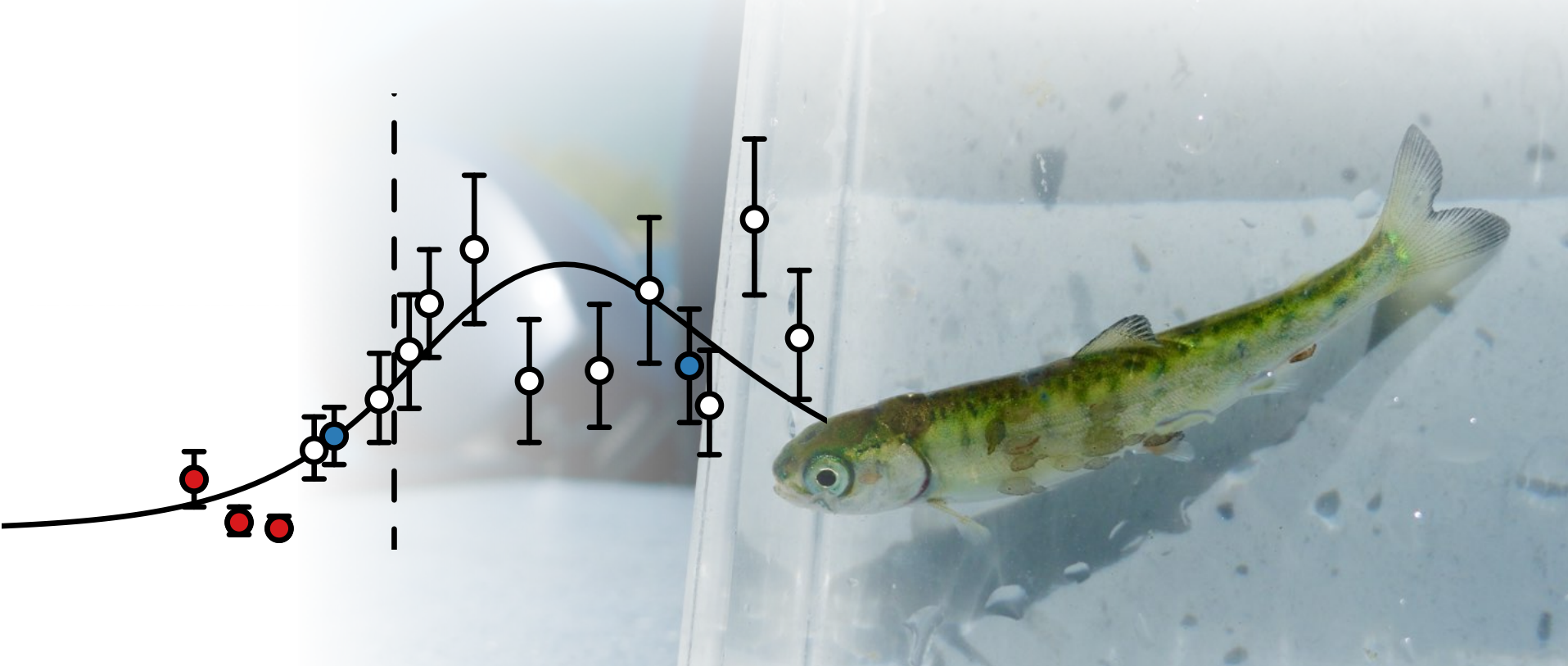


Lousy lessons learned

Study design and parameter estimability for spatial and temporal ecological models using data cloning



Mark Lewis

Stephanie Peacock, Martin Krkošek, Andrew Bateman, and Subhash Lele



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CALGARY



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TORONTO



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ALBERTA

Parameter estimability

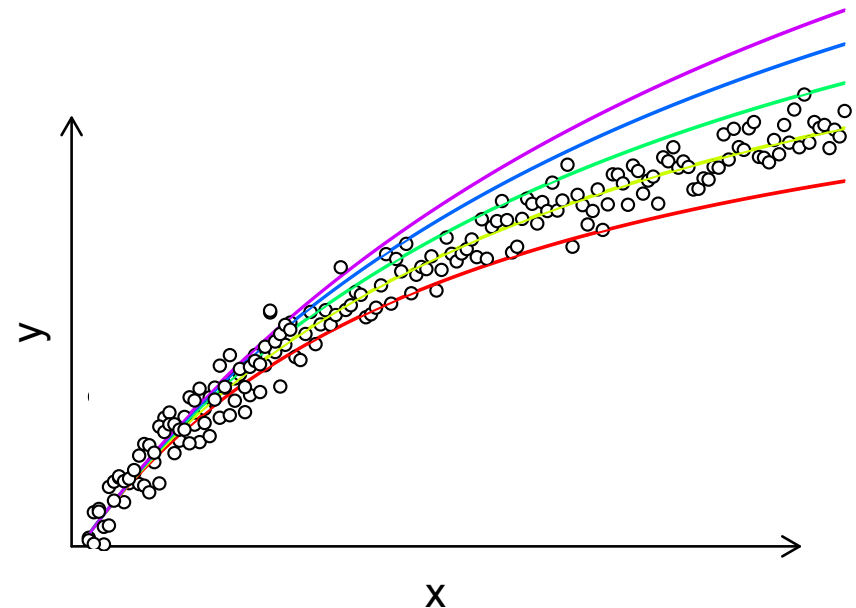
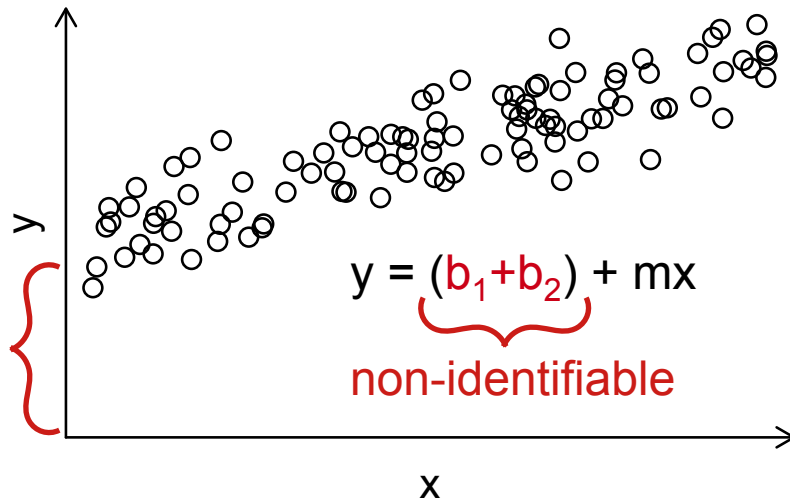
Non-identifiability

