

Using Coupled Biophysical – Particle Tracking Models Of Sea Lice in Loch Torridon

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EXTENDED ABSTRACT

Sea lice are marine ectoparasites that undergo free-living planktonic larval phases before maturing to become parasitic on fish. Salmonids are affected by lice of the species *Lepeophtheirus salmonis* and various species of the genus *Calanus*. These lice are estimated to cost US\$100M y⁻¹ to marine salmonid farms worldwide and may have contributed to declines in wild salmonid populations.

Because of their planktonic larvae, sea lice have the potential to be transported over considerable distances. Exactly where they might be transported to depends on the hydrodynamics of the water body they are in and on the biological factors that keep lice viable and infectious; viability is sensitive to salinity and temperature.

Lice infest farmed Atlantic salmon farms, whose production exceeds 1M tonnes y⁻¹, concentrated fjordic coastal regions of Norway, Chile, Scotland, Canada and other countries. Control of lice through synchronised treatment and fallowing and protection of sensitive wild salmonid populations requires an understanding of where lice are likely to be transported to.

The interaction of hydrodynamics and biology is a highly suitable subject for coupled biophysical modelling of particle transport. This has been worked on by coupling hydrodynamic models with biological particle models of sea lice dispersal in the Loch Torridon system, a small fjord in northwest Scotland. This system has been the subject of studies of larval sea lice distribution dating back to 1999 and has been the subject of several oceanographic and louse biology studies, and of studies of their sea trout wild host.

Hydrodynamic models calculate current velocities on the basis of fluid dynamics and external forcing from tidal elevation at the loch mouth, freshwater inputs and wind generated currents. Hydrodynamics of fjordic systems are much less studied than those of drowned valleys typical of

more temperate regions. Modelling of Loch Torridon has therefore required considerable development and the use of different models to provide acceptable performance.

The first model applied, GF8, provided a good description of Loch Torridon's overall hydrodynamics, but under-estimate surface current velocities. This was because the model had a fixed number of layers and required a thick surface layer to cope with Loch Torridon's large tidal range. Unfortunately these surface currents were critical to lice transport, since larval lice were commonly found near the surface.

The BOM (Bergen Oceanographic Model) that had been applied in Hardanger Fjord is therefore being adapted to Loch Torridon's bathymetry and is in the processes of validation.

Currents generated from the hydrodynamic model were used to drive movements of particles representing larval lice. Many of these particles were released from a given location (1000 in scenarios shown) and their dispersal followed as they matured through two non-infectious stages (at a rate dependent on temperature) to become infectious copepodids, which died off at a rate dependent on salinity. Plotting the location of these copepodids identified regions of high infection pressure.

Areas where infection pressure is orders of magnitude higher than the average across the Loch Sheildaig basin were identified in all scenarios so far investigated. The location was generally kilometres from the source, but the specific location was highly variable, driven mostly by wind, but was also dependent on temperature and to a lesser extent freshwater flow. Freshwater can also greatly increase mortality rates, thereby reducing time over which dispersal may occur.

1. INTRODUCTION

The constant motion of water leads to the transport of dissolved and suspended substances, sometimes over many kilometres. Movement may be entirely due to passive transport by the water, e.g. nutrients, or may include limited independent motion e.g. plankton. The substance may change status, e.g. plankton may take up nutrients and grow. The resultant distribution is the complex result of hydrodynamics and biological processes. Coupled biophysical models incorporating hydrodynamic and particle models are widely used to simulate such dispersal processes.

Sea lice are ectoparasitic copepods that infest a wide variety of marine fish species. Marine-phase salmonid fish in the North Pacific and North Atlantic are affected by the species *Lepeophtheirus salmonis*, but species of the genus *Caligus* (*C. elongatus* in the N. Atlantic, *C. clemensi* in the N. Pacific and *C. rogercresseyi* off Chile) also parasitise marine salmonids. These lice are estimated to cause US\$100M y⁻¹ damage to farmed salmonids (Johnson et al. 2004) and may contribute to declining wild salmonid populations.

Sea lice larvae have 3 planktonic stages: non-feeding Nauplii I and Nauplii II and infectious copepodid. These planktonic larvae are moved by currents but are not entirely passive, tending to be positively phototactic. The period before maturation is largely dependent on temperature and survival is particularly sensitive to salinity.

