Network models of live fish movements and disease spread in Scottish aquaculture

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BY

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Declaration

I declare that the thesis has been composed in its entirety by me. Except where specifically acknowledged, the work described in this thesis has been conducted by me and has not been submitted for any other degree.

Signature: ______________________________

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Abstract

The Scottish salmon industry is facing challenges in the control of aquatic infectious disease, as is the case in other countries such as Chile and Norway. Disease outbreaks can have an enormous economic impact and possibly affect wild fish populations. Disease transmission in an aquatic environment is complex and there are several transmission routes (vertical transmission, natural reservoirs, hydrodynamic transmission and long-distance movements). Effective control methods such as vaccines are not available in all cases and therefore disease prevention remains a priority.

In livestock, epidemiological network models have been proven to be a highly useful tool to investigate the role of different transmission routes on the course of epidemics and have the potential to provide the same utility for aquatic networks. Understanding the complex contact network will result in more effective disease prevention, surveillance systems and control strategies. The aim of this thesis was to investigate the Scottish live fish movement network and its consequences for pathogen transmission between farms in order to develop and optimize control strategies for epidemics.

The main objective of chapter 3 was to investigate the effect of different fallowing strategies on the spread of diseases with different transmission properties. A network model was constructed that included both local transmission and long-distance transmission. The basic structure of this network was a ring model where neighbours within a management area could infect each other and non-local transmission occurred at random. The results showed that when long-distance transmission was under reasonable control in comparison with local transmission risk, synchronized fallowing at the management area level was potentially a highly effective tool in the control of infectious diseases.

Chapter 4 presents a detailed description of the number of live fish movements and their timing for Atlantic salmon (*Salmo salar*) in Scottish aquaculture. For this, movement records from 2002 to 2004 were provided by Marine Scotland, Aberdeen. Salmon are anadromous and have a freshwater (FW) and seawater phase (SW). Scottish live fish movements can be divided in FW-FW, FW-SW, SW-SW, SW-FW and "other" movements. The latter are mainly movements from and to research sites. This study showed that the contact structure and timing of live fish movements are seasonal and differ largely between production phases. Disease control measures should take these differences into account to optimize their strategies.

In chapter 4, live fish movements were shown to be seasonal; therefore in chapter 5 the main aim was to quantify the effects of seasonality of live fish movements on the course of epidemics. The results showed that the sequence of salmon movements is important for the course of an epidemic. Seasonality is important when local transmission is higher than 0.05 per contact per week and when the movements are not clustered and when movements do not occur in a specific order based on the specific assumptions made in this model.

In conclusion, this thesis described the complex live fish movement structure of salmon in Scotland and showed that biosecurity in SW farms is good but could be further improved if all management areas apply synchronized fallowing. The results of this study suggest that biosecurity between freshwater sites could be improved by the application of a system similar to management areas in SW farms.

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CHAPTER 1. General introduction

Aquaculture and fisheries are important for the incomes and food supply of millions of people worldwide. Capture fisheries and aquaculture produced together 145.1 million tonnes of fish in 2009 (FAO, 2010). The proportion of fish supplied by aquaculture has increased considerably in the last 50 years; aquaculture was responsible for 38% of this total in 2009 while the contribution to the supply of fish from capture fisheries has decreased substantially (FAO, 2010). However, it appears that the growth of aquaculture has peaked (FAO, 2010).

Fish is a good source of animal protein and the majority of aquaculture production is used for human consumption (81%) followed by the manufacture of fishmeal and fish oil. Human consumption of fish has increased enormously in the last 40 years; in 1970 a worldwide average of 0.7 kg of fish was consumed per capita per year whereas in 2006 the average worldwide consumption had raised to 7.8 kg fish per capita per year (FAO, 2008). Consequently, the proportion of animal protein intake derived from fish and fish products has increased during the last 20 years and is now 15.7% (FAO, 2010).

White leg shrimp (*Penaeus vannamei*) is the most valuable cultured species worldwide (USD 9 billion), while Atlantic salmon (*Salmo salar*) is the second most valuable cultured species, grossing an estimated USD 7.2 billion in 2008 (FAO, 2008). The salmon production derived from aquaculture worldwide was 1,440,000 tonnes in 2009 (FAO, 2009).

Scotland is one of the main producers of Atlantic salmon worldwide together with Norway and Chile. The total Scottish finfish culture production was approximately 160,000 tonnes in 2010, of which 154,000 tonnes was of salmon (MSS, 2011a). The worldwide retail value of Scottish salmon production was estimated over £1 billion

(SSPO, 2011). Salmon production is important for the Scottish economy as it offers approximately 850 full-time jobs and 100 part-time jobs in remote areas (Highlands and Islands) where there are few alternative employment opportunities (SSPO, 2011; MSS, 2011a).

Chilean salmon production underwent an enormous period of growth from the late 1990s (Gallardo, 2010) and in 2006 the production was comparable with the Norwegian salmon production. In 2006, these countries together accounted for approximately two thirds of the worldwide Atlantic salmon production (below, salmon refers to Atlantic salmon). However, due to recent disease epidemics the production of salmon in Chile has decreased substantially (by approximately 40% in 2009) (FAO, 2010; Gallardo, 2010).

It is not only Chilean salmon production that is vulnerable to disease outbreaks: Aquaculture populations worldwide are under threat (OIE, 2009; MSS, 2010b). Fish suffering from disease can have a reduced appetite or growth; this results in reduced production and profitability (Murray and Peeler, 2005). Furthermore, increased mortality rates are seen on the affected farms (OIE, 2009). Fish that die from disease are not allowed for human consumption (EU Regulation No 1774/2002, 2002). The disease that affected the Chilean salmon production was infectious salmon anaemia (ISA, box 1). In Scotland, there have been two relatively recent ISA outbreaks (1998/1999 and 2009/2010). The cost to eradicate the first epidemic in Scotland has been estimated at £20 million (Hastings, et al., 1999). ISA cost the salmon farmers £6.9 million in Norway and £8.8 million in Canada in 1999 (Cipriano and Miller, 2003). ISA is not the only disease with the potential to cause substantial economic losses: for example, the costs of sea lice infections (*Lepeophtheirus salmonis,* box 2) on farmed salmonids worldwide have been estimated around €305 million per year (Costello, 2009b).

Box 1: Infectious salmon anaemia

Infectious salmon anaemia (ISA) is caused by the orthomyxovirus, infectious salmon anaemia virus (ISAv). ISA has been reported in Norway, Scotland, Ireland (in rainbow trout), USA, Canada, the Faroe Islands and Chile. This disease mainly affects farmed Atlantic salmon, which are exposed to seawater or kept in seawater (see section 1.1). In addition, subclinical infections are observed in rainbow trout and brown/sea trout. These species could act as carrier species (i.e. species which present no clinical signs after infection with the pathogen and are capable of transmitting pathogens to other fish) (Snow et al., 2001; Nylund and Jakobsen, 1995) . Daily mortalities are between 0.1% (Hammell and Dohoo, 2005) and several percent per pen and can increase over time; cumulative mortalities can rise up to 90% in severe cases (Godoy et al., 2008, Stagg et al., 2001). Usually ISA starts in one net pen and it can take several months before the disease develops in other net pens (OIE, 2009).

Box 2: Sea lice

*Sea lice (*Lepeophtheirus salmonis *and* Caligus *Spp.) are parasites that affect both wild and farmed salmon in marine waters. The life cycle of sea lice is complicated: lice go through several stages before reaching the adult stage (Boxaspen, 2006). Sea lice can cause skin lesions or open wounds (Heuch et al., 2005). These lesions result in reduced growth and reduced feed conversion efficiency. Sea lice are prevalent in the United Kingdom, Ireland, the Faeroe Islands, Norway, Chile and the USA (Costello, 2009b).*

Disease outbreaks not only result in reduced profitability; health problems also affect the welfare of the fish (Turnbull and Kadri, 2007) and welfare issues of farmed species are becoming more important for consumers (Huntingford, et al., 2006; Ashley, 2007). Moreover, pathogen build-up in fish farms may lead to transmission of pathogens to wild fish populations (Wallace, et al., 2008, Middlemas et al., 2010) as wild fish can acquire infection when they are in vicinity of fish farms (Uglem, et al., 2009). This in turn can cause declines in wild fish (salmonids) populations (Johansen et al., 2011).

Indeed, the decline of wild salmonid populations, especially near fish farms, has been linked to disease outbreaks in salmon farms (Morton et al., 2005; Krkošek et al,. 2008). For these reasons, disease control in aquaculture is important.

1.1. Aquaculture in Scotland

Scottish finfish production includes Atlantic salmon (*Salmo salar*), rainbow trout (*Oncorhyncus mykiss*), brown trout/sea trout (*Salmo trutta*), Arctic charr (*Salvelinus alpinus*), cod (*Gadus morhua*) and halibut (*Hippoglossus hippoglossus*). Atlantic salmon (154,000 tonnes per year), rainbow trout (5100 tonnes per year) and brown/sea trout (53 tonnes per year) are the most important species for the Scottish finfish culture by both volume and value (MSS, 2011a). This thesis will mainly focus on salmon, as it dominates the Scottish production in terms of biomass.

From 1987 salmon production has increased from 12,700 to 154,000 in 2009 (see figure 1.1), and a further rise is expected for 2011(MSS, 2011) despite the number of Scottish production sites having decreased over the period (FRS, 2008; MSS, 2010c) (figure 1.2). This implies a higher total production per site.

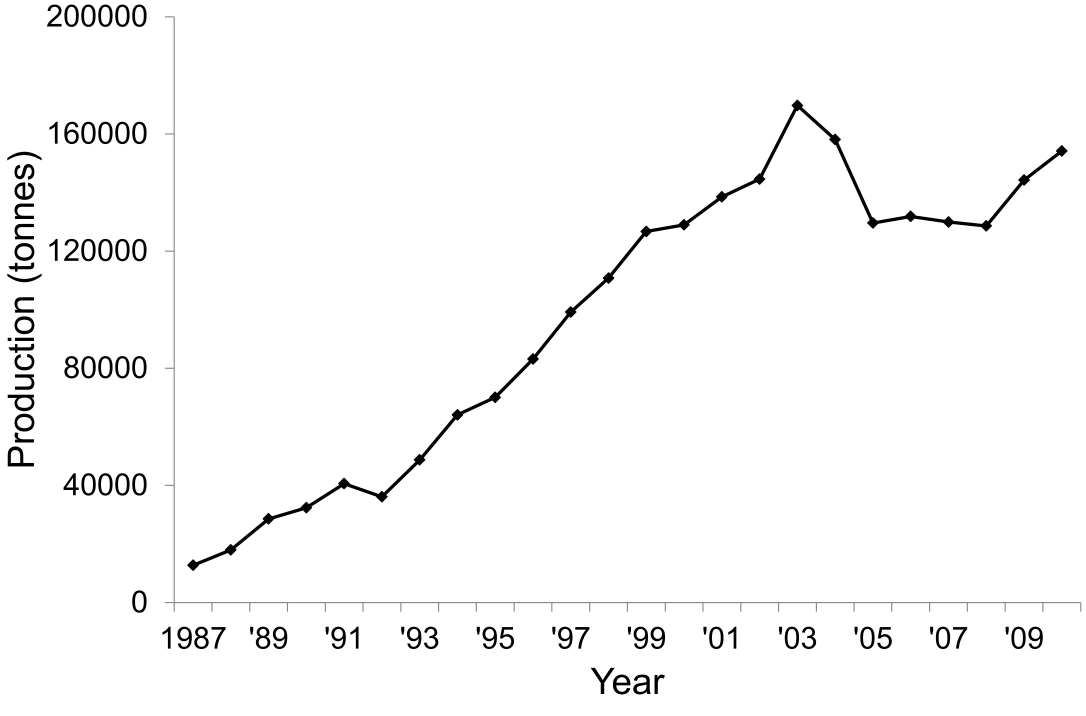

Figure 1.1. The total Scottish salmon production (tonnes) per year.

Salmon are anadromous and live in two environments: first, farmed salmon are reared in freshwater fisheries: ova (i.e. salmon eggs) are fertilized and hatched in hatcheries. Next, salmon go through the fry and parr stage in freshwater cages, tanks or raceways until they reach the smolt stage. The complete freshwater phase takes twelve to sixteen months. Smolts are then moved to marine waters, where they are kept in tanks or cages and where they will achieve their harvest size (mean 4.7 kg) after approximately another eighteen months. When salmon reached their harvest size they are moved to harvest stations or processing plants (MSS, 2011a).

Scotland is divided into five production areas; in 2009 the highest production areas for ova and smolts were Northwest, West and the Western Isles. The highest production areas for growers were Shetland, Southwest and Northwest of Scotland (MSS, 2011a). There were 105 freshwater sites and 253 seawater sites for salmon production in Scotland in 2009. Both numbers have decreased substantially in the last 10 years (figure 1.2). The main reason for this is that control strategies of infectious diseases such as ISA are aimed at limiting potential dangerous contact (such as shipping of live fish) between farms (Joint Government/Industry Working Group, 2000); this resulted in fewer but larger farms with greater separation between them. Large farms physically separated over several geographical areas could reduce the speed of transmission of pathogens (Salama and Murray 2011) as separation can act as a firebreak, especially when contact such as shipping of live fish between those areas is limited (Green, 2010).

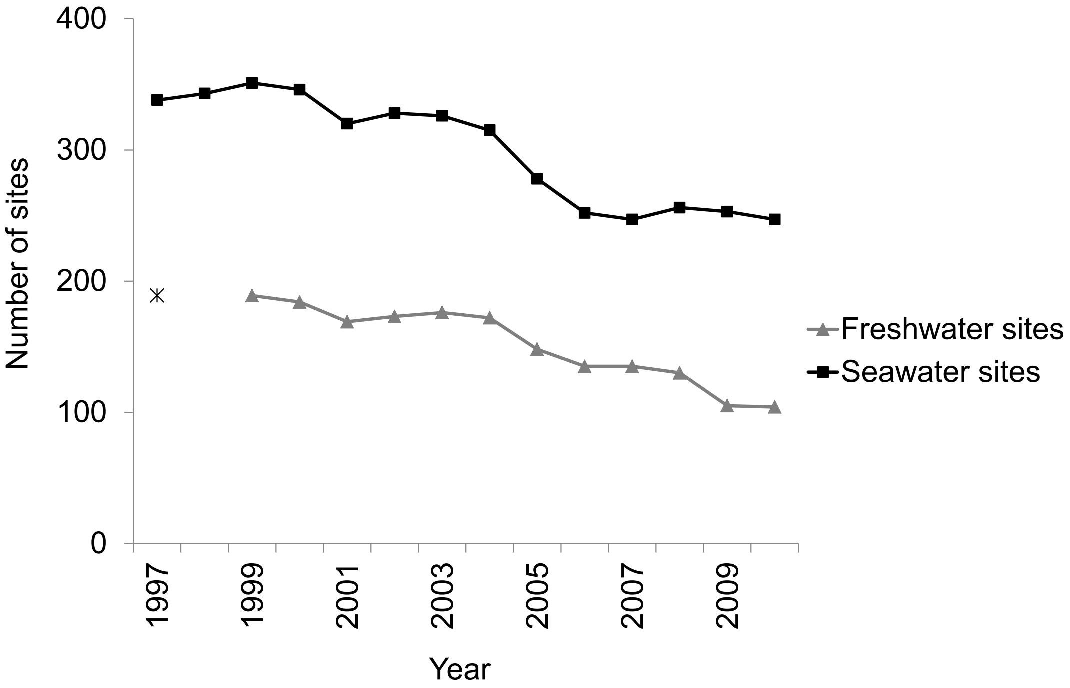

Figure 1.2. The number of active Scottish salmon sites per year.
*** No data available for these years for freshwater sites.**

1.2. Aquatic diseases

The course of an epidemic is complex and depends on many factors, such as the environment, pathogen and host (Snieszko, 1974; Reno, 1998; Turnbull, et al., 2011), (see figure 1.3). For example water temperature can play an important role in the development of clinical symptoms or transmission rates of aquatic pathogens (OIE, 2009; MSS, 2010b). Outbreaks of bacterial kidney disease (BKD, box 3), for example, usually occur in the spring when water temperatures are rising (MSS, 2010b). In addition, it is thought that water temperature is the most important factor for the development of clinical infectious haematopoietic necrosis (IHN, box 4). Outbreaks of clinical diseases of IHN mostly occur in young fish when the water temperature is between 8°C and 15°C (OIE, 2009). Water temperature does not only affect the pathogenicity and virulence of pathogens, low water temperatures also have an adverse effect on the adaptive immune system of fish (Le Morvan, et al., 1998; Rimstad and Mjaaland, 2002).

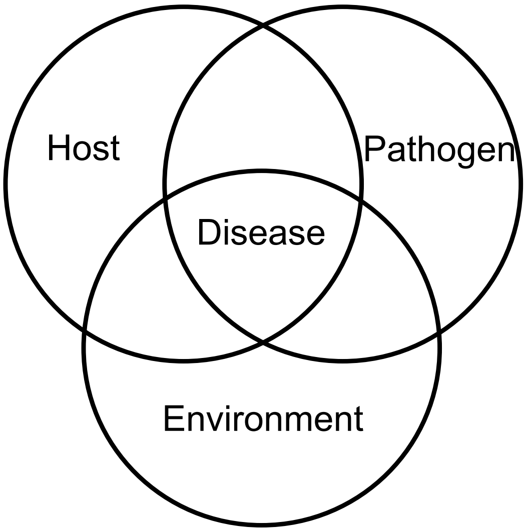

Figure 1.3. The three-circle diagram from Snieszko (1974). Only when the host is susceptible to a virulent pathogen in a suitable environment will disease occur.

Box 3: Bacterial kidney disease

Bacterial kidney disease (BKD) is a chronic disease in farmed salmon and can cause severe economic losses in salmon seawater farms. In addition, rainbow trout are also affected, but the symptoms are in general less severe compared with Atlantic salmon (Murray, et al., 2011). The agent responsible for causing BKD is Renibacterium salmoninarum. *All age groups are affected, but the disease is rare in very young fish (OIE, 2009; MSS, 2010b). Cumulative mortalities can reach up to 40% in Atlantic salmon in severe cases (CEFAS, 2011).*

Box 4: Infectious haematopoietic necrosis

This disease affects mostly salmon and trout, but all salmonid species are affected. It is caused by infectious haematopoietic necrosis virus (IHNV), which is a rhabdovirus (OIE, 2009; MSS, 2010b; CEFAS, 2011). Economic losses are observed the most in freshwater farms. The life stages that are mainly affected are fry and small fingerlings; the younger the fish the more susceptible they are (OIE, 2009; MSS, 2010b). Acute outbreaks can cause mortality rates up to 90-95% and 100% in fry. Daily mortalities exceed several percent of the population. Fish that survive an outbreak can become carriers of the virus (OIE, 2009).

Another factor that plays an important role in the development and severity of clinical diseases is the strain of the pathogen, as different pathogen strains can vary largely in their pathogenicity and virulence, for example in pancreas disease (PD, box 5) (Rodger and Mitchell, 2007). ISA strains have been found that are both virulent (Stagg, et al., 2001; Mardones, et al., 2009; OIE, 2009) and non-virulent (Nylund, et al., 2007). Moreover, different pathogens often affect specific age groups, life stages (for example fry or smolt), environments (i.e. freshwater or seawater) or species (OIE, 2009; MSS, 2010a; MSS, 2010b).

Box 5: Pancreas disease

Pancreas disease (PD) is caused by a salmonid alpha virus and has had a major economic impact in Norway, Ireland and Scotland (Rodger and Mitchell, 2007). Scottish salmon farmers have identified PD as the most important (biomass) loss caused by a disease (MSS, 2009). The most significant losses are seen when salmon are between 3.0 and 4.5 kg (MSS, 2009). This disease mostly affects salmon on their first year at sea. Mortality rates differ significantly from pen to pen, from 5% for a whole production cycle to as high as 40% in three to four months (Rodger and Mitchell, 2007). In Scotland, outbreaks normally occur between August and October (MSS, 2009).

Presence of a pathogen alone is often not enough to cause symptoms and additional factors are needed to result in clinical disease (Rimstad, 2011). Clinical infectious pancreatic necrosis (IPN, box 6) is often seen during week 5 to 19 after smolt transfer (Soares et al., 2011). The increase in mortalities during this period is most likely to be stress related, caused by sea transfer and change of environment (FRS, 2003).

Box 6: Infectious pancreatic necrosis

IPN is caused by infectious pancreatic necrosis virus (IPNV); this virus belongs to the aquatic birnavirus family (Wolf, 1988). IPNV is a very robust virus and affects a wide range of species in both fresh and seawater farms (MSS, 2010a). The virus causes clinical symptoms mainly in salmon in fry (Smail, et al., 1992) or during the first weeks after sea transfer (Bruno, 2004a; Soares, et al., 2011). Clinical signs of IPN include high mortality rates and reduced growth (Damsgård, et al., 1998). In 2003, over 80% of the Scottish marine farms were found positive for IPNV and 12 % of freshwater farms; however prevalence of IPN differed between regional areas. At most sites clinical signs were absent (Murray, 2006a). Daily mortality rates are between 0.5 and 1.0% (Soares, et al., 2011).

1.2.1. Notifiable diseases and other important diseases

Diseases can be classified into non-notifiable diseases and notifiable diseases. Notifiable diseases are diseases that have the potential to cause major economic losses or have a detrimental effect upon wild fish populations. When a farmer or veterinarian suspects one of these diseases, they are obliged to report this to the fish health inspectorate (MSS, 2010b; MSS, 2011b). The diseases classed as notifiable are listed in Part II, Annex IV of Directive 2006/88/EC (MSS, 2010b). Some diseases, for example IPN, are so widespread that the benefits of controlling those diseases are smaller than the negative effects of the control strategies such as movement restrictions have on the industry. In the following sections, important diseases for Scottish aquaculture are discussed in detail.

In cases where an outbreak of a notifiable disease occurs, movement restrictions are applied to prevent further spread. The following fish diseases are notifiable in the UK: infectious salmon anaemia (ISA); bacterial kidney disease (BKD); viral haemorrhagic septicaemia (VHS); infectious haematopoietic necrosis (IHN); gyrodactylosis caused by the parasite *Gyrodactylus salaris*; epizootic haematopoietic necrosis (EHN); epizootic ulcerative syndrome (EUS); spring viraemia of carp (SVC) and koi herpes virus (KHV) (MSS, 2010b). All diseases are notifiable in all species but EHN does not cause clinical disease in salmon. However, salmon might be a carrier species for EHN. Salmon are not susceptible to EUS, SVC and KHV (OIE, 2009). Consequently, these diseases will not be discussed in this chapter. IHN and *G. salaris* are exotic in the UK but are prevalent in other European countries (MSS, 2010b; CEFAS, 2011).

Gyrodactylosis (box 7) has caused major losses in Atlantic salmon in Northern European countries (OIE, 2009; MSS, 2010b; CEFAS, 2011). It is identified as one of the biggest potential threats for Atlantic salmon populations in the UK (Peeler and Thrush, 2004), as Scottish salmon are highly susceptible to this parasite (MSS, 2010b; CEFAS, 2011). In order to keep the UK free of *G. salaris*, susceptible live fish from areas that are affected with *G. salaris* are prohibited from being moved into the UK (MSS, 2010b).

Box 7 Gyrodactylosis.

Gyrodactylus salaris *is a parasite that causes gyrodactylosis. The parasite gives birth to live young and has a direct life cycle.* G. salaris *affects mainly Atlantic salmon, but rainbow trout and brown trout are known to be affected as well (OIE, 2009; MSS, 2010b). Mortalities are normally seen in fry and parr, but all stages are susceptible. Mortality rates up to 100% are seen in fry. The average mortality rate is 85% in farmed Atlantic salmon in untreated farms. In other susceptible species the prevalence is lower, around 10% or not observed at all (OIE, 2009).*

IHN is prevalent in North America, Europe and Asia (OIE, 2009), but has never been detected in the UK. However, were it to spread to the UK it has the potential to cause significant economic losses for the UK. The fish health inspectorate inspects farms with species susceptible to IHN annually. In addition, every two years samples of internal organs from 30 fish per farm are collected and screened for IHNV. This is important in order to maintain IHN-free status in the UK (MSS, 2010b).

There have been two outbreaks of ISA in Scotland in the past few years, the first occurring in 1998/1999 (Stagg, et al., 2001; Murray, et al., 2002) and the last one in 2009/2010 (Murray, et al., 2010). Both outbreaks only affected seawater farms. It is believed that ISA is now eradicated in Scotland, although final confirmatory testing was still being completed at the time of writing. Other countries, such as Norway (Rimstad and Mjaaland, 2002) and Chile (Mardones, et al., 2009) have been unable to eradicate the disease.

Between 1990 and 2002, there were 68 cases of BKD in Scotland. Of these cases, 27 were recorded in Atlantic salmon and the remaining cases (41) were recorded in rainbow trout (Bruno, 2004b). During recent years the prevalence of BKD in Scotland has been low in both salmon and rainbow trout farms in relation to the prevalence during 1990 to 2002 (MSS, 2010b).

It is not only notifiable diseases that can cause substantial losses for the Scottish aquaculture. Infectious pancreatic necrosis (IPN), pancreas disease (PD), furunculosis (box 8) and sea lice (both *Lepeophtheirus salmonis* and *Caligus elongatus*) are not notifiable diseases but all have the ability to cause significant losses to Scottish salmon farms (MSS, 2010a). For example, IPN accounted for 10% of the total biomass losses during 2001 to 2006 and another 10% of the losses were suspected to be caused by IPN according to Scottish salmon farmers. IPN was a notifiable disease until 2005, but due to the high prevalence (>80% in marine sites, Murray, 2006a) in Scotland, IPN is no longer controlled. IPN is not registered anymore as an OIE-listed disease (OIE, 2009). In addition to IPN, sea lice and pancreas disease cause substantial losses according to Scottish salmon farmers. Sea lice accounted for over 5% of the biomass losses while more than 45% of the biomass losses were suspected to be caused by PD (MSS, 2009).

1.3. Disease challenges

Box 8: Furunculosis

Furunculosis is caused by a gram-negative bacteria Aeromonas salmonicida *and has been resolved as a problem for salmon aquaculture in the UK due to a successful vaccination programme. Furunculosis affects all life stages and can be either chronic or acute. In the acute stage, fish show almost no symptoms and there is a sudden increase in the mortality rate. While in the chronic state the symptoms are more severe. Mortalities differ significantly from farm to farm and vary from 10% to 50% without treatment (DIPNET, 2007; MSS, 2010a).*

Aquaculture is important for Scotland; the industry had an enormous growth in the last 20 years (figure 1.1). Scottish salmon aquaculture is potentially vulnerable to disease outbreaks. Pathogens can transmit between farms by horizontal transmission such as live fish movements (Murray, et al., 2002; Murray and Peeler, 2005), wild reservoirs (Uglem, et al., 2009) and hydrodynamic contact (Jonkers, et al., 2010) or vertical transmission (i.e. from parent to egg) (OIE, 2009).

It is important to understand the different pathways of pathogen transmission in order for governmental organisations to optimise disease control strategies. If a disease is persistent on a farm or if farms get re-infected, for example by a wild reservoir, then farm-level approaches to control the disease should be considered. If a disease is not persistent i.e. previous infection is not a risk factor for a disease and the disease spreads easily to other farms, then control strategies at management-area level, or even wider, should be implemented (Murray, 2006b). In section 2.1, the ecology of diseases is discussed.

There are several methods available to control pathogens and prevent large epidemics, for example, antibiotics and vaccines are available for some pathogens (MSS, 2010b; OIE, 2009; CEFAS, 2011). Treatments are not always 100% effective due to resistance of the pathogen to the treatment (Murray, 2011). In section 2.2, possible control strategies are discussed.

In addition to antibiotics and vaccines, fallowing is thought to be an effective disease control strategy that is often used to break the disease cycle (Wheatley, 1995). However, prior to this thesis, there have been no large-scale studies performed to investigate the effectiveness of this strategy. In chapter 3, the effectiveness of different fallowing strategies is investigated.

Movement of live animals has been shown to play a big role in the transmission of diseases for varied species (Murray et al., 2002; Gibbens et al., 2001; Green et al., 2006a). Network models are a valuable tool to give a quantitative prediction of the consequences of live fish movements and can be used to assess the effects of disease control measures. More details on the use of mathematical models to study disease transmission between farms are given in section 2.3.

Livestock movement data showed that there are substantial differences in the contact structure between production phases and these differences are likely to affect the course of epidemics (Bigras-Poulin et al., 2006; Bigras-Poulin et al., 2007; Natale, et al., 2009; Lindstrom et al., 2010). However, prior to this thesis there have been no studies performed to investigate possible differences of the contact structure between production phases in salmon aquaculture. In chapter 4, the contact structures of the different salmon production phases are discussed alongside their impact on disease transmission. In chapter 5, seasonality patterns and their effects on disease transmission are discussed.

1.4. Project outline

The main objective main objective of this thesis was to investigate the Scottish live fish movement network and its consequences for pathogen transmission between farms in order to develop and optimize control strategies for epidemics. In figure 1.4 an overview of the chapters and how they are linked is shown.

CHAPTER 2: The use of mathematical models in the control and prevention of pathogen spread in the Scottish salmon industry.

Understanding how diseases are spread between farms is the first step towards developing effective control strategies. In this chapter, we discuss the ecology of aquatic diseases that have the potential to cause severe losses to the Scottish aquaculture. Next, different methods that could contribute to the control and prevention of epidemics are discussed. In some cases, control strategies other than culling all fish on a site are not available. Therefore, the emphasis should be on preventing epidemics. With the use of mathematical models it is possible to investigate the importance of transmission routes. This chapter ends, with a review about the use of mathematical models in exploring the course of possible epidemics.

CHAPTER 3: The effectiveness of fallowing strategies in disease control in salmon aquaculture assessed with an SIS model.

Scottish marine sites are located in management areas, where agreements are made about live fish movements, disease treatments and fallowing times. In this study the effectiveness of these management areas combined with three different fallowing strategies (synchronised fallowing, unsynchronised and partial synchronised at the management-area level) using a stochastic SIS model, is discussed. All seawater farms were simulated to infect two neighbouring farms within the same management area and long distance movements occurred at random, within and between management areas. The results showed that when live fish movements are under reasonable control, synchronized fallowing is a highly effective tool to control epidemics. This chapter was published in Preventive Veterinary Medicine (2011, 98:64-73).

CHAPTER 4: Seasonality and heterogeneity of live fish movements in Scottish fish farms.

In chapter 3, live fish movements between sea sites occurred at random. Data that showed how often and when these movements occurred per production phase were not available. In this study we investigated the contact structure and seasonality patterns per production phase of live salmonid movements. Movement records collected by the Fishery Health Inspectorate of Marine Scotland, Aberdeen from 2002 to 2004 were used. Data analysis demonstrated that contact structure and seasonality patterns differed between production phases. Disease control strategies and disease models should take these differences between production phases into account. This study was published in Diseases of Aquatic Organisms (2011, 96: 69–82).

CHAPTER 5: Seasonality in live fish movements and their effects on epidemics.

In chapter 4 we showed that salmon live fish movements show seasonal patterns. These seasonal patterns possibly have an effect on the course of an epidemic. In this chapter we examined the effects of seasonality on epidemics using a SIR model; the model structure was similar to the one described in chapter 3. Three different models were developed: the real-life network with the original order of movements (1), the real-life network in which the movements between freshwater sites and freshwater to seawater sites occurred with a random reordering (2) and a simulated network model (3). Seasonality had an effect when local transmission was high and movements occurred at random or when there was no clustering.

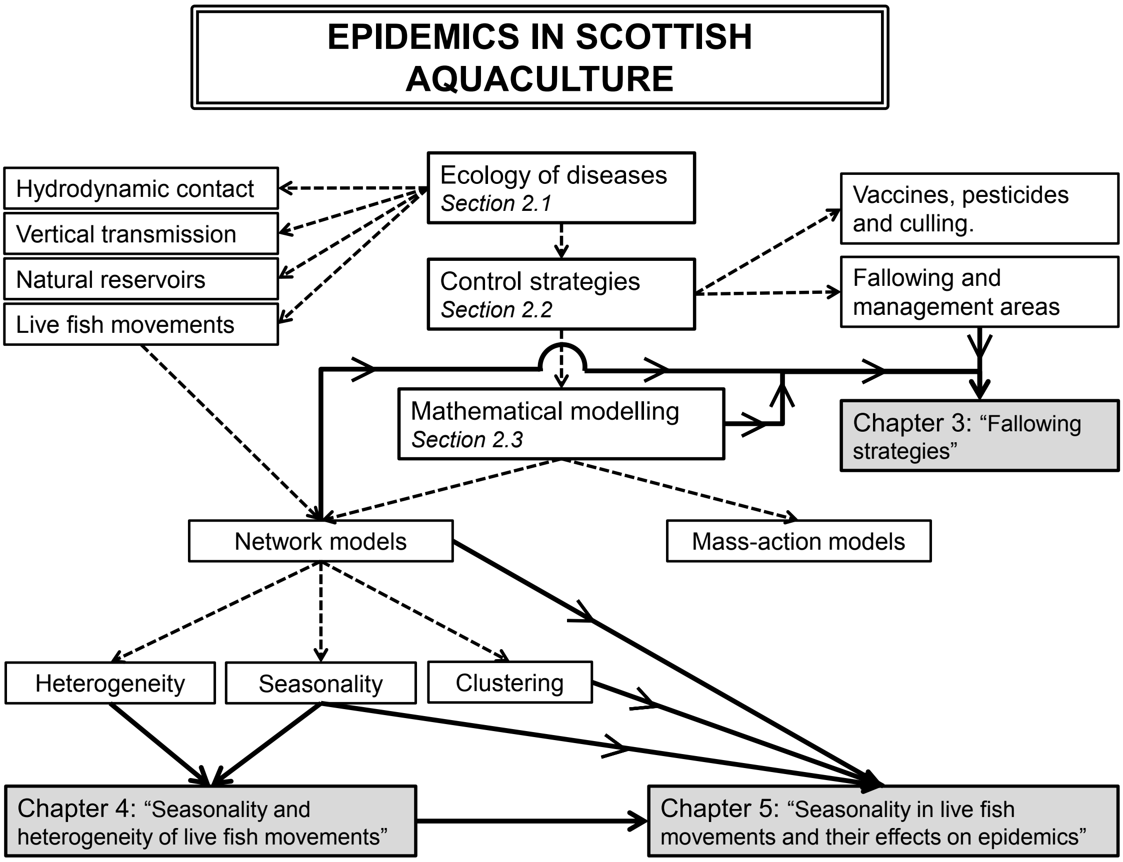

Figure 1.4. An overview of all the topics in this thesis and how these topics are linked. The dashed arrows show how topics are linked, the black lines show how these topics result in the research chapters.

This thesis consists of one literature review (chapter 2) and three scientific papers (chapter 3 to 5). Chapters 3 and 4 are already published and chapter 5 is readied for publication in a peer-reviewed journal. In chapter 6, the main conclusions of this thesis are discussed. All chapters were written by me, Marleen Werkman, with advice and proofreading by the co-authors (Dr. Darren Green, Dr. Alexander Murray, Prof. James Turnbull and Lorna Munro). The data used in chapters 4 and 5 were collected and edited by me and Lorna Munro from Marine Scotland Science, Aberdeen.

In addition, I was a co-author on two further papers, for which my contributions were collecting and processing the data and assisting with the editing of the manuscripts. These papers are included as appendices.

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CHAPTER 2. Disease transmission routes, control strategies and the use of mathematical modelling in disease control.

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In this chapter the theoretical framework of the thesis is discussed. This chapter starts with describing the main routes of pathogens between farms. Second, the most important strategies to control diseases are discussed. The last part of this chapter explains how mathematical models can be used in the control and prevention of large epidemics.

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Chapter 2. Disease transmission routes, control strategies and the use of mathematical modeling in disease control.

Aquaculture is important for the supply of food of millions of people worldwide (FAO, 2010). In Scotland salmon aquaculture is important as it supplies jobs in areas with few job alternatives (MSS, 2011a). Aquatic diseases pose a threat to Aquatic industries (OIE, 2009). Pathogens can spread between farms through several pathways (natural reservoirs, vertical transmission, hydrodynamic contact and long-distance movements). Disease control strategies are necessary to minimize the effects of diseases on the aquatic industries. In order to develop disease control strategies, it is important to understand how diseases are spread. In this section, pathogen transmission routes are discussed for pathogens that are relevant for the Scottish salmon industry. In section 2.2, possible control strategies are discussed and this chapter finishes by explaining how mathematical models can be used in testing and developing disease control strategies.