Parameter can not be estimated, no matter how many data



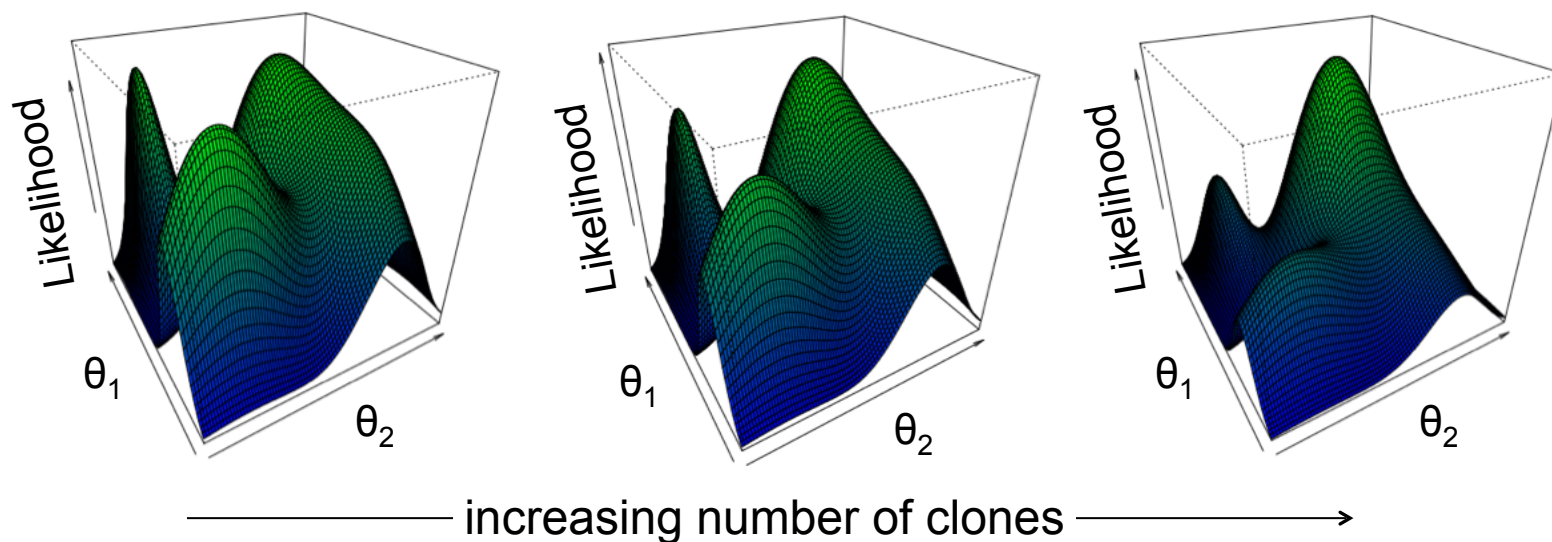
Non-estimability

Parameter can not be estimated, given the data you have



Data cloning

- Maximum Likelihood Estimates (MLEs) using **MCMC** in a **Bayesian framework** by *overwhelming* the prior
- Global MLEs when your likelihood surface may be flat or multi-modal
- Estimability of parameters in your model



How does data cloning work?

1. Create a K cloned data set
2. Using MCMC, generate draws from your posterior, based on some (proper) prior and the likelihood of the cloned data vector
3. Compute **means** and **sample variances** from the marginal posteriors from the MCMC output

$$\mathcal{D}^k = \underbrace{\mathcal{D}, \mathcal{D}, \dots, \mathcal{D}}_{k \text{ times}}$$

\mathcal{D} : data

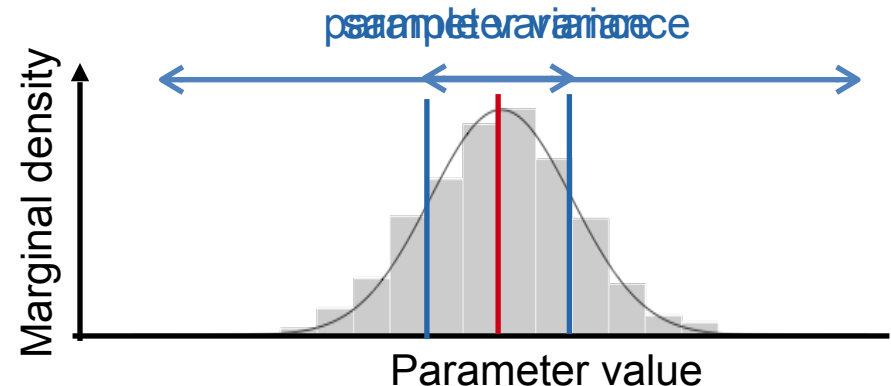
k : number of clones

\mathcal{M} : model

$$\Pr(\mathcal{M}|\mathcal{D}^k) \propto \Pr(\mathcal{D}^k|\mathcal{M})\Pr(\mathcal{M})$$

Given enough clones....

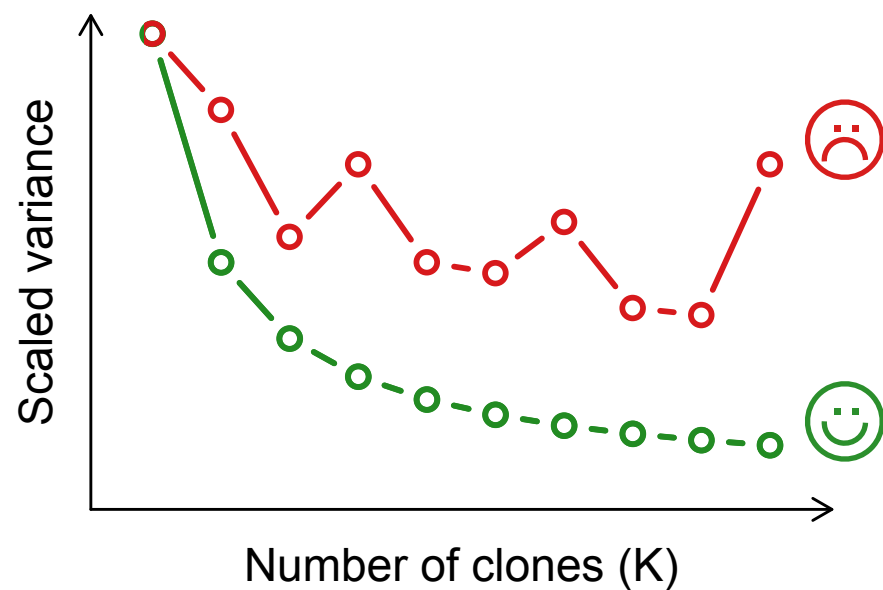
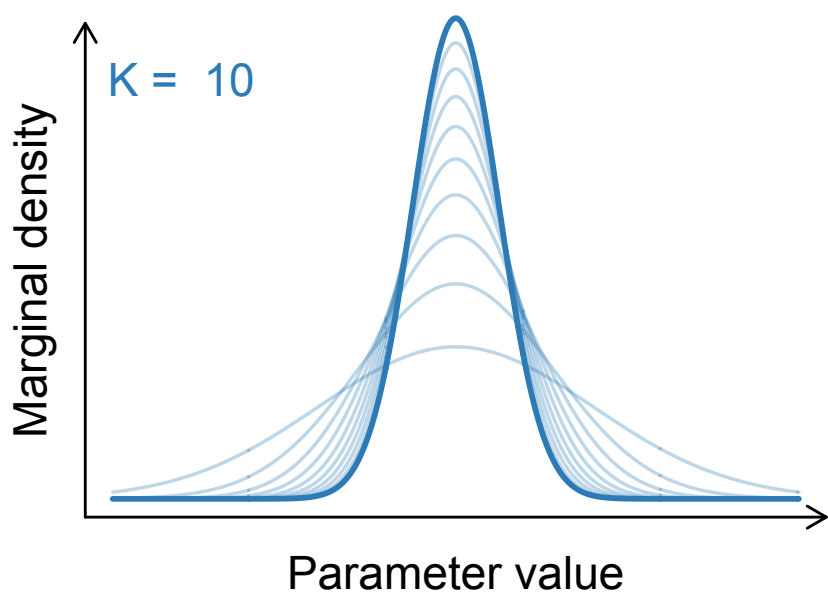
4. The MLE is the **mean** of the posterior, and the **variance is K times the MCMC sample variance**



```
> install.packages("dclone")
```

