The development of a model of the spread of the pilchard fish kill events in southern Australian waters

Dr A. G. Murray, Dr. M. O'Callaghan, Dr. B. Jones

C S I R O

MARINE RESEARCH

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OBJECTIVES

1. We will construct a 1-D SIR (Susceptible, Infected, Removed) model of the spread of the pilchard mass mortality events of 1995 and 1998/9.

2. We will produce a literature review of similar mass mortalities and the modelling approaches used to analyse them.

3. We will refine the SIR model to include different transmission process functions and data obtained by other pilchard mortality study projects, in particular the Fisheries WA lead study on viral transmission.

4. We will review the observations, including those obtained in concurrent studies, to provide the tightest possible constraints on the ranges of model parameters.

5. We will analyse the effects of fisheries management strategies on pathogen transmission, in particular we will test the viability of a 'fire break' policy.

6. We will construct a simple model of the recovery of the fishery to investigate the period required for the stocks to become vulnerable to renewed mortality.

7. We will development a Graphical User Interface (GUI) to display the local and geographical spread of pathogens.

8. We will produce an initial report detailing the approaches used both by us and other modellers of epidemics.

9. We will produce a final report detailing the final form of the model produced and incorporating analysis of model structure, parameters and results.

10. We will present this work at a nationally significant scientific meeting in 2000.

The pilchard mass mortalities of 1995 and 1998/9 were unprecedented in their rate and geographical scale of spread. Waves of mortality spread from South Australia to Western Australia and to Queensland at a rate of 10-40 km d^{-1}. In many cases, stocks were reduced by over 60%. The cause of this mortality was certainly a herpesvirus, although as it has proved difficult to infect fish with this virus Koch's postulate remains unfulfilled.

We have developed a range of models looking at disease transmission from the school to the national level. These models enable us to determine which parameters control the transmission of disease.

At the school level we conclude that small-scale fish mixing patterns do not play a dominant part in the local development of disease. Hence we are able to model the larger scale transmission without considering lower level population details.

At the larger scale we produce models that generate realistic epidemic waves. The model we have produced differs from standard forms in that it uses fixed length latent and infectious periods, rather than continuous turnover between these phases. Using analytical methods we find that three parameters control the epidemic wave's geographical spread: the rate of disease transmission, the length of the latent period, and diffusion coefficient.

We also use the observed local pattern of mortality to constrain the model. Initially, in South Australia, there is recurrent mortality over days or weeks. Later, when the epidemic is matured, mortality occurs over a few days at any given location.

The epidemic wave's speed is least sensitive to the rate of disease transmission, however this parameter could vary by orders of magnitude, so weak sensitivity does not necessarily mean low importance in explaining variation in the wave's speed. A large decline in the number of virus-containing lesions in the gills of sick fish was observed between 1995 and 1998. This would indicate reduced viral transmission. At large values of the viral transmission rate the wave's speed becomes increasingly less sensitive, so there is a value beyond which wave speed becomes independent of this parameter.

The transmission rate is multiplied by population density in our standard model, however, population density has not varied by orders of magnitude (although it has off Japan) and so the epidemic wave speed is only very weakly sensitive to changes in population density. Alternatively, because schooling effectively keeps population density constant, the viral transmission may be population density independent, in which case population density has no effect on the epidemic's speed.

Large values are inconsistent with the large wave speeds observed and small values produce unrealistic initial epidemic behaviour, so values of around 4 days give the best results. If this parameter could be experimentally evaluated the model would be very strongly constrained.

The diffusion coefficient is the parameter that reflects the large-scale spatial transmission of the virus. The diffusion coefficients generated by fish swimming patterns appear to be quite sufficient to explain the observed rate of spread of the epidemic. Indeed diffusion coefficients larger than those which fish can generate (perhaps as a result of bird transmission) result in mortality patterns that are inconsistent with the observations: several days of similar levels of mortality. This inadmissibility of very large diffusion coefficients does not rule out vector transmission, but it does make it far less likely that vectors are involved. Change in diffusion is the most likely process to explain the large difference in speed between east and west bound waves in a single epidemic.

The model generates very high levels of infection, in excess of 90% for realistic mortality distribution patterns. This means the critical parameter for determining the epidemic's longer-term impact is the proportion of those infected fish which survive infection. A model of post-epidemic population recovery indicates that this should be fairly rapid, even with high levels of epidemic mortality. However, the same model shows that persistently elevated mortality, even to a small degree, leads to serious decline in fish stocks.

Because of weak sensitivity to adult population levels, fisheries management strategies based on the manipulation of populations are very unlikely to succeed. Control of vectors is also unlikely to be effective. Juvenile pilchards appear to be confined to embayments their populations do not mix easily. This makes the preservation of as many nursery sites as possible the best means of protecting stocks from epidemics. As yet, the origin of the virus is unknown. In the longer term, exploitation of the adult population's strong degree of mixing may make it possible to inoculate the population with low mortality virus.

The development of a model of the spread of the pilchard fish kill events in southern Australian waters

BACKGROUND

In 1995, and again in 1998/9, mass mortalities of Australian pilchard occurred throughout their entire range – some 3000 km of southern Australian coast. The 1995 mass mortalities necessitated the short-term closure of the fishery (for public health reasons), caused serious damage to stocks, and had impacts on other fisheries (such as lobster) and the environment (such as little penguin breeding success). Three and a half years later similar mass mortality is recurring with similar results. If such events recur then stable exploitation of the pilchard resource will be made difficult and the economic impact may become more severe if this fishery grows. The mass mortality travelled as a wave originating in South Australia and terminating, in 1995, less than three months later in both WA and Queensland; the current kill front is travelling a little more slowly.

No environment factors are coincidental with the kills, lack of environmental cause is underlined by the winter 1995 and summer 1998/9 timing of the two events. The wave pattern is however typical of an epidemic and a herpes virus has been found in association with all the pilchard deaths. Proof that the virus is the cause of the mortality has not been obtained, but an associated transmission study will shortly address this issue.

As part of a combined proposal we propose to model the spread of this kill event. Other studies will look at viral transmission, including transmission by fish-eating bird vectors, and at the genetic characteristics of the herpes virus. Extensive ongoing monitoring of the current epidemic will also produce data valuable to the modelling.

NEED

The mass mortality events are very economically and ecologically damaging. Economic damage occurs acutely in the short-term due to the need to close the fishery during events and damage also occurs in the longer term owing to the removal of large numbers of fish during the event.

No model exists of the spatial propogation of a viral epidemic in an exploited fish population, we will derive such a model. This model will be aimed less at predicting the spread of a particular mass mortality event and more at the understanding of the dynamics of the event. Using the model we will be able to assess hypotheses concerning the factors which control the mass mortality and hence focus future study on the most sensitive processes. The model will show the conditions under which these events may recur. We will also be able to assess the potential for management intervention to halt an ongoing epidemic or prevent further outbreaks. The model will also integrate all the aspects of the spread of the mass mortality events, showing

linkages within the existing data and showing those areas for which adequate data is lacking.

It should also be noted that damaging epidemics among wild caught and farmed marine fisheries are not infrequent and that modified versions of the model may have future applications to other fisheries

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METHODS

A 1 D SIR (Susceptable, Infected, Removed) model will be developed to describe the spread of the mass mortality event around the southern Australian coast. The model will be prototype in BASIC (for convenient application on a PC) and the final version implemented in Java allowing portability. A modular approach to programming will allow modelled processes to be modified as data becomes available. This will include long-term runs in which the pilchard population recovery mass mortality is modelled

Model results will be compared statistically with observations. The best confirmed observation is the speed of the kill front and replication of this will be highest priority. Its dependence on parameters will be examined by model analysis and experimentation. Model tests will include different functional forms of the model, particularly the inclusion/exclusion of bird vector transmission. Effects of different management strategies will be analysed under model forms and parameter values which produce realistic results.

RESULTS/DISCUSSION

1   The Pilchard Epidemics, a Brief Overview

In March 1995 strandings of massive numbers of dead pilchards (*Sardinops sagax*) were first reported from the beaches of South Australia (Whittington *et al.* 1997). Three months later these deaths had spread to the extreme northern limits of pilchard distribution in both Western Australia (Fletcher *et al.* 1997) and Queensland, which are some 2500 km along the coastline from the origin, respectively west and east. Similar mortality events also occurred in New Zealand in June to September (Whittington *et al.* 1997).

In October 1998 a second outbreak of mortality began; again it started in South Australia (Ward *et al.* 1999). This mortality lasted until late May; again ceasing only when the wave of mortality had reached the limits of the pilchard's distribution. The mortality patterns were similar to those of the first event. However the mortality wave travelled at about half the speed of 1995 and at times seemed to disappear. Levels of mortality may have been even higher than in 1995. Although local mass deaths of pilchards and other fish have been reported previously, nothing on this scale appears to have occurred before 1995 (Fletcher *et al.* 1997). According to indigenous oral tradition, prior to European settlement pilchards disappeared from the Canadian Pacific for some years and then returned (Hart 1933). This temporary disappearance could indicate a massive die off possibly due to infection. However, sudden large population changes can have other causes, such as recruitment failure (Wada and Jacobson 1998).

The rates of spread of these epidemics were phenomenal. The wave travelled at over 30 km d^{-1} in 1995, while the second 1998/9 epidemic travelled at about half this speed. As a comparison, the Black Death travelled at about 0.5-1 km d^{-1} (Murray 1993). It has been argued that a vector, such as the population of piscivorous birds, is required to account for this extreme speed, we will use the models to examine this theory.

Mortality only lasted a few days, at most, at any given site. There was an exception near the South Australian point of origin where mortality persisted for weeks (Ward *et al.* 1999). This short period of mortality leads to very little scatter in the distribution of mortality about the space/time regression line (Whittington *et al.* 1997, Fletcher *et al.* 1997). By comparison the mass mortality induced by the seal virus PDV overlapped throughout its range of spread. Significant seal mortality was still occurring at its initial focus in Denmark when the epidemic had already reached Ireland, where it terminated (Swinton *et al.* 1998). The period of significant mortality was defined as the time over which 90% of local recorded mortality occurred.

Mortality showed no relationship with physical oceanographic factors (Griffin *et al.* 1997) or with toxic phytoplankton (Whittington *et al.* 1997, Fletcher *et al.* 1997). Indeed the 1995 and 1998/9 events occurred at different times of year and covered the entire Australian southern coast with environments that ranged from the edge of the tropics in Queensland to cold temperate waters in southern Tasmania. The only universal factor appeared to be the development of a herpesvirus in the pilchards' gills up to 4 days prior to death (Whittington *et al.* 1997, Fletcher *et al.* 1997).

A Polymerase Chain Reaction analysis of the virus's genes showed that the 1995 and 1998/9 viruses were related (AAHL 1999). The test only involved 180 base pair and so is not specific enough to prove that the viruses were identical on the two occasions. Few other fish died in association with the epidemics, and those fish that were found dead in association with the pilchard mass mortalities that were tested for the virus did not return positive results (AAHL 1999). It has proven very difficult to experimentally transmit the virus in tanks (Jones 1999). This difficulty makes a formal proof of the virus as the cause of mortality difficult to achieve under Koch's postulates.

Disease is the cause of substantial mortality among many fish populations (Munro *et al.* 1983). Disease agents will persist if they can produce new infections faster than infected hosts die off. If this production of new infections exceeds the rate at which new hosts become available then the disease will be epidemic. If production of infection lies between these extremes of pathogen extinction and epidemic disease, a stable endemic level of disease results (Reno 1998). Viruses that cause disease in fish include birnaviruses, notably IPNV which causes substantial mortality in farmed salmon (Hill 1982) and whirling disease in wild Atlantic menhaden (Stephens *et al.* 1980). Lymphocytosis virus causes endemic disease in North Sea estuarine flounder (Lorenzen *et al.* 1991) and over 100 other species (Möller and Anders 1986). Viruses are also associated with mass mortality in Caribbean herring (Williams and Bunkley-Williams 1990) and mortality of wild salmon (des Clers 1993).

Viral diseases of Australian fish have recently been reviewed by Mundy and Owens (1998). Viral diseases have been associated with mass mortality in Australian barramundi (Mundy *et al.* 1994) and epidemics in Australian red-fin perch (Whittington *et al.* 1996). A double stranded DNA herpes virus is the apparent cause of mass mortality of the Australian pilchard (Whittington *et al.* 1997).

The pilchard (*Sardinops sagax*) is a small (~20 cm) planktiverous clupeoid fish found in large numbers in warmer temperate coastal waters throughout the southern hemisphere and also in the northern Pacific (Parish *et al.* 1988). Pilchards are found all along the southern coast of Australia from roughly the tropic of Capricorn in both Western Australia and Queensland to 43° S in eastern Tasmania (Fletcher *et al.* 1997). Distribution is largely restricted to the narrow continental shelf.

Like other clupeoid fish, pilchards travel in large dense schools (Blaxter and Hunter 1982). These constantly change shape and composition as they form and disperse. A group of schools forms a shoal. Pilchards feed on both phytoplankton and zooplankton (van der Lingen 1998) and seek out zooplankton swarms that are separated by a few km. However, they then depart rapidly owing to the enhanced risk of predation within these swarms (Nonacs *et al.* 1994, 1998). The exact nature of the schooling and

swimming behaviour of the pilchards has very specific implications for pathogen transmission, which will be considered in more detail later.

In summary, a continental scale mass mortality of pilchards occurred in Australia and New Zealand in 1995 and a second such event occurred in 1998/9 (although New Zealand was not affected). The scale and speed of these epidemics is unique. Pilchards are commercially fished and form a critical food-chain link; as such, these epidemics are of very great importance to both fisheries and ecosystems.

2   The Aims, Limitations and Structure of the Modelling Project

It is the aim of this project to produce a range of models that give scientists and managers an understanding of the processes and parameters that controlled the transmission of the 1995 and 1998/9 pilchard herpesvirus epidemics. Models and their analysis will show the key parameters controlling the epidemic and the degree of uncertainty of this role and of the actual values of the parameters.   Using this knowledge we can predict the response, if any, of the epidemic to changes in the environment, including to management actions.

Our approach is to use a range of models to fulfil different functions. These models include very simple classical epidemic models, which prove to be useful illustrations of the basic processes driving the epidemic, but which prove to have flaws in their replication of some of the observations. More complex models still allow the derivation of analytical solutions of the basic processes controlling the rate of spread of the epidemic. Such analytical solutions are a powerful tool that allows us to rapidly determine the parameters and processes controlling basic steady-state behaviour of the system (Murray and Parslow 1999). Dynamic solutions of these models allow us to investigate the initiation of the epidemic and some of its other properties for which analytical solutions are not available. The dynamic models can also incorporate non-linear processes and varying behaviours, for which the analytical solution is not obtainable.

We develop models that cover the different spatial scales of processes involved in the spread of the epidemic. These scales are the local transmission of infection within a school; the movement of infected fish between schools in a shoal; and the large-scale intermixing of schools.

Our ability to refine the modelling is limited by the available data. The data sets available are very good. The reported mass-mortalities do give a clear indication of where the epidemic had spread to at a given time. As two similar but different epidemics have occurred we have replication and differences between the epidemics are a valuable source of insight into processes and parameters. Even these data sets do have some problems. They were not collected by the same method; instead they are based upon different reporting system ranging from systematic surveys involving ships and aircraft to public reporting. This variation in sampling allows for mortality to be missed in under-populated areas or non-epidemic coincidental mortality to be misreported. Similarly, most reports are of beached fish, offshore mortality being only occasionally

reported from survey ships or fishing boats. Because the pilchards may have drifted for a short time before beaching and because their presence may not be detected immediately, there is some uncertain difference between the reported mortality with respect to the actual time and place of death. However, the data set represents an extremely good record of an epidemic in a wild population.

More seriously, we have a lack of data on processes behind the epidemic. Attempts to infect captured pilchards or goldfish (AAHL 1999) with the disease have not been successful. Pilchards exposed to virus in food did eventually die (Jones 1999), but PCR analysis did not detect the virus in these dead pilchards. We can use some physiological evidence to support our understanding of the epidemic. In particular the formation of lesions in the gills of the pilchards a few days before their death (Whittington *et al.* 1997) may be taken as proof that the fish are infected for this period. The evidence available contains valuable clues as to the epidemic behaviour, but it does not provide direct answers to many of the questions raised in modelling processes.

Given that two epidemics have occurred, we are able to investigate commonalities and differences behind both epidemics. This comparison gives considerable insight into basic processes driving the epidemics. But we are not able to predict the behaviour of a future epidemic.

The data available is thus exceptionally good, but it does contain uncertainties. Uncertainty in the data inevitably leads to uncertainty in model predictions. However, the models are able to use the range of observations from many different fields to constrain model behaviours, allowing theories concerning the epidemic to be tested quite rigorously.

We must use the data efficiently to obtain maximum insight into underlying processes, so we do not necessarily use the simplest possible model. The simplest model of these epidemics is a linear regression of location of mortality against time. This gives a very good prediction of where the mortality front will be at a given moment. But it tells us nothing, nothing at all, about the processes driving the epidemic.

Even if there were no other data than the record of the time series of the place of peak mortality, a simple epidemiological model would tell us the potential roles of diffusion and local transmission in the spread of the epidemic. We will begin by exploring such models as valuable illustrations of the processes underlying the spread of epidemics.

In fact, of course, there is much more data than just the timing of the peak of mortality at a given location. There is evidence such as scatter of mortality about this peak - this turns out to be very limited and that proves a powerful constraint on the model. There is the initial development of the epidemic, there are gaps in the evidence of progress of the epidemic (which may or may not be valid), and there is physiological and experimental evidence. There are also clues from the study of other diseases. We use all this data to constrain and develop the model. Note that the model development and assessment process proves a powerful means of integrating a diverse range of observations concerning the epidemic.

We should not complicate the model by including too many untestable processes. Sometimes the inclusion of different forms of the model, which produce no detectable change in the validity of the performance may be reasonable - this is after all negative evidence that both the underlying theories could be valid. These different formulations may lead to substantially different predictions of response to environmental or evolutionary changes. But complication takes away from the understandability of the model and may make it dependent on parameters whose value cannot be independently assessed.

In the following chapters we will explore the development of the model from simple standard epidemic models to a form tailored to the description of these pilchard herpesvirus epidemics. We will discuss analytical solution of the wave speeds from these models. We will then present a detailed description of the dynamic model that is used to describe the model, followed by presentation of the results of the analysis of this model. We then summarise the implications of the results of model, and the modelling process, for our understanding of the disease's behaviour and the possibilities of management.

We start by analysing the available observations in order to derive the processes and parameters required for the modelling.

3 Available Data and the Characterisation and Parameterisation of the Epidemic's Spread in Space and Time

There is a considerable amount of data available on the two epidemics of 1995 and 1998/9. Most importantly there are the reports of mass mortalities, which give a very good indication of the epidemics spread in space and time. There are also physiological and experimentally obtained data which allow us to constrain certain aspects of the epidemic's development. We use this data to describe the epidemic's basic properties. We derive *a priori* constraints on model parameters which we use when we evaluate the model's sensitivity in the next chapter.

3.1 Spread of the Epidemic

In order to understand the spread of the epidemic better we plot the reported mortalities against time and space. We have the time data immediately available. Spatial position must be calculated relative to some initial point. The simplest, and most unambiguous, way to do this is to plot the locations of these events relative to an origin point, eastward spread being defined as negative (Fig. 3.1).
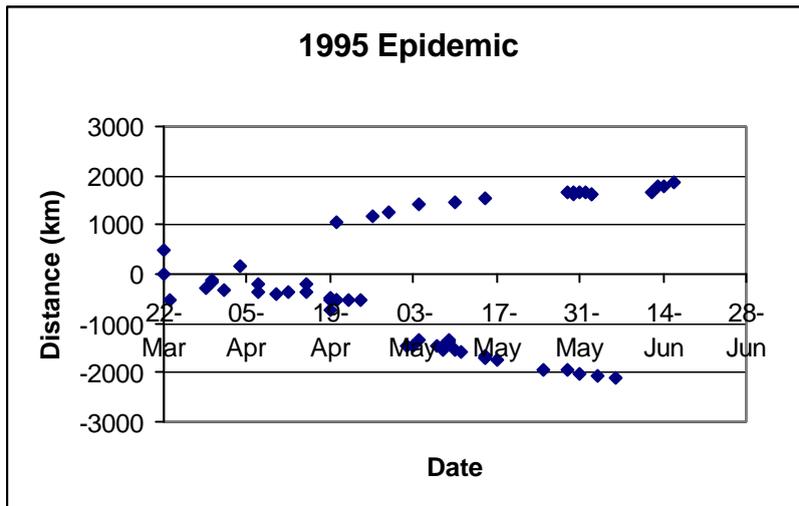
Figure 3.1   Simple Radial Spread of mortality about origin

From this radial plot we note that for a considerable period (about 2 to 4 weeks) the epidemic remains at the origin before splitting into eastbound and westbound waves.

However, this radial spread pattern does not give the speed of advance of the front because it becomes distorted when the waves are not advancing directly away from the origin. This distortion becomes a particular problem as the waves leave the south coast and advance along the east and west coasts of the continent; this motion is at right angles to the origin.

We need to describe the location of the front with respect to the distance the epidemic has actually advanced along the coast. Here we come across serious problems relating to the exact route and timing of spread. Coastal indentations, such as Spencer Gulf, add considerably to coastal length, but probably have no effect on the motion of offshore pilchards. The timing between first mortality occurring at point and a point some distance ahead is not necessarily the same time as that between the first detection of mortality at these points and hence front speed may be miscalculated if the data is incomplete.
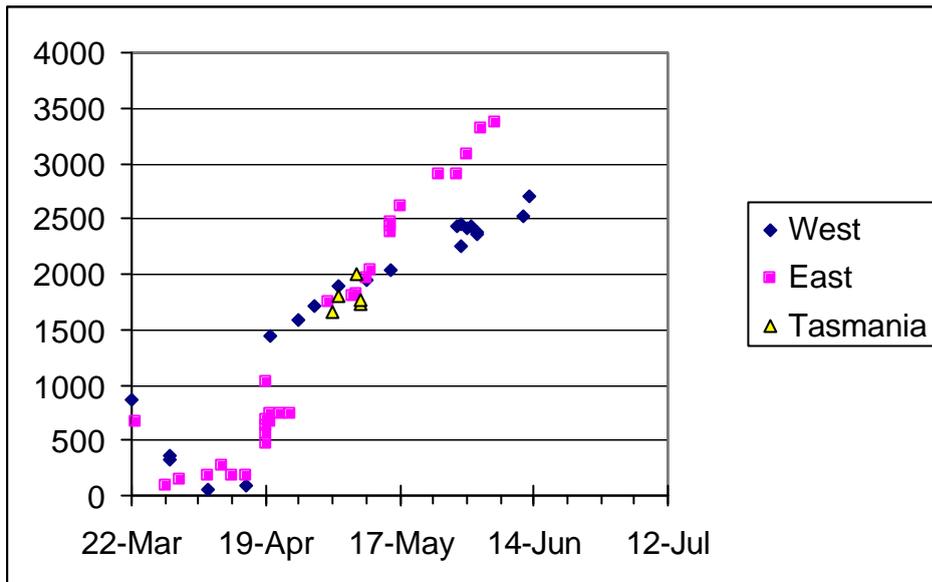
Figure 3.2   Location of mortality with time as minimum coastal travel distance from origin

Initially mortality remains in the South Australia region for a considerable period and only after about four weeks does the epidemic split into two waves travelling in separate directions (Fig. 3.2). Once it is established, the front speed is fairly constant, as we expect from the epidemiological models so far discussed, i.e. it is a typical epidemic. The eastbound wave seems to be faster and less constant than the westbound wave. This relatively constant speed is similar to the results obtained from the analyses carried out by Whittington *et al.* (1997) and Fletcher *et al.* (1997).

The simple regressions of the west and eastbound lines are 30 and 50 km d^{-1}, with R^2 of 0.85 and 0.91. However, such regressions are problematical and probably not a valid analysis (Whittington *et al.* 1997). If we exclude the South Australian data (points within 1200 km of the origin) from the figure we get regressions of 22 km d^{-1} west bound ($r^2 = 0.97$) and 49.5 km d^{-1} ($r^2 = 0.95$) eastbound (including Tasmania). Because the initial mortality was quite widely scattered, however, the speed required to get from the initial observation to the final observation of mortality is 36 km d^{-1} east and 22 kmd^{-1} west.

Eastbound expansion appears to have been somewhat variable in speed. If we exclude the Victorian and Tasmania data we obtain a gradient of 40 km d^{-1} with r^2 of 0.97, and a similar gradient applies to the data for the Victoria and Tasmania data. The region 1500 to 2000 (Bass Strait only) has a gradient of 26 km d^{-1}. A sudden leap of 400 km in 5 days appears as a break in the records between Lakes Entrance in Victoria and Sydney in New South Wales. It is this leap which gives the overall gradient of 50 km d^{-1} for eastbound expansion.

The 1995 westbound expansion proceeds at an average of 21 km d^{-1}, but has a temporal hiatus, from mid May until nearly June as the epidemic slowly rounds the south western Cape Leeuwin area of Western Australia. This area also marks the boundary between two distinct pilchard populations (Fletcher *et al.* 1997). Gradients before and after this

point are both around 24 km d^{-1}. This is similar to the rate in Bass Strait, but much slower than the eastern average.

In detail it appears from the data that the epidemic had an initial establishment period of about a month, when it remained restricted to South Australian water. After this the epidemic started to expand westward at 21 km d^{-1}, a speed which was largely maintained, but may be slightly faster with a period of slow spread in late May. Expansion also occurred eastward at about 40 km d^{-1}, with a sudden break between western Victoria and Sydney, in 5 days advancing nearly 400 km. This kink is readily apparent in the graph and appears to be real because slopes both before and after this lead have regressions of about 40 km d^{-1}. The total eastbound slope, including this leap, has a regression of around 50 km d^{-1}. It is possible that there is a lower background eastward expansion rate of about 25 km d^{-1}, with advective leaps in position. And this is similar to the speed of the west-bound wave, allowing for a delay at Cape Leeuwin.

The 1998/9 epidemic broke out in Spencer Gulf, South Australia (Ward *et al.* 1999). This is close to the origin of the 1995 epidemic, but is a few hundred kilometres to the east. In South Australian waters the epidemic showed the same pattern as in 1995, recurring several times at some locations over the course of weeks. Persistence about the origin is a little longer, some 40 days as opposed to 28 days in 1995. However, many of the later mortality event involved juvenile pilchards and, as these did not start to die until after the adults this may be regarded as almost a separate epidemic. The rate of spread was significantly slower, only being of order 10 km d^{-1}.
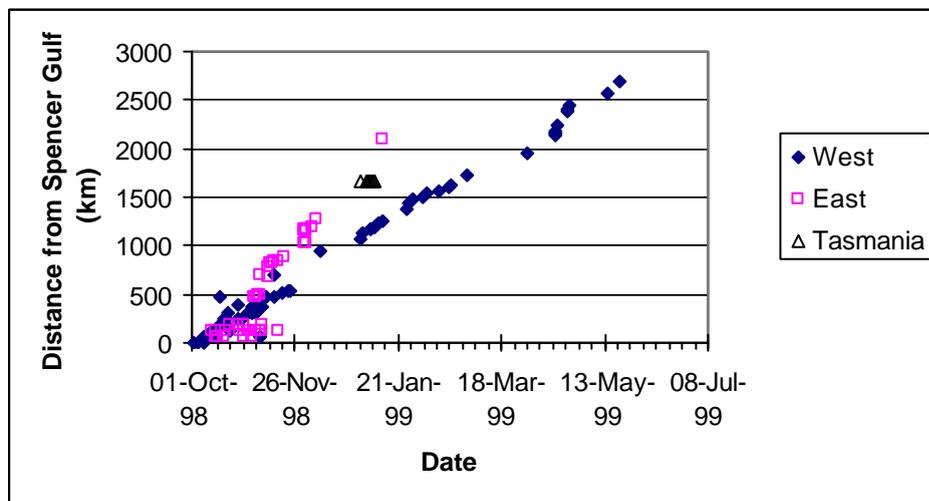
Figure 3.3   The pattern of mortality in 1999 from South Australia (Ward et al. 1999), Western Australia (Gaugin, Fisheries WA), Victoria (Neira, MAFRI), New South Wales (Geoff Gordon, NSW Fisheries) and Tasmania (Sherman, Tasmania DPI).

We have extended the analysis to include the Western Australian 1998/9 data (provided by Daniel Gaugin of Fisheries WA). We present the rate of spread of this epidemic front (fig. 3.3). The pattern of spread was similar to that obtained in 1995 with a gap at about 2000 km from the origin as the epidemic passed round Cape Leeuwin. However the speed of expansion of the second epidemic was much slower at 10.7 km d^{-1}. This speed is about half that of the western rate of expansion of the 1995 epidemic and about a third of its overall average speed. There is little variation within the 1998/9 epidemic

around this average speed and so this regression is statistically highly significant ($r^2 = 0987$). There is still evidence of variation as the epidemic first reaches Western Australia with more scatter about the regression.

We have also incorporated MAFRI's data on Victorian waters (provided to the Pilchard Scientific Working group by Francisco Neira), the reported mortality from Newcastle NSW and the Hobart area of south east Tasmania. From this we generated a similar east-bound epidemic wave. The wave travelled at a very similar speed to the westbound wave, of 10 km d^{-1} ($r^2 = 0.982$) in the eastern states. However, two very isolated points, Newcastle and Hobart, provide all the data that lies beyond Victorian waters. If the Hobart data is treated as a single point instead of five separate points then the wave speed is 20 km d^{-1}. The distance from Bass Strait to Hobart could be underestimated, since the epidemic may not have spread by the shortest route. Wave speed within Bass Strait is about 20 km d^{-1}. These data points are extremely valuable in that they show that the epidemic, while undetected, remained and was travelling at a similar rate to that which was earlier apparent.

The two westbound waves are quite similar in many features, apart from travelling at different speeds. Both terminate at around the same point, around 29°S and if we plot the position of these waves relative to the same initial point and normalise time to the total time elapsed we can see the waves share features in common (Fig. 3.4). In an initial phase observed mortality is scattered and irregular, this is much more severe in 1995, for which the epidemic's point of origin is nearer to Western Australia. There then follows a period of fairly constant expansion as the wave advances along the south coast. At about the 2000 km point there is a period of low mortality as the epidemic rounds Cape Leeuwin, an area which forms the boundary between two pilchard populations. The epidemic then reappears on the west coast and makes a final reappearance near Geraldton. The 1995 epidemic shows more sign of variation in speed than the 1998/9 epidemic.
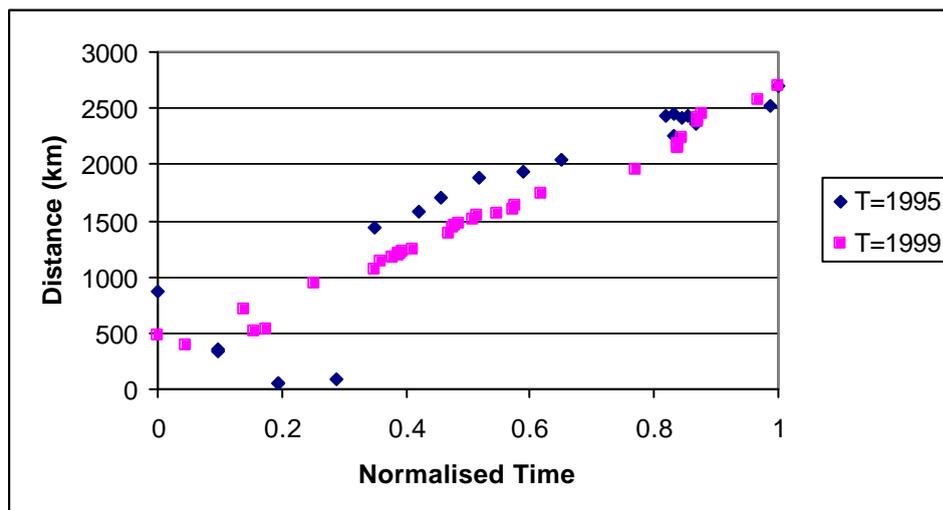
Figure 3.4   Pattern of the 1995 and 1998/9 epidemic mortality in Western Australia.

No such recurrent patterns exist for the two eastbound epidemics. In 1995 the epidemic resulted in extensive mortality in northern Tasmania, no such mortality was reported in

1998; however mortality occurred of Hobart in 1999, where none occurred in 1995. Extensive mortality was reported in New South Wales and Queensland in 1995. In these states, only a single outbreak near Newcastle was reported in 1999.

The available data gives a very detailed account of the spread of the epidemic. However, it is not perfect. Reportage of mortality depends upon different search programs in which different levels of effort were invested and so is recorded to a different level of detail and reliability on different occasions. Mortality may go completely undetected in areas of low (human) population, or when currents lead to the fish being transported offshore. Even where extensive aerial surveys have been carried out, mass mortality events may be missed (false negative) or may be incorrectly reported (false positive), on one occasion cuttle bones are believed to have been misreported as dead pilchard from an aerial survey (Ward *et al.* 1999).

