

Building a statistical spatio-temporal model for predicting the abundance of salmon louse (*Lepeophtheirus salmonis*) on salmon farms in a west coast Norwegian fjord

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Background

Rapid outbreaks of salmon louse occur predominantly during the summer and fall seasons in the west coast Norwegian fjord. The most effective measure to reduce lice levels is by synchronizing chemotherapeutic treatments between neighboring aquaculture facilities. Rising water temperatures significantly shorten the biological cycle of the salmon louse, leading to sudden and explosive increases in lice which effectively halt the implementation of synchronized treatments. Prediction of lice levels will facilitate coordination between neighboring farms.

Objective

The aim of this study is to build a model that predicts lice levels at each farm, to facilitate the coordination and synchronization of delousing treatments.

Materials & methods

- Study conducted at 33 farms in the West region of Norway between Jun. – Dec. of 2011-2012 (33 farms & 44 fish cohorts, data for modelling) and 2013 (16 farms & 16 fish cohorts, data for predictions).
- The region is divided in three sub-regions (south, mid & north), where planning of pest management activities are coordinated within each sub-region.
- Lice samplings performed biweekly in half the pens.
- Sampling lice abundance by three stages groups: chalimus, pre-adult & adult males (PAAM), adult females.
- We calculated weekly exposure (total production of lice larvae) at each farm, which includes local and neighboring farm production.
- Negative binomial (NB) Gaussian additive model (GAM) was built to model data PAAM abundances from years 2011 and 2012.
- Predictions were made for PAAM abundances in 2013.

Results

- Epidemics of salmon lice are seasonal with peaks occurring on the second half of the year coinciding with warmer temperatures.
- Peak production of calculated larvae exposure coincides with the epidemics of PAAM.

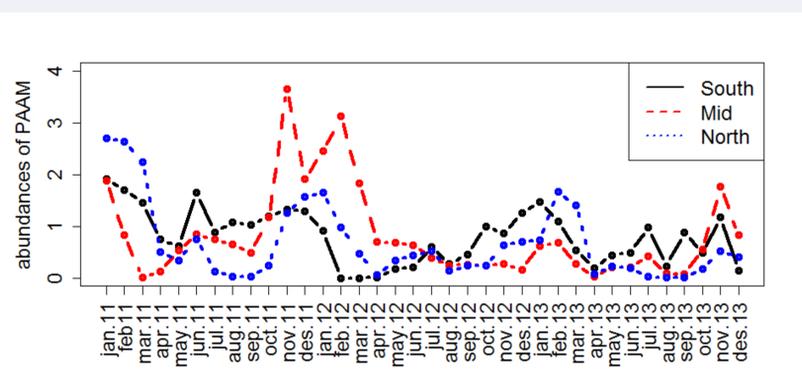


Figure1. Weekly abundances of PAAM at each sub-region.

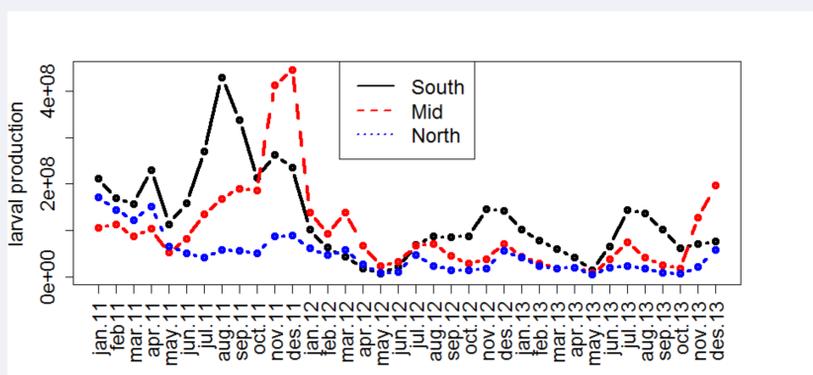


Figure2. Average weekly production of larvae at each sub-region.

Results

- The model explains 74% of the null deviance.
- Model fit include 70% of observations (2011-2012) within the 95% CI.
- The trend (one week ahead) in PAAM abundances for the year 2013 are well captured by model predictions.

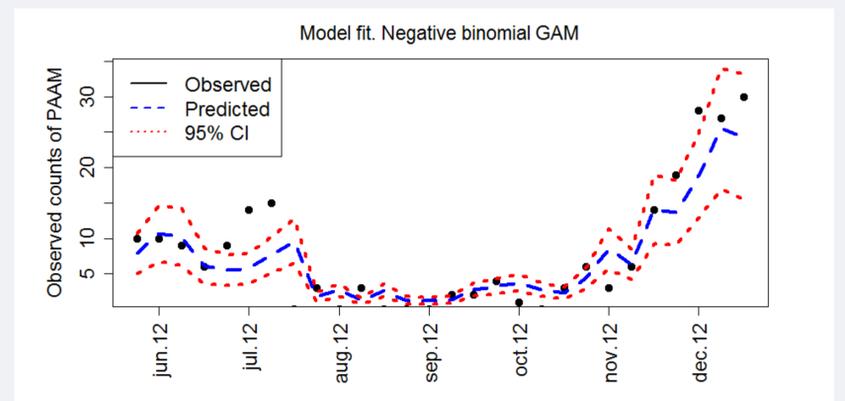


Figure 3. Model fit and 95% CI for the observed PAAM abundances in one of the 2012 fish cohorts.

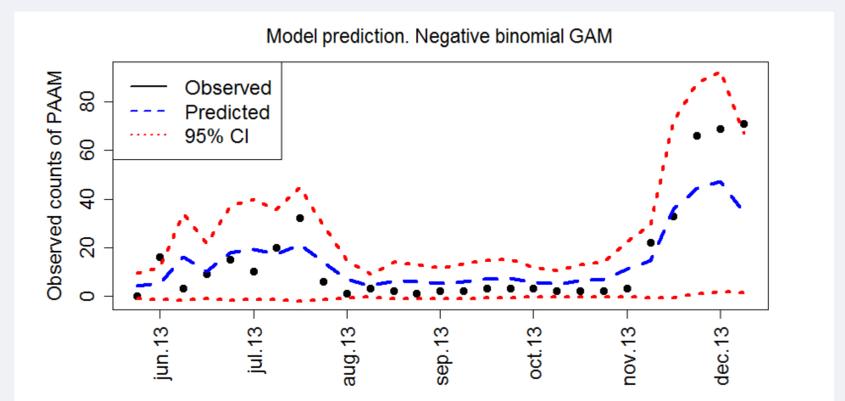


Figure 4. Predicted PAAM abundances (one week ahead) and 95% CI in one of the fish cohorts in 2013.

Variable	edf	F	p-value
s(calculated larva[t-2],temp)	16.9	39.4	0.01
s(chalimus[t-1],temp)	6.7	102.2	<0.001
s(PAAM[t-1],temp)	11.7	640.9	<0.001
s(average fish weight)	2.8	25.0	<0.001
s(total fish biomass)	2.1	15.9	<0.001
s(X,Y)	24.4	83.4	<0.001

Table 1. The numerical output of the NB GAM is summarized. All variables contain a smoother. Temp correspond to water temperatures and X and Y are the geo-coordinates.

Discussion

- We have produced a model that can reliably predict the abundance of PAAM one week ahead.
- All variables in the model have been shown to be positively associated with PAAM abundances.
- Besides a NB GAM, an option is to apply a zero-inflated GAM and to model predictions beyond one week.
- This model could be implemented to support preparedness and coordination of delousing activities within each sub-region.

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