and less on growth.

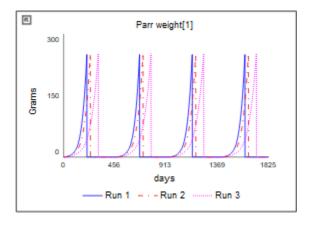


Figure 36 -Parr growth with feed conversion ratios of 1, 1.15 and 1.5

Above is a graph with parr starting at the reference mode fry weight of 0.2 and growing for around 260 days, with three different feed conversion ratios. Run 1 has an FCR of 1, assuming conversion of all food into growth. Run 2 is the reference mode FCR of 1.15 and run 3 is a

higher FCR of 1.5. The graphs shows that the higher the FCR, the longer it takes for the parr to grow to their desired weight.

It is impossible for fish to have an FCR of 1, some energy must always be used for other biological processes. The present day FCR of 1.15 over a fish's lifetime may be able to be improved slightly, though it is also possible that fish will not be able to spend less than 13% of their energy on biological functions other than growth.

The value that has been chosen for the model -1.15 – is one that comes directly from the feed producer, Skretting AS, and is likely to be very accurate. Most fish farmers today operate with a feed conversion ratio of less than 1.2 (Stead and Laird, 2002).

To test whether the feed conversion ratio is working as expected, an experiment was run where the parr started at 30 grams, and was grown over 30 days at 14c. According to the tables provided by Skretting AS (see appendix C), after 30 days at 14c the parr should have reached 64.2g

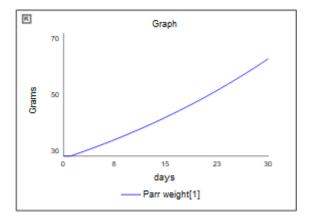


Figure 37 – Parr weight growth after 30 days starting at 30g

As shown in the graph, the parr do reach quite close to the value provided by Skretting. After 30 days in the model, the parr weigh reaches 63.2g. So, while changing this value does have a strong effect on the behaviour of fish growth, the value itself is very likely to be accurate as the model recreates the data in the feed tables quite well.

The rate of fish growth was also found to be very sensitive to these variables. Increasing them or decreasing them by a small amount can have a great impact on the rate of parr and fish growth. As an example, the variable "% of weight fed to parr at 14c" for cohort 1 has been increased by 1% - that is to say the parr are being fed 1% more of their body weight than before. Below is the effect this has on the parr weight.

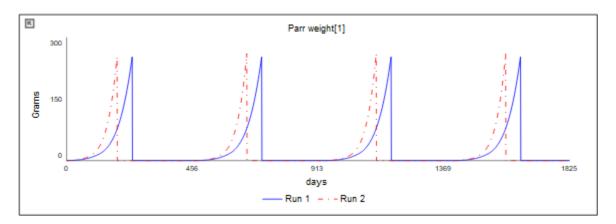


Figure 28 - Run 1 shows the reference mode behaviour, while run 2 shows an increase in feeding of 1%

Though increasing the "% of weight fed to parr at 14c" by one percentage point leads to much faster fish growth mathematically, in real life the fish would not grow faster. There is only a certain amount of food that the fish will eat before they are not hungry anymore, and if they don't eat the extra food given, they are not converting it into growth.

The graphs for the "% of fish food fed at Xc" variables are based on research by Skretting AS, a producer of fish food, and is in their opinion the recommended feeding rate for fish at a given size at a given temperature. While lowering these feeding rates would certainly slow down fish growth, there is no guarantee that raising them would speed it up, and is more likely to lead to food being wasted. These variables, though the model is quite sensitive to them, are likely to be accurate, and are the maximum amount of food a fish can eat at its respective size and temperature and cannot be increased. The feed conversion ratio, combined with these percentages of body weight, give the growth described in Skretting's feed tables.

6.23 Sensitivity analysis: temperature

Temperature data in the model is based on historical temperature readings taken by Osland Havbruk in the Sogn og Fjordane area. The temperature is prone to variation, seasonally or throughout the year. With the effects of climate change, it is possible that sea temperatures will rise overall, or that there will be more extreme periods of warm and cold temperatures.

To show the effect of a changing temperature on fish growth, the graph below shows fish growth under the reference mode temperature, and under a temperature that has increased by 2c all year round.

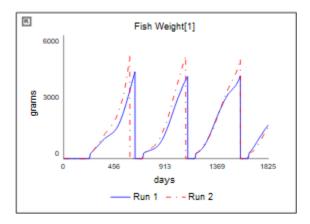


Figure 39 - Fish growth, reference mode (run 1) and 2c increase (run 2)

There is significant change in the amount the fish can grow in the same space of time.

Unfortunately, natural water temperatures are not under the control of mankind. Of all the parameters that the model is sensitive to, the temperature is the most uncertain of them.

However, there is not much that the modeler can do t improve the certainty of temperatures, aside from use the most up to date and accurate data available, and run tests to see how changing temperatures would affect fish growth, and base policy recommendations on those results.

6.24 Extreme Conditions

To test whether the model is replicating the desired behaviour for the correct reasons, a series of tests were conducted to see what would happen if there were no fish in the system, after the introduction of the initial cohorts.

To initiate this, the variable "time to next hatching" has been set to 0, so that there will be no "hatchings" – i.e. no new cohorts – after the first group has hatched.

The results of only one group of each cohort hatching are shown below, compared to the reference mode.

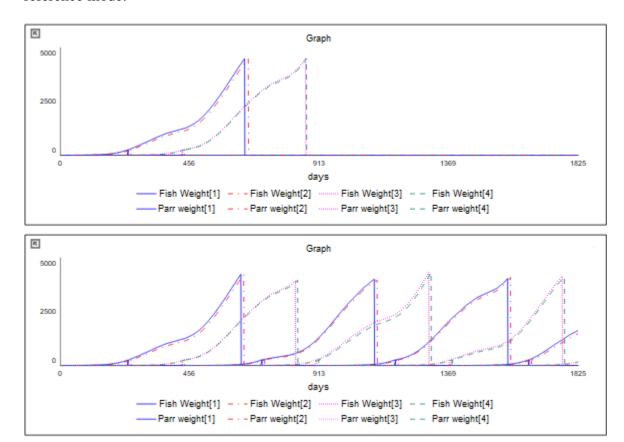
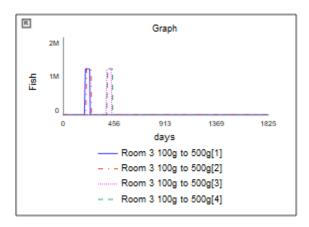


Figure 40 - One group of each cohort parr and fish weight gain versus reference mode results

In both graphs, the fish and parr weight combined grow to the reference mode "desired fish weight" of 4.5kg, before they leave the system through the slaughter flow. In the top graph, with the next hatching time set to zero, the growth does not repeat itself.



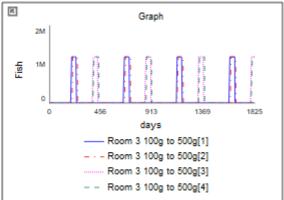
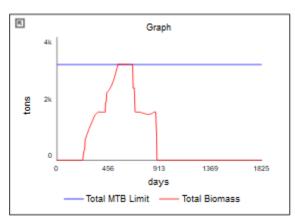


Figure 41 - Amount of time spent in room three and number of fish for one group of each cohort versus reference mode results

With the next hatching time set to zero, the parr only register in the rooms once for each cohort, the rest of the time there are no parr in the rooms. This is true for all of the rooms, and the graph above of room three shows an example of this.



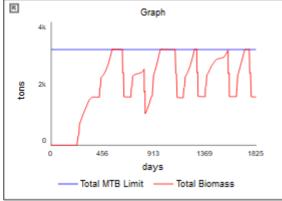


Figure 42 - One group of each cohort total biomass versus MTB limit versus reference mode results

The biomass too does not repeat itself as it does in the reference mode. Once the fish have reached the biomass limitation, their slaughter starts. Once they have reached the "desired fish weight", there is another sharp drop as the remaining fish are slaughtered. There are eventually 0 fish in the stock.

These tests show that the model behaviour is coming from the structures as intended.

7. Policy recommendations

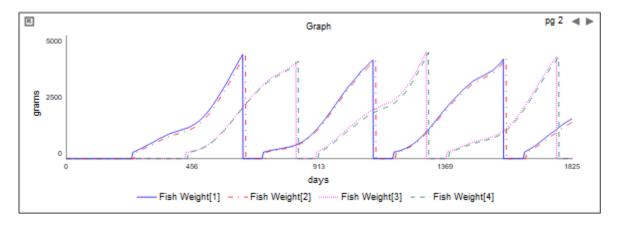
Now that the model has been tested and analysed, and its behaviour validated, it is time to look at ways in which the reference mode behaviour can be improved. This behaviour, shown at the end of section 4, shows some areas which could be improved.

- 1. Unused capacity in the smolt growth rooms
- 2. Reaching MTB
- 3. Lessening the time that fish spend in the sea

The following sections will explore two policies which could improve the behaviour of the model.

7.1 Grow smolt to a larger size

Current practices in Norway recommend growing the salmon to between 4 and 4.5kg, as larger salmon can often be sold for better prices. (Osland, 2018) The reference run of the model assumes a desired fish weight of 4.5kg, with smolt being introduced to the sea at 250g – the maximum government allowed smolt weight. For clarity, this run will also assume there are no lice effects. With this starting weight of 250g, it takes both the spring and fall cohorts around 415 days in the sea to grow until 4.5kg – with a total growing time of around 650 days from fry to 4.5kg salmon. The time in the sea varies slightly for fall and spring cohorts due to the different sea temperatures at different points in the fish's growth.



Figure~43-Reference~mode~behaviour~-~amount~of~time~it~takes~for~fall~cohorts~and~spring~cohorts~to~reach~around~4.5kg~with~astarting~smolt~weight~of~250g

The time in the sea is the riskiest part of the operation for the farmer. It is when the fish are most exposed to temperature fluctuations, disease and accidents (escapement, predators). It is

therefore beneficial to everyone involved in the industry to reduce the amount of time spent in the sea.