Farms have massively increased the population of salmonids in coastal waters of countries such as Norway, Scotland and Canada. Even when the burden of adult lice-per-fish is low, these farmed salmon contribute to greatly increase production of sea lice eggs (Heuch and Mo 2001). The question is where do the resultant larvae go?

To answer this question we have developed coupled biophysical models incorporating the hydrodynamics and lice biology. We have applied these models to Loch Torridon, a small fjordic system in northwest Scotland. This system is well characterised as divided into three basins separated by sills: upper Loch Torridon, outer Loch Torridon, and, between these, Loch Sheildaig. Data on sea lice has been collected using coastal and offshore sweeps for larval lice, lice counts from sentinel caged salmon and from wild sea trout. The wild populations of sea trout have also been extensively studied. Extensive oceanographic studies have also been carried out including deployments of current metres and of drifter

buoys. Both the physical and biological sides of this system are therefore well characterised.

2. MODELLING THE HYDRODYNAMICS OF FJORDS

Fjordic systems, such as Loch Torridon, have been modelled less than drowned valley estuaries typical of more temperate coasts. Historically low population densities and levels of development have led to lack of incentive for studies. However, such systems have proven highly suitable for marine salmon production and so modelling is required to assess impacts of this development.

The GF8 hydrodynamic model has been applied to model dispersal in Loch Torridon (Murray and Gillibrand 2005, Gillibrand and Amundrud 2007). This model has been successfully applied to systems such as the Saint Lawrence estuary and provides a good description of deeper circulation in Loch Torridon. However, GF8 has a fixed number of layers and the surface layer incorporates all the tidal change. Because tidal range in Loch Torridon is large, the surface layer is thick. Near-surface currents are faster than the currents averaged over this relatively thick surface layer and so the model can under-estimate the currents experienced by near-surface lice larvae.

Different forcing scenarios (including observed tidal elevation at the seaward end of the loch, winds and freshwater inflow, see Gillibrand and Amundrud 2007) have been run to generate files of current velocities. Although the hydrodynamic model is 3-d, its output is 2-d as only surface layer currents are used to drive the particle-tracking model. The model is rotated 49 degrees for reasons of computational efficiency. Current velocities are specified at 100 m intervals on the X and Y dimensions of the 2-d model surface grid and at 20 minute time intervals.

3. BIOLOGICAL PARTICLE MODELLING

The currents generated by the hydrodynamic models are used to drive movements of particles representing planktonic larval lice. This requires modelling of particle movement and modelling of the changes in the particles' properties with time as lice mature and die.

3.1. Particle Motion

Particles are released at a location representing a source of lice, such as a salmon farm, on the hydrodynamic grid. The default time-scale is the release of particles at 20 minute intervals over a tidal cycle. Thousands of particles may be

released and followed for a time appropriate to the length of the larval phases, see next section.

Each particle represents many lice. The initial particle value, $P_0 = 1$, is the actual number of larvae hatched divided by the number of simulated particles, this latter being a trade-off between efficiency and the degree of resolution of infection pressure distribution. Typically there are thousands of particles and millions of larvae.

The particle has motion calculated from the hydrodynamic model's output. The exact location of a particle will lie between the four nearest grid points, unless the particle lies on a grid point or a grid square edge. Local current velocity is interpolated using inverse square weighting. Velocity is also linearly interpolated in time.

The particle is also given a random turbulent motion. A simple constant diffusion coefficient of $D = 0.1 \text{ m}^2 \text{ s}^{-1}$ is used based on field observations, rather than the more complex shear-based form used in an earlier version (Murray and Gillibrand 2005).

A further simplification is that a fixed length time step is now used (rather than the variable form used earlier). This simplifies calculation, especially the interaction of turbulent diffusion with advection.

An issue that is especially critical for confined areas such as sea lochs, is the interaction of the particles with boundaries. A range of interactions have been tested but results have so far not shown significant variations in resulting distributions of particles. The default used here is a sticky boundary where particles hitting a boundary are 'stuck' in place until motion (normally diffusive) at a subsequent time step moves the particle off the boundary.

3.2. Biology of the louse larvae

Dispersal time depends on how long larvae remain viable. This depends on rates of development and mortality.

Development time from the hatching of the egg to infectious copepodid (T_m) is largely a function of temperature. The model of Stein et al. (2005)

$$T_m = [24.79/(T - 10 + 24.79 * 0.525)]^2,$$

has been adopted.