3.2   Duration of Infection in a Population

Locally, reported pilchard mortality events are confined to a short period, except in South Australia. This is reflected in the low level of scatter around the regression in figure 3.4. In the Storm Bay and adjacent areas of south-eastern Tasmania, for example, mortality events that were reported to the Tasmanian Department of Primary industries were, with one exception, reported over a five day period, with half the reports applying to mortality detected on 1 day (Fig. 3.5). Reported strandings reflect not only the time of mortality but also the processes, which transport the pilchards before they were detected, and so detection is likely to be extended over a longer period than is the mortality itself.
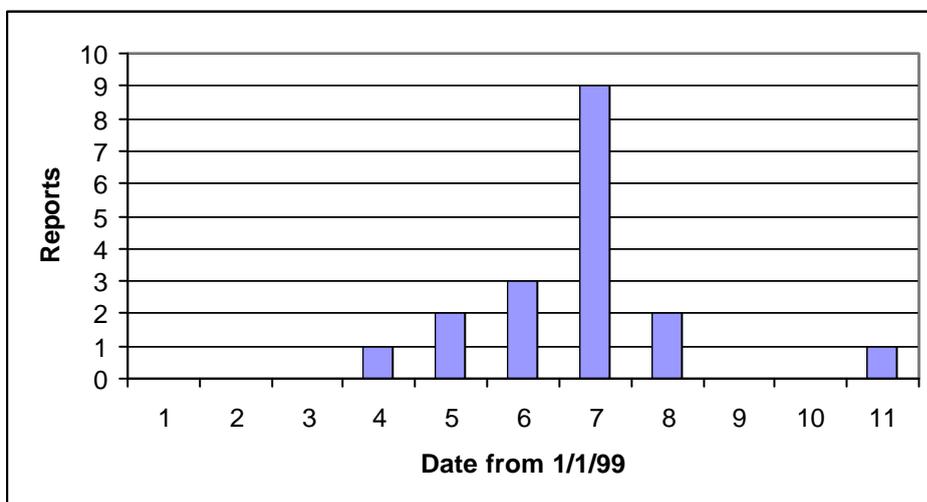
Figure 3.5   Pilchard mortality events reported in the South Eastern Tasmania (Storm Bay, Frederick Henry Bay and Derwent Area) in January 1999 (Data supplied Sharon Sherman, Senior Technical Officer, Tasmanian DPI).

Likewise, in 1995, duration of mortality in Western Australia was reported as being restricted to 1 or 2 days in each location (Fletcher *et al.* 1997).
The duration of local mortality events for 1995 has been plotted as the number of days between the first and last recorded mortality event within 250 km intervals along the coastline (Fig. 3.6). Coast stretches with 1 or zero observations are ignored. Those

stretches of coastline within 1000 km of the origin experienced mortality for over 10 days, and at the origin mortality persisted for over 30 days. Further away from the origin mortality persisted for less than 10 days, and given that the epidemic takes about a week to traverse 250 km and pilchards may be detected some time after death, this means local duration of the infection is very brief. There is an exception, off central Western Australia mortality persisted for 14 days, however this duration is due to a single event occurring 10 days after other mortality events. If this event is included the regression is still good with an r^2 of 0.67, but its exclusion brings the r^2 to 0.83.
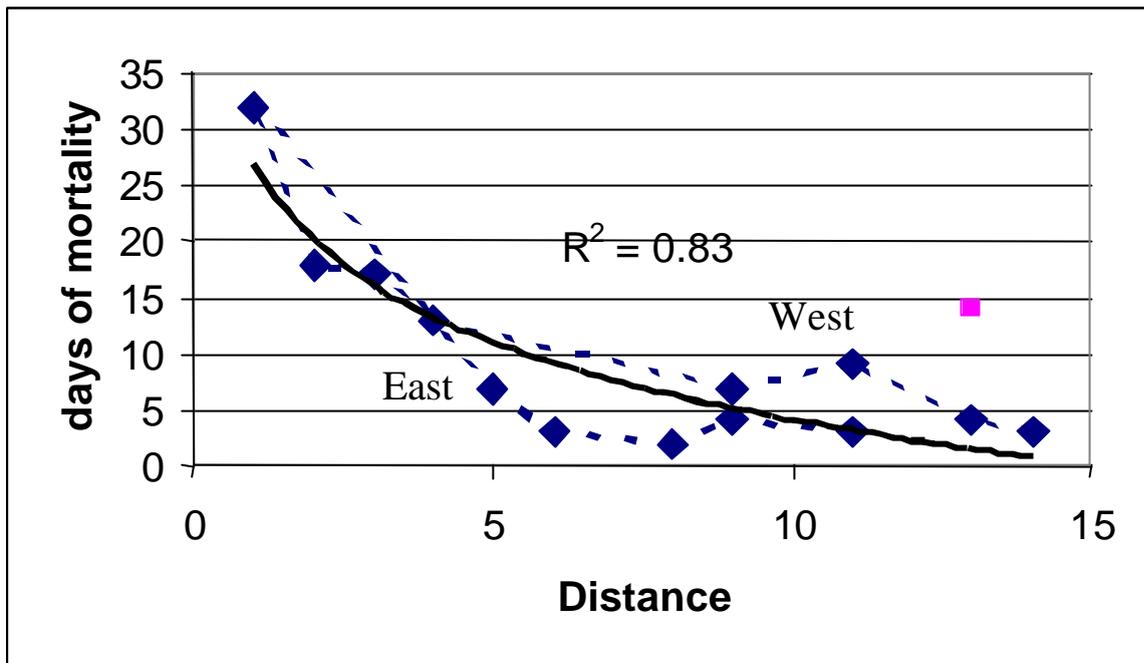
Figure 3.6 Days that mortality persisted between first and last observed events on 250 km stretches of coastline. The log regression line $-9.96\ln(x)+27.05$ has $r^2 = 0.83$.

3.3   *A Priori* Constraints on the Diffusion Coefficient

We use a diffusive model to describe the dispersal of fish. The diffusive model is simple to implement and parameterise. In this section we explore some limits to the parameter which derive from fish behaviour and from the patterns of detected mortality.

This diffusion model assumes random swimming patterns. Migration in a particular fixed direction can generate much larger mass movement. Pilchards do show such large-scale movement patterns off South America (Torres *et al.* 1985) and these patterns are sensitive to season and climatic factors such as El Niño. While we can use the model to investigate the effects of different specific swimming patterns on the epidemic's progress, a predictive model of fish swimming patterns is beyond the capacity of this project and there is a lack of data on these patterns in the field. With reference to the Telegraph Model we do show that diffusion is a good description of motion, provided fish do change direction at intervals.

Only diffusion of infected individuals affects this spatial/temporal smearing of mortality. This is also the case for the epidemic wave's speed (see chapter 7). So it is the behaviour of infected fish that controls the behaviour of the epidemic.

_____

3.3.1   Pilchard Swimming

We can use pilchard biology to obtain some constraints on the diffusion parameter, assuming fish dispersion accounts for this diffusion.

The rate of dispersal of an organism depends upon both its speed and its pattern of movement. If fish swim in legs of a given random direction for a distance L over a time T then:

$$D = L^2/2T \tag{3.1}$$

Dispersal of pilchards thus depends on both their speed and swimming pattern.

The pilchards must have a maximum sustained swimming speed of over 40 km d^{-1} or 1.66 km h^{-1} in order to account for the observed rate of spread of the epidemic of this speed (Whittington et $al.$ 1997), if bird vectors are not responsible. Beamish (1984) recorded maximum pilchard swimming speed of about 3 km h^{-1}. However, Fletcher et $al.$ (1997) note rather faster speeds for pilchards - 3 km h^{-1} being the average speed for pilchard schools while some schools moved at 2.5 times this or 7.5 km h^{-1}. Such speeds easily exceed the epidemic front's speed. Because we use this data, specifically obtained from observation of Australian pilchards in $situ$, our estimates of D (Fig. 3.7) are somewhat larger than our earlier estimates (Murray 1999). If bird vectors account for dispersal then much larger diffusion coefficients are possible. However, very high diffusion rates may not be consistent with the brief observed duration of mortality.
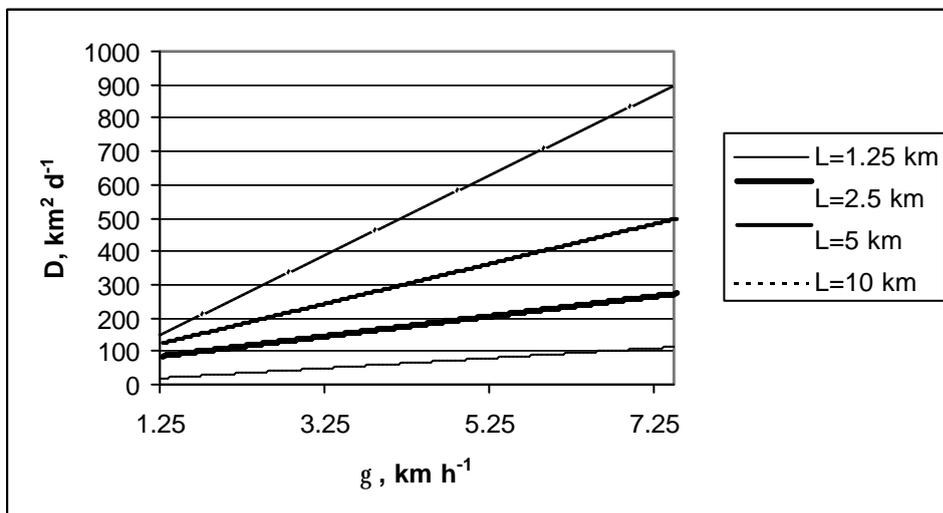
Figure 3.7   Diffusion coefficients generated by 4 different swim leg lengths for swimming speeds of 1.25 to 7.5 km h^{-1} (30 - 180 km d^{-1})

The 1995 front advanced 400 km from Lakes Entrance to Sydney over 5 days (Section 3.1). This is evidence of the potential for sustained movement of 80 km d^{-1} or 3.3 km h^{-1}. We attribute this movement to migration of fish because this is the only way to have the epidemic advance so rapidly as a coherent front. Other factors, such as

increased bird activity, could lead to increased diffusion, which could induce large velocities but would also result in mortality that was smeared out along the coast. If the pilchards seek out zooplankton patches in which to feed, then their appropriate swimming pattern will be determined by the separation of these patches. Such patches are separated by distances of a few km (2.5 km in the model of Nonacs *et al.* 1994, 1998). If pilchards swim distances of this order before changing direction diffusion will depend upon swimming speed and the distance travelled before changing direction. The length of the legs that are swum by the fish can be derived for a given value of *D* and a specific swimming speed (Eq. 3.1). The maximum swimming speed is at least 1.45 km h^{-1} if the epidemic spreads at 35 km d^{-1} (Whittington *et al.* 1997), and our estimate is slightly higher. Appropriate swimming leg lengths fit most closely with diffusion coefficients of 20 to 400 km^2 d^{-1}, while very long, but not impossible leg lengths of 10 km generate diffusion coefficients in the high hundreds of km^2 d^{-1}. We later rule out such large diffusion coefficients by reference to the local pattern of mortality (see next section).

The average diffusive displacement of pilchards in 1 dimension is $\ddot{0}$(2*Dt*) (Berg 1993). So with *D* of 50 to 400 km^2 d^{-1} the daily mean movement is 10 – 28 km, which is generally less than the speed of this front. Because this displacement is related to the square root of time it declines with time, over 4 days the average pilchard's movement would be only 5 – 14 km d^{-1} and over 100 days just 1 – 2.8 km d^{-1}. Small numbers of pilchards move larger distances, 1% of the population moves 2.58 times the average and 0.1% moves 3.39 times the average displacement. The latent period by delaying the formation of new infections acts as a substantial break on the epidemic's spread. The rates of average and outlier movement just noted are consistent with movements of tagged pilchards discussed by Fletcher *et al.* (1997). Non-random movement can lead to somewhat larger displacement, particularly over longer time periods. It is due to the difference between average displacement and maximum movement that net fish movements, particularly over longer periods, may give a very misleading picture as to the potential role of the fish themselves in spreading the mortality. Given a relatively short period between infection and death or recovery, it is only required that some individuals show efficient short-term dispersal for the epidemic to spread at maximum rate.

3.3.2 Mortality Distribution as a Limit to Diffusion

The brief local duration of the epidemic provides another limit on *D*. Dispersal must not be too large following infection if the pattern of intense local mortality over a short period is to be maintained. This dispersal depends upon both *D* and the length of the latent period and may constrain both these parameters.

Dispersion occurs over the period between infection and death. Due to this dispersion the observed mortality occurring at a point will be composed of individuals that were infected within a region whose size is dependent on this dispersion. Even if infection were instantaneous at a given point in space, because the individuals dying at that point were infected at a range of different points in space, the mortality would be spread out in time at any give location. This effect can be used to estimate limits on dispersal given that local mortality occurs over a few days.

The standard deviation of dispersion is $\sqrt{(2Dt)}$ in 1 dimension (Berg 1993). Thus dispersion depends upon diffusion coefficient and the time over which diffusion occurs. The minimum t is about 4 days, the period over which lesions exist (Whittington *et al.* 1997), but an incubation period of four or even 8 days before symptoms occur may also exist giving t values of 8 or 12. With $\pm 1.65s$ we will obtain 90% of the mortality, this is 3.3 times the standard deviation. For a wave speed of 40 km d^{-1}, 90% of mortality occurs in a time equivalent to approximately 0.0825 days per km of the standard deviation. From this we see that diffusion coefficients in excess of 400 km^2 d^{-1} will result in mortality persisting for over five to 8 days, even if infection is instantaneous at a given point. This value therefore represents a maximum D consistent with observed mortality patterns.

The maximum value of D consistent with observed mortality distributions is comparable to the larger values generated from analysis of pilchard swimming patterns. Thus it is possible that pilchard swimming unaided by vectors could account for epidemic's spread, although it is equally impossible to rule out a role for these vectors without a better knowledge of pilchard swimming patterns.

Table 3.1 Standard deviation of mortality following instantaneous infection with D of 50 to 800 km^2 d^{-1} and infection persistence times of four to 12 days.

D	$t = 4$		$t = 8$		$t = 12$	
	s	90%	s	90%	S	90%
50	20	1.7	28	2.3	34	2.8
100	28	2.3	40	3.3	49	4.0
200	40	3.3	56	4.6	69	5.7
400	56	4.6	80	6.6	98	8.1
800	80	6.6	113	9.3	138	11.4

Patterns of distribution generated under large diffusion coefficients are inconsistent with the observed short duration of the epidemic at a given locality. Thus high diffusion coefficients, which could be generated by bird-based transmission, are not appropriate. Inefficient bird-base transmission, generating low diffusion coefficients, comparable to pilchard-swimming generated diffusion coefficients cannot be ruled out. As discussed in the next sub-section, such bird-based transmission does not affect the epidemic's behaviour, but may alter its response to changing viral virulence.

We later show that these limits on diffusion coefficients do correspond to limits in the dynamic model that correspond with maximum levels of dispersal consistent with observations of brief local mortality. However the wave speed is shown to depend largely upon diffusion coefficient, latent period length and the rate infection spreads. For a given D if we increase the latent period we must also increase infection rate if we are to maintain the wave's velocity. This means that the effect of the latent period on local duration of mortality is effectively counteracted and is much weaker than this simple analysis predicts.

3.3.3 Diffusion and Telegraph Models

Diffusion is a measure of dispersal, not of actual motion. Diffusion in Fick's equations is a continuous process and speed is infinite, instantaneously some organisms or materials diffuse throughout the range. However, the numbers of individuals moving large distances are very small. Most epidemics in nature travel at a rate that is far less than their potential maximum speed and so the individuals which undergo extreme dispersion are not important. For example, rabies is spread by foxes at 30-60 km y[1] (Murray 1993), obviously foxes can travel at many times this speed. In such cases diffusion describes the epidemic's spread well. However, the pilchard herpes virus (in 1995) spread at a rate approaching the maximum swimming speed of its hosts. Increasing bS_0 in a diffusion-based model can cause the velocity V to exceed the actual swimming speed of the fish. Clearly this is not realistic and does not give a realistic prediction of what would occur if the disease were to become more virulent.
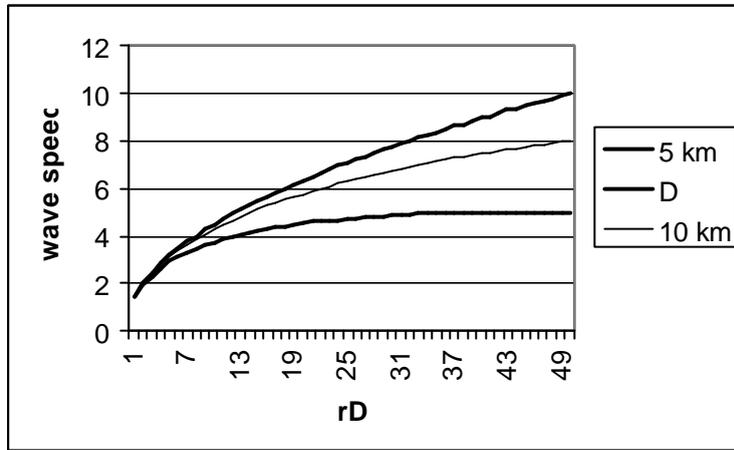
Figure 3.8   Daily progress of an epidemic wave calculated by diffusion- (D) and telegraph-based Fisher models with two maximum swimming speeds (5 and 10 km d^{-1}).

An alternative transmission is the telegraph model (Holmes 1993). Under this model the velocity of the wave's spread is limited to the maximum movement of the organism. The model is:

$$\frac{\partial S}{\partial t} = - \frac{1}{2l}\,\frac{\partial S^2}{\partial^2 t} + g^2 S\frac{\partial^2 S}{2l\partial^2 x} + \frac{1}{2l}\,\frac{\partial F}{\partial t} + F(S) \tag{3.2}$$

where $?$ is the frequency with which the organism changes direction, g is the organism's finite velocity, and r (or bS_0) is the intrinsic rate of population increase. Holmes (1993) analysed this model using the logistic growth equation for the function F(S). This is the telegraph equivalent of the Fisher equation. She derived the following relationship between diffusion and telegraph velocities:

$$C_t/C_d = 1/(rD/g^2 + 1) \tag{3.3}$$

As the wave speed calculated by diffusion ($2\ddot{O}rD$) approaches maximum swimming speed the telegraph wave reaches $0.8C_d$, ($= 1/[0.25 +1]$). As r becomes larger the

telegraph speed drops as a fraction of the diffusion speed; in fact the telegraph wave's speed is approaching the constant γ (Fig. 3.8). At epidemic wave speeds that are close to the maximum pilchard swimming velocity the diffusion-based model can lead to distorted estimates.

For birds flying at 10 km h^{-1} and with a D of 110 km^2 d^{-1}, for which the appropriate value of bS_0 is 21 d^{-1} (Murray 1999), there is only a small difference (<4%) between the solutions of the diffusion and telegraph equations. Faster flying speeds will tend to reduce the discrepancy further.

The model may respond differently to changes in the disease's infectivity or the host's population depending upon what animal is responsible for transporting the virus. For fish the speed of the epidemic wave is close to their maximum swimming speed, while birds can fly far faster than the wave travels. If fish are the major cause of spread then increase in virulence may have less effect on the wave's speed than will be the case for bird-borne viruses for which the standard diffusion model applies. The exact effect depends upon how close the epidemic wave's speed is to the pilchard's maximum swimming speed. The current epidemic certainly can be modelled using standard diffusion equations, the 1995 epidemic probably can also be so modelled, a more virulent epidemic than 1995's would require application of the telegraph model.

In conclusion, provided the fish can swim significantly faster than the epidemic's rate of spread (which they can) then a simple diffusion model should be capable of reproducing disease transmission - if this is due to the fishes' motion and this is non-migratory.

3.4   Constraints on Viral Transmission Rate

There are relatively few observations that we can use to constrain the rate of viral transmission b. In particular the maximum value may be very large because infected pilchards produce vast numbers of viral particles from their gill. Any of these viruses can, at least in theory, cause a new infection.

These is a lower limit to b, infection must be rapid because mortality at a given location occurs over a very short period. Processes such as dispersion tend to increase this minimum required value.

At a single site in an SIR model, a value of bS of 1 d^{-1} will lead to 50% of the infection occurring over 2.2 days, but with 90% of the infection over 4.5 days, while a value of 2 gives 50% in 1 day and 90% over 2.3 days. This latter is consistent with the observed pattern of mortality near Hobart. It is probably the minimum time that can be associated with the very short time scale over which mortality was locally reported. Dispersion of live fish post infection and of corpses will tend to spread mortality over longer periods at a given location.

In the SEIR models larger b values are required owing to the weakened feedback. However the value depends upon the strength of this feedback (the length of the latent period) and so *a priori* analysis is difficult. In particular, the dependence on b is complex in the fixed periods for phase duration model (Murray 1999).

Once we add the spatial element restrictions become more complex because following infection the infected individuals are dispersed from their point of infection. This prolongs the period over which mortality occurs at a given location and reduces the local peak of intensity. Conversely, the invasion of infected individuals accelerates the development of infection.

The *a priori* constraints on b are weak, we can be fairly confident that it is greater than $s1$. The principle constraint is provided by the co-constraint of the known epidemic wave speed and other parameters for which uncertainty is less (see Chapter 8).

3.5   Pilchard Population Structure and Density

The Australian pilchard's population was described as consisting of three separate sub-populations as early as 1951 (Blackburn 1951) on a morphological basis. Blackburn identified populations in New South Wales, Victoria and southern Western Australia. Subsequently Syahailatua (1992) identified a fourth population off west coast Western Australia. Genetic studies have also identified four semi-independent but contiguous populations (Dixon *et al.* 1993). A gap in pilchard egg distribution also shows in the region between southern and western WA (Fletcher *et al.* 1997).

The populations are further subdivided into local aggregations. For example the southern coast of Western Australia has three such aggregations at Albany, Bremer Bay and Esperance (Cochrane 1999). However, these local aggregations do not appear to affect the rate of spread of the epidemic.

Notably, the boundaries of these populations are associated with the anomalies that can be identified in the epidemic's rate of spread. A slowing in spread rate between the southern and western WA populations is explicable in terms of weakened contact across the boundary. However, the rapid spread from Victoria to mid New South Wales does not seem to be explicable in terms of population boundaries, quite the reverse would be expected. A possible explanation is that there is a migration from the Bass Strait region to the New South Wales region caused by the approach of winter. Pilchards have been shown to undertake seasonal migrations off South America (Torres *et al.* 1985). This response could be exaggerated if sick fish sought out warmer waters (Fletcher *et al.* 1997).

Spawning of different populations of pilchards occurs at different times of the year, such that among these different populations some pilchards are spawning on any given month (Fletcher *et al.* 1997). Even in Western Australia, for which the front exhibited a near uniform speed of progression, a complete range of breeding states (pre, post and current) existed among local pilchards at the time of the passage of the 1995 epidemic. We do not expect breeding related behaviour to explain differences in the transmission of the epidemic front.

Table 3.2 Breeding Seasons of Australian Pilchards at locations along the Australian Coast (Data from Fletcher *et al.* 1997).

Location	Spawning Season
Western WA	August and February-March
Albany	July and December to January
Bremer Bay	June to July
Eastern WA and Great Australian Bight	April to July
South Australia	February to March
Victoria	November
New South Wales	Summer, progressing northwards

Pilchard populations have been estimated from the Albany region using catch and effort data and a computer model (Fletcher 1992). Using subsequent data (1991-5) to refine the estimate, this population is now estimated to vary from 12,000 to 25,000 tonnes. Use of daily egg production method (DEPM) produced an estimated range of 15,000 to 31,000 for the same period. So regional population numbers, and hence density, varies by a factor of 2 in time. Population off Albany peaked in 1994 and declined to about 50% in 1997. Population was therefore at this location about half during the 1998/9 epidemic what it had been during the 1995 epidemic. We will later show that models show only a very weak dependence upon the pilchard's population density. Pilchard populations off Japan have shown changes of three orders of magnitude due to changes in recruitment success (Wada and Jacobson 1998), so large changes are possible.

We normalise the model population to the average pilchard population. Thus we do not need to know the exact value of this population, only relative variation about this mean. As the model is very insensitive to variation in population density, even the issue of relative population level proves only of limited importance.

The pilchard sub-populations are all of the same species and sub-species. Indeed the global pilchard population is now considered to consist of a single species without genetically distinct sub-species (Parish *et al.* 1988).

3.6   The Virus

The viruses associated with the mortality of pilchards in 1995 and 1998/9 were herpesviruses (Whittington *et al.* 1997). Herpesviruses are large double stranded DNA viruses (Cann 1997). They are similar in structure to phytoplankton viruses, which are robust and capable of surviving marine environmental stresses for hours or days (Murray and Jackson 1992). Since pilchard schools are constantly moving, while viruses do not, it is the physical separation of viruses from potential hosts, not their destruction, which leads to viruses ceasing to become an effective source of infection. In a similar situation, when Pacific herring are kept in cages hemorrhagic septicemia virus numbers are able to build up and infection becomes widespread (Hershberger *et al.* 1999).

The viruses associated with the two epidemics are similar. A comparison of DNA using PCR methods found that the 1995 virus tested positive to a test developed for the

1998/9 epidemic, but this test is not very specific as it consists of only 180 nucleic acid base pairs (AAHL 1999).

Virus numbers in the gills of fish appear to be much lower in the 1998/9 epidemic than was the case in 1995 (AAHL 1999). Electron microscopy could not always detect virus in individual gill filament of infected fish in 1998/9. This reduced presence of virus in the fishes' gills suggests a very large reduction in the value of the viral transmission rate parameter b. In spite of the low sensitivity of wave speed to b under models with fixed-length latent periods (see chapters 7 and 8), this change could be large enough to lead to a substantial reduction in the wave speed.

3.7   Length of the Infection in a Single Individual

Lesions containing viral particles appear on the fishes' gills some 2 to 4 days before mortality occurred (Whittington *et al.* 1997). The lesions are clinically different prior to the coming of the mortality wave to their condition within the mortality wave (Fletcher *et al.* 1997). This shows that the lesions developed over about 4 days (Whittington *et al.* 1997). We thus can be certain the fish were infected several days before they died. We earlier assumed that the lesions released viruses and represented an infectious stage (Murray *et al.* 1999). However it is only at the time of mortality that extensive exudation is detected (Fletcher *et al.* 1997). It is possible that the lesions are only relatively briefly a source of new infection when exudation increases just before the fish dies. Later modelling results do support a relatively brief period of exudation if the model is to replicate the pattern of the initial phase of the epidemic (see Chapter 9).

The disease may incubate for some time before symptoms occur, and this period, plus any period over which lesions are not a source of infection, forms the latent period. We lack the data to determining the length of this latent period. This data was hoped to be a result of transmission trials, however these trials do not appear to have succeeded in transmitting viable virus (AAHL 1999). Because during the incubation period the infected individuals lack symptoms it is difficult to determine if fish are incubating in the field. We therefore have little data to support any particular value.

We do have some suggestive data however. The initial period of mortality, in South Australia, shows clumping of mortality events. After the first three reports on 22 and 23rd of March there was a gap of about 8 days before the mortality broke out again (Fig. 3.9). This was followed by reduced mortality, followed by further peaks at eight-day intervals; the waves becoming less distinct with time. This is suggestive of a gap between infectious periods, i.e. a latent period, of 8 days. However, such a long latent period proves to be inconsistent with very high velocities of the 1995 epidemic.
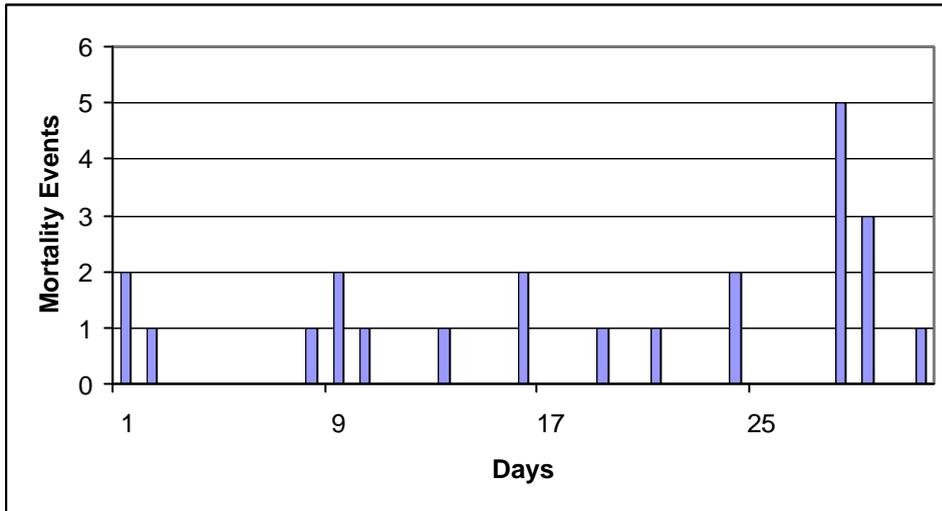
Figure 3.9   Reports of pilchard mortality events in the early part (from 22 March) of the 1995 epidemic. Note a possible tendency to peak at 8 day intervals.

Similar data from the initial month (October) of the 1998/9 epidemic (Ward *et al.* 1999) shows similar gaps in the initial build up of that epidemic (Fig. 3.10). This data appears to show peaks in mortality at a slightly shorter time interval of about 6 days. Records of mass mortality are much denser for the 1998 period than for 1995, possibly due to better reporting. If so there may be much missing data from 1995. It is also possible that the gap is due to the spread of the disease from relatively isolated Spencer Gulf into the Southern Ocean.
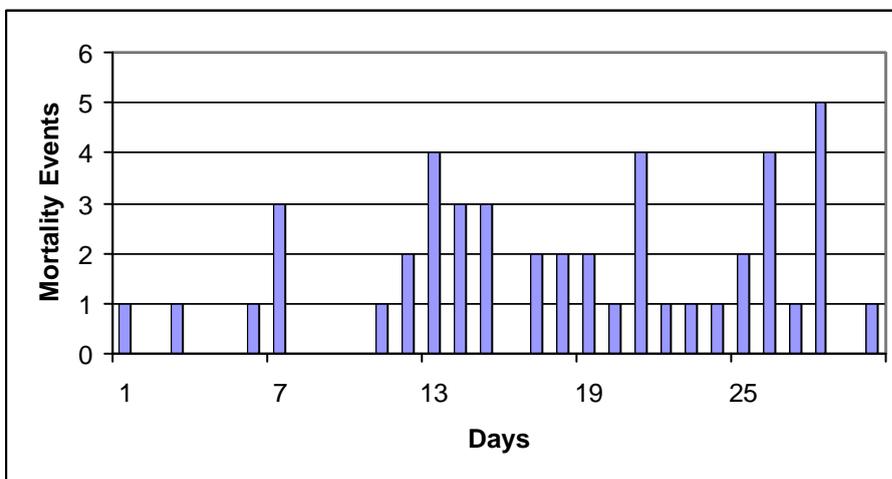
Figure 3.10   Reports of pilchard mortality events in the early part (from 1 October) of the 1998/9 epidemic. Note a possible tendency to peak at 6 day intervals.

A fairly long latent period would also be consistent with delayed mortality of caged pilchards, although this may well not be due to the virus (AAHL 1999) and therefore irrelevant.   It is also consistent with the observation of lesions in small numbers of pilchards considerably in advance of the active front and the identification as PCR positive of a pilchard isolated from advance of the front (AAHL 1999). However, the available evidence concerning the length of the incubation period remains weak. Mild

lesions were apparent 13 days after exposure to viruses of pilchards in tanks (Jones 1999), which may indicate that the incubation period was just ending. However, these pilchards did not test positive for virus (AAHL 1999), so this is very doubtful evidence for the length of the latent period.

As we have already noted, these longer latent periods allow fish to disperse following infection and this is difficult to reconcile the brief local duration of the infection in the mature wave. Although these observations of gaps are interesting, they are very inconclusive evidence, while the brief duration of local infection away from the origin is clearly demonstrated.

Actual infection takes place some time before the deaths occur. The length of this period is equal to the sum of the lengths of the infective and latent periods. This gives a total period of 4 to 12 days and the front progresses during this time. If the front is travelling at 35 km d^{-1} then the infection is actually occurring at least 140 km in advance of the current position of the mortality front, possibly over 400 km in advance of the apparent front. This must be borne in mind for the development of any control strategy and is in line with the isolation of infected pilchards far in advance of the observed mortality (AAHL 1999).

3.8   Survivorship and Mortality

Estimates of the proportions of the adult pilchard population that was killed by the herpesvirus are very variable in space and between the two epidemics.

In 1995 the estimate for pilchard mortality in Western Australia was around 10-15% of the population (Whittington *et al.* 1997). Estimates for mortality in Western Australia following the 1998/9 epidemic are of the order of 60% (Jones, personal communication), some local mortality is estimate at 40 - 90% at Bremer Bay (Gaughan, personal communication). However, the pilchard population at Albany only appeared to receive 2% mortality, such a large difference is unlikely to be the case - indicating that there are major uncertainty in the mortality estimates.

In South Australia, mortality of 60% was estimated for the 1995 epidemic on the basis of fish stock estimates for 1995 and 1996 (Ward *et al.* 1999). A similar decline occurred in South Australia following the epidemic of 1998 (Jones 2000).

 It is difficult to explain how large proportions of the adult population could avoid the disease if schools interact at realistic rates (see chapters 8.4) and in any case, the high 1999 mortality indicates that a large proportion of the host population is exposed to the virus. This is particularly the case since the pathology indicates more viruses were present in the gills of the pilchards in 1995 than was the case in 1998/9 (AAHL 1999) and the disease spread more rapidly in space in 1995. This would suggest that the 1995 epidemic was more easily spread than the 1998/9 one. Therefore a significant proportion of the hosts in 1995 must have been exposed and yet survived that infection, if the Western Australian mortality levels of 1995 were correctly estimated.

3.9   Conclusions

The epidemics of 1995 and 1998/9 were similar with extremely rapid spread and brief local duration. But they had significant differences, including differences between the east and west bound spread of the 1995 epidemic. Our estimates of the rate and nature of the spread of the 1995 epidemic are similar to those of Whittington *et al.* (1997).