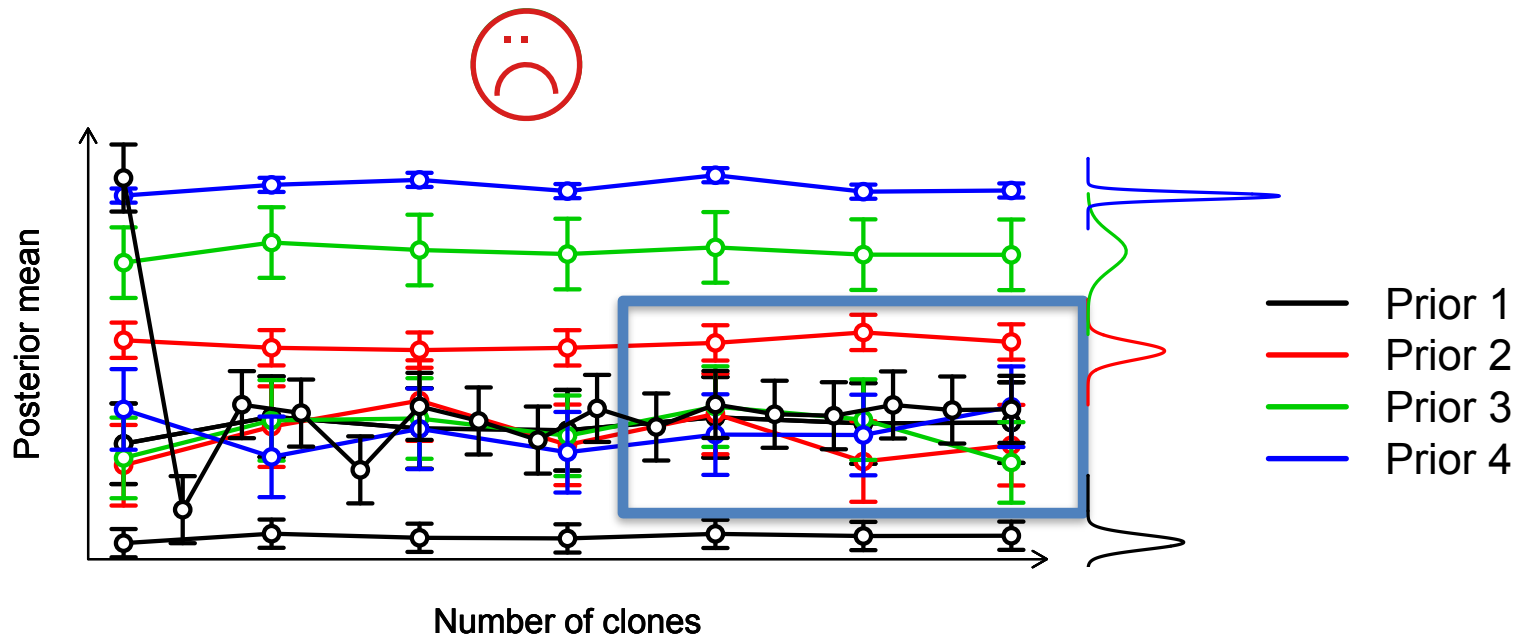
Data cloning and estimability

Variance in posterior should decrease at a rate of $1/K$



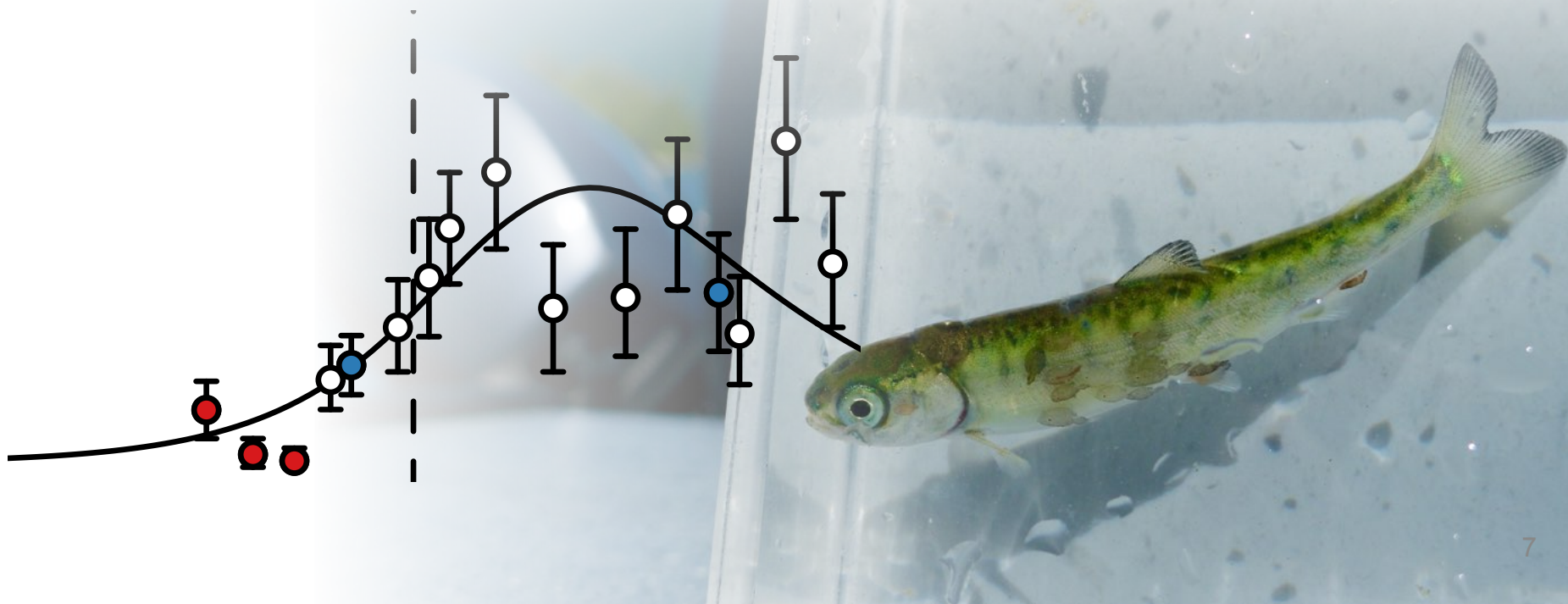
Data cloning and estimability

Variance in posterior should decrease at a rate of $1/K$
Posterior mean should be invariant to the choice of prior

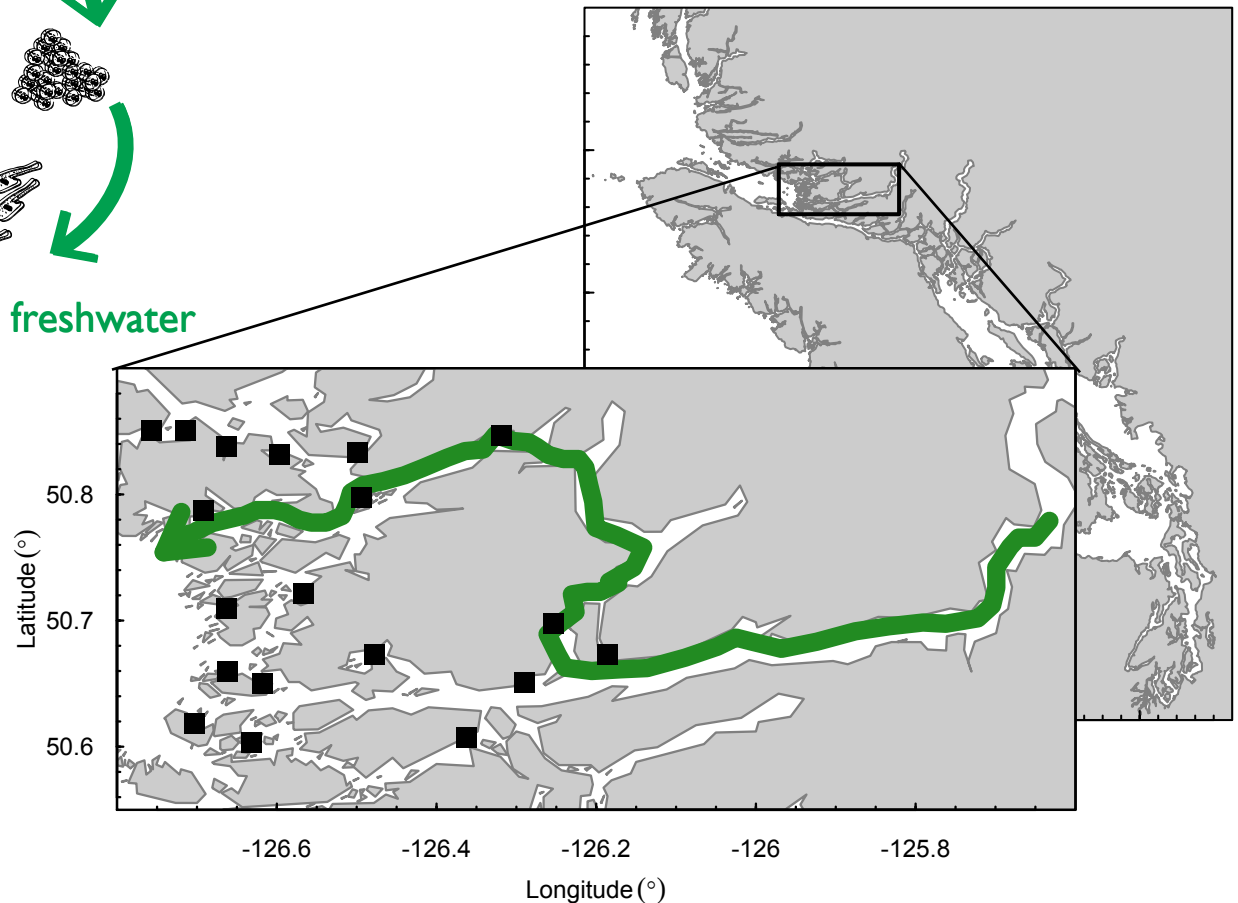
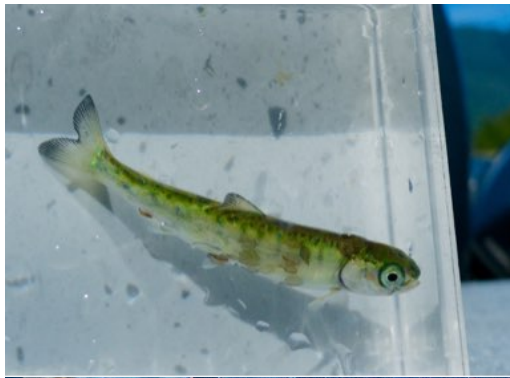
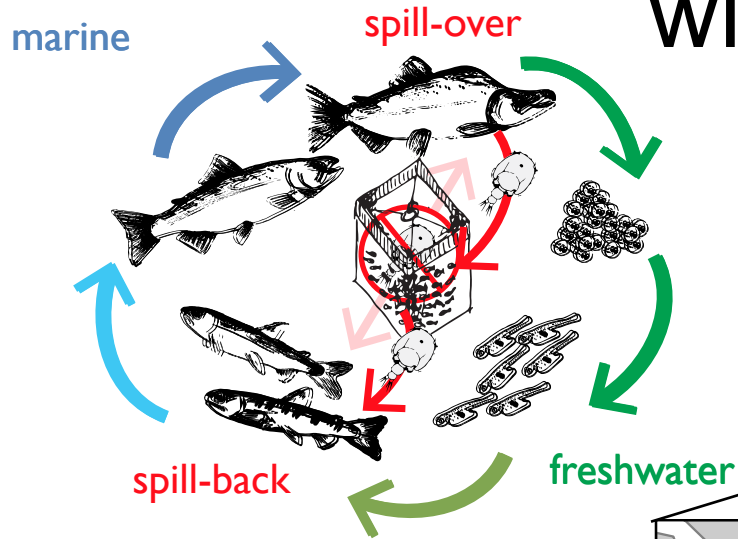


