Estimation of spatiotemporal transmission dynamics and analysis of management scenarios for sea lice of farmed and wild salmon

**Supplementary material**

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**Simulations**

![Graph showing daily outmigration of pink salmon from Glendale River in Knight Inlet from 2007-2012](image)

Figure S1: Daily outmigration of pink salmon (millions of fry) from Glendale River in Knight Inlet from 2007-2012, used to estimate migration paths through time in simulations. Source: Glendale Creek Juvenile Downstream Program 2012 Bulletin #4 (Pieter vanWill, personal communication).
Model fitting

Farm dynamics

We estimated the growth rate of sea louse populations on three salmon farms from time-series of counts of the number of sea lice on farmed salmon (Krkoshek et al. 2010). For Farm 1 and Farm 2, we had multiple raw counts of sea lice per salmon from each sampling date and for Farm 3 we had only average counts for each sampling date. Because of these different response variables, we had to assume two different data models when estimating parameters. For Farm 1 and Farm 2, we assumed that counts were distributed according to the negative binomial distribution with an expected value equal to the model prediction (equation 2) and overdispersion parameter, $k$, to be estimated. For Farm 3, we assumed Gaussian error between the average count and model prediction, with the variance in the error term to be estimated.

We fit the model using data cloning (Lele et al. 2007) to ensure the estimability of parameters. Data cloning was implemented in JAGS (Plummer 2003), with an adaptation phase of 1000 MCMC iterations, burnin of 1000 iterations, and posterior samples from the subsequent 5000 iterations. Priors on parameters and resulting estimates from 10 clones of the data are given in table S1. We checked parameter estimability by plotting the variance in the posterior estimates against the number of clones (Lele et al. 2010). The results suggest that parameters were estimable, with the variance declining at the rate of $1/K$, where $K$ is the number of clones (Figure 2).

Table S1: Parameter estimates (± 95% confidence intervals) for equation 2 fit to lice counts on farm salmon at three different salmon farms.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Prior</th>
<th>Farm 1</th>
<th>Farm 2</th>
<th>Farm 3</th>
</tr>
</thead>
<tbody>
<tr>
<td>$r_1$</td>
<td>Norm(1, 0.1)</td>
<td>0.045 (0.041, 0.048)</td>
<td>0.008 (0.005, 0.011)</td>
<td>0.013 (0.011, 0.016)</td>
</tr>
<tr>
<td>$r_2$</td>
<td>Norm(1, 0.1)</td>
<td>-0.056 (-0.06, -0.053)</td>
<td>-0.024 (-0.027, -0.022)</td>
<td>-0.048 (-0.062, -0.033)</td>
</tr>
<tr>
<td>$f_0$</td>
<td>logNorm(0, 0.1)</td>
<td>6.848 (6.121, 7.574)</td>
<td>2.861 (2.444, 3.279)</td>
<td>6.177 (5.524, 6.83)</td>
</tr>
<tr>
<td>$k$ or $\sigma$</td>
<td>logNorm(0, 0.1)</td>
<td>1.547 (1.231, 1.863)</td>
<td>1.284 (0.986, 1.582)</td>
<td>0.638 (0.494, 0.781)</td>
</tr>
</tbody>
</table>

Parameters in the prior distributions are the mean and precision (precision = 1/variance). For Farm 1 and Farm 2, $k$ is the dispersion parameter of the negative binomial distribution, whereas for Farm 3, $\sigma$ is the residual standard deviation of Gaussian errors.
Figure S2: Data cloning results for parameters of the temporal sea louse dynamics on farms. Scaled variance is the variance in the posterior estimate divided by the variance in the posterior estimate for K=1, where K is the number of clones. If parameters are estimable given the available data, the scaled variance should decline at the rate of 1/K (Lele et al. 2010).
Figure S3: Comparison of total number of motile *L. salmonis* versus average motile *L. salmonis* per farmed salmon on Farm 1 (top), Farm 2 (middle) and Farm 3 (bottom). The total *L. salmonis* (red, left axis) was calculated as the average number of motile *L. salmonis* (black, right axis) multiplied by the number of farmed salmon (Marty et al. 2010). Patterns for the two metrics are similar.
Spatiotemporal infection dynamics

The infection model was fit to counts of copepodid, chalimus and motile sea lice on juvenile salmon throughout their migration. We also fit this part of the model using data cloning, as described above. Because of the increased complexity of this part of the model, we allowed a longer adaptation and burnin phase of 5000 and 20 000 MCMC iterations, respectively. Inferences were drawn from the subsequent 2000 iterations. Convergence diagnostics suggested that three parallel chains had converged (Figure 4). We fit the model to $K = 1$-$6$, 8, and 10 clones of the data. Because of the number of data and complexity of the model, the fitting took 7 days on four processors. The resulting maximum likelihood estimates from 10 clones of the data are given in Table 1 of the main text. Data cloning suggested that these parameters were estimable (Figure 5).
Figure S4: Trace plots from the MCMC algorithm. The trace plots for each parameter (left column) show the values sampled by the MCMC algorithm for three different parallel chains (black, red, and green). The resulting posterior density of the samples for each parameter is shown on the right. These samples correspond to the fitting with 10 clones, but diagnostic summary suggests that convergence was obtained for other numbers of clones as well (i.e., $\hat{R} < 1.1$) (Gelman and Rubin 1992).
Figure S5: Data cloning results for parameters of the spatiotemporal infection model fit. Scaled variance is the variance in the posterior estimate divided by the variance in the posterior estimate for \( K = 1 \), where \( K \) is the number of clones. If parameters are estimable given the available data, the scaled variance should decline at the rate of \( 1/K \) (Lele et al. 2010).
Figure S6: The spatiotemporal pattern in the ratio of farm over ambient larval density, calculated as $\phi_L(x,t)/\kappa$, ranging from zero to 30. The red lines are contours indicating the date and distances corresponding to a ratio of 1 (equal farm and ambient larval densities) and a ratio of 10 (the density of larvae from farms is 10 times greater than the density of larvae from ambient sources).
Figure S7: The abundance of (a) copepodid, (b) chalimus, and (c) motile sea lice per wild juvenile chum salmon along their migration corridor (distance \( x \), km) from April 10, 2006 (day \( t = 100 \)) to May 24, 2006 (day \( t = 144 \)). The grey surface is the model prediction based on the fitted parameter estimates (Table 2), and the points are the observed mean number of copepodid, chalimus, or motile sea lice on juvenile salmon at each location and date of sampling (\( \pm 95\% \) bootstrapped confidence intervals). Observations are coded blue when they are higher than model predictions and red when they are lower than model predictions. See Figure 5 of main text for corresponding figure showing fits to data from pink salmon.
Figure S8: a) Sea surface temperature (°C; mean ± SD) for each day of wild-salmon monitoring from April 10th to May 22nd, 2006. Between one and six sites were sampled in each day. The transmission model parameters are based on the developmental time of attached louse stages at 10° C (dashed red line) from Stien et al. (2005). As an example, the development time (x-axis) as a function of temperature (y-axis) for copepodites from Stien et al. (2005) is shown on the right. B) Sea surface salinity (psu, mean ± SD) for the same sampling as in (a). The relationship shown on the right is the proportion of copepodites successfully attaching to hosts (x-axis) over salinity, where the proportion incorporates the impact of salinity on both survival and behaviour of copepodites (Groner et al. 2016). The dashed blue lines show the range in attachment success that may be encountered given the range in mean temperatures we observed. The values of naupliar and copepodid survival assumed in our model were based on a different calculation (Krkošek et al. 2005) that assumed a salinity of 30 psu (dashed red line).
References