From these observations we draw the following constraints upon the model. The epidemic wave speed in 1995 was 40 km d^{-1} east-bound and 21 km d^{-1} west-bound, while in 1998/9 the speed was around 11 km d^{-1}. Our estimates of the rate and nature of the spread of the 1995 epidemic are similar to the 35 km d^{-1} of Whittington *et al.* (1997), except that we emphasise the differences in speed between the two fronts. These rates are 2.4 and 4.6 m s^{-1}, very similar to the 0.3 - 0.5 m s^{-1} estimated by Griffin *et al.* (1997).

The value of *D* is constrained to a range of 20 - 400 km^2 d^{-1} this is a very important constraint upon the model. On occasions pilchards may exhibit non-diffusive movement. The value of ***b*** is only weakly constrained to values >1. It is later constrained with reference to other parameters and the epidemic wave speed. The length of the infection must be at least 2 - 4 days, because of observational evidence based on lesion formation. However, these lesions may not be a source of infection until they are mature so the infectious period may be shorter (but not longer) than this. The length of the latent period is highly uncertain. Some, weak, evidence suggests periods of up to 8 days, but other constraints suggest a short latent period. This lack of data on the latent period is the most significant gap in direct data constraining the model. We later use the initial behaviour of the epidemic to indirectly investigate latent and infective periods.

4   Local Epidemic Models

Epidemics travel and develop in both space and time. We start our analysis by considering the development of the epidemic at a single point in space. We use very simple models of the spread of an epidemic in a single population, the local school and in an interacting shoal of schools. In the following chapters (6+) we consider the effect of large spatial scales on the epidemic's development.

Simple epidemic models were reviewed as an initial stage in the development of the modelling project (Murray 1999, Murray *et al.* 1999). However, it is worth summarising these simple models again. This summary is useful for a development of understanding of the basic modelling process and because there have been further developments in our use of simple models to describe the pilchard herpesvirus epidemics.

4.1   Continuous Turnover

The simplest epidemic model is the susceptible-infected model. In this model a population of initially susceptible individuals is exposed to a small number of infected individuals. These infected individuals spread infection to the susceptible individuals

increasing the number of these infectious individuals. Meanwhile infected individuals recover or die - joining an implicit or explicit pool of individuals that are removed from the infection (see Anderson and May 1979).

$$dS/dt = -SI\boldsymbol{b} \tag{4.1}$$

$$dI/dt = SI\boldsymbol{b} - I\boldsymbol{a} \tag{4.2}$$

$$dR/dt = I\boldsymbol{a} \tag{4.3}$$

Because of the extremely rapid spread of the pilchard herpesvirus and the short duration of mortality at a particular location, other slower processes such as population growth and non-disease based mortality can be neglected from the modelling of the epidemic.

This model has a critical threshold value of $S = \boldsymbol{b}/\boldsymbol{a}$. If S is less than this threshold then production of new infections is less than their removal rate and hence the disease will decline.

In practice, infected individuals do not immediately become sources of new infection. A latent phase E must be added between the S and I phases. Due to the very rapid transmission and spread of the pilchard herpesvirus it is likely that any delays due to period for which infection is in this latent phase play a critical role in the disease's dynamics.

$$dS/dt = -SI\boldsymbol{b} \tag{4.4}$$

$$dE/dt = SI\boldsymbol{b} - E\boldsymbol{s} \tag{4.5}$$

$$dI/dt = E\boldsymbol{s} - I\boldsymbol{a} \tag{4.6}$$

$$dR/dt = I\boldsymbol{a} \tag{4.7}$$

4.2   Fixed Infection Phase Period Lengths

These simple models are extremely valuable for interpreting the behaviour of epidemics, and we will use them in the analysis of the pilchard herpesvirus' spread. However, for the replication of the pattern of mortality inflicted by the pilchard herpesvirus these models exhibit a fundamental flaw. Observed mortality induced by the herpesvirus was extremely rapid, with vast numbers of fish dying over a short time. This sudden coincidental death resulted in the observed mass strandings, which for a given location usually occurred over a very short period (see later). This mortality occurred about 4 days after lesions indicated the fish had become infective (Whittington *et al.* 1997).

The pattern of mortality that the SIR and SEIR model generates (Fig. 4.1) is rather different to these observed sharp peaks of mortality. Modelled mortality is spread over a period of several of days, even if infection is instantaneous. This modelled mortality only occurs on average 4 days after infection and is spread over many days while the

number of individuals that were infected at a given time decays exponentially. Further, the highest probability of mortality occurs immediately after infection developed, observed infection (lesions) is apparent for days before mortality begins. Death under the SEIR model includes this spread due to continuous mortality plus a further spread due to the variable delay in the onset of the infectious period caused by the latent period; although mortality in this model does peak some time after the initiation of infection.

The pattern of development of infection that is generated by these standard models is not biologically reasonable. There must be some finite time required for an infection to develop and become infectious. It will be some time after infection that there will be a maximum probability of the infection developing to the infectious stage - and there is zero probability of this occurring immediately following infection. The same applies to mortality or recovery, it takes time for the fish to fight off or succumb to the disease and so the probability of death or recovery will vary as the infection develops. For example, when shrimp are infected with the virulent viruses White Spot Syndrome Virus or Yellow Head Virus no mortality occurs for 4 or 8 days respectively. High levels of mortality then follows over the course of 3 or 4 days and after this, if there are any survivors, mortality ceases (Lightner *et al.* 1998). The pattern of pilchard mortality suggests that mortality occurs over an even briefer period.

The real probability pattern for phase changes in a developing infection thus has some sort of distribution clustered about a time of maximum mortality. But we have no information on the distribution of probability about the time of maximum mortality, except that it must be highly concentrated around that peak given the short duration of observed mortality. For numerical modelling it is thus much easier to simply use an infection period of a fixed length. We have adapted such a model from the work of Dwyer and Elkington (1983).

$$dS/dt = -SI\boldsymbol{b} \qquad\qquad (4.8)$$

$$dE/dt = SI\boldsymbol{b} - S_{t-b}I_{t-b}\boldsymbol{b} \qquad\qquad (4.9)$$

$$dI/dt = S_{t-b}I_{t-b}\boldsymbol{b} - S_{t-c}I_{t-c}\boldsymbol{b} \qquad\qquad (4.10)$$

$$dR/dt = S_{t-c}I_{t-c}\boldsymbol{b} \qquad\qquad (4.11)$$

In this case the infective period is of length b and the latent period is of length $c - b$, the total infection being of length c. The pattern generated by this model is of a spike of mortality at a fixed interval after infection (Fig. 4.1). Since infection is non-instantaneous, mortality will in practice be spread over a finite period even under this model.
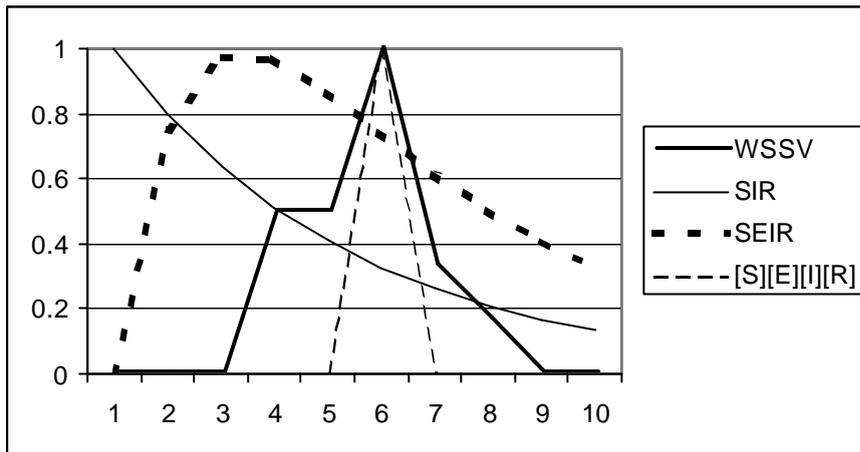
Figure 4.1   Distribution of mortality, normalised to maximum, following infection under the SIR, SEIR and [S][E][I][R] models and mortality of prawns caused by White Spot Syndrome Virus. The first two models result in mortality that is either spread over a long period or occurs immediately after infection. The fixed infection length model results in a peak after an interval; observed mortality inflicted by WSSV is of this pattern, although with some spread about the maximum

The standard continuous turnover SEIR (or SIR) model does not work well as a description of the brief burst of mortality occurring after a delay as occurs in these pilchard herpesvirus epidemics or in the WSSV mortality of prawns. However, in most other epidemics mortality is spread over a long period because the infection builds up over a relatively long period. Most epidemics incorporate several cycles of infection before burning out. It makes little difference to the pattern of mortality generated whether this mortality is modelled as occurring at a fixed time after infection or at a constant rate following infection. Hence the more mathematically tractable continuous turnover models are acceptable in other cases.

Another feature of the fixed period phase-length model is that mortality may occur as a series of peaks, particularly if $c < 2b$, i.e. the length of the latent period is longer than the infectious period. These peaks are generated because of the time gap between infection and mortality. Such peaks appear to occur at the initial focus of the disease near Adelaide, where mortality peaked, with intervening gaps, about three times before the epidemic started to spread spatially (see later). Continuous turnover models cannot reproduce this pattern of gaps in the mortality, which stems naturally from the fixed-period phase length model. We will look at the pattern of initiation of the epidemic in spatially explicit models in more detail later.

4.3   Effect of Schools on Transmission

Disease dynamics are usually modelled on the basis of the random interaction of infected and susceptible organisms. However, most organisms have a tendency to aggregate (Okubo 1980) and hence do not interact randomly.

The effect on epidemics of spatial variation in host population density has been examined extensively. This spatial variation may consist of regionally varying population density as in the fox hosts of rabies (Murray *et al.* 1986) or of interacting patches as in the case of seals subject to phocine distemper virus (Swinton *et al.* 1998).

In patchy populations, the epidemic spreads both within and between patches (Ball *et al* 1997). At the local level, the spread of rabies is also patchy, due to higher degrees of interaction among related foxes (Thulke *et al.* 1999). The population structure of the model may thus depend upon the level of spatial resolution required by a model, which depends upon the problem being investigated.

Many fish populations form large shoals that are subdivided into schools. In this case variation is not spatial, the schools in a shoal do not have a specific spatial relationship to each other and interact randomly (see Blaxter and Hunter 1993). This is different from the continuous interactions of individual members of households (Ball *et al.* 1997) or patches (Swinton *et al.* 1997) with their neighbouring household or patch; the interaction of schools occurs as a discrete mass interaction.

Within schools the population density is fixed and independent of school size, the fish maintain a constant spacing from their neighbours. Clupeoid fish, for example, occupy a volume equivalent to approximately $(body\text{-}length)^3$ (Blaxter and Hunter 1993). Therefore, as the shoal's population increases the size and/or number of the schools can increase and the reverse applies as population declines, but the density of fish in these schools does not change.

We analyse transmission of disease at the levels of the school, shoal and larger spatial scales. We use this analysis to derive a numerical model encompassing both school and shoal scale transmission and consider the larger scale transmission of epidemic waves.

In the creation of this model we are hampered by a lack of knowledge of the details of behaviour in the interaction of individuals within and between schools. We therefore aim to make models that are not sensitive to assumptions of patterns of behaviour and to note and describe the areas that are sensitive to unknown behaviours.

4.4   Transmission at the School Level

There are basically two mechanisms by which fish diseases can be transmitted: directly by close contact with infected individuals, and indirectly through the medium of the water. The two mechanisms lead to substantially different responses of epidemics to changes in school sizes. The mechanisms are respectively density dependent and density independent, or more strictly, school population dependent and school population independent.

The simplest mechanism is direct contact, requiring susceptible fish to come into close proximity to an infected fish. In this case transmission is density independent, since the infected fish has the same number of neighbours regardless of the size of the schools. The identity of these neighbours can, and almost certainly will, vary with time. There is an exception in that individuals on the edge of the school have fewer neighbours, and the proportion of the population at the edge of the school does decrease as the school size increases, but (except for very small schools) the number of these fish is insignificant. Transmission (at the school level) is

$$\boldsymbol{b}_z\, I_z\, S_z\, /N_z \tag{4.12}$$

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where $\boldsymbol{b}$ is the contact rate, I the infected population, S the susceptible population and N the total population. Subscript z indicates that these are the school populations. Note that these are populations, not densities, since the school density is independent of the population. It is however often convenient to normalise these populations to a standard total shoal population, i.e. $N = 1/Z$ where Z is the number of schools in the shoal.

This patch (school) size independent transmission approach was used by Swinton *et al.* (1998) to model the transmission of PDV between seals. Transmission of the disease occurred when seals rested at communal haulouts due to interaction between immediate neighbours; the number of which was independent of haulout size.

If the water is a major conduit for transmission within the school then transmission efficiency can increase with school size. At the simplest, the virus mixes through the whole school and so the number of susceptible fish that encounter the virus increases with the school size

$$\boldsymbol{b}_z\, I_z\, S_z \qquad\qquad\qquad\qquad (4.13)$$

This is the simplest classical form of the disease transmission model (Anderson and May 1979). However, non-random mixing within the school complicates school size dependent transmission. Non-random mixing in the water in a school, such as concentration of viruses in trails immediately behind infected fish, may lead to a dependence of transmission rate on a power of school size (Murray 1999). Under water-bourne transmission, if fish are immobilised then viral numbers can accumulate allowing for more transmission within a trapped population (Hershberger *et al.* 1999).

To reproduce the full range of complete independence of transmission from school size to linear dependence, we can use the formula

$$\boldsymbol{b}_z\, I_z\, S_z\, [N_z^{\,x}/N_z] \qquad\qquad\qquad\qquad (4.14)$$

Where x lies between 0 and 1, and hence the extremes of school size independent ($x = 0$) and school size dependent transmission ($x = 1$) are brought into a single formula.

Notice, however, if the number of schools increases with population density, so that the size of individual schools is constant, then transmission at the school level does not change with the shoal's total population size whatever the value of x. Maintaining constant school size is a second means of introducing density independence to local transmission.

4.5   Transmission between Schools

Like individuals, schools interact. Unlike spatially fixed patches or populations, the schools do not have fixed neighbours and so interact randomly with other schools in the shoal. The rate at which schools come into contact depends both upon the probability of contact and the number of schools within the shoal. So the number of schools containing infected individuals contacts individuals consisting entirely of susceptible individuals is

$$\boldsymbol{g} Z_i\, Z_s \qquad\qquad\qquad\qquad\qquad\qquad (4.15)$$

If, on encounter the fish exchange some proportion of their populations then infected individuals will be spread through the population. So if infected individuals are introduced into one school then random encounters will lead to infected fish reaching all other schools at a rate controlled by school encounter rate. As the number of schools containing infected fish increases, the rate of the spread of infection to uninfected schools increases; and then declines as the number of uninfected schools become limiting.

The shoal itself may increase in density as numbers increase, or it may be of constant density and the schools spread over a larger area as their numbers increase. In the latter case the encounter rate between two particular schools may drop as total population increases, although this is counteracted by the increased number of schools.

The interaction between infected and clean schools is thus similar to the interaction between infected and susceptible individuals. There is a difference, however, in that infection can persist in schools for longer than in individuals. Infected schools can contain uninfected individuals and these act as a target for new infections, allowing the disease to persist. For the whole period infection lasts within the school then school may act as a source of new infection to other schools.

At the start of infection in a shoal a small number of infected individuals will be introduced to one of the schools. The source will be an adjacent shoal or, if the epidemic is starting then a local source of a novel mutant, introduced virus or resurrected virus (e.g. viable virus released from sediments) will similarly introduce the virus to one of the schools.

At the initial stage of the epidemic within a school the rate of production of new infections per infected fish is at its most rapid because the population of the initially infected school is still mostly susceptible and any other school the school may encounter will consist entirely of susceptible fish. The rate of production of new infections per infected fish from then on declines, although with temporary increases as new untouched schools are encountered.

In the next chapter we develop these ideas on viral transmission and pilchard schooling into a formal model which we analyse to determine the effect of schooling the local development of an epidemic.

5   A Numerical Model of Intra- and Inter- School Transmission

To analyse the interaction of school and shoal level effects that we discussed in the previous chapter we derive a model including both intra-school and and inter-school level activity.

5.1   The Model Structure

5.1.1   The school-level models

At the local level, transmission is modelled using a standard SEIR model (Fig. 5.1) based on the methods described by Anderson and May (1979)

$$dS_z/dt = -b_z S_z I_z \, [N_z^{\,x}/N_z] \tag{5.1}$$

$$dE_z/dt = b_z S_z I_z \, [N_z^{\,x}/N_z] - s E_z \tag{5.2}$$

$$dI_z/dt = s E_z - a I_z \tag{5.3}$$

$$dR_z/dt = a I_z \tag{5.4}$$

The subscript z denoting that this is the local school population. The epidemic in question persisted at most sites (apart from its origin) for only a few days. Therefore factors such as birth and non-disease death of the pilchards are not included in the model.

Such SEIR models also have problems in replicating the short duration of mortality observed at any given location. They tend to spread the mortality over a long period even if infection is near instantaneous.
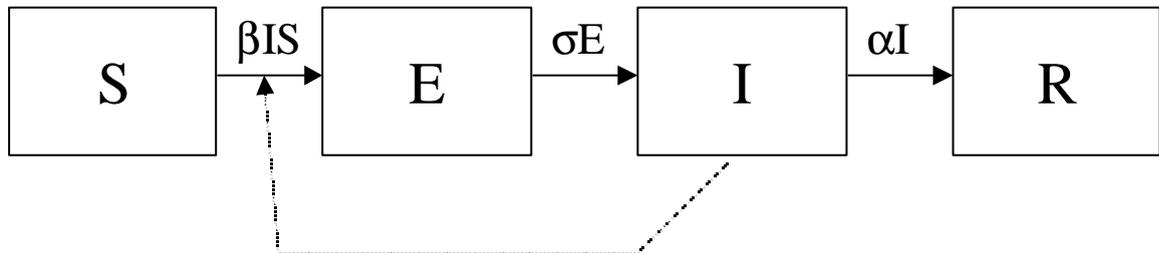
Figure 5.1   The SEIR model's structure

In order to produce a short period of high mortality, as is observed for the pilchard epidemics (Fletcher *et al.* 1997) we also use a version of the model with fixed infection period lengths. This model has the same structure as before (Fig. 5.1) and approximates to

$$dS_z/dt = -b_z S_{zt} I_{zt} \, [N_{zt}^{\,x}/N_{zt}] \tag{5.5}$$

$$dE_z/dt = b_z S_{zt} I_{zt} \, [N_{zt}^{\,x}/N_{zt}] - b_z S_{zt-b} I_{zt-b} \, [N_{zt-b}^{\,x}/N_{zt-b}] \tag{5.6}$$

$$dI_z/dt = b_z S_{zt-b} I_{zt-b} \, [N_{zt-b}^{\,x}/N_{zt-b}] - b_z S_{zt-c} I_{zt-c} \, [N_{zt-c}^{\,x}/N_{zt-c}] \tag{5.7}$$

$$dR_z/dt = b_z S_{zt-c} I_{zt-c} \, [N_{zt-c}^{\,x}/N_{zt-c}] \tag{5.8}$$

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Similar models have been used by Dwyer and Elkington (1993) to study viral epidemics in moth populations. We will refer to this as the [S][E][I][R] model because the phases of infection persist for periods of fixed length.

Implementation of this model can present a computational problem because of the need to keep track of exactly when infection occurred. If the model were simply implemented with short time steps then E and I could require to be specified as hundreds or thousands of sub-variables and these would be required in each school in the model; this could present very large computation overheads.

To avoid such vast numbers of model components, we implement the basic model with fewer categories integrating the infection occurring over a given period. Typical periods are 0.05 to 0.2 days, thus for each day that the phase E or I persists we require 5 to 20 variables. The model then acts as a conveyer belt, inputs for the period are place in the initial variable subcomponent of the school (e.g. E_{z1}) continuously. Once the time interval is complete these are transferred to the next subcomponent so that infection in category E_{z1} is transferred E_{z2} which in turn is transferred E_{z3}; where E_{zt} is the infection in school z which occurred at time t.

When the transfer is between different phases of the infection, for example when the contents of the last E are transferred to the first I, there is a potential problem of sudden influx if updating were done on this longer-term basis. To ameliorate this problem the transfer is continuously between categories $S \rightarrow E$, $E \rightarrow I$ and $I \rightarrow R$, implemented with short time steps the model requires. Indeed it is precisely because of the high rates of infection and so rapid transmission from S to E within schools, that the model needs to use short time steps.

This hybrid mechanism of occasional updates within infection phases and continuous updates between infection phases works well. It can produce problems when transmission is extremely fast if the updating interval is too long, these problems may occur at the end of the infection when I is already large and therefore the epidemic is already reaching its final phase. Even if numerical problems do occur, they have little effect on earlier phases of the development of infection. Hence, to avoid any possible numerical problems, we tend to use infection rather than mortality as a measure of the epidemic's behaviour. Defining mortality is in any case problematic since a includes both mortality and recovery from infection. Sensitivity analysis shows no effect of the length of the update period for periods of less than 0.2 days.

One other problem with the hybrid mechanism is that it is not easily analysed. Indeed, the values of E or I can mean quite different things for the development of the epidemic depending upon how these are distributed between their sub-categories. However, it generally behaves in a similar manner to the SEIR model, and so this forms a good basis for initial analysis.

5.1.2   Stochastic Interaction between Schools

The number of schools in a shoal is variable and may be large, but it is small enough that interaction of these schools is not continuous, instead it is governed by chance. This is particularly true in the initial and final phases of the spread of infection between the schools. The initially infected school may simply not interact with any other school

for a long period of time, alternatively it may rapidly come into contact with a second school. Once the initial exchange has occurred the probability of the two schools that now carry infections coming into contact with another school is almost doubled. Thus it would seem that stochastic interaction between schools in the initial phase of the epidemic may shape its development.

The schools interact at random with the probability of any two schools coming into contact being defined by a parameter, the event being determined stochastically. On contact the schools exchange a fixed proportion of their populations of all the classes.

$$Sc_xy(X_x - X_z)\ x = 1\ \text{to}\ Z \tag{5.9}$$

$$\text{\pounds}\ p,\ c_x = 1 \tag{5.10}$$

$$z > p,\ c_x = 0 \tag{5.11}$$

The parameter y is the proportion of populations exchanged by schools that come into contact, X is the set of S, E, I and R contained in a school x or z. Exchange over a given time occurs at random if the stochastic variable z (lying between 0 and 1) is less than the probability p of contact. If schools tend to merge and split on contact, this is equivalent to large values of y.

5.1.3   Model Parameters

The model therefore has 6 parameters, the within-school b_z, s and a plus between school contact probability p, exchange quantity y and the number of schools, Z. The phase lengths b and c-b are the logical equivalents of s and a. Note, however that b_z is the local infection rate within a school. The value of b at the shoal population level (and higher levels) emerges from this value and the interaction of the schools.

We have observational evidence with regards to a (or c-b) that this turnover of the infectious phase occurs over less than 2 – 4 days, although we experiment with periods of up to 6 days. It is in this period that viral containing lesions are present in the fishes' gills (Whittington *et al.* 1997), but these may not be a source of viruses until they mature (see Chapter 9). We assume that s (or b) is of the same order, but lack direct evidence and so experiment with a larger range of 1 -10 days, $s = 0.1$ - 1 d^{-1}.

The value of b_z is uncertain, but it must be high enough to allow for rapid development of infection within a school if mortality is to occur over a short period. The value required for this depends upon the within-school model used. The value of b derived from b_z must be consistent with the observed epidemic wave speed, this relationship can be found directly for SEIR models, but not the [S][E][I][R] version. From the analysis of Murray *et al.* (1999) the appropriate range of b in the SEIR model was 20 - 200 d, implying 600 - 6000 d for b_z with 32 schools; higher values of b are valid only for very low D values.

The mixing parameters are highly uncertain, but schools in a shoal interact frequently, so a rate which allows for, on average, the daily contact of all schools within a shoal,

1 d^{-1}, seems reasonable particularly if schools dissolve overnight and reform at random. Schools do dissolve at night in the case of some clupeoid fish species (Blaxter and Hunter 1982). We experiment with a range of rates of contact of 0.125 to 2 d^{-1}. Similarly the amount of exchange of population on contact is uncertain and we look at the range of 1 - 10% exchange of population per contact.

We also have the choice of school size independent or school size-dependent virus transmission within the school; this we can attain by varying x from 0 to 1. This factor is only important if we are varying the sizes of the schools.

Table 5.1   Model parameter values

Parameter	Default	Min	Max	Units	Function
b_z	1000	250	4000	d^{-1}	Infection rate
a	0.25	0.166	1	d^{-1}	Mortality/recovery rate
s	0.25	0.1	1	d^{-1}	Infectivity onset rate
p	1	0.125	2	d^{-1}	School contact probability
y	0.05	0.01	0.1		Proportional exchange
x	1	0	1		Densisty dependence factor

5.1.4   Evaluating the Model Output

We need a means of comparing runs with a few simple statistics. The model produces a very large number of raw outputs in the form of S, E, I and R time series and these must somehow be condensed.

One good measure of the length of the epidemic is the number of days over which infection of 50% of the population occurs. This is not the days from the start of the epidemic, but rather the number of days around the peak of the epidemic. We find this by sorting the infection calculated at 0.01 day intervals and summing until we have reached a total population in excess of 50% have been or are infected. The value of the length of time over which modelled infection occurs is that it can related to observations of mortality, whereas the time required for the infection to reach its peak cannot since the time of the initial arrival of infected individuals cannot usually be known.

Another interesting, although less compact, measure of the effect of schooling on the models is apparent b. By this we mean the value of b that can be calculated from *S, I* and the rate at which new infections are created at the shoal level, relative to the b_z value actually used in the model at the school level.

5.2   Model Results

5.2.1   Overall Parameter Sensitivity of Infection Transmission

The period over which 50% of the susceptible hosts become infected that occurred in the SEIR and [S][E][I][R] models after a 20 day run is plotted in figure 5.2 for a range of parameter values. The values plotted are the means of five runs, however only under

conditions of low contact probability or low numbers of schools was their much stochastic variation.

Unsurprisingly, the period required to induce 50% infection of the pilchards is highly sensitive to the infection rate parameter in both the SEIR and [S][E][I][R] models.
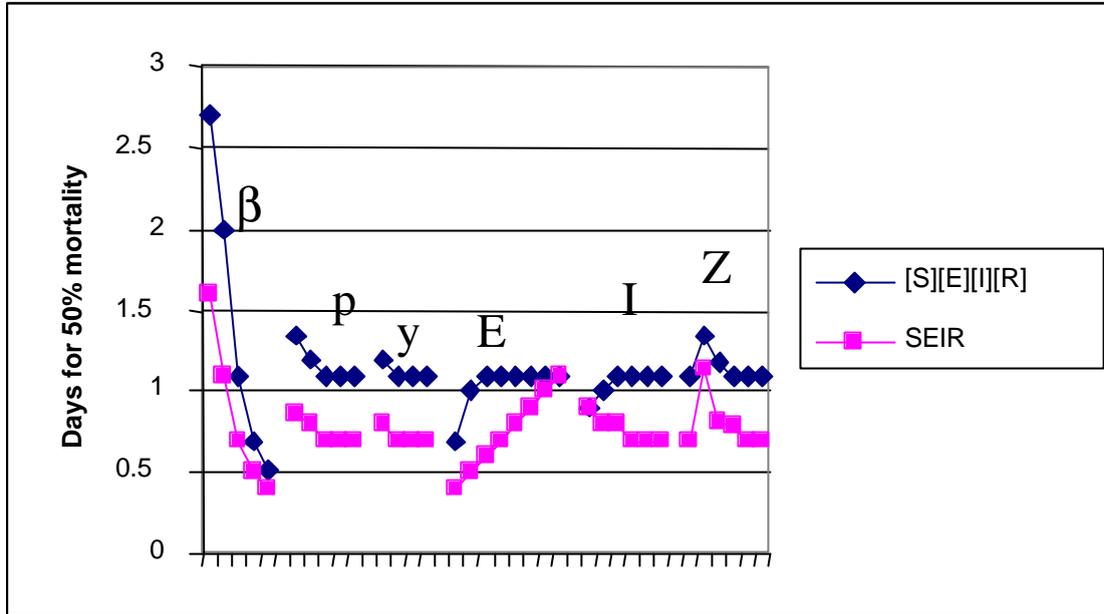
Figure 5.2   Parameter sensitivity of the period required for 50% infection in the SEIR and [S][E][I][R] models. $\boldsymbol{b}_z$ =[250, 500, 1000, 2000, 4000 d^{-1}], p=[12.5, 25, 50, 100, 200% d^{-1}], y =[1.25, 2.5, 5, 10%], E = [1, 2, 3, 4, 5, 6, 7, 8, 10 d], I =[1, 2, 3, 4, 5, 6 d], Z =[1, 2, 4, 8, 16, 32 schools] density independent (or school size constant).

The effect of changes in contact rate of schools is significant only for low contact rates. If contact rate between any pair of schools is less than about 50% per day then the infection peak is increasingly spread over a long period as contact rate drops. However, for higher rates of contact there is no effect of increase in the contact rate. This lack of response is highly significant since it suggests that the details of the dynamics of inter-school interact may not be important provided interaction is reasonably frequent.

The period over which infection occurs does show some sensitivity to the proportion of fish that exchange between two schools following interschool contact. This effect of this is generally less than changes to the contact rate and is only significant if exchange is very small (<2.5% per contact). This lack of effect at higher exchange levels means that the wholesale merging (and splitting) of schools would not change the epidemics dynamics, because this is simply equivalent to high values of y.

Intuitively, reducing the number of schools into which the population is divided would be expected to have a major impact on the epidemic, since this reduces the frequency of contact but increases the proportion of the population exposed as each new school receives infected individuals. Note that we reduce $\boldsymbol{b}_Z$ as the number of schools declines, in order to maintain the value of $\boldsymbol{b}$. On the whole, there is remarkably little effect in changing the number of schools. When the population is combined into one school infection spreads very rapidly, as expected. With two schools the period over which

infection spreads is prolonged. This is because, with only two schools, contact is infrequent and so infection in one school is likely to be advanced before contact occurs with the second school, this leads to prolonged low levels of infection. At larger numbers of schools reduced transmission within the schools is counteracted by more frequent contact between schools and so transmission rate does not change with the number of schools. If there are few schools then the model's behaviour between runs is highly variable, but at larger numbers the runs are all similar. This lack of dependence on the number of schools provided their number is not small, like the lack of dependence on contact rate, suggests that details of the schooling behaviour can be neglected.

The lack of effect of school numbers on transmission tends to support the use of transmission models that are population independent at the larger scale. This applies regardless of whether transmission is dependent on population size at the school level or not if the total population tends to break up into more schools as population rises. Breakup into more schools is very likely to be the case if there is an optimal school size for feeding and defence. We will explore the effect of the number of schools in more detail later.

We might expect the behaviour of the SEIR and [S][E][I][R] models to differ over their response to changes in the length of the latent and infective periods, since it is the representation of the exchange between these stages that is the specific difference between the two models. This is indeed the case (but is not related to schooling behaviour).

The effect of latent period length on the SEIR model is largely linear, because changes in s change the rate at which infection develops and hence the period over which mortality is spread. Under the [S][E][I][R] model there are two phases to the response to the length of E. Initially increase in E increases the period over which mortality occurs. This is because at low E there is a rapid development of I and hence feedback of new infections occurs. Once E is sufficiently long, the initial infected of individuals (as discussed before) drives infection and lacking feedback from new infections the process is independent of E.

The models are both less sensitive to changes in I than in E and respond qualitatively differently. Under the SEIR model increased I (reduced a) reduces the period of over which infection occurs because more transmission occurs if the infective stage lasts longer, the effect is quite weak. Under the [S][E][I][R] model the spread of infection is largely independent of the length of I, but low levels reduce the length slightly by delaying this until feedback can occur.

As described earlier, the exchange between infection stages in the [S][E][I][R] model was carried out at discrete intervals. Test model runs updated at intervals of 0.01 to 0.2 d showed no variation at all, we therefore conclude the model is not numerically sensitive to this process at the default level of resolution of 0.05 d.

As a general conclusion we see that the model is largely independent of the details of inter-school transmission, provided the number of schools and their interaction rates are not small. Schools of many clupeoid fish, such as pilchards, do indeed appear to be

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numerous and continuously interacting (Blaxter and Hunter 1982). The initial analysis also indicates that infection in the SEIR and [S][E][I][R] models shows similar dependence upon parameters, but with important exceptions, largely relating to the nature of the feedback between infection and further infection in the two models. We can expect largely similar behaviours in the two models.

We examine the effects of contact probability and the number of schools on the details of the epidemic's regional behaviour in more detail in the following section.

5.2.2   Transmission Between Schools

The random encounters between schools lead to changing rates of contact between infected and uninfected schools as the proportion of schools carrying infection changes (Fig. 5.3). Initially the average time required to spread the infection to another school is long because there is only one infected (source) school. Stochastic events are also important for the same reason. Once infected school numbers build up the frequency of encounters between schools containing infected individuals and schools completely clean of infection increases, peaking when 50% of schools contain infected individuals. The frequency of encounters then drops because of a lack of 'clean' schools, until the last school without any infected members is equally unlikely to encounter infected individuals as the first school containing infected individuals was to encounter an uninfected school.