2.1. Ecology of diseases

2.1.1. Natural reservoirs of pathogens

Natural pathogen reservoirs (or microbes capable of evolving pathogenicity) can cause infection or re-infection of farms. The most important natural reservoir is probably wild fish. Marine farms located on migration routes of wild fish face an increased risk of becoming infected by wild fish. Farmed and wild fish share the same water and are only separated by nets, therefore there is a risk of wild fish acquiring infection (Wallace, et al., 2008; Johansen et al., 2011; Kurath and Winton, 2011) and transmitting pathogens to farmed populations when they are in close proximity to a farm (Uglem, et al., 2009). Tagging studies show that wild fish, such as saithe (*Pollachius virens*) stay close to fish farms for several months because they are attracted by the large amounts of food available. Wild fish have been identified as a risk factor for the introduction and re-infection of aquatic diseases such as ISA (Nylund, et al., 2002; Plarre, et al., 2005) and sea lice (Rae, 2002; Costello, 2009).

Fish can be infected with a disease without showing symptoms (Plarre, et al., 2005) and infections in wild populations typically stay undetected unless a big decline in the population is noticed (Frazer, 2009). A Scottish study showed positive ISAv results for wild fish populations during the 1998/1999 outbreak. ISAv-positive samples were sometimes found during this outbreak in large quantities, indicating that there was a pattern in the transmission of the virus between wild fish (Raynard, et al., 2001).

In addition to ISA, wild fish might also be responsible for introducing sea lice into susceptible salmon farms (Bron, et al., 1993; Butler, 2002). This applies both to low-level external inputs that kick-start outbreaks of *Lepeophtheirus salmonis* on farms (Revie et al. 2005) and seasonal spikes of *Caligus elongatus* potentially associated with wild fish migration (Revie et al. 2002). The larvae of the lice are planktonic (Johnson and Albright, 1991) therefore they can easily be transmitted between farmed and wild fish populations by passive drift. Environmental factors such as tidal currents and wind are important factors in transmission of lice larvae between the wild population and farmed population (Murray and Gillibrand, 2006; Amundrud and Murray, 2009). Infections of sea lice are found to be correlated with ISA outbreaks, as vector-borne transmission of the virus might occur by sea lice (Hammell and Dohoo, 2005; OIE, 2009) and being infected by sea lice might increase the severity of the symptoms of ISA (Gustafson, et al., 2005). Sea lice are thought to have a negative effect on the non-specific immune system of their hosts (Mustafa, et al., 2000). Therefore, controlling the spread of sea lice could also be beneficial in the control of ISA and other diseases.

IPNV is also detected in wild fish, however the estimated prevalence of IPNV in wild fish in Scotland is low, around 0.15%; prevalences of IPNV in wild fish populations in the vicinity of salmon farms are found to be higher (0.58%) (Wallace, et al., 2008). Higher prevalence in samples taken from wild fish in close proximity of salmon farms indicates that there is probably transmission from salmon farms to wild fish populations. However, there is insufficient evidence to prove that transmission is in the direction of wild populations to farmed populations as opposed to farmed populations to wild populations.

Wild fish are probably not responsible for transmission of IPNV to farmed populations (Murray, 2006). This could be due to the high prevalence in Scottish marine farms (>80%), though wild fish populations might become important for re-infecting farmed populations when the prevalence of IPN on farms drop to very low levels (Wallace, et al., 2008).

Although some studies suggest the possibility of pathogen transmission from wild fish to farmed populations (Rae, 2002; Kurath and Winton, 2011) other studies doubt whether wild fish are responsible for disease transmission to farmed fish such as ISA and sea lice and this possible transmission route needs further investigation (Uglem, et al., 2009). Farmed fish are likely responsible for transmitting pathogens to wild fish (Wallace, et al., 2008) causing declines in wild fish populations (Costello, 2009; Frazer, 2009) depending on the pathogen.

2.1.2. Vertical transmission

Some diseases can transmit vertically through reproductive fluids (OIE, 2009), therefore Scottish broodstock are screened for key pathogens (Bruno, 2004a). Vertical transmission could be important, particularly for long-distance imports into pathogen-free countries as this mechanism could be responsible for the index case (i.e. first infected farm in a susceptible and naive population). Vertical transmission is only important on a country-wide scale when other pathways such as hydrodynamic contact and long-distance movements do not overtake the effects of vertical transmission.

BKD can be transmitted vertically; therefore broodstock originating from BKD-positive farms are not allowed to be used for the production of ova and must be culled (MSS, 2010). Furthermore, since transmission of *Aeromonas salmonicida* can occur vertically, disinfection of ova infected with these bacteria is important in the control of furunculosis (DIPNET, 2007).

Vertical transmission is uncommon or entirely unknown for IPN (Robertsen, 2011) and PD (Rimstad, 2011); evidence regarding vertical transmission of ISA is, as yet, inconclusive. Nylund et al (2007) suggested that non-virulent strains of ISA can be transmitted vertically, and it is thought that ISAv was introduced in Chile by infected embryos originating from Norway (Vike, et al., 2009). However, it is generally assumed that vertical transmission is unlikely to play a role in the transmission of ISA (Cipriano and Miller, 2003; Lyngstad et al., 2008). Virulent and non-virulent strains might differ in their transmission routes. Nylund et al (2007) were the first to publish a study that indicated vertical transmission of ISA; however, these results were only valid for non-virulent strains, with virulent strains not included in this study. Lyngstad et al. (2008) concluded that vertical transmission is unlikely to occur for ISA, however this study only included virulent strains. The findings of Vike et al (2009) were based on two isolates, one coming from a marine farm and one from a freshwater farm. However, infections of ISA are generally only in seawater farms and have in a few cases been seen on freshwater farms mixed with seawater (OIE, 2009). Further research is needed to give conclusive evidence on the possibility of vertical transmission of ISAv.

2.1.3. Hydrodynamic contact

Fish can shed pathogens by urine, blood, gut contents, mucus, reproductive fluids (such as ova) and material from dead fish (OIE, 2009). These products are assumed to be transmitted passively to neighbouring farms by water flow, especially in downstream directions or with the prevailing current (Sharkey, et al., 2006). Therefore, close proximity to an infected farm could be a risk factor for a susceptible farm in the watercourse to become infected. In this thesis, proximity reflects the shortest physical distance between farms via the water column.

Close proximity to an infected farm has been identified as a risk factor for the transmission of PD (Kristoffersen, et al., 2009; Viljugrein, et al., 2009; Aldrin, et al., 2010). For example, in a Norwegian study, close proximity was found to be important in the transmission of PD and explained 80% of PD transmission between farms (Aldrin, et al., 2010). In addition, close proximity to ISA-infected farms has been identified in many studies as a risk factor in the spread of ISAv (Aldrin et al., 2010; Mardones et al., 2009; McClure, et al., 2005; Jarp and Karlsen, 1997). In 2008/2009 the second ISA outbreak occurred in Scotland, but this outbreak was limited to six farms located at the Shetland Islands with the rest of Scotland remaining free of the disease. The most likely transmission pathway of infection between farms during this outbreak was thought to be through local transmission (Murray, et al., 2010).

Harvest stations and processing plants could pose a threat to fish farms in close proximity to these sites. If infected fish are transported to a harvest site and the site does not dispose of infected fish and their waste products hygienically, then they can become a serious threat (Munro, et al., 2003). Improved biosecurity on Norwegian processing plants reduced the risk of neighbouring salmon farms becoming infected with ISA (Vagsholm, et al., 1994; Jarp and Karlsen, 1997). However, close proximity to a harvest station or processing plant could still be a serious risk for ISA (Jarp and

Karlsen, 1997; Murray, et al., 2002) when water from a well boat is released. Furthermore, escaped live fish from harvest plants infected with a disease might pose a risk if they come in close contact with salmon farms (Munro, et al., 2003). Escape of live fish from harvest stations is uncommon, however if it does happen it may result in transmission of ISA to neighbouring farms in case of contact with infected fish (Munro, et al., 2003).

2.1.4. Long-distance movements

Live animal movements play an important role in pathogen transmission and can lead to epidemics covering a large geographical area as shown in the British foot–and–mouth disease (FMD) epidemic in 2001 (Gibbens, et al., 2001; Green, et al., 2006a; Kiss, et al., 2006a) and have the potential to play an important role in the transmission of avian influenza (Dent, et al., 2008) and bovine tuberculosis (Green, et al., 2008).

Salmon production has increased substantially in the last 20 years (MSS, 2011a), therefore an increased number of movements has become necessary; this makes the Scottish salmon industry more vulnerable to pathogens (Murray, et al., 2003). Live fish movements between farms are necessary for biological reasons as salmon are anadromous and have a freshwater and seawater phase (see section 1.1.). However, live fish movements might also be necessary for economic reasons. For example, in Shetland there are insufficient freshwater sites to provide the seawater farms in Shetland with smolts. Therefore, smolts are sourced from Yorkshire and ova from Norway (Murray, et al., 2010).

Live fish movements are associated with an increased risk of disease transmission between fish farms (Stagg, et al., 2001; Murray, et al., 2002; Peeler and Thrush, 2004; Murray and Peeler, 2005; Thrush and Peeler, 2006; Mardones, et al., 2009; Branson, 2011; Murray, et al., 2011). Transportation of smolt is identified as a major risk factor for transmission of ISA over great distances and has been associated with the Scottish ISA outbreak in 1998/1998 (Stagg, et al., 2001; Murray, et al., 2002). These movements caused the epidemic to spread over a large geographical area (Murray, et al., 2002). Live fish movements have also been linked to the transmission of ISA in Chile (Mardones, et al., 2009) and other diseases, such as BKD (Murray, et al., 2011), sleeping disease (Branson, 2011) and VHS (Thrush and Peeler, 2006). In addition, live fish movements are considered the most important risk for introduction of the exotic parasite *Gyrodactylus salaris* in the UK (Peeler and Thrush, 2004).

Scottish fish farmers are obliged to register live fish movements going onto and off their farm. The fish health inspectors at Marine Scotland (Aberdeen) keep these records (MSS, 2011b). These records have been used to examine the risks of live fish movements on pathogen transmission (Green, et al., 2009; Munro and Gregory, 2009; Green, 2010; Green, et al., 2011), see section 2.3. Live fish movements have also been used in Chile to study the spread of ISAv (Mardones et al., 2009).

Farms infected with a notifiable disease are not allowed to move live fish from the farm (Joint Government/Industry Working Group, 2000). However, pathogens are hard to detect at low prevalence or when the fish do not show clinical symptoms (Murray and Peeler, 2005; Graham, et al., 2006; Lyngstad, et al., 2008). Therefore, infected fish may be moved from the farm while they are infected with a notifiable pathogen (Jonkers, et al., 2010).

2.2. Control strategies

2.2.1. Fallowing and management areas

It is recommended that marine sites have a fallowing period between cycles (Joint Government/Industry Working Group, 2000), where farms are left unstocked for a period of time in order to let pathogens die out in the absence of hosts (Wheatley, et al., 1995; Bruno, 2004b). Multiple generations of fish overlapping on one farm is thought to be a risk factor for BKD in rainbow trout farms, where BKD can persist for several years. Salmon farms commonly hold one generation of stock and have a fallowing period before the next cycle starts; in salmon farms BKD is less persistent compared with rainbow trout farms (Bruno, 2004b). Furthermore, fallowing appears to be effective in the control of *L. salmonis* sea lice (Bron, et al., 1993; Rae, 2002). However, it is not effective with another type of sea louse, *Caligus elongates* (Bron, et al., 1993; Revie, et al., 2002) which has a large wild-fish reservoir population.

Fallowing seems to be effective in the control of PD (Wheatley, et al., 1995; MSS, 2009; Rimstad, 2011). However the evidence is not conclusive; some studies did not find fallowing to be beneficial in the control of PD (McLoughlin, et al., 2003; Rodger and Mitchell, 2007). It might be that farmers facing major problems with PD are more motivated and more likely to integrate fallowing strategies in their management this could explain why fallowing does not appear to be beneficial in some studies. Furthermore, natural reservoirs could be responsible for re-infection of the farm or re-infection may occur through other farms that are in close proximity and are not fallowed (McLoughlin, et al., 2003; Rodger and Mitchell, 2007).

After the Scottish ISA outbreak in 1998/1999 the workgroup, “Joint Government/Industry Working Group” (JGIWG) was established to develop control strategies for future ISA outbreaks. A code of practice was developed with agreements on husbandry and bio-security measures such as management areas, fallowing strategies and limiting movements between marine sites (Joint Government/Industry Working Group, 2000). The use of management areas was shown to be effective during the Scottish ISA outbreak in 2009/2010 (Murray, et al., 2010): infections were limited to one management area, in contrast to the Scottish outbreak in 1998/1999 where infected farms covered a large geographical area (Murray, et al., 2002).

According to the JGIWG, in case of a suspected outbreak of ISA, movement restrictions are applied to the suspected farm. Depopulation of the farm should be undertaken as soon as possible after the confirmation of ISA (Joint Government/Industry Working Group, 2000) because it is thought that the time period in which a farm is depopulated after confirmation of ISA is important in eradicating pathogens (Mardones et al., 2009). Fish that survive ISA can shed the virus for another month (OIE, 2009). The viral load reduces when hosts are removed from an infected site as there are no viral particles shed by hosts and the virus will die out in the absence of hosts (Wheatley, et al., 1995). This will also reduce the risk of infection to neighbouring sites. After depopulation, the fallowing period should at least be six months in case of confirmed ISA (Joint Government/Industry Working Group, 2000). When there are no substantial problems on the farm, the fallowing period is normally between 4 to 8 weeks, but can take up to a year (MSS, 2011a).

Pathogens might spread from infected farms by wild fish movements or through passive drift and can cause re-infection of farms after a fallowing period. Therefore, synchronised fallowing at management area level might be beneficial over unsynchronised fallowing. Some farms in Scotland have applied synchronised fallowing and treatments at management area level for some years (Rae, 2002), and recently synchronized fallowing has been applied in Norway (Rimstad, 2011). However, prior to this thesis there have been no studies performed to investigate the advantages of synchronised fallowing over unsynchronised fallowing at a management area level.

There are no biosecurity measures between freshwater sites comparable to management areas between seawater sites. Therefore, in case of a disease outbreak in a freshwater site, there is a possibility that a geographical widespread epidemic might occur, as occurred with the first Scottish ISA outbreak in seawater. However, this depends on the contact structure of salmon farms. So far there have been no studies performed to investigate the contact structure of Scottish salmon freshwater sites specifically. Biosecurity measures such as movement restriction should be strategic because of the biological and economic importance of live fish movements between freshwater sites.

2.2.2. Other treatment options

Control of many diseases is often only possible with restricted movements of live fish, good hygiene, stress control, quarantine of infected stocks, culling of infected brood stock or total hatchery depopulation followed by disinfection (in case of vertical transmission) (OIE, 2009). In some cases, vaccines, antibiotics or pesticides are available. However, there are no licensed vaccines or antibiotics available in the UK for the treatment of BKD, ISA and gyrodactylosis (OIE, 2009; MSS, 2011b; CEFAS, 2011).

Vaccines are sometimes used to prevent epidemics; in Scotland 68 salmon freshwater farms were vaccinated in 2009. The majority of vaccinations were against furunculosis. A small number of sites vaccinated their stock against enteric red mouth disease, PD, IPN and vibriosis (MSS, 2011a). Vaccines are not available or not effective in all cases (Rodger and Mitchell, 2007; Kibenge, et al., 2004). The most important features of vaccines are that they prevent clinical disease and transmission of the pathogen and should offer protection against multiple serotypes. Vaccinations are rarely 100% effective but do not need to be in order to prevent an epidemic (Glass et al., 2002) as long as they decrease the number of secondary cases caused by a primary case to below 1. However, if protection against a pathogen is incomplete at individual fish level there might be a risk for vaccinated fish to become carriers of the pathogen (OIE, 2009).

In addition to vaccines, pesticides are used in some cases to eradicate pathogens. For example, rotenone is used in Norwegian rivers that are infected with *G. salaris*. Rotenone eradicates not only the parasite but also kills all the fish in a river and therefore restocking is necessary. Treatment of rivers with rotenone is unlikely to be possible in most parts of the United Kingdom, due to the complex hydrography of the river systems and ecological concerns (Peeler and Thrush, 2004).

Another problem that might occur with the use of pesticide treatments is that parasites, such as sea lice, can become resistant to the treatment (Rae, 2002; Murray, 2011). As pesticides often lose their effects due to resistance in the sea lice (Murray, 2011), vaccination programs might be a better solution to prevent sea lice infections (Rae, 2002). Several organisations are trying to develop effective treatments to protect salmon from sea lice such as vaccines that stimulate the production of antibodies that damage important organs of the sea lice (Rae, 2002), but so far without success. Some other treatments against sea lice are highly effective in eradicating the lice, but can also damage their hosts such as hydrogen peroxide (Rae, 2002).

The effectiveness of control strategies depends largely on the complexity of the transmission pathways and the knowledge about these pathways. In case of a disease outbreak at site level, culling might be the only solution to prevent an epidemic occurring on a larger scale. However, culling infected sites is very expensive and can cause huge financial difficulties to fish farmers. In addition, as seen from ISA infections in Norway (Nylund, et al., 2007; Vike, et al., 2009) and Chile (Mardones, et al., 2009), culling is not always effective. Nevertheless in some cases it is the only available option. However, as shown during the foot-and-mouth disease (FMD) outbreaks in Great Britain and the Netherlands, where culling was applied, public tolerance for these methods are low (EU, 2001). Therefore, more emphasis should be made upon preventing diseases by fallowing strategies, vaccine development and strategic movements between farms.

2.3. Mathematical modelling

Pathogens, especially viruses, can be hard to control in aquaculture due to a lack of effective treatments such as antibiotics, vaccines or the existence of natural reservoirs causing re-infection. Understanding how pathogens spread within a population or country is important in order to develop effective surveillance strategies. Mathematical models can help us to understand how pathogens are spread and can be a useful tool to investigate the role of live fish movements in the spread of disease.

Mathematical models show a simplification of reality with which it is possible to explore the behaviour of – for example – biological processes that cannot be tested in reality because it is unethical, too expensive or impractical (Kiss et al., 2005; Webb et al., 2005). In these models only the essential elements that are necessary to test hypotheses or explore the behaviour of epidemics should be included (Jorgensen and Bendoriccho 2001; Murray 2008).

2.3.1. Mass-action vs. network models

There are two types of mathematical models that are used most often to study disease dynamics: mass-action and network models. Mass-action models are used to investigate the course of epidemics in random well-mixed populations. These models are normally divided into compartments (susceptible, exposed, infected, recovered, etc), representing fractions of the population.

Susceptible individuals are those that are not infected with the causal agent, but which have the potential to become infected. If individuals infected with the pathogen but are not infectious then they belong to the *exposed* compartment and after the latent period (i.e. the time period in which individuals are infected with the pathogen become infectious), individuals move to the *infected* compartment in which they have the potential to infect other individuals. When individuals are moved to the *recovered* class, they are not able to infect other susceptible individuals anymore, as they are immune or dead, or otherwise removed from the population. In some cases recovered individuals can become susceptible again, but this depends on the pathogen and other circumstances (Anderson and May, 1992) and also the level of study. For example, if farms are the epidemiological unit, the animals on the farm can reach a state of immunity, but when a new population replaces these animals, this farm will become susceptible again. These compartments are examples, compartments can be added and removed.

Models can be stochastic or deterministic. Stochastic means that moving between compartments occurs by chance and in this case many outcomes are possible. For example, if the removal rate is 0.25 per time step, there is a 1 in 4 chance that an infected individual is removed or recovered per time step. In a deterministic model there is only one outcome when all parameter values are fixed, while stochastic models provide multiple outcomes when all parameter are fixed. Stochastic models are a better choice when contact structures between individuals are complex (Keeling, 2005). In addition, stochastic models are more appropriate to use when the population size is small as with the use of stochastic models only ‘complete’ animals are moved to the next compartment (Anderson and May, 1992).

One of the main assumptions of most mass-action models is that all epidemiological units (for example farms or individual animals) are mixed randomly i.e. if farm is the unit, the number of contacts per farm is homogenous and there is an equal risk of connection between any two farms. Thus, they all have an equal risk of becoming infected and spreading the infection (Anderson and May, 1992; Keeling, 2005). However, in reality infected farms do not have the potential to reach all farms and thus they do not have the potential to infect every susceptible farm in a population. For example, poultry (Cox and Pavic, 2010), pigs (Lindstrom, et al., 2010) and salmon movement networks are “pyramidal” in structure (figure 2.1). In these networks there are more movements going from the top (hatcheries) to the bottom (growers) than from the bottom to the top. In this case smolt suppliers are less likely to infect hatcheries, while infections that started in hatcheries are likely to reach smolt suppliers. There is also a tendency for the top of the pyramid to be narrow and for the bottom to be wide. The number of susceptible farms that can be infected by one infected farm is limited and shows large differences amongst farms (Keeling, 2005; Martinez-Lopez, et al., 2009). Several studies in livestock show that there are differences in the contact structure between production phases (Bigras-Poulin, et al., 2006; Bigras-Poulin, et al., 2007; Natale, et al., 2009; Lindstrom, et al., 2010). Farms that have as their main purpose the breeding of animals, normally have more movements going off their farm compared with gathering farms and abattoirs (Bigras-Poulin, et al., 2007). This is likely to influence the course of an epidemic as farms at the top of the pyramidal structure are more likely to be sources of infection, while farms on the bottom are more likely to be sinks. Including the stage of production is therefore important to assess the infection risks of (salmon) farms. Prior to this thesis, no studies have examined the differences in contact structure amongst production phases for salmon farms; however differences in contact structure amongst production phases are expected due to the complex structure of salmon farming.

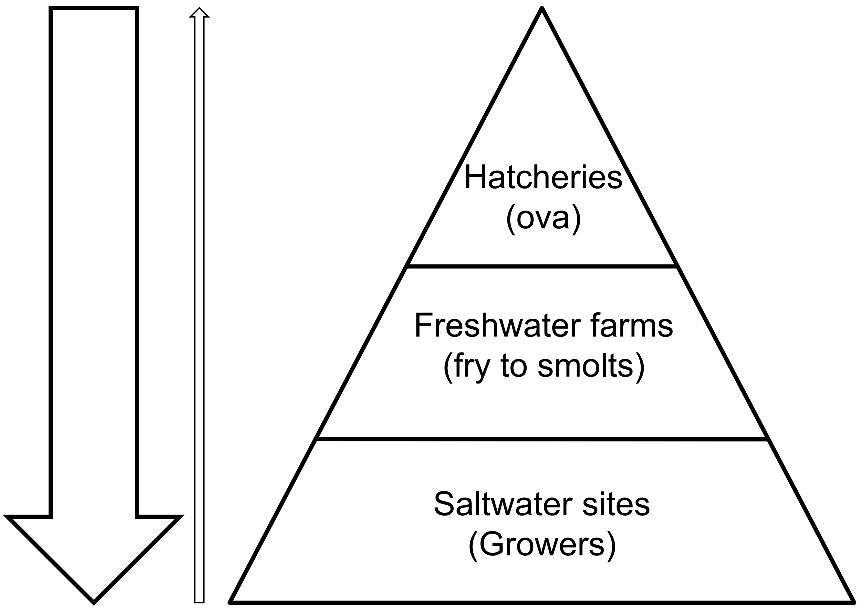

Figure 2.1. Graphical representation of a pyramidal network. The size of the arrows represents the number of movements going from the top to the bottom and from the bottom to the top.

Epidemiological network analysis is a technique that allows description of contact patterns between individuals in a population. Network models can easily take into account heterogeneity (i.e. the variation in the number of contacts per farm) and the direction of movements (Newman, 2003b; Christley, et al., 2005; Keeling and Eames, 2005; Martinez-Lopez, et al., 2009). Network models consist of nodes (for example, farms or animals). Connections amongst nodes can be represented in a graph or by an adjacency matrix A_{ij}. When $A_{ij} = 1$ there is a connection between two nodes. $A_{ij} = 0$ implies no connection between nodes (Newman, 2003b; Keeling and Eames, 2005). Nodes are connected by edges (undirected connections, figure 2.2A) or arcs (directed connections, figure 2.2B), resulting in an undirected network (i.e. P can infect Q, Q can infect P) or directed network (i.e. Q cannot infect P). One of the main assumptions in mass-action models is that contacts are undirected (Martinez-Lopez, et al., 2009).

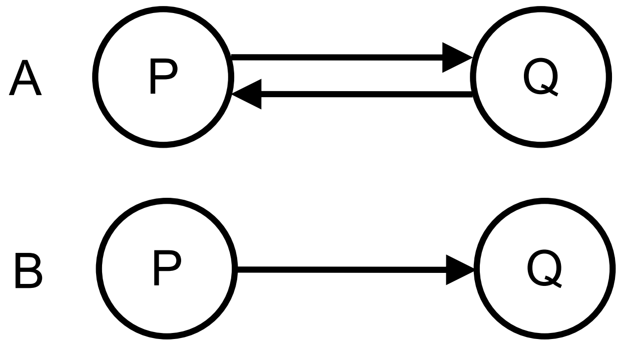

Figure 2.2. Graphical representation of an undirected network (A) and a directed network (B).

With the use of network analysis it is possible to identify potential high-risk farms (farms that have many connections to other farms) (Woolhouse, et al., 1997; Christley, et al., 2005; Keeling, 2005; Lloyd-Smith, et al., 2005; Kiss, et al., 2006a; Ortiz-Pelaez, et al., 2006; Green, 2010).

In human epidemiology, social network modelling has been applied often, for example to investigate the role of contact networks in the spread of severe acute respiratory syndrome (SARS) (Meyers, et al., 2005), HIV (Pivnick, et al., 1994; Amirkhanian, et al., 2005), and tuberculosis (Cook, et al., 2007; Klovdahl, et al., 2001). Social network analysis has been applied to preventive veterinary science from approximately 2003 and its use has been expanding since (Martinez-Lopez, et al., 2009). For example, network analysis was used to study the role of live animal movements on the British FMD epidemic in 2002 (Green, et al., 2006a; Kiss, et al., 2006a; Ortiz-Pelaez, et al., 2006) and avian influenza (Dent, et al., 2008).

Although there are some disadvantages of using mass-action models, these models are often used and are thought to often give a good approximation of disease dynamics (Anderson and May, 1992; Keeling, 2005; Murray 2006). Nevertheless, network models should be used when it is thought that heterogeneity, direction or spatial scale of contact between nodes exists and are thought to play an important role in the course of an epidemic (Keeling, 2005; Keeling and Eames, 2005). This is the case with live fish movements occurring between farms (Thrush and Peeler 2006; Munro and Gregory, 2009).

2.3.2. Heterogeneity

Network models can easily take into account the farms that pose the most risk and those that are most at risk, the direction of the contacts and heterogeneity. This is a big advantage over simple mass-action models. However, mass-action models can take into account heterogeneity in host susceptibility (Green et al., 2006b). In this context, heterogeneity is the variation in the number of contacts per epidemiological unit. In several studies it is shown that 20% of the population with the most contacts is responsible for 80% of the infection, this is known as the 20/80 rule (Anderson and May, 1992; Woolhouse, et al., 1997; Volkova, et al., 2010). Nodes (i.e. here farms) that have many connections with other nodes are more like to become infected, and when they are infected they have the ability to spread the infection to a large number of nodes. These nodes are called "super-spreaders" (Keeling, 2005; Keeling and Eames, 2005; Lloyd-Smith, et al., 2005), and generally comprise a small number of the total nodes in a network. Targeting these super-spreaders for surveillance is effective in detecting pathogens and preventing large epidemics (Christley and French, 2003; Christley, et al., 2005; Lloyd-Smith, et al., 2005; Kiss, et al., 2006a; Green, 2010). For example, during the ISA outbreak in 1998/1999, many cases could be linked to one processing plant (Murray et al., 2002).

Heterogeneity has been shown to have a substantial impact on epidemics of FMD (Kiss, et al., 2006a) and avian influenza (Dent, et al., 2008) by reducing the epidemic threshold (Keeling, 1999; Kiss, et al., 2005; Kiss, et al., 2006b). Variation in the number of connections between nodes is shown in several livestock networks, such as cattle in the UK (Brennan, et al., 2008), Danish cattle (Bigras-Poulin, et al., 2006), Belgian pig farms (Ribbens, et al., 2009), Danish pig farms (Bigras-Poulin, et al., 2007). Heterogeneity in the number of contacts has also been shown in fish farms in Wales and England (Thrush and Peeler, 2006) and in a Scottish company with 68 farms (Munro and Gregory, 2009).

2.3.3. Seasonality

Seasonality is likely to play an important role in the course of an epidemic. During times where the network is highly connected it is more likely that an epidemic will be initiated and become widespread in a short time period (Kiss, et al., 2006a). For example, the timing of agricultural shows in the UK is highly seasonal and peaks during August. The late summer months and early autumn therefore pose an extra risk for the start and establishment of an epidemic (Gibbens, et al., 2001; Webb, 2006). Prior to this thesis, there have been no studies performed that investigate the seasonality of live fish movements or that quantify the effects of seasonality in aquaculture.

2.3.4. Clustering

R_0 is often used in epidemiology to describe the number of secondary cases caused by a typical primary case in a susceptible population. This parameter indicates if an epidemic is likely to occur. For $R_0 < 1$ epidemics have the tendency to die out and the size of these epidemics will not scale with epidemics having $R_0 > 1$ in this case a large epidemic is more likely to occur (Anderson and May, 1992; Keeling, 2005). R_0 depends on both the transmission rate of the disease and the contact network structure and is relatively easily derived for homogenous networks. For complex structured network models it is often problematic to calculate R_0 (Keeling, 2005; Meyers, et al., 2005), even though it is regarded as a useful concept. For example, when the population is divided into epidemiologically distinct subpopulations, then a one-size fits all R_0 is not useful.

Clusters are triangular connections or cliques in a network (figure 2.3); a clustering coefficient represent the probability that two connected nodes have another common neighbour (Newman, 2003a; Christley, et al., 2005; Keeling, 2005; Keeling and Eames, 2005; Martinez-Lopez, et al., 2009). Clustering decreases R_0, slows the speed of infections and decreases the final size of an epidemic (Newman, 2003a; Keeling, 2005) as infected nodes compete to infect the same neighbouring nodes.

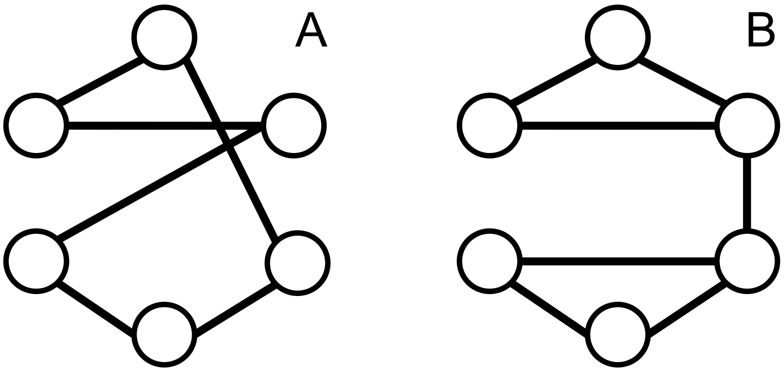

Figure 2.3. Graphical overview of an unclustered (A) and clustered (B) network.

2.3.5. Types of network models

There are several idealised network approaches that help us to understand disease dynamics, such as random graphs, small-world networks, lattice networks and scale-free networks (Watts and Strogatz, 1998; Newman, 2003b; Keeling, 2005; Martinez-Lopez, et al., 2009), explanations of these networks and examples are given below. In random graphs (figure 2.4A), nodes are connected by edges at random. Random graphs are characterized with a short path length (i.e. the smallest number of steps to get from node i to node j), and a low cluster coefficient (table 2.1) (Watts and Strogatz, 1998; Newman, 2003b; Christley, et al., 2005; Keeling, 2005; Martinez-Lopez, et al., 2009). In lattice networks (figure 2.4C), nodes are distributed in a grid, where each node has the same number of neighbours. Lattice networks have a long path length and are highly clustered (Table 2.1) (Keeling and Eames, 2005). Small-world networks (figure 2.4B) are ring-models with a small number of extra connections that are randomly allocated (Newman, 2003b; Keeling and Eames, 2005; Martinez-Lopez, et al., 2009). These extra long-distance connections have a large effect on the disease transmission in a network: all nodes can be reached within a few steps (Christley, et al., 2005; Keeling and Eames, 2005). Networks with small-world network characteristics (short path length and high cluster coefficient, table 2.1) are seen in British racing horses (Christley and French, 2003) and the British sheep movement network (Kiss, et al., 2006a); local transmission between sheep farms is likely to be more regular compared with long-distance movements and trading markets represent the extra long-distance contacts (Webb, 2005).

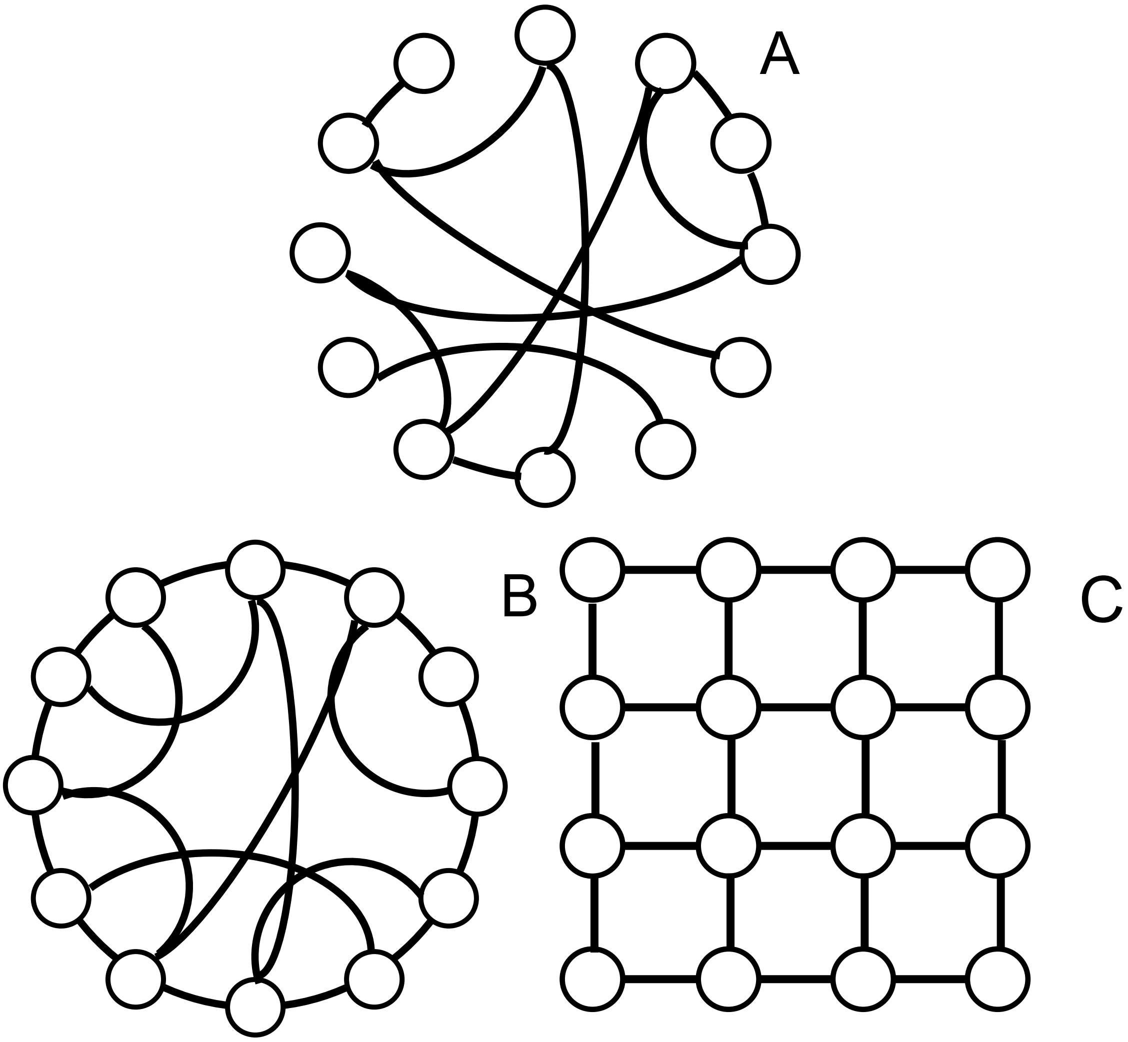

Figure 2.4. Graphical overview of a random (A), small-world (B) and lattice (C) network.

Network models that are used are often static, meaning that adding or removing nodes or connections is not considered. Furthermore, they assume that the connections between nodes are independent of each other (which occurs in a random network), except for lattice-type networks (Martinez-Lopez, et al., 2009). This is often not the case as, for example, a Swedish study showed that movements of cattle within a county are more likely to occur than between counties (Noremark, et al., 2009). In the UK local sheep trading markets are quite common and these trading markets played an important role in the British FMD outbreak in 2001 (Eales, et al., 2002; Kiss, et al., 2006a; Webb, 2006). Market-trading connections could be treated as new connections between farms that are present for a short period of time with a high number of connections. Network models are capable of being dynamic and thus to include temporary connections such as trading markets.

Table 2.1. Overview of theoretical network models and their most important characteristics.