Case study: sea lice on juvenile salmon

1. How does one address problems of parameter non-estimability?
2. How does one avoid such problems to begin with?

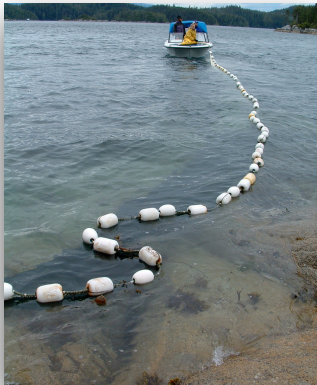
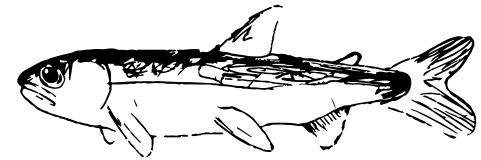
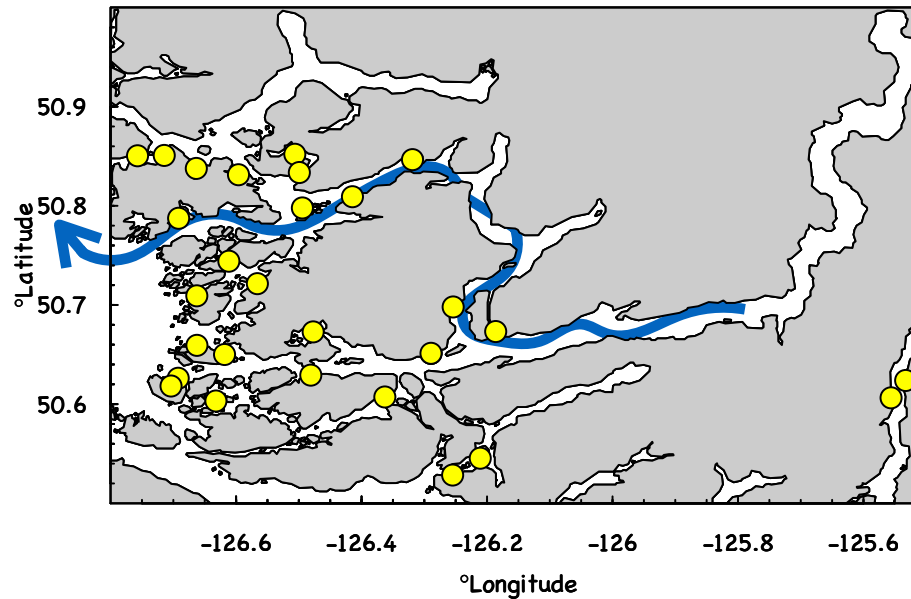


Sea louse transmission from farmed to wild salmon

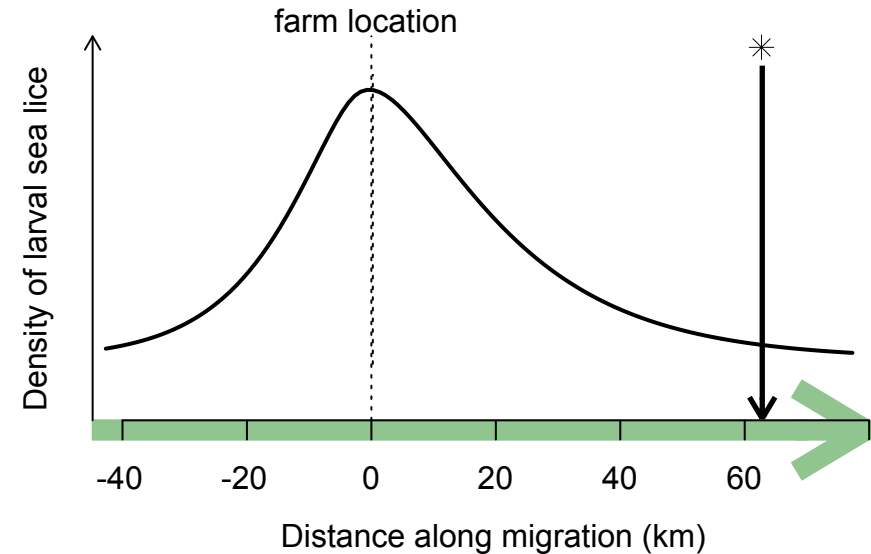
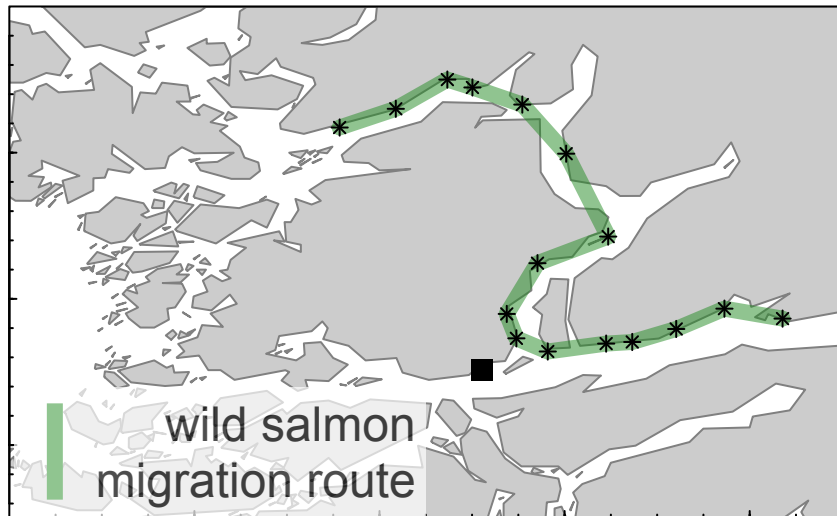


