Sea lice epidemiology update and development of infection models

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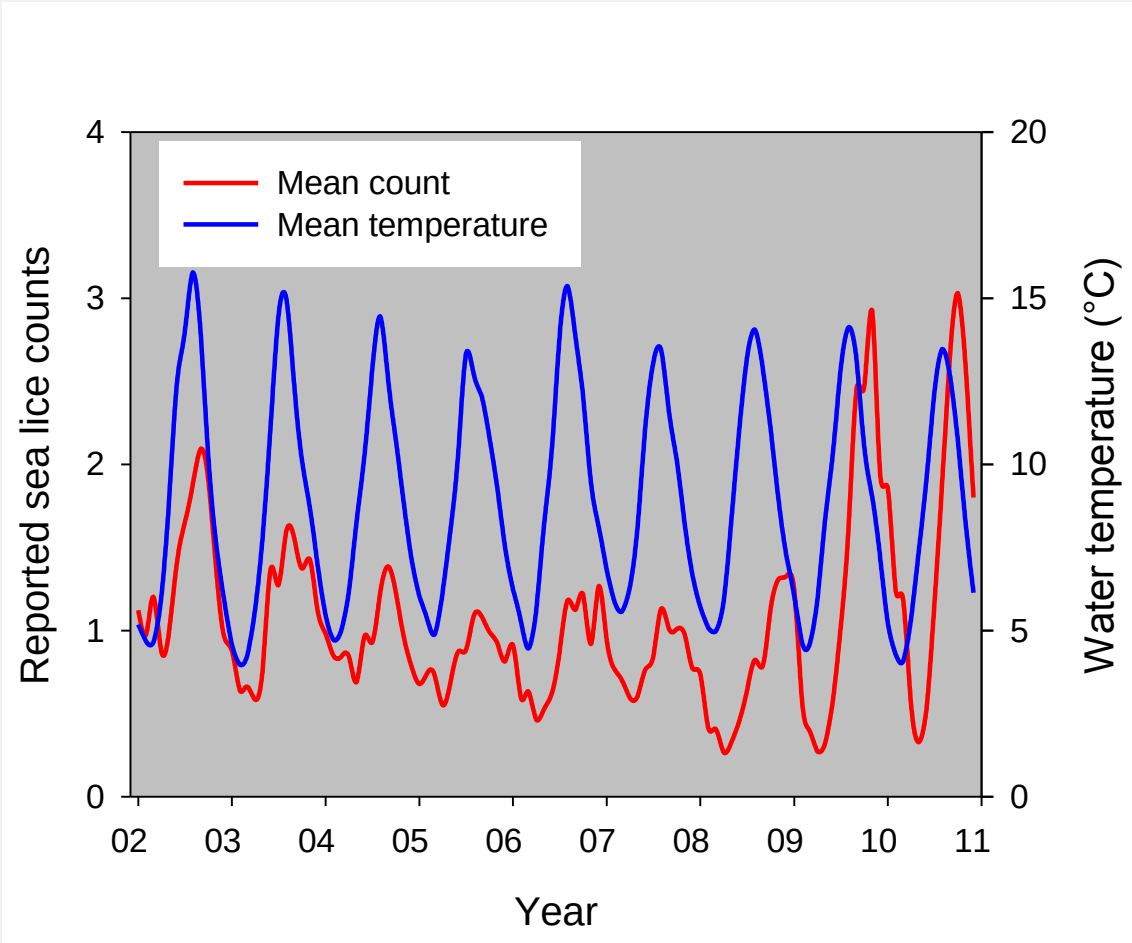
Are lice-infections on farmed fish predictable or chaotic?



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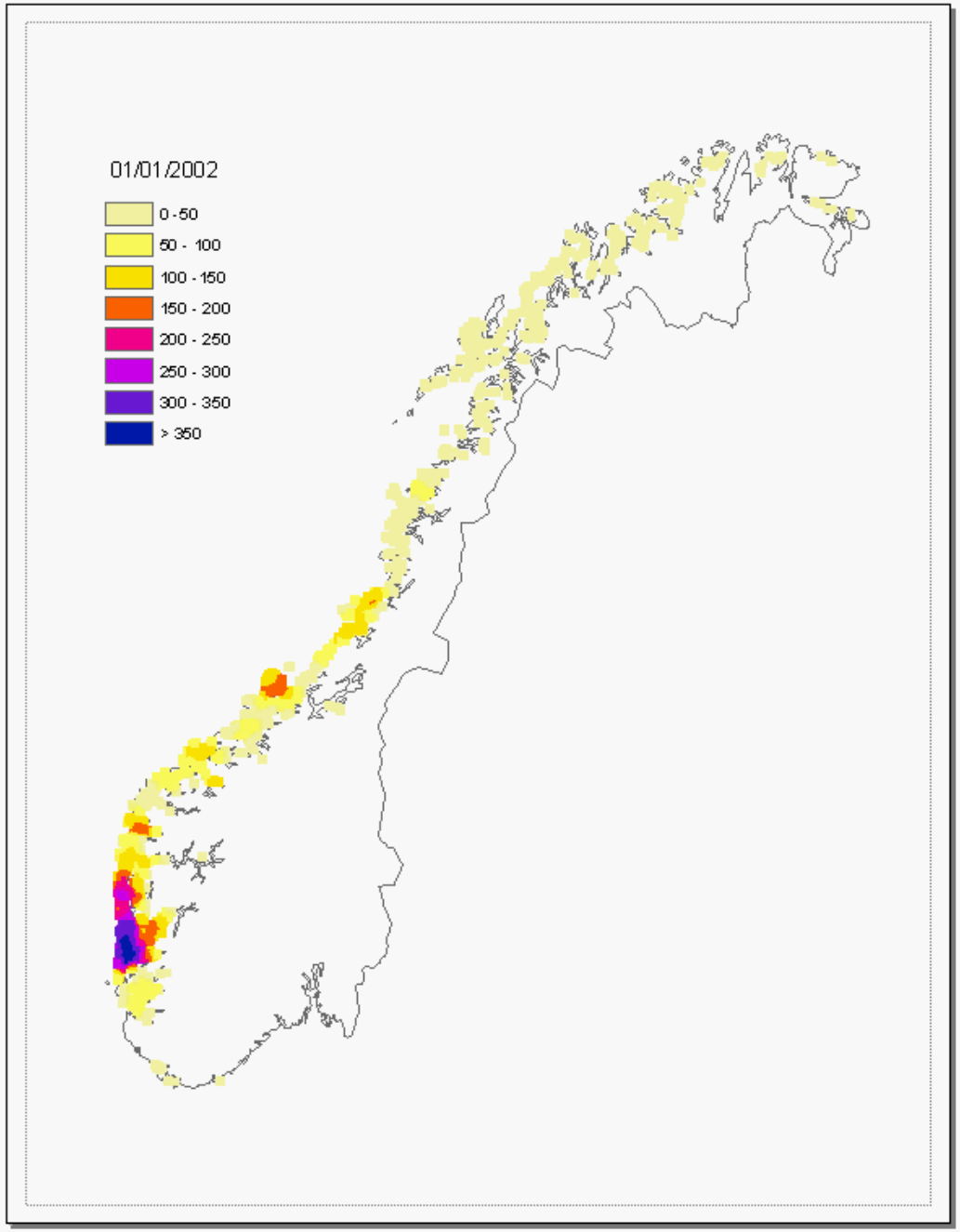