		Path length	
		Short	*Long*
Cluster coefficient	*Low*	Random graph	*
	High	Small-world network	Lattice graph

2.4. Conclusion

Diseases can spread through several pathways. Live fish movements are found the most ‘dangerous’ contact between farms as they almost definitely causes infection at the receiving site when the source farms is infected. Natural reservoirs, vertical transmission and hydrodynamic contact are all important transmission routes and should not be neglected in disease control strategies.

Vaccines, antibiotics and pesticides are in some cases available to eradicate pathogens. However, side-effects can cause problems to the host of the parasites or to their surroundings. In addition, not all eradication tools are 100% effective or pathogens are becoming resistant to the treatment. Therefore emphasis should be made on disease prevention.

Mathematical models, especially network models, are increasingly being used to investigate and study the effects of control strategies. Epidemiological network models can easily take into account heterogeneity, clustering and seasonal patterns and therefore are more appropriate to use in complex networks such as the live fish movement network.

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CHAPTER 3. The effectiveness of fallowing strategies in disease control in salmon aquaculture assessed with an SIS model.

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This chapter describes the effects of three different fallowing strategies on disease control in salmon aquaculture. This study was a theoretical study, however real data were used in the form of management area maps compiled by Marine Scotland, Aberdeen. This chapter forms a base for the network model used in chapter 5.

The main author, Marleen Werkman, constructed the disease model together with A.G. Murray and D.M. Green. All co-authors provided supervisory and editorial support throughout the whole study.

This work was published as shown in Preventive Veterinary Medicine 98, 64-73 (2011). Furthermore, results of this chapter have been presented at the European Workshop of PhD and Post-Doctoral fellows on anadromous Salmonids (NoWPaS) and the PhD workshop “Mathematical Modeling in the Life Sciences” at Glasgow University.

CHAPTER 3. The effectiveness of fallowing strategies in disease control in salmon aquaculture assessed with an SIS model.

Werkman, M.; Green, D.M.; Murray, A.G.; Turnbull, J.F.

3.1. Abstract

Salmon production is an important industry in Scotland, with an estimated retail value >£1 billion. However, this salmon industry can be threatened by the invasion and spread of diseases. To reduce this risk, the industry is divided into management areas that are physically separated from each other. Pathogens can be spread between farms by local processes such as water movement or by long-distance processes such as live fish movements. Here, network modelling was used to investigate the importance of transmission routes at these two scales. We used different disease transmission rates (β), where infected farms had the probability of 0.10, 0.25 or 0.50 per month to infect each contacted farm. Interacting farms were modelled in such a way that neighbours within a management area could infect each other, resulting in two contacts per farm per month. In addition, non-local transmission occurred at random. Salmon are input to marine sites where they are raised to harvest size, the site is then fallowed; in the model the effects of different fallowing strategies (synchronised, partial synchronised and unsynchronised fallowing at the management area level) on the emergence of diseases were investigated. Synchronised fallowing was highly effective at eradicating epidemics when transmission rate was low ($\beta = 0.10$) even when long distance contacts were fairly common (up to 1.5 farm^{-1} month^{-1}). However for higher transmission rates, long distance contacts have to be kept at much lower levels (0.15 contacts month^{-1} where $\beta = 0.25$) when synchronised fallowing was applied. If fallowing was partially synchronised or unsynchronised then low rates of long-distance contact are required (0.75 or 0.15 farm^{-1} month^{-1}) even if

$\beta = 0.10$. These results demonstrate the potential benefits of having epidemiologically isolated management areas and applying synchronised fallowing.

Keywords: Fallowing, disease transmission, Atlantic salmon, SIS-model, epidemiology.

3.2. Introduction

Scottish production of Atlantic salmon was around 130,000 tonnes per year in the years 2005-2009 (Marine Scotland Science, MSS, 2009b). In 2006 the worldwide retail value of Scottish Atlantic salmon production was estimated to be >£1 billion (Scottish Salmon Producers' Organisation, SSPO, 2009). Scottish salmon production created 849 full-time jobs and 100 part-time jobs in 2008 (MSS, 2009b) in remote areas with few alternative employment opportunities. For these reasons, salmon production is important for the Scottish economy. Diseases such as infectious pancreatic necrosis (IPN) and pancreas disease (PD) can cause anorexia and high mortalities (Bruno 2004a; McLoughlin and Graham, 2007; World Organisation for Animal Health, OIE, 2009), infectious salmon anaemia (ISA) is subject to controls under EU legislation (Murray et al., 2010), and all pose an economic threat to the industry (Murray and Peeler, 2005). For example, the cost of the ISA outbreak in 1998/1999 was estimated to be >£20 million (Hastings et al., 1999).

Preventing aquatic diseases is not only important from an economic perspective. Diseases also have an impact on (farmed) fish welfare (Huntingford et al., 2006), which can affect markets given growing awareness of fish welfare among consumers (Ashley, 2007). In addition, it is possible for pathogens of farmed fish to be transmitted to wild fish populations (Wallace et al., 2008).

Pathogen transmission between farms can occur on a local level, as hydrodynamic transmission can be responsible for pathogens spreading between farms for short distances (McClure et al., 2005; Gustafson et al., 2007; Amundrud and Murray, 2009; Viljugrein et al., 2009). Close proximity to an infected farm has been indentified as a risk factor for transmission of, for example, ISA (McClure et al., 2005; Gustafson et al., 2007; Lyngstad et al., 2008; Aldrin et al., 2010) and PD (Kristoffersen et al., 2009; Aldrin et al., 2010). Local transmission also occurs through wild fish movement between farms (Uglem et al., 2009). Wild fish may be infected in the vicinity of infected farms (Wallace et al., 2008) and transmit those pathogens from farm to farm (Uglem et al., 2009).

Anthropogenic activities, such as sharing equipment between sites, visits from well boats, or movement of live fish can increase the risk of transmission of pathogens between farms (Murray et al., 2002; Munro et al., 2003; Munro and Gregory, 2009). Live fish movements can be over long-distance, for more than 100 km (Murray et al., 2002) or even international (Ruane et al., 2009), which can cause more dispersed disease patterns.

The effects of hydrodynamic movements were shown in the recent (2008/2009) outbreak of ISA in the Shetland area of Scotland, infecting six farms in a geographically confined area (Murray et al., 2010). This may be contrasted with an outbreak in 1998/1999, which spread between areas through the use of well boats for transporting live fish or for harvest (Murray et al., 2002). Data from the ISA outbreak in Chile (2007/2008), showed clusters of outbreaks appearing around the index case, suggesting hydrodynamic transmission has caused the local spread of the virus. However, at the early stage of the ISA epidemic in Chile, anthropogenic activities were found to be important, which caused a highly dispersed pattern (Mardones et al., 2009).

To reduce the risk of local disease transmission in Scotland, management areas were established in 2000 based on the maximum spring-tide current speeds (Joint

Government/Industry Working Group, JGIWG, 2000). All active farms were divided between 46 management areas (but the numbers change as farms are opened, closed or relocated), with a minimum distance of 13 km between management areas, except for Shetland where it is 7.6 km due to lower tidal currents (JGIWG, 2000). Wild fish movements are also typically at the same scale (Uglem et al., 2009). Separation between management areas is intended to form adequate ‘firebreaks’ to reduce the risk of pathogen transmission between management areas (JGIWG, 2000). Concentration of production in separate areas may help in the control of pathogens (Green, 2010). Management areas are used for the control of epidemics. For example under current control schemes a new ISA outbreak would result in all the fish on the affected farm being slaughtered and other farms in the same management area would be placed under strict surveillance. Suspected ISA-infected farms would be controlled and fish movements from suspected farms would be restricted (JGIWG, 2000) to prevent spread of pathogens between management areas.

An important strategy used to reduce the risk of disease emergence is fallowing, whereby sites are emptied and not restocked for a period of time. The hypothesis is that pathogens will die out due to the absence of hosts (Wheatley et al., 1995; Bruno, 2004b). There is strong evidence that fallowing a whole site can reduce the risk or at least the severity of infections (JGIWG, 2000). The effectiveness of fallowing is linked to the persistence of the pathogen in the water with a reduced biomass of hosts and the length of the fallowing period (JGIWG, 2000). However, as diseases can spread from adjacent farms it is important that farmers in a management area make agreements regarding synchronised fallowing. In general, coordinated management of farms at the management area level is recognised as an effective method of managing diseases and parasites. For example coordinated treatments are applied to control sea lice infestation (Code of Good Practice, CoGP, Working Group, (CoGP

Working Group, 2010). By 2008, 18 management area agreements had been signed and many include coordinated fallowing (Tripartite Working Group, 2010).

The presence of external hosts such as wild fish is also relevant as they can become infected (Wallace et al., 2008) and possibly cause re-infection (Rae, 2002; Plarre et al., 2005; Costello, 2009). Fallowing period length is normally at least four weeks, but can be up to a complete year (MSS, 2009b). Fallowing takes place for at least six months when a farm is confirmed with ISA (JGIWG, 2000). A history of infection on a site is not a significant risk factor for recurrence of IPNV (seawater) in Scotland, where farms are commonly fallowed after every cycle (Murray, 2006a). This suggests that fallowing is effective for these cases. Individual farms may fallow at different times or fallowing of farms in a management area can be synchronised.

The objective of this study was to identify the importance of local and long-distance contact for the transmission of pathogens, which we simplified as a network of contacts at these two levels as has been modelled by Watts and Strogatz (1998). In addition, we examined the effectiveness of different fallowing strategies on controlling disease transmission. This study focuses on transmittable diseases in seawater, such as IPN and PD. However, to estimate and validate parameters, data from the last Scottish ISA outbreak were used. This model is flexible and can be used to assess factors that may lead to emergence of new diseases as well. The model does not explicitly include vertical or freshwater transmission and does not allow for change in practices when the pathogen is detected and so best describes marine non-notifiable diseases. This is a theoretical study (and sensitivity analysis), though grounded in real data in the form of the amount and sizes of management areas, which were based on the management area maps compiled by the Fisheries Research Services (FRS), Aberdeen (now Marine Scotland Science, 2009a).

3.3. Materials and Methods

3.3.1. Contact structure

A stochastic SIS model (susceptible – infectious – susceptible) was constructed to investigate the effect of local (within a management area) and long-distance contacts (directed movements both between and within management areas) and different fallowing strategies on the spread of diseases between farms. This model was restricted to Scottish marine farms. There were $n = 263$ marine farms dispersed among 53 management areas, each containing 1 to 30 farms (MSS, 2009a), as shown in figure 3.1. See table 3.1 for an overview of all model parameter and their description use din this study. An undirected adjacency matrix A (i.e. wherever there is contact from node i to node j, there is contact in the opposite direction) was constructed of size $n \times n$ an element A_{ij} contains either 1 (potentially infectious contact exists from farm i to j) or 0 (no contact). Matrix A was based on the management area maps compiled by MSS (MSS, 2009a). The basic structure of each modelled management area was a ring model where each farm can infect two neighbour farms (figure 3.2A) except for small management areas where $n = 1$ or $n = 2$. This resulted in 243 edges (undirected contacts) by hydrographical connections.

Table 3.1. Description of the model parameters used in this stochastic SIS-model to describe the spread of pathogens between Scottish marine fish farms.

Parameter symbol	Description
β	Transmission rate per month.
n	Number of Scottish marine sites
t	Time step
d	Length production cycle
m	Time since last fallowing
A	Adjacency matrix of undirected hydrographical connections
L	Adjacency matrix of directed long distance connections (i.e. live fish movements
v	The pairwise probability of directed contact between all farms, both between and within management areas.
g	A pairwise probability of connections between all farms in the same management area.
h	Permeability of management area boundaries $(0 \leq h \leq 1)$. Boundaries are 100% impermeable when $h = 0$ and ineffective for $h = 1$.

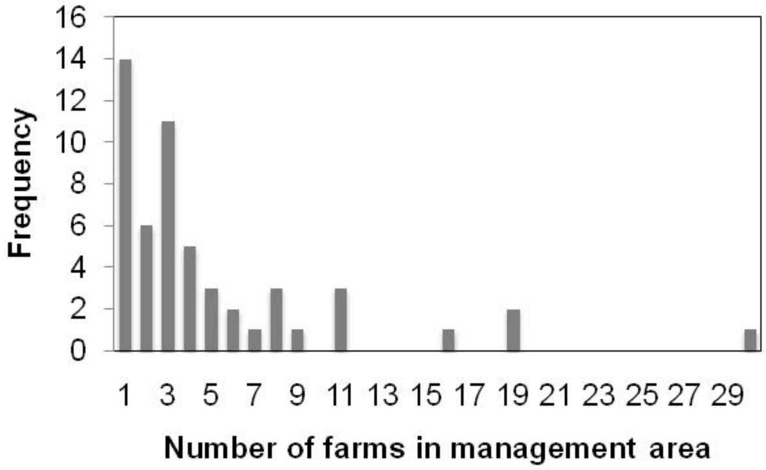

Figure 3.1. Frequency of number of farms per management area. Management areas with eight or fewer farms were classified as small management areas, while management areas containing nine or more farms were classified as large management areas.

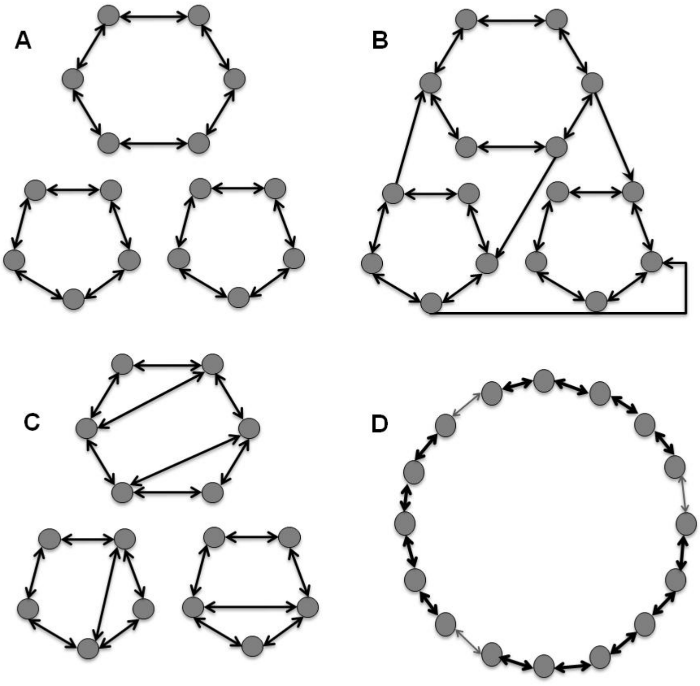

Figure 3.2. Graphic representation of the models used in this study: basic structure (A), adding long-distance movements (directed) to basic structure (B), adding local contacts (undirected) to basic structure (C), imperfectly sealed management areas. The grey arrows represent the weakened boundaries between management areas (D).

In this model the transmission rate (β) was defined as the monthly probability of an infected farm infecting a susceptible farm when there was contact between an infected and a susceptible farm. We modelled β for 0.10, 0.25 and 0.50 per month. A minimum rate to cause an epidemic for β is 0.028, because otherwise the basic reproductive rate $R_0 < 1$ even in ideal conditions for transmission of the pathogen, assuming an eighteen-month production cycle ($d =$ 18) and transmission in two directions $(0.028 \times d \times 2 = 1.008)$. Maximum transmission rate can be high: for example ISA spread from an index case to five other sites in eight months by local spread (Murray et al., 2010), which is equivalent to $\beta = 0.3$ per month, assuming each farm is connected with two others as described earlier.

In this model, susceptible farms became infected through potentially infectious contact from a connected infected farm, subject to transmission rate β; there was no change in status when an infected farm was subject to further infectious contact. The length of production cycles as modelled was eighteen months and proceeded through five production cycles (time, $0 < t \leq 90$) with a time step size of one month. Farm infectious status (0 for susceptible sites, 1 for infected) at time t was stored in a vector I of size n farms. At time $t = 1$ one farm was selected at random as the index case. ISA outbreaks, for example, are normally traced back to one index case (Stagg et al., 2001; Mardones et al., 2009; Murray et al., 2010).

3.3.2. Infection between management areas

Long-distance contacts were included in a second adjacency matrix (L). These contacts were directed: contact from node i to node j does not imply contact from j to i (figure 3.2B). Long-distance contacts were fixed and chosen randomly at the beginning of each simulation. The timing of these contact events was random, but occurred on average once in every cycle (five times per simulation). This means that $L_{ij} = 1$ does not imply a constant connection. The pairwise probability of directed contact between all farms (v) varied between 0.0025 and 1.00. For $v = 0.0025$, there were $\frac{1}{d}0.0025 \times \big(n(n-1)\big) = 9.6$ directed long-distance contacts for the whole industry per month and $9.6/n = 0.036$ directed contacts per farm per month. In addition, when $v = 1.00$ every possible connection between farms existed, which resulted in 14.6 contacts farm^{-1} month^{-1}. Epidemiological investigations into a recent ISA outbreak on the Shetland Islands (Scotland) showed eighteen farms had a total of seven live fish movements to or from sites in other management areas in 2008 (Murray et al., 2010), this equalling 0.03 contacts farm^{-1} month^{-1}. Other long-distance contacts could have occurred via movements of well boats, however these are less likely to spread infection, even if the boat is contaminated, although the risk is not negligible (Murray et al., 2002; Murray et al., 2010).

For the stochastic model vector B of size n was derived containing the number of inward contacts from infected farms.

$$B_i = \sum_j I_{j,t}\left(A_{ji} + L_{ji}\right)$$

Risk depends on the number of contacts and associated probability of transmitting infection, however the probability of infection can never exceed 1.0. Therefore, we define p_i as the probability of receiving pathogens either through long-distance movement or hydrodynamic connections at time t. Variable $Q_i = 1$ represents stochastically the receipt of pathogens through contact.

$$p_i = 1 - (1 - \beta)^{B_i}$$

$$Q_i \sim \text{Bernouilli}(p_i)$$

The new infectious status of each farm was stored in the vector $I_{i,t+1}$ of size n.

$$I_{i,t+1} = I_{i,t} + \left(1 - I_{i,t}\right)Q_{i,t}$$

3.3.3. Adding contacts within a management area

In this model all farms in a management area could infect two neighbouring farms within the same management area (see section 3.3.1). After examining the location of the farms this assumption did not appear realistic in every case, because multiple farms were within close proximity (MSS, 2009a) and as a result could potentially spread pathogens to more than two other farms. Therefore, we investigated how the proportion of additional local contacts (within a management area) affected the spread of disease and its persistence. For this an undirected contact matrix was compiled, which represented the contacts within a management area (figure 3.2C). A pairwise probability of connection between all farms in the same local area (g) was considered. These connections were added to contact matrix A. Parameter g was modelled for values between 0 and 1.00; if $g = 1$ all local connections between nodes existed resulting in a total of 1089 additional undirected local connections.

3.3.4. Imperfect management area separation

The previous model (section 3.3.1) assumed that management areas were perfectly separated, meaning there was no contact between adjacent management areas, except through long-distance movements (see section 3.3.2). However, diseases can spread between adjacent management areas when the separation distance is not great enough and the pathogen is sufficiently persistent in the environment (Aldrin et al., 2010). For this reason we examined how effective management area boundaries need to be in order to prevent disease transmission by hydrodynamic contact to adjacent management areas. Here, management area boundaries imply sufficient separation by seaway distance to prevent spread of pathogens.

In this ring model, all farms had two neighbouring farms as in the other models, except those farms on the boundary of a management area. These farms could transmit diseases by hydrodynamic contact to the adjacent management area (figure 3.2D). However, such between-management-area contacts were subject to a multiplier h $(0 \leq h \leq 1)$. Models were simulated for $h =$ 0, 0.25, 0.50 and 1.0, where $h = 0$ means the boundaries are 100% impermeable, while $h = 1.0$ means the boundaries have no effect on transmission rate. We preferred this approach as it keeps the number of neighbouring farms similar to the model as described in section 3.3.1. Management area sizes were once again based on the management areas maps that were compiled by MSS (MSS, 2009a), however the proximities of the management areas were chosen arbitrarily.

We investigated the effects of both extra local contacts (section 3.3.3) and imperfect management area boundaries for transmission rates β =0.10 and 0.25, along with long-distance movements proportions v =0.0025 and 0.01 (see section 3.3.2).

3.3.5. Fallowing

Farms were assumed to have an eighteen-month production cycle between input of smolts and restocking the farm. Other species such as rainbow trout do have a shorter production cycle, and so diseases would have less time to spread before harvest. If fish of different species with different production times are farmed in the same management area then coordinated fallowing will be more problematic. However, salmon occupy by far the majority of sea cages in Scotland: there were 256 marine salmon salmon farms in 2008 (MSS, 2009b). As a simplification we assumed that all farms had the same production cycle. After harvesting, the farms were fallowed and left without fish for a short period. The fallowing period was one month (one time step). It was assumed that after fallowing, farms were free from infection, as all fish used for restocking were free of disease. Consequently farms were susceptible once more at the following time-step of the simulation. Time since last fallowing at time t is represented for farm i by $m_{i,t}$.

$$m_{i,t+1} = m_{i,t} + 1$$

At $m_{i,t} = 18$ farms became clear of infection so that $I_{i,t+1} = 0$ and $m_{i,t+1} = 1$.

In this model, fallowing occurs after infection and therefore may occur in the same time step. The maximum median prevalence could therefore never be 1.00, as prevalence was counted after fallowing, which means there was a 5.56% chance $(1/d)$ that the index case was fallowed at $t = 1$. In this case the index case could not infect other farms.

The effects of three fallowing strategies were investigated. Timing of fallowing could be different between sites. However, length of production cycle and fallowing period was similar for all sites and all three fallowing strategies: synchronised fallowing (SYN, all farms in one management area were fallowed simultaneously), unsynchronised fallowing (UNS, the start of fallowing period occurred randomly inside management areas) and partial synchronised fallowing (PAR). In this last management strategy, areas with eight or fewer farms were subject to synchronised harvesting and management areas of nine or more farms were subject to unsynchronised harvesting. We used this cut-off point as approximately 50% of the farms were divided over small (or large) management areas. This results in an intermediate strategy between synchronised fallowing and unsynchronised fallowing. Because larger areas may contain multiple companies, agreement to synchronise fallowing is more difficult, for example the 2008/2009 ISA outbreak occurred in a large management area that had never been synchronously fallowed (Murray et al., 2010). Using the Scottish marine farms as a base, there were eight large management areas and 45 small management areas, containing in total 126 and 137 farms, respectively (figure 3.1). Furthermore, we investigated the differences in epidemic size between initiating an epidemic in a small or large management area for the most realistic scenarios ($\beta = 0.10$ and $\beta = 0.25$ and for $v = 0.0025$ to 0.01).

The model was run 1000 times for each parameter set and the median prevalence over time, percentage of runs where the epidemic was eradicated prior to $t = 90$ and the 90th percentile of the median prevalence at $t = 90$ was recorded. Analyses were performed in R (R Development Core Team, 2005) and Excel (Microsoft excel, 2008).

3.4. Results

In this section, we use the term equilibrium, by which we mean the point in the graph where the line visually levelled off, as variation is always present in a stochastic model. Increasing the transmission rate β increased the median prevalence over time (figure 3.3A and 3.3B). Similarly, increasing the proportion of long-distance movements v increased the median prevalence. However, β and v were not related to each other. Increasing β increased the probability of infection when there was a contact, while increasing v simply increased the number of long-distance contacts between farms.

3.4.1. Median prevalence and eradication of epidemics

Fallowing strategies had a clear effect in reducing the median prevalence and the probability of eradicating an epidemic when the proportion of directed long-distance movements (v) was between 0 and 0.10 (=1.5 movements per farm per month) especially for $\beta = 0.10$. For $v = 0.10$ and $\beta = 0.10$, the equilibrium prevalence was 0.65 (PAR) and 0.68 (UNS), while the epidemic died out prior to $t = 90$ for SYN. For $v \geq 0.25$ $(\geq 3.6$ movements farm^{-1} month^{-1}) equilibria were established at 0.75 or higher for all three fallowing strategies $(\beta = 0.10)$. In general, equilibria were established earlier and median prevalence was higher for $\beta = 0.50$ compared with $\beta = 0.25$ (figure 3A and 3B). For $v \geq 0.25$, median equilibria were 0.90 or higher for all the fallowing strategies for both β =0.25 and 0.50, but there were no important differences found between fallowing strategies.

We investigated if an epidemic would die out prior to $t = 90$ (five production cycles), to examine in which situations an epidemic is likely to be controlled. SYN increased the probability of eradicating an epidemic prior to $t = 90$ compared with PAR and UNS, when $v \leq 0.10$ for $\beta = 0.10$ and $v \leq 0.05$ (0.073 movements farm^{-1} month^{-1}) for

$\beta = 0.25$ (figure 3.4A). For $\beta = 0.10$ the proportion of eradicated epidemics was ≥ 0.90 for PAR and $v \leq 0.01$. However, for the same scenarios but with $v = 0.05$ the proportion of eradicated epidemics dropped to 0.59. Similar reductions in the proportions of eradicated epidemics were seen for the other fallowing strategies for $\beta = 0.10$ and $\beta = 0.25$, except for SYN and $\beta = 0.10$, where the reduction of the proportion of eradicated epidemics was seen between $v = 0.05$ and $v = 0.10$ (figure 3.4A). Probabilities of eradicated epidemics prior to $t = 90$ were lower for $\beta = 0.50$ compared with $\beta \leq 0.25$. For $\beta = 0.50$, 100% (SYN), 54.9% (PAR) and 17.7% (UNS), of epidemics died out prior to $t = 90$ when there were no long-distance movements added. For $v = 0.01$, 44.6% (SYN), 27.2% (PAR) and 14.8% (UNS) of the epidemics died out prior to $t = 90$ $(\beta = 0.50)$; for $v \geq 0.05$ less than 14% of the epidemics died out. When $v \geq 0.50$, fallowing strategies had no substantial effect on the proportions of eradicated epidemics, therefore there were too many movements.

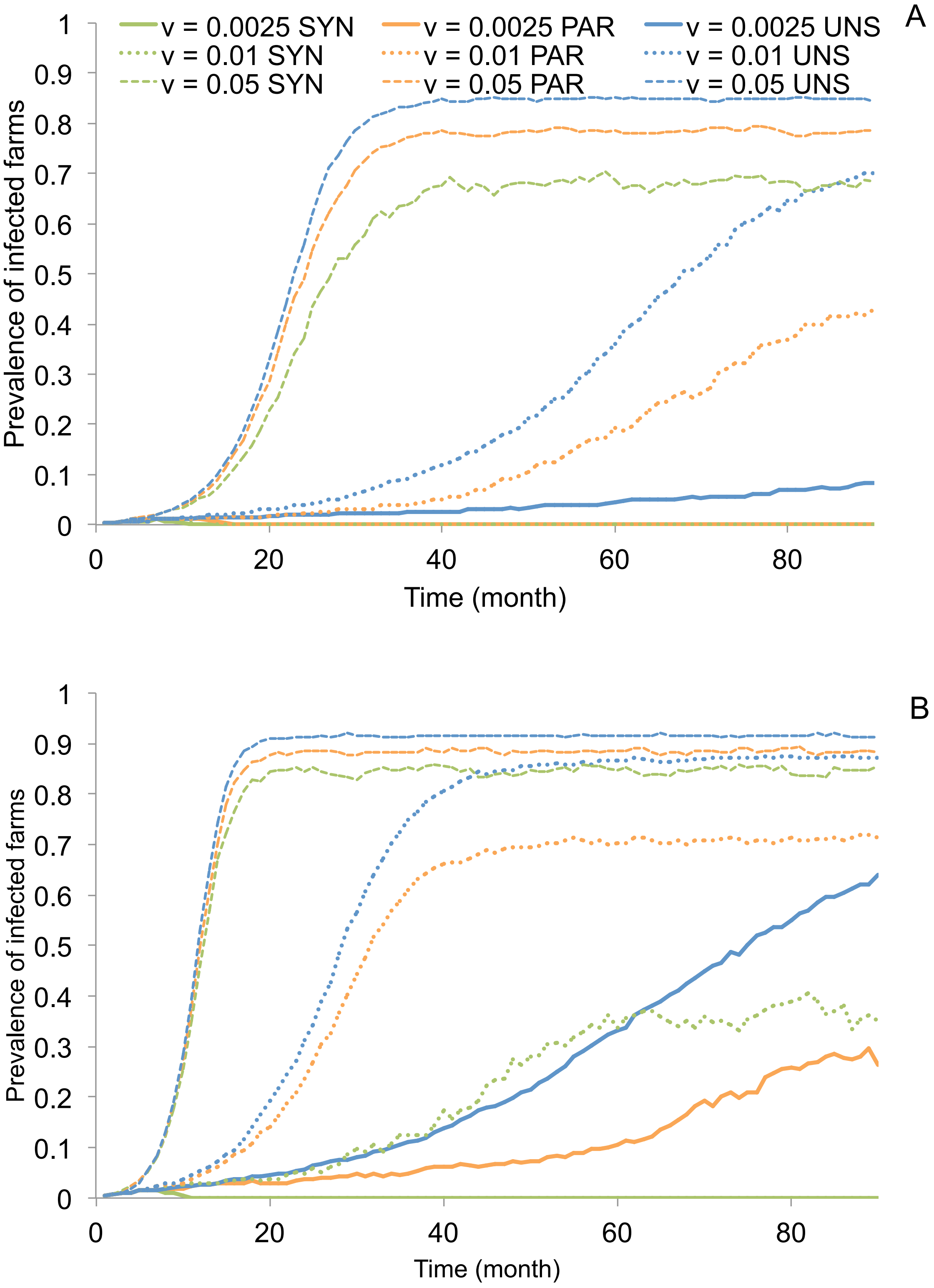

Figure 3.3. Median prevalence over time for three different fallowing strategies: synchronised (SYN), partial synchronised (PAR) and unsynchronised (UNS) and for transmission rates, $\beta = 0.25$ (A) and $\beta = 0.50$ (B). Median prevalences are shown for the probability of long-distance contact, $v = 0.0025$ to $v = 0.05$.

There were no differences in epidemic size between initiating an epidemic in a small or large management area at $t = 90$ for all SYN scenarios $(v = 0.0025$ to $v = 0.01)$ and for PAR and UNS when $\beta = 0.10$. For $\beta = 0.25$ and when PAR was applied, median prevalence was 0 when the index case was in a small management area $(v = 0.0025$ to $v = 0.01)$ and varied from 0.11 $(v = 0.0025)$ to 0.50 $(v = 0.01)$ when the index case was in large management areas. When UNS was applied, median prevalence was also higher when epidemics were initiated in large management areas (varied from 0.15 to 0.73, for respectively $v = 0.025$ and $v = 0.01$) compared with small management areas (varied from 0.02 to 0.68, for respectively $v = 0.0025$ and $v = 0.01$), however this difference was relatively smaller when v increased. The chance to eradicate an epidemic was larger when the index case was in small management areas compared with large management areas. The largest difference was noticed when PAR was applied; the chance to eradicate an epidemic for $\beta = 0.25$ dropped from 93.4% to 19.9% $(v = 0.0025)$; 84.1% to 18.2% $(v = 0.005)$; 70.8% to 16.0% $(v = 0.01)$ for respectively initiating an epidemic in small and large management areas. For PAR and $\beta = 0.10$, the chance to eradicate a pathogen was between 16% and 18% lower when the index case was in large management areas compared with small management areas. For UNS and $\beta = 0.10$ and $\beta = 0.25$ the chance to eradicate an epidemic was between 5% and 17% lower when the index case was in large management areas.

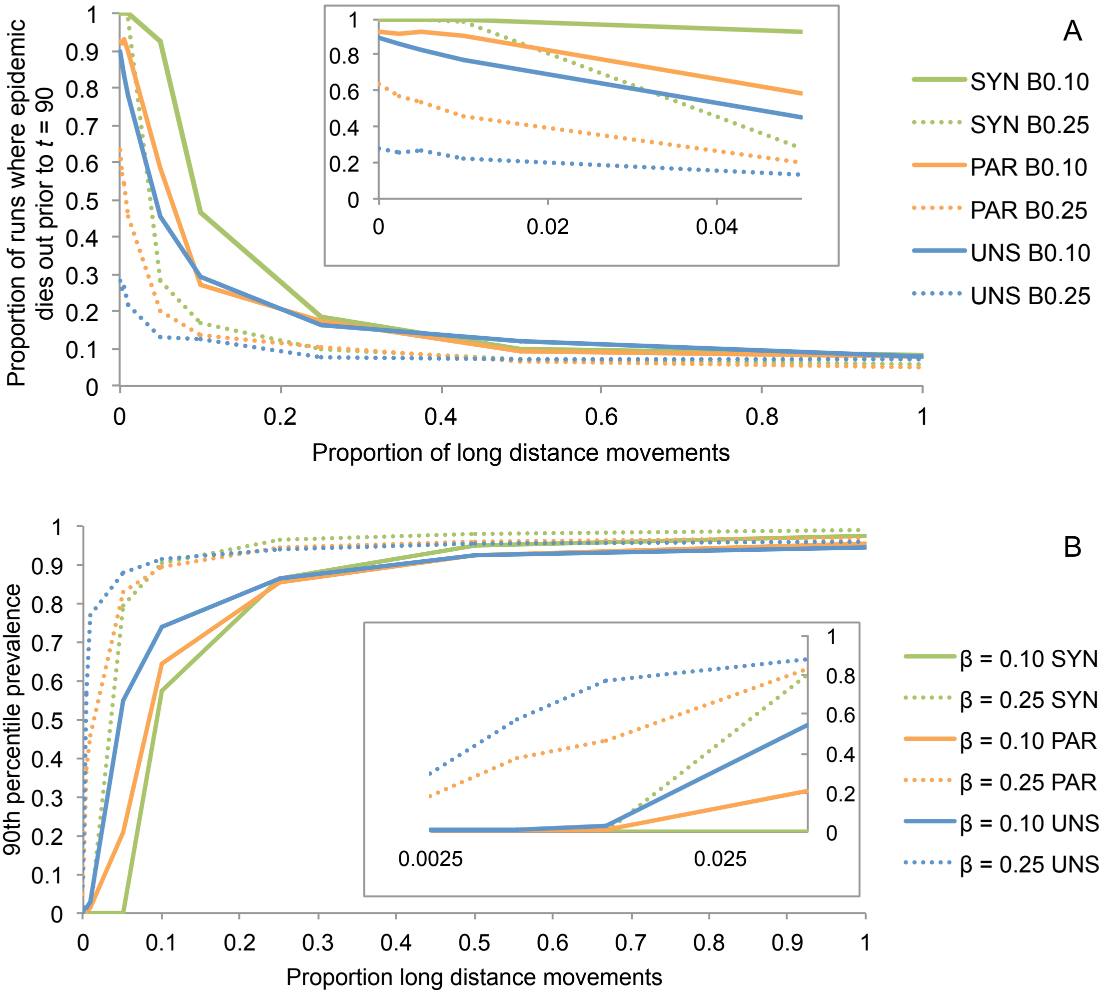

Figure 3.4. Proportion of runs where the epidemic died out prior to $t = 90$ (A) and worst-case scenarios presented by the 90th percentile at $t = 90$ (B). Both are represented for different proportions of long-distance movements v and different fallowing strategies synchronised (SYN), partial synchronised (PAR) and unsynchronised (UNS) and two different transmission rates $\beta = 0.10$ and $\beta = 0.25$.

3.4.2. Worst-case scenario

Worst-case scenarios as defined as 90th percentile (figure 3.4B) were in general lower for $\beta = 0.10$, compared with $\beta = 0.25$. As seen with median prevalence and epidemic persistence to $t = 90$, SYN has a beneficial effect, especially for $v \leq 0.05$ and $\beta = 0.10$. For $v = 0.05$, 90th percentiles were 0 (SYN), 0.21 (PAR) and 0.55 (UNS) for $\beta = 0.10$, there was no difference seen for this scenario for $\beta = 0.25$. However, fallowing had a substantial effect for $\beta = 0.25$ and $v = 0.01$. For this scenario, 90th percentiles were 0 (SYN), 0.46 (PAR) and 0.77 (UNS). The required parameters for a 90th percentile below 0.1 for UNS were $v < 0.01$ and $\beta = 0.10$, and when no long-distance movements were added for $\beta = 0.25$. There were no substantial differences noticed in the worst-case scenario between initiating an epidemic in small or large management areas, except when PAR was applied and for $\beta = 0.25$. However, this difference decreased when v increased. Worst-case scenarios increased from 0 to 0.25 $(v = 0.0025)$; 0.20 to 0.42 $(v = 0.005)$ and from 0.51 to 0.58 $(v = 0.01)$ for respectively initiating an epidemic in small and large management areas.