Data: Spatial surveys of sea louse abundance

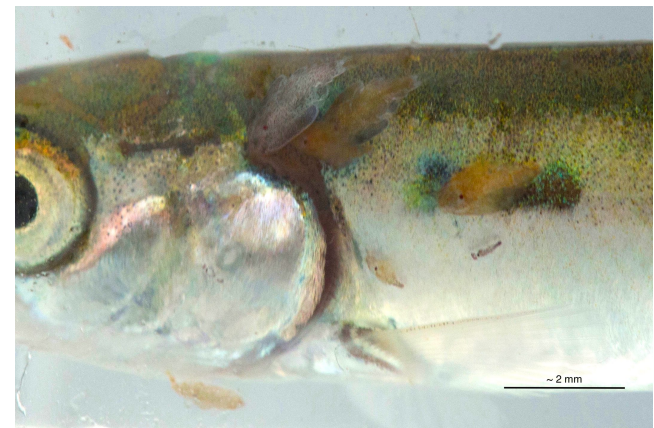
- location of salmon farms
- ↑ wild salmon migration route



The model

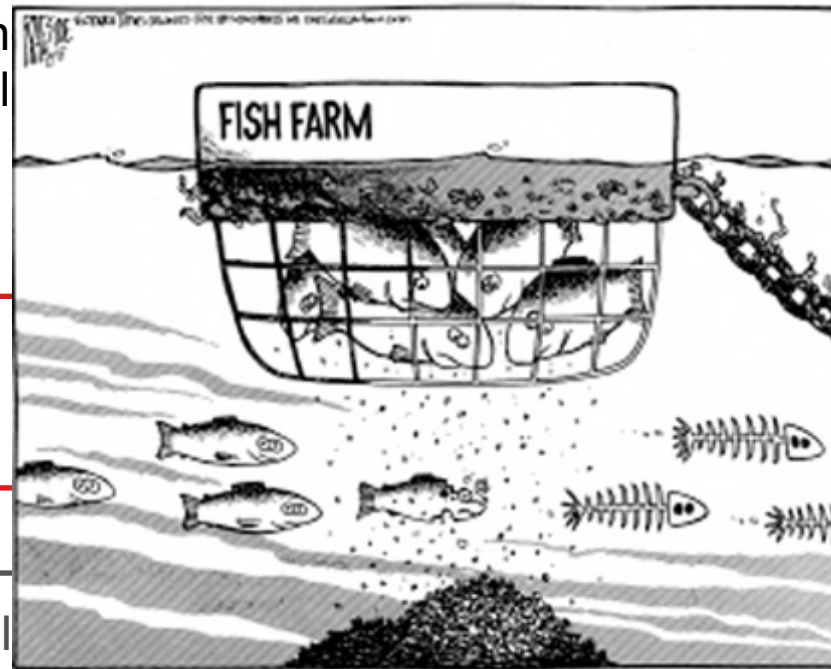
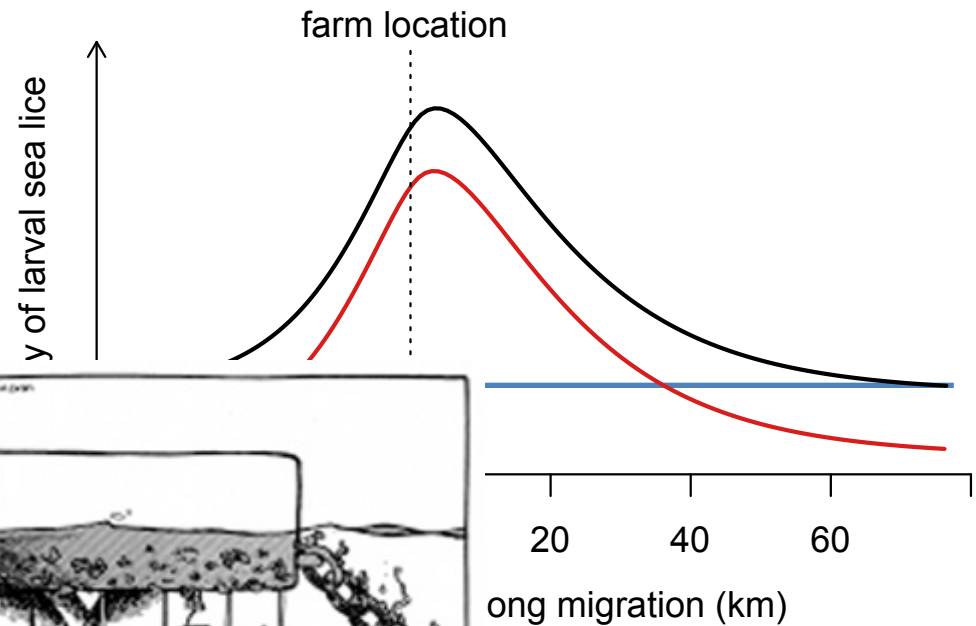


What is the relative contribution of farm and ambient sources of sea lice?



Three hypotheses:

1. No effect of farms
2. Point source of sea lice at location of farm
3. Both background sources of sea lice



infection → host migration + development + survival (s_c, s_h)

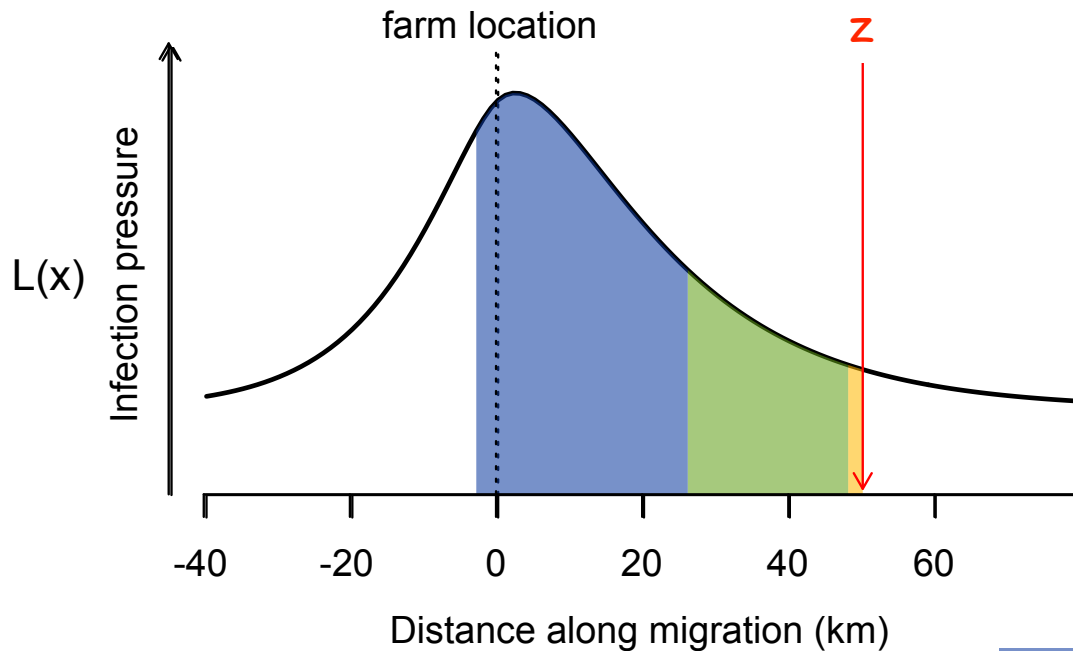
Constants
 D, g, m_n, m_p, q_n

Wild data
 c_i, h_i, m_i

background sources of parasites

Estimated parameters
 $f, k, l_c, l_h, l_m, s_c, s_h$

The math



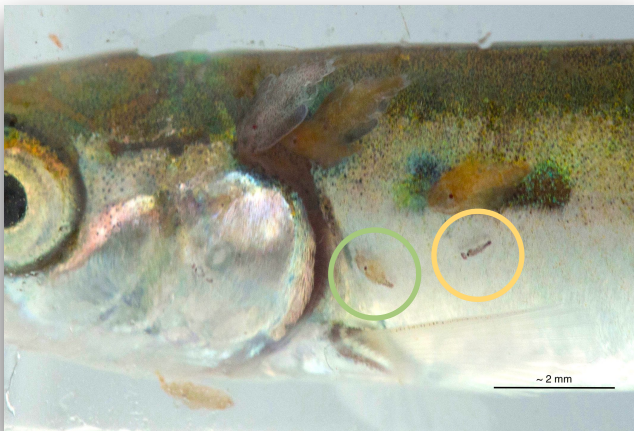
$$L(x) = k + f f(x)$$

Expected number of lice of each stage:

$$C(z) = \beta \int_{z-\lambda_c}^z L(x) dx$$

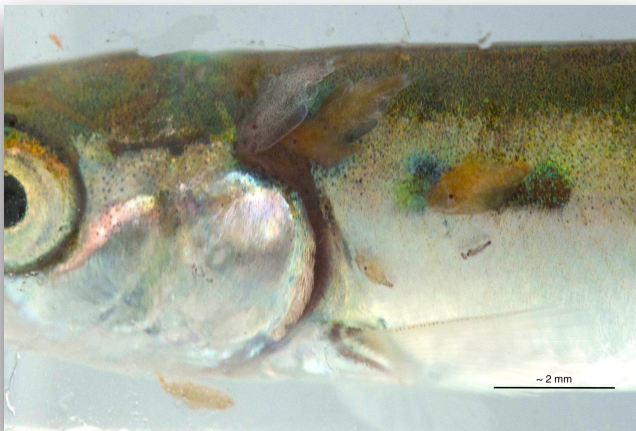
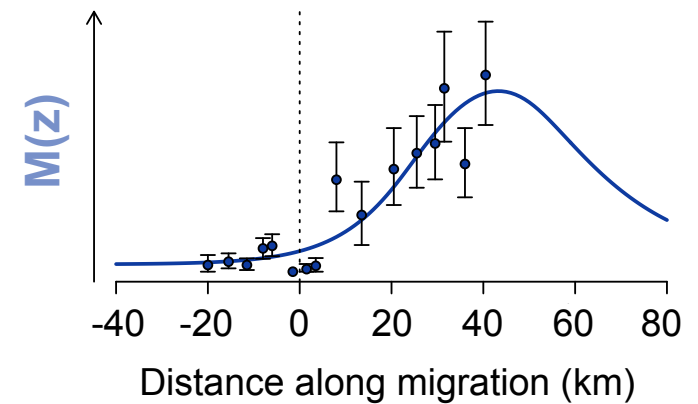
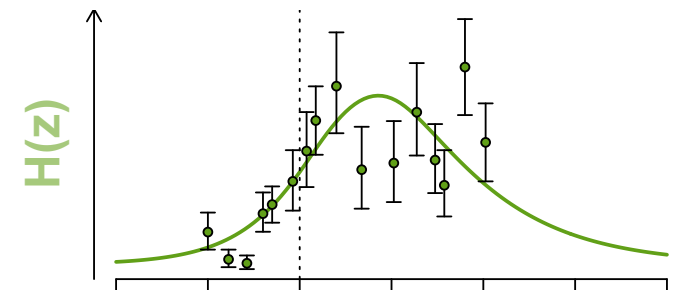
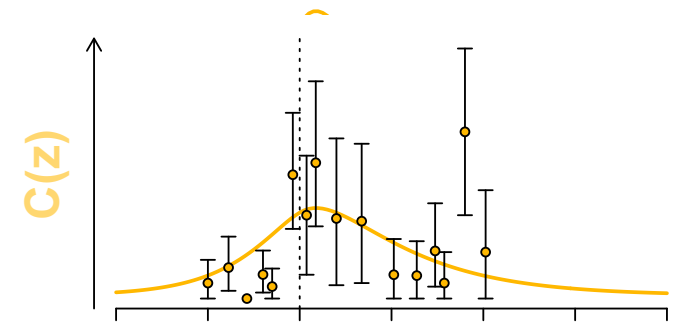
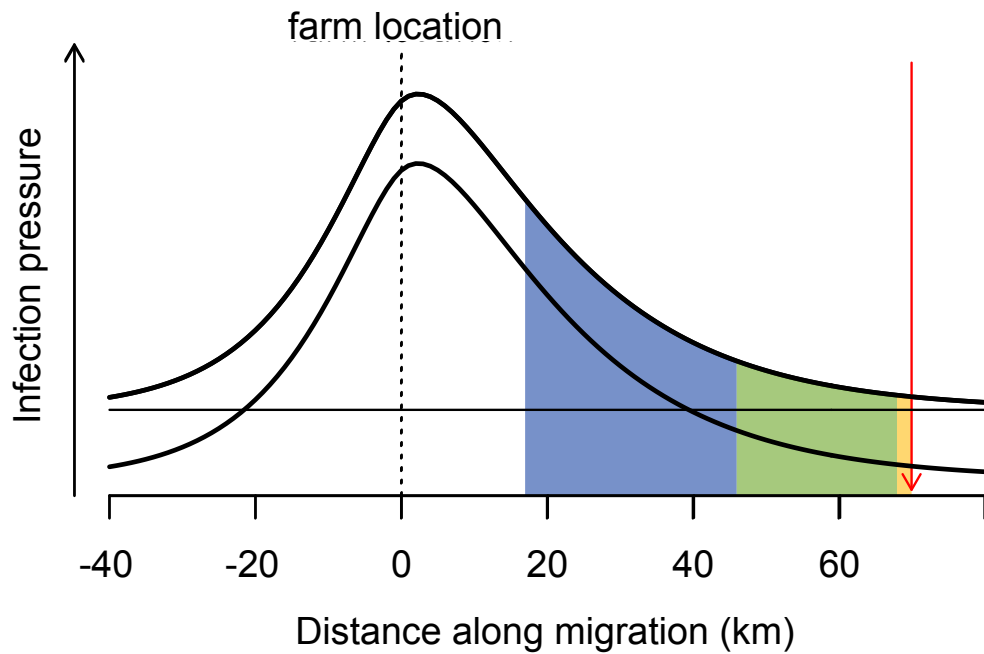
$$H(z) = \beta s_c \int_{z-\lambda_c-\lambda_h}^{z-\lambda_c} L(x) dx$$

$$M(z) = \beta s_h s_c \int_{z-\lambda_c-\lambda_h-\lambda_m}^{z-\lambda_c-\lambda_h} L(x) dx$$



- b transmission coefficient (unknown)
- l_i distance migrated during stage i (days)
- s_i survival of lice from stage i to $i+1$

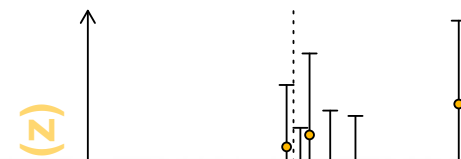
The math



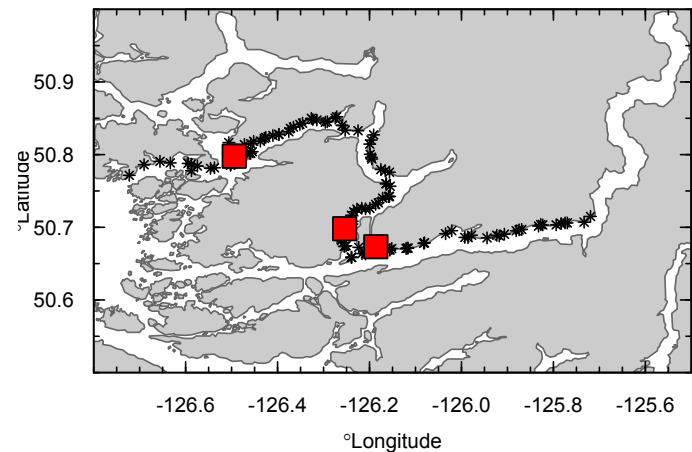
Model results

“Farm salmon were the primary source of lice, raising the density of infective parasite larvae

Can we apply the model to test if we can measure effects of multiple farm sources of lice (f)?