To see if this time could be reduced, experiments were run using the model with different desired smolt weights (250g, 350g and 500g). The chart of the results for the fall introduction is below.

Table 7 – Results of different smolt weight introduction, Fall

Smolt Introduction at Different Starting Weights – Fall					
<u>Variable</u>	Run 1 (250g)	Run 2(350g)	Run 3 (500g)		
Hatching time	0 (Jan 1)	0 (Jan 1)	0 (Jan 1)		
Transfer to sea	239 (Aug 27)	257 (Sept 14)	278 (Oct 5)		
Reached desired weight of 4.5kg	647 (Oct 9)	645 (Oct 7)	641 (Oct 3)		
Amount of days spent at sea	408	388	363		

Larger smolt, then, spent less time at sea, and had a slightly shorter total growing period (641 days with 500g smolt vs 647 days with 250g smolt). To minimize the amount of time spent then in the risky sea environment, it is worth investigating growing the smolt to larger sizes. The same can be said for fish put to sea in the spring

Table 8 – Results of different smolt weight introduction, Fall

Smolt Introduction at Different Starting Weights – Spring					
<u>Variable</u>	Run 1 (250g)	Run 2(350g)	Run 3 (500g)		
Hatching time	192 (July 11)	192 (July 11)	192 (July 11)		
Transfer to sea	431 (March 7)	449 (March 25)	470 (April 15)		
Reached desired weight of 4.5kg	862 (May 11)	845 (April 25)	827 (April 7)		
Amount of days spent at sea	431	396	357		

The smolt spend less time at sea, and have a slightly shorter total growing period (670 days for 250g smolt vs 635 days for 500g smolt).

The model shows that learning how to work with smolt that are that size can be quite beneficial to the environment, fish health and welfare. Fish that spend less time in the sea produce less

waste that goes into the fjord. They also spend less time exposed to sea lice, which is detrimental not only to their health but the health of wild stocks of salmon.

It is also important to see if these policies have any effect on the lice sector. For these next graphs, the model was run both with and without treatments in the lice sector, and the production sector was changed to have smolt starting at 250g, 350g and 500g. The results for the fall cohorts are below. The model was initialised with some fish in cohorts 3 and 4 in order to give more lice data for those locations.

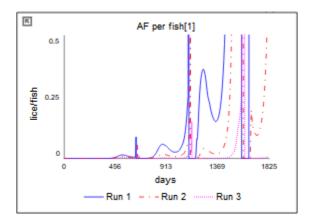
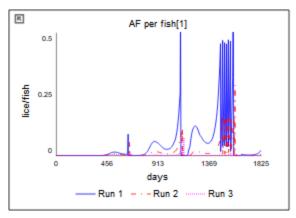


Figure 44 - Adult female lice per fish, with smolt starting weights of 250g, 350g and 500g

The graph above shows the number of adult female (AF) lice per fish, with smolt starting weights of 250g (run 1), 350 g (run 2) and 500g (run 3), and no treatment. The maximum allowed female lice per fish is 0.5 (1/2 louse) (Bruland, 2016). Introducing larger smolt seems to have a positive effect on the number of adult female lice per fish, with run 2 and run 3 often showing lower levels of lice. This is due to the fish spending less time in the sea when they are introduced at larger weights, and therefore reducing the time they are available hosts to which the lice can attach.

As levels do exceed 0.5 female louse per fish even in the case of 250g smolt, there does need to be treatment to keep the farm legally compliant. Below are the graphs of adult female lice per fish when treatments are turned on and the number of treatments. With the treatment function turned on, the lice level falls to within the allowed level. With lower lice per fish levels as smolt weight increases, less treatment is needed when larger smolt are introduced.



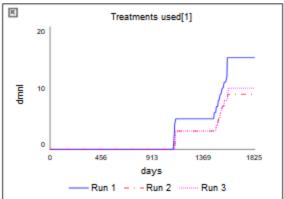
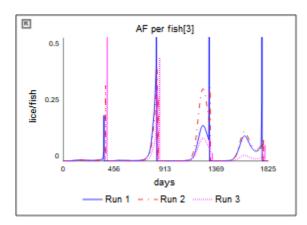


Figure 45 - Adult female lice per fish when treatments are turned on, and number of treatments, with smolt starting weights of 250g, 350g and 500g and fall introduction

The results of spring introduction are similar, the level of lice is often lower with larger smolt weight, but there is not as great a variation in the amount of treatments needed.



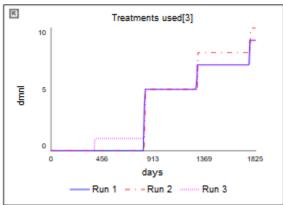


Figure 46 - Adult female lice per fish when treatments are turned on, and number of treatments, with smolt starting weights of 250g, 350g and 500g and spring introduction

The policy of growing smolt to a larger size indoors seems to be a viable policy that can have advantages in terms of shorter growing periods in the sea, and this policy should be studied further.

7.2 Year-round sea introduction

The reference mode behaviour shows unused capacity in the juvenile growth sector. The graphs of the four rooms in which juvenile fish are grown are below.

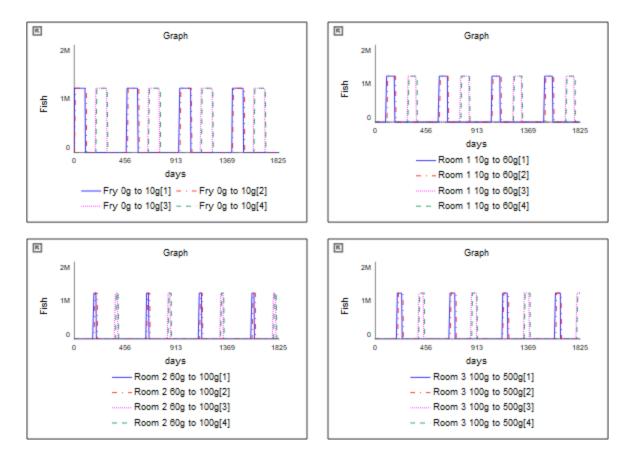


Figure 47 - Reference mode (seasonal introduction), 250g smolt, time smolt spend in rooms

To make use of the unused capacity in these rooms, an experiment has been run where there is constant production of smolt. That is, when one cohort leaves a room, another cohort immediately makes use of the room. To do this, a new cohort is introduced every 100 days, as 100 days this is the longest time a cohort spends in any room. The results of this simulation are below.

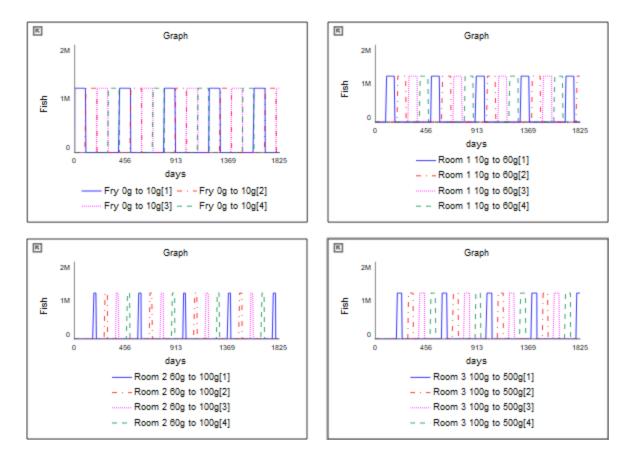
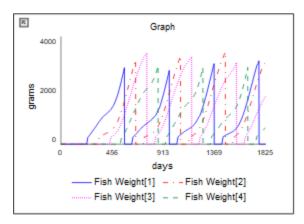


Figure 48 - Year-round introduction, 250g smolt, time smolt spend in rooms

With year-round production of smolt, there is much less unused capacity in the juvenile growth sector. The farm is able to use its capacity on a full-time basis and avoid periods of stagnation with no production.

It is also important to look at how this will affect other sectors and key indicators of the model behaviour. Below are the graphs for fish weight and total biomass vs MTB in both the reference mode and the new year-round juvenile growth mode.



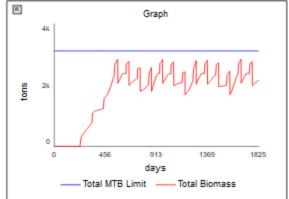
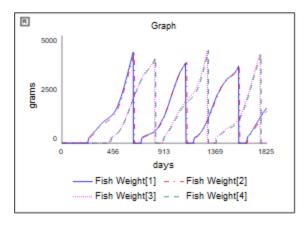


Figure 49 - Year-round introduction, 250g smolt, fish weight and total MTB limit vs total biomass



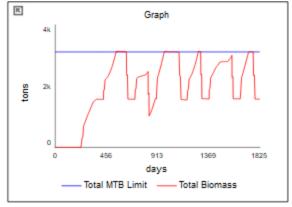


Figure 50 - seasonal introduction, 250g smolt, fish weight and total MTB limit vs total biomass

The year-round introduction alone does seem to grow smaller fish, with the cohorts only reaching between 2.9kg and 3.4kg, weight as opposed to between 4.3kg and 4.5kg when there is seasonal introduction. The MTB average is the same, both the reference mode and this simulation reach on average 71% of the MTB. This is due to the fact that there are more fish in the water at one time with year-round introduction, keeping the biomass high. Even with a similar average biomass, this year-round introduction with 250g smolt is less ideal than seasonal introduction with 250g smolt as the fish do not grow as large as in the reference mode.

To make year-round introduction work then, the smolt need to be grown to a larger size indoors. Growing the smolt to larger sizes has been shown to have benefits in the seasonal introduction scenario and has benefits too in a year-round introduction scenario. It is possible to do this as there is some unused capacity in room 3, and upping the weight to which the smolt are grown indoors would use this unused capacity and improve fish weight and biomass. Below are the

graphs of the fish weight and MTB with year-round introduction when the smolt are grow up to 500g before going to sea.