3.4.3. Adding contacts at local level

Adding contacts at a local level decreased the chance of eradicating an epidemic prior to $t = 90$ for $\beta = 0.10$ when PAR and UNS was applied (figure 3.5A). Adding 54 undirected local contacts on the whole network ($g = 0.05$, equivalent to 0.2 extra local out contacts per farm) reduced the chance of eradicating an epidemic compared with the original model where every farm has two local contacts (except for small management areas, see section 3.3.1). For example, for $\beta = 0.10$, using PAR and UNS decreased the chance of eradicating an epidemic prior to $t = 90$ by 0.15 to 0.20 ($g = 0.05$, figure 3.5A), for this scenario, compared with the original network with two contacts per farm $(g = 0)$. However, when applying SYN, additional contacts at a local level had no substantial effect. Conversely, with $\beta = 0.25$ and $v = 0.01$ the proportion of eradicated epidemics was reduced from 0.98 (no extra local contacts) to 0.89 when local connections were added $(g = 0.05)$ and SYN was applied. No reduction was observed for this scenario and $v = 0.0025$ (figure 5B). Using PAR or UNS showed no substantial reduction in the probability to eradicate an epidemic for $\beta = 0.25$ and $g = 0.05$.

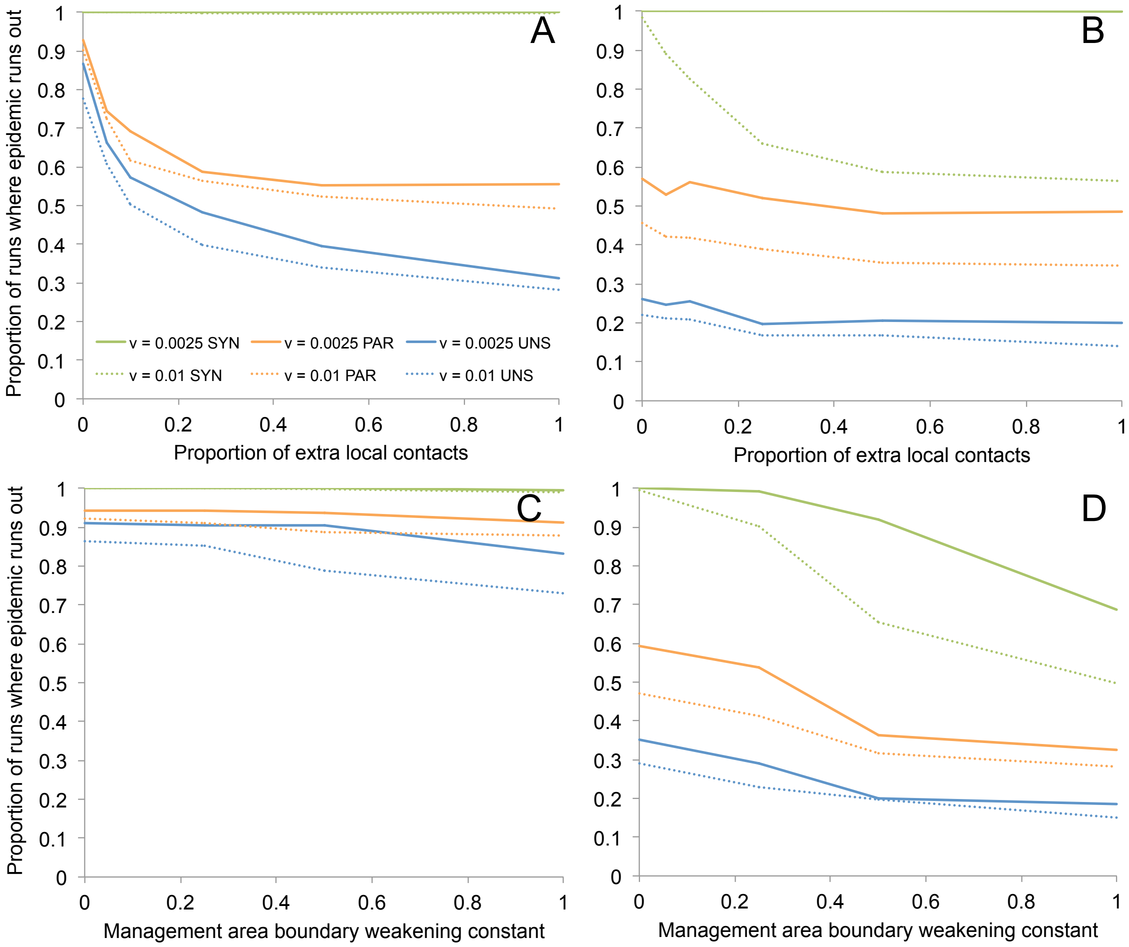

Figure 3.5. Percentage of runs where the epidemic died out prior to $t = 90$ in order to investigate the effects on epidemics when adding extra local contacts (in addition to the two neighbours). For the proportions of long-distance movements, $v = 0.0025$ and $v = 0.01$ and different fallowing strategies synchronised (SYN), partial synchronised (PAR) and unsynchronised (UNS) and for $\beta = 0.10$ (A) and $\beta = 0.25$ (B). The effects of weakening the management area boundaries on the amount of epidemics that die out prior to $t = 90$ for $\beta = 0.10$ (C) and $\beta = 0.25$ (D).

3.4.4. Imperfect management area boundaries

Weakening the management area boundaries with constant h had no substantial effect on eradicating epidemics for $\beta = 0.10$ and for the three different fallowing strategies (figure 3.5C). However, for $\beta = 0.25$, the proportion of eradicated epidemics at $t = 90$ decreased from 0.54 $(h = 0.25)$ to 0.36 $(h = 0.50)$, for PAR and $v = 0.0025$ (figure 3.5D). For SYN and $\beta = 0.25$ the proportions of epidemics that were eradicated prior to $t = 90$ was 0.91 when $h = 0.50$ and decreased to 0.69 when $h = 1.00$. Similarly, for UNS fallowing the ability to control an epidemic became smaller when the management area boundaries were weakened, although less dramatically (figure 3.5D).

3.5. Discussion

The significance of long-distance movements in disease transmission has been shown before in, for example, foot–and–mouth disease (Green et al., 2006a) and for ISA in Atlantic salmon (Murray et al., 2002). Movement of live fish between sites would almost certainly transmit pathogens if the source site was infected, but movement of fish infected with a notifiable disease such as ISA is prohibited (JGIWG, 2000). However, subclinical infections might go undetected (Murray and Peeler, 2005). IPNV is often subclinical (Bruno, 2004a) and there is evidence that even ISAv may persist for months on sites sub-clinically (Murray et al., 2010) which makes it harder to detect pathogens. In such circumstances long-distance movements can unknowingly spread pathogens (Murray and Peeler 2005). Contact by vessels might be a low risk, but there may be many of such contacts. Long-distance contacts are likely to be rare relative to local spread and therefore lower values of v will be more realistic. For example, ISA tends to occur in clusters, indicating higher rates of local spread compared with pathogen transmission over long-distances (Mardones et al., 2009). In this study we found that the amount of long-distance movements should not exceed 0.073 per farm per month assuming synchronised fallowing is not commonly used in all Scottish marine farms. Higher probabilities of long-distance movements (v) decreased the chance of eradicating an epidemic substantially with high transmission rates $\beta \geq 0.25$. This emphasises the value of epidemiologically isolated management areas. Even pathogens with slow rates of local spread being managed by synchronised fallowing were unlikely to be eradicated if long-distance transmission events were more common than 3.6 movements per farm per month.

The higher median prevalence and decreased chance of eradicating an epidemic when an epidemic is initiated in large management areas compared with small management areas when unsynchronised fallowing is applied occurs because pathogens can spread more easily between farms and persist longer at a local level. Local spread will be more important if long-distance movements occur less often than two movements per farm per month. Because large management areas have simply more farms, there is a higher prevalence when the index case is in large management areas. The difference between median prevalence and the chance to eradicate an epidemic is larger between an index case in small and large management areas when partial synchronised fallowing is applied. This is because synchronised fallowing is only applied in small management areas and large management areas apply unsynchronised fallowing.

For the assumptions used in this specific model, ideally, local contacts should be fewer than 2.2 local contacts per farm, for Scottish marine sites. However, it is likely that the results differ when the number of farms within a management area differs, since reducing contacts by the same number in small and large management areas results in a too small reduction of contacts in large management areas. In this study we assumed that neighbouring farms within the same management area had an equal risk of infection. We did not take into account the site-to-site distance by sea, currents or wind direction. The direction of spread is complicated by such considerations as described in Amundrud and Murray (2009).

The importance of local contacts was also seen in the ISA epidemic in Chile where long-distance movements and local transmission were both found to contribute to the transmission of the virus (Mardones et al., 2009). In addition, it is likely that if pathogens are persistent in the environment or in wild hosts, that they would re-infect farms (Rae, 2002; Plarre et al., 2005), which makes it harder to eradicate pathogens. Synchronised fallowing can increase the probability of eradicating an epidemic as synchronised fallowing quickly removes local spread.

Moreover management areas must have epidemiologically appropriate boundaries. If separation does not prevent at least 75% of spread then eradication becomes substantially less likely for pathogens with high rates of spread $(\beta \geq 0.25)$ as described in section 3.4.4.

In the model, the first production cycle after a disease outbreak is critical for control. If the pathogen is not eradicated during this time period, it is likely that a large number of farms will have been infected (figure 3.3). In this case, the disease is likely to become established as an endemic disease and eradication is unlikely or at least expensive. The Scottish ISA outbreaks of 1998/1999 which became widespread before detection (Murray et al., 2002), and 2008/2009 which was localised due to early detection, illustrate this point (Murray et al., 2010). During the British FMD outbreak in 2001, there was a delay in detecting the index case which resulted in a major epidemic (Gibbens et al., 2001). For this reason it is necessary to control emerging diseases at an early stage.

Pathogens may transmit vertically through ova, as well as horizontally. For vertical transmission to be important after introduction the risk of transmission has to be significant relative to horizontal transmission. In Norway the spread of ISA did not appear to be related to vertical transmission (Lyngstad et al., 2008). In Scotland parent fish are screened for key pathogens and ova are disinfected (Bruno et al., 2004a). This model can be applied to diseases where vertical transmission is a relatively small risk compared with horizontal transmission, although vertical transmission, even at low risk, might be a source of infection to the index case. Not including vertical transmission is a limitation of this model; however this model involves the site level rather than fish level. Therefore, not including vertical transmission is appropriate in this case.

Moreover, farms owned by the same company do have an increased risk of infection when a farm in that company is infected as shown with the ISA outbreak in Chile (Mardones et al., 2009). The random transmission in this model was a simplification and did not include the network structure.

Clearing farms has been proven to reduce the risk of re-infection of *Salmonella* infections in poultry (Namata et al., 2009) and in pigs (Beloeil et al., 2004; Lo Fo Wong et al., 2004), where all-in/all-out systems are commonly used. There are few studies of the effectiveness of fallowing strategies in aquaculture. Wheatley et al. (1995) demonstrated a reduced mortality rate in cycles where farmers applied fallowing strategies. Furthermore, it is believed that fallowing helps to control the sea louse *Lepeophtheirus salmonis* (Bron et al., 1993; Rae, 2002), however, is seems that fallowing is less effective in the control of the other sea louse species *Caligus elongatus* (Bron et al., 1993; Revie et al., 2002). From the experience of ISA outbreaks in the past, the time between diagnosis and clearing and fallowing the farms seems to be highly influential on subsequent spread (Mardones et al., 2009). So far, Scotland is the only country where an ISA outbreak has been eradicated. During the ISA outbreak in Scotland (1998/1999), farms were cleared within one month after confirmed diagnosis of ISA (Stagg et al., 2001). However, time between confirmed diagnosis and depopulating the affected farms has been estimated to be four to five months in the ISA outbreak in Chile (Mardones et al., 2009). In this study the fallowing time was one month, which is realistic when pathogens are not diagnosed (MSS, 2009b), as may occur when there are no clinical signs.

The use of this simple SIS model was valuable for showing the effectiveness of different fallowing strategies and the importance of reducing long-distance movements. However, the real-life situation is more complex in both pattern of contact between farms and disease characteristics. Long-distance movements occurred at random in this study, while reality is more complex and shows a high variance in the number of contacts between farms (Thrush and Peeler, 2006; Munro and Gregory, 2009; Green et al., 2009). Heterogeneity, i.e. variance in the number of contacts, is likely to affect the transmission pattern of disease significantly. It has been suggested that 80% of the infections are in general caused by 20% of the population (Anderson and May, 1992). The assumption of homogenous spread has been used to model the spread of IPNV through the salmon farming industries of both Scotland (Murray 2006b) and Ireland (Ruane et al. 2009). In this study, we assumed that long-distance movements were homogenous as unpublished data showed that variation in the number of contacts is substantially smaller between seawater contacts compared with contacts between freshwater sites.

Live fish movements do not occur at random, but are dependent on the size of the fish and the season. Timing of movements will be important for disease transmission. For example BKD outbreaks are more likely to occur during spring (MSS, 2010) and IPN outbreaks occur mainly after transfer to sea (May-August) (Bruno, 2004a). Therefore movements during spring may be more risky for BKD transmission compared with other periods of the year.

Different model types could be more appropriate for diseases with different characteristics, different modelling objectives, or different management systems. In this study we choose an SIS model, however, a SEIS (susceptible-exposed-infectious-susceptible) can take into account the variations of latent periods, which may vary largely between different diseases. In our SIS model a farm becomes infectious after one month. However, in the real-life situation this varies. For example, IPN outbreaks occur mainly after transfer to sea (Bruno, 2004a). During this vulnerable stage, transmission rates of IPN could be higher, and it is likely that this effects the time for a farm to become infectious. Furthermore, our model assumes that all farms were similar, excepting their membership of a particular management area, whereas Scottish farms have different stocking sizes (from <50 to >1000 tonnes, MSS, 2009b) and stocking densities. Stocking density can be important, as an outbreak of a viral disease is sensitive to a minimum effective concentration, which is influenced by stocking densities in farms (Hammell and Dohoo, 2005; Thrush and Peeler, 2006).

3.6. Conclusion

This simple model demonstrates the importance of long-distance movements in the spread of pathogens. In this model, even applying synchronised fallowing in combination with a low transmission rate could not prevent an epidemic when there were high numbers of long-distance movements between farms. However, when long-distance contacts are rare compared with local contacts, synchronised fallowing greatly improves the chance of controlling outbreaks. Therefore, it is important both to reduce the number of long-distance movements and to implement good bio-security measures to reduce disease spread and to synchronise fallowing to enhance eradication.

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CHAPTER 4. Seasonality and heterogeneity of live fish movements in Scottish fish farms

Werkman, M.; Green, D.M.; Munro, L.A.; Murray, A.G.; Turnbull, J.F

In chapter 3, live fish movements occurred at random between seawater sites, in this chapter the contact structure of the Scottish salmonid industry is discussed in detail. Movement records from 2002 to 2004 were collected from Marine Scotland (MSS), Aberdeen.

Data were collected and edited by the main author, Marleen Werkman, and L.A. Munro (MSS). This chapter was constructed by the main author and all co-authors provided assistance during the writing process and edited the manuscript.

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CHAPTER 4. Seasonality and heterogeneity of live fish movements in Scottish fish farms

Werkman, M.; Green, D.M.; Munro, L.A.; Murray, A.G.; Turnbull, J.F.

4.1. Abstract

Movement of live animals is a key contributor to disease spread. Farmed Atlantic salmon *Salmo salar*, rainbow trout *Onchorynchus mykiss* and brown/sea trout *Salmo trutta* are initially raised in freshwater (FW) farms; all the salmon and some of the trout are subsequently moved to seawater (SW) farms. Frequently, fish are moved between farms during their FW stage and sometimes during their SW stage. Seasonality and differences in contact patterns across production phases have been shown to influence the course of an epidemic in livestock; however, these parameters have not been included in previous network models studying disease transmission in salmonids. In Scotland, farmers are required to register fish movements onto and off of their farms; these records were used in the present study to investigate seasonality and heterogeneity of movements for each production phase separately for farmed salmon, rainbow trout and brown/sea trout. Salmon FW–FW and FW–SW movements showed a higher degree of heterogeneity in number of contacts and different seasonal patterns compared with SW–SW movements. FW–FW movements peaked from May to July and FW–SW movements peaked from March to April and from October to November. Salmon SW–SW movements occurred more consistently over the year and showed fewer connections and number of repeated connections between farms. Therefore, the salmon SW–SW network might be treated as homogeneous regarding the number of connections between farms and without seasonality. However, seasonality and production phase should be included in simulation models concerning FW–FW and FW–SW movements specifically. The number of rainbow trout FW-FW and brown/sea trout FW-FW movements were different from random. However, movements from other production phases were too low to discern a seasonal pattern or differences in contact pattern

Keywords: disease transmission, epidemiology, contact structure, aquaculture

4.2. Introduction

Finfish culture in Scotland produces Atlantic salmon *Salmo salar*, rainbow trout *Oncorhynchus mykiss*, brown/sea trout *Salmo trutta* and other species such as arctic charr *Salvelinus alpinus* and halibut *Hippoglossus hippoglossus*. Brown trout and sea trout belong to the same species, and are not distinguished in this study. Hereafter, brown trout refers to both brown and sea trout.

Scottish production includes ca. 144,000 tonnes of salmon, 6800 tonnes of rainbow trout and 200 tonnes of brown trout per year (Marine Scotland Science 2010b). Salmon (and some brown trout) are anadromous and have a freshwater (FW) and a seawater (SW) phase. In FW, salmon eggs are fertilized and hatched in a hatchery. Next, fry are transported to FW farms. After approximately 12 to 16 mo, the fish (smolts) are moved to marine waters, where they achieve their harvest size after approximately a further 18 mo. Occasionally, salmon are moved between farms during the marine phase. Furthermore, SW–FW movements are needed to provide FW farms with broodstock (i.e. mature fish kept for breeding).

Rainbow trout can also be anadromous and their life cycle is similar; however, most rainbow trout are reared in FW without a marine phase. Live rainbow trout movements mainly occur between hatcheries and on-growing farms where juvenile fish are kept till harvest or moved to fisheries for re-stocking. The movement structure of these cultured fish species is pyramidal, with more movements going from the top (hatcheries) to the bottom (smolt producers or on-growers), which can be compared with the movement structure of industries such as of pigs (Lindstrom et al. 2010) and poultry (Cox & Pavic 2010).

Live fish movements are a risk for pathogen transmission between farms (Murray et al. 2002, Murray & Peeler 2005). Pathogens can also be introduced by other pathways such as well-boat visits (Murray et al. 2002) and on a local level by water movement (Jonkers et al. 2010) or by wild fish movements (Uglem et al. 2009). Disease outbreaks can cause reduced appetite, reduced growth and increased mortality rates, depending on the disease (OIE 2009), reducing production and profitability (Murray & Peeler 2005). In addition, disease outbreaks can cause welfare problems (Turnbull & Kadri 2007), and pathogen accumulation in fish farms may lead to transmission of pathogens to wild fish populations (Wallace et al. 2008).

If fish are infected and transported there is a great risk that the receiving farm will become infected (Murray & Peeler 2005). Therefore, movements from source farms known to be infected with a notifiable disease are prohibited (Joint Government/Industry Working Group 2000). However, notifiable and other infections can go undetected (Murray & Peeler 2005, Graham et al. 2006, Lyngstad et al. 2008). Therefore, pathogens may spread through live fish movements before pathogens are detected (Jonkers et al. 2010). For example, the spread of infectious salmon anaemia virus (ISAv) between regions during the 1998–1999 outbreak in Scotland was largely due to live fish movements (Murray et al. 2002), and movements are also thought to have played an important role in other outbreaks such as those in Chile (Mardones et al. 2009). Live fish movements have been identified as a risk factor for pathogen transmission for diseases such as viral haemorrhagic septicaemia (VHS) (Thrush & Peeler 2006), sleeping disease (Branson 2003) or for potential introduction of *Gyrodactylus salaris* in the UK (Peeler & Thrush 2004).

Some fish pathogens are only infectious in one environment (either FW or SW) or during a specific life stage. For example, *G. salaris* can survive only in FW, and ISAv causes clinical diseases only in SW (OIE 2009). Infectious pancreatic necrosis virus (IPNV) and bacterial kidney disease (BKD) affect salmonids in both FW and SW; initially, both these diseases emerged in FW and only later were the pathogens observed to cause disease in SW. IPNV causes clinical outbreaks in fry or during the first weeks after transfer to sea (Smail et al. 1992, Bruno 2004). BKD affects almost all age groups, especially when the water temperatures are rising, except in very young salmonids (Marine Scotland Science 2010a). Where diseases affect one species more than another, carrier species could play an important role in spreading a pathogen, as infections are likely to be hard to detect. For example, potential undetected sub-clinical spread of *G. salaris* with trout movements can lead to infection of salmon, where it causes serious disease (Peeler & Thrush 2004). This combination of environment and host will determine which species or life stage is most relevant for disease transmission.

Network models are often used to understand the transmission of pathogens between epidemiological units, e.g. animals or farms. They have been used for modelling foot–and–mouth disease (FMD) (Green et al. 2006, Kiss et al. 2006) and avian influenza (Dent et al. 2008), amongst other diseases. These models are valuable because they can identify farms that are important in the spread of pathogens and provide a valuable tool for designing and investigating the effectiveness of control strategies (Green et al. 2011).

Contact between farms often shows a large variation in the number, timing and direction of contacts (Thrush & Peeler 2006, Munro & Gregory 2009, Green et al. 2009). Heterogeneity, i.e. variation in the number of contacts, affects the transmission pattern in a network (Anderson & May 1992). It is often stated as a rule of thumb that 20% of the population can cause approximately 80% of the infections (Anderson &

May 1992, Woolhouse et al. 1997, Volkova et al. 2010). Previous work has shown a high variation in the number of contacts between farms for live salmon movements (Munro & Gregory 2009) and that a targeted surveillance strategy in a small number of farms will substantially decrease the risk of an epidemic (Green et al. 2009). Basic reproduction number (R0, i.e. the average number of secondary infections caused by one primary infection in a fully susceptible population) and clustering are both likely to affect the final epidemic size. When R0 < 1, there will be a small epidemic, whereas when R0 > 1, this is likely to result in a large epidemic (Anderson & May 1992). A high degree of clustering will reduce the final epidemic size and R0 (Keeling 1999, Kiss et al. 2005).

Sheep movement data in the UK (Kiss et al. 2006), Italian cattle movement data (Natale et al. 2009) and Swedish cattle data (Noremark et al. 2009) show clear seasonality. Seasonality is commonly not included in aquatic network studies. However, epidemics are more likely to start and to become widespread during a period of high movement activity (Kiss et al. 2006), which was illustrated during the FMD epidemic in the UK in 2001 (Gibbens et al. 2001). Moreover, studies in cattle (Bigras-Poulin et al. 2006, Natale et al. 2009) and pigs (Bigras-Poulin et al. 2007, Lindstrom et al. 2010) showed differences in the contact structure across different production phases, which are likely to affect the course of an epidemic. This suggests that there is value in studying aquaculture network structures in more detail.

The aim of the present study was to provide a detailed description of the number of live fish movements per farm and their timing for Atlantic salmon, rainbow trout and brown trout in Scottish aquaculture stratified by production phase. This can be used to improve and develop pathogen transmission models in Scottish aquaculture. It is of interest whether we can treat the movement network as static or whether we need to include seasonality or production phase. Because of the differences in husbandry conditions, there was a need to investigate whether there were differences in the timing of movements and contact structure between salmon, rainbow trout and brown trout movements. This could have implications for biosecurity strategies, including timing of official surveillance.

4.3. Data analysis

In Scotland, fish farmers are required to record the live fish movements onto and off of each farm (including movements that occur between farms of the same owner). The fish health inspectors at Marine Scotland, Aberdeen, hold these records. We used the movement records from 1 January 2002 to 31 December 2004 for salmon and from 1 January 2003 to 31 December 2004 for rainbow trout and brown trout. More recent data were not available in a database format. These records included both ova and fish. Confirmed records (i.e. movements recorded at both source and destination farm) were entered in a database. Movements onto or off unregistered sites (such as fisheries), or movements only recorded at either the source or destination farm, could not be validated and were excluded. For example, fisheries can be treated as sinks, as they only receive fish and do not move fish off the site; fisheries were therefore excluded from this study. Movements onto or from sites outside Scotland and movements to harvest stations were recorded separately. An overview of the different stages of data organisation from movements between registered farms is given in figure 4.1.

Movements were divided into five categories: freshwater to freshwater (FW–FW), freshwater to seawater (FW–SW), seawater to seawater (SW–SW), seawater to freshwater (SW–FW) and ‘other’. ‘Other’ includes movements onto and off of farms that have both FW and SW facilities (N = 10). These farms were mostly research facilities (N = 7), which transport relatively small numbers of fish; 3 farms were commercial hatcheries with both FW and SW capabilities. The classification of these movements was based on the facilities available on the farms.

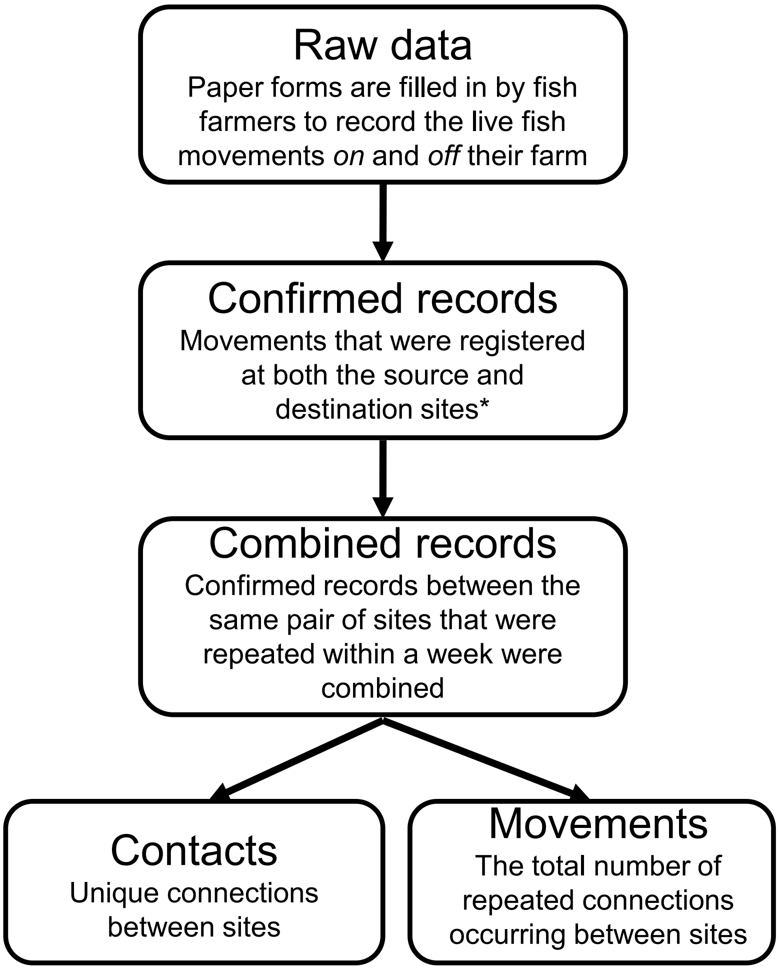

Figure 4.1. An overview of the different data levels. *Movements onto and off of Scottish farms from outside Scotland and harvest movements could not be validated and were entered into a different data set; these movements were not included in the on and off counts in the data described in this figure.

A degree of consistency in the live fish movement network structure is shown in a previous study for the years 2002 to 2004 (Green et al. 2011); therefore, the Scottish live fish movement network is somewhat stable and it is likely some contacts will repeat across years. To investigate the concordance of contacts between the years 2003 and 2004, we calculated the mean arc persistence (MAP) by dividing the number of contacts present in both years (a) divided by the geometric mean of the numbers of contacts present in each year (x = 2003 and y = 2004):

$$mean\ arc\ persistence = \frac{a}{\sqrt{xy}} \quad (1)$$

This was performed for the different movement types of salmon and ‘all’ movements of rainbow trout and brown trout.

4.3.1. Salmon

During 2002 to 2004, 3730 salmon movement records were confirmed. However, approximately 36% of these movements were multiple movements between the same pairs of farms within the course of a week. The infection status of the source farm is relatively unlikely to have changed over such a short period; we therefore decided to combine the movement records that occurred within 1 wk between the same pair of farms and to record them as one movement (figure 4.1). Moreover, in some cases the receiving farm recorded multiple movements whereas the source farms recorded the same movements as one movement (or vice versa). To be consistent, we combined the multiple movements in these cases and recorded them as one movement. The movement dates of these combined records were the starting date of these series of movements and numbers of fish were added together. This resulted in 2401 salmon movements. The proportion of movement records that were combined were similar across the different types of movement and varied from 32% in FW–SW movements to 39% in SW–FW movements.

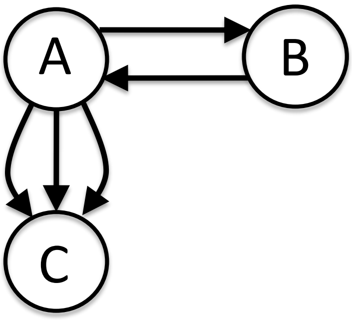

Figure 4.2. Simplified graphical view of part of the network to explain the differences between movements and contacts. In this example, farm A has 4 movements off the farm divided over 2 contacts (Farm B and C) and has 1 movement (and contact) onto the farm. Farm B has 1 movement (and contact) onto and 1 movement (and contact) off of the farm. Farm C has 3 movements onto the farm coming from 1 contact.

We made a distinction between contacts and movements. Contacts in this study are unique connections between farms and lack temporal perspective, whereas movements are the total number of repeated connections occurring between farms, which may occur more than once (figure 4.1). In figure 4.2, a simplified network is shown. We made this distinction as live fish movements to different farms are presumed to have a different impact on pathogen transmission in the network than multiple movements between the same pair of farms.

During 2002 to 2004, 499 salmon farms were active (i.e. farms in a production growing cycle either having stock or fallowing), of which 186 were FW farms, 304 were SW farms and 9 farms had both FW and SW facilities. The majority of movements occurred between FW farms, whereas FW–SW movements contained more contacts (table 4.1).

Table 4.1. Number of movements and contacts between farms stratified by type of movement. FW: freshwater; SW: seawater; other: movements/contacts are onto or off a farm with both facilities.

Type	Movements	Contacts
Salmon (total)	2401	1208
FW–FW	1181	400
FW–SW	810	595
SW–SW	237	154
SW–FW	54	22
Other	119	37
Rainbow trout (total)	343	69
FW–FW	310	59
FW–SW	30	9
Other	3	1
Brown trout (total)	82	31
FW–FW	60	22
FW–SW	12	5
SW–SW	6	1
SW–FW	2	2
Other	2	1

4.3.2. Rainbow trout

There were 432 confirmed rainbow trout movement records during the years 2003 and 2004. Combining the movement records that occurred within 1 wk resulted in 343 combined records. During the study period there were 55 active rainbow trout farms: 46 FW farms, 7 SW farms and 2 farms with both FW and SW facilities. The majority of rainbow trout movements occurred between FW farms; the remaining movements were classified as FW–SW and ‘other’ (table 4.1).

4.3.3. Brown trout

Of the confirmed movement records, 36% occurred within 1 wk; after combining those movement records, 82 combined brown trout records remained. Recorded movements took place between 34 active brown trout farms, of which 28 were FW farms, 5 were SW farms and 1 had both facilities. Again, the majority of movements were between FW farms, followed by FW–SW, SW–SW, SW–FW and ‘other’ movements (table 4.1).

4.3.4. Harvest movements and movements to and from Scotland

Salmon were often not processed at the marine farm where they achieved their harvest weight, but were transported to harvest stations for processing. The live fish movements towards these harvest stations are listed as harvest movements. Movements to harvest stations should not be epidemiologically relevant if fish are maintained in biosecure transport and blood is disposed of hygienically (Munro et al. 2003). However, if harvest sites become contaminated, they can be a very serious focus for disease spread (Murray et al. 2002).

In addition to the movements mentioned above, there were 1980 salmon harvest movements recorded during the period 1 January 2002 to 31 December 2004. Movements to the same harvest station that re-occurred within 1 wk were combined and reported as 1 movement, which resulted in 829 combined harvest records. The number of movements to harvest stations is likely to be larger than that obtained in our data set as many harvest movements may not have been recorded as live fish movements. We have no records of dead fish moved to processing plants.

Records of Scottish imports and exports of live fish were treated similarly as the harvest records, which reduced the number of movement records from 331 to 253. There were 192 movements onto Scottish farms from outside Scotland and 61 Scottish exports in 2002–2004 (see table 4.2). These international movements are in addition to the national and harvest movements.

Table 4.2. Number of Scottish salmon import and export movements per year

	2002	2003	2004	Total
Imports	77	59	56	192
Exports	17	18	26	61

4.3.5. Seasonality

To test whether the number of movements per month was significantly different from random, we performed a chi-square test for all types of movements that had an expected number of movements (total number of movements/time period) of ≥ 5 per month (which were salmon: all movements, FW–FW, FW–SW and SW–SW; rainbow trout: all movements and FW–FW). For the less common movements, we combined the movements belonging to the same season (salmon: other, brown trout: all movements and FW–FW). The expected numbers of salmon SW–FW, rainbow trout FW–SW and other, and brown trout FW–SW, SW–SW, SW–FW and other were <5, even after combining the months belonging to the same season; therefore, there was no chi-square test performed on these movements.

In addition, we investigated by least-squares regression whether there was a significant sinusoidal seasonal trend with a period of 1 yr (for all types of movements with an expected number of movements >5 per month). In the regression model, we fitted the number of movements (y) as follows:

$$y = a + b\cos\frac{2\pi m}{t} + c\, sin\frac{2\pi m}{t} + d\, cos\frac{4\pi m}{t} + e\, sin\frac{4\pi m}{t} + \varepsilon \qquad (2)$$

where ε is the error term, a is the mean, and b,c,d and e together determine the magnitude and phase for yearly (b,c) and twice-yearly $(d,\ e)$ seasonal patterns. The variable m represents the time step, which relates to $t =$ 12 mo. If the residuals did not follow a normal distribution, data were square-root-transformed (salmon: all movements and SW–SW) or log10-transformed (salmon FW–SW) to normalise the residuals. We performed the analysis in Minitab 16.

4.4. Results

4.4.1. Timing of movements

The highest total number of salmon movements per month was in April (372 movements; figure 4.3A). The number of movements per month was significantly different from random (chi-square, $p < 0.001$, df = 35) and showed a significant seasonal trend ($F_{4,31} = 12.96$, $p < 0.001$, $r^2 = 62.6\%$).

Timings of salmon movements differed among the type of movements (figure 4.3A). The number of salmon FW-FW movements was increased during May ($n = 146$), June ($n =$ 152) and July ($n =$ 142). SW farms were supplied with smolts mainly in March and April ($n =$ 149 and $n =$ 275) and October and November ($n =$ 84 and $n =$ 81). Salmon SW–SW movements were more constant throughout the year; however, they showed seasonal variation between years. Salmon SW–FW movements occurred mainly during September ($n =$ 12) and October ($n =$ 17). The number of movements per month from FW–FW, FW–SW, SW–SW (chi-square, $p < 0.001$, df = 35) and other (chi-square, $p < 0.001$, df = 11) were significantly different from random. FW–FW ($F_{4,31} = 17.80$, $p < 0.001$, $r^2 = 69.7\%$) and FW–SW movements

($F_{4,31}$ = 20.96, p <0.001, r^2 = 73.0%) showed a significant seasonal trend. Salmon SW–SW movements did not show a significant seasonal trend ($F_{4,31}$ = 0.37, p = 0.827, r^2 = 4.6%).

Timing of rainbow trout movements were more constant throughout the year compared with salmon movements; however, fewer rainbow trout movements occurred during the winter period (December, $n =$ 6; January, $n =$ 13 and February, $n =$17; figure 4.3B). The number of movements per month for the total number of rainbow trout movements and rainbow trout FW–FW movements were significantly different from random (chi-square p < 0.001, df = 23) and showed a seasonal trend for both total number of rainbow trout movements ($F_{4,19}$ = 8.72, p < 0.001, r^2 = 64.7%) and rainbow trout FW–FW movements ($F_{4,19}$ = 7.81, p = 0.001, r^2 = 62.2%). The residuals of both rainbow trout models showed a temporal trend. Rainbow trout FW–SW movements peaked at different times compared with salmon movements, namely during June and September–October. However, the numbers of movements were too low to discern any seasonal patterns.

Brown trout FW–FW movements mainly occurred in June ($n =$ 11), November ($n =$ 15) and December ($n =$ 8) during the period studied (figure 4.3C). The numbers of movements per season were significant different from random (chi-square, p < 0.001, df = 7) for both all movements and FW–FW movements.