2006:



Ecological Applications, 23(3), 2013, pp. 606–620
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Cessation of a salmon decline with control of parasites

STEPHANIE J. PEACOCK,^{1,2,6} MARTIN KRKOŠEK,^{3,4} STAN PROBOSZCZ,⁵ CRAIG ORR,⁵ AND MARK A. LEWIS^{1,2}

¹Department of Biological Sciences, University of Alberta, Edmonton, Alberta T6G 2G1 Canada

²Centre for Mathematical Biology, Department of Mathematical and Statistical Sciences, University of Alberta, Edmonton, Alberta T6G 2G1 Canada

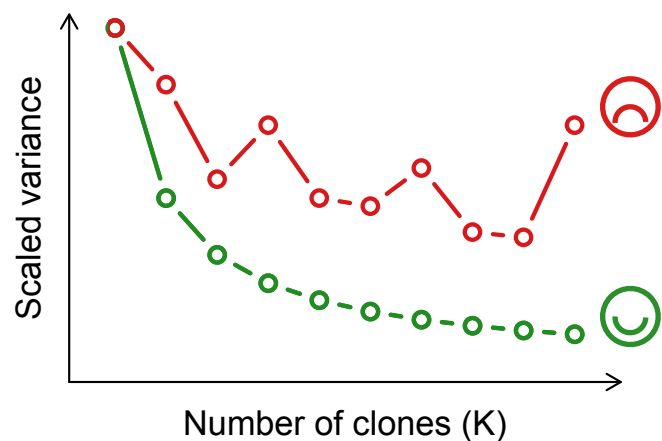
³Department of Zoology, University of Otago, Dunedin, New Zealand

⁴Salmon Coast Field Station, Simoom Sound, British Columbia V0P 1S0 Canada

controversial and unresolved th
ecosystems and fisheries. We re
the spread and impact of farm-origi
wild fish populations. We mathemat
sets of native parasitic sea lice (*Lepe
corhynchus gorbuschae*) and chum (*O
Farm-origin lice induced 9–95% mortality in several sy
juvenile pink and chum salmon populations. The epiz
through a mechanism that is new to our understandi
ing infectious diseases: fish farms undermine a functio
host migration in protecting juvenile hosts from paras
ated with adult hosts. Although the migratory life cycle
salmon naturally separate adults from juveniles, fish far
L. salmonis novel access to juvenile hosts, in this ca
infection rates for at least the first ~2.5 months of t
marine life (~80 km of the migration
between juveniles and
fishes.*



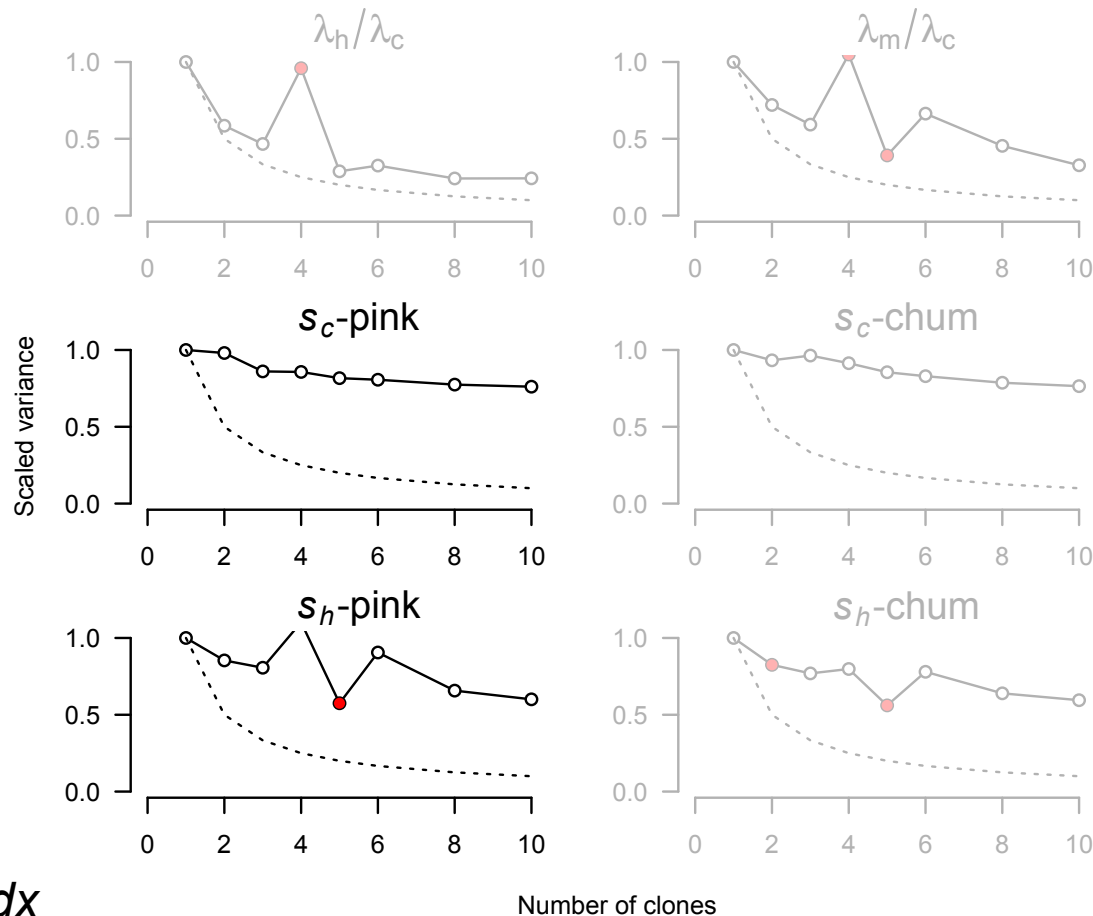
Non-estimability of parameters



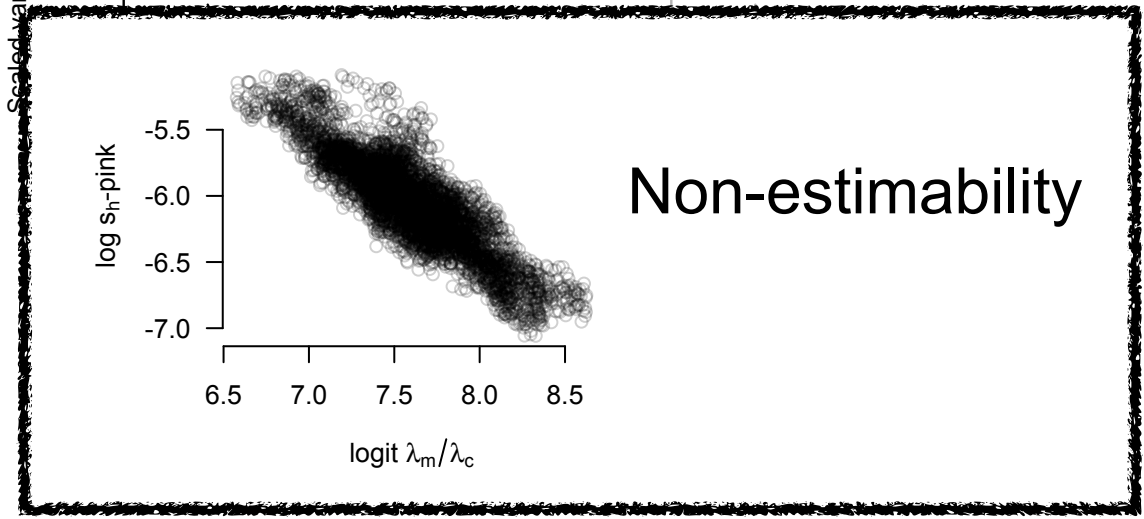
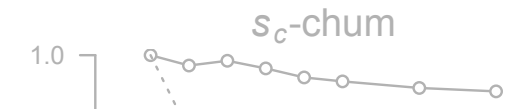
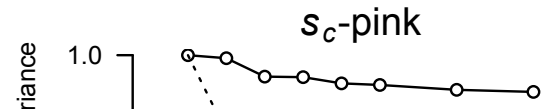
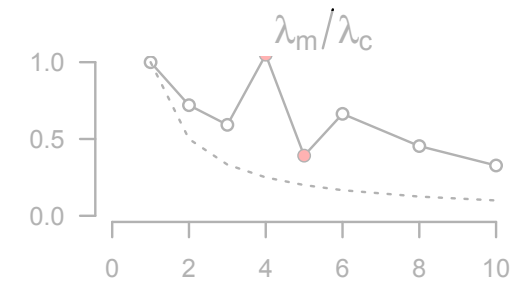
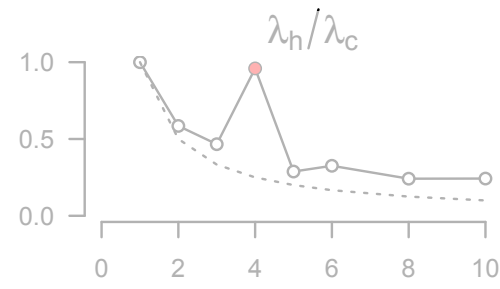
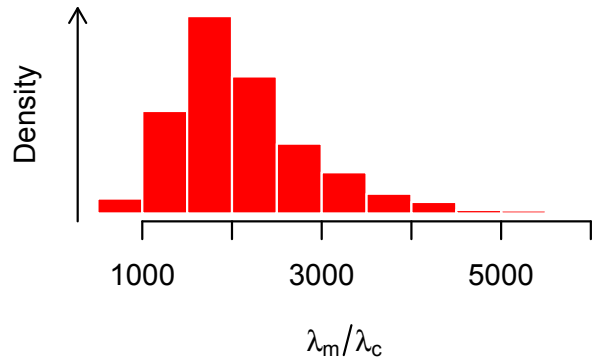
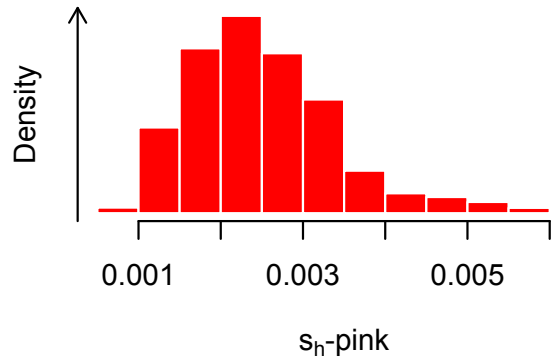
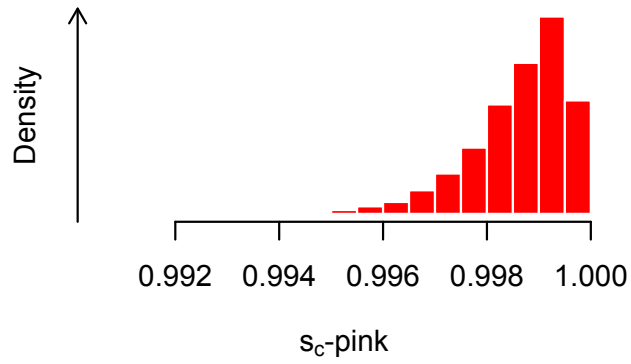
$$H(z) = \beta s_c \int_{z-\lambda_c-\lambda_h}^{z-\lambda_c} L(x) dx$$