Despite the low probability of encounter with the last clean school it cannot serve as a refuge because the probability of avoiding contact is equally low as was the probability of propagation of the disease to a second school after it was initially introduced to the shoal. Therefore, only if there is a high chance of the disease failing to transmit initially is there a significant possibility for refuge populations to avoid infection. The rapid and smooth observed propagation of the epidemic along the Australian coast indicates that transmission is not weak. Further, there is only one initially infected school and if the infection dies out in this school the epidemic ceases locally and must be reintroduced. The final school is only safe from infection once the epidemic has burnt out in all the other schools in the shoal.
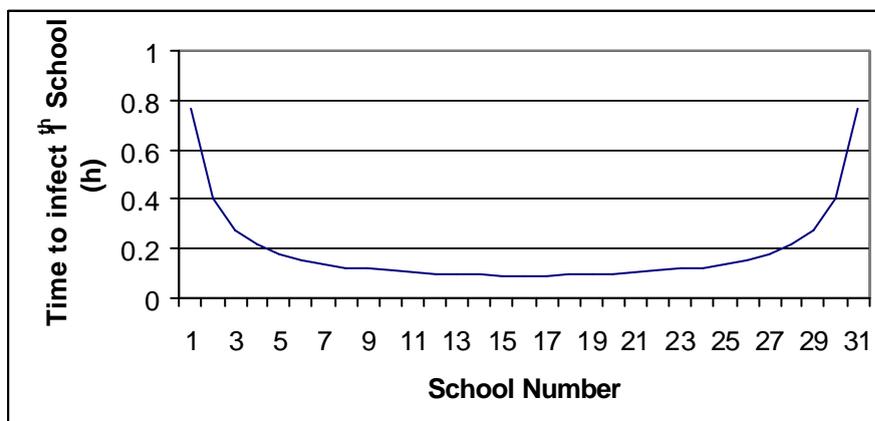
Figure 5.3   Average time required for the Ith of 32 schools to become infected at 1 contact for each pair of schools per day.

The probability of transmission between schools depends upon both the contact probability and the number of schools. The dependence is relatively simple and is close to linear, i.e. if we take four times the number of schools with a quarter the contact rate we have to similar contact patterns to the original situation (Figure 5.4). The initial phase of the infection is prolonged as is the transmission of infection to the last of the schools, but the exposure of the bulk of the population occurs at the same rate in both situations (p = 1, schools = 8 and p = 0.25, schools = 32).
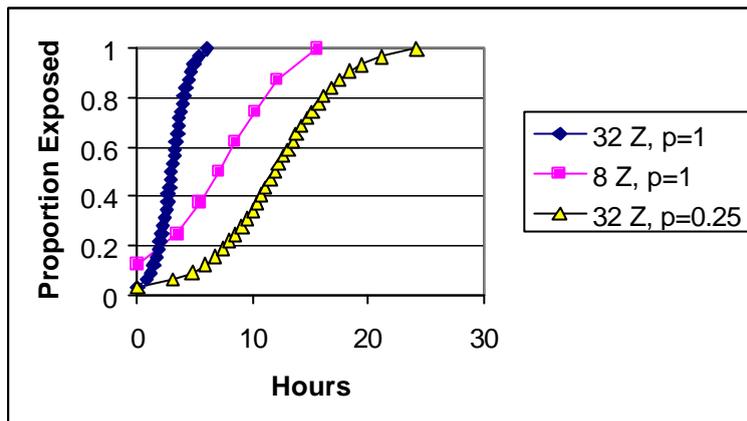
Figure 5.4   Time required for a given proportion of the fish population to be exp osed to the risk of infection (i.e. in schools containing infected individuals). 32 or 8 schools (*Z*) with contact probabilities of 1 or 0.25 d^{-1}.

The rapid mixing of infected and clean schools which occurs in the midpart of the curves (Fig. 5.4) means that the bulk of the mixing of infected and uninfected schools occurs over a relatively short period. Hence the effect of schooling may be to delay the initiation of the epidemic, but it does not dilute its force when it arrives under even moderate rates of mixing. The population even though it is divided into schools is effectively well-mixed for the critical phase of transmission of infection, except at very low rates of interaction or numbers of schools. Pilchard shoals appear to consist of abundant and frequently interacting schools.

5.2.3   Transmission Efficiency and the Spread of Infection

We are interested in how schooling affects transmission at all stages of the epidemic as this develops. To look at this we examine the apparent value of *b* versus *S* for these runs. The apparent value of *b* is the value of *b* calculated from the rate at which infection spreads averaged over the whole shoal's population relative to *S* and *I*, again over the whole shoal.

In the SEIR model we see that initially (when *S* = 1) all *b* values are the same, at the value close to that one would expect from uniformly distributed I (Fig. 5.5). This is because initially *I* is very small and so infection rate is close to maximum. The rate is close to maximum, but not quite there because the initial *I* is not zero, particularly as a proportion of the school. The infection rate rapidly drops off as a large proportion of individuals in the initial school become infected. This decline in infection is counteracted by mixing to other schools, but *b* can remain substantially depressed when contact between schools is limited. In this early phase stochastic influences may be

important. As *S* falls, the values of **b** begin to increase and, at very low S values, **b** is again back to the perfectly mixed value (1000/32 schools = 31.25). At high mixing rates apparent **b** is always close to the value of **b** predicted for a perfectly mixed population. At lower mixing rates, apparent **b** may actually overshoot the predicted uniform population **b** value just before returning to this value. The overshoot occurs because, if contact rate is low, then by the time the epidemic spreads to the last of the schools it has already burnt itself out in some schools which received infection early on. These schools mostly consist of R individuals. As a result *S* and *I* are both relatively concentrated in the schools that received infection later and hence contact rate is higher than expected from averaged population.
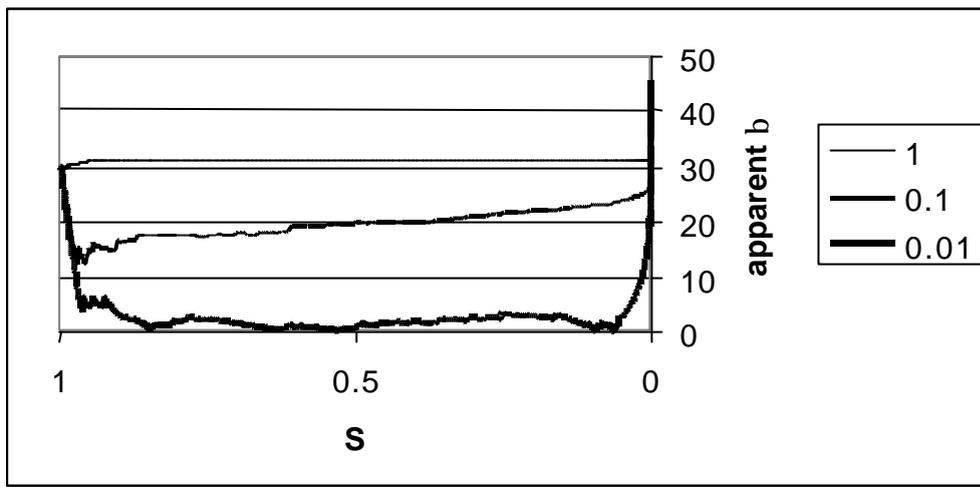
Figure 5.5   SEIR model apparent **b**, the infection rate in the population as a whole, versus the proportion of the total population that are susceptible to infection under three inter-school daily contact probabilities.

We also apply the analysis of apparent **b** versus *S* to the [S][E][I][R] model (Fig. 5.6) obtaining results that are similar in general principles, but different in detail. The model starts off and ends with the uniform effective **b** value. However, rates drop off rapidly, then recover to a fairly constant level, and only at extremely low *S* do they finally recover completely. At very high mixing rates the constant value of apparent **b** reached rapidly is the value expected for uniform population with $1/32^{nd}$ of the transmission rate ($= 31.25$ d^{-1}). At lower school contact rates the intermediate apparent **b** value is proportional to mixing and so is strongly impacted by inter-school mixing. The general sensitivity analysis (Fig. 5.2) indicates that only as p falls below 0.25 d^{-1} (25%) does this parameter have any effect on transmission, so at p = 0.1 d^{-1} there is only a small deviation from the well mixed situation. However, there is a large decline in **b** if mixing is further inhibited. A population whose subgroups interacted at, on average, greater than 10 day intervals would not be considered a coherent shoal.
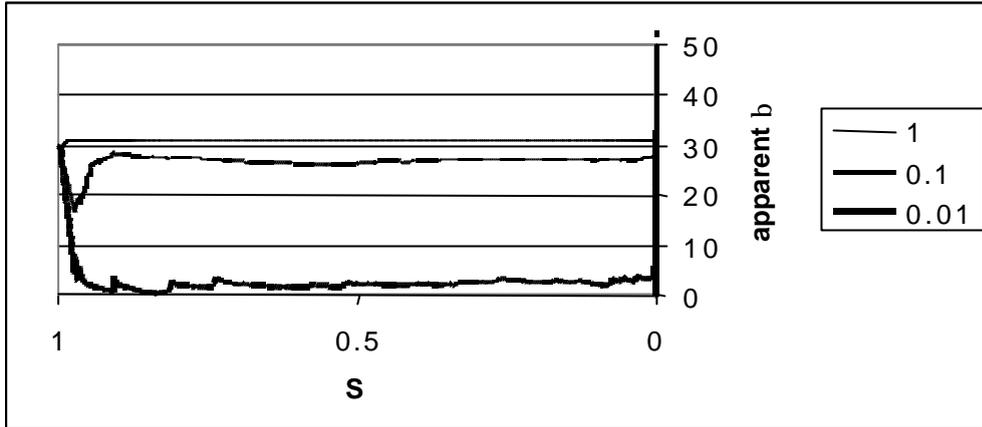
Figure 5.6 [S][E][I][R] model apparent β, the infection rate in the population as a whole, versus the proportion of the total population that are susceptible to infection under three inter-school contact probabilities.

Neither model gives a significant threshold value for a minimum S. Given the very rapid local transmission rate of the virus, the much lower mortality/recovery rate of infected fish a minimal threshold would be expected: $S_t = a/b = 0.008$ or 0.00025 in each school (Anderson and May 1979). The decoupling between infection and the end of that infection, enhanced by the E phase, leads to an overshoot of the threshold so infection does not cease until virtually all susceptible fish have been infected. This overshoot is more extreme under the [S][E][I][R] model.

The critical point about both the SEIR and [S][E][I][R] models is that both initially, when S is large, and finally, when S is small, contact rates are similar to those predicted under uniform population with the within-school transmission rate b_z divided by the number of schools. If mixing within the school is density independent then the patterns in apparent b still apply, it is just that $b = b_z$ when S is close to 1 or 0. The apparent value of b when $S \to 1$ determines speed of transmission of the epidemic front. Suppression of apparent b for intermediate values of S only occurs to a large extent at low levels of interaction.

5.3   Discussion

We have developed a simple dynamic model to explore the effect of the interaction within a shoal of schooling fish. We apply models of the effect on transmission of both the local interactions within the school and of the interaction between the schools of a shoal. Our approach has been to develop a robust model with stochastic interactions which allows us to look at different local model structures and extents of interschool interaction.

The results from this model are highly significant for our understanding of the effect of interaction at local and regional levels on the spread of epidemics and in particular the spread of herpesvirus among pilchards.

Firstly, epidemic wave speeds do not depend upon mixing processes between schools. Epidemic wave speeds are calculated by linearising equations at the point where $S_0 = 1$ (Murray 1993), i.e. at the time when very small numbers of infected individuals are

initially introduced. The initial infection rate is independent of inter-school contact rate (Fig. 5.4), so the speed of the epidemic wave does not depend upon the nature of the interaction between schools.

Secondly, schooling does not provide a refuge for avoidance of infection as the epidemic draws to a close. As S tends to zero, the apparent infection rate increases back up to the uniform populations mixing rate (the overshoot is illuminating of the processes, but does not have much effect on infection). This recovery of the infection rate means that schooling does not provide any refuge for susceptible fish to escape infection. Since apparent b is the same as S tends to 1 and S tends to 0, avoidance of infection by the last clear school is only possible if there is a significant possibility of infection not escaping from the first infected school. This is inconsistent with the easy transmission of the virus to adjacent shoals that the rapid spread of the epidemic shows (Whittington *et al.* 1997).

Small schools could form a refuge, if transmission were school size dependent and the schools were persistent. But this would be balance by higher exposure in larger schools. Variation in school size will increase variation in the rate of spread of the infection, but not alter the epidemic's basic properties. In any case, because b is much larger than a, the schools would have to be very small indeed for threshold to significantly impact transmission

Between these extremes of low initial levels of infection and high late-stage infection, schooling may potentially weaken viral transmission at intermediate levels of infection. This weakening of transmission could result in a less intense but more prolonged epidemic. However, when intermediate numbers of schools contain infected fish, the rate of contact between infected and uninfected schools is at its peak. This means that mixing of infected individuals into the population is highly efficient and hence any suppression of transmission is strongly mitigated, unless b is very large and c is very small. For the pilchard herpesvirus b is very large (Murray 1999), but there is still a lack of dependence on c and y. This indicates that for other diseases, with lower transmission rates, the effect on transmission of subdivision of local populations is likely to be weak if these interact on reasonably frequent time scales.

Schooling does tend to make disease transmission less population density dependent. The individual schools may be of a similar size even if the total population changes. If so, transmission rates may not change with total population, and instead transmission may depend upon the proportion of hosts infected, rather than their numbers. Even if school size does change with shoal size, it is possible that local transmission is independent of the school size anyway, this too would mean density dependent shoal-level transmission. Density independent transmission would mean that the speed of long-distance propagation of epidemic waves would be independent of apparent population density at the larger spatial scale. Explicit modelling of schools is not required to reproduce this effect of schooling.

Schooling may affect the effective value of viral transmission b as a function of the actual local transmission rate b_z because their values are related by the number of schools in the shoal. However, we estimate β directly from the epidemic's observed rate of spread and so it is the value of b_z that we are uncertain of owing to our lack of

knowledge of the school structure. If we dispense with modelling the school-level structure, uncertainty in this parameter is not important.

The initial input of infected individuals is in the form of *I*. If these individuals were input in their *E* phase of infection then mixing into other schools would occur before they became a source of new infections. This pre-infectious mixing would further weaken the effect of schooling on transmission.

These conclusions do not appear to be dependent upon the structure of the model adopted. Details may be different owing to the role of the *E* phase and fixed period length versus continuous turnover in delaying feedback between the occurrence of one infection and the initiation of further infection from this infected individual. However the generally limited role of schooling is apparent in all model forms for realistic school interaction rates.

We can think of models under which the interaction among schools is nonrandom, effectively adding another layer of population organisation to the model. Juvenile pilchards school separately from adults, and this may explain an observed relatively low vulnerability in this age group (Fletcher et al 1997). Adult pilchards do form separate breeding populations, but these seem to intermingle spatially. There is no evidence that the adult population within a region is subdivided into mutually exclusive groups. Relatively low levels of mortality (10-15%) recorded for 1995 in Western Australia (Fletcher *et al.* 1997) appear to have been replaced by very high levels of mortality (up to 90%) in 1999. Unless the mixing behaviour within the shoals has changed substantially, this high mortality would not support the concept of internally separate populations.

Our overall conclusion is that, in the case of the pilchard epidemic, we can dispense with the direct modelling of schooling behaviour. Transmission rate at the shoal and larger levels is likely to be independent of the shoal's size. Since we lack adequate data to model schools and their interactions in detail, this lack of dependence greatly reduces uncertainty in our model results.

6   Modelling Large Scale Dispersion in a Spatially Structured Dynamic Model

The 1995 and 1998/9 pilchard herpesvirus epidemics spread along some 5000 km of coastline. The spread of infection at this scale cannot be considered as a single well-mixed population and so an explicit large-scale spatial structure must be incorporated into the model.

6.1   The Models

We therefore developed 2 basic dynamic model structures - one for the SEIR model and the other for the [S][E][I][R] version. Other structures have also been experimented with, including a model with a fixed length latent period but with continuous turnover of infectious phase. This model is used to derive an analytical solution of the wave speed (next chapter), which we are able to apply to it and to the [S][E][I][R] model to determine the wave's parameter sensitivity.

The basic equations of these models are those described before, with the addition of diffusive transport.

Continuous Turnover Model

$$\partial S/\partial t = -\boldsymbol{b}IS + D\,\partial^2 S/\partial x^2 \tag{6.1}$$

$$\partial E/\partial t = \boldsymbol{b}IS - \boldsymbol{s}E + D\,\partial^2 E/\partial x^2 \tag{6.2}$$

$$\partial I/\partial t = \boldsymbol{s}E - \boldsymbol{a}I + D\,\partial^2 I/\partial x^2 \tag{6.3}$$

$$\partial R/\partial t = p\boldsymbol{a}I + D\,\partial^2 R/\partial x^2 \tag{6.4}$$

$$\partial D/\partial t = (1-p)\boldsymbol{a}I \tag{6.5}$$

Fixed latent period

$$\partial S/\partial t = -SI\boldsymbol{b} + D\,\partial^2 S/\partial x^2 \tag{6.6}$$

$$\partial E/\partial t = SI\boldsymbol{b} - S_{t-x}I_{t-x}\boldsymbol{b} \qquad + D\,\partial^2 E/\partial x^2 \tag{6.7}$$

$$\partial I/\partial t = S_{t-x}I_{t-x}\boldsymbol{b} - \boldsymbol{a}I + D\,\partial^2 I/\partial x^2 \tag{6.8}$$

$$\partial R/\partial t = p\boldsymbol{a}I + D\,\partial^2 R/\partial x^2 \tag{6.9}$$

$$\partial D/\partial t = (1-p)\boldsymbol{a}I \tag{6.10}$$

Fixed latent and infection, the [S][E][I][R] model, periods

$$\partial S/\partial t = -SI\boldsymbol{b} + D\,\partial^2 S/\partial x^2 \tag{6.11}$$

$$\partial E/\partial t = SI\boldsymbol{b} - S_{t-x}I_{t-x}\boldsymbol{b} + D\,\partial^2 E/\partial x^2 \tag{6.12}$$

$$\partial I/\partial t = S_{t-x}I_{t-x}\boldsymbol{b} - S_{t-y}I_{t-y}\boldsymbol{b} + D\,\partial^2 I/\partial x^2 \tag{6.13}$$

$$\partial R/\partial t = pS_{t-y}I_{t-y}\boldsymbol{b} + D\,\partial^2 R/\partial x^2 \tag{6.14}$$

$$\partial D/\partial t = (1-p)S_{t-y}I_{t-y}\boldsymbol{b} \tag{6.15}$$

Analytical solutions allow the speed at which the epidemic expands to be evaluated; this greatly speeds model analysis. However they do not describe the dynamical nature of the epidemic's spread, particularly at its origin. They cannot be used to describe non-linear features of the epidemic and must be re-evaluated for every different model structure.

6.2 Model Implementation

The models have to be implemented as a computer program before it can be fully used. Programming is a complex process involving a large range of implementation decisions from basic design strategy to output formats (see Murray *et al.* in press). We will not describe the coding process in detail, but we will describe some of the major strategies and problems involved in programming and describe the use of the program.

6.2.1 Program Design

The pilchard mortality model has been coded in Java. The program used is Object Orientated with five separate files, which contain classes describing: the main program plus output routines, parameter values, the fish population structure, records of model fluxes and the output file stream (Fig. 6.1). These classes hold major data objects and associate processing routines.
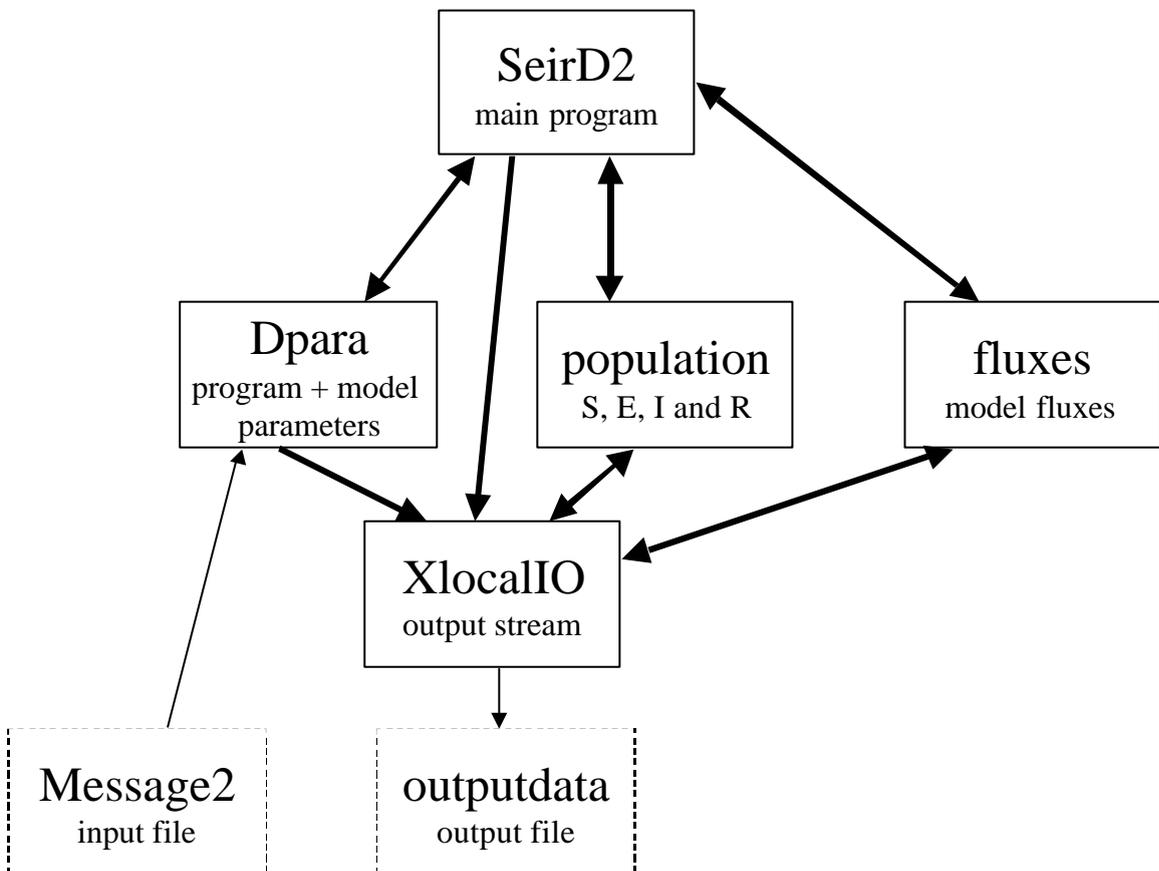
Figure 6.1 Basic class structure of the pilchard epidemic model showing input and output files.

The main program SeirD2 creates instances of the other four classes and then initialises their values. It then inserts an initial infection at a spatial point in the population packages. The program then calls an internal routine which calculates model process for a day, this routine being called as many times as the days model is to run for.

For each daily time step the model routine calls a routine handling local processes in each spatial box. It then calls a routine within the population class which handles diffusion between the boxes. If an update stage is completed the model updates the sub-

stages of the *E* and *I* variables (see next section). Finally, it selects between 5 output routines, if conditions are appropriate. These routines are held in XlocalIO and their functioning is described in subsection C.

The Dpara class holds all the parameter values. It handles their input from the parameter file. Time sensitive rates parameters are adjusted to fit the model time step and the diffusion rate is also adjusted to fit the spatial structure adopted. This internal conversion enables standard parameter files with fixed units of days and km to be used. Parameter values are recorded via XlocalIO in the output file. Numerical issues are discussed in the next subsection.

The population class holds the spatial and infection stage (S, E, I or R) and substage structure of the model. It handles the updating of the substages and diffusion between the spatial boxes and is adjusted in response to local fluxes calculated in SeirD2. It also contains a routine to find the size and location of the largest number of infected individuals, this is used in the output of epidemic wave location with time, allowing calculation of wave speeds.

The detailed structure of the population *E* and *I* sub-stages is hidden from outside routines. This means the population class can be switched with those holding other population structures in the most straightforward possible manner.

The flux packages stores the model fluxes: infection, onset of infectious phase (*E* to *I*) and recovery plus mortality. Data is stored on both the instantaneous (as rates per day) and summed total values. This data may be used by program output routines.

Output is to a file handled in class XlocalIO, which is initialised to the file "outputdata.txt" by the main routine in class SeirD2. This class records model parameters on input. It also records outputs as selected by the SeirD2 class, reaching into the data classes population or fluxes to obtain the values for output.

6.2.2   Numerical Issues

The models are solved on a fixed grid of time and space using simple Eulerian integration methods. These temporal and spatial grids are set up at model initialisation using parameters. The model's parameters are in units of days, km and normalised fish population density. Rates are converted within the program of the model to rates per time-step. Diffusion is divided by the time step size and the square of the space step size to create a proportional exchange between adjacent boxes.

The *E* and *I* variables are subdivided into sub-phases. The fixed period length model is required to keep track of when infection occurred, so it can update phases at the appropriate time. This means keeping separate variables containing the individuals that received infection at a given time. If a new variable were created for each model time-step this could lead to very large numbers of variables, leading to inefficient computation. To avoid this problem, the model is implemented using the same approach to time stepping as was used in the schooling model (chapter 5). The phases of infection *E* and *I* are subdivided into sub-phases which are N time-steps long. Only after N time-steps are the phases updated and infection is transferred among the subphases. Interaction between the first or last sub-phases and other model phases are

handled at the level of the model's fine time steps. These interactions with outer sub-phases are infection from S to $E(1)$, onset of infectivity from $E(\text{last})$ to $I(1)$, and the removal phase $I(\text{last})$ to R or D.

A potential numerical problem could occur if the number of time steps per day were such that there was not an exact integer number per model update time. On initial input of parameters, the model checks that these values are consistent and, if not, alters the number of time-steps to a value such that there are an integer number per update time. If the number of time-steps per day is less than the number of phase updates, the model adjust the time step length so that it equals that of phase updates.

A second numerical problem may emerge if the spatial scale used is too fine relative to the diffusion coefficient and time scales. In this case the diffusive flux can become large and ultimately it may lead to values > 0.5, which results in diffusion more than equilibrating the concentration gradient, analogous to water flowing up hill. If the flux value exceeds 1 it can lead to negative quantities being produced. The program detects this situation and gives a warning message and aborts the run if the flux exceeds 0.25. The flux varies with the inverse square of the spatial scale and so when this is reduced flux may increase rapidly. Excess flux can be avoided by decreasing the model time step or increasing the spatial scale. Since there are two option, the computer aborts the run allowing the user to select which to adjust.

Another numerical issue related to the spatial scale is that the initial dose of infection is described as a concentration at a particular location. If the spatial scale is adjusted the initial dose is also adjusted. This does not affect the ultimate development of infection, but it may delay its initial development.

The use of a fixed time scale is problematic but probably unavoidable. Because of the close link between infection processes and diffusion, particularly once the wave starts moving, we need to use the same time step for all boxes. Experimentally, we have found the model can be numerically sensitive to box sizes of > 4 km, which is not surprising considering wave speeds are of the order of 10 km d in 1998/9. This means we use a spatial scale of 2 km. As discussed earlier this use of a relatively fine spatial structure requires small time steps in order to avoid numerical problems with diffusion. The model is not sensitive to changes in sub-phases lengths of around 0.2 day or less, we use 0.1 day as standard.

Results obtained from the model agree strongly with analytical predictions (Chapter 7 and 8) and therefore are not subject to numerical errors.

6.2.3   Using the Model

The model is quite simple to operate it has only one input file and produces output to an output file or that is viewed on the screen. Shell scripts have been set up which select different input files and directing the output to a common file. This allows multiple model runs.

The input file contains a column of input numbers and a column of descriptive text. There are 15 input parameters that control the model and the program's operation. These parameters are the infection rate, the diffusion coefficient and a switch describing

linear (standard) or quadratic (see chapter 11) infection. The pilchards' spatial range in km and the spatial scale are then input. From this the model derives a spatial structure. The lengths of the *I* (infectious) and *E* (latent) periods, in days, together with an update resolution (per day) are used to calculate the numbers of *I* and *E* sub-phases in the infection periods. There then follows the initial dose of infected individuals, which is $<=1$, and the site at which infection first occurs. This is usually box 0, but for investigation of the initial stages of the epidemic a central box should be used. There then follow some program control parameter, the length of the run (in days) the time steps per day, the interval between I/O events, a parameter used to define the limits of I/O option 3, and the selection of I/O options. These will be detailed shortly.

Rate parameters are adjusted to the model time step on input. A diffusive flux is calculated from the diffusion coefficient on the basis of the inverses of the time step and the square of the spatial scale. If sub-phase update resolution time-step is not an integer number of the main model time step size then this latter is adjusted. Problems with diffusion are also detected. The details are as described in the previous sub-section.

The model has 5 output options. The first four are exercised at an interval determined by the output resolution parameter. The first is simply a dump of all the S, E, I and R values; *E* and *I* being the sums of their sub-phases. The second is an output of the current wave location, as determined by the site with the maximum value of the sum of local *I*. The third option is the size and location of the wave of mortality, with sensitivity limits describing the spatial envelope within which mortality rate exceeds a specified level. The fourth output option is the wave shape which is dumped at the I/O resolution and at intervals of 0, 0.25, 0.5 and 0.75 along the spatial scale. The fifth output option is spatial, not temporal and is not controlled by the I/O resolution parameter. This option detects the time at which the wave of *I* reaches target milestones that are spaced at intervals 0.1 of the spatial resolution. This is used for evaluating the epidemic wave's speed.

6.3   Analytical Solution of the Model's Wave Speeds

The results of the model depend upon the parameter values that it is given. We investigate the model's dependence upon parameters by means of analytical solutions which can give us strong insights into the basic behaviour of the model (Murray and Parslow 1999).

Epidemics travel as a wave. The epidemic stars at a source location and spreads out, but behind this front the epidemic dies down and may die out. In certain simple models the epidemic wave has a surprisingly simple dependence upon a few parameters. These include local transmission terms and also long distance dispersal (*D*). Dispersal depends upon the concentration gradient and this dispersal term, for example the dispersal of infected individuals in 1-dimension depends on $D \partial I / \partial x$.

Epidemic wave speed speeds are found by linearising the differential equations around the origin, where *I* tends to zero (Murray 1993), i.e. at the point when the first few infected individuals are introduced. We will not detail the derivation of these wave speeds, we have discussed them in more detail elsewhere (Murray 1999).

_____

In a simple SIR (susceptible infected, removed) model described by Murray (1993) to look at the spread of the Black Death, the following (1-dimensional) velocity of the epidemic is derived:

$$V = 2\ddot{0}(bS_0D)\ddot{0}[1 - a/bS_0] \tag{6.16}$$

In this case α is the mortality/recovery rate of infected individuals.

For a more complex model presented by Yachi *et al.* (1989), to describe (one-dimensional) fox rabies and involving a latent phase, the following velocity speed was derived.

$$V = \ddot{0}(2D\{\ddot{0}[(s - a)^2 + 4sbK)] - (s + a + 2a)\}) \tag{6.17}$$

In this case *s* is the rate at which animals with latent infection develop into the full blown infectious state, K is population maximum, equivalent to S_0, and a is the non-disease mortality. The 1-dimensional model is particularly appropriate to pilchards, which inhabit a strip along the relatively narrow Australian continental shelf (Fletcher *et al.* 1997). There are some simplifications that can be made for the fish disease. If *s* and *a* are small, as they are in fast developing disease, the $(s - a)^2$ is very small, particularly if the two are similar. The value of a is also small relative to *a*. Allowing for these corrections leaves the simplified equation:

$$V = \ddot{0}(2D\{\ddot{0}[4sbS_0)] - (s + a)\}) \tag{6.18}$$

As just discussed, the rate of transmission, per infected fish, is at its highest when the infection is first introduced. This means that transmission rate is high when I tends to 0 and hence the linear approximations of travelling wave solutions apply.
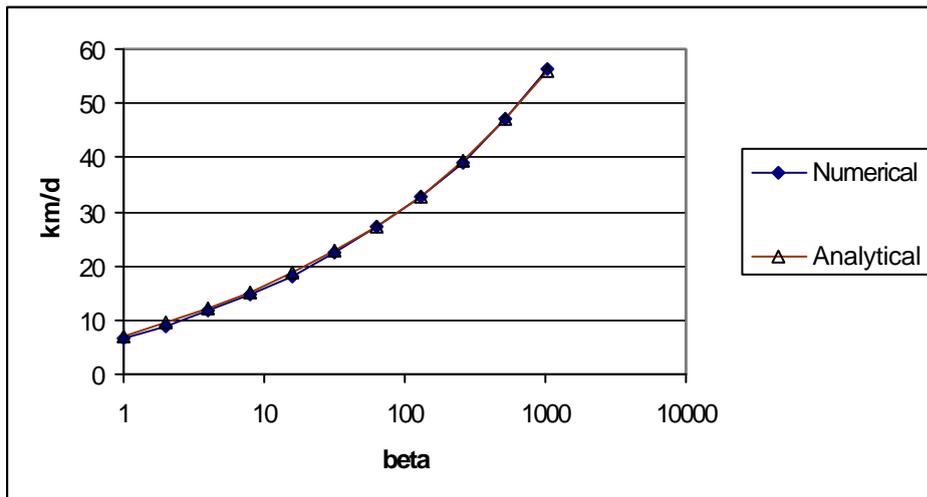
Figure 6.2   The speed of the wave front calculated from the modified version of Yachi *et al.* (1986) model and the wave speed as determined by the numerical SEIR model.

Experimentally, we find that the modified Yachi formula provides a very good description of the numerically generated wave speeds (Fig. 6.2).

These analytical solutions allow us to rapidly assess the sensitivity of the model's wave speed to parameterisation and so to concentrate upon more detailed analysis of other features such as the duration of mortality at a given point.