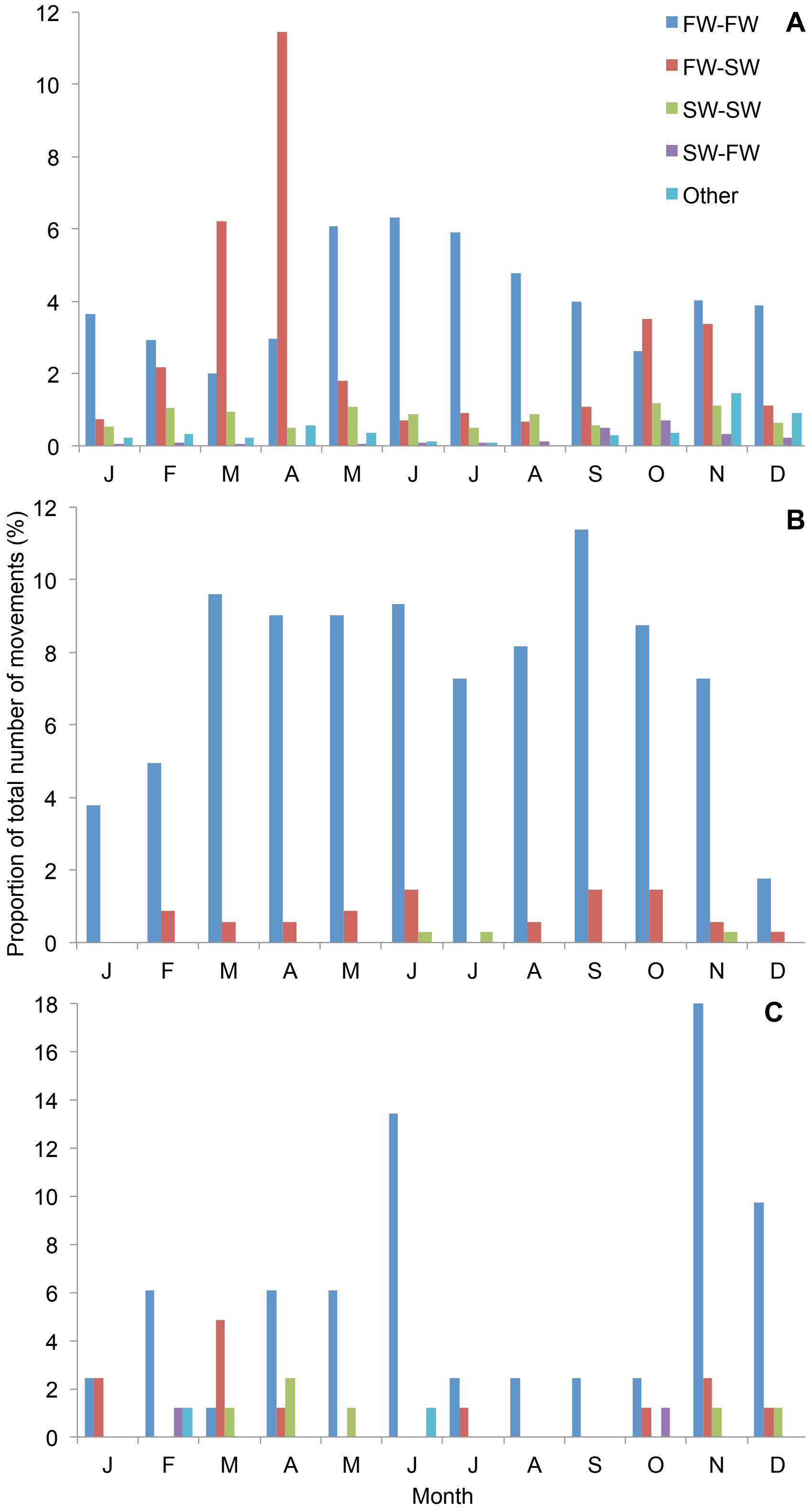

Figure 4.3. Seasonal patterns of live fish movements of Scottish aquaculture, stratified by production phase (FW: freshwater; SW: seawater). 'Other' movements are movements onto or off farms with both FW and SW facilities. (A) Data for 2002–2004 for salmon ($n =$ 2401). (B) Data for 2003–2004 for rainbow trout ($n =$ 434). (C) Data for 2003–2004 for brown trout ($n = 82$). Numbers of movements per month are represented as the percentage of the total number of movements of the specified species

4.4.2. Variation in contact structure

During 2002–2004, 299 salmon farms had movements off the farms. As was anticipated from the industry structure, there were more farms that had movements onto their farms $(n = 471)$; however, the number of movements and contacts per farm was lower (table 4.3). Many movements were repeated between the same pairs of farms. The number of unique contacts per farm was therefore lower compared with the total number of movements per farm (figure 4.4A); there was a larger variation in the number of movements per farm than in the number of contacts per farm (table 4.3).

The variation in number of movements and contacts differed across the salmon production phases (table 4.3). Salmon FW–FW movements had the largest range of total number of movements onto (min = 1, max = 38) and off (min = 1, max = 52) per farm, whereas FW–SW movements had the highest number of contacts going onto (min = 1, max 11) and off (min = 1, max = 24) their farms. Approximately 40% of the salmon SW farms received smolts from 3 or more different suppliers (figure 4.5).

We did not stratify the rainbow trout and brown trout movements to study the contact structure across production phases because by far the majority of movements were between FW farms. Forty-four rainbow trout farms had movements onto their farms and 28 farms had movements off their farms during 2003–2004. The maximum number of movements and contacts onto farms was higher than the number of contacts and movements off farms (table 4.3).

Table 4.3. Descriptive statistics for movements and contacts per farm for salmon (2002–2004 data, stratified by production phase), rainbow trout and brown trout (2003–2004 data)

		MOVEMENTS		CONTACTS	
		ON	OFF	ON	OFF
Salmon (ALL)	Median	4	4	2	2
	Mean	5.1	8.0	2.6	4.0
	Variance to mean ratio	13.3	4.9	1.1	5.0
	Maximum	38	65	11	24
Salmon (FW–FW)	Median	5	7	2	2
	Mean	7.3	10.9	2.5	3.7
	Variance to mean ratio	5.8	11.8	1.0	3.7
	Maximum	38	52	8	20
Salmon (FW–SW)	Median	3	4	2	3
	Mean	3.4	6.3	2.5	4.6
	Variance to mean ratio	2.0	6.5	1.0	3.4
	Maximum	16	44	11	24
Salmon (SW–SW)	Median	1	2	1	1
	Mean	2.1	2.1	1.4	1.3
	Variance to mean ratio	2.6	1.0	0.5	0.3
	Maximum	22	10	6	4
Salmon (SW–FW)	Median	3	3	1	1
	Mean	3.4	4.2	1.4	1.7
	Variance to mean ratio	1.4	3.3	0.3	1.1
	Maximum	8	15	3	6
Salmon ('Other')	Median	4.5	1	1	1
	Mean	6.0	5.4	1.9	1.7
	Variance to mean ratio	2.9	14.8	0.8	1.4
	Maximum	13	36	5	6
Rainbow trout (ALL)	Median	4	4.5	1	1
	Mean	7.8	12.3	1.6	2.5
	Variance to mean ratio	11.6	23.3	0.5	2.7
	Maximum	45	62	4	12
Brown trout (ALL)	Median	1	2	1	1
	Mean	2.9	3.9	1.1	1.5
	Variance to mean ratio	3.0	3.5	0.1	0.3
	Maximum	11	13	2	3

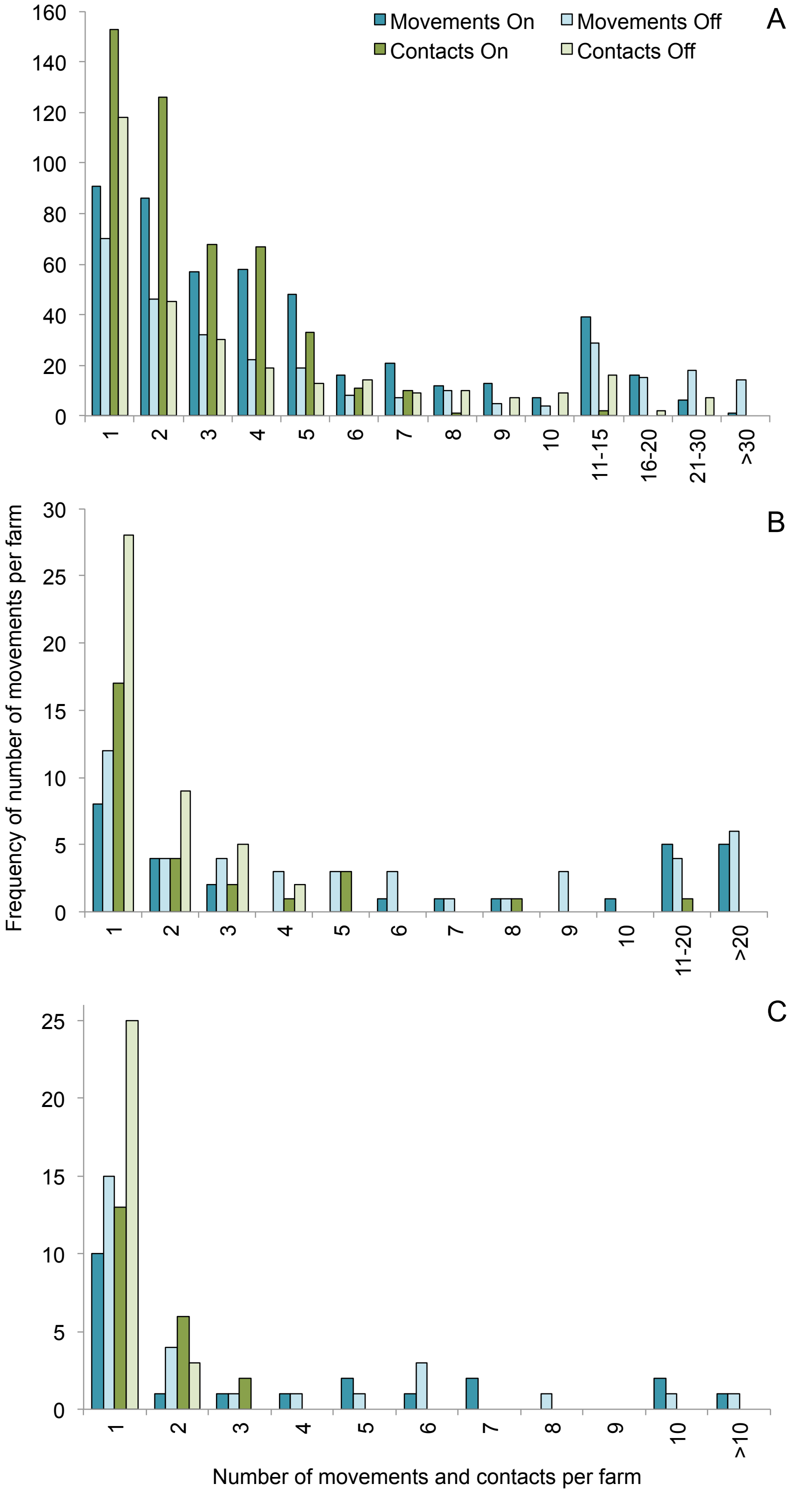

Figure 4.4. Number of movements and contacts per farm for (A) salmon ($n = 2401$), (B) rainbow trout ($n = 434$) and (C) brown trout ($n = 82$). The majority of the farms had multiple movements from one contact; therefore, a distinction was made between the total number of movements per farms and the number of contacts per farm. Farms often had multiple movements going onto or off their farm; therefore, there are more farms with a lower number of contacts than number of movements

There were fewer brown trout farms than rainbow trout or salmon farms. During 2003 to 2004, 28 farms had brown trout movements onto their farm and 21 farms had movements off of their farm. The number of movements and contacts per farm were lower for movements onto farms than for movements off of farms.

There was a moderate concordance in the contacts between years 2003 and 2004 for salmon FW–FW contacts (mean arc persistence, MAP = 0.51) and other contacts (MAP = 0.55), as well as for all rainbow trout contacts (MAP = 0.50) and all brown trout contacts (MAP = 0.56). The MAP for the remaining salmon contacts was low; 0.05 for FW–SW, 0.18 for SW–SW and 0.20 for SW–FW.

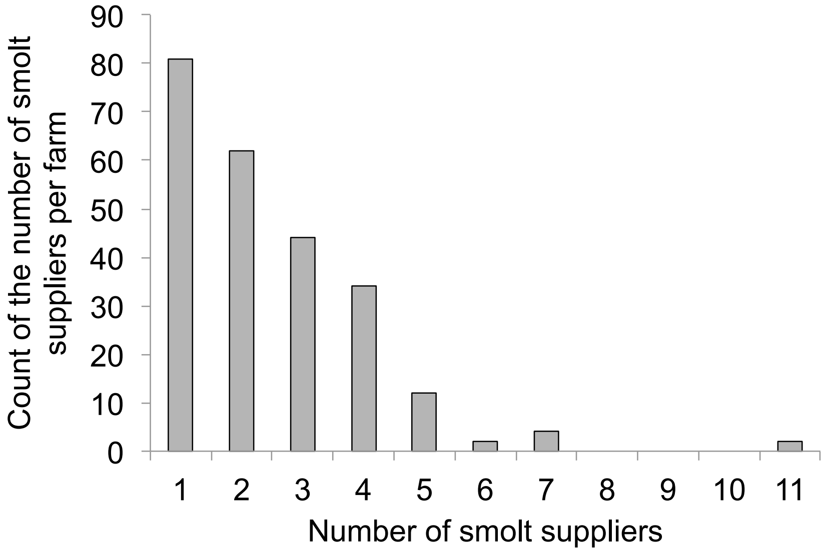

Figure 4.5. Distribution of the number of smolt suppliers per farm for salmon farms.

4.4.3. Harvest movements

The majority of the harvest movements (540) were recorded in 2004, compared with 94 in 2002 and 195 in 2003 (figure 4.6). In 2003 and 2004, the number of harvest movements increased during August and December, which made these months an extra risk of a source of infection for farms in close proximity to harvest stations.

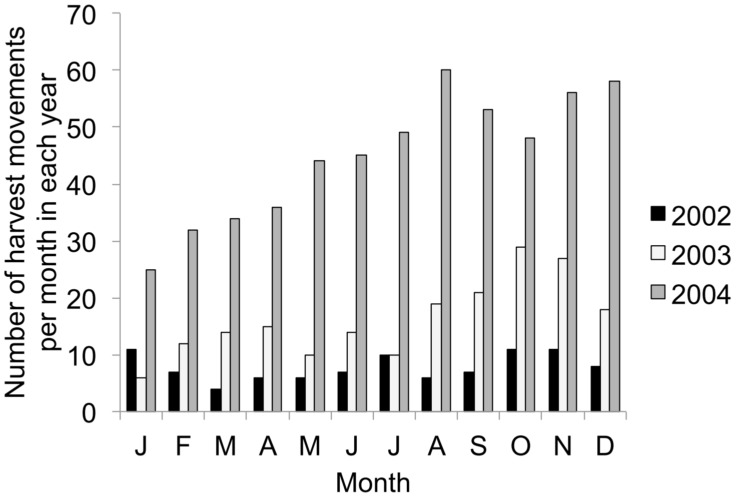

Figure 4.6. Number of salmon harvest movements per year.

4.3.4. Movements to and from Scotland

There are strict biosecurity measures for live fish imported from other countries, with the exception of movements to or from Wales and England; however, there is still a risk of introduction of pathogens. This might have occurred with IPNV in Ireland (Ruane et al. 2009).

There were 192 movements going onto Scottish farms (figure 4.7A) originating from outside of Scotland. Imports of live fish occurred from Ireland, the Isle of Man and England, whereas imports of ova occurred from Iceland, Australia, Denmark (trout ova only), Norway (salmon ova only) and the USA. There were also 61 movements to farms outside Scotland (figure 4.7B). Destinations for live fish were England and Ireland, whereas ova were exported to EU member states and Chile. Eight farms had movements going on or off the farms outside Scotland. In January and December, there was a peak of both the export and import of live salmon. The lowest numbers of imports were during August to November. Epidemic models that simulate the introduction of exotic diseases introduced by international movements should take into account the seasonality of these movements. However, the timing of these movements showed differences between the years studied (figure 4.7A).

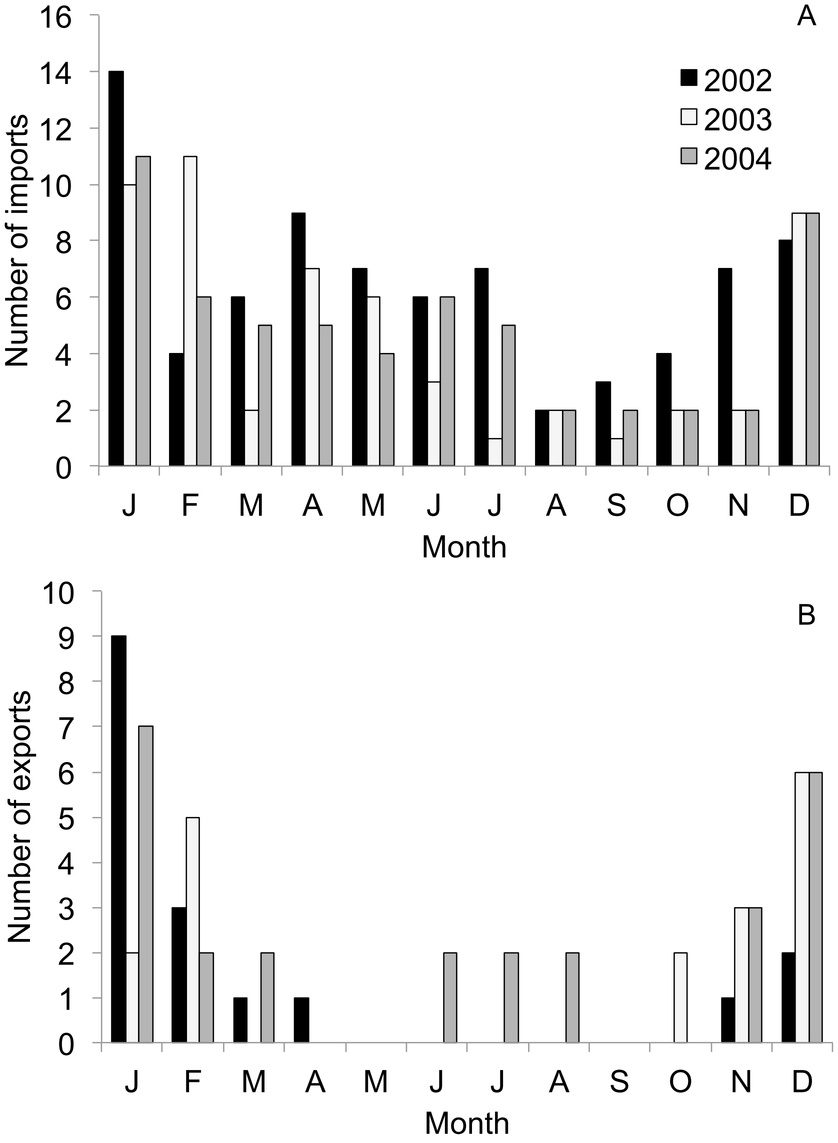

Figure 4.7. Salmon movements in/out of Scotland. (A) Imports; (B) exports

4.5. Discussion

To our knowledge, this is the first study describing seasonality and contact structure stratified by production phase of live fish movements.

4.5.1. Contact structure

These data show heterogeneity in the number of movements and contacts across different production phases; these differences could change the course of an epidemic considerably (Bigras-Poulin et al. 2006, Bigras-Poulin et al. 2007, Natale et al. 2009, Lindstrom et al. 2010). Salmon SW–SW, SW–FW and other movements had lower numbers of movements and contacts per farm compared with salmon FW–FW and FW–SW movements and contacts. An index case in a salmon hatchery or other salmon FW farm is likely to result in a larger epidemic (especially when farms with many off contacts are infected) than an epidemic that starts in a salmon SW farm because of differences in direction and number of contacts. Salmon FW farms are likely to be sources for infections, whereas salmon SW farms are more likely to be sinks. Because of the low numbers of FW–SW and SW–SW movements compared with FW–FW movements in rainbow trout and brown trout, differences in contact structure between the different types of movements were not distinguished.

The number of smolt suppliers supplying a farm has often been identified as a risk factor for disease outbreaks on salmon production farms, such as for IPN (Jarp et al. 1995, Murray 2006) and ISA (Vagsholm et al. 1994, Jarp & Karlsen 1997). In the present study, FW–SW movements showed a large range of contacts per farm. Although it might not always be possible to limit the number of smolt suppliers, a further reduction of the number of FW–SW contacts per farm is likely to decrease the risk of infections in SW farms.

The reduced risk of pathogen transmission between SW farms is mainly because of reduced movements of fish between SW farms, which has been improved since the

Scottish ISA outbreak in 1998–1999. Scottish sea farms are now divided into management areas, and good code of practice prohibits fish farms from moving post-smolts between management areas (Joint Government/Industry Working Group 2000). The use of management areas combined with fallowing strategies has proven to be effective in reducing epidemic spread in a theoretical study (Werkman et al. 2011) [chapter 3] and in the field during the recent ISA outbreak in 2009, where the outbreak affected only one management area (Murray et al. 2010).

Broodstock could theoretically be a source of vertical infection, as ova can become infected with, for example, BKD (Marine Scotland Science 2010a). Broodstock were only moved occasionally and these fish movements are under strict surveillance. Furthermore, the number of contacts for SW–FW was low during the period studied compared with FW–FW contacts. A decrease in the number of contacts reduces the chance of infection. This, in combination with the strict biosecurity measures, protects broodstock from infection. If broodstock are infected, transmission to other freshwater farms is extensive. And, from these freshwater farms, transfer may occur to multiple seawater farms, which underlines the importance of strict surveillance of broodstock.

Large numbers of movements occurred between FW farms. The data presented here showed that the number of total movements and contacts in salmon SW–SW movements was considerably lower than salmon FW–FW and salmon FW–SW movements. This suggests that there is a need to investigate the possibilities of biosecurity measures for FW farms, similar to the management areas applied to SW farms. Some of these movements are essential to aquaculture; fish must be moved off hatcheries to on-growing sites and smolts must be moved to sea. Receiving farms minimise the costs of fish moved onto them, which may involve sourcing from different locations, and this is essential for their economic sustainability. Use of stocks from different sources increases genetic variability; this may increase the risk of pathogen introduction but reduce its impact, should this occur. However, pathogen transfer risk may be reduced by removing strategic nodes that link clusters of farms (Green et al. 2009), so a strategic review of movement, rather than blanket reduction, may be the most effective modification of the network.

Despite the lower number of total rainbow trout live fish movements compared with salmon, the numbers of movements per farm were comparable for rainbow trout and salmon. However, the numbers of contacts per farm were considerably lower for rainbow trout because movements between pairs of rainbow trout farms occurred more frequently compared with the salmon movements. The salmon movement network had more connections between farms and diseases could therefore spread more easily between salmon farms than between rainbow trout farms, all other factors, such as the transmission rate of the pathogen, being equal. However, multiple movements between the same pair of farms increase the risk of the receiving farm becoming infected from the source farm, as multiple movements occur during the year. It should be kept in mind that only 2 yr of data were considered for rainbow trout data and 3 yr for salmon data.

In this study we did not include the effects of size of farms (i.e. production) on the number of movements or contacts. However, it is likely that larger farms would have more movements and contacts onto and off their farm, and, therefore, have a higher risk of becoming infected and transmitting pathogens to a large number of farms.

4.5.2. Seasonality

The timing of movements is important, as a peak in the number of live animal movements has been shown to increase the size of an epidemic considerably (Gibbens et al. 2001). During peak periods of movements, fish farmers should be extra vigilant for clinical signs of diseases before moving live fish; this is important in order to prevent potential transmission of pathogens to other farms and, in some cases, large numbers of farms.

Salmon data showed a high degree of seasonality, particularly for FW–FW and FW–SW movements, as would be expected because of the seasonal nature of smolt transfers. During periods of high peak in activity there are increased numbers of movements between contacts, and epidemics are more likely to become widespread in a network containing more (direct) connections between farms (Kiss et al. 2006). Targeted biosecurity aimed at identifying pathogens before the increased activity will help to prevent or reduce pathogen spread to other farms. However, eradication strategies might have less of an effect when outbreaks are widespread before detection (Keeling 1999, Kiss et al. 2005, Thrush & Peeler 2006, Natale et al. 2009, Ward et al. 2009, Werkman et al. 2011) [chapter 3]. This was shown during the 2001 FMD outbreak, where 57 farms were infected with FMD before the disease was detected (Gibbens et al. 2001, Eales et al. 2002). This was also the case with ISA in Scotland, where the 1998–1999 outbreak spread nationwide before detection (Murray et al. 2002), whereas the 2008–2009 outbreak was limited to a relatively small area of southwest Shetland (Murray et al. 2010). Thrush & Peeler (2006) estimated that in case of introduction of *Gyrodactylus salaris*, 50% of the catchments in England could be infected before diagnosis of the parasite, in the worst-case scenario. However, this study did not include seasonality of movements. Subclinical infections can go unnoticed (Bruno 2004, Graham et al. 2006, Lyngstad et al. 2008, Murray et al. 2010). Performing clinical tests increases the change of detecting subclinical infections and movements can be stopped when a farm tests positive. Therefore, performing clinical tests during periods of a high peak in activity of movements can minimise the risk of spreading pathogens. The control of widespread diseases can be very difficult if the necessary resources and infrastructure are not available, such as the lack of trained personnel, which exacerbated the UK FMD outbreak in 2001 (Eales et al. 2002).

Because salmon FW–FW and FW–SW movements and rainbow trout movements are seasonal, control strategies performed before these high peak seasons will have a positive impact on disease control. This strategy prevents farms from having many movements off (during a relatively short period of time) with possibly infected fish. As SW–SW movements occur more constantly through the year, targeted control surveillance has less of an effect compared with targeted control for FW–FW and FW–SW movements.

Some diseases, such as BKD, are more likely to occur during the spring when water temperatures are rising (Marine Scotland Science 2010a). The spring is also a period with an increased number of FW–FW and FW–SW movements, which increases risk of this disease.

The inclusion of seasonality or timing of movements in simulation models will not only include peaks of live fish movement activity during specific periods of the year, but will also include sequence of movements. For example, if movements occur from A to B and from B to C and A is the source of infection, C will only get infected if movement from A to B occurred first. Therefore, the sequence of movements is important for predicting the course of epidemics in more complex dynamic models when compared with static networks. Further studies are needed to quantify the effects of seasonality on the course of epidemics.

4.5.3. Harvest data

Close proximity (<5 km) to a harvest station has often been identified as a risk factor for disease transmission (Vagsholm et al. 1994, Jarp & Karlsen 1997, Munro et al. 2003). Harvest stations could be a source of infection to adjacent farms via pathogens and escaped live fish from the harvest station contacting fish in adjacent farms (Munro et al. 2003). Well boats transporting live fish to harvesting plants can also be responsible for pathogen transmission to farms en route to the harvest stations (Munro et al. 2003, McClure et al. 2005). During periods of increased movement activity towards harvest stations, disease risk is increased to farms adjacent to or en route to harvest stations.

Some farms transported salmon to more than one harvest station. To reduce the risk for farms in close vicinity of the harvest station, it would be better to transport live fish to one harvest station, because in case of infection only one harvest station will be affected, although this might not be possible in all cases for logistical and economic reasons. Companies will seek to sell their fish to the processor offering the best price; this is especially the case for small independent companies, whereas larger companies are more likely to own and operate company processing plants. The specific harvest stations could not be validated in all cases in this study, as in some records only the area was included and the name of the harvest station was missing.

During the studied period, as a result of the ISA outbreak of 1998–1999, improving practices led to fewer fish being slaughtered on site and hence more live fish movements to harvest stations. This could have led to the increased harvest movements in 2004. However, we believe this increase could also be partly due to improved record keeping, also as a result of the ISA outbreak, as some movements to slaughter may not have been recorded because these fish were not being moved to another farm.

4.5.4. Other routes of infection

Live fish movements are not the only route of pathogen transmission between fish farms. Pathogens can also spread at a local level, as wild fish can become infected and transfer pathogens when they are in the vicinity of infected farms and susceptible farms (Uglem et al. 2009). In addition, diseases such as ISA and pancreas disease are known to spread at a local level (<10 km; McClure et al. 2005, Lyngstad et al. 2008, Aldrin et al. 2010). Effects of local transmission are likely to be reduced when the distance between the susceptible farm and the source farm is increased (Aldrin et al. 2010). In the present study, spatial analysis was not conducted. However, movements occur to and from farms; therefore, the number of movements and contacts is likely to be positively correlated with the number of farms in an area. This can have a substantial effect on pathogen transmission and makes areas with a high production more vulnerable to disease outbreaks, both through local transmission and long-distance movements.

Depending on the infectivity of the disease, long-distance transfer of live fish have a high risk to cause infection on the receiving farms when the transferred fish are infected (Murray & Peeler 2005). Furthermore, long-distance movements are easier to control than local transmission pathways such as movements of water and wild animals. Controlling and decreasing long-distance movements can therefore have a substantial impact in reducing the risk of epidemics in Scottish aquaculture (Werkman et al. 2011)[chapter 3]. Moreover, local transmission tends to have a lower R0 than long-distance transmission: Because of clustering of infection on a local level, infected farms are competing for the same neighbours to infect (Keeling 1999, Kiss et al. 2005). However, economic reasons may mean that fish are sourced some distance from the receiving site. For example, in Shetland, the area of FW production is small relative to the area for SW production; in this case, salmon smolts may be sourced from Yorkshire and ova from Norway (Murray et al. 2010).

4.5.5. Data collection

It would be useful to collect movement data electronically. Movement records are currently documented on paper forms and held by fish health inspectors at Marine Scotland. Collecting the data electronically would improve the traceability of the movements and makes it easier to check whether data are recorded at both the source and destination farms. Furthermore, electronic data collection will increase the speed of identifying the movements on and off the index case or other infected farms. Collecting the movement data physically causes a delay in identifying the possible secondary infections. As a consequence, movement restrictions might have to be applied across the whole country in the case of an outbreak of an exotic disease such as *Gyrodactylus salaris*, at least until data are collected and analysed. This is especially relevant when the disease is subclinical, and when the source (e.g. wild reservoir or international movement) cannot be identified, which means that the duration of infection and degree of spread is unknown.

4.6. Conclusion

In this study we have shown variation in the timing of movements and number of movements and contacts across different species and production phases (for salmon). Therefore, it is important to include seasonality, heterogeneity of the number of contacts and production phase in simulation models. Salmon movements between SW farms show less heterogeneity in the timing of movements and contacts. Therefore, simulation models considering these networks only may be treated without seasonality of live fish movements.

Disease outbreaks affecting mainly FW farms can spread easily throughout the network because of the high number of contacts per farm. If the number of these movements can be reduced, then disease risk from pathogens with a FW phase might be reduced substantially, as has occurred for SW farms. Simulation models should consider disease-specific parameters and include network properties affecting the relevant subpopulation.

4.7. Acknowledgements

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CHAPTER 5. Seasonality in live fish movements and its effects on epidemics

Werkman, M.; Green, D.M.; Munro, L.A.; Murray, A.G.; Turnbull, J.F

This chapter used the data of chapter 4 and the network model of chapter 3 as a base. The objective of this chapter was to quantify the effects of seasonality patterns of live fish movements on the course of an epidemic.

The main author, Marleen Werkman, developed the network models in this study with assistance of D.M. Green. Data were collected by the main author and L.A. Munro. D.M. Green, A.G. Murray and J.F. Turnbull provided assistance during the writing process and edited the manuscript. The body of the text is written as a publication-ready manuscript.

CHAPTER 5. Seasonality in live fish movements and its effects on epidemics

M. Werkman, D.M. Green, A.G. Murray, L.A. Munro, J.F. Turnbull

5.1 Abstract

Live fish movements between salmon farms risk spreading pathogens at a country-wide scale. Salmon movements between freshwater farms and movements from freshwater to seawater for smolt supply show clear seasonality. Seasonality could have a substantial impact on the course of disease. In this study, we quantify the effects of seasonality of live fish movements on epidemic dynamics, using a network model populated with live fish movements between Scottish fish farms of 2002 to 2004. We used three types of networks: A) the real-life situation in which timing and pair-wise movements between farms were as observed as in the data; B) as network A, but with a random reordering of all movements between freshwater farms and movements from freshwater to seawater farms; C) simulated networks in which the number of movements per farm were kept the same as in the data but connection between nodes was random. We compared the time-course of simulated epidemics in all three networks. In each network seasonality was included and excluded to investigate the effects of seasonality of live fish movements on the course of an epidemic. For this a stochastic susceptible-infected-recovered (SIR) model was used. Here we showed that seasonality mainly has an effect when local transmission is > 0.05 per week per contact for network B and C and did not have a strong effect in network A. The effects of seasonality of live fish movements were stronger for seawater farms, compared with freshwater farms. The order of salmon movements appears to be important for disease dynamics.

5.2. Introduction

Scotland is the third-largest producer of Atlantic salmon (*Salmo salar*) after Norway and Chile and produced approximately 154,000 tonnes in 2010 (MSS, 2011). The Scottish salmon industry is threatened by potential disease outbreaks such as pancreas disease and infectious salmon anaemia (ISA). Movements of live fish provide a route for spreading pathogens between otherwise isolated farms. However, these movements are common in aquaculture and are required for both economic and biological reasons (e.g. movement of salmon smolts from freshwater to marine farms). Movement of live fish has been associated with the spread of ISA (Mardones et al., 2009) and bacterial kidney disease (BKD) (Murray et al., 2012) and as an important risk factor for possible introduction of the parasite *Gyrodactylus salaris* into the UK (Peeler and Thrush, 2004).

Epidemic network models can be used to assess the risk of these live fish movements on transmission of pathogens on a countrywide scale. A movement network can represent live animal movements between farms. These farms are connected by “edges” or “arcs” representing potentially infectious contact, for example through animal movements. Edges represent undirected contact between farms and arcs represent directed contact between nodes (Martinez-Lopez et al., 2009); movements are inherently directed. Network models can easily take into account heterogeneity in the number of movements between farms (Kiss et al., 2005; Webb et al., 2005). As a ‘rule of thumb’, 20% of the population contribute to infecting 80% of the population due to high number of contacts with the susceptible population (Volkova et al, 2010; Woolhouse et al., 1997; Anderson and May, 1992).

Epidemics that start during periods with increased movement activity have a higher probability to become widespread than epidemics starting during other periods of the year (Kiss et al., 2006). For example, the British FMD outbreak in 2001 was large because it started during a time of year with many sheep movements going onto and off livestock markets (Kiss et al., 2006; Gibbens et al., 2001). In a previous study, Scottish live fish movements were shown to be seasonal in the number of live fish movements, but these seasonality patterns differed across production phases (Werkman et al., 2011b). Movements between freshwater (FW) farms mainly occurred from May to July (figure 5.1A), while seawater (SW) farms were supplied with smolts mainly during February to March and October to November (2002 to 2004 data, figure 5.1B). However, there was no overall seasonality in movements between SW farms (Werkman et al., 2011b). During periods of increased movement activity, the salmon industry might be more vulnerable to large epidemics. Therefore, fish farmers should be particularly vigilant for clinical symptoms of their fish during periods of increased live fish movements between farms.

Network clustering could have a big impact on the course of an epidemic. In a highly clustered network, there is a high probability that two neighbours (nodes in contact) have another common neighbour (Christley et al., 2005; Keeling and Eames, 2005; Newman, 2003). Furthermore, clustering decreases R_0 (the average number of new infections caused by a typically infected individual in a susceptible population) and this slows the spread of an epidemic. Epidemics are more likely to die out in a highly clustered network (Keeling and Eames, 2005; Newman, 2003).

During periods of the year when many movements occur, and for farms that are likely to become infected and spread the infection of pathogens, early recognition of disease is important. Fish known to be infected with a notifiable disease are prohibited from moving fish to other farms (Joint Government/Industry Working Group, 2000), but are allowed to move fish off their farm for processing. However, diseases can go unnoticed when the prevalence is low (i.e. low infectivity at within-farm level) or when there are no clinical signs (i.e. low pathogenicity and low virulence) and fish might therefore be moved while they are infected with a notifiable disease (Jonkers et al., 2010; Lyngstad et al., 2008; Graham et al., 2006; Murray and Peeler, 2005).). An example is *Renibacterium salmoninarum*, the causative agent of BKD, whose persistent subclinical phase reduces the effectiveness of controls. When diseases have a high pathogenicity or high virulence, infections will be noticed earlier and there is a lower chance of accidentally transporting infected animals.