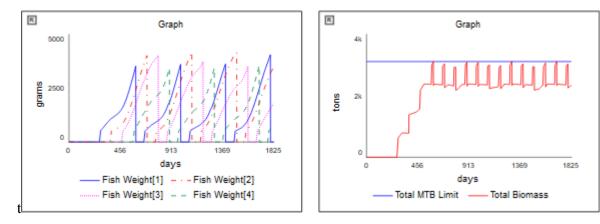


Figure 51 - Year-round introduction with 500g smolt, fish weight and total MTB limit vs total biomass

The fish weight and the biomass vs MTB are much improved in this scenario, with the fish reaching maximum weights of between 3.9 and 4.1 kg, and biomass reaching on average 78% of MTB.

To see whether the year-round introduction has any affect on the lice population, the lice population without treatments for seasonal introduction and year-round introduction has been compared below. As in the last section, the model was initialised with some fish in cohorts 3 and 4 in order to give more lice data for those locations.

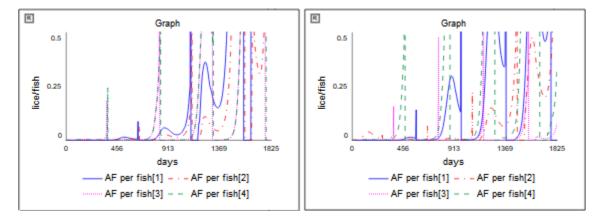
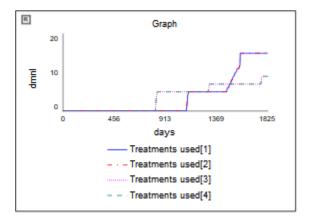


Figure 52 - Adult Female Lice per fish, on the left is seasonal introduction and on the right is year-round introduction, with an initial smolt weight of 250g.

The year-round introduction seems to have more spikes of lice levels reaching above the allowed legal threshold of 0.5 female louse per fish. This is to be expected as the amount of fish in the sea

is higher. The locations close to each other which used to be fallowed at the same time are now fallowed at different times, allowing the lice infestation to continue at a high level in the neighbouring location while the first location is fallowed.

Below, are the comparisons of the amount of treatments needed with year-round introduction and seasonal introduction.



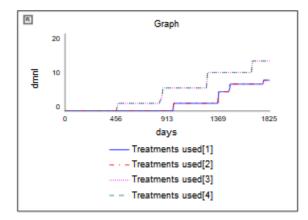


Figure 53 - Number of treatments, left is seasonal introduction, right is year-round. Smolt 250g

In total, the seasonal introduction over five years shows 48 treatment periods, while the year-round introduction shows only 42. It seems then that the treatment policy that has been built to treat the neighbouring farms to an infected location is especially effective at keeping the lice population down year-round.

As year-round introduction was more effective with 500g smolt, below is the graph of treatment needed when smolt are 500g and introduced year-round. There are even fewer lice treatments in this scenario (40 total) which fits with the lower lice levels seen in section 7.1 when 500g smolt were introduced.

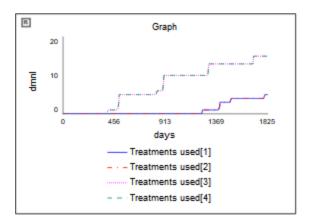


Figure 54 - Year-round introduction number of treatments uses, 500g smolt.

It seems then that year-round smolt growth and introduction is a viable policy that should be explored in order to improve unused capacity.

8. Implementation

The policies in chapter 6 seem to be helpful in reducing the three main problems – idle capacity, long growth periods in the sea and reaching the MTB. Though they may be good in theory, there are practical considerations that must be taken into account in order to implement the policies in real life. These practical considerations will be discussed below.

8.1 Year round smolt introduction

The largest barrier to year-round smolt introduction is a change in the current practices of salmon farming. Currently, normal practice is to introduce smolt in the spring and the fall. Suggesting that farmers change a practice that has served them well for generations may be a hard sell, and further research will need to be done to confirm that this policy is beneficial to the farmer, the environment and the regulatory body (the government).

There is also a concern about temperature shock. The smolt indoors are kept at 14c, and introducing them in the winter would mean putting them in water as low as 5-6c. When there is a large sudden change in water temperature, the mortality of salmon often increases due to the

shock. To prevent this increase in mortality, a policy should be introduced that lowers the temperature gradually indoors in the days before sea introduction, to lessen the shock.

8.2 Growing smolt to a larger size

The largest barrier to implementing this policy, is government regulations. Normally, fish farmers are only allowed to grow smolt up to 250g (Bruland, 2016). However, it is possible to apply to the government to be allowed to grow smolt even larger than this, up to 1000g. However, the purpose must be "to gain experience of management forms, production methods and techniques that can give benefits in terms of the environment, fish health and fish welfare" (Bruland, 2016, pg 72, trans.). This regulation would have to be modified in order to allow farmers to grow their smolt to above 250g for other purposes.

There is of course a limit to how large fish can grow on land. After a certain size, it becomes difficult to maintain facilities that pump enough water and provide enough electricity for heating the tanks (Osland, 2018). Research from the Norwegian agency Nofima shows that after 600g, the costs of growing smolt on land start to outweigh the benefits, both to the farmer and to the fish (Kraugerud, 2018). The parr will be spending more time indoors when grown to a larger size, so the additional cost of operating the smolt growth facility for a longer period of time will need to be calcuated and weighed against the benefits of less time in the sea.

Fully land-based aquaculture systems are still in their infancy and growing the smolt to larger size before putting them into the sea seems like a good compromise between the system farmers use now and moving the operation entirely to land.

9. Conclusion

The model built to recreate the production operations of a single fish farm, owned by Osland Havbruk, has provided insight into the workings of this operations. After ensuring that the model was as accurate as possible within the limits and simplifications necessary, the behaviour generated showed the same problems that the literature and those involved in the fish farming industry have concerns about: idle capacity, long periods of sea-based growth, and not being able to reach the maximum allowed biomass.

By simulating the behaviour of the farm with the model, these three problems and their causes have been better understood. With this better understanding, two policies were created that can help improve the problematic behaviour of the model – growing the smolt to larger sizes indoors to help alleviate idle capacity and long periods of sea-based growth, and introducing year-round introduction to help reach a higher percentage of MTB. These policies were also found not to aggravate the lice population problem, and in some cases actually improved the levels of lice and number of treatments.

The policies created were also fairly feasible, with the largest barriers being the changes to government regulations and the normal practises of fish farmers. Many industries are averse to change, and fish farming is among them. Further research will need to be conducted in order to confirm the results of this analysis. There is also room for expansion of the model, and the building of further sectors to investigate the wider-reaching effects of these new policies.

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Appendix A - Equations — Production Sectors

Juvenile Growth Sector

Equations and Comments	Unit
Death_Rate = 20	Fish per day
Desired_Smolt_weight[1] = 250	Grams
Desired_Smolt_weight[2] = 250	
Desired_Smolt_weight[3] = 250	
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
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	Fish
$Fry_0g_to_10g[2](t) = Fry_0g_to_10g[2](t - dt) + (Fish_egg_Hatching[2] - Moving_to_Room_1[2] - Death_Rate_Fry[2]) * dt \\ INIT Fry_0g_to_10g[2] = 0$	
$Fry_0g_to_10g[3](t) = Fry_0g_to_10g[3](t - dt) + (Fish_egg_Hatching[3] - Moving_to_Room_1[3] - Death_Rate_Fry[3]) * dt \\ INIT Fry_0g_to_10g[3] = 0$	
Fish_egg_Hatching[1] = PULSE (Number_of_Fry_per_Cohort, First_hatching, Time_to_next)	Fish per day

Fish_egg_Hatching[2] = PULSE (Number_of_Fry_per_Cohort, Second_hatching, Time_to_next)	
Fish_egg_Hatching[3] = PULSE (Number_of_Fry_per_Cohort, Third_Hatching, Time_to_next)	
Fish_egg_Hatching[4] = PULSE (Number_of_Fry_per_Cohort, Fourth_Hatching, Time_to_next)	
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
Room_1_10g_to_60g[Cohorts](t) = Room_1_10g_to_60g[Cohorts](t - dt) + (Moving_to_Room_1[Cohorts] - Moving_to_Room_2[Cohorts] - Death_Rate_Room_1[Cohorts]) * dt	Fish
INIT Room_1_10g_to_60g[Cohorts] = 0	
Moving_to_Room_1[Cohorts] = IF Parr_weight >= 10 THEN PULSE (Fry_0g_to_10g-Death_Rate_Fry*DT) ELSE 0	Fish per day
Moving_to_Room_2[Cohorts] = IF Parr_weight >= 60 THEN PULSE (Room_1_10g_to_60g-Death_Rate_Room_1*DT) ELSE 0	Fish per day
Death_Rate_Room_1[Cohorts] = IF Room_1_10g_to_60g > 0 THEN Death_Rate ELSE 0	Fish per day
Room_2_60g_to_100g[Cohorts](t) = Room_2_60g_to_100g[Cohorts](t - dt) + (Moving_to_Room_2[Cohorts] - Moving_to_Room_3[Cohorts] - Death_Rate_Room_2[Cohorts]) * dt	Fish
INIT Room_2_60g_to_100g[Cohorts] = 0	
Moving_to_Room_2[Cohorts] = IF Parr_weight >= 60 THEN PULSE (Room_1_10g_to_60g-Death_Rate_Room_1*DT) ELSE 0	Fish per day
Moving_to_Room_3[Cohorts] = IF Parr_weight >= 100 THEN PULSE (Room_2_60g_to_100g-Death_Rate_Room_2*DT) ELSE 0	Fish per day
Death_Rate_Room_2[Cohorts] = IF Room_2_60g_to_100g > 0 THEN Death_Rate ELSE 0	Fish per day