In the next chapter a method is developed which allows solutions of the fixed latent period length model to be determined analytically. The solution of the model is very insensitive to the turnover of the infectious phase. The fixed latent and fixed infectious period lengths version of the model turns out to have very similar solutions, we are thus able to use the analytical method as a tool to investigate both models in the relevant region of parameter space.

7 A Tractable Deterministic Multiple Diffusion Coefficient Model With Latent Period For Virus Epidemics In Pilchards

7.1 Introduction

Having demonstrated by simulation work that the existence of a latent period implies that the effect of schooling on the spread of disease may be neglected, we exhibit in this chapter a tractable deterministic model with a fixed length latent period and different diffusion coefficients for healthy fish as compared to infected fish and show how we may obtain analytic formulae for both the population threshold for the onset of an epidemic and the speed of the resulting infection front.

7.2 The Model

Let us assume that the virus has a latent period and let

$$S = S(x,t), E = E(x,t), I = I(x,t), R = R(x,t), M = M(x,t)$$

be the densities of susceptibles, latent, infectives, recovered and dead, respectively. If the latent period is a constant duration b for every infected fish then we obtain a system of equations thus

$$\frac{\partial S}{\partial t}(x,t) = -\boldsymbol{b}S(x,t)I(x,t) + D\frac{\partial^2 S}{\partial x^2}(x,t) \tag{7.1}$$

$$\frac{\partial E}{\partial t}(x,t) = \boldsymbol{b}S(x,t)I(x,t) - \boldsymbol{b}S(x,t-b)I(x,t-b) + B\frac{\partial^2 E}{\partial x^2}(x,t) \tag{7.2}$$

$$\frac{\partial I}{\partial t}(x,t) = \boldsymbol{b}S(x,t-b)I(x,t-b) - (\boldsymbol{a}+\boldsymbol{m})I(x,t) + B\frac{\partial^2 I}{\partial x^2}(x,t) \tag{7.3}$$

$$\frac{\partial R}{\partial t}(x,t) = \boldsymbol{a}I(x,t) + D\frac{\partial^2 R}{\partial x^2}(x,t) \tag{7.4}$$

$$\frac{\partial M}{\partial t}(x,t) = \boldsymbol{m}I(x,t) \tag{7.5}$$

subject to the initial conditions

$$\begin{cases} S(x,0) = S_0 > 0 \; \textit{for all } x \\ E(x,0) = I(x,0) = R(x,0) = M(x,0) = 0 \; \textit{for all } x \end{cases} \tag{7.6}$$

where

$\boldsymbol{b}$ = transmission rate,

$\boldsymbol{a}$ = recovery rate for infectives,

$\boldsymbol{m}$ = death rate for infectives,

B, D are diffusion coefficients. Here we have allowed for the possibility that infected fish may, due to some panic or terror reaction to the virus, dart about more quickly than do normal healthy fish, or even move more slowly, but we assume that upon recovery they return to normal behaviour. However, in order to get the solution set out below, we must assume that latent hosts behave similarly to infectives. We assume also that schooling plays no significant part affecting the speed of progress of the disease through the inhabited space and may be neglected.

Unfortunately, the above system of differentio-functional equations is quite beyond our powers of analysis in the form given. However, if we modify the postulate of a fixed latent period to one in which it shows random variation then we may find the resulting system of differential equations tractable.

Replacing equation (7.2) for the latent phase by a differential equation with input to the phase at a rate $\boldsymbol{b}SI$ and transference to the infective phase at a rate $\boldsymbol{s}E$, say, gives the deterministic equivalent of a model in which the time spent in the latent phase is a random variable with a negative exponential distribution with parameter $\boldsymbol{s}$. This then becomes tractable but at the cost of realism because the negative exponential distribution favours small values of the variate far too much to accord with the reality of a latent period which is nearly constant.

We will instead reformulate the model with the latent phase represented *artificially* as a concatenation of distinct though similar subphases. The model then becomes the deterministic equivalent of one in which the latent period is a random variable with reasonably realistic distribution. Ultimately, in fact, we make its variance extremely small while keeping its mean fixed so as to obtain, for all practical purposes, behaviour indistinguishable from that of the above model.

Let us suppose that the density of latent hosts decomposes thus

$$E(x,t) = E_1(x,t) + E_2(x,t) + ... + E_n(x,t). \tag{7.7}$$

and replace the system (7.1)-(7.6) with

$$\frac{\partial S}{\partial t} = -bSI + D\frac{\partial^2 S}{\partial x^2} \tag{7.8}$$

$$\frac{\partial E_1}{\partial t} = bSI - sE_1 + B\frac{\partial^2 E_1}{\partial x^2} \tag{7.9}$$

$$\frac{\partial E_i}{\partial t} = sE_{i-1} - sE_i + B\frac{\partial^2 E_i}{\partial x^2} , i = 2,...,n \tag{7.10}$$

$$\frac{\partial I}{\partial t} = sE_n - (a+m)I + B\frac{\partial^2 I}{\partial x^2} \tag{7.11}$$

$$\frac{\partial R}{\partial t} = aI + D\frac{\partial^2 R}{\partial x^2} \tag{7.12}$$

$$\frac{\partial M}{\partial t} = mI \tag{7.13}$$

subject to the initial conditions

$$\begin{cases} S(x,0) = S_0 > 0 \ for\ all\ x \\ E(x,0) = I(x,0) = R(x,0) = M(x,0) = 0 \ for\ all\ x \end{cases} \tag{7.14}$$

The system (7.7)-(7.14) is the deterministic equivalent of a model in which the latent period is random with distribution that of the sum of n independent variates each having a negative exponential distribution with parameter s. In other words, it is as if the latent period has a Gamma distribution with mean n/s and variance n/s^2. See, for example, Feller (1965, pp 8-10).

We *do not* postulate that the latent phase consists *physically* of a concatenation of distinct though similar subphases. This is merely a mathematical device to give the latent phase's duration a realistic distribution and thus achieve both realism and tractability.

7.3   Travelling Wave Solutions

Introducing a variable $z = x - ct$ where c is a constant velocity, we seek travelling wave-form solutions of the form

$$S = S(z), E = E(z), E_i = E_i(z), I = I(z), R = R(z), M = M(z)$$

whereupon (7.8) – (7.14) transform to the ordinary system

$$-cS' = -bSI + DS''$$ (7.15)

$$-cE_1' = bSI - sE_1 + BE_1''$$ (7.16)

$$-cE_i' = sE_{i-1} - sE_i + BE_i'' \, , i = 2,...,n$$ (7.17)

$$-cI' = sE_n - (a + m)I + BI''$$ (7.18)

$$-cR' = aI + DR''$$ (7.19)

$$-cM' = mI$$ (7.20)

subject to the conditions

$$\begin{cases} S(z) \to S_0 \; as \, z \to \infty \\ E(z) \to 0, E_i(z) \to 0, I(z) \to 0, R(z) \to 0, M(z) \to 0 \; as \, z \to \pm\infty \end{cases}.$$

Now, making E_{i-1} the subject, we can represent (7.17) as

$$E_{i-1} = D_1 E_i$$ (7.21)

where D_1 is a linear differential operator with constant coefficients. Similarly, making E_n the subject, we can represent (7.18) as

$$E_n = D_2 I$$ (7.22)

where D_2 is a linear differential operator with constant coefficients.

Also, as $z \to \infty$, we have $bS \to bS_0$ so, making I the subject, we can represent (7.16), asymptotically as $z \to \infty$, as

$$I \approx D_3 E_1$$ (7.23)

where D_3 is also a linear differential operator with constant coefficients.

Now, appealing to the associativity of linear differential operators, we find recursively from equation (7.21)

$$E_1 = D_1 E_2 = D_1^2 E_3 = D_1^{i-2} E_{i-1} = D_1^{n-1} E_n \; , i = 2,...,n \, .$$ (7.24)

Then, taking the first and last members of (7.24) and substituting first for E_n from (7.22) and then for I from (7.23) we get

$$E_1 = D_1^{n-1} D_2 I$$
$$\approx D_1^{n-1} D_2 D_3 E_1 . \tag{7.25}$$

Similarly, beginning with (7.23) and substituting for E_1 from (7.24)

$$I \approx D_3 E_1$$
$$\approx D_3 D_1^{n-1} E_n$$
$$\approx D_3 D_1^{n-1} D_2 I . \tag{7.26}$$

Similarly from (7.22)

$$E_n = D_2 I$$
$$\approx D_2 D_3 E_1$$
$$\approx D_2 D_3 D_1^{n-1} E_n . \tag{7.27}$$

And, finally, from (7.21)

$$E_{i-1} = D_1 E_i$$
$$= D_1^{n-i+1} E_n$$
$$= D_1^{n-i+1} D_2 I$$
$$\approx D_1^{n-i+1} D_2 D_3 E_1$$
$$= D_1^{n-i+1} D_2 D_3 D_1^{i-2} E_{i-1}$$
$$= D_1^{n-1} D_2 D_3 E_{i-1} . \tag{7.28}$$

Looking now at equations (7.25)-(7.28), taking the first and the last member in each case, and comparing the equations using the commutativity of differential operators, we see that I and all of the E_i satisfy, asymptotically as $z \to \infty$ one and the same linear differential equation with constant coefficients. Therefore, recalling that $I \to 0, E_i \to 0$ as $z \to \infty$ for $i = 1,...,n$, we see that those variables must each be asymptotic to a multiple of one and the same exponential function corresponding to the real negative eigenvalue closest to zero. Hence we can write

$$I \approx g_i E_i , i = 1,...,n \tag{7.29}$$

for some constants $g_i > 0$, $i = 1,...,n$ which are now to be determined.

We deduce from (7.29) that

$$E_{i-1} \approx \frac{g_i}{g_{i-1}} E_i , i = 2,...,n . \tag{7.30}$$

Substituting into (7.16), (7.17), (7.18) from (7.29), (7.30) and rearranging the terms we get

_____

$$BE_1{}''+cE_1{}'+(bS_0g_1 - s)E_1 \approx 0 \tag{7.31}$$

$$BE_i{}''+cE_i{}'+s(\frac{g_i}{g_{i-1}} - 1)E_i \approx 0 \, , i = 2,...,n \tag{7.32}$$

$$BI''+cI'+[\frac{s}{g_n} - (a + m)]I \approx 0 \, , \tag{7.33}$$

respectively, which three equations must share at least one real negative eigenvalue. Their discriminants must therefore be equal and so we must have

$$bS_0g_1 - s = s(\frac{g_i}{g_{i-1}} - 1) = \frac{s}{g_n} - (a + m) \, , i = 2,...,n \, . \tag{7.34}$$

This immediately means that

$$\frac{g_2}{g_1} = \frac{g_3}{g_2} = ... = \frac{g_n}{g_{n-1}} = r \, , \tag{7.35}$$

say, for some $r > 0$. So we may write

$$g_i = r^{i-1}g_1 \tag{7.36}$$

and, in particular,

$$g_n = r^{n-1}g_1. \tag{7.37}$$

But, substituting from (7.35) into (7.34) now gives

$$bS_0g_1 - s = s(r - 1) \tag{7.38}$$

which reduces to

$$g_1 = \frac{s}{bS_0}r \, . \tag{7.39}$$

Taking just the first and last members of (7.34) gives

$$bS_0g_1 - s = \frac{s}{g_n} - (a + m) \tag{7.40}$$

and, substituting into that from (7.37), (7.38), (7.39) gives

$$s(r - 1) = \frac{bS_0}{r^n} - (a + m) \tag{7.41}$$

or, more usefully,

$$r^{n+1} - [1 - \frac{(a+m)}{s}] r^n = \frac{bS_0}{s} . \tag{7.42}$$

For reasons to become clear later s will be sufficiently large that the quantity in square brackets will be positive.

According to the principle established by Kolmogorov et al (1937) the system can represent an epidemic if and only if the discriminants of equations (7.31)-(7.33) can, as c is varied, possibly become negative so that the equations admit some oscillating solutions, requiring simply that the members of (7.34) be positive. Fisher (1937) showed, by considering the random motion of individuals near the wavefront, that in such a case waveform solutions will travel with a speed c chosen so as to render those discriminants zero and thus be given by

$$c = 2B^{\frac{1}{2}} \left(\frac{bS_0}{r^n} - (a+m) \right)^{\frac{1}{2}} = 2B^{\frac{1}{2}} s^{\frac{1}{2}} (r-1)^{\frac{1}{2}} . \tag{7.43}$$

Clearly then, the existence of an epidemic requires that

$$1 < r < (\frac{bS_0}{a+m})^{\frac{1}{n}} \tag{7.44}$$

which in turn requires that S_0 satisfy the threshold criterion

$$S_0 > \frac{a+m}{b} . \tag{7.45}$$

Recall now that the model is the deterministic equivalent of a model in which the latent period is a random variable with a Gamma type probability density, actually given specifically by

$$g(t) = s \frac{(st)^{n-1}}{(n-1)!} e^{-st} , \tag{7.46}$$

viz e.g. Feller (1965 pp 8-10), with mean value n/s and variance n/s^2 .

To approximate to the model expressed in equations (7.1)-(7.6) we assign to the latent period of this second model a mean value of b and a variance v, say, the latter having some quite small value.

Thus, setting

$$\frac{n}{s} = b \tag{7.47}$$

$$\frac{n}{s^2} = v \tag{7.48}$$

we can solve to obtain

$$s = \frac{b}{v} \tag{7.49}$$

$$n = \frac{b^2}{v}. \tag{7.50}$$

Substituting in (7.42) for s, n from (7.49), (7.50) we obtain

$$r^{1+\frac{b^2}{v}} - [1 - \frac{v(a+m)}{b}]r^{\frac{b^2}{v}} = \frac{bS_0 v}{b}. \tag{7.51}$$

Thus, from (7.43), we can say that if the latent period is a Gamma variate with mean b and variance v then the speed of waveform solutions will be

$$c = 2\left(\frac{Bb(r-1)}{v}\right)^{\frac{1}{2}} \tag{7.52}$$

where r is the unique root of (7.51).

To use Newton's method to solve (7.51) we let, say,

$$f(r) = r^{1+\frac{b^2}{v}} - [1 - \frac{v(a+m)}{b}]r^{\frac{b^2}{v}} - \frac{bS_0 v}{b} \tag{7.53}$$

from which

$$f'(r) = (1 + \frac{b^2}{v})r^{\frac{b^2}{v}} - \frac{b^2}{v}[1 - \frac{v(a+m)}{b}]r^{\frac{b^2}{v}-1} \tag{7.54}$$

and, taking $r = 1$ as an initial estimate, we successively replace r by $r - \frac{f(r)}{f'(r)}$ until the process converges. Because a small percentage error in the value of r leads to a much larger percentage error in the value of c it is necessary to compute the former to very high accuracy.

By arbitrarily choosing the variance v to be quite small we may obtain the front speed for a system which, for all practical purposes, is indistinguishable from the system described in (7.1)-(7.6). We verify this solution in the next chapter with respect to the numerical model.

8   Parameter Sensitivities of the Speeds and Duration of Model Mortality Waves

Perhaps the single most significant model outcome is the speed of the wave generated from a model run. This is a single clear result which can be tested against observations. The wave's speed can be found numerically or by the analytical solution methods described earlier in chapters 6 and 7.

Observed values of the wave-speed were discussed earlier (chapter 3). These varied substantially between eastern and western bound waves in 1995, between the two epidemics and probably between the two waves of the 1998/9 epidemic. Maximum sustained speed was about 40 km d^{-1}, while the minimum was about 10 km d^{-1}. We also consider the intermediate speed of 20 km d^{-1} for analysis as this is close to the speed of the westbound 1995 wave and of the eastbound 1998 wave. Analysis of the parameter sensitivities indicated by the models will give us insight into the factors controlling the variation in this speed.

8.1   Wave Speed

We earlier derived an analytical solution of the continuous turnover model based on work by Yachi *et al.* (1989)

$$V = \sqrt{(2D\{\sqrt{[4sbS_0]} - (s + a)\})} \tag{8.1}$$

As we showed earlier, this formula gives a very good description of the wave's speed as generated numerically in this model.

We thus are able to see exactly what parameters this model's predicted wave speed depends upon. Essentially it depends upon the square root of D, and the fourth roots of bS_0 and s the rates of infection of susceptible and of the onset of the infectious period among infected individuals. This indicates that inclusion of the latent period gives a much lower sensitivity to transmission rate and population density than in simple SIR models.

In the previous chapter we derived an analysis method which allows rapid evaluation of the wave speed generated by the model version containing a fixed latent period length. In this chapter we use this method to show how the wave speed depends upon parameter values. We then compare the results obtained by the analytical method to those obtained numerically to analyse models with a fixed latent and infectious period lengths and show that the analysis works well for the parameter ranges appropriate to the pilchard epidemic.

In chapter 3 we showed that the epidemic wave's observed speed varies from about 10 to 40 km d^{-1}. We wish to find an appropriate parameter space for waves with velocities in this range based on the three parameters singled out above. The analytical solution depends only upon the latent period length, b, the rate of turnover of infectious individuals, a, infection rate b and susceptible population S_0 and upon diffusion.

The wave velocity is largely independent of the rate of turnover of infected individuals (mortality or recovery). We used the analytical solution to find the effect of varying a + m from 0.125 to 0.5 d^{-1} that is an infective period of 8 to 2 days, which is the extremes

of what might be consistent with the observed timing of lesion formation. We found the wave speed varied from 31.8 to 31.1, about 2%. Effects of changes in these parameters become larger for small values of b, but at such small values of b produce unrealistic local patterns of mortality (see 8.2).

The epidemic wave's development is independent of the fate of fish post infection. Whether infected fish eventually recover or die is unimportant at this stage, although this of course determines the longer term impact. We therefore set p equal to 0, so that all infected fish die. This means model mortality results presented here describe mortality not as a fraction of population but of total mortality. In terms of population, the mortality must be multiplied by p, which lies between 0.6 and 0.15.

Because the wave speed shows little variation with the parameterisation of the turnover rate of infected individuals it may also be independent of the formulation of that turnover. Since we are also interested in models with fixed infection period length, we have also tested the wave speeds generated from that model against the analytical method in the hope that we will be able to use it to analyses this model. As we show in the next three figures the analytical solution does indeed turn out to describe the fixed infection period length model very well although it was not developed for this version of the model.

As demonstrated in the previous chapter, the wave speed depends only upon the rate of diffusion of infected individuals, not uninfected ones. We confirmed this in the numerical model by turning off diffusion in S and R fish. There was, as predicted, no change in the speed of propagation of the epidemic front. However for this analysis we use a single diffusion coefficient, since behaviour of uninfected fish has no effect on the epidemic wave's properties we do not need to consider these parameters separately and lack the data to do so.

We use a model population that is normalised to the average initial population N_0 $(N_0 = S_0 = 1)$ and also normalise $\boldsymbol{b}$ to the average population density, so these two are essentially a combined parameter. We have no means of evaluating b independently, and thus must evaluate it for current population. Although variation in the population may affect the wave, we do not need to explicitly determine the average population.

Thus the critical parameters to which epidemic wave speed is sensitive are D, $\boldsymbol{b}$ and b. Using the analytical method we find that the parameter values $D = B = 200$ km^2 d^{-1}, $\boldsymbol{b} = 200$ d^{-1}, and $b = 4$ d and $\boldsymbol{a} + \boldsymbol{m} = 0.25$ d^{-1} gives a wave speed of 31.5 km d^{-1}. We use this as our initial point for our extended sensitivity analysis and investigation of the applicability of the analytical solution.

Our first test of the model is of the calculated epidemic wave speed against the infection transmission efficiency $\boldsymbol{b}$. The analytical solution fits both numerical solutions very closely over four order of magnitude of $\boldsymbol{b}$ and a factor of 4 change in wave speed (Fig. 8.1). It is an effective analysis tool. The wave speed is only weakly dependent on $\boldsymbol{b}$, increasing at a rate slightly less than proportional to the log of $\boldsymbol{b}$. We are very uncertain about the range of $\boldsymbol{b}$, the weakness of the wave's dependency on this parameter means that uncertainty in this parameter does not translate into large uncertainties in the model results. If transmission *per se* were very efficient then there

would be a maximum limit imposed by the rate of mixing of schools at some large but unknown value. Because of the saturation in response to change in **b** for large **b** the existence of such a maximum value is not a problem that could affect the model results. At very low values of **b** the wave speed becomes much more sensitive to **b**'s value.
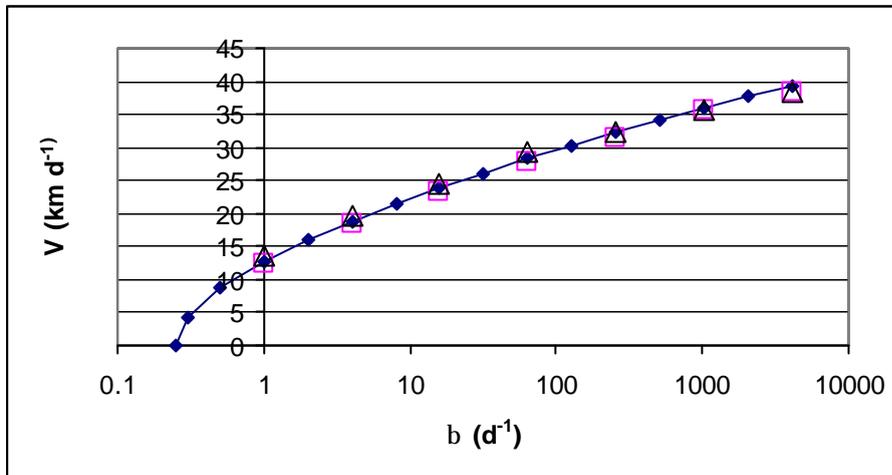
Figure 8.1   Analytical solution (solid diamonds) and numerical solution (open squares) of the epidemic wave speed versus infection transmission **b** for the fixed latent period length model. Also shown is the fixed latent plus fixed infectious period lengths (open triangles) model's wave speed.

It must be emphasised that the transmission efficiency is normalised to the average population density. Because of this, the rate of transmission of the disease depends on population density in the same way that it depends upon the actual transmission efficiency. Hence the wave's speed will respond significantly to changes in population density only if these are very large and will only cease if these changes are of several orders of magnitude. While changes of three orders of magnitude have occurred in Japanese pilchard populations following recruitment failure (Wada and Jacobson 1998), changes in Australian waters have been much smaller. Changes of the order of 50% may have occurred off Albany between the two epidemics and not driven by the mass mortality (Fletcher 1992, Cochrane 1999).

The model solutions show a much stronger relationship with the diffusion coefficient. The relationship is linear with the square root of the diffusion coefficient (Fig. 8.2); this is the same relationship as exhibited by all the other standard epidemic wave models (Murray 1999). In fact, as discussed in the previous chapter, it is the diffusion of infected individuals which control the wave's speed. To test this, we have run the numerical model with *D* set to zero, while the value of *B* is maintained. As predicted, this was found to have no effect on wave speed as predicted under the analytical method.
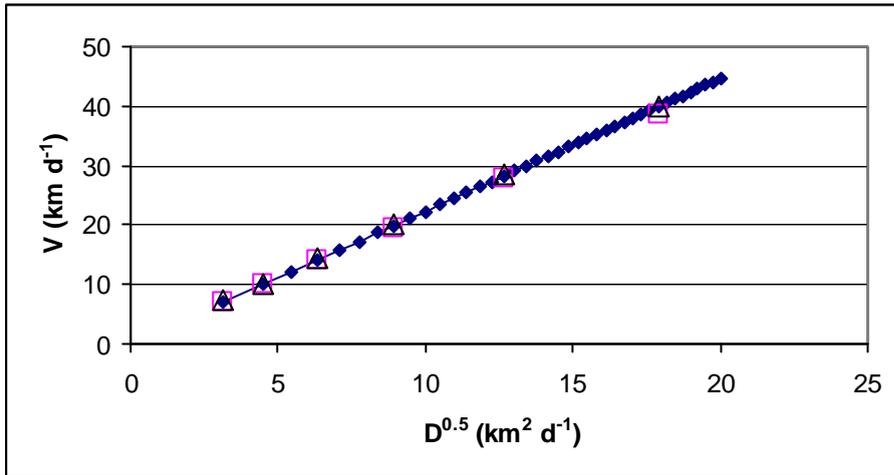
Figure 8.2 Analytical solution (solid diamonds) and numerical solution (open squares) of the epidemic wave speed versus the square root of diffusion coefficient D (= B) for the fixed latent period length model. Also shown is the fixed latent plus fixed infectious period lengths (open triangles) model's wave speed.
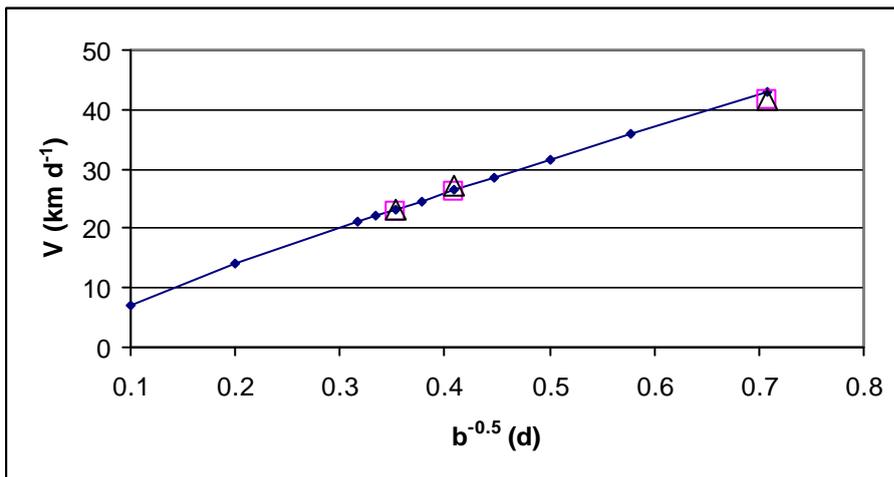
Figure 8.3 Analytical solution (solid diamonds) and numerical solution (open squares) of the epidemic wave speed versus the inverse of the square root of the latent period for the fixed latent period length model. Also shown is the fixed latent plus fixed infectious period lengths (open triangles) model's wave speed.

The final parameter that the model wave speed is strongly sensitive to is the length of the latent period (Fig. 8.3). The model wave speed depends linearly on the inverse of its square root. Because of the dispersion of infected fish, large values of b are not consistent with the observed restricted period of mortality at any given location (see section 8.3) so we have a relatively restricted range for this parameter. If the latent period is reduced towards zero (not shown) the wave speed tends towards 400 km d^{-1}. This is the wave speed predicted from a simple SIR model which the model is in this case equivalent to. The numerically calculated speed of an SIR model is, as discussed earlier, $2\ddot{o}(Db)$.
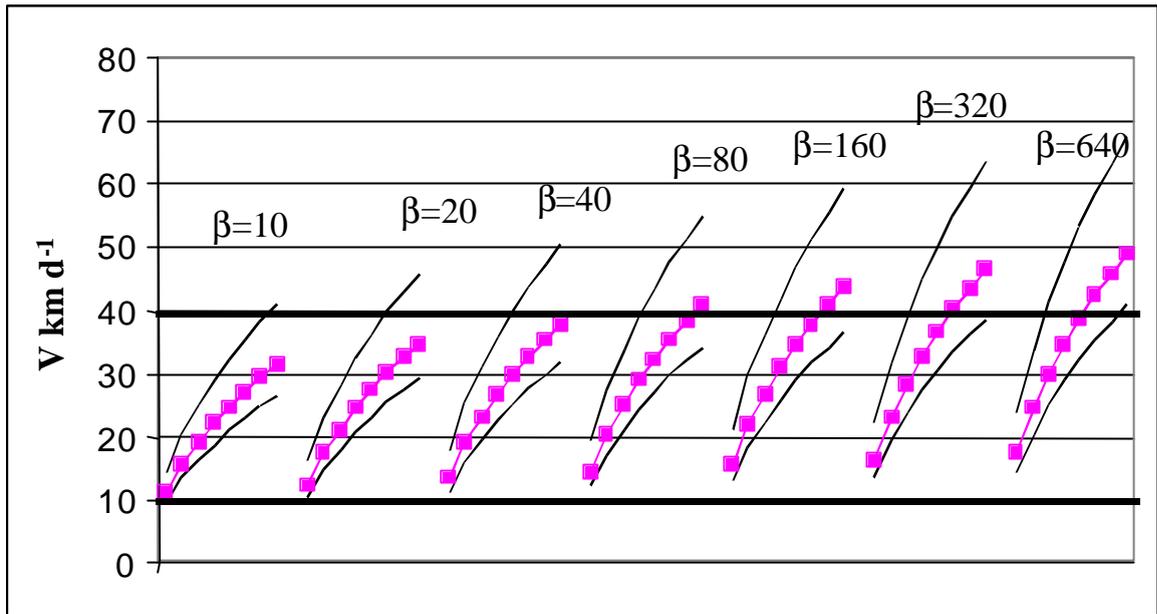
Figure 8.4   Speed of epidemic waves calculated using **b** as shown and *D* of 50, 100, 150, 200, 250, 300, 350 or 400 km^2 d^{-1}. Default latent period is 4 days; ranges shown by empty lines indicate the effect of varying latent period from 2 (faster) to 6 (slower) days. Bold lines mark the 10 and 40 km d^{-1} limits of observed wave speeds.

We bring this information together to show how the wave speed varies with the three parameters acting in combination. As can be seen from Fig. 8.4 even over large changes of **b** there is little change in wave speed. Change in latent period, *b*, seems to be not enough to account for the large changes in wave speed on it own. For large *D* and/or **b** (i.e. for fast waves) the wave speed becomes more sensitive to *b*. Only *D* seems to be able to vary enough and the wave speed is sensitive enough for this parameter to be able to account for the observed variation in wave speed on is own.

We summarise wave speed parameter sensitivity. As Yachi *et al.* (1989) determined, the presence of a latent period makes wave speed far less sensitive to the local rate of spread of the infection than in simple SIR models. But we also show that by making this latent period of a fixed length the sensitivity is even further reduced. This weak sensitivity applies particularly for large **b**, as is the case of the pilchard herpesvirus. Sensitivity to the latent period is greatly increased from the fourth root (Yachi *et al.* 1989) to the square root of turnover time. All versions of the model are sensitive to the square root of the diffusion coefficient. As demonstrated in the previous chapter, it is the diffusion of infected animals only that affects the wave's speed, so any change in their behaviour may be very important to the spread of an epidemic.

8.2   Duration of Mortality Waves

Observed mortality in the mature epidemic wave lasted for only about a day or two at any given location (Fletcher *et al.* 1997). It is possible that small amounts of mortality are going undetected before or after this peak. However, we would expect one or 2 days to exhibit significantly higher rates of mortality than occur on other days.

We can look at wave shapes directly by using the numerical model. Using a diffusion coefficient of 200 km^2 d^{-1} and a range of latent periods b of 1 to 4 days, we use the analytical method to select a $\boldsymbol{b}$ value that produces a 40 km d^{-1} wave velocity (Fig. 8.5). We then record total the daily mortality at a point 1500 km from the start of the run (similar records were made at 500 and 1000 km to verify that the wave shape was constant). Over this considerable range of b and $\boldsymbol{b}$ we find the wave's shape to be remarkably similar. The time required for initialisation of the wave increases as incubation period increases. The wave's speed is the same because it has been so parameterised. There is a slight increase in the length of time over which the peak arises as b increases, and a slight decline in peak size. However, in all cases 50% of mortality occurs in <2 days and 80% in <4, so this level of diffusion is consistent with observations. Therefore, for a given wave velocity, D is the critical parameter for determining the wave's shape. This is perhaps not too surprising because, for a given value of D, the wave must maintain the same slope if diffusive flux and hence the rate of motion is to remain the same.
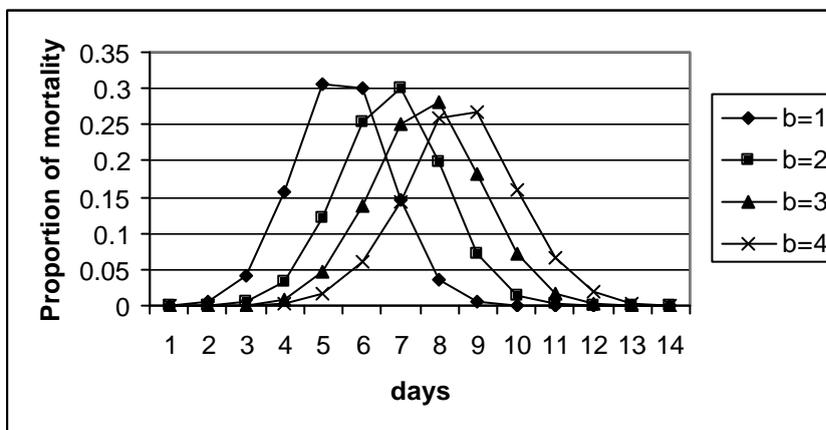
Figure 8.5   Distribution of mortality for 40 km d^{-1} waves at a point (1500 km from origin) for model runs with diffusion coefficients of 200 km^2 d^{-1}. Runs have been executed for latent periods of 1, 2, 3 and 4 days with $\boldsymbol{b}$ values of 13.9, 102, 750 and 5527 d^{-1} which gives a 40 km d^{-1} velocity.

A similarly weak dependence on incubation period length, over the range in this parameter of 1 to 4 days, has been derived for waves with velocities of 10 and 20 km d^{-1}.