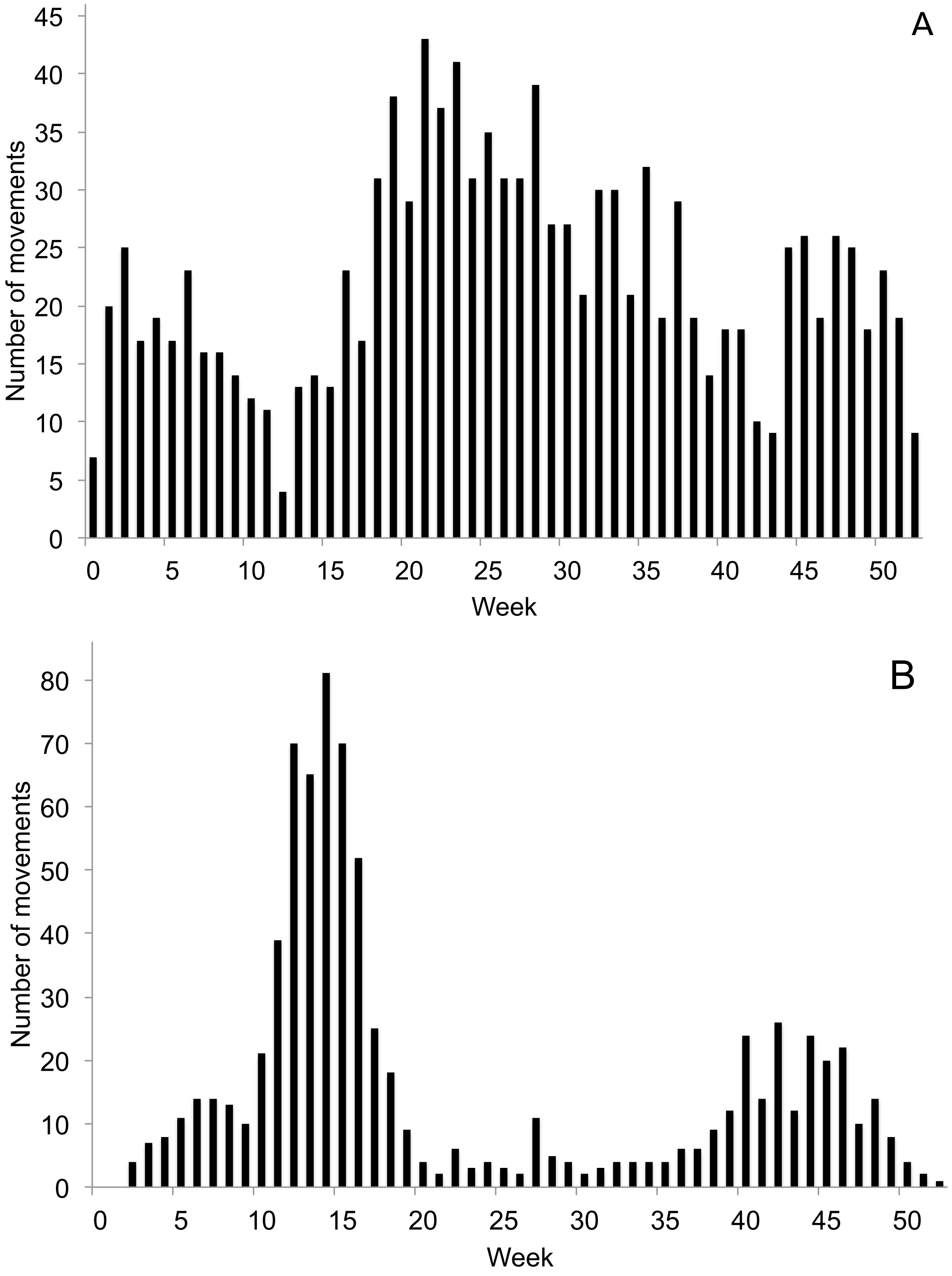


Figure 5.1. Timing of movements between freshwater farms (A) and movements from freshwater to seawater farms (B).

In addition to fish movements, pathogens may also be transmitted between farms through the environment, e.g. by water movement (Jonkers et al., 2010; OIE, 2009). Survival time of the pathogen outside of its host, in water, differs between pathogens and is dependent on factors such as water temperature and water chemistry (OIE, 2009). The persistence of pathogens also depends on natural reservoirs (such as wild fish) in the proximity of fish farms; wild fish can be responsible for (re-)infection of fish farms when they become infected and come into close proximity of fish farms (Uglem et al., 2009).

Seasonality was found in Scottish salmon movements between freshwater farms and movements from FW to SW farms. In the current study, we investigated the effects these seasonal patterns of live fish movements on the course of epidemics. We used the descriptive statistics from Werkman et al. (2011b) as a base to estimate parameter values for seasonality in the numbers of movements per farm. As the transmission of pathogens between farms can vary largely depending on the characteristics of the environment, host, and pathogen itself, we studied the transmission of pathogens with a range of different pathogen characteristics (i.e. transmission rates and removal times). Models generally should aim to be as parsimonious as possible, while being capable of describing the features of interest in a particular system (Jorgensen and Bendoriccho 2001; Murray 2008), which means identifying the relevant details for a particular problem.

5.3. Materials and methods

To investigate the effects of seasonality of live fish movements on the course of an epidemic, we modelled pathogen transmission through both live fish movements (see section 2.1) and due to local spread (see section 2.2).

5.3.1. Long-distance movements

Scottish fish farmers are obliged to record the live fish movements *onto* and *off* their farms. The records from 1 January 2002 to 31 December 2004 were used in this study; the movements were edited as described in Werkman et al., 2011b. In total there were 2401 movements between salmon farms over this three year period.

There were $N_{fw} = 186$ active FW farms (i.e. farms in a production cycle either having stock or fallowing) during 2002 to 2004, and $N_{sw} = 314$ active SW farms of which 304 farms had movements onto or off their farm. Nine farms had both facilities available on their farm; for the purpose of this study we counted these farms as SW farms. The total number of SW farms (N_{sw}) was 323, and the total number of all salmon farms (N_{total}) was 509.

We studied the effects of seasonality of live fish movements on three different types of networks, these are discussed below.

For all situations, a directed contact matrix A_{ijt} was developed of size N_{total} by N_{total} by t, in this study t is $1 \leq t \leq 159$ weeks. An element A_{ijt} contained 1 when there was a movement between farm i and j at time t and 0 otherwise.

For all three networks, we compared the scenario where the original seasonality of live fish movements was left as shown to occur in the data with one where the timing of these movements was altered such that the number of FW-FW movements and FW-SW movements were both distributed homogeneously over the time period. The timing of the movements between SW farms, SW-FW and 'other' were kept the same to the raw data as these data did not show seasonal patterns (Werkman et al., 2011b). Movements that were between research farms or onto or off research farms were classified as 'other'.

Network A: Real-life network

Network A included the real-life situation, in this network nothing was altered after the data manipulation and cleaning as described in Werkman et al., 2011b. The movement network structure and the sequence of movements were kept the same as in the original data in both the seasonal and non-seasonal network (table 5.1).

In the non-seasonal network, all movements were placed in chronological order based on the date they occurred. The study period was 3 years and each year contained 53 weeks, this resulted in 159 time steps. The total number of movements per production phase divided over the total number of time steps was allowed per week. For FW-FW movements this resulted in $1181/t \approx 7$ movements per week. For the first week, the first 7 FW-FW movements of the chronological movement list were selected. For week 2, movements 8 to 14 were selected, etc.

Movements were only allowed once a week; when network A was transformed to a non-seasonal network it resulted, in a few cases, in two movements between the same pair of farms in the same week. In the case where two movements between the same pair of farms occurred in one week, movements were changed to the first movements in the following week in order to keep the sequence of the movements in the non-seasonal network as close as possible to the sequence of the movements in the seasonal network. For example, in the non-seasonal network there were two movements between farm A to farm B in week 17 (movement 1 and 2). In week 18 no movements occurred between farm A and B, but a movement occurred from farm D to E (movement 3). In this scenario, movement 2 and 3 were exchanged. In this way the sequence of the movements changed as little as possible while keeping the same number of total movements. This problem only occurred in the non-seasonal version of network type A as the sequence of movements was left unaltered in this network type, in contrast to network B and C where the sequence of movements was random.

Table 5.1. Characteristics of each type of network, * was placed when the characteristic was included in the designed network.

	Network A	Network B	Network C
Number of movements *onto* and *off* per farm	*	*	*
Clustering	*	*	
Order of movements	*		

Network B: Real-life network with random order of movements

For the seasonal version of network B, the original movements of network A were matched to a new timing list. In this list the original timings of movements (i.e. week numbers) were put in a random order and one-by-one matched to a movement. The movement network structure and seasonal pattern of network B was the same as network A, but the sequence of FW-FW and FW-SW movements was altered by letting them occur in a random order (table 5.1). The sequence of these movements was altered, to investigate the importance of the sequence of live fish movements on disease dynamics. SW-SW, SW-FW and 'other' movements was left unaltered.

For the non-seasonal version of network B another timing list was made where each week number was listed as often as there were movements of a particular production phase per time step. Movements were only allowed to occur once a week, so movements were only allowed to occur when $A_{ijt} = 0$. When $A_{ijt} = 1$, the next time point on the timing list was used until the criteria were met or until there were no further possibilities available. In this case, this movement was removed without replacement. This resulted in a network where the movements were randomized and the numbers of movements per week were equal over the whole time period.

Network C: Simulated network

The last network, network C, was designed in such a way that the number of movements going onto and off farms were preserved. Clustering was removed and also the order of movements was not taken into account in this network. The clustering coefficient was calculated as suggested by Opsahl and Panzarasa (2009) and was based on 10,000 simulated networks. The clustering coefficient was based on the static, directed and weighted network, where all the connections of all time steps were added together. The mean clustering coefficient for network C was 0.09 (range 0.08 to 0.11). Network A (and B) had a cluster coefficient of 0.20.

During 2002 to 2004, there were in total 1181 movements between FW farms registered. To build the long-distance movement network between FW farms, two lists of farms were constructed. The first list contained 1181 stubs (i.e. one half of an arc) which represented the source farms. There were 108 farms with movements off their farm which were selected at random from the FW farms and were repeated as often as they had movements off the farm (varying from 1 to 38 times).

The second list contained the destination farms, 161 were selected and repeated as often as they had movements on their farms (varying from 1 to 52 times), again resulting in 1181 stubs. Of these 161 farms, 92 farms were also in the source list and 69 farms were selected at random from the remaining FW farms. Nine farms remained without any simulated FW-FW movements on or off their farm. As in the original data, these farms had only movements to SW farms, to or from farms with both FW and SW facilities, or were supplied with broodstock from SW farms. These nine farms were included in FW-SW, SW-FW or movements to and from research farms (farms with both FW and SW facilities). In this way the in-out degree correlation were partly preserved compared with random assignment of the edges.

An additional list was made which included the timings of the movements and contained the week numbers from 1 to 159. Each week number was included as many times as movements occurred during 2002 to 2004 $(N = 1181)$. Movements were allowed to occur only once a week between the same pair of farms.

The source list, destination list and the timing list were each put in a random order. One by one, each farm from the source list was connected to one farm from the destination list and one week number from the timing list. The farms were only matched when $A_{ijt} = 0$ and $i \neq j$. Otherwise, the next farm on the source list was selected until the criteria were met or after 50 unsuccessful attempts, in which case the second movement between i and j at time t was removed without replacement (producing less than the desired number of movements).

A similar approach was used for the other classes of movements: FW-SW $(N = 810)$, SW-SW $(N = 237)$, SW-FW $(N = 54)$ and other movements $(N = 119)$.

5.3.2. Local contacts

An additional undirected contact matrix (B_{ij}) of size N_{total} by N_{total} was developed that represented spread between farms by local contact other than recorded movements. To create this matrix, the maps from the Scottish salmon and sea trout catches (FRS, 2003) were used in conjunction with geolocation data for the farms and management area maps from Marine Scotland Science (MSS, 2003). Scotland is divided into 62 salmon fishery statistic districts, which can contain single or multiple river catchments which were combined with adjacent coastlines. Salmon FW farms were dispersed over 39 salmon fishery statistic districts each containing between one and 23 farms (figure 5.2).

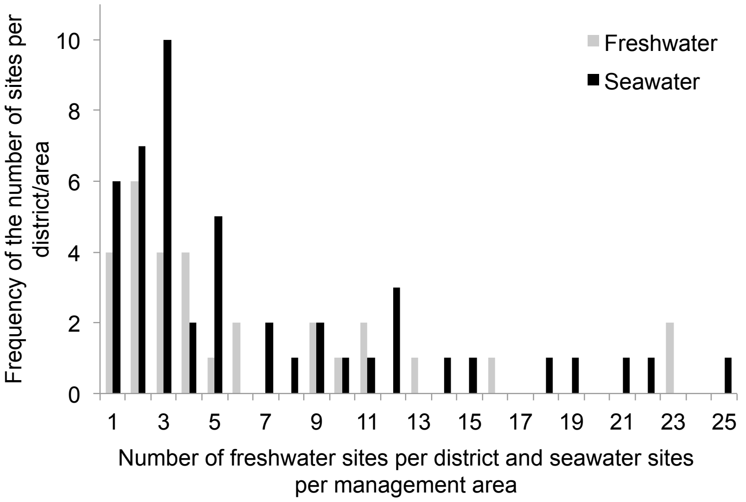


Figure 5.2. Number of freshwater farms per district.

After the Scottish ISA outbreak in 1998/1999, SW farms were divided into management areas with “firebreaks” between them (Joint Government/Industry Working Group, 2000; MSS, 2003). For this study the management area maps of 2003 were used as this corresponds with the time period of the movement records used. Scottish SW farms were divided over 47 management areas, each management area containing between 1 to 25 SW farms (figure 5.2).

Farms that had both FW and SW facilities were not assigned to a district or management area; local contact was not present between these farms.

In this contact matrix B, we assumed that all farms in a district were located in a ring and could infect two adjacent farms by local contact, except farms located in a district containing one farm (no adjacent farms) or two farms (one adjacent farm) as described in Werkman et al. (2011a).

5.3.3. Transmission model

A susceptible-infected-removed (SIR) model was developed to investigate the effects of seasonality on disease transmission, similar to the methods as described in Werkman et al. (2011a). The local transmission rate (β_{local}) was defined as the weekly probability of an infected farm to infect a susceptible farm when there was local contact. Parameter β_{local} was varied between zero and 0.25. Transmission rates caused by long-distance movements (β_{long}) were set to 1 as receipt by a susceptible farm of fish from an infected farm almost always causes infection at the susceptible farm owing to the large numbers of fish moved in aquaculture operations (Murray and Peeler, 2005).

For the local contacts, a vector of size N_{total} was derived to include the contacts of infected farms at time t:

$$C_i = \sum_j I_{j,t} B_{ji}$$

The more (local) contacts a farm has the higher the likelihood that a farm becomes infected. However, the risk of becoming infecting can never be over 1.0. Therefore vector P_i was introduced, which represents the probability of becoming infected through local contacts. Vector Q_i represents stochastically the receipt of pathogens through local contact and is 1 if the farm becomes infected and 0 otherwise.

$$P_i = 1 - (1 - \beta_{local})^{C_i}$$

$$Q_i \sim \text{Bernouilli}(P_i)$$

For long distance movements a vector of size N_{total} was derived containing the number of inward contacts:

$$D_i = \sum_j I_{j,t}(A_{j,i})$$

$$F_i = 1 - \left(1 - \beta_{long}\right)^{D_i}$$

The new infectious status at time $t + 1$ was stored in a vector of size N_{total}:

$$I_{i.t+1} = I_{i,t} + \left(1 - I_{i,t}\right)\left(1 - (1 - Q_{i,t})(1 - F_{i,t})\right)$$

The average duration of infection per farm was following an exponential distribution:

$$R_i \sim \text{exponential}(r)$$

After a farm reached the removal/recovered state we assumed immunity and there were no further infection events for farms reaching this state.

The index cases were selected at random from all FW farms and we initiated the epidemic at two different times: week 17 and week 41 as these time point were just before and after the increase in movement activity (figure 5.1A). Each model was run for three years (159 time steps). As this is a stochastic model, there is always a possibility that the index case will be removed in the first time step. To prevent this, we chose to start an epidemic with 5 index cases, which were randomly selected during each simulation from all FW sites. When seeding multiple index cases it is likely that the probability that an epidemic takes off is overestimated, so it does not take into account situations in which an epidemic dies out quickly after introduction. For this study, this was not important, as we wanted to investigate the importance of seasonality patterns in case of an epidemic.

The epidemics that were run in network A without seasonality were initiated in week 13 and 43. Simulations were started at a specific point in the sequence of movements, rather than the calendar month and thus in this scenario the simulations started on a different date. When the simulation reached week 159, the following time step was week 1 and continued from that week until the simulation reached all 159 time steps.

Simulations of all networks were run 1000 times. However, the real-life network did not change: simulations were run over the same network for network A in all cases. In contrast to network A, networks B and C changed every simulation. Therefore, the results of the real-life network showed less variation compared with the other two networks.

5.4. Results

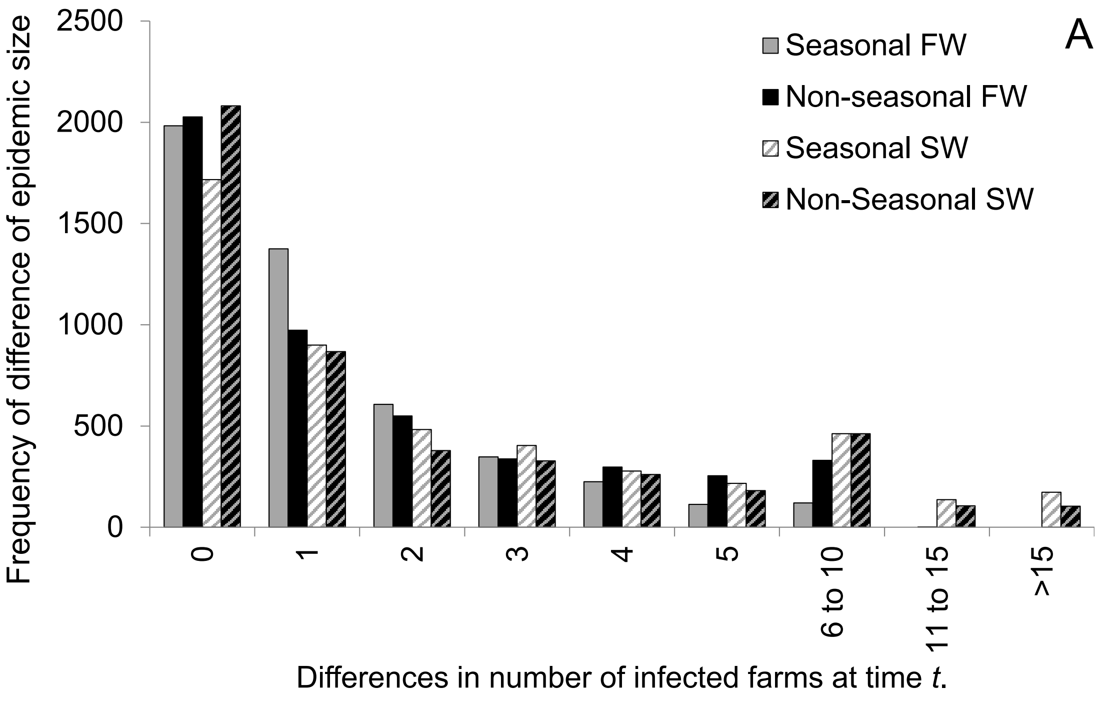
Networks B (real-life networks with movements in a random order) and C (simulated networks) were created every simulation. Multiple movements occurring in the same week from i to j were deleted and movements were also removed without replacement when $i = j$, this resulted in < 2401 movements (see section 2). The number of movements in each network should be similar in order to make a fair comparison between networks. Therefore we first investigated how successful the creations of these networks were. For each type of network, 10,000 networks were created and the total numbers of movements were recorded. For both networks and for both the seasonal and non-seasonal version there were a maximum of two movements missing over a three-year period (table 5.2). In 95% of the cases for all networks, all 2401 movements were included (table 5.2).

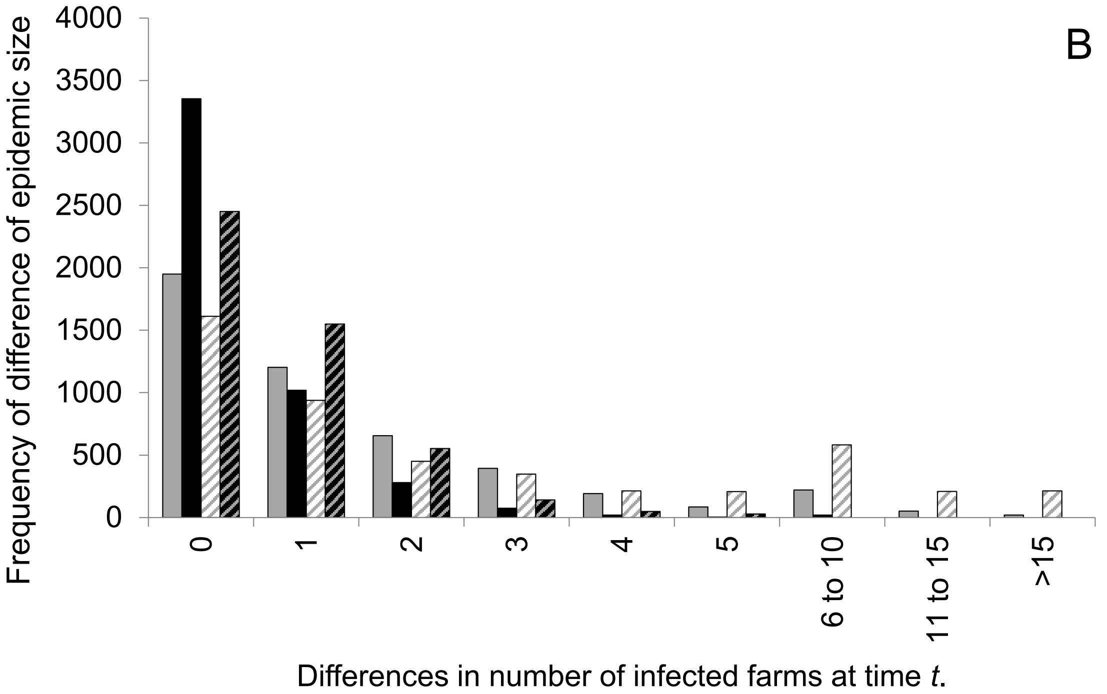
Table 5.2. Proportion of real-life networks with movements in random order (network B) and simulated networks (network C) that included all 2401 movement or had 1 or 2 movements missing. Both networks were run 10,000 times for both a seasonal and non-seasonal network.

	Real-life network with movements in a different sequence (network B)		Simulated network (network C)	
	Seasonality	No seasonality	Seasonality	No seasonality
No movements missing	95.5%	96.2%	97.1%	97.1%
1 movement missing	4.4%	3.7%	2.8%	2.9%
2 movements missing	0.01%	0.01%	0.03%	0.00%

5.4.1. Mean prevalence

A higher local transmission rate increased the epidemic size and the speed at which an epidemic occurred. While an increased removal rate reduced the chance of an epidemic. When the removal rate was 0.075, an epidemic only occurred with the highest local transmission rates (> 0.10 per week). The difference in the mean number of infected farms when epidemics were initiated at week 17 and 41 (and week 13 and 43 for network A without seasonality) was calculated and followed over the 159 time steps for all the local transmission rates (0 to 0.25 per week), removal rates (0 to 0.075) and time steps (1 to 159). Figure 5.3 shows the accumulated differences over all parameter values at all time points. The time of year in which an epidemic started had a clear effect on the course of the epidemic in both freshwater (FW) and seawater farms (SW) when epidemics were initiated at two different time points (week 17 or week 41) for network B, (figure 5.3B) network C (figure 5.3C). In the real-life network with the original sequence (network A), differences in the mean prevalence were less obvious when epidemics were initiated at these time points (figure 5.3A).





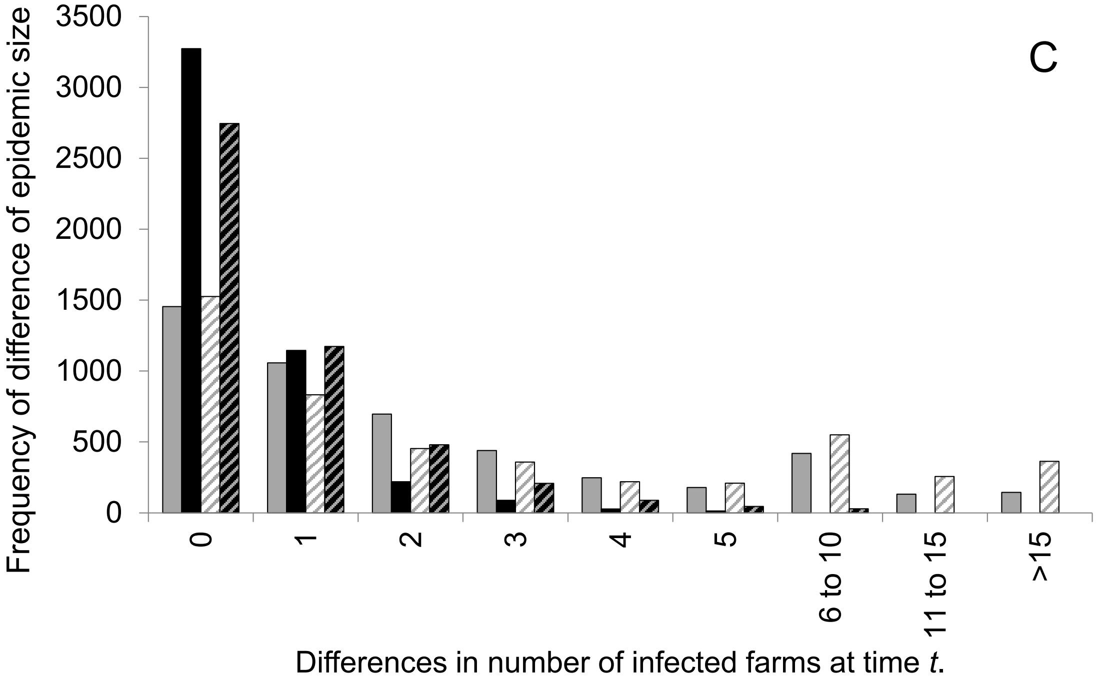


Figure 5.3. These graphs show the accumulated difference of the mean number of infected farms when an epidemic is initiated at week 17 or week 41 over all parameter values at all time points (A = real-life network, B = real-life network with movements in different order, C = simulated network).

For networks B and C, the difference of the mean prevalence when initiated at two different time points was larger when seasonality was included in both FW and SW farms. The maximum difference for network C was 36 farms when seasonality was included and 5 without seasonality for FW farms. For SW farms, the maximum difference was 41 with seasonality and 9 without seasonality. For network B, the maximum difference was smaller. For FW farms the maximum difference was 19 when seasonality was included and 7 when seasonality was excluded. For SW farms, the maximum difference was 35 and 5 for respectively with and without seasonality.

In network A, differences in the mean prevalence between the different timings of the start of the epidemic were slightly higher for FW farms when live fish movements were seasonal (maximum difference was 8) compared with non-seasonal (maximum difference was 9). In SW farms, the maximum difference was 70 when seasonality was included and 39 when seasonality was excluded.

Difference in mean prevalence was most clear during the first one-and-a-half years as most epidemics peaked during this time course (figure 5.4 for FW farms and figure 5.5 for SW farms). Furthermore, higher local transmission rates were positively correlated with difference in epidemic size when initiated at week 17 and 41 (figure 5.4 and 5.5). Increasing local transmission itself does not cause the difference on its own; seasonal patterns in live fish movements cause these differences as prevalences in non-seasonal networks were similar when started in week 17 and week 41.

Epidemics that started after the peak period of live fish movements (week 41) needed longer to peak compared with epidemics starting in week 17 (figure 5.6). Local transmission rates were positively correlated with the size of the epidemic. Mean prevalence was lower for network A and B compared with the simulated network (network C), see figure 5.6.

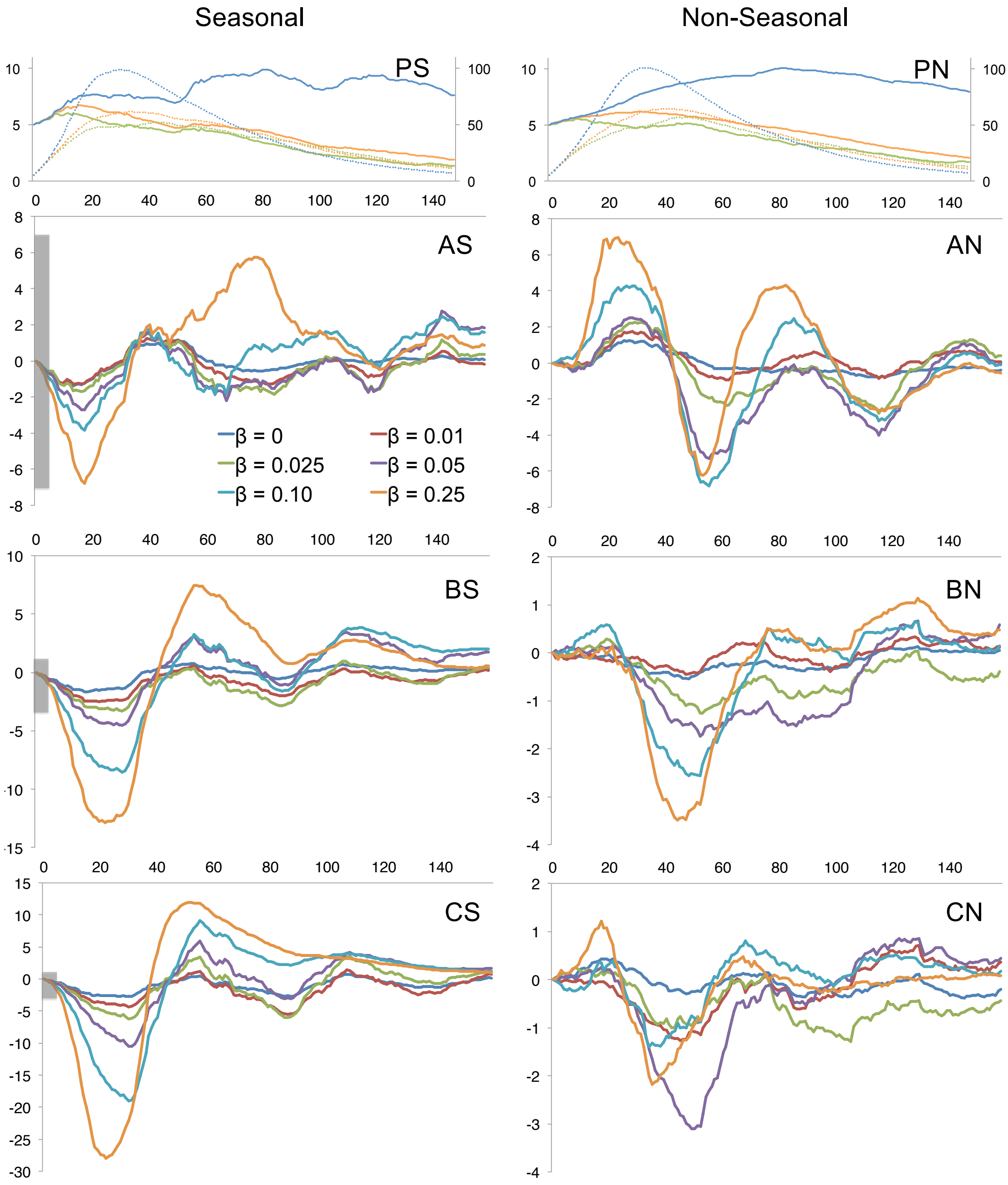


Figure 5.4. Graphs PS and PN show the mean prevalence for respectively seasonal and non-seasonal networks with local transmission rate 0 (solid lines) and local transmission rate 0.25 (dashed lines) for network A (green), B (orange) and C (blue) for freshwater farms. The x-axis shows the time steps (1 to 159) and the y-axis shows mean prevalence for local transmission rate 0 (y1) and 0.25 (y2). Graph AS, BS and CS show the difference in mean prevalence of freshwater farms when an epidemic was initiated in week 17 or 41 with removal rate 0.025 and all local transmission rates, graph AN, BN and CN do not account for seasonality in movements between freshwater farms. The y-axis shows the difference of the mean time step at time *t*. The grey bars on AS, BS and CS show the variation of epidemic size in the non-seasonal networks.

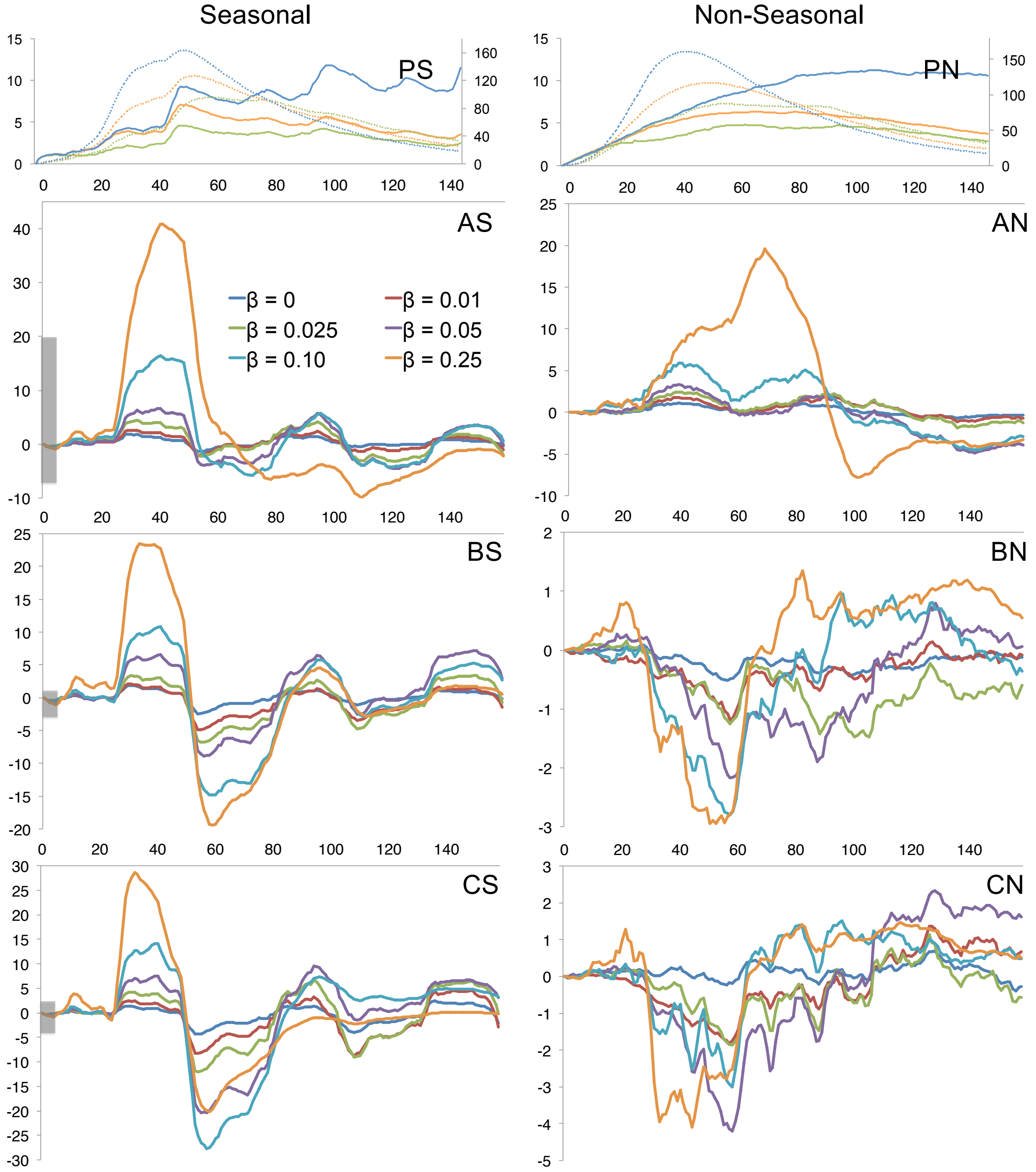
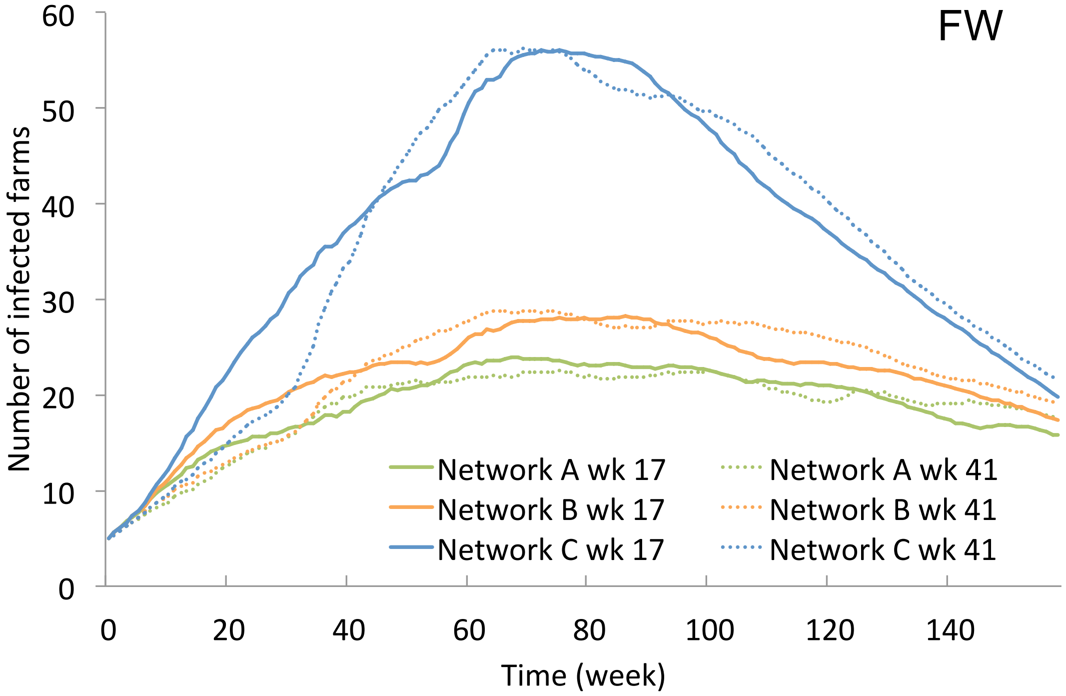


Figure 5.5. Graphs PS and PN show the mean prevalence for respectively seasonal and non-seasonal networks with local transmission rate 0 (solid lines) and local transmission rate 0.25 (dashed lines) for network A (green), B (orange) and C (blue) for seawater farms. The x-axis shows the time steps (1 to 159), while the y-axis shows mean prevalence for local transmission rate 0 (y1) and 0.25 (y2). Graph AS, BS and CS show the difference in mean prevalence of seawater farms when an epidemic was initiated in week 17 or 41 with removal rate 0.025 and all local transmission rates, graph AN, BN and CN do not account for seasonality in movements between seawater farms. The y-axis shows the difference of the mean time step at time t. The grey bars on AS, BS and CS show the variation of epidemic size in the non-seasonal networks.