To simulate variability in maturation, once a particle has reached the age T_m it has a probability

in each subsequent time-step of maturing into an infectious copepodid. Data to constrain this probability are limited, but a default value of $10\% \text{ hr}^{-1}$ is used, which is consistent with observations (C. Pert pers. comm.). Rates of $50\% - 1\% \text{ hour}$ have also been applied.

Based on data from Johnson and Albright (1991) copepodids suffer mortality at a rate of $1\% \text{ h}^{-1}$ in seawater (Stein et al. 2005). Bricknell et al. (2006) found mortality equivalent to $2.9\% \text{ h}^{-1}$. Much higher rates of mortality occur at salinity <29 (Bricknell et al. 2006). However, most of Loch Sheildaig is close to full seawater.

Data on mortality of nauplii are limited, but mortality rates derived by Stein et al. (2005) for copepodids and nauplii were similar and so we use the same rate in the scenarios illustrated.

Due to mortality of larvae, a particle's value declines at rates of mortality appropriate to the particular scenario. The value of the particle P at time t depends on time and larval mortality rates, $P_0 = 1$ as defined in 3.1

$$P_t = P_0^{-td}.$$

3.3. Model outputs

The outcome of the model is the location, status (nauplii or copepodid, i.e. if infectious) and survival of lice represented by particular particles at particular times. These outcomes can be used to identify areas of relatively high risk of infection. The spatial distribution of this risk for a single particle is the number of time steps the particle was in a particular 100 m model grid square, with each time step weighted by the proportion of lice still surviving in that particle: i.e. P_t . These risk distributions are summed over all the particles followed in the scenario simulation to generate a risk map with units referred to as "particle time-steps".

4. RESULTS

The coupled models have been applied to the replication of high concentrations of sea lice larvae found near the mouth of the Sheildaig River if farm 1 is assumed to be a source.

Hydrodynamics: Hydrodynamic currents within the surface layer (ranging from 2 – 6 m in depth, depending on tides) are generated using the GF8 model and are discussed in detail in Gillibrand and Amundrud (2007).