Room_3_100g_to_500g[Cohorts](t) = Room_3_100g_to_500g[Cohorts](t - dt) + (Moving_to_Room_3[Cohorts] - To_Sea[Cohorts, Location] - Death_Rate_Room_3[Cohorts]) * dt	Fish
INIT Room_3_100g_to_500g[Cohorts] = 0	
Moving_to_Room_3[Cohorts] = IF Parr_weight >= 100 THEN PULSE (Room_2_60g_to_100g-Death_Rate_Room_2*DT) ELSE 0	Fish per day
To_Sea[Cohorts, Location]> Sea_and_Slaughter_Sector: Death_Rate_Room_3[Cohorts] = IF Room_3_100g_to_500g > 0 THEN Death_Rate ELSE 0	Fish per day

Juvenile Feeding Sector

Equations and Comments	Unit
"%_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) Graphs for all of the "% of weight fed at Xc" converters created using tables	Per day
from Skretting AS, document provided by Osland Havbruk	
"%_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)	Per day
"%_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)	Per day
"%_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)	Per day
"%_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)	Per day

"%_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)	Per day
"%_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)	Per day
"%_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)	Per day
Feed_conversion_ratio_parr = 1.15	Dimensionless
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 "%_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 Feeding rate chooses the percentage of body weight fed to the fish per day based on the temperature and the size of the fish.	Dimensionless per day
Initial_Fry_weight = 0.2	Grams
Parr_weight[Cohorts](t) = Parr_weight[Cohorts](t - dt) + (Parr_Weight_Gain[Cohorts]) * dt INIT Parr_weight[Cohorts] = Initial_Fry_weight	Grams
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 This formula includes a condition to reset the parr weight gain when the	Grams/Day
cohort has left the juvenile growth sector	

Temperature_Parr = 14	Degrees C
Total_Amount_of_parr_Food[Cohorts](t) =	Grams
Total_Amount_of_parr_Food[Cohorts](t - dt) +	
(Amount_of_parr_food_per_day[Cohorts]) * dt	
INIT Total_Amount_of_parr_Food[Cohorts] = 0	
Amount_of_parr_food_per_day[Cohorts] = IF Fry_0g_to_10g > 0 OR	Grams per day
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	
This formula includes a condition that there must be parr in the rooms in order for them to be fed	

Fish Feeding Sector

Equations and Comments	Units
"%_of_weight_fed_at_4c_1"[Cohorts] = GRAPH(Fish_Weight)	Per day
(30, 0.805), (100, 0.7705), (200, 0.713), (300, 0.6555), (400, 0.598), (500,	
0.552, $(600, 0.5175)$, $(700, 0.483)$, $(800, 0.4485)$, $(900, 0.4255)$, $(1000, 0.4255)$	
0.4025, $(1100, 0.3795)$, $(1200, 0.368)$, $(1300, 0.345)$, $(1400, 0.3335)$, $(1500, 0.4025)$	
0.322, $(1600, 0.3105)$, $(1700, 0.299)$, $(1800, 0.2875)$, $(1900, 0.276)$, $(2000, 0.322)$	
0.276, $(2250, 0.253)$, $(2500, 0.2415)$, $(2750, 0.230)$, $(3000, 0.2185)$, $(3250, 0.230)$	
0.207, $(3500, 0.207)$, $(3750, 0.1955)$, $(4000, 0.1955)$, $(4250, 0.184)$, $(4500, 0.1955)$	
0.184), (4750, 0.1725), (5000, 0.1725), (7000, 0.1725)	
Graphs for all of the "% of weight fed at Xc" converters created using tables	
from Skretting AS, document provided by Osland Havbruk	
"%_of_weight_fed_at_6c_1"[Cohorts] = GRAPH(Fish_Weight)	Per day
(30, 1.2535), (100, 1.219), (200, 1.127), (300, 1.035), (400, 0.9545), (500,	1 CI day
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)	
0.5105), (1750, 0.257), (5000, 0.257), (7000, 0.2075)	
"%_of_weight_fed_at_8c_1"[Cohorts] = GRAPH(Fish_Weight)	Per day
(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)	
"%_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)	Per day
"%_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)	Per day
"%_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), (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)	Per day
Feed_conversion_ratio_fish = 1.15	Dimensionless
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	Per day

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.	
Historical_temperature = GRAPH(TIME) (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) The ghost variable "temperature" in the fish feeding sector is the same as the historical temperature above	Degrees C
Fish_Weight[Cohorts](t) = Fish_Weight[Cohorts](t - dt) + (Fish_Weight[Cohorts] = 0	Grams
Fish_Weight[Cohorts] = 0 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 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 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 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 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	Grams per day

Total_Amount_of_Fish_Food[Cohorts](t) = Total_Amount_of_Fish_Food[Cohorts](t - dt) + (Amount_of_fish_food_per_day[Cohorts]) * dt INIT Total_Amount_of_Fish_Food[Cohorts] = 0	Grams
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	Grams per day
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	
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	
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	
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.	

Sea and Slaughter Sector

Equations and Comments	Units
Avg_lifespan_in_sea[1] = Normal_Life_in_sea-	Days
(Treatments_used[1]*Eff_of_treatments_on_mortality)	
Avg_lifespan_in_sea[2] = Normal_Life_in_sea-	
(Treatments_used[2]*Eff_of_treatments_on_mortality)	
Avg_lifespan_in_sea[3] = Normal_Life_in_sea-	
(Treatments_used[3]*Eff_of_treatments_on_mortality)	
Avg_lifespan_in_sea[4] = Normal_Life_in_sea-	
(Treatments_used[4]*Eff_of_treatments_on_mortality)	
Biomass_per_location_check[1] = IF Location_Biomass[1] >	Tons
Maximum_biomass_per_location THEN 1 ELSE 0	