Since the critical parameter determining wave shape at a given velocity is the diffusion coefficient, we therefore carried out a series of tests of the effect of diffusion coefficient on wave shape (Fig. 8.6). The result is an increasingly prolonged wave as D rises and $\boldsymbol{b}$ falls. For D of 50 km^2 d, most mortality occurs within 1 day and >80% over a 2 day period. The period over which 80% mortality occurs rises to about 3 and 4 days and 50% in less than 2 days for D of 100 to 200 km^2 d^{-1}, which is still consistent with observations. However, for D of 400 km^2 d^{-1} 80% mortality is spread over 5 days, and this is beginning to become inconsistent with observed short-lived mortality. Also the days with the two highest rates of mortality are not much greater than mortality on the third highest day, and only a little higher than that occurring on the fourth highest day. This value is similar to the simple estimate of the maximum limit for D that was made in Chapter 3.
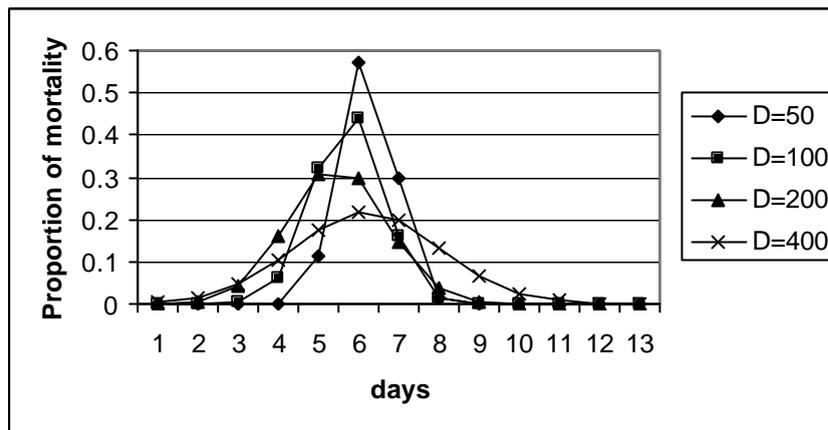
Figure 8.6   Distribution of mo rtality for 40 km d^{-1} waves at a point (1500 km from origin) for model runs with diffusion coefficients of 50 to 400 km^2 d^{-1}. Runs have been executed for latent periods of 1 day with **b** values of 2945, 123, 13.9 and 3.24 d^{-1} which gives a 40 km d^{-1} velocity.

Therefore, for a given wave velocity, *D* is the critical parameter for determining the wave's shape. A maximum value of of less than 400 km^2 d^{-1} seems consistent with observed patterns of mortality. This maximum value is well within the possible maximum value due to pilchard swimming and therefore vectors such as birds are not necessary to account for the observed transmission. This does not mean they can be ruled out. Surprisingly the length of the latent period has little effect on wave's shape, given that diffusive dispersion depends upon $\ddot{O}(Dt)$. However, for a given diffusion coefficient the epidemic wave must have the same gradient to maintain the same velocity. Hence the latent period and transmission coefficient tend to counterbalance and result in a similar distribution of mortality.

Westbound, the epidemic travelled at about 20-25 km d^{-1}. The eastbound 1998 epidemic appears to have travelled at a similar speed; we use 20 km d^{-1} as a reference point midway between the slowest and fastest observed wave speeds (Fig. 8.7). By about *D*= 150 km^2 d^{-1} the model is unable to produce the observed brief duration of mortality, mortality being fairly evenly spread over several days. Thus for the 1995 epidemic westbound diffusion is less than 200 km^2 d^{-1}. It is greater than 10 km^2 d^{-1}, since **b** must be very large to produce an epidemic speed of 20 km when *D* is <20 km^2 d^{-1} (see next section). In any case, such values of *D* are at the low end of those predicted from an analysis of pilchard behaviour (Chapter 3).
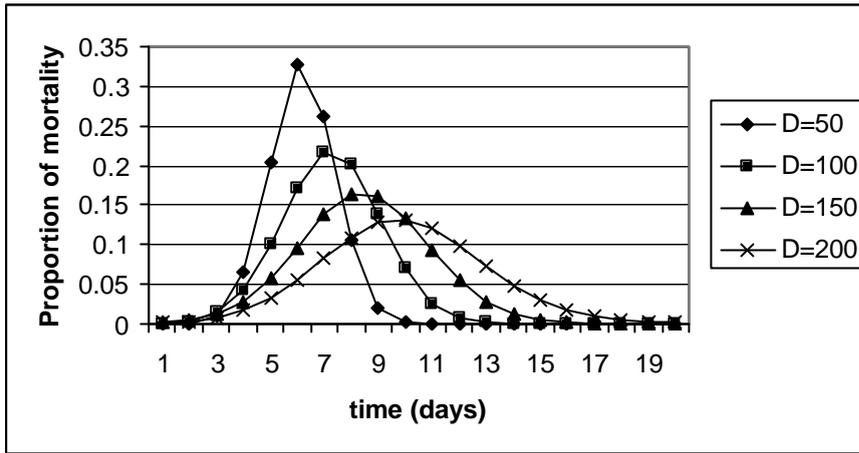
Figure 8.7 Distribution of mortality for 20 km d^{-1} waves at a point (1500 km from origin) for model runs with diffusion coefficients of 50 to 200 km^2 d^{-1}. Runs have been executed for latent periods of 1 day with **b** values of 13.9, 3.24, 1.75 and 1.22 d^{-1} which gives a 20 km d^{-1} velocity.

The westbound 1998/9 epidemic travelled at a little over 10 km d^{-1}. There was little scatter of mortality about the regression line and this is only explicable in terms of low diffusion coefficients (Fig. 8.8). Even 50 km^2 d^{-1} results in mortality being smeared across a period of around 10 days, which is incompatible with the observations. A *D* of about 30 km^2 d^{-1} appears to be the upper limit, as by this level of dispersion mortality is already spread over several days.

The only way to obtain the 1995 epidemic's rate of spread with this level of diffusion (30 km^2 d^{-1}) is to use very short latent periods, < = 2 days. The response of the wave's velocity to increase **b** is effectively saturated. We have no direct evidence to constrain the parameterisation of the latent period, but some finite time is required for infection to mature. Such brief latent periods result in a single continuous wave which differs little between the origin and at distance from the origin, this does not reproduce differences in persistence (see next chapter). So change in *D* seems likely to have been an important driver of differences in wave speed, particularly given the difference between eastern and western spread of the 1995 epidemic.
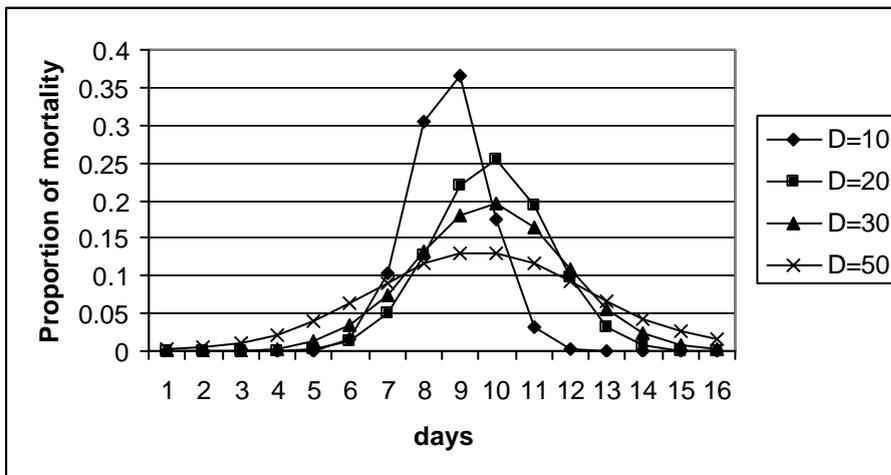
Figure 8.8 Distribution of mortality for 10 km d^{-1} waves at a point (1500 km from origin) for model runs with diffusion coefficients of 10 to 50 km^2 d^{-1}. Runs have been executed for latent periods of 1 day with **b** values of 25.6, 4.87, 2.41 and 1.22 d^{-1} which gives a 10 km d^{-1} velocity.

8.3 A Maximum Limit on Latent Period Length

We have been able to limit the value of *D* by reference to the observed local duration of infection. Wave speed at a given value of *D* depends essentially upon the transmission coefficient **b** and the latent period *b*. However, the modelled wave velocity becomes very weakly dependent on **b** as this parameter becomes large. We can combine these two facts to find a maximum reasonable length for the latent period.

The maximum epidemic wave speed appears to be up to 40 km d^{-1}. We apply the analytical method with a binary search algorithm to find **b** values which generate this wave speed given *D* and *b* values (Fig. 8.9). Because of the weak dependence on **b** for large **b** there is, for a given latent period, a value of *D* at which increase in **b** fails to offset further change in *D*. Thus if *D* = 200 km^2 d^{-1}, it is almost impossible to generate a 40 km d^{-1} wave if the latent period is much more than 4 days long.
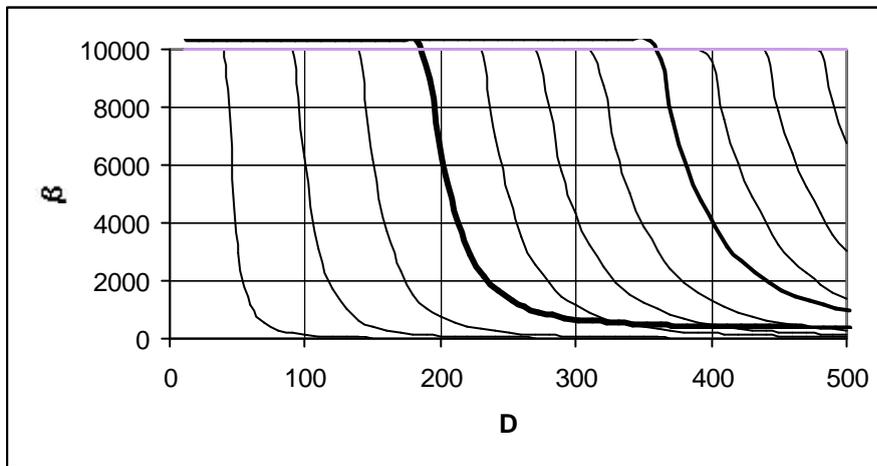
Figure 8.9 Values of **b** and *D* required to generate wave speeds of 40 km d^{-1} for latent periods of 1 to 11 days (4 days = treble line, 8 days = double line)

The 20 km d^{-1} westward rate of expansion appears to be consistent for a latent period of up to four times that of the 40 km d^{-1} wave with a given diffusion rate (Fig. 8.10). This is expected from the linear sensitivity to the inverse square root of the latent period shown in the earlier sensitivity analysis. This velocity of wave is consistent with *D* of up to 100 km^2 d^{-1}. This would place an absolute maximum limit on the latent period of about 8 days, double that of the 40 km d^{-1} wave's maximum *b*. However, we do not expect the disease to be significantly different between two waves of the same epidemic.

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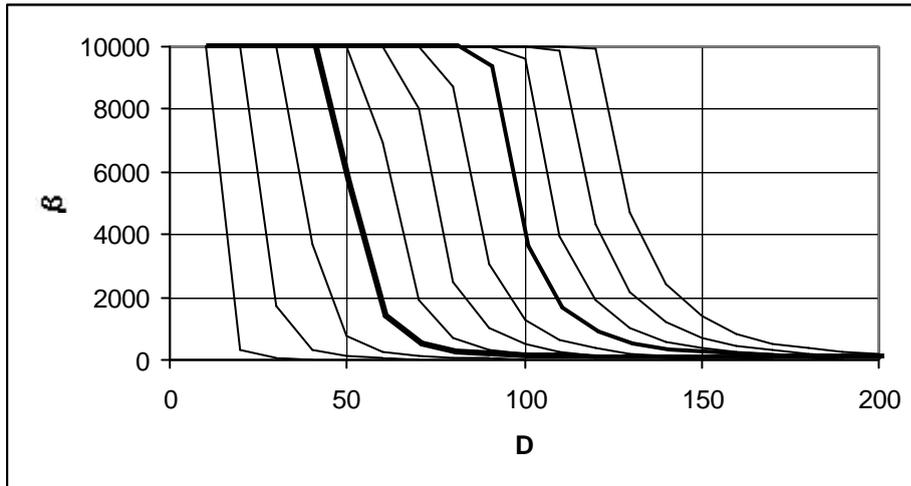
Figure 8.10 Values of **b** and *D* required to generate wave speeds of 20 km d^{-1} for latent periods of 1 to 11 days (4 days = treble line, 8 days = double line)
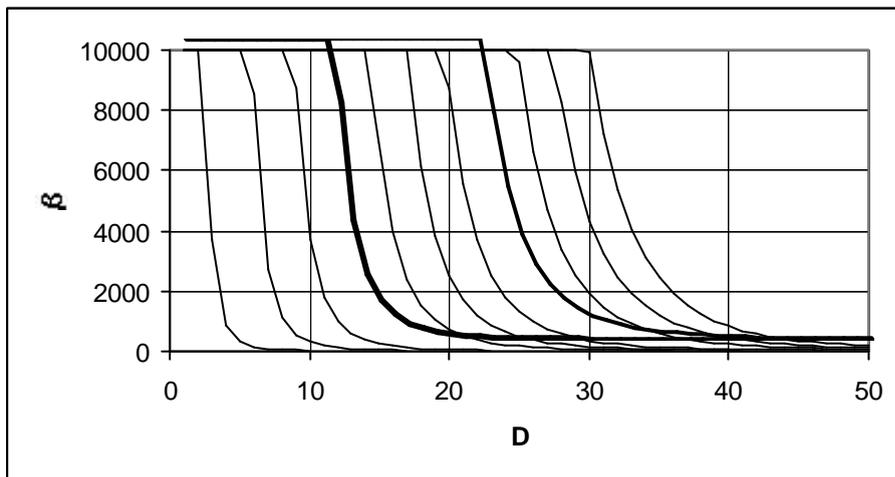
Figure 8.11 Values of **b** and *D* required to generate wave speeds of 10 km d^{-1} for latent periods of 1 to 11 days (4 days = treble line, 8 days = double line). Note change in *D* scale.

The 10 km d^{-1} 1998/9 epidemic speed with a *D* of < 30 km^2 d^{-1} is consistent with latent periods of up to about 12 days, thereafter the transmission rate **b** value's effect on wave speed begin to saturate (Fig. 8.11). It is quite possible that the disease changed the length of its latent period substantially between the 1995 and 1998/9 epidemics. However, the diseased fish exhibited substantially more virus containing lesions in 1995 than in 1998/9. We therefore would not expect the incubation period to have increased by so much that **b** had to rise to obtain the observed wave speed.

8.4   Levels of Infection and Mortality

In most model runs the proportion of the host that is subjected to infection is in excess of 90%. Exceptions can occur for runs in which **b** is small, but in these runs infection develops too slowly resulting in unrealistically prolonged periods of mortality.

Infection levels are reduced if the length of the infectious phase is cut. This reduction is small unless b is small.

We have tabulated the levels of infection obtained for the waves analysed in figures 10.6 to 10.8, but with an infectious period of only 1 day instead of 4 days in order to find maximum levels of infection (Table 8.1). The value of b is adjusted slightly to maintain the wave speed. Except for the 10 and 20 km d^{-1} waves with the lowest b, which produced unrealistic mortality wave shapes, the levels of infection exceed 90%. Under the runs with an infectious period of 4 days length, all the infection levels exceeded 98%. The level of infection generated is the same regardless of wave speed, and hence D, for a given b value, provided that the infectious period is of the same length.

Table 8.1   Levels of infection obtained under model conditions used to generate figure 8.6 to 8.8, with infectious period cut to 1 day.

40 km		20 km		10 km	
b	Infection	b	Infection	b	Infection
3213	100.00%	18.57	100.00%	32.58	100.00%
144	100.00%	5.18	98.07%	7.31	99.56%
18.57	99.99%	3.17	90.53%	4.08	95.61%
5.18	98.03%	2.44	81.14%	2.44	81.22%

The high levels of infection generated by the model mean that lower observed levels of mortality must be due to the survival of significant fractions of the infected hosts. The relatively low mortality in Western Australia in 1995 occurs under conditions of higher wave speeds and larger b (more lesions) than 1999. Under these conditions the model predicts higher levels of infection (as would all standard model formulations). Because all model runs generate high levels of infection the critical parameter for determining the long-term impact of the epidemic is thus the fraction of infected individuals which go on to die. The data indicates that this lies between 0.15 and 0.6, but the cause of variation in this parameter is uncertain. This uncertainty leads to uncertainty in the impact of an epidemic and makes prediction of the effect of any future epidemics difficult.

8.5   Conclusions

The model wave's speed is well described by the analytical solution; the existence of this solution greatly speeds up the process of model analysis. The speed is sensitive to three parameters: the length of the latent period (b), the infection spread rate (b), and the diffusion coefficient D, or rather to the diffusion of sick fish only. There is very little sensitivity to the turnover of infectious fish (mortality + recovery). For this reason the analytical solution applies to the fixed infectious period length model too.

Analysis shows that sensitivity of the epidemic wave speed to infection's rate of spread is relatively weak. Sensitivity to further change declines as this parameter becomes larger. This weak response also means the epidemic's spread is not very sensitive to population density because the transmission rate is normalised to average population density, and it is the only parameter for which this applies. Thus changing population

density and changing infection spread rates are equivalent and only very large changes in this affect the epidemic.

The model is strongly sensitive to the latent period, depending upon the inverse square root of this parameter. This is far more sensitive than the equivalent continuous model, for which sensitivity depends upon the fourth root of the rate of turnover of the latent phase infection (Yachi *et al.* 1989).

The model's epidemic wave speed also depends upon the square root of the diffusion coefficient. All of the waves generated in the standard epidemic models do so. We have been able to derive some rough limits on the diffusion coefficient by observing the effect of high diffusion coefficients upon the stabilised for of the epidemic wave. Large diffusion coefficients lead to long wavelength waves, such waves are not consistent with the brief observed mortality at any given location.

Because the model depends almost entirely on three parameters, we have devised diagrams to show the entire possible parameters space for waves of a given velocity. These consist of plots of diffusion coefficient versus infection, for a given latent period length. We use these plots to locate the diffusion coefficient at which the model becomes very insensitive to increase in *b*. Because we have derived a maximum value of *D* for any epidemic velocity and we can use the diagrams to derive minimum values of *D* that are compatible with a given latent period, we derive maximum possible latent period lengths.

In the next chapter we examine the observed and predicted behaviour of the epidemic at its point of origin in South Australia to find further constraints upon the model.

9   The Initialisation and Stabilisation of Wave Speeds

There are substantial differences between the initial behaviour of the epidemic and its mature form. Locations near the origin of the disease may be revisited by episodic infection over prolonged periods, whereas at a distance from the source the epidemic strikes only once and for a brief period before moving on.

The model also exhibits differences in behaviour at its origin and when it matures. This is because epidemic waves coalesce from several peaks at the origin to a single peak as the wave matures. The process is controlled by the lengths of the latent and infectious periods and by the transmission rate.

9.1   Wave Speed and Stability under Different Latent Periods

One aspect of wave speed that cannot be found analytically, is the nature of the unstable initial development phase of the wave from a localised infection. The initial development phase is of particular importance for the pilchard herpes virus epidemic, given the relatively short duration of the mortality. It also has the potential to provide clues about appropriate model parameterisation which are not apparent once the wave has stabilised.
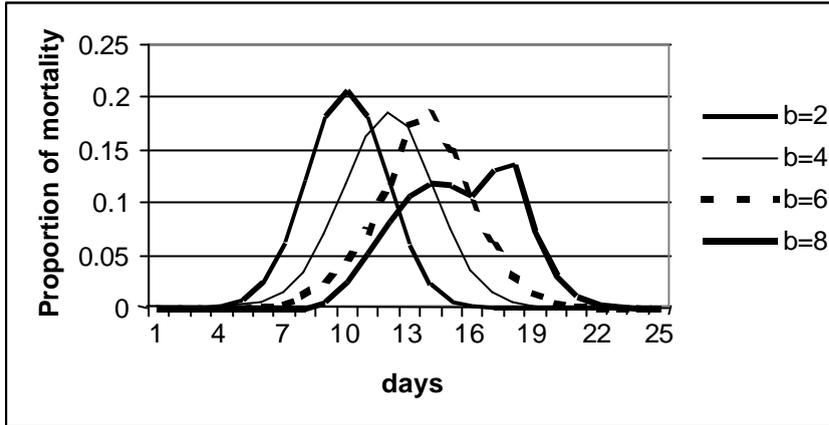
Figure 9.1   Mortality wave shape at 1500 km for $D = 400$ under a range of latent periods, b days, and appropriate infection transmission $\boldsymbol{b}$ to generate a wave velocity of 40 km d^{-1}. A period of 40 days (in which no mortality occurs at 1500 km) has been removed from the start of the time series)

In the previous chapter we looked at the shape of waves that existed after a long period of stabilisation. Specifically we examined the wave shape after the wave had travelled 1500 km and we ensured this was the stable form by checking the wave shapes were the same at 500 and 1000 km from the origin. We found that, for a given D (or rather B) value, the wave's shape was similar over a range of b and $\boldsymbol{b}$ values that gave a speed of 40 km d^{-1} (Fig. 9.1). However, as we increase the latent period, b, we find that wave shape at 1500 km deforms. Using $D = 400$ km^2 d^{-1} we find that the wave shape changes little for b = 2, 4 or 6, from that described in the previous chapter (at $b = 1$). However, at $b = 8$ a quite different wave with two peaks emerges.

The reason that the wave shape is different at $b = 8$ days is that the wave has not yet stabilised. As a result quite different wave patterns are present at 500, 1000 and 1500 km from the origin (Fig. 9.2). In this chapter we will investigate the pattern of mortality generated by the model in the vicinity of the South Australian origin point and the origin of the wave.
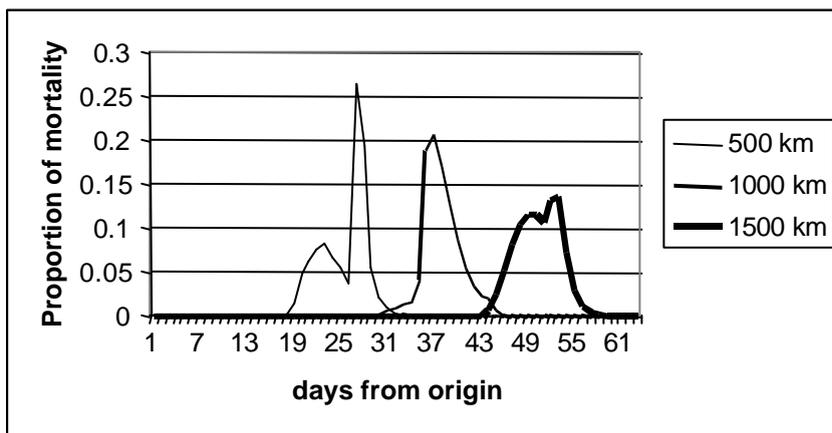
Figure 9.2 Mortality wave shape at 500, 1000 and 1500 km from the epidemic's origin for $D = 400$ km^2 d^{-1}, $b = 8$ days and $\boldsymbol{b}$ (3540 d^{-1}) is selected to give a wave velocity of 40 km d^{-1}.

Even though the wave form has not stabilised for $b = 8$ days, the wave still travelled at 40 km d^{-1}, as is predicted from the analytical solution for the stable wave's velocity.

This means that we can use the analytical solution to predict appropriate parameters for a given average velocity of the unstable wave.

We can also see that the wave does not take off immediately, there is a delay in reaching 500 km which is far longer than the period required for mortality to transfer from 500 to 1000 or 1000 to 1500 km. This is in line with the observed occurrence of mortality is South Australian waters for several weeks before the wave develops and spreads to other states.

9.2   The Initial Formation of the Epidemic

The mortality pattern at the point of origin in South Australia differs from that in the mature wave. In 1995 mortality was observed to persist and recur near the point of origin for several weeks (Whittington *et al.* 1995). In 1998 mortality again recurred over the course of several weeks in areas of South Australia near the point of origin. Although the epidemic did not recur at its point of origin in Spencer Gulf it did persist for some time in nearby waters (Ward *et al.* 1999).

We follow the development of the epidemic at the origin by plotting mortality (at 0.1 day intervals) in the spatial point of the initiation of the epidemic. We cannot use point zero for this initial location of the infection in the model because the initiation of the epidemic is affect by dispersal both to the east and west of the original location (although this effect is relatively weak). The behaviour depends both quantitatively and qualitatively upon the latent period and transmission efficiency (Fig. 9.3).
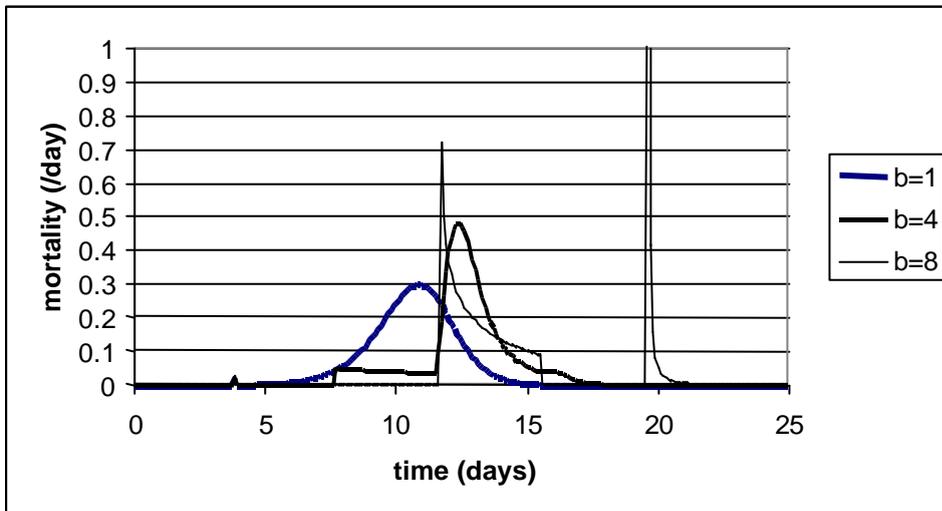
Figure 9.3   Mortality at the origin of the epidemic. $D = 30$ km^2 d^{-1}, infectious period (*c-b*) 4 days. Latent period (*b*) 1, 4 or 8 days with appropriate **b** (2.4, 29 and 821 d^{-1}) for a 10 km d^{-1} wave speed. Note the initial blip 4 days after the run begins, it is then that the initial group of infected individuals die.

When the latent period is short, mortality shows a smooth increase and then decrease with time. The wave is similar to the steady state wave and so mortality would be

expected to be detected over a similarly short period as occurs away from the origin. Mortality was observed for several weeks at or near the origin.

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Too long a latent period requires that the infection rate be rapid to produce the observed wave speed. We are using the maximum *D* value that is consistent with mortality wave shape, so this parameter cannot be increased. This high value of **b** means that infection is near instantaneous, and thus so is mortality. The result is isolated intense peaks of mortality. Although the mortality observations do hint at peaks, they are not the occasional isolated peaks but rather slight increases and decreases in reported mortality.

The observed pattern is best replicated by an intermediate latent period of about 4 days. This produces mortality over a period of about a week.
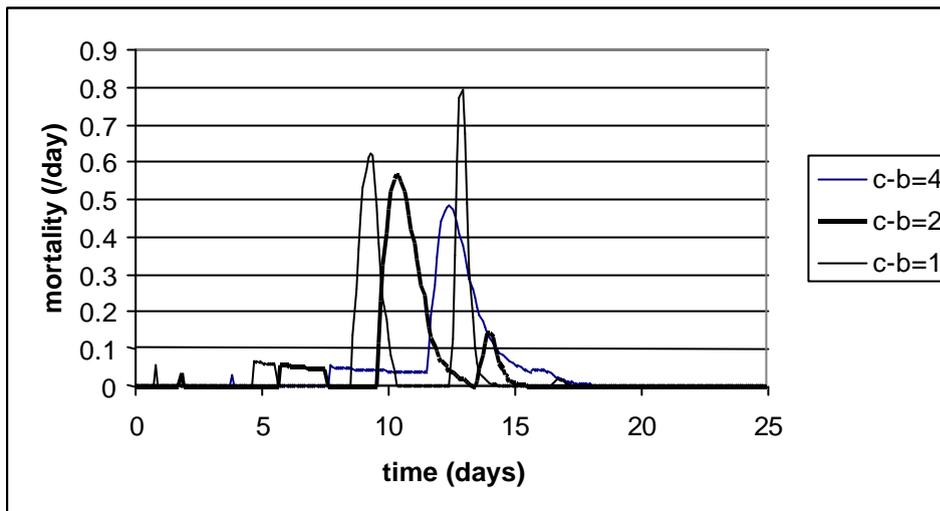
Figure 9.4   Mortality at the origin of the epidemic. $D = 30$ km^2 d^{-1}, Latent period (*b*) 4 days. infectious period (*c-b)* 1, 2 or 4 days with appropriate **b** (29 d^{-1}) for a 10 km d^{-1} wave speed.

The duration of mortality at the origin can be enhanced if the length of the infectious period is cut (Fig. 9.4). This parameter has only a small effect on the wave's stabilised speed (see previous Chapter). In this case infection has less time to spread and so each generation of infection (and hence peak of mortality) is smaller. The result is prolongation of the mortality. The pattern generated under an infectious period of 2 days and latent period of 4 days is strongly reminiscent of the observations, although mortality appears to persist near the origin for longer than predicted. An infectious period of 1 day results in large isolated peaks, which would not appear to be consistent with observations. Such isolated peaks occur whenever the infectious period is substantially shorter than the latent period.

We need a systematic way of looking at the effect of latent and infectious periods on the length of time that infection persist at the origin of the epidemic. We have therefore plotted the time between the first time mortality exceeds 5% and the last time this occurs in a systematic search of parameter space of the 10 km d^{-1} wave with $D = 30$ km^2 d^{-1} (Fig. 9.5). This method is not perfect, the difference to the figure caused by a small peak of about 4%, rather than 5% may be substantial, but is not important. We generate an overall pattern of lengths of mortality periods but the value in individual cases may not be significant. We have used latent periods of 1 to 5 days and **b** values appropriate to generate 10 km d^{-1} waves.
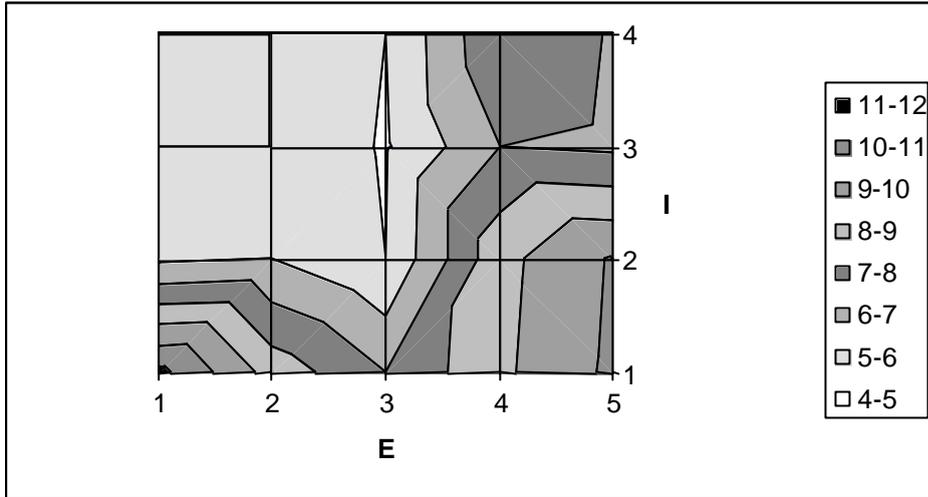
Figure 9.5   Time between first and last instances of mortality at rates of >5% day at the point of origin for a 10 km d^{-1} wave, $D = 30$ km^2 d^{-1}, for a range of latent (E) and infectious (I) period lengths.

The result of this analysis is to show that waves are short lived when $E < I$ and that there are two areas of prolonged wave persistence. The first is for very short latent and infectious periods; the second is for long latent periods with short infectious periods. To distinguish between these we look at the time series generated both at the origin and some distance from this.
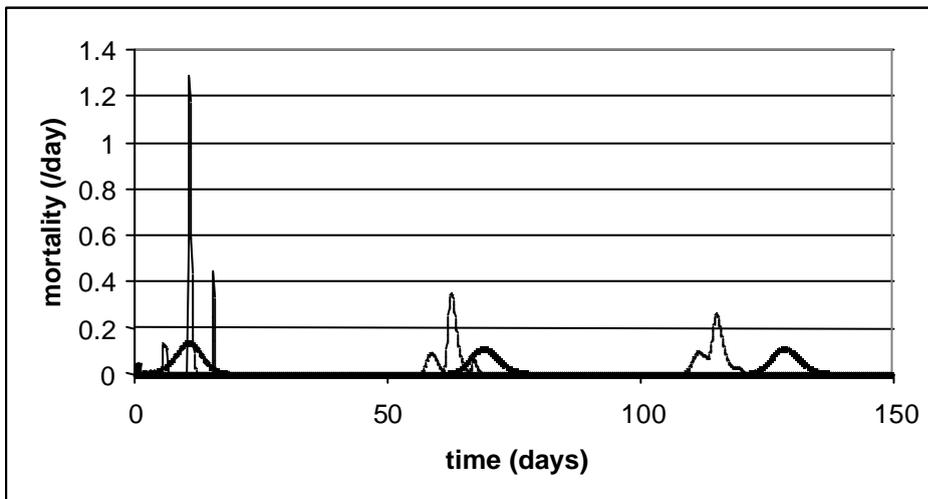
Figure 9.6   Development of mortality waves at 0, 500 and 1000 km from the origin of the epidemic. Thick line = 1 day latent period, thin line = five day latent period.