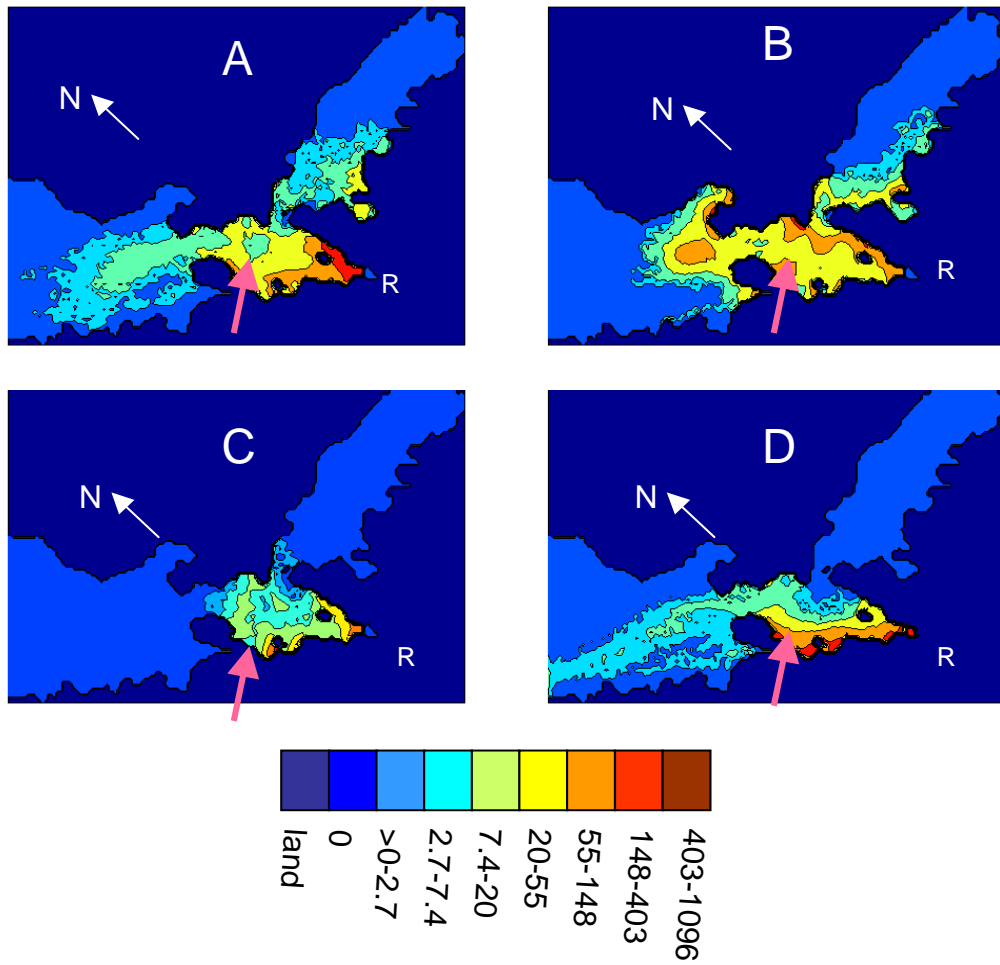


Figure 1. Copepodid concentration (particle time-steps scale) pattern in Loch Torridon under 4 quasi-realistic but unvalidated examples of wind forcing. Pink arrow shows location of release into Loch Sheildaig, the central basin of the Loch Torridon system. R = Sheildaig river mouth.

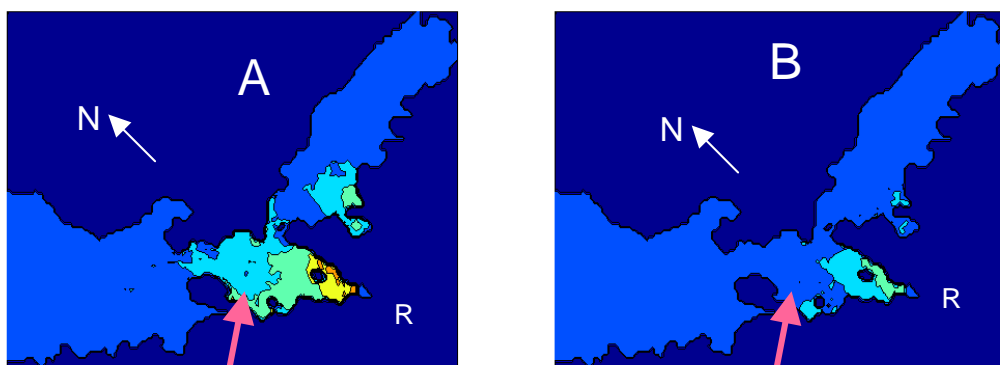


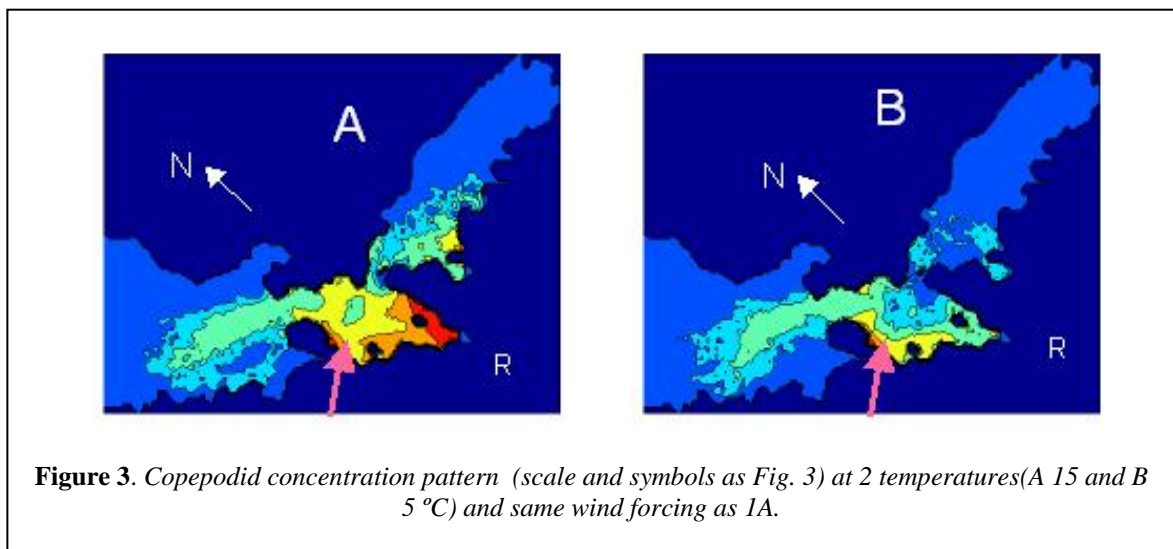
Figure 2. Effect of salinity (increased mortality) on distribution of copepodids (scale and symbols as Fig .3). A = 3% h^{-1} , B = 6% h^{-1} for wind forcing equivalent to Fig. 1 A (where mortality = 1% h^{-1}).