Biomass_per_location_check[2] = IF Location_Biomass[2] > Maximum_biomass_per_location THEN 1 ELSE 0	
Biomass_per_location_check[3] = IF Location_Biomass[3] > Maximum_biomass_per_location THEN 1 ELSE 0	
Biomass_per_location_check[4] = IF Location_Biomass[4] > Maximum_biomass_per_location THEN 1 ELSE 0	
Desired_Fish_Weight = 5000	Grams
Fallowing_period = 60	Days
Grams_per_ton = 1000000	Grams/to ns*fish
Last_Slaughter_time[Location](t) = Last_Slaughter_time[Location](t - dt) + (cLST[Location]) * dt	Days
INIT Last_Slaughter_time[Location] = 0	
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.	
cLST[Location] = IF Time_when_Slaughter_occurs>0 THEN (Time_when_Slaughter_occurs-Last_Slaughter_time)/DT ELSE 0	Dimensio nless
Location_Biomass[1] = Locations[1]*Fish_Weight[1]/Grams_per_ton	Tons
Location_Biomass[2] = Locations[2]*Fish_Weight[2]/Grams_per_ton	
Location_Biomass[3] = Locations[3]*Fish_Weight[3]/Grams_per_ton	
Location_Biomass[4] = Locations[4]*Fish_Weight[4]/Grams_per_ton	
Location_MTB_Limit = 780	Tons
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	Fish
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	

```
Locations[3](t) = Locations[3](t - dt) + (To_Sea[1, 3] + To_Sea[2, 3] + To_Sea[3, 3])
3] + To_Sea[4, 3] - Weight_Slaughter[3] - Slaughter_based_on_Biomass[3] -
Sea_based_mortality[3]) * dt
  INIT Locations [3] = 0
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
To_Sea[1, 1] = IF Parr_weight[1] >= Desired_Smolt_weight[1] AND
                                                                             Fish per
Locations[1] < 100 AND TIME >= Next_introduction_Date[1] THEN PULSE
                                                                             day
(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
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
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
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
These equations contain structures which ensure that all the necessary parameters
are in place before fish can enter a location
    Weight_Slaughter[1] = IF Parr_weight[1] >=
                                                                             Fish per
parr_weight_60_days_before_sea_introduction[1] AND Locations[1] > 10 THEN
                                                                             day
Locations[1]/Slaughter time ELSE
Slaughter_based_on_weight[1]/Slaughter_time
    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 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	
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 Slaughter_based_on_Biomass[Location] =	Fish per
Number_of_fish_slaughtered_exceeding_biomass/Slaughter_time	day
$Sea_based_mortality[1] = MAX(0, (Locations[1]/Avg_lifespan_in_sea[1]) - Slaughter_based_on_Biomass[1])$	Fish per day
$Sea_based_mortality[2] = MAX(0, (Locations[2]/Avg_lifespan_in_sea[2]) - Slaughter_based_on_Biomass[2])$	
Sea_based_mortality[3] = MAX(0, (Locations[3]/Avg_lifespan_in_sea[3])-Slaughter_based_on_Biomass[3])	
$Sea_based_mortality[4] = MAX(0, (Locations[4]/Avg_lifespan_in_sea[4]) - Slaughter_based_on_Biomass[4])$	
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_amou nt_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+ Fallowing_period ELSE 0	Days
Normal_Life_in_sea = 400	Days
Number_of_cages_120 = 8	Cages
Number_of_cages_160 = 0	Cages

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 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	Fish
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	
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	
number_of_locations = 4	Dimensio nless
parr_weight_60_days_before_sea_introduction[1] =	Grams
0.2*Desired_Smolt_weight[1]	
parr_weight_60_days_before_sea_introduction[2] = 0.2*Desired_Smolt_weight[2]	
parr_weight_60_days_before_sea_introduction[3] = 0.2*Desired_Smolt_weight[3]	
parr_weight_60_days_before_sea_introduction[4] = 0.2*Desired_Smolt_weight[4]	
Slaughter_amount_based_on_total_MTB = MAX((Total_Biomass-Total_MTB_Limit), 0)	Tons
Slaughter_amount_per_location[1] = MAX((Location_Biomass[1]-Location_MTB_Limit), 0)	Tons
Slaughter_amount_per_location[2] = MAX((Location_Biomass[2]-Location_MTB_Limit), 0)	
Slaughter_amount_per_location[3] = MAX((Location_Biomass[3]-Location_MTB_Limit), 0)	
Slaughter_amount_per_location[4] = MAX((Location_Biomass[4]-Location_MTB_Limit), 0)	

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
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	
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	
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	
These equations contain a condition to make sure there are fish in the location before slaughter.	
Slaughter_of_Exceeding_Biomass[Location] = (Slaughter_amount_based_on_total_MTB+Slaughter_amount_per_location)	Tons
Slaughter_time = 2	Days
Time_when_parr_are_in_room_3[1] = IF Room_3_100g_to_500g[1] > 194000 THEN TIME ELSE 0	Days
Time_when_parr_are_in_room_3[2] = IF Room_3_100g_to_500g[2] > 194000 THEN TIME ELSE 0	
Time_when_parr_are_in_room_3[3] = IF Room_3_100g_to_500g[3] > 194000 THEN TIME ELSE 0	
Time_when_parr_are_in_room_3[4] = IF Room_3_100g_to_500g[4] > 194000 THEN TIME ELSE 0	
Time_when_Slaughter_occurs[1] = IF Weight_Slaughter[1] > 0 THEN TIME ELSE 0	Days
Time_when_Slaughter_occurs[2] = IF Weight_Slaughter[2] > 0 THEN TIME ELSE 0	
Time_when_Slaughter_occurs[3] = IF Weight_Slaughter[3] > 0 THEN TIME ELSE 0	

Time_when_Slaughter_occurs[4] = IF Weight_Slaughter[4] > 0 THEN TIME ELSE 0	
Total_Biomass = Location_Biomass[1]+Location_Biomass[2]+Location_Biomass[3]+Location_Biomass[4]	Tons
Total_MTB_Limit = Location_MTB_Limit*number_of_locations	Tons

Appendix B - Equations — Lice Sector

Lice reproduction, Treatment and Cleaner Fish Sectors

Cleaner Fish Sector

Cleaner Fish MR = 0,028	1/days
$Cleaner_fish[Location](t) = Cleaner_fish[Location](t - dt) + (Cleaner_fish_increase[Location] - dt) + (Cleaner_fish_i$	fish
Cleaner_fish_mortality[Location]) * dt	
INIT Cleaner_fish[Location] = 0	fish
INFLOWS:	fish/day
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	
OUTFLOWS:	fish/day
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	
Cleaner_Salmon_Ratio[1] = MIN(MAX(0; Cleaner_fish/(Locations[1]+0,0001)); 1)	dmnl
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)	
mortality_from_cleaner_fish[1] = 1-EXP(-0,0823*Cleaner_Salmon_Ratio[1])	dmnl
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])	
number_of_cleaner_fish_introduced[1] = 10000	fish
number_of_cleaner_fish_introduced[2] = 10000	
number_of_cleaner_fish_introduced[3] = 10000	
number_of_cleaner_fish_introduced[4] = 10000	
refilling_time = 50	days
Time_of_introduction[1] = 250	days
Time_of_introduction[2] = 250	
Time_of_introduction[3] = 250	
Time_of_introduction[4] = 250	

Infection Pressure Sector

alfa_test = 1/360*20	dmnl
alfa_val_in_dir_of = 0,0556	dmnl
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	
Attachment_rate[1] =	lice/days
$(IP_i[1]*Copepodid[1]+IP_j[1]*Copepodid[2]+IP_k[1]*Copepodid[3]+IP_l[1]*Copepodid[4])$	
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] =	
$(IP_i[4]*Copepodid[1]+IP_j[4]*Copepodid[2]+IP_k[4]*Copepodid[3]+IP_l[4]*Copepodid[4])$	
The rate at which infectious stage lice are able to develop, find a host and attach to a fish.	
host_availability_P[1] = IF(Host_population[1]>1000) THEN 1 ELSE 0	dmnl
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_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[3] = Locations[4]+Wild_hosts/4 Host_population[4] = Locations[4]+Wild_hosts/4 IP_i[1] = "Si_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[1] Dmnl/days 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] IP_i[4] = "Si_x_P(B)"[4]*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] IP_i[4] = "Si_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[2] IP_i[1] = "Si_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[2] IP_i[1] = "Si_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[2] IP_i[4] = "Si_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[2] IP_i[4] = "Si_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[3] IP_k[1] = "Sk_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[3] IP_k[4] = "Sk_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[3] IP_k[4] = "Sk_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[3] IP_k[4] = "Sk_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[3] IP_k[4] = "Sk_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[3] IP_k[4] = "Sk_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[4] IP_k[4] = "Sk_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[4] IP_k[4] = "Sk_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[4] IP_k[4] = "Sk_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[4] IP_k[4] = "Sk_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[4] IP_k[4] = "Sk_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_	host_availability_P[4] = IF(Host_population[4]>1000) THEN 1 ELSE 0	
Host_population[3] = Locations[3]+Wild_hosts/4 Host_population[4] = Locations[4]+Wild_hosts/4 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] 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 lumbda 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 the model behavior and so drive the exponential growth processes associated with the outbreak of a contagious disease." Duggan (2016) 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. IP_j[1] = "Sj_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[2] IP_j[3] = "Sj_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[2] IP_j[4] = "Sk_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[2] IP_j[4] = "Sk_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[3] IP_k[4] = "Sk_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[3] IP_k[4] = "Sk_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[3] IP_k[4] = "Sk_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[3] IP_k[4] = "Sk_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[4] IP_l[1] = "Sl_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[4] IP_l[1] = "Sl_x_P(B)"[1]*alfa_val	Host_population[1] = Locations[1]+Wild_hosts/4	fish