We can see that there are very different time series patterns under the two latent periods (Fig. 9.6). These time series strongly support the long latent period parameter value. The short latent period produces a wave which shows hardly any difference between the origin and the more distant locations. This cannot be consistent with the observations of prolonged mortality at the origin and a brief phase of mortality once the wave has matured. The long latent period, by contrast, shows an evolution from several peaks of mortality scattered over a long period towards a single peak. In any case the very short latent, very short infectious period model would appear to be inconsistent with the observed presence of viral lesions up to 4 days prior to mortality. This result does

indicate that our initial assumption, that viral lesions were a sign of infectiousness is not true. Viral release appears to occur only at a late stage of lesion formation when inflammatory exudates appear (Fletcher *et al.* 1997).

Runs for which the latent period is shorter or equal to the infectious period had essentially only one peak. Under long latent periods in excess of 3 days the peak can show some distortion. Multiple (>2) peaks in excess of 5% mortality, were a feature of runs with infectious periods of one or 2 days and with longer latent periods. Long latent and infectious periods produce two brief peaks of mortality at the origin. These require very high **b** values to produce appropriate wave speeds, and so the infection is very rapidly spread. The runs with only one peak can be ruled out, this peak propagates unchanged and so cannot account for the initial long persistence of mortality while at the same time producing a short-lived mature wave. The two intense peaks produced under longer infectious and latent periods would appear to be unlikely, the observations do not indicate mortality events to be this isolated. An intermediate form with moderate to long latent (2 - 4 days) plus a brief infectious period (1 - 2 days) appear most in line with the observations.

We also apply the model to the origin of a $(1-p)\alpha I$ wave. If we systematically analyse the persistence of the initial infection, as days between first and last incidence of 5% d^{-1} mortality (Fig. 9.7), we find a similar pattern to the persistence of mortality to that obtained under the 10 km d^{-1} wave. The persistence is somewhat lower than for the 1998/9 wave, which is in line with observations.
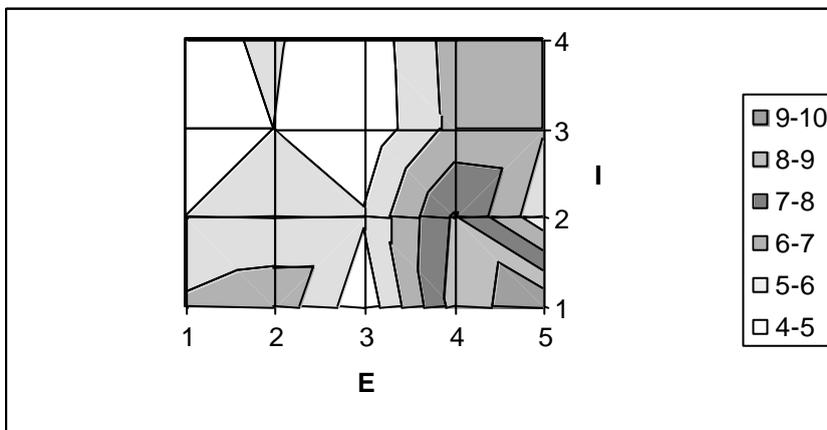
Figure 9.7   Time between first and last instances of mortality at rates of >5% day at the point of origin for a 20 km d^{-1} wave, $D = 100$ km^2 d^{-1}, for a range of latent (*E*) and infectious (*I*) period lengths.

The pattern of wave peaks is also similar to that found under the 10 km d^{-1} wave. That is, there is a single peak when the infectious period is equal or longer than the latent period, isolated brief peaks when the latent and infectious periods are both long, and multiple peaks when *I* is one or two and less than *E*.

Faster waves, with larger infection rates tend to produce one or two intense pulses of mortality at the point of initiation. This is not in line with observations, but if the initial speed of the 1995 epidemic were 20 km d^{-1}, and it subsequently speeded up as it travelled towards the east the fast waves are not relevant to initial behaviour.

We have found that if we change only *D*, leaving infection and latent periods unchanged to replicate the east and west bound waves of the 1995 epidemic, then there are only small differences in the initial behaviour of the epidemic. The development of infection at the origin largely depends upon local processes.

We are able to obtain, under this model, a period of relatively prolonged mortality consisting of a number of peaks that occur over a period of up to two weeks. This is considerably less than the persistence of the observed mortality in South Australia, but it is qualitatively the correct behaviour. Our estimate of the persistence of mortality is perhaps excessive. The residual from linear regression that was obtained at the origin by Fletcher *et al.* (1997) was 20 days, reasonably close to the model results. Our estimate of residual of 30 days (Figure 3.5) is based rather crudely on 250 km stretches of coastline. The 1998 epidemic appears to have persisted for even longer, up to 40 days, within a short distance from its origin. However, many of the later, and none of the early, mortality incidents involved juvenile pilchards (Ward *et al.* 1999). A delay in the spread of the epidemic from adults to juveniles may have increased the to local persistence of mortality. As we will discuss in the next section, oscillating waves will recur within a short distance of the origin so the total period of the epidemic may be prolonged.

The model tends to support an infectious period that is a little shorter than we expected from the pathological evidence. Possibly lesions only become significant sources of virus as they mature and so the lesions observed up to 4 days before mortality occurs were not initially contributing to new infections.

The observed prolonged infection at one point at the origin of the epidemic supports a relatively low rate of transmission of infection, $b < 100$ d^{-1}. Larger rates lead to one or two brief and isolated peaks of mortality. That pattern does not accord with the observations.

9.3   The Initial Formation of Epidemic Waves

The epidemic starts at a point, but develops as waves travelling respectively east and west. We look at the initial nature of the wave that arises within a short distance of the origin.
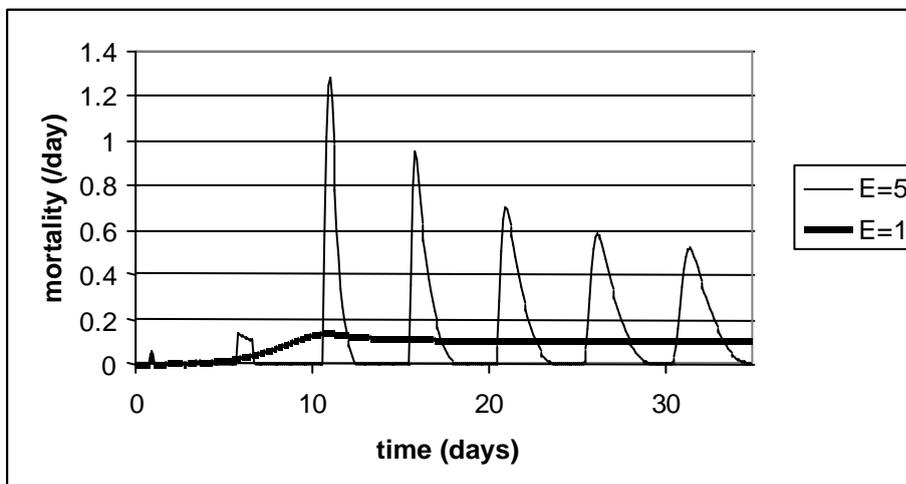
Figure 9.8   Peak level of mortality with time under the 10 km d^{-1} waves, $D = 30$ km^2 d^{-1}, infectious period = 1 day, latent period 1 or 5 days.

We see that in the model run for which both latent and infectious periods are short, and similar, the model rapidly reaches a constant maximum level of mortality. This reflects the smooth development of the wave as discussed earlier. Peaks persist within the run for which the latent period is much longer than the infectious period, producing strong oscillations. These are extreme versions, when the latent period is only moderately longer than the infectious period the waves will run together. Even under this extreme the wave is showing signs of coalescing into a single wave, as was apparent in Fig 9.6. If the infectious period length is increased, or the latent period cut, the wave will coalesce more rapidly.

The persistence of the oscillation when the infectious period is much shorter than the latent period would appear to put a limit on the shortness of the infectious period I. If this is much shorter than the latent period E then the waves will persist as brief isolated mortality events for longer than observations would indicate. These persistent oscillations would appear to limit the extent to which rapid travelling waves can be explained by very short infectious periods. It is possible that variation in the incubation period length could smear waves together, while allowing for short infectious periods.

We look at how the mortality wave originates under the two parameter sets. With a short latent period the model smoothly develops a narrow wave of mortality with a constant period of time over which mortality exceeds 5% per day occurs at any given location (Fig. 9.9). The oscillating wave shows short-term variation in speed, but on average it travels at the speed that the stabilised wave will settle at (Fig. 9.10). These short-term variations in speed are unlikely to be distinguishable from a constant wave speed.
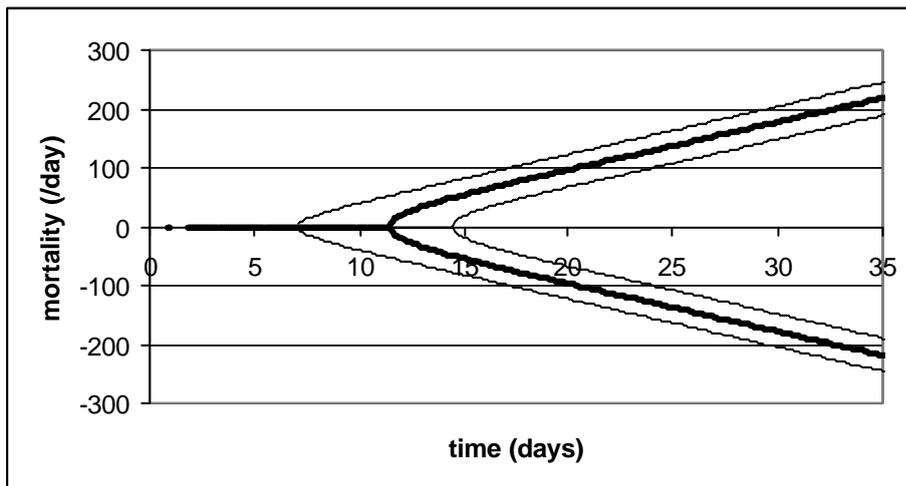
Figure 9.9   Development of 10 km d^{-1} waves with a 1 day latent period in the vicinity of the origin of the epidemic, thick line is the centre of the wave, thin lines show 5% mortality envelope ($D = 30$ km day^{-1}, $b = 1$ day, b-$c = 1$ day).
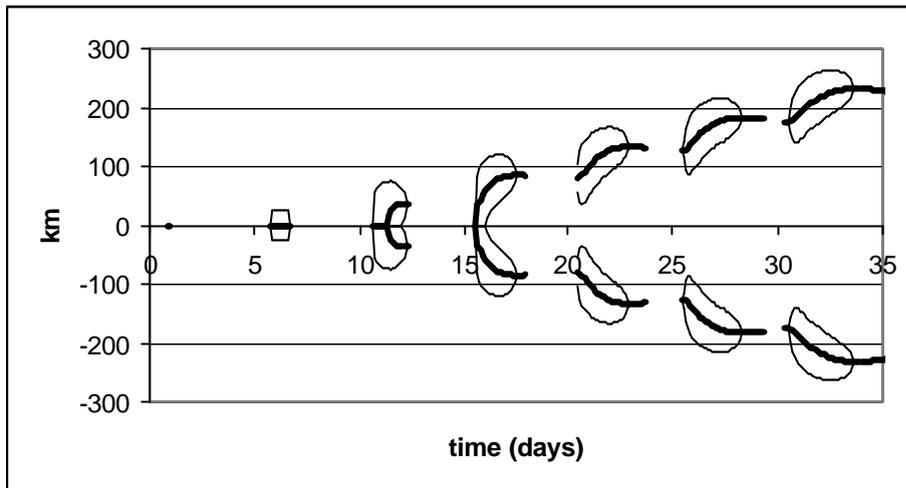
Figure 9.10   Development of 10 km d^{-1} waves with a 5 day latent period in the vicinity of the origin of the epidemic, thick line is the centre of the wave, thin lines show 5% mortality envelope (D = 30 km day^{-1}, b = 5 days, b-c = 1 day).

We see that, even though the wave moves away from the origin after about 2 weeks, it takes a similar period for the 5% mortality envelope (the region in which mortality exceeds 5% day) to reach 250 km from the origin. Mortality could occur within 100 km of the origin for a period of over 20 days. This is very much in accordance with the observations, particularly if currents or net fish movements lead to the focus of the epidemic waves being moved relative to the coast. We cannot take this argument too far however, because if such movements were important, the mature waves would exhibit more distortion. Both model versions are quite similar in average behaviour. However, the regular peaks and troughs of mortality should be detectable and indeed the evidence suggests that the epidemic recurs over a substantial period.

While oscillations persist the epidemic wave's speed varies, but from the moment it starts to move the wave speed averages 10 km d^{-1}, as predicted analytically. Because variation is very short term and the average speed is constant it is difficult to distinguish between the model versions.

The short-latent, short-infectious period model resembles the continuous turnover models. In this version of the model there are no oscillations. Even a very long latent period does not produce significant oscillations (Fig. 9.11). The wave develops smoothly without prolongation of the epidemic around the origin relative to later waveforms. Note also the very low maximum mortality (and resultant long time scale of mortality) caused by the gradual mortality of infected individuals in the continuous turnover versions of the model. This prolonged mortality is made worse by the adoption of a long latent period.
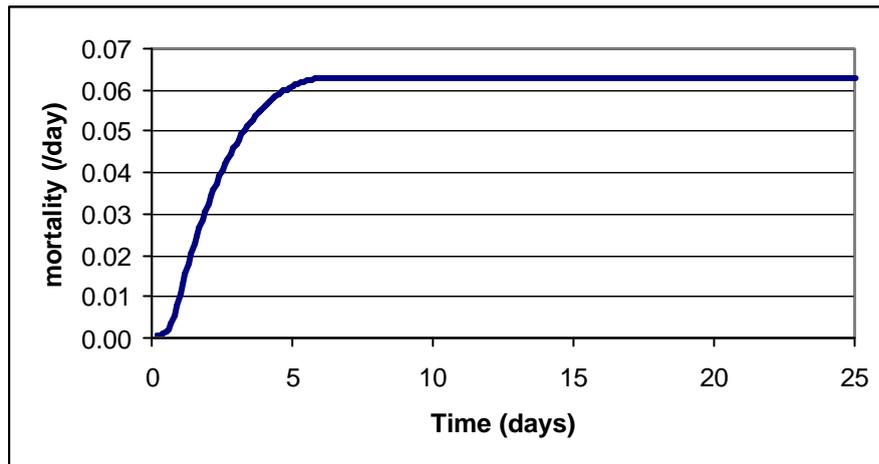
Figure 9.11   Maximum daily mortality in a continuous turnover SEIR model with eight day latent period (0.125 d^{-1} turnover). $D = 50$ km^2 d^{-1} and $\boldsymbol{b} = 500$ d^{-1} to give a 40 km d^{-1} wave.

This pattern of oscillation in mortality levels that the fixed period-length models produce does appear to resemble the observed initial pattern of reported epidemic mortality. Gaps of several days occurred between the first reports of mortality and subsequent reports. A six day oscillation may well be consistent with the 1998/9 epidemic. However the 1995 epidemic appeared to show a gap of about 8 days between the first and second peaks. A latent period of this length is inconsistent with the speed of the subsequent epidemic wave. A latent period of 4 days would be consistent with the epidemic disappearing, and possibly the second peak was then missed - the model predicts the initial peaks to be intense but brief so it is quite possible that a peak could have been missed.

9.4   Conclusions

At their point of origin, the epidemics persisted for several days before waves developed and travelled away to east and west. This persistence was for considerably longer than the time that mature waves lasted at a given location. There is also some evidence of gaps between initial recurring mortality events.

It does not appear that fish or current motions can explain this persistence, because otherwise the position of the epidemic wave would show similar distortion at distance from the origin. It may be that pilchard populations are isolated in the complex topography of the central South Australian coast. In 1998, mortality was most persistent around the complex Gulf St Vincent, Kangaroo Island, Victor Harbour area; but the area of most persistent mortality in 1995 was the western Eyre Peninsula, which provides few obstacles to the mixing for pilchard populations. In 1998, pilchards died in Port Phillip Bay only 3 days after deaths occurred at the entrance to that semi-enclosed bay (Neira, personal communication). We therefore expect that the recurring early epidemic behaviour is, at least in part, an intrinsic part of the epidemic's initiation.

The most realistic versions of the model appear to be moderate to long fixed-length latent-period with a short infectious period. This produces a wave with near constant speed and a short-lived peak after a long initial period of irregular mortality at the origin. The nature of this initial behaviour depends partly upon initialisation conditions.

The short latent period version produces a wave of constant speed but has similar mortality patterns at the origin and at distance from the epidemic, not consistent with the evolving wave. Traditional continuous turnover epidemic models produce similar results, again failing to reproduce the evolution of the epidemic waveform.

If the latent period is made too long relative to the infectious period, this leads to very intense isolated mortality events. These regular oscillations in the mortality events persist if the ratio is large. Observed mortality appears to rapidly become more spread out. This limits the possible ratio of the two period lengths.

The results challenge our earlier interpretation of the presence of lesions as being indicative of the infection having reached an infectious stage. It may only be in the later stages of their development that they become a significant source of new infection. However, the lesions, as they contain viruses, are certain evidence that infection has occurred and therefore the total infectious plus latent periods must be at least 4 days, the duration of the lesions.

We are thus able to use the initial observations to provide evidence for the most appropriate model structure and to further constrain parameters. The existence of a latent period allows the epidemic to recur over a prolonged period at the origin while coalescing into a single wave later. The period of recurring outbreaks is less than observed, but it is qualitatively reproduced by this form of the model - and not by other model formulations.

10 Non-Linear Transmission and the Epidemic Spread

In this chapter we consider a non-linear transmission of infection model. This model has major implications for the origin of the epidemic since it requires a large initial dose of infection to induce the epidemic, whereas under the standard model any dose may induce an epidemic provided the environment is suitable.

Viral transmission may depend on a threshold concentration of viruses that is required to induce infection. The immune systems of hosts that are exposed to small numbers of viruses may be able to fight this off, but a massive dose is another matter. This appears to be the case for IPNV for which a minimum challenge dose of virus may be required to trigger infection (Hill 1982). Confinement of Pacific herring in cages allowed VHSV (viral hemorrhagic septicemia virus) to build up in the water and thus an epidemic to take off (Hershberger *et al.* 1999). Free herring, from which the caged stock was taken, did not develop disease at this time. This may be an effect of linearly higher infection probability caused by the local retention of the fish in the vicinity of accumulating virus numbers, but it is suggestive of the minimum viral dose effect.

If there is such a dependence of infection on high viral density then infection may depend upon a higher power of I, perhaps bSI^2 (Liu *et al.* 1986). Infectivity, the rate at which new infections are produced per infected host, is low both when I is low and when it is high because then S is low as a proportion of the population. This situation means that there is a minimum product of both susceptible and infective host populations required for an epidemic to take off (Fig. 10.1). Under the standard linear model the number of infections produced per infected individual is only low when I is

high and hence S is small. The actual number of infections produced when I is low is also low, but the infections produced per infected host are then maximal.

$$[SI]_t = a/b \qquad\qquad (10.1)$$

This relationship of infection rate to I has particular significance for the origin of the epidemics. Under the quadratic (I^2) model a locally stressed host population may have an infection induced by this stress that can then spread freely to adjacent unstressed populations. A localised environmental shock could thus be the trigger of a wide-ranging epidemic. However, the presence of a small amount of virus in an unstressed host population will not trigger disease. This is in contrast to the standard linear model, under which any presence of virus will trigger the disease, provided the initial host population exceeds the threshold.
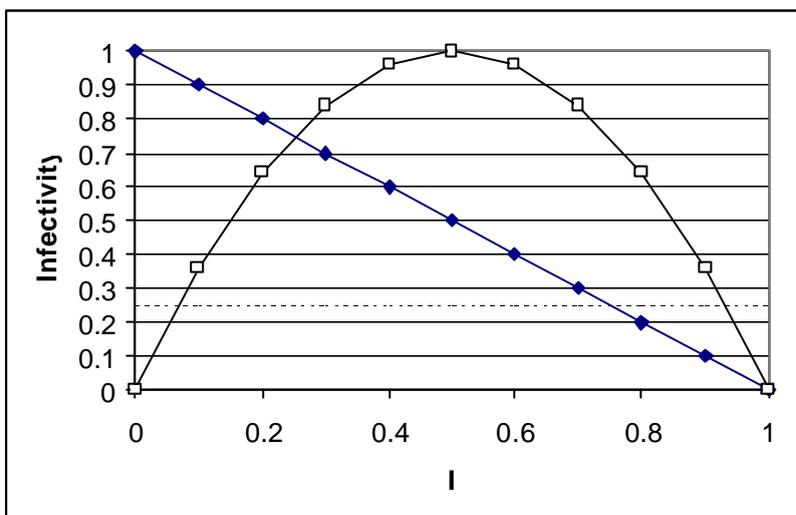
Figure 10.1   Infectivity (normalised to maximum infectivity) under bIS and bI^2S models (while R and $E = 0$). The dashed line gives an example threshold population for net infection. The maximum infectivity = bS_0 under bIS and $0.25bS_0$ under bI^2S model.

There is no evidence of any environmental shock that could have initiated an infection of the non-linear transmission type. There was a cold upwelling prior to the 1995 epidemic, but events on a similar scale occur every three-four years (Griffin *et al.* 1997). No upwelling occurred prior to the 1998/9 epidemic (Ward *et al.* 1999).

The transmission of the epidemic to caged pilchards, physically isolated from the wild stock, is evidence supporting the linear transmission model since it is unlikely that very large number of viruses would be transmitted to this isolated population. Similarly, the coincidental outbreak in New Zealand in 1995 supports the linear model. It would be unsurprising if the disease were transported to New Zealand given its then prevalence in Australia, but it would be less likely that a similar environmental shock occurred coincidentally in the same year and not in some other year.

The linear model is the form of transmission that is almost invariably used to model epidemics (e.g. Anderson and May 1979). However, because of the significant differences between the two models, both linear and quadratic transmission we examine the latter formulation here as well

We can apply the quadratic version of non-linear infection (i.e. infection dependent on I^2) to the spatially resolved model. We can thus generate waves of infection which are similar to those generated under the linear model. However, with the initial intrusion of the wave of infection I is small and I^2 is very small. This means, in the quadratic model the forward front of the infection is an area of low production of infection. The speed of the wave is driven by the area of high production, when I becomes large and where S is still not small. But by this point the relative gradient of the distribution of I has declined and so diffusive flux is weakened. Hence the epidemic wave progresses more slowly. The dispersal of E and I still limits maximum diffusion rates consistent with observations. Hence, for a given latent period, the value of b selected must be much larger than under the linear model.

We lack an analytical solution of the quadratic model, but we have been able to find curves for various latent periods under the two speeds by fitting the value of b required to produce the appropriate wave speed (Fig. 10.2). These waves are of constant speed. However, longer latent periods result in the need for even higher infection rates. The high infection rates results in waves that mature very rapidly, hence these waves depart from the origin only a few days after infection. Indeed the wave forms only a couple of days after the first mortality, which occurs at 4 days after the infection is introduced. Mortality does continue at the origin for a short while.
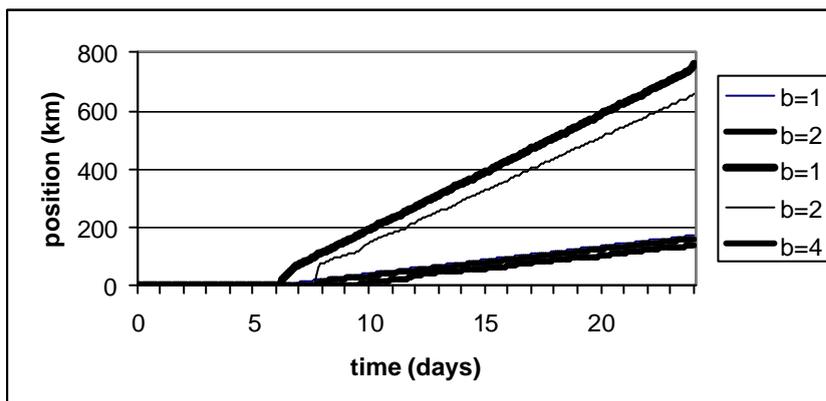
Figure 10.2   Development of 10 and 40 km d^{-1} waves under quadratic infection. For the 10 km d^{-1} waves $D = 20$ km^2 d^{-1} and $b = 1$ $b = 100$, $b = 2$ $b = 1000$, $b = 4$ $b = 40000$. For the 40 km d waves $D = 200$ and $b = 1$ $b = 1000$, $b = 2$ $b = 20000$.

The quadratic model also produces a similar mature wave shape (Fig. 12.3) to that obtained under the linear mortality model. Mortality is spread over a few days, as observed. There are similar peaks for the two diffusion coefficients to the values obtained under the linear infection model.
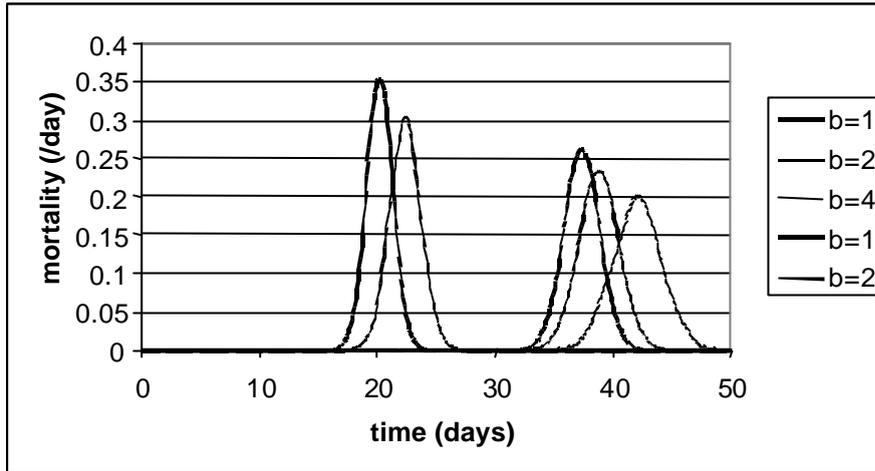
Figure 10.3   Shape of stable 10 and 40 km d^{-1} waves under quadratic infection. For the 10 km d^{-1} waves $D = 20$ km^2 d^{-1} and $b = 1$ $\boldsymbol{b} = 100$, $b = 2$ $\boldsymbol{b} = 1000$, $b = 4$ $\boldsymbol{b} = 40000$. For the 40 km d waves $D = 200$ and $b = 1$ $\boldsymbol{b} = 1000$, $b = 2$ $\boldsymbol{b} = 20000$.

The quadratic infection model can also produce oscillations similar to those obtained under the linear model. However, due to the relatively short latent periods that in this model are compatible with the observed wave speeds, given limits to diffusion imposed by the short-lived pattern of mortality in the mature waves, only brief periods of oscillation occur (Figs. 10.4, 10.5). For latent periods of 1 day, these peaks are spaced at daily intervals and so would be undetectable given the necessary limits to the resolution of observational data, except possibly as initially high mortality. Only the slower waves can be made compatible with a significant gap between first and secondary mortality events.
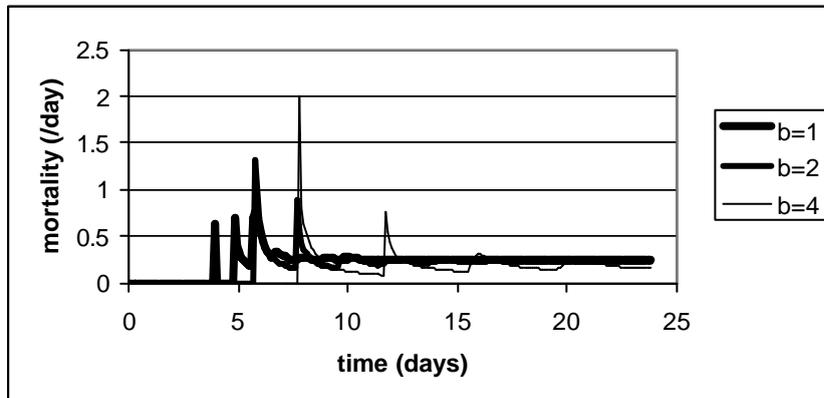
Figure 10.4   Initial development of the 10 km d^{-1} quadratic epidemic wave under three latent period lengths.
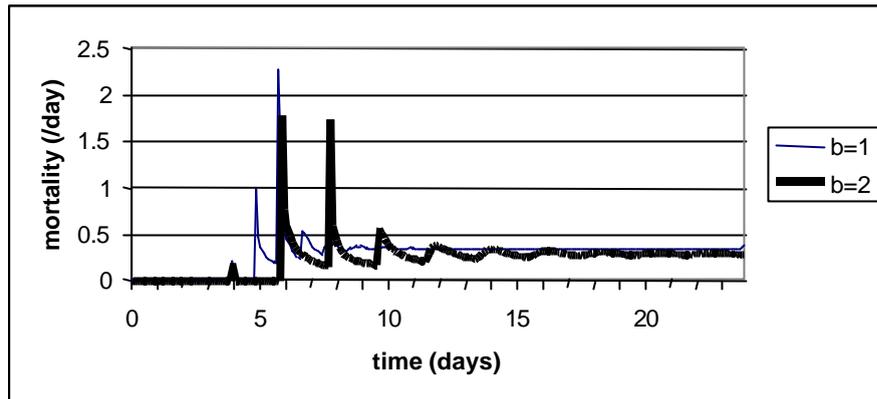
Figure 10.5   Initial development of the 40 km d^{-1} quadratic epidemic wave under two latent period lengths.

The quadratic model appears less compatible with the evidence than is the standard linear model. It can be made to produce stable epidemic waves whose behaviour is identical to those obtained under linear infection models, although higher transmission coefficients are required. However, the initial persistence at the origin under this model is too short lived. This occurs because of the requirement for rapid viral transmission rates. Initial gaps or oscillations in the observed mortality also cannot be reproduced, except for the slower wave speeds because long incubation periods are not consistent with observed wave speeds. The quadratic model would be entirely ruled out in its current form if it were shown that latent periods do exceed two to 3 days.

Because quadratic infection spreads more rapidly as the number of infected individuals increases it gives an inherent tendency for epidemics to take off suddenly and so not to persist near the origin as was observed.

The difference between the linear and quadratic models is largely in their implications for the origin of the epidemic. Under the linear model any initial dose of viable virus can lead to the epidemic taking root. The quadratic model requires a large initial viral dose and so is less easy to introduce. Since it is precisely the behaviour at the origin that the quadratic model fails to reproduce the linear model would appear to be a better choice.

11   Discussion of the Modelling, Impacts and Management of Epidemics

11.1   General Discussions on the Modelling

We have developed a new approach to modelling the pilchard epidemics of 1995 and 1998/9, which gives a better replication of the observations than existing models, particularly at the point of origin of the epidemic. We are able to derive several important conclusions derived from the model we have developed. Analysis has been greatly simplified by the development of an analytical method for finding wave speed.

Traditional continuous turnover models do not work as a description of the pilchard epidemic. Such models generate continuous mortality over long periods; the observed pattern is quite different. Lesions are apparent up to 4 days before mortality occurs and this mortality then occurs suddenly over a short period. The continuous models would predict mortality would begin at the same time as the first lesions became apparent and would tail off slowly as the number of infected fish gradually declined. Alternatively, if mortality were very rapid then there could be a very rapid die off, if infection were even more rapid. If this turnover were rapid then infected fish would not be present in significant numbers, as evidenced by lesions, days prior to detected mortality. The lesions present in fish sampled ahead of the front are qualitatively different from those at the front (Fletcher *et al.* 1997). This means that they are at an earlier pre-lethal stage of development, not simply that there are a few infected fish with mortality going undetected. Such a rapidly turning over epidemic would develop a mature waveform rapidly. The epidemic would not persist near the origin for much longer than the 1 or 2 days that the mature epidemic wave persists.

We therefore adopted another model based on fixed length periods of infection. This model can generate sharp mortality events and have infection apparent in the form of lesions for days prior to these events. The model is also biologically reasonable in that infection must take time to develop, no fish will die the instant it is infected, the disease must develop first. But continuous models predict this is possible and indeed in the SIR model the most probable time of death is immediately after infection, the probability then drops since dead animals cannot die again.

We split the time course of the development of infection into an infectious period and a latent period while the disease develops within the fish but it does not act as a significant source of new infection. The latent period is a standard component of disease models. In this case it appears to be necessary that the infectious period is quite short in order to reproduce the behaviour of the epidemic at its point of origin.

A method of solving the wave speed from this model analytically has been developed. This is a major advance in that it enables wave speeds for a given parameter set to be determined almost instantaneously. When combined with a binary search algorithm, the method can be used to find an unknown parameter value required to generate a specific wave speed, if two of the diffusion coefficient, transmission coefficient and latent period length are specified. This enables a systematic search of parameter space to be conducted in minutes, a process that would take days under the numerical model.

11.2   What Controls Epidemic Behaviour?

Model epidemic wave speed has been found to depend essentially on three parameters: the infection rate, the diffusion coefficient and the length of the latent period. Two other factors have surprisingly little effect on wave speed. These are the duration of the infectious phase and population density.

11.2.1 Infectious Period

Duration of the infection has little effect on the mature waves speed, although it has significant effects on its initiation. The effect is so small that the analytical solution derived under a continuous turnover of infected individuals works just as well for the

version with a fixed length infectious period. The infectious period length does become a significant constraint when b is small.   The model has provided unexpected evidence that the infectious period only applies to a short period towards the end of the infection. This has significant effect on the pattern of origin of the epidemic.

11.2.2   Population Density

Change in population density actually has as much effect on wave speed as do changes in viral transmission rate in the model. However, changes of an order of magnitude are required to have large effects on wave velocity, and while this may be possible for viral transmission rate such large changes are not consistent with known changes in population density in Australia. One need only examine the near constant rate of spread of either epidemic in Western Australia to see how constant the speed is over a couple of thousand km, a range in which there must surely be variation in population density. Populations in Western Australia declined between 1994 and 1997, for reasons other than the epidemics (Cochrane 1999).