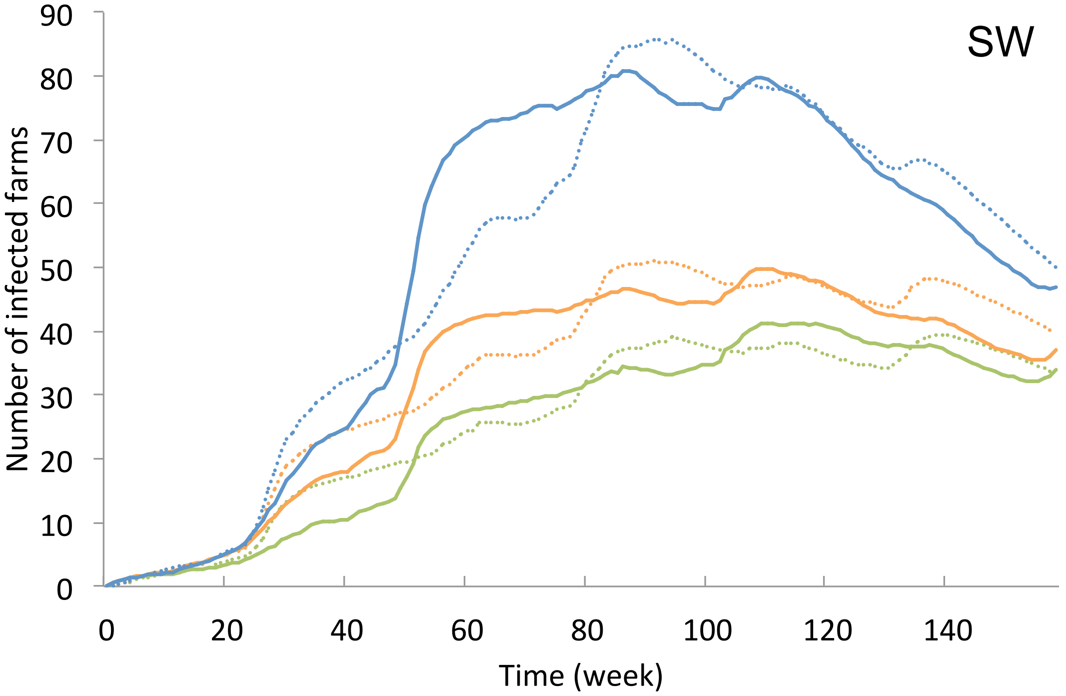


Figure 5.6. The mean number of infected farms per time step for freshwater (FW) and seawater farms (SW). Results are shown for Network A (real-life network), Network B (real-life network with movements in a random order) and Network C (simulated network) when epidemics were initiated in week 17 and 41 and removal rate 0.025 and local transmission rate 0.05 per week.

5.5. Discussion

This study provides a first attempt to quantify the effects of seasonality in live salmon movements upon epidemic risk. Epidemics were larger in network B (real-life network where movements were put in a random order) and network C (simulated network) compared with network A (real-life network). The original movement network used in network A and B did include clustering. This is in contrast to network C where clustering was removed and this is likely the cause of the larger epidemics in network C compared with network A (Keeling, 2005; Newman, 2003).

The effects of seasonality were stronger in SW farms compared with FW farms, this is probably a result of a stronger seasonal pattern in the FW to SW movements Differences in the mean prevalence when initiating an epidemic in week 17 and 41 for the real-life network were less extensive in proportion to the simulated network in both FW and SW farms. In the real-life network (network A) there were still differences in the mean prevalence when original seasonal patterns were removed in both FW and SW farms. While in the non-seasonal networks B and C, no substantial differences were observed between the mean prevalences. This suggests that network properties and the order and direction of movements are more important than seasonality patterns when considering the mean or average prevalence over a time period. However, the order and direction might be less important for movements from FW to SW farms compared with movements between FW farms. This is because differences between epidemic size were similar in FW farms for the seasonal and non-seasonal network for network A (figure 5.3A), but the difference in epidemic size was almost half of the difference in the seasonal network compared with the non-seasonal network for FW-SW movements (figure 5.3B).

5.5.1. Transmission model

In this study we chose an SIR model and the disease prevalence was recorded over a three-year period. We believe that an SIR model was the most suitable model to investigate the effects of seasonality of live fish movements on the course of epidemics. However, there are limitations of this choice: for example, it is implied that the removal period is open-ended and farms do not again become susceptible. Using a SIS model would however assume that farms immediately become susceptible after the infection phase ends; this is unlikely. In addition, allowing farms to become susceptible after the removal phase (using a SIRS model) would make the transmission model unnecessarily complicated.

In this study we did not include fallowing of farms, which is an effective method to control diseases (Werkman et al., 2011a; Murray et al., 2010). Fallowing is often applied in marine farms, where farms are emptied and left unstocked (Wheatley et al., 1995). Synchronized fallowing of management areas has a positive effect on disease control (Werkman et al., 2011a). Fallowing is likely to reduce the impact of an epidemic and therefore the effects of seasonality on the epidemic. However, seasonality could still play a very important role when a farm moves fish to many other farms in a short period of time.

5.5.2. Contact structure

In a previous study we investigated the number of movements between farms and their frequency (Werkman et al., 2011b). This study showed that many movements (approximately 40%) occurred between the same pair of farms. Therefore, a distinction was made between the number of contacts (i.e. unique connections between farms) and number of movements (i.e. total number of repeated connections between farms) per farm. This was because many movements between the same pair of farms are likely to increase the risk of the receiving farm to become infected. But if a farm moves fish to many different farms, the source farm can infect many different farms (until the disease is detected); this can have enormous implications on the course of an epidemic. During 2002 to 2004, there were in total 400 contacts and 1181 movements between registered FW farms and 595 contacts and 810 movements from FW to SW farms. In the simulated network (network C), to keep the network model as parsimonious as possible the number of movements per farm were kept similar to the real-life situation rather than the number of contacts. This possibly resulted in the higher prevalence in network C compared with the real-life situation.

In the current study we showed that network properties are very important to the course of an epidemic and that control strategies should consider clustering, and the sequence and direction of movements, as this appeared to be important in the spread of pathogens between farms.

We started the epidemics of the real-life network only in one year. Previous studies showed that there was some degree of consistency in the movement data between years (Werkman et al., 2011b; Green et al., 2011) and we do not expect any substantial changes during this time frame. We expect similar results for epidemics if those were initiated during the two other years.

5.5.3. Local transmission

The course of an epidemic depends on both local contact and anthropogenic activities (such as live fish movements and well boat movements). In this study the effects of seasonality were increased proportionally when the local transmission rate was increased. One of the assumptions of the transmission model was that every farm was linked to two neighbouring farms by local contact (by water movement), except for farms that had only one or two farms in the district or management area. In a previous study we showed that increasing the number of farms that are reached by local contact had a substantial effect on the course of an epidemic (Werkman et al., 2011a). As increasing local transmission rate increases the effects of seasonality, we expect that if the number of farms reached by local contacts in the simulation were increased, the effects of seasonality will increase as well.

In addition, the number of farms that can be reached by local contact is very important for the course of an epidemic. As seen in Werkman et al. (2011a), epidemics are larger when they are initiated in large management areas (areas with 9 or more SW farms) compared with small management areas (8 or less SW farms), all other parameters being the same. Therefore, control strategies should target areas where the number of farms is highly concentrated.

Local transmission rate can also be influenced by environmental factors such as water temperature. In the current study, we did not take into account differences in (local) transmission rates during the year. This would have made it difficult to distinguish the influence of seasonality in live fish movements from seasonal effects of environmental factors on the course of the epidemic. However, environmental factors are likely to affect local transmission rates. For example, the transmission rate of BKD is known to increase when water temperatures are increasing during spring (MSS, 2010) and water temperature is also important in the development of clinical disease of infectious haematopoietic necrosis (IHN) (OIE, 2009). Outbreaks of IHN are normally seen when the water temperature is between 8°C and 15°C (OIE, 2009). With targeted surveillance or control strategies, not only should the seasonality of movement activity between farms be taken into account, but also those seasonal factors that favour the survivability and infectivity of the pathogen, such as water temperatures. Different pathogens have a different environment that is beneficial for their reproduction and infectivity (OIE, 2009); disease-specific models can take environment factors into account.

For such pathogens with a seasonal, or temperature driven, expression of disease if this expression co-incides with periods of movement of fish it is likely that detection will occur before the pathogen is spread too widely, however if the movement co-incides with a period of low probability of expression of disease then imposition of control will have to rely on laboratory diagnostic testing in the absence of disease and this means the potential for uncontrolled spread is greater.

5.5.4. Subclinical infection

In this model, movements off a farm still occurred after a farm was infected. In real life, movements are restricted when a notifiable disease is found on a farm (MSS, 2010). The time period in which diseases are notified is crucial in controlling epidemics (Kiss et al., 2006) and is thought to have been important during the British foot–and–mouth epidemic in 2001 (Gibbens et al, 2001). Being able to recognize a disease in an early stage depends on the time period in which clinical signs occur after being infected and the clinical symptoms caused by the infection (pathogenicity). However, this varies highly between pathogens, it can be acute as sometimes occurs with infectious haematopoietic necrosis virus (OIE, 2009) or chronic as could be the case with bacterial kidney disease (Murray et al., 2012). If epidemics are detected before an increase of animal movement activity, then this could benefit control of epidemics. Therefore, surveillance strategies should be targeted to just before any increase of live animal movements and should also take into account the direction of movements.

If carrier species are infected with an (exotic) disease, they could play an important role in the course of an epidemic as they can transmit infections without showing clinical symptoms. If infected carrier species are not detected, they can infect a susceptible species on a wide scale before the disease is detected. In fish, rainbow trout could spread *G. salaris* to salmon (which are clinically affected by this parasite) without showing clinical symptoms (Peeler and Thrush, 2004).

5.6. Conclusion

This study provided more insight into the network properties of the Scottish salmon network. Seasonality in the number of movements and the direction of the movements has a large effect on the course of an epidemic. Clustering in real network limits epidemic spread. Targeting surveillance should not only be performed for farms but also for the time of year. Higher prevalence during certain periods of the year is not only due to environmental factors, but likely also due to the seasonality patterns in live fish movements between farms.

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CHAPTER 6. General discussion

6.1. Summary

In this final chapter, the main conclusions of this thesis and possible future studies are discussed.

This project was sponsored by University of Stirling and Marine Scotland Science (MSS); MSS provided the live fish movement database. The general aim of this thesis was to provide more insight into the contact structure of live fish movements within the Scottish salmonid industry and to investigate control strategies for diseases. Through live fish movements, infected fish can contact disease-free populations (Murray, et al., 2002; Murray and Peeler, 2005; Thrush and Peeler, 2006; Mardones, et al., 2009).

In the first research chapter, chapter 3, we looked at three different fallowing strategies (synchronized, partial synchronized and unsynchronized fallowing at the management area level). The results showed that synchronized fallowing is a highly effective tool when long-distance movements are under reasonable control.

The main aim of chapter 4 was to provide a detailed description of the number of live fish movements going onto and off a farm and the timing of these movements stratified by production phase. Seasonal patterns of live fish movements differed between production phases. Movements between freshwater (FW) sites peaked from May to July and showed the highest number of movements that were going on and off per farm. Movements from FW to seawater (SW) sites mostly occurred during March and April and the median number of movements going onto and off was higher compared with movements that occurred between SW sites. SW-SW movements did not show a clear seasonal pattern.

In chapter 5, the results of chapter 4 and the transmission model of chapter 3 were used to investigate the effects of seasonality on the course of an epidemic with a dynamic network. The results showed that seasonal patterns of live fish movements are likely to have a substantial impact on the course of an epidemic. This is especially the case when the local transmission is high and when the movement network does not include clustering. These results emphasize the importance of early detection of pathogens especially during periods when many movements occur between sites.

6.2. General discussion

6.2.1. Data

The data used in chapter 4 and 5 originated from 2002 to 2004. These data were the most recent data that were available due to logistic and convenience reasons. During 1998 to 1999 an ISA outbreak occurred in Scotland (Murray, et al., 2002) and this changed the management practice of seawater sites considerably (Joint Government/Industry Working Group, 2000). These management changes were already adapted in 2002 and therefore we do not expect any substantial differences in the network properties compared with more recent years. Structure might have changed slightly due to the merging of companies, but the overall properties of the network should be the same as in more recent years. The data used in chapter 4 and 5 showed continuity between the years (Chapter 4; Green et al., 2011).

Farmers record their own movement records on paper and these records are collected by the fish health inspectors (MSS, 2011). These records are filled by hand; during data collection some data were lost due to being recorded illegibly. Other records were not included in the dataset because they were not registered at both the source and destination site. Although these problems did not occur often, there is still a need for recording movements in an electronic dataset. Introducing an electronic dataset will improve the traceability, speed and accuracy from movements going off infected farms. During the FMD epidemic in the UK, it appeared that the time period in which ‘dangerous’ contacts were identified was highly important (Tildesley and

Keeling, 2009). Introducing an electronic dataset will help to shorten the time period in which all dangerous contacts will be identified.

Surveillance resources are costly and limited and should be used efficiently. Chapter 4 showed that movements between salmon farms are directed and show heterogeneity in the number of movements per farm. This indicates that targeted surveillance will be possible to detect diseases and ultimately prevent epidemics (Green, 2010). Disease surveillance should target farms that have a high risk of becoming infected and have the potential to spread the infection to a relatively large number of farms (Christley and French, 2003; Christley, et al., 2005; Lloyd-Smith, et al., 2005; Kiss, et al., 2006). In this way, ‘dangerous’ contact between two farms can be controlled to prevent pathogen transmission between high-risk farms. However, to investigate which farms or edges should be targeted, the most recent data available should be used.

6.2.2. Disease transmission

In chapter 2 we discussed several routes for pathogen transmission. Pathogens can spread by vertical transmission (parents to offspring) (OIE, 2009; MSS, 2010), natural reservoirs (i.e. wild fish) (Rae, 2002; OIE, 2009; MSS, 2010; Kurath and Winton, 2011), hydrodynamic contact (McClure et al., 2005; Gustafson et al., 2007; Lyngstad et al., 2008; Aldrin et al., 2010, Mardones, 2009) and live fish movements (Murray, et al., 2002; Mardones, et al., 2009), the importance of each transmission route depends on the pathogen. Controlling live fish movements will reduce the risk of large epidemics as moving fish from a disease infected farm will almost certainly result in infecting the receiving farm (Murray and Peeler, 2005). Banning movements is not possible as that makes it for the industry impossible to operate. However, if movements are structured strategically, even for the same number of overall movements, this can be beneficial in reducing the risk of large epidemics (Bigras-Poulin et al., 2007)

Although live fish movements are the most dangerous contact, infected eggs can possibly result in an index case and wild fish might be responsible for (re-)infection of farms or for transmission between farms on local level (Uglem, 2009). Consequently, to reduce the risk of transmission from pathogens between farms, we should not only reduce live fish movements, but also aim to site new farms strategically, where there is minimised contact with wild fish, and to screen broodstock for diseases that are known to transmit vertically.

In addition, pathogens can simply be transported by water flow. For example, ISA is known to spread on a local level, as happened during the ISA outbreak in 2009 in Scotland, and also in Chile (Mardones et al., 2009), Canada (McClure, et al., 2005) and Norway (Aldrin, et al., 2010). Furthermore, during the ISA outbreak in Chile, outbreaks occurred in clusters, which were initiated by long-distance movements and then spread at a local level (Mardones, et al., 2009). Close proximity to PD-infected farms also increase the risk of becoming infected with PD (Kristoffersen et al., 2009; Aldrin et al., 2010) and other diseases (OIE, 2009). In chapter 3, an increase in the number of farms that could be reached by local contact reduced the effectiveness of synchronised fallowing. And when epidemics were started in large management areas (9 or more farms per management area), it resulted in larger epidemics compared with epidemics that were initiated in small management areas (eight or less farms). In chapter 5, it was shown that increasing the transmission rate of local contacts increased the size of an epidemic and the speed in which an epidemic occurred.

Spatial clustering appears to be important in the course of a disease (Tildesley, et al., 2010). As the closer farms are to an infected farm the more likely it is that they become infected; ideally, contact network studies should take this into account. Spatial structure is also important for bio-security: larger farms localized in epidemiologically separated areas will decrease the risk of large epidemics as these ‘firebreaks’ prevent disease transmission between areas (Green, 2010). However, firebreaks are only effective if the firebreak distance is sufficient to prevent pathogen spread between areas. If this is not the case concentrating production might increase the risk of epidemics.

6.2.3. Number of fish moved

The number of fish moved per movement was not included in this study. At this stage of the study it would make the network analysis unnecessary complicated; however the number of fish moved per movement is highly dispersed (figure A in appendix I at the end of this chapter). Heterogeneity in the number of animals moved per movement was also seen in the Danish cattle movement network (Bigras-Poulin, et al., 2006). There have been no studies published in fish that look at the effects of the number of fish moved per movement, but it is likely that the more fish are moved, the higher the probability that the receiving farm will become infected if the source farm is infected. A weighted network can take this into account; repeated movements between the same pair of sites are essentially a weighted network. However, this might not be a simple linear effect and the prevalence at the source is likely to be important.

In addition, the number of fish present on a farm and stocking densities could play a role in disease transmission. There may be a minimum viral load needed to cause an outbreak, and viral load depends on the infected stocking density (Hammell and Dohoo, 2005; Thrush and Peeler, 2006). When there is a large number of fish moved from an infected farm to a naive farm (relative to the current stock) this might increase the likelihood of disease outbreaks.

6.3. Future work

6.3.1. Biosecurity in freshwater farms

Farms or regions that supply animals to a relatively large number of farms/regions should be targeted for monitoring strategies (Noremark et al., 2009). This can reduce the financial costs of biosecurity and control measures as part of a surveillance program or in the event of a disease outbreak (Kiss et al., 2005). As shown in chapter 3, management areas are an important biosecurity strategy in Scottish seawater sites to prevent and control large epidemics.

It is recommended that movements between seawater sites only occur within management areas (Joint Government/Industry Working Group, 2000). However there are no such recommendations for movements between FW sites or for FW to SW sites. The live fish movement data showed that there are many movements occurring between regions and catchments (Green et al., 2012) [appendix B]. This indicated the need to develop biosecurity strategies for FW sites similar to those in SW sites. The Scottish industry should aim to make agreements on movements that occur on regional level. If fish are moved between and within a large number of regions, pathogens can spread easily throughout the country. So far, there is no detailed information describing the geographical distribution regarding live fish movements of Scottish salmon, brown and rainbow trout stratified by production phase.

Management areas are only effective when the boundaries between areas are strong enough to prevent pathogen spread between areas. In order to minimize the chance of an epidemic, management area boundaries should prevent pathogen transmission of a minimum of 75% between management areas based on the model assumptions used in chapter 3. However, the management areas cease to be effective when many movements occur between them. There are considerably more movements occurring between freshwater sites compared with movements between seawater sites as shown in chapter 4. The number of movements between seawater sites is relatively low ($N = 237$) compared with movements between freshwater sites ($N = 1181$) and movements from freshwater to seawater sites ($N = 810$). The relatively high number of movements occurring between FW sites forms a concern to the effectiveness of zoning strategies (such as management areas in seawater sites). Therefore, it is likely that the zoning boundaries need to be more effective in FW sites compared with management area boundaries in SW sites, however further studies are necessary to investigate the practicality of zoning strategies for FW sites.

Because of the risk of local transmission, if supply of fry or smolts is needed from another region, all farms in the region should be supplied from the same region. Ideally, movements should occur within the same region; however this might not be possible as some sites produce insufficient smolts for their region (Murray et al., 2010). Movement restriction between regions should be strategic in order to allow farms to be supplied with sufficient fish without increasing risk unnecessary

6.3.2. Disease data

Disease dynamics show substantial differences amongst pathogens; the timescale over which symptoms appear; the transmission rate and routes; or the spatial scale over which they operate. For example, bacterial kidney disease can transmit through vertical transmission (MSS, 2010), which is unlikely to occur for other diseases (OIE, 2009).

The practicality of using network models to study epidemics depends largely on disease characteristics. The timescale of the course of diseases should correspond with the timescale of changes in the network. For example, applying network models to study disease dynamics is less appropriate for diseases with a long incubation period (Kao, et al., 2007), as the movement network might have changed during the disease time scale. If movements are on a scale faster than disease transmission, also makes contact tracing harder. For these reasons, disease-specific models should be developed.

6.3.3. Well-boat movements

Well-boat movements could transmit pathogens between farms (Murray et al., 2002) as in some cases it might be necessary to open the valves of the well-boat and water exchange between the well-boat and seawater can occur (Munro et al., 2003). Boats can make “tours” between several places; in case of bad weather well-boats might have to shelter en route and open the valves in order to keep the fish alive. If this occurs in close vicinity of a fish farm, this increases the risk of these farms to become infected should the fish on the well-boat be infected. Integrating well-boat movements into the live fish movement contact network might help to identify possible important connections between farms.

6.4. Conclusions

- Networks models are an effective tool to identify high-risk farms or connections between farms (Kiss, et al., 2006) and to investigate disease control measures (Tildesley, et al., 2009; Green, 2010).
- Reducing the number of long-distance movements combined with synchronized fallowing will reduce the risk of epidemics (chapter 3).
- Seasonality patterns of live fish movements and contact structure differ between production phases (chapter 4). Disease control measures should take this into account to optimize control strategies.
- Seasonality patterns of live fish movements are shown to have a large effect on the course of epidemics. Especially when local transmission is high and when there is no clustering.
- Pathogens can spread by different transmission routes depending of the pathogen and for an optimal control policy all possible transmission routes should be considered.
- Biosecurity in freshwater sites could be improved by using zoning strategies similar to management area strategies in seawater sites.
- More detailed contact-network studies could be performed when disease data are available.

Effects of diseases are not as detrimental for the Scottish industry as compared with disease outbreaks such as ISA, in Chile (Mardones et al., 2009) and Norway (Rimstad, 2011), due to disease control measures applied in the Scottish industry (Murray et al., 2010). For example, this thesis showed that synchronized fallowing, which is often applied in Scottish marine sites, is highly effective. Diseases might always pose a threat to the Scottish industry, but mathematical models have great potential for investigating and developing biosecurity measures for the control of epidemics. This thesis constitutes a strong foundation to improve biosecurity measures and increases the knowledge and effects of live fish movement network properties on disease dynamics. The results of this thesis are applicable to aquatic industries in other countries and even to other species.

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Chapter 6: Appendix I

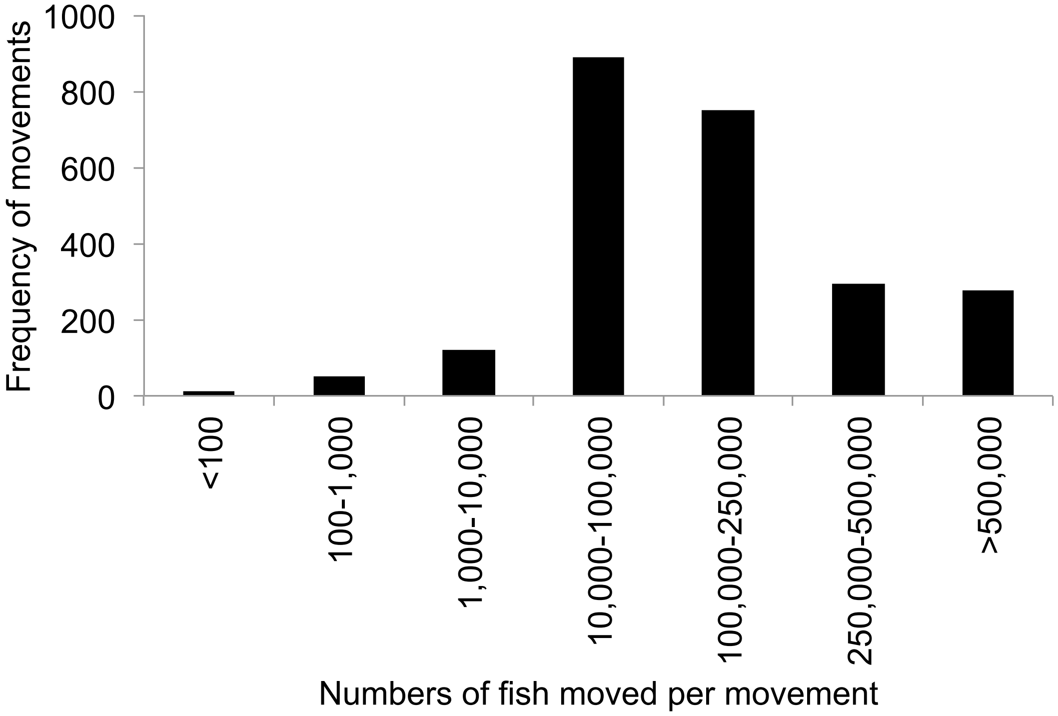

Figure A. The number of fish moved per live fish movement during 1 January 2002 to 31 December 2004 $(N = 2401)$**.**

APPENDIX

In this appendix, two published articles are presented on which Marleen Werkman is co-author. The first article discusses continuity of live animal movements between years of two datasets. The continuity of live fish movements are studied over a three-year period and the livestock data (pigs, sheep and cattle) is studied over a two-year period. The results are published in Preventive Veterinary Medicine 99, 225-228 (2011). The second article investigates the network structure of the movements of live fish in the Scottish aquaculture industry. This article is published in Journal of Fish Diseases 35, 29-37 (2012).

APPENDIX A: Tools to study trends in community structure: application to fish and livestock trading networks

Green, D.M.; Werkman, M.; Munro, L.A.; Kao, R.R.; Kiss, I.Z.; Danon, L.

A.1. Abstract

Partitioning of contact networks into communities allows groupings of epidemiologically related nodes to be derived, that could inform the design of disease surveillance and control strategies, e.g. contact tracing or design of 'firebreaks' for disease spread. However, these are only of merit if they persist longer than the timescale of interventions. Here, we apply different methods to identify concordance between network partitions across time for two animal trading networks, those of salmon in Scotland (2002 to 2004) and livestock in Great Britain (2003 to 2004). Both trading networks are similar in that they moderately agree over time in terms of their community structures, but this concordance is higher – and therefore community structure is more consistent – when only the 'core' network of nodes involved in trading over the whole time series is considered. In neither case was higher agreement found between partitions close together in time. These measures differ in their absolute values unless appropriate standardisation is applied. Once standardised, the measures gave similar values for both network types.

Keywords: aquaculture, community, network, graph, movements

A.2. Introduction

Movement of farmed animals is an important route for disease spread in what are highly structured industries. For example, sheep, cattle, and pigs were all involved in the UK epidemic of foot-and-mouth disease in 2001 (Shirley & Rushton, 2005), and movements of salmon were involved in the spread of infectious salmon anaemia (Murray et al. 2002). A network representation, where farm sites are represented by ‘nodes’, and potentially infectious contact by directed ‘arcs’ or undirected ‘edges’ is a powerful tool for studying the potential for disease spread and control (for a review of networks in preventive veterinary medicine, see Martínez-López et al., 2009).

Network communities represent partitions of nodes with a high level of within-partition connectivity (for a review, see Fortunato, 2010). In a strongly community-organised network, contact between communities may be relatively weak, and community algorithms can provide us with natural groupings of epidemiologically related nodes, derived from the network itself rather than artificially imposed. Uncommon inter-community links might furthermore be considered as potential targets for proactive targeted surveillance, or reactively in disease control (Kao et al. 2006; Green et al. 2009; Salathé & Jones, 2010). That is to say, removing the disease transmission risk of such contacts could reduce the size of potential epidemics by creating ‘firebreaks’, particularly where these contacts are long distance. However, these analyses are only of merit if partitions can be used predictively; that is, if community structure changes more slowly than we collect data in order to inform surveillance or disease control strategy.

A key problem here is that objective measures of the rate of change of large-scale network structure are not clearly defined, nor how large a change must be to heavily compromise disease control strategies. In this short paper, we consider the first part of this question, by comparing different methods for determining how network community structures change, or not, over time. We apply these methods to two movement networks of farmed animals, to investigate whether networks closer in time have more similar network structure. The two networks are that of live Atlantic salmon *Salmo salar* movements within Scotland 2002 to 2004, and that of livestock (pigs, sheep, cattle) in Great Britain for 2003 to 2004.

A.3. Method

A.3.1. Data

The network of live fish movements in Scotland has been described for salmonid species (brown trout *Salmo trutta*, rainbow trout *Onchorhynchus mykiss*, Atlantic salmon *S. salar*) by Green et al. (2009) and Munro & Gregory (2009). Here, we extend and refine their analysis to a three-year dataset of Atlantic salmon alone for 2002-4. In brief, these data comprise movements of live fish (egg to adult) between registered sites in Scotland, where paper records of both off and on movements were legible and in agreement. Data are held by the Fish Health Inspectorate of Marine Scotland.

For the network of livestock movements, the partitions used here are derived from the data extract used by Kao et al. (2006). Their data set comprised data from January 2003 to December 2004 for cattle (Cattle Tracing System) and sheep and pigs (Animal Movements Licence System, England and Wales; Scottish Agricultural Movements System, Scotland). A full description is given by Kao et al. (2006).

Both data sets provide source and destination premises, species and number moved, and date. Data were segregated into time periods (years for fish, four-week periods for livestock), with each network described by an adjacency matrix A. Here, $A_{ij} = 1$ implies movement of animals from node (site) i to node j (zero for no contact). The number of in and out connections for node$i$ are given by k_i^{out} and k_i^{in}, the total number of nodes by n, and the total number of arcs by M.

A.3.2. Graph partitioning

Communites were identified for the two datasets using related partitioning algorithms. For the fish network, the measure of community fit used is that defined by

$$Q = \frac{1}{M}\sum_{i,j}\left(A_{ij} - \frac{k_i^{out}k_j^{in}}{M}\right)[X_i = X_j]$$

Where X_i is the community 'label' of node i. The Iverson bracket $[\cdot = \cdot]$ returns one if the condition inside is true, and zero otherwise. This formulation – as described by Kao et al. (2006) and Leicht & Newman (2008) – accounts for the strong directed nature of the fish network. Higher Q indicates a larger fraction of arcs within communities. 'Lone' nodes in a network, with no movements during the period of interest, gain a unique label. However, it could be argued that without network activity, such nodes are not part of the network at all (further discussed in the Results section A.4). The livestock network was treated similarly, except that the partition data available were based on undirected edges.

For both systems, we employ a 'hill-climbing' algorithm (Newman, 2004; Danon et. al. 2005). This begins by assigning each node a unique community label $X_i = i$. Each possible merger of two communities is considered, with that providing the largest positive change in Q accepted. This step is repeated until a maximum Q is reached, for which the corresponding community assignments are taken as the 'best fit'. Though other algorithms may find improved partitions, this one has the benefit of being practicable on very large networks such as that for livestock movements.

A.3.3. Entropy measures

Borrowing concepts from information theory, entropy-based measures can be used to compare multiple partitions of the same network (Strehl et al. 2002; Vinh et al. 2009). Beginning with two vectors X and Y containing community labels for two partitions, two vectors U and V are built containing the number of nodes present in each community in X and Y:$U_u = \sum_i [X_i = u]$; $V_u = \sum_i [Y_i = u]$. Also, an $n \times n$ matrix is defined containing the frequency combinations of communities in both X and Y: $W_{uv} = \sum_{i,j} [X_i = u][Y_j = v]$. For two networks with congruent partitions, this matrix contains only a single non-zero element in each row and column. The Shannon entropy (a measure of the information content of a dataset) is calculated for the partitions of each network $(H(U))$ and $(H(V))$, and that of the matrix of community combinations, the 'joint entropy' $H(U,V)$.

$$H(U) = -\sum_{u} \frac{U_u}{n} \log\left(\frac{U_u}{n}\right)$$

$$H(U,V) = -\sum_{u,v} \frac{W_{uv}}{n} \log\left(\frac{W_{uv}}{n}\right)$$

Choice of logarithm base does not affect the end result below, and by definition, $0 \times \log 0 = 0$. The mutual information $I(U,V) = H(U) + H(V) - H(U,V)$ then measures the amount of information shared between the two partitions – and thus their similarity – with a lower bound of zero, but no upper bound. For comparison between networks, a normalised measure of similarity is required. A simple approach is to scale I by its maximum potential value (it cannot exceed the minimum of $H(U)$ and $H(V)$), giving the normalised mutual information $0 \leq NMI_1 \leq 1$:

$$NMI_1 = \frac{I(U,V)}{\min\left(H(U), H(V)\right)}$$

Alternatively, we can scale by the geometric mean of these two quantities (Strehl et al. 2002), $0 \leq NMI_2 \leq NMI_1$:

$$NMI_2 = \frac{I(U,V)}{\sqrt{H(U)H(V)}}$$

For correlation coefficients such as Pearson's or Spearman's, a value of zero is obtained where there is no relationship, i.e. under the null hypothesis. However here, under a reasonable null hypothesis that communities are assigned randomly, the expectation of $I(U,V), E_0\left(I(U,V)\right)$ is not generally zero and depends upon the size distribution of communities (Vinh et al. 2009). A further approach is to normalise I against this expectation, providing the adjusted mutual information AMI (Vinh et al.

2009), with a maximum of one, zero under the null hypothesis, and negative where there is less agreement between network communities than would be expected by chance.

$$AMI = \frac{I(U,V) - E_0\big(I(U,V)\big)}{\min\big(H(U),H(V)\big) - E_0\big(I(U,V)\big)}$$

This definition of AMI is similar in form to that of Cohen's Kappa statistic, and has a lower value than NMI_1 except where $E_0\big(I(U,V)\big)$ is vanishingly small. Vinh et al. (2009) suggest using $\max(\cdot,\cdot)$ not $\min(\cdot,\cdot)$, however the min term has more in common with the formula for NMI_2 above. Unlike correlation coefficients, its minimum possible value is not defined to be -1. A permutation test was employed to determine the mean and distribution of $E_0(I)$ allowing for calculation of AMI and its significance. One of the vectors X and Y is repeatedly shuffled, removing association between the node labels in X and Y. On each permutation, $I(U,V)$ is recalculated. The original $I(U,V)$ can be compared with the distribution of these permuted versions.

A.3.4. Pair-based measures

Pairs of nodes can be examined with respect to whether or not they are in the same communities. Pairs of nodes that were in the same community in the two partitions were counted: $x = \sum_{ij\neq i}\big[X_i = X_j\big]$ and $y = \sum_{ij\neq i}\big[Y_i = Y_j\big]$, as well as pairs that were in the same community in both partitions: $a = \sum_{ij\neq i}\big[X_i = X_j\big]\big[Y_i = Y_j\big]$, or in different communities in both: $b = \sum_{ij\neq i}\big[X_i \neq X_j\big]\big[Y_i \neq Y_j\big]$.

From these values, the probability that a pair of nodes present in the same community in partition$X$ are also in the same community in partition$Y$ was calculated: $P(\text{pair in } Y|\text{pair in } X) = \frac{a}{x}$. However, this metric is not necessarily symmetric with respect to $X$and Y, unlike the earlier measures. Instead, the geometric mean of both possible probabilites was taken: $\bar{P} = a/\sqrt{xy}$ (Wallace, 1983; quoted in Meilă, 2007).

These probabilities benefit from being easily interpretable. A further pair-based measure of clustering similarity, the Rand index $R = (a + b)/\big(n(n - 1)\big)$ (Rand, 1971), was also calculated.

Again, these measures do not equal zero under the null hypothesis that the two partitions are independent. The statistical significance of both was determined through a permutation test and – as with the mutual information – standardised according to $[\varphi - E_0(\varphi)]/[1 - E_0(\varphi)]$, where φ is the measure of interest, giving an adjusted Rand index AR and an adjusted probability related to $\bar{P}$, $A\bar{P}$.