Host_population[4] = Locations[4]+Wild_hosts/4 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] 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 the model behavior and so drive the exponential growth processes associated with the outbreak of a contagious disease." Duggan (2016) 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. IP_j[1] = "Sj_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[2] IP_j[3] = "Sj_x_P(B)"[2]*alfa_val_in_dir_of*host_availability_P[2] IP_j[4] = "Sk_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[2] IP_j[4] = "Sk_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[3] IP_k[4] = "Sk_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[3] IP_k[4] = "Sk_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[3] IP_k[4] = "Sk_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[3] IP_k[4] = "Sk_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[4] IP_l[1] = "Sl_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[4]	Host_population[2] = Locations[2]+Wild_hosts/4	
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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] 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 the model behavior and so drive the exponential growth processes associated with the outbreak of a contagious disease." Duggan (2016) 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. IP_j[1] = "Sj_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[2] IP_j[3] = "Sj_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[2] IP_j[4] = "Sj_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[2] IP_k[1] = "Sk_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[3] IP_k[2] = "Sk_x_P(B)"[2]*alfa_val_in_dir_of*host_availability_P[3] IP_k[4] = "Sk_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[3] IP_k[4] = "Sk_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[3] IP_k[4] = "Sk_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[3] IP_k[4] = "Sk_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[3] IP_k[4] = "Sk_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[4] Dmnl/days IP_l[2] = "Sl_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[4] IP_l[1] = "Sl_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[4] IP_l[1] = "Sl_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[4]	Host_population[4] = Locations[4]+Wild_hosts/4	
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] 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 the model behavior and so drive the exponential growth processes associated with the outbreak of a contagious disease." Duggan (2016) 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. IP_j[1] = "Sj_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[2] IP_j[3] = "Sj_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[2] IP_j[4] = "Sj_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[2] IP_k[1] = "Sk_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[3] IP_k[2] = "Sk_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[3] IP_k[3] = "Sk_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[3] IP_k[4] = "Sk_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[3] IP_k[4] = "Sk_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[3] IP_l[1] = "Sl_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[4] Dmnl/days IP_l[1] = "Sl_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[4] Dmnl/days IP_l[1] = "Sl_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[4]	IP_i[1] = "Si_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[1]	Dmnl/days
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numbers of infected. This is a reinforcing process, and the positive feedback loop can quickly dominate the model behavior and so drive the exponential growth processes associated with the outbreak of a contagious disease." Duggan (2016) 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. IP_j[1] = "Sj_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[2] IP_j[2] = "Sj_x_P(B)"[2]*alfa_val_in_dir_of*host_availability_P[2] IP_j[3] = "Sj_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[2] IP_j[4] = "Sj_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[2] IP_k[1] = "Sk_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[3] IP_k[2] = "Sk_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[3] IP_k[4] = "Sk_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[3] IP_k[4] = "Sk_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[4] IP_l[1] = "Sl_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[4] IP_l[3] = "Sl_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[4] IP_l[3] = "Sl_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[4]	loop polarity in the SIR model. As the number of infected cases increase, so too does lambda. An	
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Duggan (2016) 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. IP_j[1] = "Sj_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[2] IP_j[2] = "Sj_x_P(B)"[2]*alfa_val_in_dir_of*host_availability_P[2] IP_j[3] = "Sj_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[2] IP_j[4] = "Sj_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[2] IP_k[1] = "Sk_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[3] IP_k[2] = "Sk_x_P(B)"[2]*alfa_val_in_dir_of*host_availability_P[3] IP_k[3] = "Sk_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[3] IP_l[1] = "Sl_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[3] IP_l[1] = "Sl_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[4] IP_l[3] = "Sl_x_P(B)"[2]*alfa_val_in_dir_of*host_availability_P[4] IP_l[3] = "Sl_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[4]	the model behavior and so drive the exponential growth processes associated with the outbreak of a	
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. IP_j[1] = "Sj_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[2] IP_j[2] = "Sj_x_P(B)"[2]*alfa_val_in_dir_of*host_availability_P[2] IP_j[3] = "Sj_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[2] IP_j[4] = "Sj_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[2] IP_k[1] = "Sk_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[3] IP_k[2] = "Sk_x_P(B)"[2]*alfa_val_in_dir_of*host_availability_P[3] IP_k[3] = "Sk_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[3] IP_k[4] = "Sk_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[4] IP_l[1] = "Sl_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[4] IP_l[3] = "Sl_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[4]	contagious disease."	
EIP is significant correlated with louse counts. IP_j[1] = "Sj_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[2] IP_j[2] = "Sj_x_P(B)"[2]*alfa_val_in_dir_of*host_availability_P[2] IP_j[3] = "Sj_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[2] IP_j[4] = "Sj_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[2] IP_k[1] = "Sk_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[3] IP_k[2] = "Sk_x_P(B)"[2]*alfa_val_in_dir_of*host_availability_P[3] IP_k[3] = "Sk_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[3] IP_k[4] = "Sk_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[3] IP_l[1] = "Sl_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[4] IP_l[2] = "Sl_x_P(B)"[2]*alfa_val_in_dir_of*host_availability_P[4] IP_l[3] = "Sl_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[4]		
IP_j[1] = "Sj_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[2] IP_j[2] = "Sj_x_P(B)"[2]*alfa_val_in_dir_of*host_availability_P[2] IP_j[3] = "Sj_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[2] IP_j[4] = "Sj_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[2] IP_k[1] = "Sk_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[3] IP_k[2] = "Sk_x_P(B)"[2]*alfa_val_in_dir_of*host_availability_P[3] IP_k[3] = "Sk_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[3] IP_k[4] = "Sk_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[3] IP_l[1] = "Sl_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[4] IP_l[3] = "Sl_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[4] IP_l[3] = "Sl_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[4]		
IP_j[2] = "Sj_x_P(B)"[2]*alfa_val_in_dir_of*host_availability_P[2] IP_j[3] = "Sj_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[2] IP_j[4] = "Sj_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[2] IP_k[1] = "Sk_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[3] IP_k[2] = "Sk_x_P(B)"[2]*alfa_val_in_dir_of*host_availability_P[3] IP_k[3] = "Sk_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[3] IP_k[4] = "Sk_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[3] IP_l[1] = "Sl_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[4] IP_l[2] = "Sl_x_P(B)"[2]*alfa_val_in_dir_of*host_availability_P[4] IP_l[3] = "Sl_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[4]		
IP_j[3] = "Sj_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[2] IP_j[4] = "Sj_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[2] IP_k[1] = "Sk_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[3] IP_k[2] = "Sk_x_P(B)"[2]*alfa_val_in_dir_of*host_availability_P[3] IP_k[3] = "Sk_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[3] IP_k[4] = "Sk_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[3] IP_l[1] = "Sl_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[4] IP_l[2] = "Sl_x_P(B)"[2]*alfa_val_in_dir_of*host_availability_P[4] IP_l[3] = "Sl_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[4]		Dmnl/days
$IP_j[4] = "Sj_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[2]$ $IP_k[1] = "Sk_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[3]$ $IP_k[2] = "Sk_x_P(B)"[2]*alfa_val_in_dir_of*host_availability_P[3]$ $IP_k[3] = "Sk_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[3]$ $IP_k[4] = "Sk_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[3]$ $IP_l[1] = "Sl_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[4]$ $IP_l[2] = "Sl_x_P(B)"[2]*alfa_val_in_dir_of*host_availability_P[4]$ $IP_l[3] = "Sl_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[4]$		
IP_k[1] = "Sk_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[3] IP_k[2] = "Sk_x_P(B)"[2]*alfa_val_in_dir_of*host_availability_P[3] IP_k[3] = "Sk_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[3] IP_k[4] = "Sk_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[3] IP_l[1] = "Sl_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[4] IP_l[2] = "Sl_x_P(B)"[2]*alfa_val_in_dir_of*host_availability_P[4] IP_l[3] = "Sl_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[4]		