It is also possible that transmission is population density independent, in which case there would be no response at all to changes in population density.

Because of non-linear effects of population density it is possible that the degree of dispersal of the pilchard population could impact on the averaged rate of transmission. A population that was denser in some local areas and less dense in others would be less effective at transmission than would a population that travelled across all areas. The weak response to population density means this effect is likely to be small, but in other epidemics which are more responsive to population density, this factor could be significant.

11.2.3   Viral Transmission Rate

The model wave speed shows a weak but significant dependence on the viral transmission rate b. Sensitivity declines as the transmission rate increases. At large values of this parameter wave speed almost ceases to respond to further increases in transmission rate.

The viral transmission rate is only weakly constrained and so may vary by orders of magnitude; indeed there is evidence that it does so vary in that the lesions on infected fish's gills in 1998/9 were much fewer than in 1995. So it may remain a significant control on changes in the epidemic's behaviour provided it is not very large.

The population mixing rate does not affect moderate viral transmission rates but it does impose an ultimate cap on the maximum value of the transmission rate. The value of the cap depends upon fish behaviour and so is unknown. Sensitivity analysis shows that the rate at which the epidemic wave propagates in this model becomes increasingly insensitive to the transmission coefficient as this becomes large. Therefore our ignorance as to the exact value of the maximum transmission is not important even when transmission rate is large, so long as the maximum is large.

Behaviour at the origin is probably a much stronger constraint on the viral transmission parameter. Large values of this parameter are inconsistent with mortality occurring at

intervals near the origin for two-three weeks. Low values produce a single smooth peak, which is similar to the mature wave. Again, this is inconsistent with a long initial period of mortality.

11.2.4 Diffusion Coefficient

The model wave speed responds strongly to the diffusion coefficient, in fact response is controlled by the diffusion of infected fish alone. The control of epidemic speed by the behaviour of infected individuals is an important insight that is applicable epidemic models in general. However, we have generally used a single diffusion coefficient for this model. We have no data to separate the behaviours of infected and uninfected fish and as no detectable effects occur when diffusion is at a different rate for uninfected fish

Diffusion coefficient can be constrained with reference the briefness of local mortality in the stabilised epidemic wave. We are able to find a maximum diffusion coefficient because as this becomes large infected fish spread out before dying. The degree to which this occurs is surprisingly insensitive to the latent period over the range of 1 to a few days. We find that the 40 km d^{-1} eastbound 1995 wave has a maximum D of about 200 km^2 d^{-1}, the 20 km d^{-1} westbound wave a D of 100 km^2 d^{-1} and the 10 km d^{-1} 1998/9 wave has a maximum D of only 30 km^2 d^{-1}.

The movement of fish alone can easily generate these values and so no vector is required to explain them. The pattern of infection, killing adults but usually avoiding juveniles, also suggests that it is fish-to-fish contact which spreads the disease. However, the fact that D can be generated without a vector does not mean that birds or other organisms do not sometimes transport the virus.

11.2.5 The Latent Period

Epidemic wave speed in this model with its fixed length latent period is far more sensitive to the length of the latent period than is the model with a continuous turnover formulation. This model responds to the square root of the latent period, while the traditional model responds to the fourth root (Yachi *et al.* 1988).

Because wave speed becomes essentially independent of *b* for large *b*, we have a maximum latent period that is consistent with the maximum diffusion coefficient and wave speed. For the 40, 20 and 10 km d^{-1} waves this latent period is four, eight or 12 days. However, we lack direct data for the length of the latent period and infectious period other than observed lesions present for two to 4 days before mortality (Whittington *et al.* 1997). Direct data should be obtainable experimentally, and if it were available it would be a highly valuable test of, and constraint on, the model.

The latent period is a major factor in the pattern of recurrent persistent mortality during the initial phase of the epidemic. This recurrence pattern would tend to support latent periods of around the 4 days that can still reproduce the observed wave speed.

The existence of the latent period gives time for infected fish to mix among schools before they become infectious. As a result the details of the mixing of fish populations are of less importance as a control on the epidemic's spread than is fish-to-fish infection.

This result greatly simplifies modelling, since we can dispense with models of the local structure and dynamics of the fish population.

11.2.6 Mortality

The proportion of mortality, as opposed to recovery, of infected individuals does not impact on the epidemic's behaviour in terms of the speed and local persistence of the mortality. It is of great significance for its longer-term impact (see 11.4). The model produces very high levels of infection and so the epidemic's long-term impact is largely controlled by the fraction of those infected individuals that die. We do not have a good handle on this value. The average value in Western Australia varied from 15% in 1995 to 60% in 1999 and showed very large local variation. In 1995 in South Australia mortality was 60% of the population. This figure is the fraction of the population killed, but with infection levels of over 90% the fraction of the population killed is not very different from the fraction of infected fish killed.

11.3 Differences Between and within Epidemics

The eastbound waves of both epidemics travelled at twice the speed of the coincident westbound epidemic wave in both 1995 and 1998/9. There is considerable uncertainty in the speed of the eastbound wave, which showed variation in 1995 and for which few data points are available beyond Victoria in 1999. The two waves of the 1998/9 epidemic travelled at less than half the speed of that occurring in 1995.

There are three possible explanations for the differences between the eastern and western wave speeds, physical advection leading to an eastward drift, changes in diffusion due to differences in the behaviour of the fish or vectors, or there could be changes in the properties of the virus and infection. Only the last two, changes in diffusion or properties of the infection, could apply to the interannual differences. These processes could apply under any model formulation and indeed the effects of changes in advection or diffusion would be exactly the same under any considered model formulation. These are thus robust conclusions.

11.3.1 Physical Advection

Net east flowing currents could lead to advection towards the east leading to a reduction in the rate of westward flow and an increase in the rate of eastward flow of the epidemic. Thus the 1995 epidemic could be characterised by a 30 km d^{-1} wave combined with a 10 km d^{-1} eastward advection, while the 1998/9 epidemic would require a 15 km d^{-1} wave and 5 km d^{-1} advection. Since the flux would be in a consistent direction this motion would not lead to no excess diffusion and hence no change in the wave's shape.

This model is simple and consistent. However, if pilchards had a net movement that were consistently in one direction the entire Australian pilchard population would gradually move east. Clearly this is impossible. It is possible that infected fish are unable to swim as efficiently as uninfected fish and therefore are carried by the current. However, the infected fish do not appear to show any behavioural differences from uninfected fish until a few minutes before death (Whittington *et al.* 1997).

There are also problems with assuming a constant east-flowing current. The epidemic wave speed, if driven by advection, would respond linearly to changes in current speed. The very limited variation from the linear regression of the epidemic's progress in Western Australia shows that there were no such distortions. Propagation rate was unaffected by several storms (Fletcher *et al.* 1997), surely these events would lead to variation in advection rate. The rapid northward development of the epidemic along the eastern coast of Australia appears to be directly against the prevailing current (Griffin *et al.* 1997). In 1999 rapid expansion of the epidemic occurred simultaneously north to Newcastle and south to Hobart, which presents obvious problems for this theory.

The speed of the advection would have to have halved between 1995 and 1998/9. This process would only lead to the differences in the speeds of the two wings of the epidemic. It can not explain the difference in the total rate of spread between the two epidemics.

11.3.2   Viral Evolution

Two parameters, viral transmission rate and the latent period of the infection, may be changed resulting in changes in the wave speed. The epidemic wave speed is very sensitive to these parameters, particularly to the latent period's length. Evolution of viruses can occur over a few generations if selective pressures are strong (Ebert 1998).

Evolution in the virus's properties almost certainly did occur between the two epidemics. Viral lesions were much less abundant in the 1998/9 epidemic than they were in 1995 (AAHL 1999). Therefore the production of viruses, and hence probably *b*, seems to have dropped.

It would seem strange for the virus to evolve such that one wing of a single epidemic travelled at twice the speed of the other, while these epidemic wings were internally highly consistent in speed. There would have to be some environmental difference to drive such evolution. In any case the major difference in the appearance of lesions between the two epidemics would suggest major differences would be apparent in pathology.

Such viral evolution is very likely to be a cause of differences between the speed of the two epidemics, but it is questionable that it explains the large differences within the epidemics.

Changes in the viral transmission rate cannot alone account for the variation in the wave speed. This is because the slower wave speed is only consistent with low diffusion coefficients, while faster wave speeds are not consistent with such low diffusion coefficients, for a given latent period. The initial behaviour of both epidemics seems to be consistent with a longer four or more days latent period length. Extreme changes in latent period length do not appear appropriate, but the wave speed is very sensitive this parameter, so small changes may have significant effects. The transmission rate and latent period could evolve in parallel.

11.3.3 Differences in Diffusion due to changes in Fish or Vector Behaviour

All epidemic models considered produce epidemic wave speeds that respond to the square root of diffusion. A change in this parameter by a factor of four leads to a change in speed by a factor of two.

The final option is thus that there is some difference between fish (or vector) behaviour east and west. This would result in changes in the diffusion coefficient, which would have to be some four times greater towards the east. This explanation would be consistent between the epidemics. However, the cause of any such difference must be explained.

The evidence suggests that pilchard movement, not that of vectors, is responsible for the epidemic's spread. Diffusion coefficients are within the values that can easily be generated by pilchards – large diffusion coefficients are not consistent with the tightly focus mortality wave observed. Mortality only occasionally affects juvenile pilchards, which suggests fish to fish mixing rather than vectors at least some of which would be likely to feed on adults or juveniles with less discrimination.

Pilchard movement on the east coast of Australia may be less inhibited by boundaries than on the west coast. Indeed the evidence appears to show a very rapid progression between the Bass Strait and east coast populations. Towards the west, Cape Leeuwin forms a strong boundary to the mixing of pilchard populations.

Pilchards off South America exhibit substantial differences in their patterns of movement between El Niño years and other years (Torres *et al.* 1984). It is therefore quite possible that the behaviour of pilchards could be different in different environments in the west and east. Long migrations exhibited by South American (Torres *et al.* 1984) and southern African (Newman 1970) pilchards appear quite different from the behaviour of Western Australia where populations and sub-population (Cochrane 1999) appear to be restricted to well defined localities. The eastern Australian population is divided into two populations (Bass Strait and east coast) but it is quite possible that they are more mobile. Yardin *et al.* (1998) noted a high degree of mixing in south eastern Australian pilchard stocks. Their distribution varies with time (Hobday 1992, Neira *et al.* 1999), so these populations are mobile. Mortality patterns also indicate a mobile population, on both occasions mortality occurred at similar locations in Western Australia while in the east mortality occurred in quite different areas, such as northern Tasmania in 1995 but not 1999, and south-east Tasmania in 1999 but not 1995. It is therefore possible that eastern Australia's pilchards could behave quite differently to those in the west.

Inter-annually, 1995 was at the end of an El Niño year and this was associated with low rainfall leading to low nutrient inputs and hence low production in coastal waters such as Port Phillip Bay (Neira *et al.* 1999). This could have lead to fish searching for food over larger distances, hence leading to higher diffusion rates.

Small diffusion coefficients maintain the sharply focused wave of mortality in the advancing front. It is possible that in 1998 the diffusion in the eastbound wave is too

large relative to lower production in the second epidemic, causing the wave to become dispersed and thus only rarely detectable once it was mature.

The epidemic advanced up the east coast less regularly than the western advance. In 1998/9 the epidemic was only apparent irregularly. This could be evidence that diffusion was larger and involved larger scale movements of the fish, leading to dispersal of peaks and random advective components to the movement; this advection is due to the motion of fish not the water. Dispersion of peaks by strong diffusion could lead to low continuous rates of mortality that might be undetectable if scavengers removed the small numbers of dead fish.

11.3.4   Conclusions

There are two explanations for the differences between epidemics waves to the east and west. Under one model, there is a 10 km advection in 1995 and 5 km advection in 1998/9. The alternative explanation is that diffusion coefficients in the east are inherently four times larger than those in the west. The properties of the epidemic are unlikely to be very different within a single outbreak. The population density has only a minimal effect on the epidemic's speed.

Which cause is more likely? If advection drove the differences in wave speed then this would respond linearly to changes in advection, it seems unlikely that advection would be constant for months and yet change in speed by a factor of two in different years. The very high degree of constancy of the westbound propagation rate would show any fluctuations in current speed if advection were important. On the east coast the currents run against the epidemic in spite of rapid advance along that coast (Griffin *et al.* 1997).

The diffusion explanation relies on fundamentally different behaviour in pilchard populations. This is certainly possible. Pilchard population in Western Australia appears to consist of specific populations and sub populations which, while mixing, live in restricted areas. On the other hand, South American and southern African pilchards migrate over 100s or even 1000s of kms on a regular basis. Therefore other pilchard populations behave quite differently and it is perfectly possible that the eastern pilchards are more mobile than those in the west are. The wave speed only responds to the square root of diffusion, so small changes would have little effect on the wave's speed. This would allow the highly constant advance of the westbound wave.

Interannual variation is due either a drop in the diffusion coefficient by a factor of four, or a large increase in b combined with an increase in the latent period. Advection cannot affect the speed in both directions in the same way; increase in one direction must lead to decrease in the other. The large change in the abundance of lesions in infected fish between 1995 and 1998 indicates that transmission efficiency has changed, so this is at least part of the explanation for the interannual change in the epidemic. Changes in the nature of the infection could be combined with changes in diffusion. Since 1995 was the end of a severe El Niño it is possible that low nutrients, leading to increased movement of pilchards as they searched for more isolated food sources.

In conclusion, we attribute difference between the eastern and western behaviours of the epidemic are due to differences in diffusion owing to different fish behaviours in

different populations. Interannual variation is due to changes in viral properties, probably with further changes in diffusion coefficient.

11.4   Longer Term Impacts of the Epidemics

Very high levels of infection are generated under all model scenarios and this is consistent with the observations. The level of mortality inflicted is thus largely controlled by the fraction of infected individuals that die rather than recover. Regional average mortality levels have been estimated for Western Australia as 15 and 60%. There is thus a substantial variation in the degree of mortality inflicted, and the effect of a subsequent epidemic could be quite different.

Population recovery following the epidemics depends upon the production of the pilchards (Wada and Jacobson 1998). The recruitment of clupeoids is extremely variable and difficult to predict (Cole and McGlade 1998). These fish do have variable populations and may be well adapted to recovering from sudden negative impacts such as the epidemics. Reduced population may reduce competition, and even cannibalism, and hence improve survival (Cole and McGlade 1998). However, pilchard populations in some areas appear to be declining, particularly near Albany, even without the epidemics and it is possible that pilchards could be replaced by some other small planktiverous fish that competes for this resource (Cochrane 1999, Kawasaki 1982). If such a replacement were to happen population changes are likely to be very long term.

We have developed a simple model of the pilchard population, based on a model developed by Fletcher (1992). This model illustrates recovery from the effects of the epidemic. The basic structure of the model is:

$$dP/dt = \textbf{\textit{m}}A/(A + r_a) - mP \tag{11.1}$$

Where P is the pilchard population, A is the adult pilchard population, $\textbf{\textit{m}}$ is the population growth rate and m is mortality rate. Typical annual mortality m is 0.4-0.5 y^{-1} (Fletcher 1997, McCall 1979). Parameter r_a is a Beverton-Holt parameter which allows production to saturate as the population becomes large. We use a value of 1.

Existing data suggests that the pilchard populations recovered rapidly from the mortality inflicted by the epidemics. Adult population estimates for South Australia are, in thousands of tonnes): 1995, 59; 1996 18; 1997 59; 1998 95; and 1999 38 thousand tonnes (Jones 2000). This shows the ability to triple population in one year - net growth. Allowing for mortality we use a gross growth $\textbf{\textit{m}}$ of 7 y^{-1}. This is at odds with the records from California, from which a maximum population growth of 8.5% y^{-1} was deduced (McCall 1979). However, there is a lot of scatter about the average growth rate.

The model divides the population into nine year classes, reflecting the maximum nine year lifespan of pilchards (Fletcher *et al.* 1997). The first year class consists of sexually immature juveniles into which new recruits are placed, while other year classes are breeding adults. Equations are solved with an annual time step. Individuals in the oldest year class die. This is obviously a simplified simulation; in reality breeding may

take place twice a year and occurs at different times at different locations (Fletcher *et al.* 1997).

We have run this model until the population structure is stable and then imposed an additional epidemic mortality on one year (Fig. 11.1), populations are normalised to the stable population. The background mortality rate is 0.4 y^{-1} and with an epidemic mortality of 0.15 or 0.6 y^{-1} the total mortality in the epidemic year is 0.49 or 0.76 y^{-1}. We find that when subjected to such epidemics the model shows a fairly rapid recovery, even under the extreme case biomass recovers from 40% to 80% within three years. Observed recovery is even faster, but this may reflect the large degree of stochasticity in the recruitment (Cole and McGlade 1998, Wada and Jacobson 1998). A second epidemic three years after the first causes a further decline in population, but recovery remains rapid.
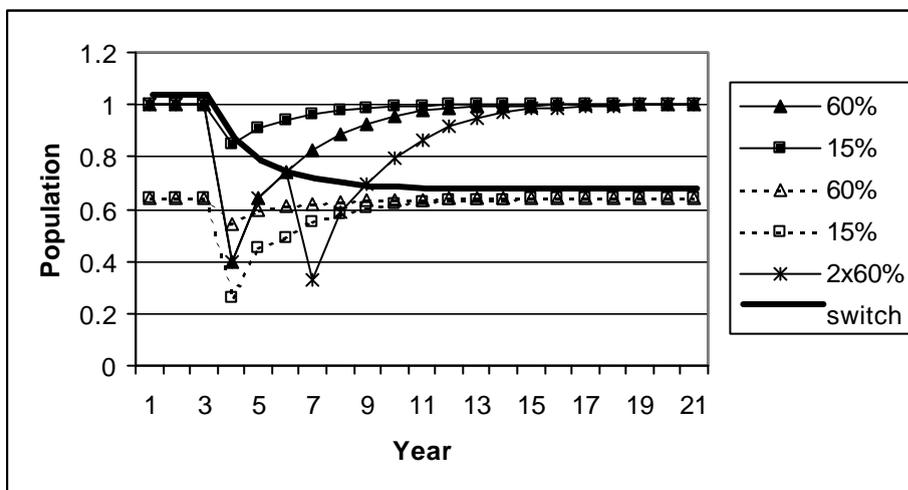
Figure 11.1   Populations of pilchards under background mortality of 0.4 y^{-1} (solid line) or 0.5 y^{-1} (dashed line) subjected to epidemic mortality of 15% (squares) or 60% (triangles) after year 3. Line with crosses shows the effect of repeated 60% epidemic mortality on a population with 40% background mortality. Bold line shows effect of switching from 40% to 50% background mortality.

The fish stocks can recover from large levels of epidemic mortality and are hardly affected by small levels of mortality. This leads to the question - can the stocks sustain high levels of exploitation? Increases in catch equivalent to the 15% epidemic mortality increases the background mortality from 40 to 50% y^{-1}. To this increase in mortality the population reacts quite differently, falling to 64% of its original biomass over about five years; at 76% mortality the population is cut to only 12.8% of the original. This high degree of sensitivity to increase in catch mortality is the same behaviour as found by Fletcher (1992). At this low biomass, the model shows a similar relative response to epidemics, with a slightly more rapid recovery than under lower background mortality.

This model is a simple model adapted from the work of Fletcher (1992). It is not intended to give an accurate description of the speed of recovery of the population following a particular epidemic. Stochastic effects are likely to be very large and therefore exact recovery time is unpredictable. The model is intended to illustrate the difference in response of the pilchard's population to one off (even repeated at intervals) and consistent levels of mortality.

Pilchards are a major food source for larger fish, seabirds and mammals (reviewed by Murray 1999, Ward and Jones 1998). A species that shows a particular dependence is the little penguin (Hobday 1992). Low stocks of pilchards are likely to result in low recruitment of their predators. However, provided the epidemic is not so severe, and alternative food sources are unavailable, as to cause adults to die of starvation, the impact of short-lived events on long lived large predator populations is likely to be moderate if the pilchard population can recover. If starvation of adults does occur, then the populations of these large predators may take a very long time to recover, resulting in persistent instability in the ecosystem.

11.5   Management Options

Because the pilchard is a highly mobile schooling fish it seems inherently vulnerable to disease. Unstable populations are a hallmark of many schooling clupeoid fish (Blaxter and Hunter 1982, Wada and Jacobson 1998). The disease appears to exist in its host for several days before killing it, this means that it can disperse freely. Such a virulent disease can be transmitted effectively even at low population density, a fact enhanced by schooling, which maintains high contact rates at low densities.

Manipulation of the adult population does not appear to be a practical management option. Even if very low densities can be maintained, the disease is still transmitted quite effectively as transmission is only very weakly dependent on population density. Firebreak management is unlikely to be effective. Note that, even if it is effective, the actual position of the epidemic front is far ahead of the point of high mortality because in the time taken for the disease to develop the epidemic front moves on. The unlikelihood of a successful firebreak is consistent with the propagation of disease around Cape Leeuwin, in spite of low local populations (Fletcher *et al.* 1997).

Juvenile pilchards found close to infected adult pilchards may avoid infection (Whittington *et al.* 1997), even though, at least in 1998/9, the juveniles were vulnerable to the disease (Ward *et al.* 1999). Juveniles and adults do not shoal together. This suggests exchange of population is required for effective transmission between schools.

If birds, or other predators, acted as a vector for the disease we would expect to see it spread as a matter of course between adult and juvenile populations. Very high diffusion coefficients, consistent with bird movements, also appear to produce mortality distribution patterns at odds with the observations. This appears to mean such vectors lack a critical role in transmission and that the culling of birds, mammals or large fish is unlikely to be an effective means of limiting the spread of the pilchard herpesvirus.

The disease's spread is much more sensitive to patterns of movement than it is to population density. If pilchard movement through specific areas could be discouraged this would be more likely to contain the disease. However, no mechanism exists for this. If a barrier could be formed, then vectors might be able to transport the virus over the barrier, even if they are not normally important in transmission.

Juvenile pilchards appear to live in coastal embayments (Neira *et al.* 1999). This would argue much weaker mixing of populations is possible than for shelf-living adults.

Mortality of juveniles either does not occur or is limited in spread. Preservation and separation of juvenile stocks would appear to be the most effective means of ensuring rapid pilchard recovery. This may be achievable by limiting fisheries based on juveniles, currently such a fishery occurs in Port Phillip Bay and Spencer Gulf (Jackson *et al.* 1999), and by ensuring as many pilchard nursery areas as possible are preserved as healthy environments. It is better, for this purpose, to preserve many ecosystems in reasonable condition than a few in pristine condition.

Populations appear to recover quite robustly following even high levels of epidemic mortality. Repeated large epidemics increase the impact on populations to a moderately large level. However, sustained increase mortality at even moderate levels leads to a large decline in fish populations. Failure of recruitment, as observed off Japan, has the largest impact of all; the disease has less impact on juvenile than adult populations and therefore it does not prevent recruitment.

Inoculation may, in the long-term be a possible route to achieve protection. Since isolation is unlikely to succeed probably the most effective strategy for preservation of pilchards may be to take advantage of their well-mixed populations. The model shows that few adult fish can avoid infection, hence survivors must be resistant individuals. The 1995 epidemic in Western Australia appears to have caused only moderate levels of mortality and to have spread far faster than the 1998/9 epidemic; part of this change in speed must be due to different fish movement patterns, but part is due to increased viral production. Had it been possible to introduce the 1995 virus ahead of the 1998/9 virus and if it caused immunity to the latter, then mortality levels could have been drastically reduced. Ideally a third virus with the elevated transmission of the 1995 epidemic, but inflicting lower levels of mortality could potentially be used to immunise the population in the event of a subsequent epidemic. We would need to know much more about why the virus kills (high levels of mortality were recorded in South Australia in 1995) before such a strategy is even remotely practicable. It will also be noted that currently we have no effective means of assessing mortality until the epidemic is well developed, in that case we cannot tell if the 'cure' is more deadly than the 'disease'. We would also need to ensure the virus induces immunity and that surviving pilchards have not evolved immunity to the older viral strain, thus preventing its spread. This requires more experimentation on pilchards and tissue cultures, but has a lot of long-term potential.

More data is required on the epidemic in order to constrain the model. The disease has to be propagated *in vivo* in order to allow the evaluation of the lengths of the latent and infectious phases. Such information should be obtainable experimentally and would strongly constrain the model. Tagging experiments could be used to determine whether there are large differences in the behaviour of different pilchard populations.

The recommendations therefore, are maintain vigilance against introduction of viruses, and protect the juveniles' habitat and populations. In the longer term, the high rate of spread of the 1995 epidemic may be used to produce a low mortality inoculum. Reduction of the fish population and culling of birds are specifically ruled out as effective controls by the results of the model.

12   Benefits, Future Developments and Conclusions of Research

12.1   Benefits

The research has lead to the development of a series of models which provide insight into the epidemiology of the pilchard herpesvirus and the behaviour of the pilchard. Exploitation of these results is of benefit to researchers and managers.

The most direct benefit is in the demonstration that the epidemic cannot be controlled by controlling sea birds or by adoption of 'fire-breaks' or other forms of fishing down the pilchard population. The epidemic's spread is shown to be consistent with pilchard movements, and local development of the epidemic is inconsistent with very high dispersal that could result from bird-based transmission. The impracticality of fire-breaks is due to the very high efficiency of transmission and the resultant extremely low threshold and due to the latent period of infection, which means that effective transmission is occurring some considerable distance in front of the detectable mortality.

Maintenance of juvenile pilchard stocks is recommended to speed the post-epidemic recovery.

The model also shows that pilchard stocks mix very freely and that degrees of large-scale mixing are different in different areas. This difference has implications for fisheries management in different parts of Australia.

The model thus provides managers with evaluations of several control and recovery strategies for managing epidemics. Experimental evaluation of these strategies would be extremely expensive and only partial.

The model is also of value to researchers. This model is the first to investigate the spatial spread of an epidemic in a fish stock and generates an evolving epidemic wave whose properties change with time, which is a novel feature of this epidemic. Since diseases are of increasing concern to marine environmental scientists (Harvell *et al.* 1999). This model may be of use in evaluating spread in this growing number of reported diseases. Disease spread is also of increasing importance to the aquaculture, and models may be adaptable to the needs of this industry.

The initial phase of the modelling has been presented at the conference MODSIM 99 (Murray *et al.* 1999), which resulted in an invitation to publish this work internationally (Murray *et al.* 2000b). Putting a dollar value on this scientific outcome is even harder, but given the scale of the emerging disease problem and the limited scope for experiments, formal modelling and analysis is of very great value. Models can be used to combine observations from the field with process rates derived experimentally and to suggest the areas of research where experimental analysis is most cost effective.

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12.2   Future Developments

The model presented here is potentially strongly constrained by data on the development of disease. Unfortunately, there is a lack of experimental data which could be used to characterise latent period and the total length of infection in more detail. If these parameters were strongly constrained by observation, then the other parameters involved in the epidemics spread (D and b) could also be restricted more strongly. This would allow the model to be investigated in more detail, particularly the origin and evolution of the epidemic. We therefore appeal for support for the continued experimental evaluation of disease transmission.

Post epidemic recovery of the pilchard population could be investigated in more detail using the model presented in this report. With only two epidemics we were not in a position to confirm modelled description of the population's recovery in any detail. However, this model of the interaction of epidemic mortality with background mortality could be extended and developed as a theoretical analysis of the interaction of disease with other forms of mortality.

Application and adaptation of the existing model to other diseases awaits the acquisition of future data sets, unfortunately a quite likely occurrence.

Further peer reviewed publication of the existing model is intended and has been discussed with the PSWG members. Particularly, the model of school level transmission and of the analytical solution of wave speeds, already have been submitted as a manuscript and the main model will also be developed for scientific publication. Further publication may be possible.

12.3   Conclusions

The project 99/225 objectives have been met or exceeded in most cases. The original objectives are described below with a description of how these objectives were met. This includes an analysis of local transmission, which was formally dropped but was fulfilled anyway.

1   We will construct a 1-D SIR (Susceptible, Infected, Removed) model of the spread of the pilchard mass mortality events of 1995 and 1998/9. *This has been met, a model of the epidemic has been developed, also see objective 4*.

2   We will analyse the effect of different modes of local transmission on the mass mortality's dynamics. *This objective was dropped as a result of the cut in available funding. However, we do include an analysis of the local inter- and intra- school transmission in chapters 4 and 5 of the final report*.

3   We will produce a literature review of similar mass mortalities and the modelling approaches used to analyse them. *This was completed at an early stage, and was incorporated in the initial report*.

4   We will refine the SIR model to include different transmission process functions and data obtained by other pilchard mortality study projects, in particular the Fisheries WA lead study on viral transmission *The model has been refined to incorporate an incubation phase in infection, fixed length phase structures, and the*

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option of non-linear transmission. We have used observations, particularly the initial behaviour of the epidemic to select the model structure; however transmission data was not available. The resultant model is substantially novel and we have derived a formal method for its analytical solution.

5   We will review the observations, including those obtained in concurrent studies, to provide the tightest possible constraints on the ranges of model parameters. *We review the observations (chapter 3) and use them to refine the model (chapters 8 and 9).*

6   We will analyse the effects of fisheries management strategies on pathogen transmission, in particular we will test the viability of a 'fire break' policy. *We included an analysis of the effectiveness of fire breaks in the initial report. We further analyse management options in chapter 11 of the final report in the light of the results of the full model.*

7   We will construct a simple model of the recovery of the fishery to investigate the period required for the stocks to become vulnerable to renewed mortality. *Such a model has been derived from a model developed by Fletcher and is used to investigate post-epidemic recovery patters (chapter 11).*

8   We will development a Graphical User Interface (GUI) to display the local and geographical spread of pathogens. *A GUI has been derived that allows model output to be plotted on a map. However, the nature of the epidemic, a sharp focus at a single location at a given time, means that there is little spatial pattern and so we have used a variety of other graphical display tools to present model outputs.*

9   We will produce an initial report detailing the approaches used both by us and other modellers of epidemics. *This initial report was presented to the PSWG last year.*

10 We will produce a final report detailing the final form of the model produced and incorporating analysis of model structure, parameters and results. *This report has just been provided to the PSWG.*

11 We will present this work at a nationally significant scientific meeting in 2000. *The modelling was discussed at the conference MODSIM 99. Three scientific papers on the modelling have been prepared, in excess of the plans for extension of results.*

As an extra objective that was also discussed in the planned extension of results, a www page has been set up on the CSIRO Marine Research projects pages.

Our initial objectives have thus been largely achieved of exceeded. This has been in spite of problems with the experimental transmission trials, which deprived us of data that could have strongly constrained the model. We identified this possibility as a serious risk at the start of the study and designed our study to be able to take advantage of the existing data in the absence of further transmission data. The model actually suggests a possible reason for this failure of transmission trials, that there may only be a relatively narrow window for infection during the development of the disease.

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ACKNOWLEDGMENTS

APPENDIX 1

Intellectual Property and Valuable Information

The principle outcomes of this project are novel epidemiology models based on a fixed length infection. These models, which are described in this text, include:

A series of simple epidemiological models adapted to describe the epidemic.

Interaction of schools and the local level spread of infection

The main model detailing continental scale spread of infection

The analytical method of determining the epidemic's speed of spread

A model describing post- epidemic population recovery

Further valuable outcomes include

A collected data set describing the spread of the 1995 and 1998/9 epidemics

A review of epidemiological models (presented to the JPSWG)

The model produced several valuable outcomes. Some of these are negative but this does not prevent their being important outcomes which can inform management of future epidemics:

Discounted the role of vectors in virus transmission, making control irrelevant. This was certainly not obvious *a priori.*

The very high transmission efficiency required shows 'fire-break' control methods to be impracticable. There was considerable doubt *a priori*, but this formal evaluation which confirmed these doubt was still valuable.

The model showed the value of maintaining juvenile stocks to ensure recovery.

The model indicates that the pilchards in eastern Australia are more mobile than those found in the west. This has important implication for the scale of management of stocks.

APPENDIX 2

Staff

Staff directly involved on this project were:

Dr Alexander G. Murray of CSIRO Marine Research, Hobart

Dr Michael O'Callaghan of the Inland Mathematics Research Network, Eugowra

Dr Brian Jones of Fisheries Western Australia, Perth

Dr Sergui Sokolov of CSIRO Marine Research. Hobart

Many other people provided data, support and suggestions. These include members of the Joint Pilchard Scientific Working Group, researchers at CSIRO and at state fisheries laboratories and members of the public who reported mass mortality events to state authorities.

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APPENDIX 3

Algorithm to find the wave speed of an epidemic with a fixed length latent period

Michael O'Callaghan derived this algorithm on the basis of the analysis described in chapter 7.

```
'Set model parameters (in units of km and days)
set D_ie            ' Diffusion coefficient for E and I phase
set b               ' Latent period length
set α               ' Turnover rate of infective phase
set S_0             ' Initial population, default value is 1
set β               ' Transmission coefficient

'Set control criteria
v = .1              'variance of latent period (day^2)
crit = .0001        'convergence criterion


'Begin algorithm to compute wave speed

relerr = 2 × crit     'ensures we perform loop first time
a = 1 - α × v / b
n = b^2 / v
rhs = β × S_0 × v / b
ρ = 1
WHILE relerr > crit
  numer = ρ - a - rhs / ρ^n
  denom = n + 1 - n × a / ρ
  δ = numer / denom
  ρ = ρ - δ
  relerr = ABS(δ / ρ)
WEND


' Finish by computing speed

Speed  = 2 × √(D_ie × b × (ρ - 1) / v)

' End of algorithm
```