Modelled currents were tested against observed motion of GPS-tracked drifters deployed in Loch Shiel, the central basin. Drifters are 3-m in length and stretch from 0.5 to 3.5m within the surface layer. This allows for direct comparison with the modelled currents in the surface layer. For a dataset collected in August 2005, the model simulated the direction of currents, but underestimated surface current velocities. This is because the thick surface layer, necessary to simulate the large tidal range in Loch Torridon. However, these non-validated hydrodynamic models results allow us to investigate the dispersion of particles under varying scenarios as long as the results are not considered accurate for management purposes (due to the errors in

population should be assessed using a validated hydrodynamic model.

Increased mortality rate, reflecting reduced salinity (Fig. 2), leads to reduction in infection pressure, but the zone of greatest relative infection pressure is not significantly altered

Temperature, by altering the duration of the planktonic phases alters the distribution of infection pressure (Fig. 3). At 15 °C maturation is rapid and occurs near the river Shiel, while at 5 °C copepodids only mature once the particles had been transported to the mouth of Loch Shiel, by which time fewer lice survive. The



predicted current speeds).

Because of this underestimation of velocity the Bergen Ocean Model (BOM) is now being applied to model surface currents in more detail (Asplin et al. 2004). BOM has the advantage of variable layer depths, allowing for finer resolution of the surface to better represent wind driven velocities.

Lice distribution: Modelled infection risk is mapped in terms of the copepodid distribution over a simulation (particle-hours per model grid square as defined in 3.3). The major cause of variation is wind, under different wind scenarios high concentrations are generated in different locations (Fig. 1), but under many scenarios there are high concentrations near the River Shiel. This is a river inhabited by wild sea trout which congregate in nearby coastal areas and can become infected with lice. However, we stress that these distribution maps were calculated using non-validated hydrodynamic models and a full understanding of the risk to wild sea trout

distribution in Fig. 1A, which has the same forcing at 10 °C, is similar to that at 15 °C, but not 5 °C. This reflects the large change in maturation time between 10 and 5 °C.

Variation in rate of maturation has relatively little effect on distribution of infection risks. A range of simulations over nearly 2 orders of magnitude did show moderate effects on absolute, but not on relative, levels of infection pressure (not shown).

Simulations result in infection pressure concentrated often at considerable distance from the source. The concentration is often orders of magnitude higher than the loch-wide average but location varies considerably from scenario to scenario.

5. DISCUSSION

Because sea lice have planktonic larval stages, coupled biophysical modelling is showing great potential for identifying infection risks posed by these economically important parasites.

The specific complication of modelling surface layer currents in fjordic systems has proved particularly difficult. In Loch Torridon, wind driven surface currents appear particularly important for generating transport regimes. Tidal flow is important in the shorter term, while freshwater inflows are relatively small

Larval maturation and mortality rates define how long the larvae are transported before and after becoming infectious

The models' ability to generate high concentrations of infectious larvae at considerable distance from their source is robust; it occurs under all scenarios examined so far, including non-validated runs under different hydrodynamic models. However, the location of these high concentrations is variable, owing to wind-driven surface dispersal.

The modelling of larval lice dispersal in Loch Torridon is now proceeding in collaboration with work in Norway and Canada. Hardanger fjord is a much larger system than Torridon that is being modelled by the institute of Marine Research, Bergen, Norway. The Broughton Archipelago is similarly large and consists of a maze of channels and is home to several species of pacific salmon (modelled by the Department of Fisheries and Oceanography, Nanaimo, Canada). Differing issues of scale, temperature, salinity and host populations, yet with fundamentally the same *L. salmonis* – farmed Atlantic salmon system make these three areas highly suitable for mutually-supporting studies.

6. CONCLUSION

Larval lice may cause infection at locations several kilometres distant from their source. Simple assumptions about dispersal of larval lice with distance are not an accurate description of this pattern. Therefore coupled biophysical modelling is proving the way ahead for assessment of risk patterns.

More modelling is required to predict exactly where concentrations form. Collaboration is proceeding with Norwegian and Canadian researchers.

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