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Predictable on a large scale

- Yearly cycles:
  - max ~ October
  - min ~ May
- Lice densities build up first in the south, later in the north
- Local «epidemic» episodes

The kernel density model for salmon lice infection pressure (IP)

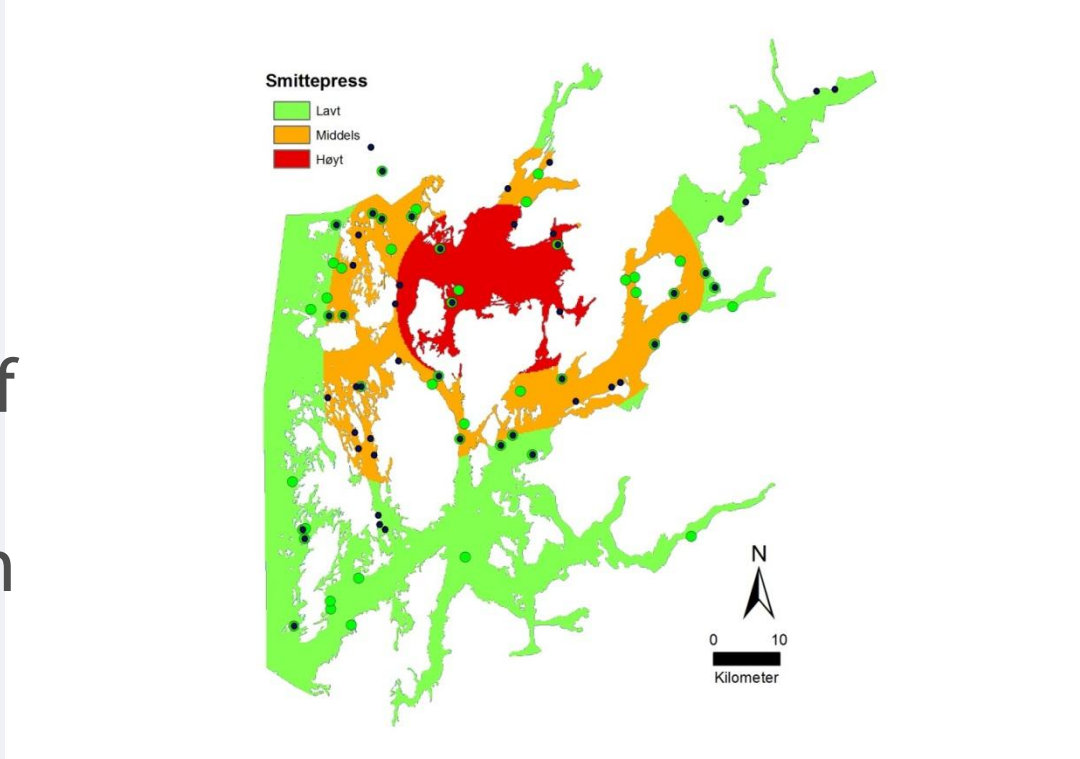
- Model focusing on the potential for transmission in space and time
- Use lice counts, farm numbers of fish and temperatures to estimate production and development of infectious copepodites
- Use seaway distance relationships to estimate farm exposure to infection
- Test if exposure predicts: new settlements of chalimus ⇨ pre-adults and adult male abundance ⇨ adult female abundance

Estimating IP I

Data:

- Adult female lice
- Number of fish

→ Total number of reproducing lice on given farms and given times



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Population dynamics of salmon lice *Lepeophtheirus salmonis* on Atlantic salmon and sea trout

Audun Stien[1,*], Pål Arne Bjørn[2], Peter Andreas Heuch[3], David A. Elston[4]

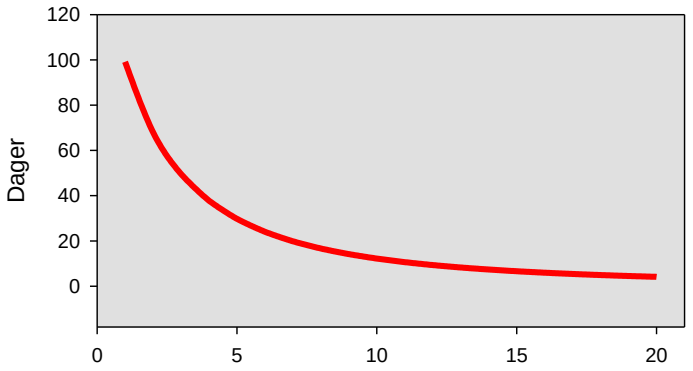
Estimating IP II

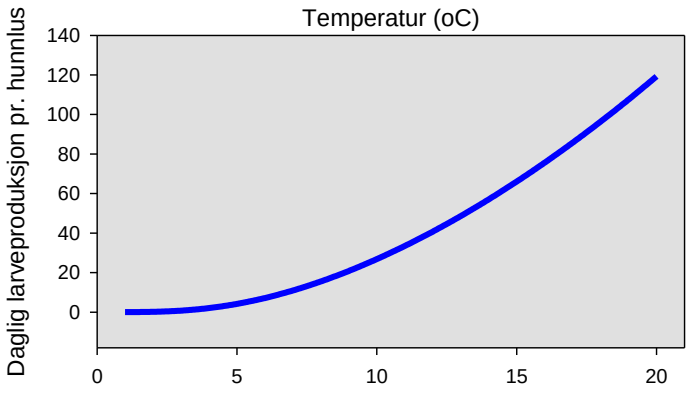
Data: Temperature

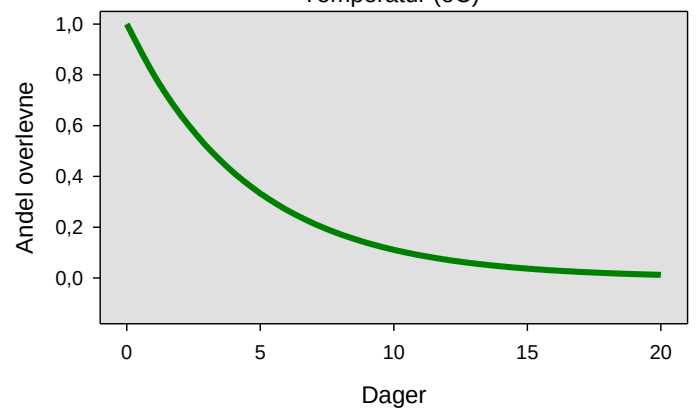
Deterministic calculations:

- Development time
- Reproduction
- Survival rates

→ Production of copepodites, infectious some time ahead depending on temperature







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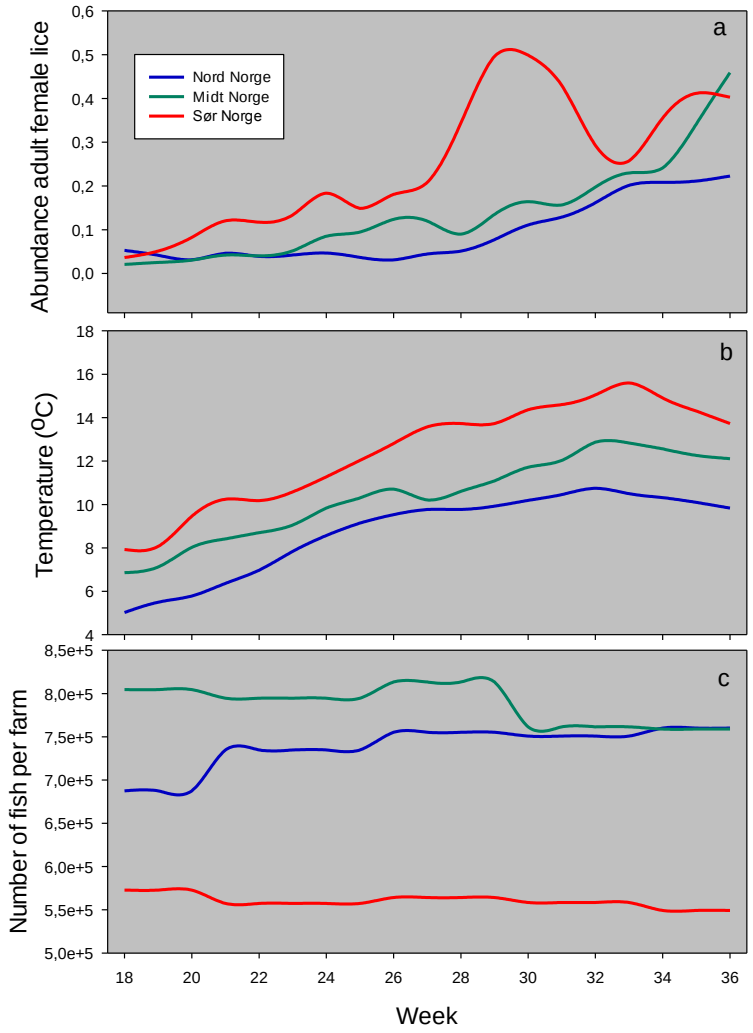