IP_k[2] = "Sk_x_P(B)"[2]*alfa_val_in_dir_of*host_availability_P[3] IP_k[3] = "Sk_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[3] IP_k[4] = "Sk_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[3] IP_l[1] = "Sl_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[4] IP_l[2] = "Sl_x_P(B)"[2]*alfa_val_in_dir_of*host_availability_P[4] IP_l[3] = "Sl_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[4]	$IP_{j}[4] = "Sj_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[2]$	
$IP_k[3] = "Sk_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[3]$ $IP_k[4] = "Sk_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[3]$ $IP_l[1] = "Sl_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[4]$ $Dmnl/days$ $IP_l[2] = "Sl_x_P(B)"[2]*alfa_val_in_dir_of*host_availability_P[4]$ $IP_l[3] = "Sl_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[4]$	$IP_k[1] = "Sk_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[3]$	Dmnl/days
$IP_k[4] = "Sk_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[3]$ $IP_l[1] = "Sl_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[4]$ $Dmnl/days$ $IP_l[2] = "Sl_x_P(B)"[2]*alfa_val_in_dir_of*host_availability_P[4]$ $IP_l[3] = "Sl_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[4]$	$IP_k[2] = "Sk_x_P(B)"[2]*alfa_val_in_dir_of*host_availability_P[3]$	
IP_l[1] = "Sl_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[4] IP_l[2] = "Sl_x_P(B)"[2]*alfa_val_in_dir_of*host_availability_P[4] IP_l[3] = "Sl_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[4]	$IP_k[3] = "Sk_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[3]$	
IP_l[2] = "Sl_x_P(B)"[2]*alfa_val_in_dir_of*host_availability_P[4] IP_l[3] = "Sl_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[4]	$IP_k[4] = "Sk_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[3]$	
IP_l[3] = "Sl_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[4]	$IP_1[1] = "Sl_x_P(B)"[1]*alfa_val_in_dir_of*host_availability_P[4]$	Dmnl/days
	$IP_1[2] = "Sl_x_P(B)"[2]*alfa_val_in_dir_of*host_availability_P[4]$	
$IP_l[4] = "Sl_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[4]$	$IP_1[3] = "Sl_x_P(B)"[3]*alfa_val_in_dir_of*host_availability_P[4]$	
	$IP_1[4] = "Sl_x_P(B)"[4]*alfa_val_in_dir_of*host_availability_P[4]$	

$"Si_x_P(B)"[1] = Survival_from_i[1]$	Dmnl/days
$"Si_x_P(B)"[2] = Survival_from_i[2]$	
$"Si_x_P(B)"[3] = Survival_from_i[3]$	
$"Si_x_P(B)"[4] = Survival_from_i[4]$	
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.	
$RR \ i,j=$	
e^(-1.444-0,351(D i,j ^(0,57)-1/0,57)/	
e^(-1,444-0,351(0-1)/0,57)	
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.	
$Sj_x_P(B)$ [1] = Survival_from_j[1]	Dmnl/days
$"Sj_x_P(B)"[2] = Survival_from_j[2]$	
$"Sj_x_P(B)"[3] = Survival_from_j[3]$	
$"Sj_x_P(B)"[4] = Survival_from_j[4]$	
$"Sk_x_P(B)"[1] = Survival_from_k[1]$	Dmnl/days
$Sk_xP(B)''[2] = Survival_from_k[2]$	
$"Sk_x_P(B)"[3] = Survival_from_k[3]$	
$"Sk_x_P(B)"[4] = Survival_from_k[4]$	
"Sl_x_P(B)"[1] = Survival_from_l[1]	Dmnl/days
$"Sl_x_P(B)"[2] = Survival_from_l[2]$	
$"Sl_x_P(B)"[3] = Survival_from_l[3]$	
$"Sl_x_P(B)"[4] = Survival_from_l[4]$	
Survival_from_i[1] = 0,3104	Dmnl/days
Survival_from_i[2] = 4,148E-07	
Survival_from_i[3] = 2,584E-13	
Survival_from_i[4] = 3,260E-14	

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	
Survival_from_j[1] = 4,148E-07	Dmnl/days
Survival_from_j[2] = 0,3104	
Survival_from_j[3] = 1,377E-14	
Survival_from_j[4] = 1,928E-13	
Survival_from_k[1] = 1,928E-13	Dmnl/days
Survival_from_k[2] = 1,377E-14	
$Survival_from_k[3] = 0,3104$	
$Survival_from_k[4] = 4,148E-07$	
Survival_from_l[1] = 3,260E-14	Dmnl/days
Survival_from_l[2] = 1,928E-13	
Survival_from_l[3] = 4,145E-07	
Survival_from_l[4] = 0,3104	

Lice Sector

$Adult[1](t) = Adult[1](t - dt) + (Maturing[1] - Mature_Mortality[1] -$	Lice
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 $[2] = 100$	
$Adult[3](t) = Adult[3](t - dt) + (Maturing[3] - Mature_Mortality[3] -$	
Treatment_Mortality_AL[3]) * dt	
INIT Adult[3] = 100	

Treatment_Mortality_AL[4]) * dt INIT Adult[4] = 100 INFLOWS: Maturing[Location] = MAX(0; Chalimus_and_Preadult/Maturing_time_PAAM) 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)) "Attached_Lice_stages_per_fish,_all_locations" = Lice/fish (lice_pr_fish[1]+lice_pr_fish[2]+lice_pr_fish[3]+lice_pr_fish[4])/4 Avg_development_time = 17 days Preadult[Location](t) = Preadult[Location](t - dt) + (Developing[Location] - lice Maturing[Location] - Pa_Mortality[Location] - Treatment_MR_on_PA[Location]) * dt INIT Preadult[Location] = 150 INFLOWS: Dayslopine II costion] = Chalimus (Day, time, to, PA)
INFLOWS: Maturing[Location] = MAX(0; Chalimus_and_Preadult/Maturing_time_PAAM) 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)) "Attached_Lice_stages_per_fish,_all_locations" = (lice_pr_fish[1]+lice_pr_fish[2]+lice_pr_fish[3]+lice_pr_fish[4])/4 Avg_development_time = 17 days Preadult[Location](t) = Preadult[Location](t - dt) + (Developing[Location] - Maturing[Location] - Pa_Mortality[Location] - Treatment_MR_on_PA[Location]) * dt INIT Preadult[Location] = 150 INFLOWS: Lice/days
Maturing[Location] = MAX(0; Chalimus_and_Preadult/Maturing_time_PAAM) OUTFLOWS:
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)) "Attached_Lice_stages_per_fish,_all_locations" = (lice_pr_fish[1]+lice_pr_fish[2]+lice_pr_fish[3]+lice_pr_fish[4])/4 Avg_development_time = 17 Preadult[Location](t) = Preadult[Location](t - dt) + (Developing[Location] - Maturing[Location] - Pa_Mortality[Location] - Treatment_MR_on_PA[Location]) * dt INIT Preadult[Location] = 150 INFLOWS: Lice/days
Mature_Mortality[Location] = Adult/life_span Treatment_Mortality_AL[Location] = MAX(0; (Adult*Treatment_MR)-Mature_Mortality- (Lice_removed_with_slaughtered_fish*Ad_fraction)) "Attached_Lice_stages_per_fish,_all_locations" = Lice/fish (lice_pr_fish[1]+lice_pr_fish[2]+lice_pr_fish[3]+lice_pr_fish[4])/4 Avg_development_time = 17 days Preadult[Location](t) = Preadult[Location](t - dt) + (Developing[Location] - lice Maturing[Location] - Pa_Mortality[Location] - Treatment_MR_on_PA[Location]) * dt INIT Preadult[Location] = 150 INFLOWS: Lice/days
Treatment_Mortality_AL[Location] = MAX(0; (Adult*Treatment_MR)-Mature_Mortality- (Lice_removed_with_slaughtered_fish*Ad_fraction)) "Attached_Lice_stages_per_fish,_all_locations" = Lice/fish (lice_pr_fish[1]+lice_pr_fish[2]+lice_pr_fish[3]+lice_pr_fish[4])/4 Avg_development_time = 17 days Preadult[Location](t) = Preadult[Location](t - dt) + (Developing[Location] - lice Maturing[Location] - Pa_Mortality[Location] - Treatment_MR_on_PA[Location]) * dt INIT Preadult[Location] = 150 INFLOWS: Lice/days
(Lice_removed_with_slaughtered_fish*Ad_fraction)) "Attached_Lice_stages_per_fish,_all_locations" = Lice/fish (lice_pr_fish[1]+lice_pr_fish[2]+lice_pr_fish[3]+lice_pr_fish[4])/4 Avg_development_time = 17 days Preadult[Location](t) = Preadult[Location](t - dt) + (Developing[Location] - lice Maturing[Location] - Pa_Mortality[Location] - Treatment_MR_on_PA[Location]) * dt INIT Preadult[Location] = 150 INFLOWS: Lice/days
"Attached_Lice_stages_per_fish,_all_locations" = Lice/fish (lice_pr_fish[1]+lice_pr_fish[2]+lice_pr_fish[3]+lice_pr_fish[4])/4 Avg_development_time = 17 days Preadult[Location](t) = Preadult[Location](t - dt) + (Developing[Location] - lice Maturing[Location] - Pa_Mortality[Location] - Treatment_MR_on_PA[Location]) * dt INIT Preadult[Location] = 150 INFLOWS: Lice/days
(lice_pr_fish[1]+lice_pr_fish[2]+lice_pr_fish[3]+lice_pr_fish[4])/4 Avg_development_time = 17 days Preadult[Location](t) = Preadult[Location](t - dt) + (Developing[Location] - lice Maturing[Location] - Pa_Mortality[Location] - Treatment_MR_on_PA[Location]) * dt INIT Preadult[Location] = 150 INFLOWS: Lice/days
Avg_development_time = 17 Preadult[Location](t) = Preadult[Location](t - dt) + (Developing[Location] - lice Maturing[Location] - Pa_Mortality[Location] - Treatment_MR_on_PA[Location]) * dt INIT Preadult[Location] = 150 INFLOWS: Lice/days
Preadult[Location](t) = Preadult[Location](t - dt) + (Developing[Location] - Maturing[Location] - Pa_Mortality[Location] - Treatment_MR_on_PA[Location]) * dt INIT Preadult[Location] = 150 INFLOWS: Lice/days
Maturing[Location] - Pa_Mortality[Location] - Treatment_MR_on_PA[Location]) * dt INIT Preadult[Location] = 150 INFLOWS: Lice/days
INIT Preadult[Location] = 150 INFLOWS: Lice/days
INFLOWS: Lice/days
Davidoning [Location] - Chalimus/Day time to DA
Developing[Location] = Chalimus/Dev_time_to_PA
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)))
Chalimus[Location](t) = Chalimus[Location](t - dt) + (Attaching[Location] - Lice
Developing[Location] - CH_Mortality[Location] -
Treatment_Mortality_Chalimus[Location]) * dt
INIT Chalimus[Location] = 100
INFLOWS: Lice/days
$Attaching[1] = MAX(0; Attachment_rate[1])$
Attaching[2] = Attachment_rate[2]
Attaching[3] = Attachment_rate[3]
Attaching[4] = Attachment_rate[4]

UNITS: lice/days	
OUTFLOWS:	
Developing[Location] = Chalimus/Dev_time_to_PA	
CH_Mortality[Location] = Chalimus/CH_life_dur	
Treatment_Mortality_Chalimus[Location] = MAX(0; (Chalimus*	Lice/days
treatment_effect_on_mortality/treatment_effect_delay)-CH_Mortality)	
$Copepodid[1](t) = Copepodid[1](t - dt) + (Infectious_development[1] - Attaching[1] - (Infectious_development[1] - (Infectious_deve$	lice
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	
INFLOWS:	Lice/days
Infectious_development[Location] = "Nauplii_(larvae)"/Development_time	
OUTFLOWS:	Lice/days
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	
Copepodid_stage_time = Normal_stage_time/(1/Effect_of_temperature_on_stage_time)	days
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.	

Development_time = norm_dev_time/(1/Effect_of_temperature_on_stage_time)	days								
Effect_of_season_on_wild_hosts = GRAPH(season)	dmnl								
(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)									
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.									
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.									
	dmnl								
(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, 10,13), (10,00, 10,13), (1									
5,96), (14,00, 5,33), (15,00, 4,79), (16,00, 4,32), (17,00, 3,93)									
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								
$Eggs[Location](t) = Eggs[Location](t - dt) + (LS_Eggs_in[Location] - Hatching[Location] - H$	lice								