A.4. Results and Discussion

For the salmon movement network $(n = 502)$, the unadjusted indices NMI_1, $\bar{P}$ and R gave numbers of different magnitude, despite their apparent normalisation (table A.1). This reflects their different values under their null models. A $\bar{P}$ index of ~0.3 is easily interpretable as the proportion of same-community node pairs that persist across both partitions. Once 'adjusted', the range of values was narrower, with the pair-based indices giving almost coincidental values (table A.1). This coincidence was also evident for the livestock network, thus in figure A.1 only the index R is shown. The null model for the permutation test was amended for the fish network to account for variation in the activity of nodes between years: Those nodes with no links were not considered during the reshuffling process to prevent their single-node communities being spuriously reassigned to other nodes.

Table A.1. Adjusted and unadjusted measures of agreement for communities between pairs of years 2002-2004 for the live salmon movement network in Scotland. All measures were statistically significant at P=0.05. Shown are the normalised and adjusted mutual information NMI_1 and AMI, the (adjusted) Rand index $(A)R$, and the (adjusted) pair-based measure $(A)\bar{P}$.

	2002,2003	2003,2004	2002,2004
Whole network			
NMI_1	0.71	0.78	0.78
$\bar{P}$	0.23	0.29	0.29
R	0.94	0.95	0.96
AMI	0.51	0.61	0.43
$A\bar{P}$	0.20	0.26	0.26
AR	0.20	0.25	0.25
Core network			
AMI	0.55	0.65	0.62
$A\bar{P}$	0.39	0.54	0.47
AR	0.38	0.54	0.47

For the much larger livestock network (n =141607; see supplementary animation), networks were built from four-week periods of data. As with the fish network, all correlations were statistically significant ($P < 0.05$). These networks show a marked seasonal pattern (Kao et al. 2006) with a higher density of arcs due to an autumn peak in sheep trading. This seasonality was still noticeable despite normalisation as a peakin AMI values for networks 13 four-week periods (i.e. one year) apart (figure A.1). Though this peak may represent a real similarity in the trading structure at particular times of year, Meilă (2007) raises concerns over the use of adjusted indices for comparison purposes where the baseline and actual values may vary non-linearly.

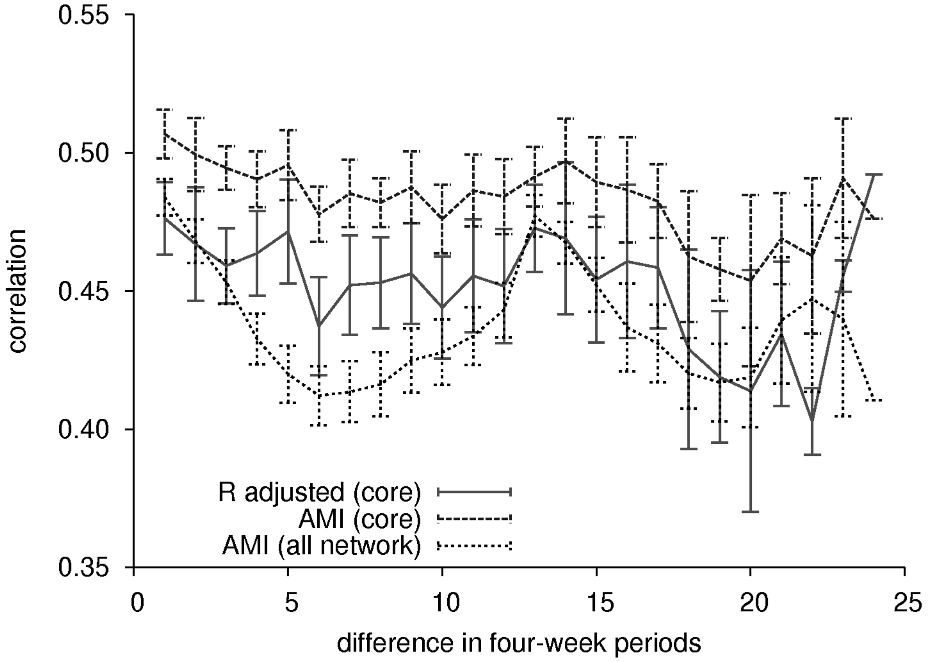

Figure A.1. Measures of agreement for network communities based on livestock movements of cattle, sheep and pigs in Great Britain (2003–2004). Means and standard errors of measures for all possible combinations of 4-week periods are shown, stratified by time difference in periods (1–24). Shown are the adjusted Rand index R (solid line) and entropy measure AMI (dashed line) for the 'core' network, with AMI for the entire network (dotted line). Probability $\bar{P}$ coincided with R and is not shown.

To explore this further, we accounted for seasonality in trading volume by considering only a 'core' sub-network of nodes that were active in each of the 25 networks examined ($n = 6424$). The AMI values together with the Rand index R are shown for this core network in figure A.1, showing close agreement between the three statistics and much reduced seasonality in community structure. Taking the 'core' network of $n =$ 208 nodes for the salmon network, a similar result is found as for the whole fish network, albeit with higher values (table A.1).

Though both sets of networks show moderate agreement between partitions at different time points, in neither case was a higher agreement between networks closer in time apparent. One possible explanation of this is that there are no significant long-term trends in community structure for either network, or that any such trends operate on timescales either longer or shorter than examined in this study. There may also be other trends and patterns within the data that remain observed. For example, the partitions above are not absolutes: different measures and algorithms could produce different groupings. Also, no allowance is made in this approach for the potential for sub- and super-community network structure (Kao et al. 2006; Green et al. 2009).

The unadjusted indices give a wide selection of values for the same network, however once adjusted they are more similar. Those for $\bar{P}$ coincided with R. However, whether this is in general the case or is network dependent remains to be established. The computational efficiency of the measures varies: Despite their apparent complexity, the entropy-based measures are relatively fast to compute, particularly for large networks, since they do not rely on counting edges.

A.5. Conclusions

In conclusion, for both networks a significant and non-trivial level of concordance between network partitions over time was seen. Dissimilarity in partitions, however, appears to represent random variation rather than decay in partition similarity over time for both networks. Characterising the way networks change over time remains a challenging problem. Our results suggest that despite the fact that many features change, a large part of the intermediate structure is conserved over time, particularly in the core network. Nevertheless, the how stable a contact network must remain over time to be epidemiologically useful for disease surveillance and control remains to be explored, potentially through simulation of dynamic disease control measures on dynamic network epidemic models.

A.6. Acknowledgements

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A.7. References

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APPENDIX B: The potential for targeted surveillance of live fish movements in Scotland

Green, D.M.; Werkman, M.; Munro, L.A.

B.1. Abstract

The network structure of the movements of live fish in the Scottish aquaculture industry has recently been demonstrated for 2003. In this paper, we enlarge this analysis to a longer three-year period from 2002 to 2004, the new data allowing complete coverage of at least one production cycle. The resulting network contains slightly more sites than that for a single year, and is denser with more arcs (directed site-to-site connections) present, but otherwise features recognisable in the one-year network are still recognisable in the three-year network. Arc removal algorithms (a proxy for targeted surveillance) were identified that could successfully reduce the portion of the network reachable from a node (a proxy for potential epidemic size) by approximately one third by removing as few as four arcs. This results from the high centrality of particular nodes and arcs. A strong community structure was identified in the network, corresponding with species farmed but only weakly geographical, with a high proportion of arcs occurring between management areas and catchments.

Keywords: aquaculture, network, graph, transmission

B.2. Introduction

Three species of salmonid fish dominate aquaculture production in Scotland: brown trout *Salmo trutta*, rainbow trout *Oncorhynchus mykiss*, and Atlantic salmon *Salmo salar*. Of these, Atlantic salmon is by far the largest sector with *c.* 130,000 tonnes per year of production over the last decade, over a gradually decreasing number of distinct sites (Scottish Government, 2011a). With production aggregated into a relatively small number of sites, in turn clustered in distinct geographic areas, the risk of spread of disease from site to site, and its management, are of importance both to producers and to the government. Under recent EU legislation, EU directive 2006/88/EC (implemented Aug 08), EU countries are required to implement risk-based surveillance. In Scotland, the competent authority for implementing this is Marine Scotland through the Fish Health Inspectorate, to whom records of live fish movements are already required to be submitted by those registered farming enterprises (under *The Registration of Fish Farming and Shellfish Farming Businesses Order* 1985).

In epidemiological systems with complex population structure, network models have been used widely to study patterns of contact through live animal movements, including in aquaculture (e.g. Thrush & Peeler, 2006; Munro & Gregory, 2009; Green et al. 2009). Epidemiological questions that can be asked of networks include *inter alia*, which sites are at risk of spreading infection, should an epidemic arise? And which sites are at risk of being infected? These are not necessarily the same. And where should we concentrate effort to help reduce epidemic spread? Live fish movements are an important potential route for disease transmission, as has been demonstrated in the cases of both infectious salmon anaemia (Murray et al., 2002) and bacterial kidney disease in rainbow trout (Bland, 2007).

Recently, Green et al. (2009) explored the network structure of movements of live fish within the Scottish aquaculture industry for 2003 (see also Munro & Gregory, 2009), with a view to informing targeted surveillance policy for infectious disease prevention and control. They reported how several algorithms could be used to identify contacts between sites that might prove suitable targets for targeted surveillance. This aids efficient application of limited resources towards high-risk farms, locations, and farm types as part of risk-based surveillance (Stärk et al., 2006). Since publication of this paper, further work has consolidated movement data into an electronic database for the additional years 2002 and 2004, representing the largest dataset for salmonid movements available for Scotland. This brings further sites and connections into the network, and importantly, covers one complete production cycle for marine salmon production. In this paper, we extend the earlier analyses of network structure and targeted surveillance approaches onto this, more complete, dataset. We investigate whether the conclusions of the earlier analysis are robust to being applied on a considerably larger network.

B.3. Method

B.3.1. Data

Data were obtained from the Fish Health Inspectorate at Marine Scotland, Aberdeen, and converted into an electronic database. Only ‘validated’ data were used, i.e. where fish movements were confirmed by paper records from both exporting and receiving sites and could be cross referenced. These data included all life stages from egg to adult, for all three species, for all registered sites within Scotland. Movements to unregistered sites (predominantly freshwater fisheries; please note that this dataset precedes the legislation introduced under EU directive 2006/88/EC which requires the registration of a wider range of aquaculture production businesses) and imports and exports out with Scotland (e.g. to England) were not included in the dataset (Munro & Gregory, 2009). The dataset was extended forwards and backwards by a year giving a three year time series, enough to cover complete production cycles of the salmon industry. However, for 2002, only salmon movement data had been converted to electronic format.

Location and river catchment data were available for each site. Inland sites may be categorised according to ‘supercatchment’ (i.e. sites connected by any route through freshwater: the whole drainage basin) and 11 official Salmon Fishery Statistical Regions (below, ‘Statistical Regions’, see figure B.1 inset). Marine sites are divided into 20 Management Areas (Scottish Government, 2011b), which are in turn subdivided (up to four-way). Management Area boundaries are determined by site locations, and are reviewed periodically if sites open and close, but did not straddle the coastline of adjacent Statistical Regions. Here, Management Area boundaries as of 2003 were used. ‘Live’ management areas are detailed by the Scottish Government (2011b) but the historical data are not reported online.

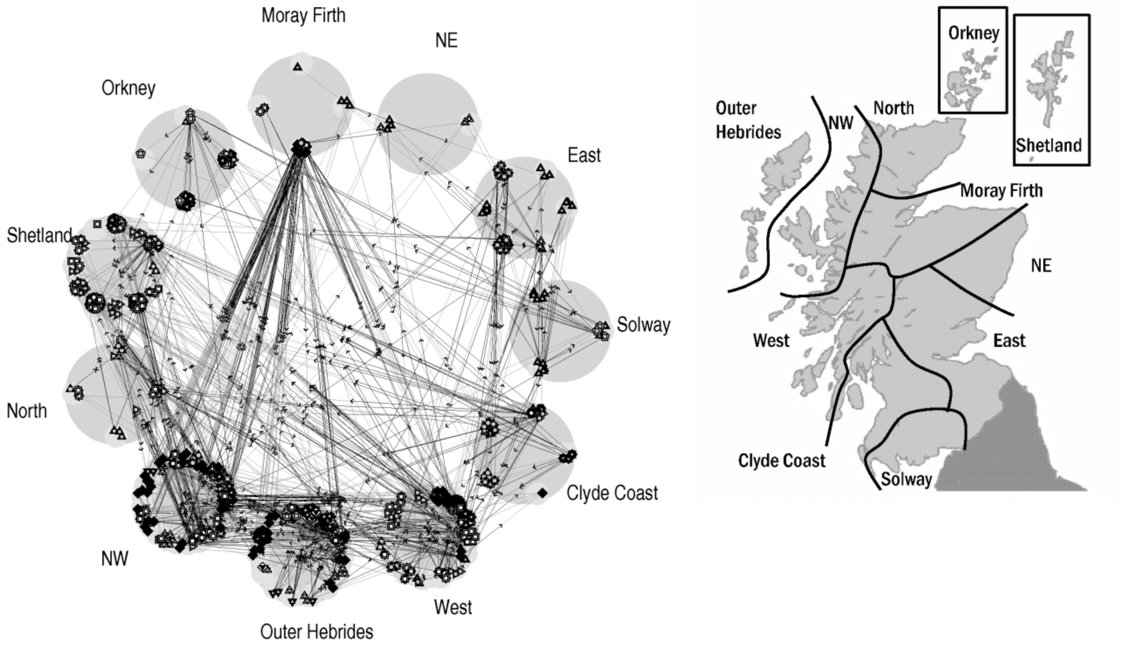


Figure B.1. Geographical representation of network community structure. Large circles of nodes represent regions; sites belonging to the same management area (and sub-area) or catchment are drawn in the same small circle. Inset: schematic showing official Salmon Fishery Statistical Regions.

B.3.2. The contact network representation

Data analysis broadly followed the approach of Green et al. (2009). Each of n sites is represented by a **node**, with potentially infectious contact from a site i to a site j represented by directed **arcs** (i,j). A matrix element $A_{ij} = 1$ indicates that at some point over the period of interest, movement of live fish occurred from site i to j; $A_{ij} = 0$ indicates no such receipt of live fish. Any (erroneous) self loops were removed $(A_{ii} = 0)$. The simplest node properties are the numbers of connections – in, out, and total (undirected) – enjoyed by each node, i.e. the node **degree**, k: $k_i^{in} = \sum_j A_{ji}$; $k_i^{out} = \sum_j A_{ij}$; and $k_i^{undir} = k_i^{in} + k_i^{out} - \sum_j A_{ij}A_{ji}$. The means of node statistics averaged across all nodes are denoted using angled brackets, e.g. $\langle k^{in} \rangle = \frac{1}{n}\sum_{i,j} A_{ij}$.

Some epidemiologically useful measures can be taken from the network topology. The shortest distance in network steps from node$i$ to node$j$ is represented by the matrix of shortest paths L_{ij}, which is zero if i and j are the same node, and undefined where no suitable path exists. The number of such paths passing through arc (i, j) is its **betweenness** B_{ij} (undefined where $A_{ij} = 0$). Additional measures of network structure included the clustering coefficient C as used by Keeling (1999), amended for a directed network as the proportion of ordered node triples (i, j, k) with arcs (i, j) and (j, k) that also have arcs (i, k). The level of assortativity (preferential mixing between nodes of relatively high or low degree) r_{assort}, was defined as the correlation between the *in* degree of node$i$ and *out* degree of node$j$ across all arcs (i, j) (Newman, 2003).

From these and other values, estimates can be obtained for the implications of network topology on the basic reproduction number R_0 of a propogating epidemic, that is the number of secondary cases generated by a typical case over its infectious period, where $R_0 > 1$ represents the transmission threshold for a large epidemic in a large network (Anderson & May, 1991). Several network measures are demonstrated on the small ‘toy’ network shown in Box B.1.

Box B.1. Demonstration of network statistics. For simplicity, the small undirected network shown is analysed in the table showing key network statistics referred to in the paper. On the network diagram, nodes are indicated and edges are marked by their betweenness$\boldsymbol{B_{ij}}$.

	A	B	C	D	E	F	mean
k	1	3	2	3	1	0	10/6
$L_{A,i}$	0	1	2	2	3	∞	
D_i	4	4	4	4	4	0	

Summary statistics

$\mathbf{max}(\boldsymbol{D}) = \mathbf{4}$

$\langle \boldsymbol{D} \rangle = \mathbf{20/6}$

$\langle \boldsymbol{k} \rangle = \mathbf{1.67}$

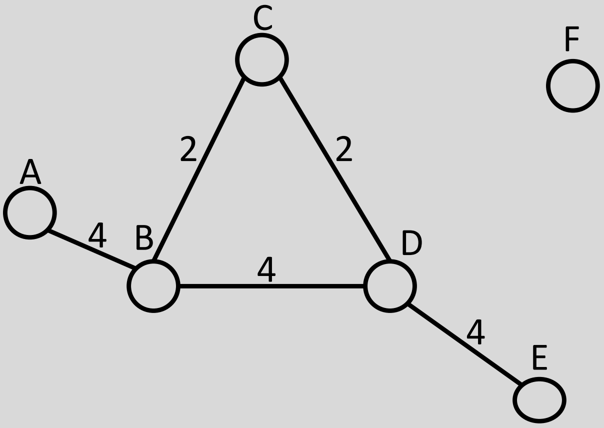
$\langle \boldsymbol{k}^2 \rangle = \mathbf{4}$

$\boldsymbol{R_0} \approx \langle \boldsymbol{k}^2 \rangle / \langle \boldsymbol{k} \rangle = \mathbf{2.4}$

Triples: ABC ABD BCD CBD CDB BDE CDE.

Triangles: BCD CBD CDB.

$\boldsymbol{C} = \mathbf{3/7}.$



B.3.3. Targeted surveillance algorithms

Several algorithms, as described by Green et al. (2009), were used to identify arcs of high importance in the network structure, whose removal from the network effectively limits the potential spread of disease. These algorithms are introduced briefly below. One such algorithm identifies arcs which bridge network **communities**. A network community is a group of nodes (sites) with a relative high density of arcs within the group, with relatively few connections to other such groups. As with the earlier study, a ‘modularity’-maximising algorithm was used (Newman, 2004; Leicht and Newman, 2008) to identify communities, with each node a member of a single community. The ‘greedy’ algorithm used is efficient though does not necessarily find an absolute global maximum for modularity Q, which is a hard problem for large networks. Greedy algorithms proceed through a set of steps, always choosing the locally best solution at each step.

$$Q = \frac{1}{M}\sum_{i,j}\left(A_{ij} - \frac{k_i^{out}k_j^{in}}{M}\right)\left[c_i = c_j\right]$$

Calculation of Q requires the total number of arcs$M = \sum_{i,j} A_{ij}$. For two variables x and y, the Iverson bracket $[x = y]$ has the value of one where the condition $x = y$ is true, and zero otherwise. Therefore the summation for Q above is only performed for combinations of nodes i and j which belong to the same community. Modularity Q penalises placing disconnected nodes with high degree in the same community, and rewards placing together those nodes with low degree which are connected.

The resilience of the network to arc removal was expressed in terms of maximum or mean node ‘reach’ (Green et al. 2009) D, which can be defined as the number of nodes downstream from a focal node, following directed paths, that are potential targets for epidemic spread, $D_i = \sum_{j \neq i}\left[L_{ij} \neq \infty\right]$. All the algorithms, listed below (see also Green et al. 2009), attempt to identify an ordering of arcs from the most to the least important for maintaining network structure. A successful algorithm will result in the fastest disassembling of network structure by removing the least number of arcs, either in terms of maximum reach max (D) (an estimate of worst-case epidemic size) or mean reach $\langle D0 \rangle$ (an estimate of typical epidemic size).

Arbitrary The null model, with a non-intelligent selection of arcs, was to choose arcs purely at random, representing non-purposeful (but potentially limited) surveillance.

Highly connected (degree) A node with many *in* connections is at high risk of infection; a node with many *out* connections poses a high risk of further connection. The second algorithm therefore ranked arcs (i,j) according to how well they fulfilled both criteria, using the metric $k_i^{in} \times k_j^{out}$. Networks with many arcs with a high value for this expression are assortative (see above), and assortativity leads to a higher value of R_0.

High betweenness Arcs were ranked according to their betweenness, B_{ij}. After each sequential removal of an arc, betweenness must be recomputed for the whole network as shortest paths are frequently rerouted.

Community-bridging Arcs bridging communities as identified above were prioritised for removal. Within-community and between-community arcs were chosen arbitrarily, aside from this criterion.

Greedy max & greedy mean In these algorithms, arcs are removed one at a time, always choosing that arc which causes the greatest reduction to either maximum or mean reach. Though this sounds ‘optimal’, as with many algorithms—including that for assigning communities above—this locally optimal choice by no means ensures finding a globally optimal solution.

Eigenvector-based Network eigen analysis provides an eigenvector V which is a measure of node centrality, and an eigenvalueλwhich in some conditions can be used to obtain an estimate of R_0. Two algorithms as used by Green et al. (2009) chose *out* arcs arbitrarily within nodes, ranking nodes according to highest eigenvector centrality V_i. The adjacency matrix was modified (Bonacich & Lloyd, 2001) in two ways before eigenanalysis, assuming either additional contact between all nodes of strength β/n (**eigen spread** algorithm), or constant total weight of *out*ward contact from all nodes (**eigen walk** algorithm).

For the most successful algorithms, the ten arcs were identified that appeared most frequently amongst the first ten arcs removed (due to the stochastic nature of the algorithms, the chosen arcs may vary between runs). The properties of these arcs were then compared with the average arc properties across the whole network.

B.4. Results

B.4.1. Small- and large-scale network structure

With the new larger movement dataset presented in this paper (compared with Green et al., 2009), a larger network is obtained with n =561 nodes and a higher density of links (figure B.1 and B.2). Mean degrees (and their coefficients of dispersion, i.e. the variance-to-mean ratio) were $\langle k^{in} \rangle =$ 2.39 (1.23), $\langle k^{out} \rangle =$ 2.39 (6.36) and $\langle k^{undir} \rangle =$ 4.53 (4.24) for an undirected network (see figure. S.1 in electronic supplementary material for a histogram of node degree). Other simple measures of network shape remained relatively unchanged from the earlier analysis with correlation between *in*- and *out* degree of nodes of $r =$ 0.238, a clustering coefficient $C = 0.069$ and a coefficient of assortativity of $r_{assort} =$ 0.164 (assortative). With a higher k, the eigenvalue approach to estimating R_0 also gives a higher value, with $R_0 =$ 4.59 for $\beta =$ 0.5. Again, this is higher than the degree-based estimate of $R_0 \approx \langle k^{in} k^{out} \rangle / \sqrt{\langle k^{in} \rangle \langle k^{out} \rangle} =$ 3.05.

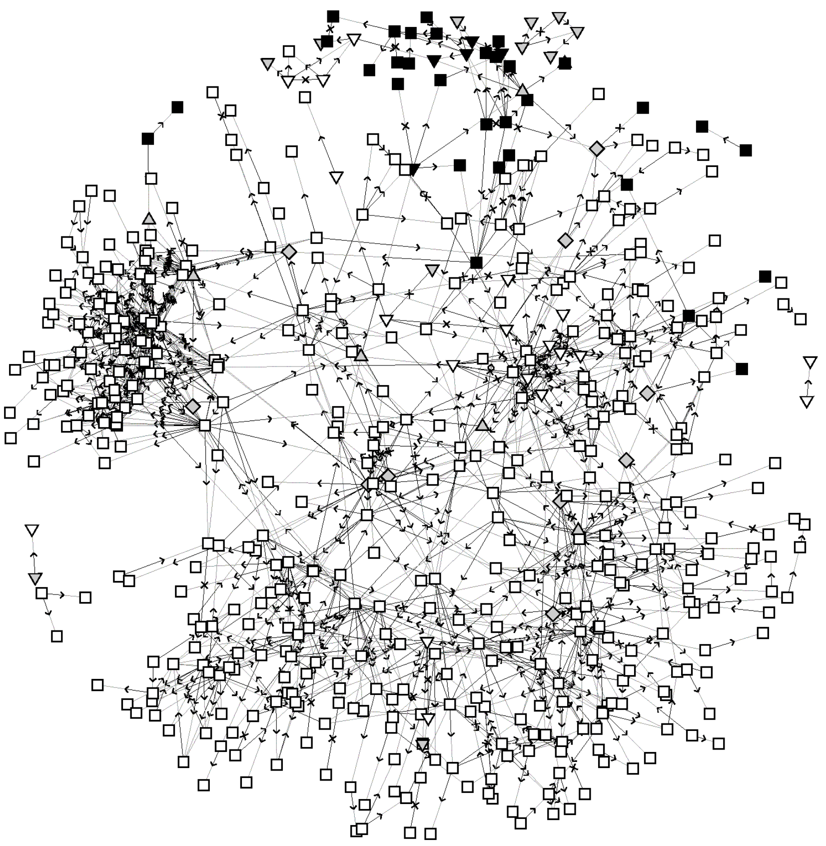


Figure B.2. The Scottish live fish movement network (2002 to 2004), according to species moved to/from sites. □ salmon only (S); ▪ rainbow trout only (R); S+R; ▾ brown trout only (T); ▾ T+R; ▿ T+S; ▴ T+S+R. Arrows indicate movement direction (sometimes bidirectional).

The higher arc density has a large impact on the overall connectivity and community structure of the entire network. Considering large-scale measures of network structure, as opposed to the node- and arc-level measures reported above, mean shortest path length (where defined and non-zero) was 5.92, with such paths accounting for 0.105% of the $n(n-1)$ possible. As in Green et al. (2009), a rewiring algorithm was employed to provide null-model networks for comparison, equivalent to a null hypothesis of no large-scale structure to the network and random connection (notwithstanding that nodes have different degree). For rewired networks, mean shortest path length was similar, 5.13, with finite non-zero paths accounting for 0.598% of those possible (see figure S.1 in electronic supplementary material for histograms of path lengths in the original and rewired networks).

The community-joining algorithm to find an optimal partition of the network to maximise modularity found partitions with maximum modularity of $Q = 0.75$, similar to that found for the one-year network data. The community assignments and joining dendrogram associated with this maximum modularity are shown in figures B.3 and S.2 (in electronic supplementary material). This community distribution consists of several large communities well defined in the dendrogram, with a small number of nodes belonging to smaller communities or disconnected. This community algorithm produces a partition with a higher modularity index than that using shared membership of a supercatchment or management area as criteria for membership of the same 'community' ($Q = 0.41$). This reflects a relatively large proportion of arcs occurring between such communities (43 %), as can be seen in figure B.1.

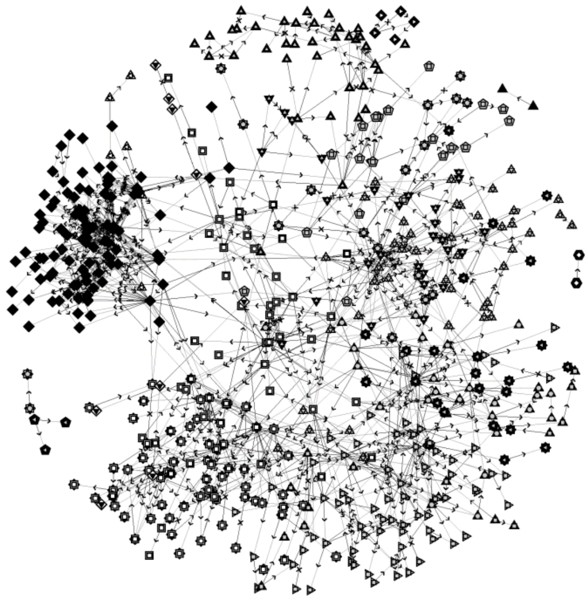


Figure B.3. Community assignment for the live fish movement network for Scotland for 2002-4. Community membership is indicated by different symbols.

B.4.2. Reducing network reach

The effects on network reach of removing up to 100 arcs is shown in figure B.4 for both maximum reach and mean reach, and for the eight algorithms explored in Green et al. (2009) and described above. With only a small number of extra nodes, but considerably more connections, network density is higher and this is reflected in different efficiencies amongst the algorithms. The two greedy algorithms perform well for both measures, with betweenness being comparatively successful. The other algorithms (degree-, community-, and eigenvalue-based) perform relatively poorly. Degree- and community-based measures are somewhat effective but only if a large number of arcs are removed.

Arcs having been ranked in order of ability of importance to network structure, the properties of high importance arcs and the average arc were compared for the greedy (both) and betweenness algorithms. For the greedy max algorithm, four out of ten selected arcs were shared with the greedy mean algorithm, and two with the betweenness algorithm, which in turn shared four with the greedy mean algorithm. Overall, 22 arcs were represented involving 33 nodes with some nodes being both source and destination nodes for these arcs. Compared with the whole network, these arcs left nodes with a higher *in* degree (3.8) than average (3.1) and led to nodes with a considerably higher *out* degree (10.8 versus 3.1). A fraction 0.52 of arcs joined nodes in different communities, compared with 0.12 for the whole network. They are also more likely to join nodes in different regions (0.52 versus 0.43).

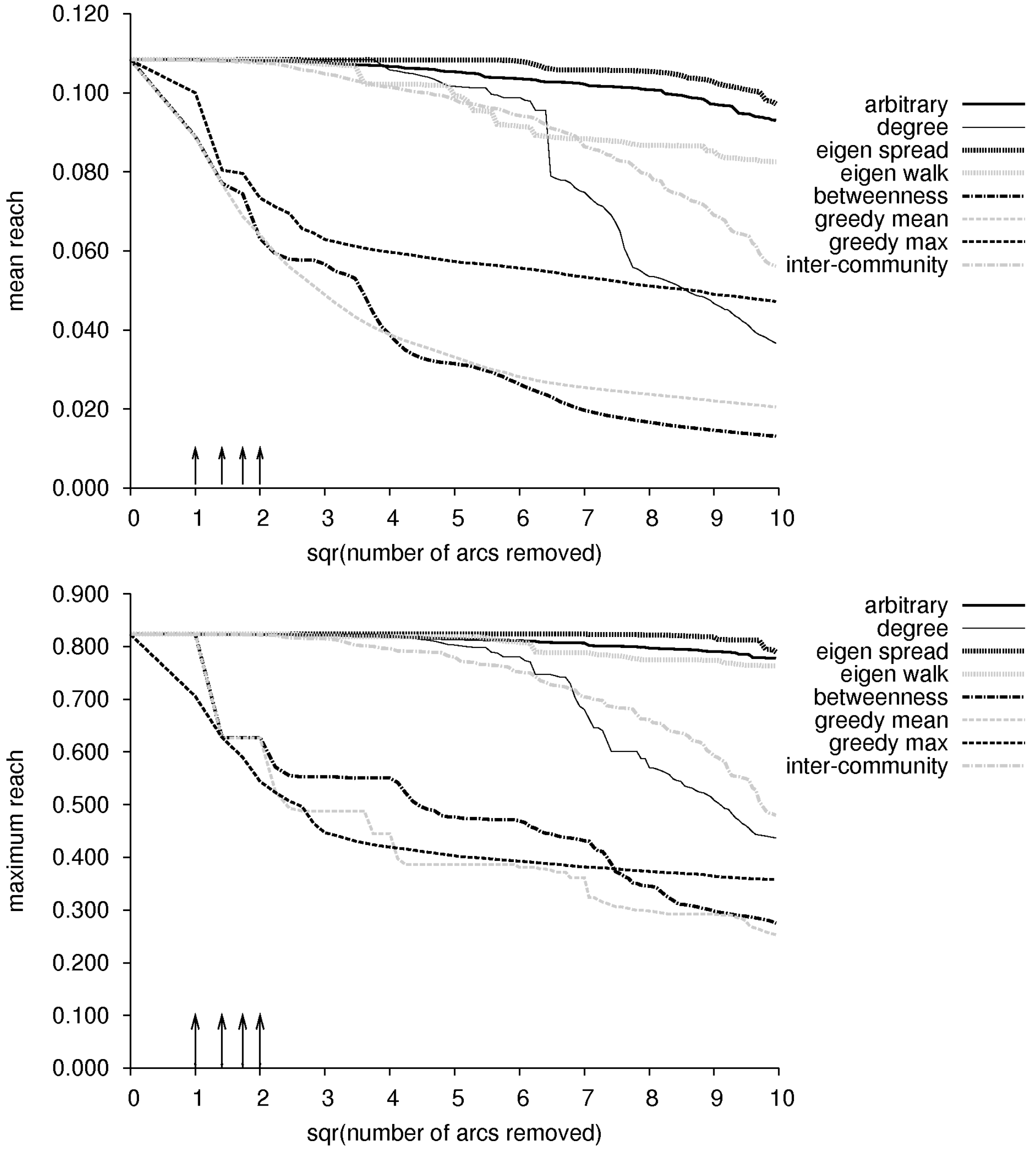


Figure B.4. Mean and maximum reach from all nodes, versus proportion of network arcs removed (plotted on a square-root scale), for eight different algorithms for determining precedence of arc removal. Arrows indicate *x*-axis values corresponding to the removal of 1, 2, 3, and 4 arcs.

B.5. Discussion

Compared with analysis of the 2003 data alone (Green et al. 2009), the 2002-2004 network shows a modest increase in the number of nodes, but a large increase in the number of arcs. This is demonstrated by the more densely connected network picture, with few poorly connected or disconnected node pairs. Community structure however remained strong. Compared with the 2003 network, the full network has a distribution of path lengths with higher mode, but with a shorter tail, as expected with a more compact network. Maximum degree is also higher. A caveat concerning the movement data raised in Green et al. 2009, remaining important here, is that only movements between registered sites are recorded (Munro & Gregory, 2009). Unregistered sites consist mainly of trout fisheries, which although they may pose a risk of disease spread by other means than fish movements, are likely to be primarily ‘sinks’ for live fish movements with no onward network connections. These data will be available in future since sites are required to be registered as of August 2008 under EU directive 2006/88/EC. Electronic recording of movement data in a database format will also aid in future analyis: the scope of the study reported here was necessarily limited in breadth by the large amount of effort involved in processing the paper movement records, particularly as these are in duplicate (off and on pairs). The complexities of analysing this data source have been recently discussed by Werkman et al. (2011b) [chapter 4].

Arc-removal methods of fragmenting the network remain effective, with c. 10 arcs removed reducing both mean and maximum network reach by about one half. This is less effective than with the 2003 data alone (Green et al. 2009), but this is to be expected given the more tightly connected network: its denser structure is held together by single arcs in fewer places. Lower betweenness values for arcs are found for similar reasons (data not shown), as a larger number of paths between nodes exist, lowering the centrality of a particular path. Though the successful arc-removal algorithms targeted arcs with a tendency towards high degree, joining communities, algorithms based on degree or community assignment alone behaved relatively poorly, demonstrating the benefit of a more technical, model-based approach to targetting surveillance. This contrasts with the earlier analysis on the smaller network (Green et al. 2009): there, the degree-based measure performed less poorly, and the eigenvalue-based measures performed at least as well as arbitrary removal. Here, the **eigen spread** measure performed worse than random removal.

The ability to identify high-centrality nodes is only beneficial for disease control if the network structure is sufficiently stable: a rapidly changing network means the predictive power of network properties for future disease control will be low. Recently, algorithms for determining the stability in time of trading networks, using both the aquaculture network fully described here, and the network for large livestock movements in the UK for 2003-2004, have been examined (Green et al. 2011). These authors concluded that though temporal autocorrelation existed in both networks, it is difficult to make a judgement on the utility of this without an objective baseline for comparison. One way of defining this baseline may be by through simulating real disease problems and their control measures on (dynamic) networks.

However, when considering the spread of disease within the aquaculture industry, live fish movements are far from the only means of disease transmission between sites. Other transmission routes include fomite, well-boat associated (Murray et al. 2002), or direct spread through the water column in sea or freshwater, for example for infectious salmon anaemia virus (ISAv; Jarp & Karlsen, 1997, Gustafson et al., 2007), with differences in risk between diseases. Where Management Areas are relatively well sealed due to infrequent movements between them and separation in water distance, synchronisation in fallowing may provide a benefit in clearing disease from specific areas. The effectiveness of such fallowing strategies has been explored by Werkman et al. (2011a) [chapter 3], which contrasts the effects of partial or fully synchronised fallowing in simulated epidemics of the Scottish salmon industry (marine sites) based on the distribution of sites within Management Areas.

In conclusion, the network of live fish movements in Scotland shows itself to be strongly organised into communities, with potential for targeted surveillance to focus on high centrality arcs, to aid in the development of risk-based surveillance programmes where resources are necessarily limited (Stärk et al., 2006). Nevertheless, utility of such approaches is limited by the lack of real-time data in a continuously changing industry.

B.6. Acknowledgements

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Electronic appendices can be found at http://onlinelibrary.wiley.com/doi/10.1111/j.1365-2761.2011.01321.x/suppinfo.

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