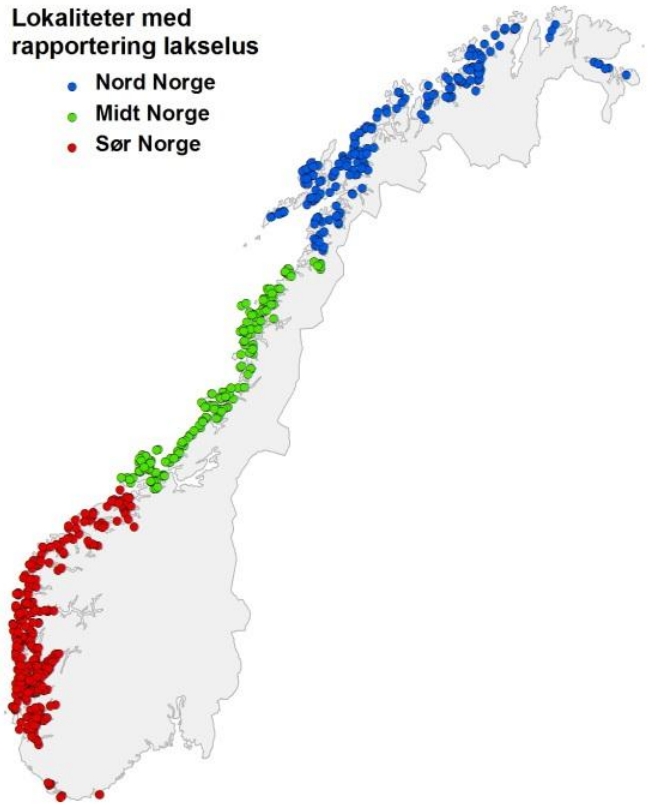

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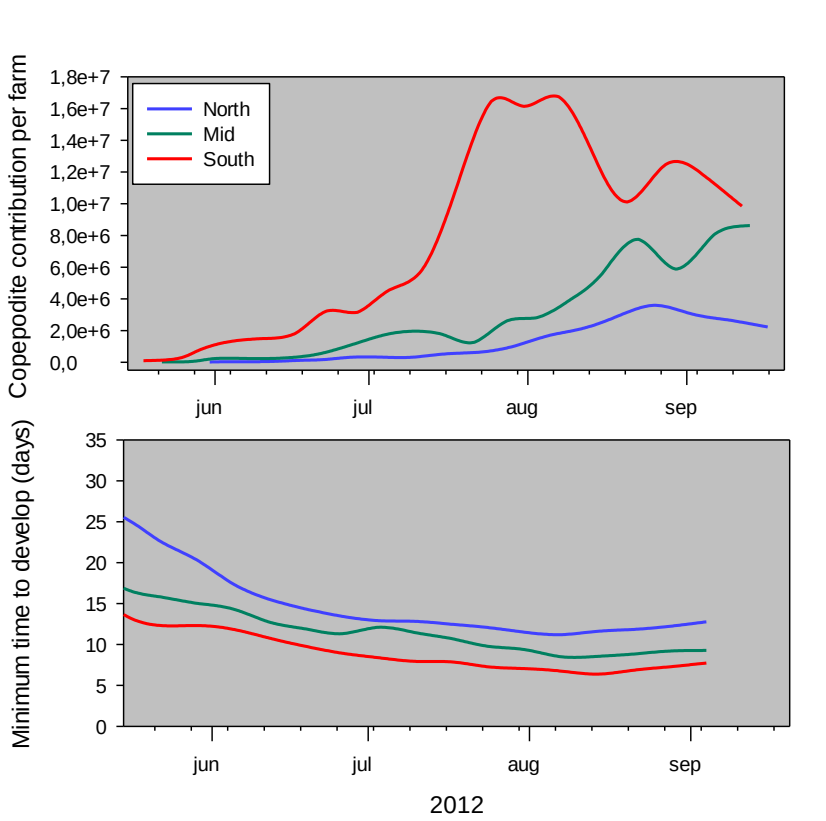
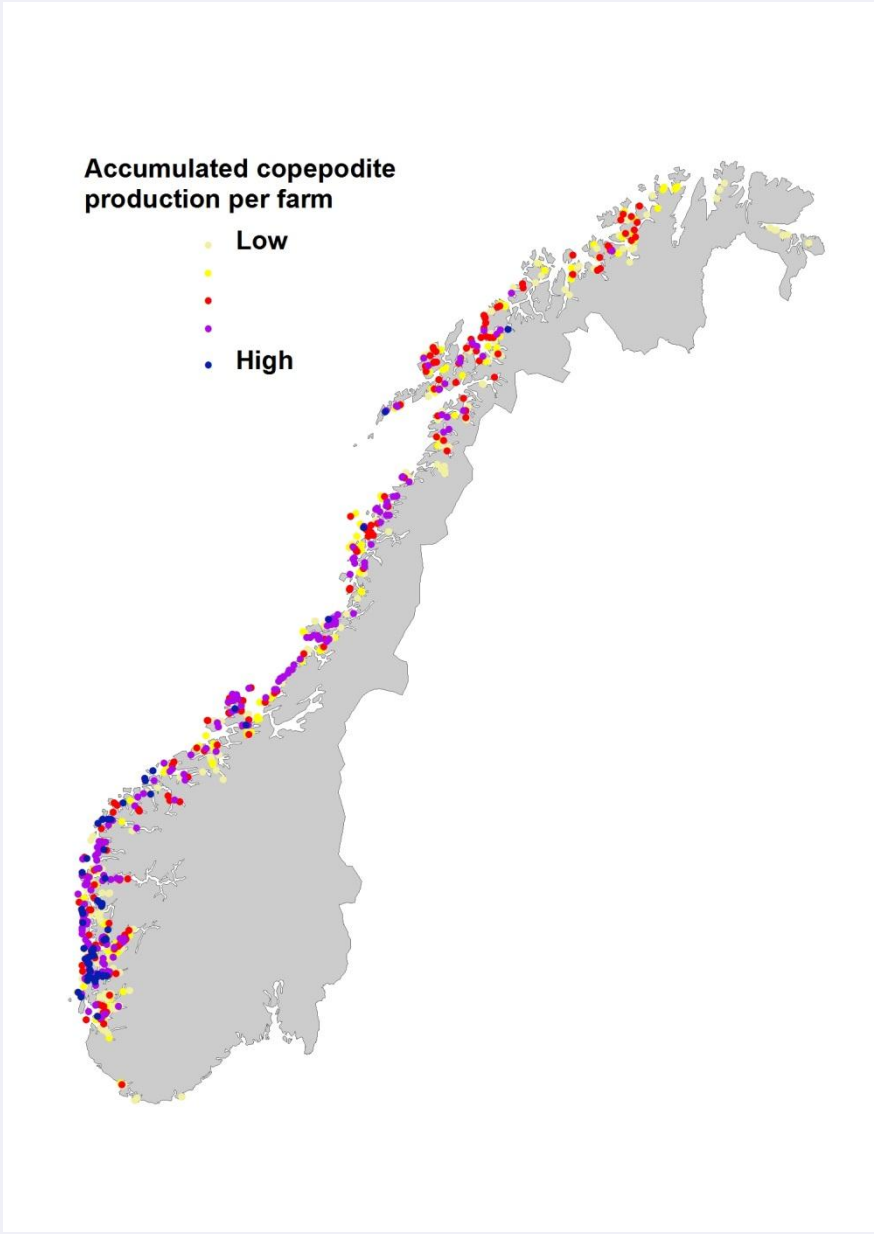
Average production, development times and accumulated farm-specific production of copepodites





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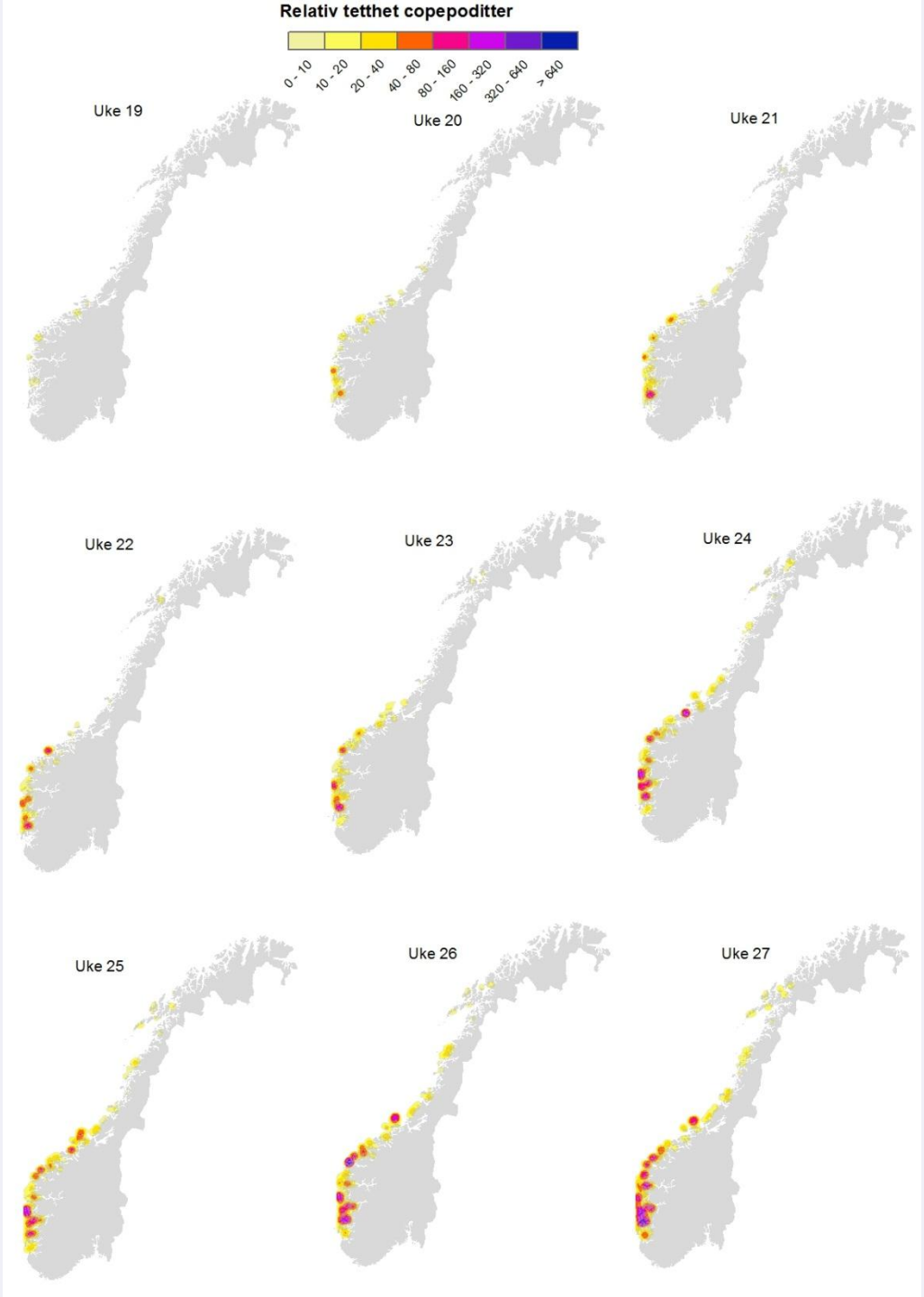