Eggs_mortality[Location]) * dt									
INIT Eggs[Location] = 100									
INFLOWS:	Lice/days								
LS_Eggs_in[Location] = eggs_produced									
OUTFLOWS:	Lice/days								
Hatching[Location] = Eggs/Hatching_time									
Eggs_mortality[Location] = Eggs/Egg_survival_time									
Eggs_pr_louse_per_day = GRAPH(Historical_temperature)	Dmnl/days								

(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, 10,13), (10,00, 10,13), (1	
5,96), (14,00, 5,33), (15,00, 4,79), (16,00, 4,32), (17,00, 3,93)	
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, 10, 10, 10, 10, 10, 10, 10, 10, 10, 10	
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	Lice/fish
"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_removed_with_slaughtered_fish[Location] = MAX(0;	Lice/days
MIN(("Mob_/_Mot_lice_in_locations"/Slaughter_time); lice_pr_fish*Weight_Slaughter))	
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]))	lice
"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]))	
"Nauplii_(larvae)"[1](t) = "Nauplii_(larvae)"[1](t - dt) + (Hatching[1] -	lice
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	
"Nauplii_(larvae)"[4](t) = "Nauplii_(larvae)"[4](t - dt) + (Hatching[4] -	
Nauplius_Mortality[4] - Infectious_development[4]) * dt	
INIT "Nauplii_(larvae)"[4] = 100	
INFLOWS:	Lice/days
Hatching[Location] = Eggs/Hatching_time	
OUTFLOWS:	Lice/days
Nauplius_Mortality[Location] = "Nauplii_(larvae)"*Nauplii_Mortality_R	
Infectious_development[Location] = "Nauplii_(larvae)"/Development_time	
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	Degrees C
Historical_temperature+Temperature_change	
Same as Historical Temperature. Variable exists incase we want to test the effect of	
temperatures other than the historical temperature	
Temperature_change = 0	Degrees C
Times_when_fish_reach_their_desired_fish_weight[1] = IF Fish_Weight[1] >=	Grams
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	
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
$Closest_Neighbour[1] = CN_Switch*((treatment_initiation[1] + treatment_initiation[2]))$	dmnl
$Closest_Neighbour[2] = CN_Switch*((treatment_initiation[2] + treatment_initiation[1]))$	
$Closest_Neighbour[3] = CN_Switch*((treatment_initiation[3] + treatment_initiation[4]))$	
$Closest_Neighbour[4] = CN_Switch*((treatment_initiation[4] + treatment_initiation[3]))$	
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.	
$CN_Switch = 0$	dmnl

effect_gap[Location] = Treatment_effectiveness*treatment_effect_on_effectiveness	Dmnl/days
Feeding_pause_time = 5	days
fraction_female_lice = 0,5	dmnl
$Last_treatment_time[Cohorts](t) = Last_treatment_time[Cohorts](t - dt) +$	days
(C_Treatment[Cohorts]) * dt	
INIT Last_treatment_time[Cohorts] = 0	
INFLOWS:	dmnl
C_Treatment[Cohorts] = IF Time_when_treatment_occurs >0 THEN	
(Time_when_treatment_occurs-Last_treatment_time)/DT ELSE 0	
life_span_reduction_during_treatment[Location] = PULSE	1/days
((treatment_effect_on_mortality); treatment_effect_delay	
$Single_Loc[1] = SL_Switch*treatment_initiation[1]$	dmnl
$Single_Loc[2] = SL_Switch*treatment_initiation[2]$	
$Single_Loc[3] = SL_Switch*treatment_initiation[3]$	
$Single_Loc[4] = SL_Switch*treatment_initiation[4]$	
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	
SL_Switch = 1	dmnl
Time_when_feeding_starts_again[1] = IF Last_treatment_time[1] > 0 THEN	days
Last_treatment_time[1] + Feeding_pause_time ELSE 0	
$Time_when_feeding_starts_again[2] = Last_treatment_time[2] + Feeding_pause_time$	
$Time_when_feeding_starts_again[3] = Last_treatment_time[3] + Feeding_pause_time$	
$Time_when_feeding_starts_again[4] = Last_treatment_time[4] + Feeding_pause_time[4] + Feeding_pause_t$	
Time_when_treatment_occurs[1] = IF treatment_increase[1] > 0 THEN TIME ELSE 0	days
$Time_when_treatment_occurs[2] = IF\ treatment_increase[2] > 0\ THEN\ TIME\ ELSE\ 0$	
Time_when_treatment_occurs[3] = IF treatment_increase[3] > 0 THEN TIME ELSE 0	
$Time_when_treatment_occurs[4] = IF\ treatment_increase[4] > 0\ THEN\ TIME\ ELSE\ 0$	
Time_with_no_feeding_due_to_treatment[1] = IF TIME >= Last_treatment_time[1] AND	days
TIME <= Time_when_feeding_starts_again[1] THEN 1 ELSE 0	

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	
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	
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	
Tot_Treatments_used =	dmnl
Treatments_used[1]+Treatments_used[2]+Treatments_used[3]+Treatments_used[4]	
treatment_effect_delay = 2	days
treatment_effect_on_effectiveness[Location] = Treatment_regularity*0,00000001	Dmnl/days
Diminishing effect from high chemical use. More data is needed for the correct weight of this	
phenomenon.	
treatment_effect_on_mortality[1] =	dmnl
Single_Loc[1]+All_delayed[1]+Closest_Neighbour[1]*Treatment_effectiveness	
+mortality_from_cleaner_fish[1]	
treatment_effect_on_mortality[2] =	
Single_Loc[2]+All_delayed[2]+Closest_Neighbour[2]*Treatment_effectiveness	
+mortality_from_cleaner_fish[2]	
treatment_effect_on_mortality[3] =	
Single_Loc[3]+All_delayed[3]+Closest_Neighbour[3]*Treatment_effectiveness	
+mortality_from_cleaner_fish[3]	
treatment_effect_on_mortality[4] =	
Single_Loc[4]+All_delayed[4]+Closest_Neighbour[4]*Treatment_effectiveness	
+mortality_from_cleaner_fish[4]	
Treatment_effectiveness(t) = Treatment_effectiveness(t - dt) + (Increase_in_eff -	dmnl
Decrease_in_effectiveness) * dt	
INIT Treatment_effectiveness = 1	
INFLOWS	Dmnl/days
Increase_in_eff = 0	
OUTFLOWS	
Decrease_in_effectiveness = effect_gap[1]+effect_gap[2]+effect_gap[3]+effect_gap[4]	
	_1

treatment_indicator[Location] = MAX(0;	dmnl
lice_pr_fish*fraction_female_lice/allowed_lice_pr_fish)	
treatment_initiation[1] = treatment_switch* (IF(treatment_indicator[1]>0,9) THEN PULSE	dmnl
(1; 1,) ELSE 0)	
treatment_initiation[2] = treatment_switch* (IF(treatment_indicator[2]>0,9) THEN PULSE	
(1; 1,) ELSE 0)	
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	Dmnl/days
Treatment_regularity[2] = Treatments_used[2]/treatment_intervals	
Treatment_regularity[3] = Treatments_used[3]/treatment_intervals	
Treatment_regularity[4] = Treatments_used[4]/treatment_intervals	
treatment_switch = 1	Dmnl
$Treatments_used[1](t) = Treatments_used[1](t - dt) + (treatment_increase[1]) * dt$	Dmnl
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	
INFLOWS:	Dmnl/days
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	

Appendix C – Fish Weight table from Osland Havbruk and Skretting AS

20		61.5	130.1	336.6	478.7	614.2	741.0	865.8	986.4	1104.2	1220.3	1335.9	1447.8	1560.8	1670.8	1778.1	1888.1	1996.1	2108.2	2212.4	2321.4	2429.1	2692.3	2956.0	3222.6	3484.2	3752.1	1016.6	1277.9	1535.9	1805.1	5057.4	5322.4	5585.8	5847.6
19		65.4	0.161	354.9	503.4	642.1	774.6	8.668	022.2	144.2	1260.8	1376.2				1831.7	1939.4	2050.3	2159.1	2265.7	2377.4	2487.7	2757.3					4077.1	1342.3	1604.2	1877.4	133.5	402.5	6.6998	5935.7
18		67.5	0.661	97.9			795.5	924.1		171.7	_				1752.2 1				2198.0 2:				2790.3 2	10	3330.1 3.	3600.4 33		126.0 40	1394.4 43	1659.5 4/	1921.2 41	195.2 5	451.2 5	721.0 5	5989.1 59
17			203.1						,,	.,									2217.6 21									•	_	4	5			5755.2 57.	
16									.,														2815.4					•	4	,	~	9 5226		_	_
										7 1192.7															3370.0			Ī			4		1 5516.7		1 6061.1
15	30	.99	202	375.	530.0	675.	812.	940.6	1068.6	1192.7	1310	1430	1545.	1661									2832	3100	3370.0	3643.6	3912.1	4188.0	4447.2	4715.	4995.2	5257.6	5533.	5789.	6061.1
14		64.2	198.4	369.8	524.6	667.2	802.6	932.3	1059.1	1182.1	1302.6	1421.8	1536.4	1651.4	1767.9	1881.4	1992.0	2105.9	2217.6	2327.2	2442.0	2547.6	2823.8	3100.4	3370.0	3632.8	3912.1	4175.5	4447.2	4715.4	4980.3	5257.6	5516.7	5789.7	6061.1
13		61.5	192.7	361.2	513.8	655.5	790.8	918.6	1043.6	1168.2	1287.2	1405.0	1522.8	1636.7	1752.2	1864.7	1980.2	2087.2	2198.0	2313.4	2420.3	2532.5	2807.0	3081.9	3350.0	3622.0	3888.9	4163.1	4433.9	4701.4	4965.5	5241.9	5516.7	5772.4	6043.0
12		58.7	186.0	350.7	500.4	640.2	772.4	8399.8	1025.2	1147.6	1264.5	1384.3	1500.4	1617.4	1731.5	1842.7	1956.7	2068.7	2178.4	2286.1	2398.7	2510.0	2782.0	3054.5	3330.1	3600.4	3865.7	4138.3	4407.6	4673.4	4950.7	5210.7	5483.8	5755.2	6025.0
11		55.6	178.5	338.6	484.4	621.5	752.1	878.7	1001.2	1124.0	1242.2	1359.9	1473.9	1588.8	1700.9	1815.5	1927.9	2038.1	2146.2	2259.0	2370.3	2480.3	2749.1	3027.3	3290.6	3568.4	3831.3	4101.5	4368.3	4645.6	4906.6	5179.7	5451.2	5721.0	5989.1
10		52.6	170.3	325.8	467.5	9.709	730.1	855.6	7.776	1094.4	1213.1	328.0	443.5	556.1	1670.8	778.1	893.7	005.0	2114.5	225.6	335.3	443.6	716.5	982.5	251.6	3526.0	3797.2	6.490	1329.3	1604.2	862.8	133.5	402.5	6.699	5953.4
6			161.9						_		_					_			2070.9								<u>"</u>	4	•	1549.5 4	4	5 67.7 5	354.3 5		5882.7 5
60			153.6 1					801.5		-	1146.4 11	.,																Ī	1227.1 42	,	•	61	_	-	
7					Ī																								•		,		61		
9										1001.0								7 1875.0				5 2302.1				3361.5			Ī	•	_	_	8 5212.		4 5743.6
			137.2			512									1509.8							2254.5	2513.6		3035.7	3301.8	"	3829.1	4090.3	4350.0	4608.1	4879.	5134.8	5405.	5658.4
2		39.1	129.3	254.0	373.2	488.7	601.9	713.7	822.7	931.9	1039.0	1147.6	1254.9	1360.8	1465.4	1568.7	1675.7	1782.1	1887.9	1987.0	2097.4	2201.2	2461.6	2718.8	2981.7	3243.0	3502.8	3761.0	4017.6	4272.6	4539.6	4792.3	5058.5	5308.9	5574.3
4		37.0	122.2	240.7	355.8	467.3	577.2	686.5	793.8	899.1	1005.4	1110.5	1214.3	1320.7	1422.2	1527.1	1631.3	1734.8	1837.7	1940.0	2041.7	2149.1	2403.3	2662.4	2919.9	3175.8	3430.2	3694.0	3946.0	4209.1	4458.8	4721.1	4968.5	5230.0	5491.5
m		34.9	115.4	228.8	339.2	446.9	553.6	660.4	763.5	867.4	972.9	1074.6	1178.5	1281.8	1384.4	1486.5	1587.9	1688.7	1794.2	1894.1	1993.3	2098.3	2353.5	2607.2	2859.3	3119.2	3369.1	3628.2	3875.7	4134.1	4392.5	4650.9	4894.6	5152.2	5409.8
2		33.1	109.1	217.5	323.3	428.5	532.5	635.2	738.8	839.3	941.4	1042.9	1143.7	1244.0	1347.6	1446.9	1550.3	1648.7	1751.7	1849.2	1952.0	2054.7	2304.6	2560.7	2808.3	3063.6	3318.9	3574.3	3818.1	4072.6	4327.2	4581.7	4836.2	5090.8	5345.3
1		31.6	103.7	207.3	310.1	412.2	513.7	614.6	714.9	814.5	913.6	1015.1	1113.3	1214.5	1315.7	1412.7	1513.6	1614.5	1715.4	1816.3	1917.2	2018.1	2263.5	515.0	2766.5	3018.1	3269.6	521.1	8783.9	1036.2	1288.4	1540.7	1792.9	5045.2	5297.5
	dager	30	100	200	300	400	200	900	200	300	006	1000	.,		1300 1	1400	1500 1		1700 1	1800 1	1900	2000	2250 2		2750 2	3000	3250 3	3500 3	3750 3	4000 4	4250 4	4500 4	4750 4		5250 5
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Appendix D - Picture of the model