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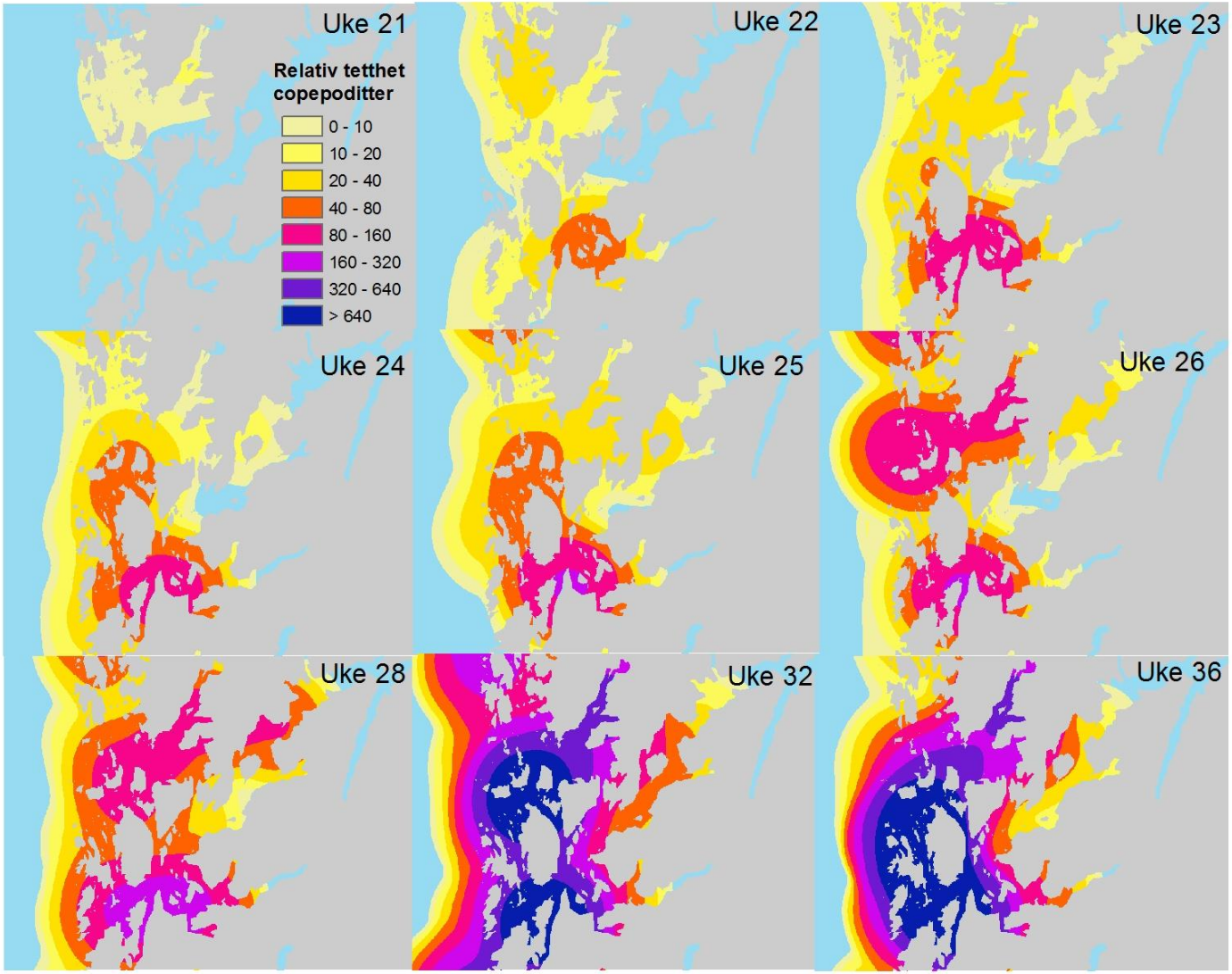
Estimated kernel density of copepodites in Hordaland 2012



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So long so good, but does it work and is it useful? VALIDIATION

- Have to derive at an expression of farm specific exposure to IP

- Test if exposure contributes to predict: new settlements of chalimus ⇨ pre-adults and adult male abundance ⇨ adult female abundance

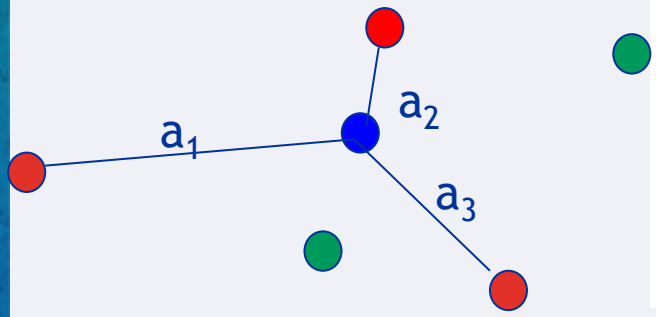
Space-time modelling of the spread of salmon lice between and within Norwegian marine salmon farms

Magne Aldrin[1,2,*], Bård Storvik[1], Anja Bråthen Kristoffersen[3,4] Peder Andreas Jansen[3]

Sources of infection:

The relationship between seaway distance and relative risk of infection between farms used to approximate exposure:

$$IP = \sum_{j} rel.risk_{(j)}$$



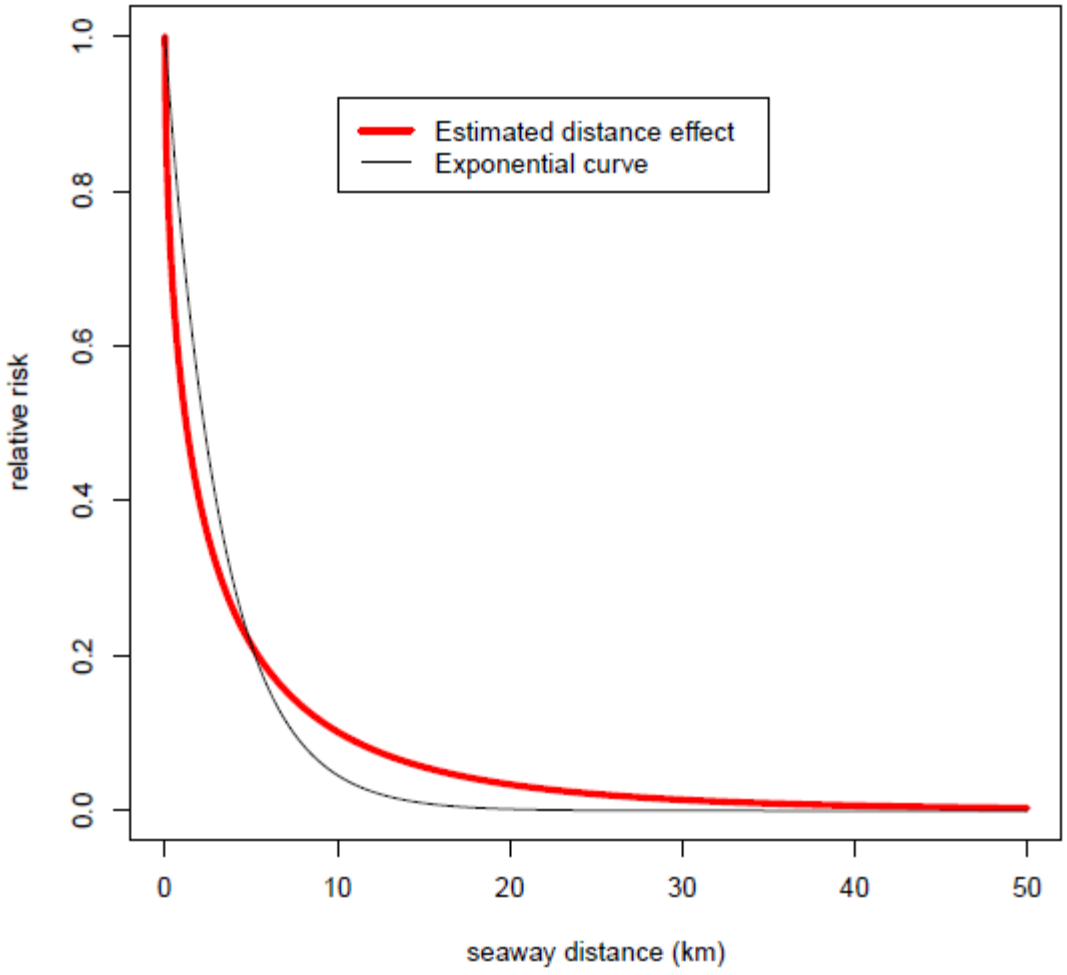


Figure 2. Estimated relative effect of the seaway distance.

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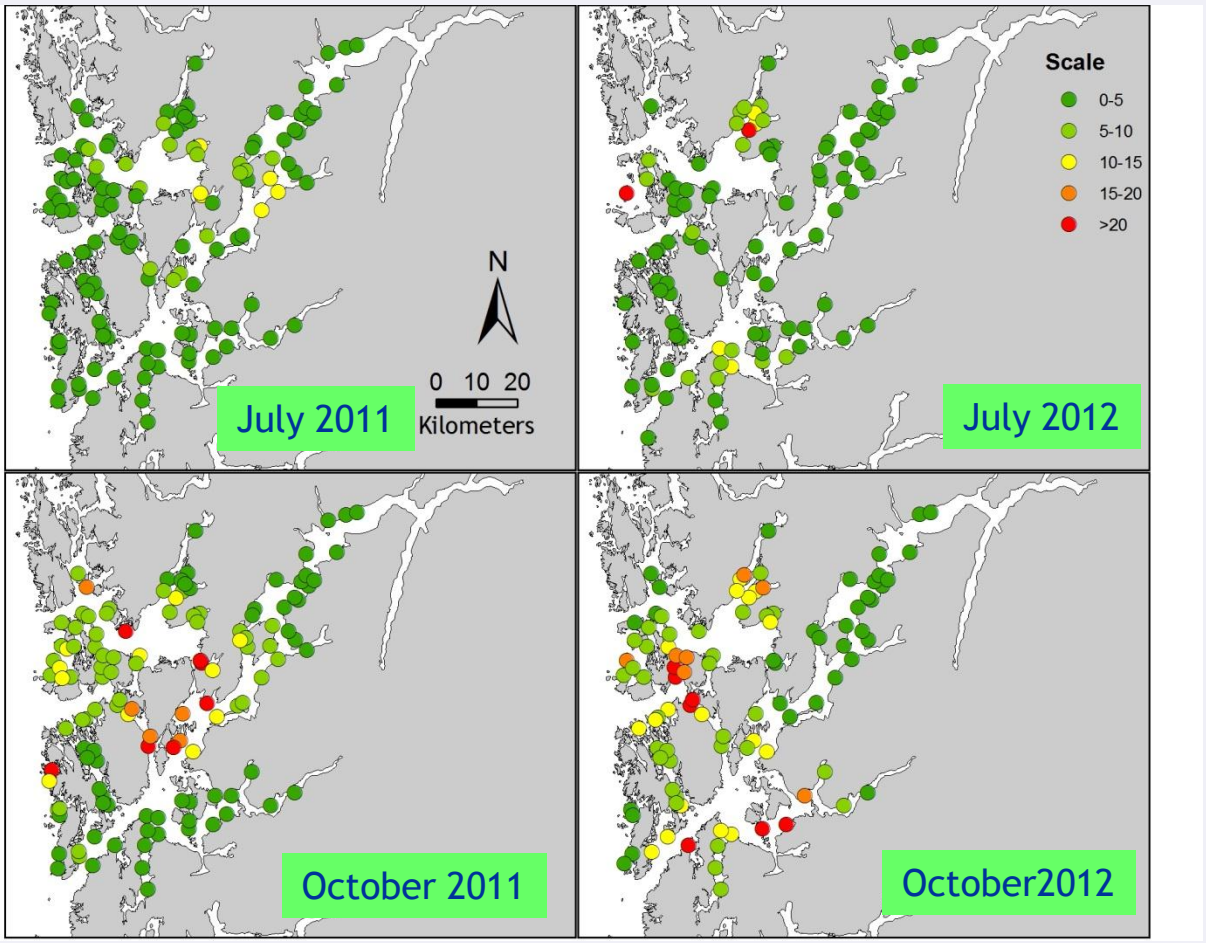
Exposure to IP



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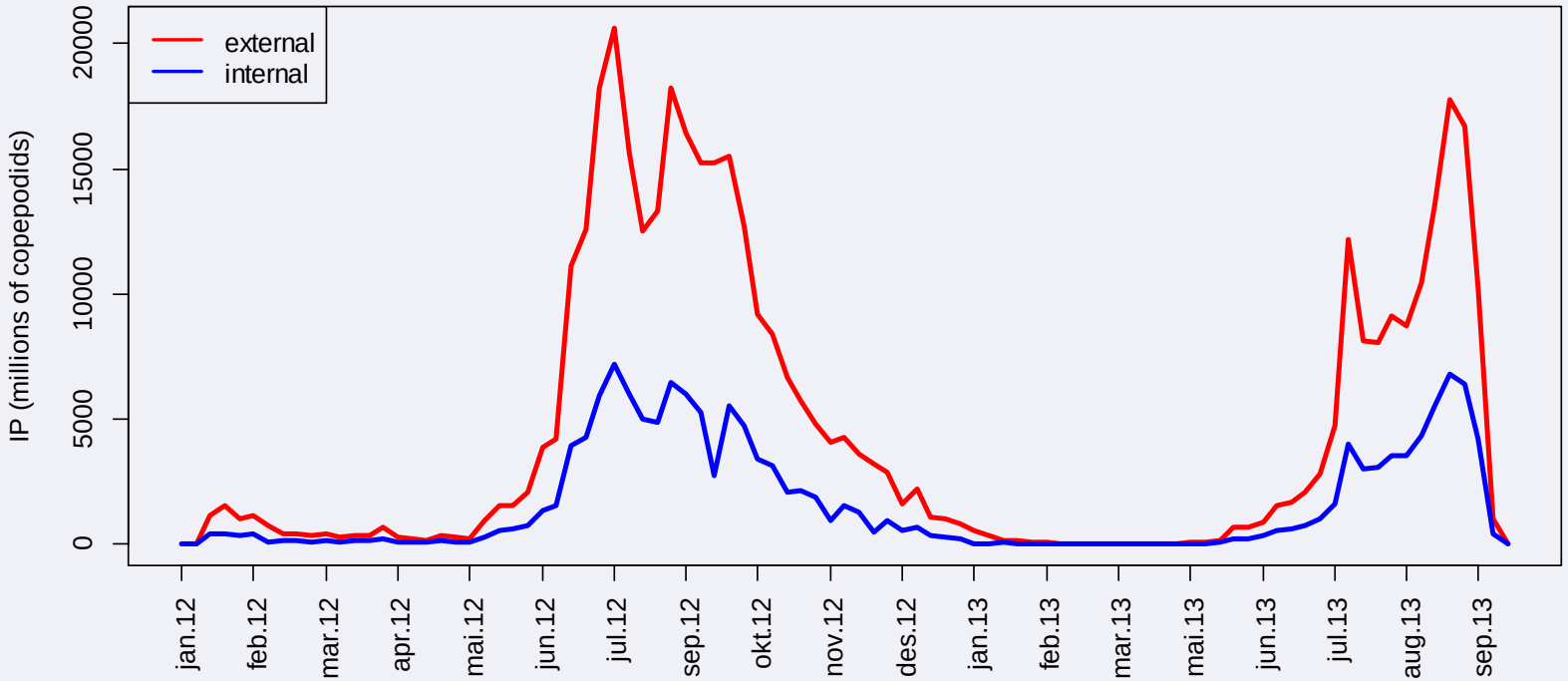
Cumulative IP from fish < 5 months old
External from all neighbours
Internal = self



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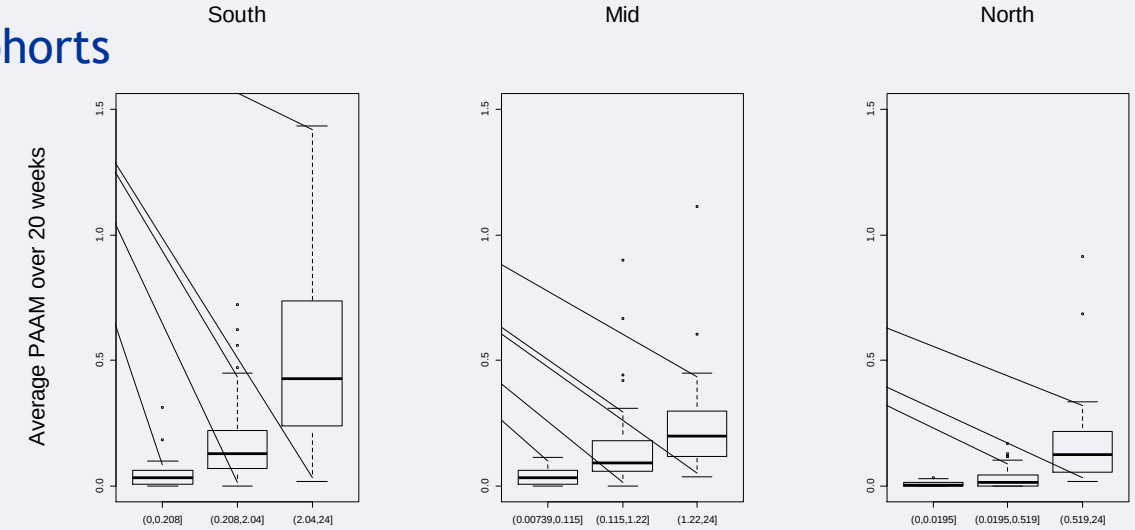
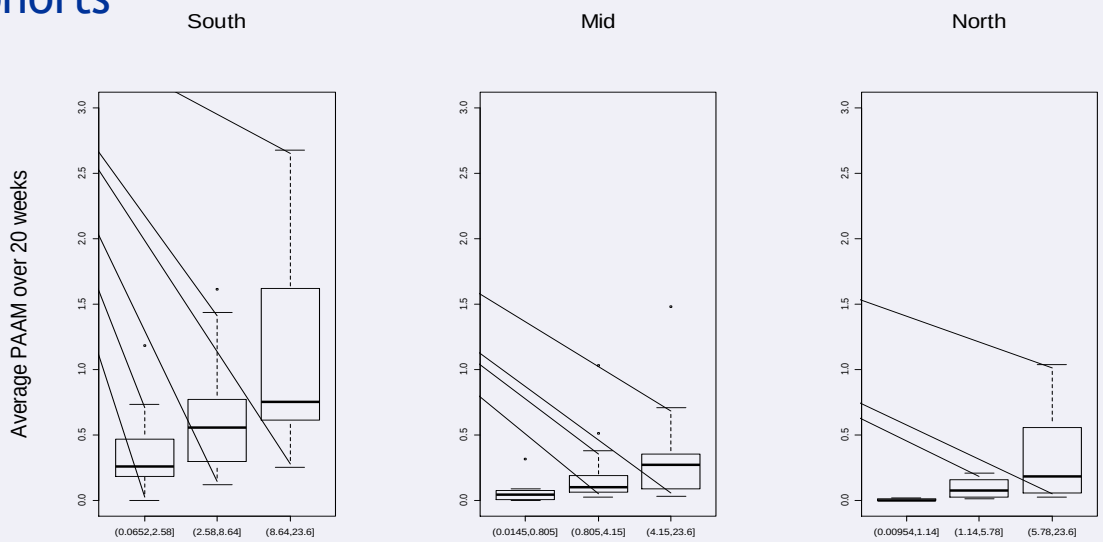
Spring cohorts



IP quantiles (<25% , 25-75%, >75%)

Autumn cohorts



IP quantiles (<25% , 25-75%, >75%)

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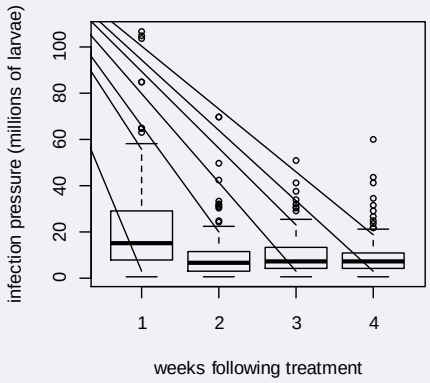
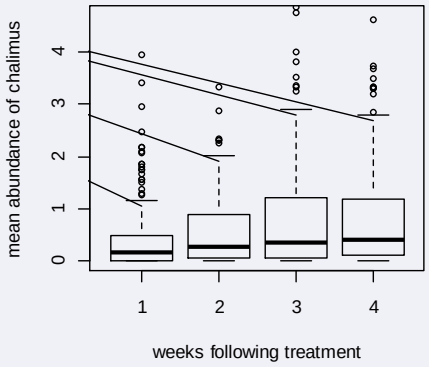
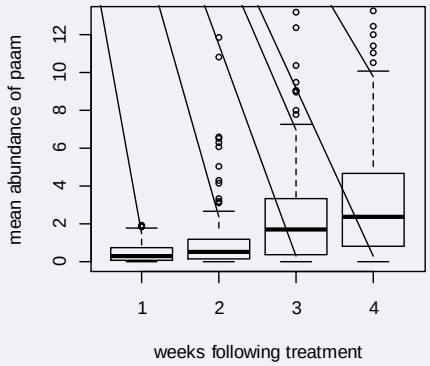
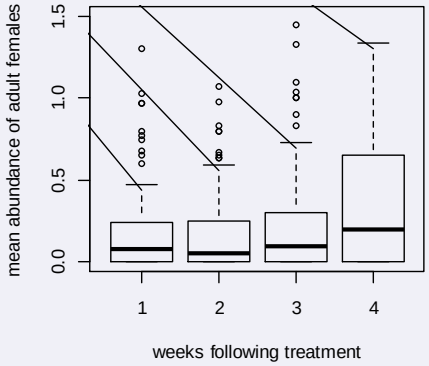
Estimated infection pressure and development of different stage categories of lice following bath treatments









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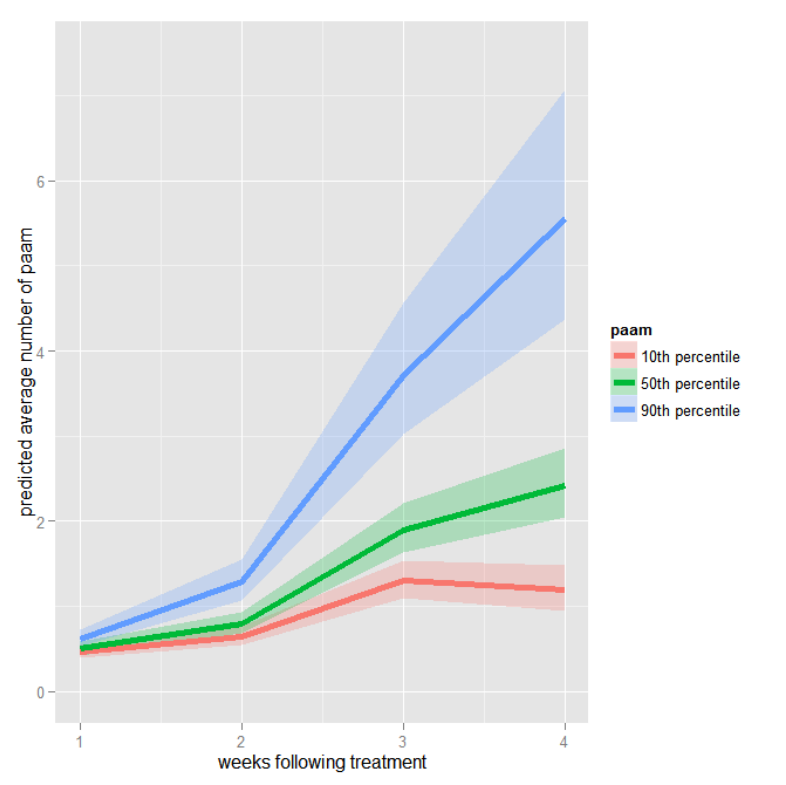
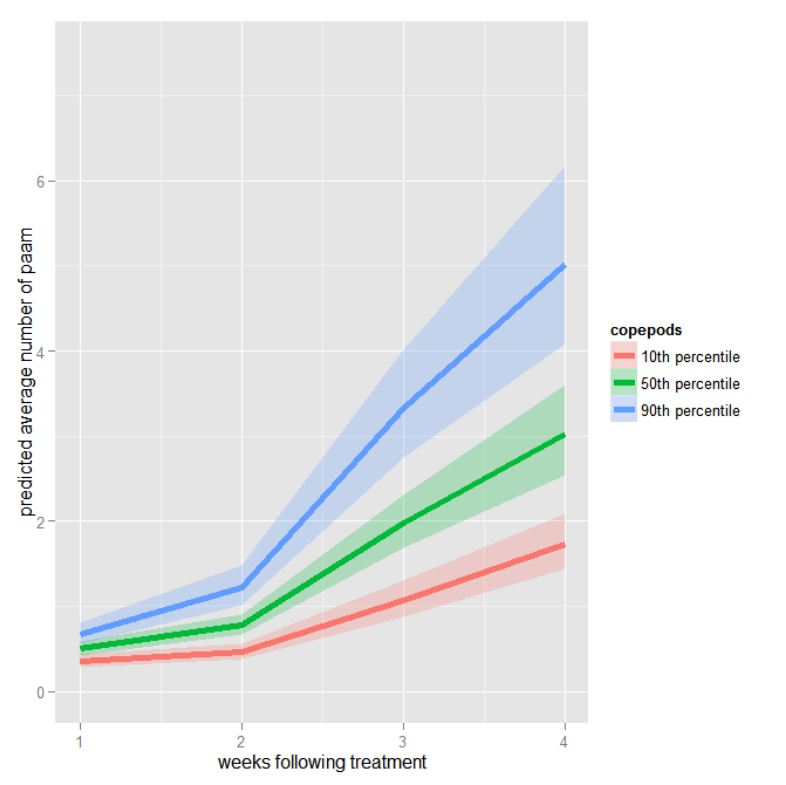
Predictions varying the PAAM category at week – 1; IP at week -2





Conclusions

- The kernel density approach focuses on the potential for transmission in space and time
- Predicts new settlements of chalimus ⇨ pre-adults and adult male abundance ⇨ adult female abundance
- Transparent, reproducible and can easily be calculated (displayed) in «real time»
- Can form the basis for regulations addressing farm discharges of infection, local IP
- Can be used by farms to evaluate risks of transmission
  - Especially when coupled to hydrodynamic models?