$$M(z) = \beta s_h s_c \int_{z-\lambda_c-\lambda_h-\lambda_m}^{z-\lambda_c-\lambda_h} L(x) dx$$

2006 data

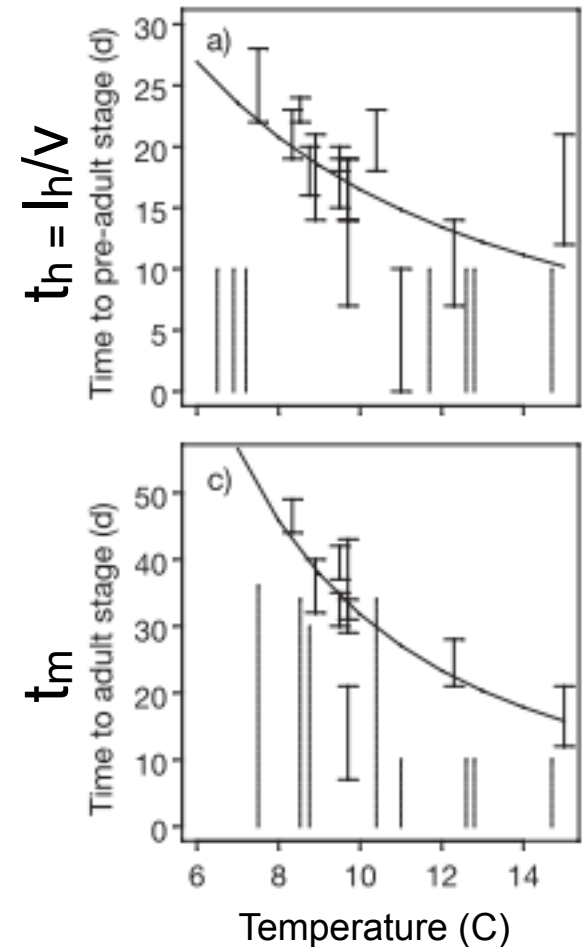


Non-estimability of parameters

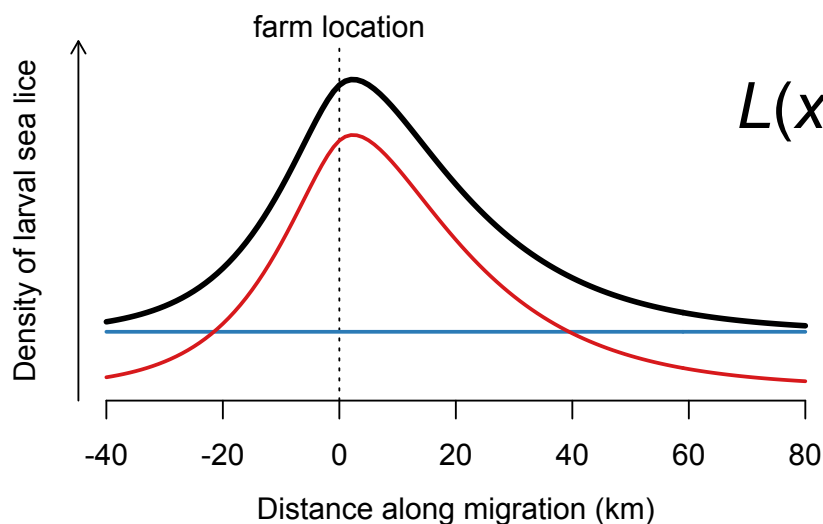


What to do about non-estimability?

- Fix parameters if information is available
 - Previous study
 - Parameters for different host species not significantly different
- Revisit model structure
 - Is something missing?
 - Can additional parameters be included?



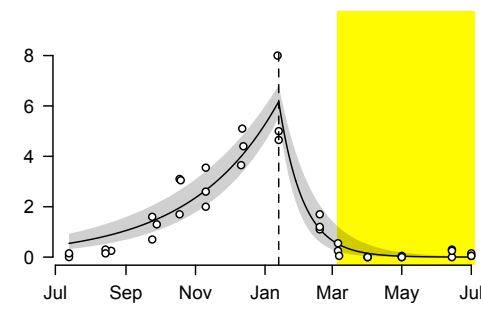
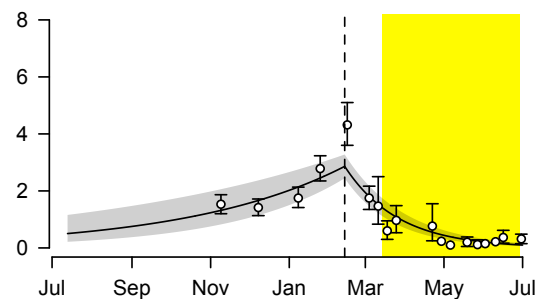
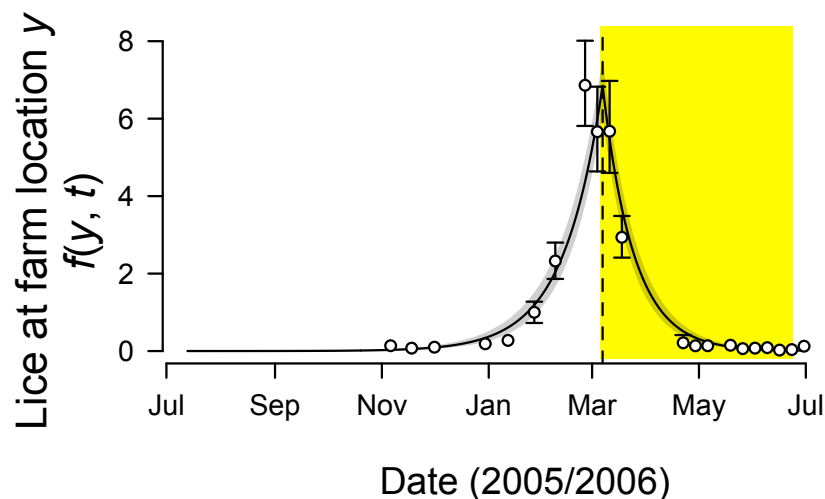
Revisiting model structure



$$L(x) = k + f f(x)$$

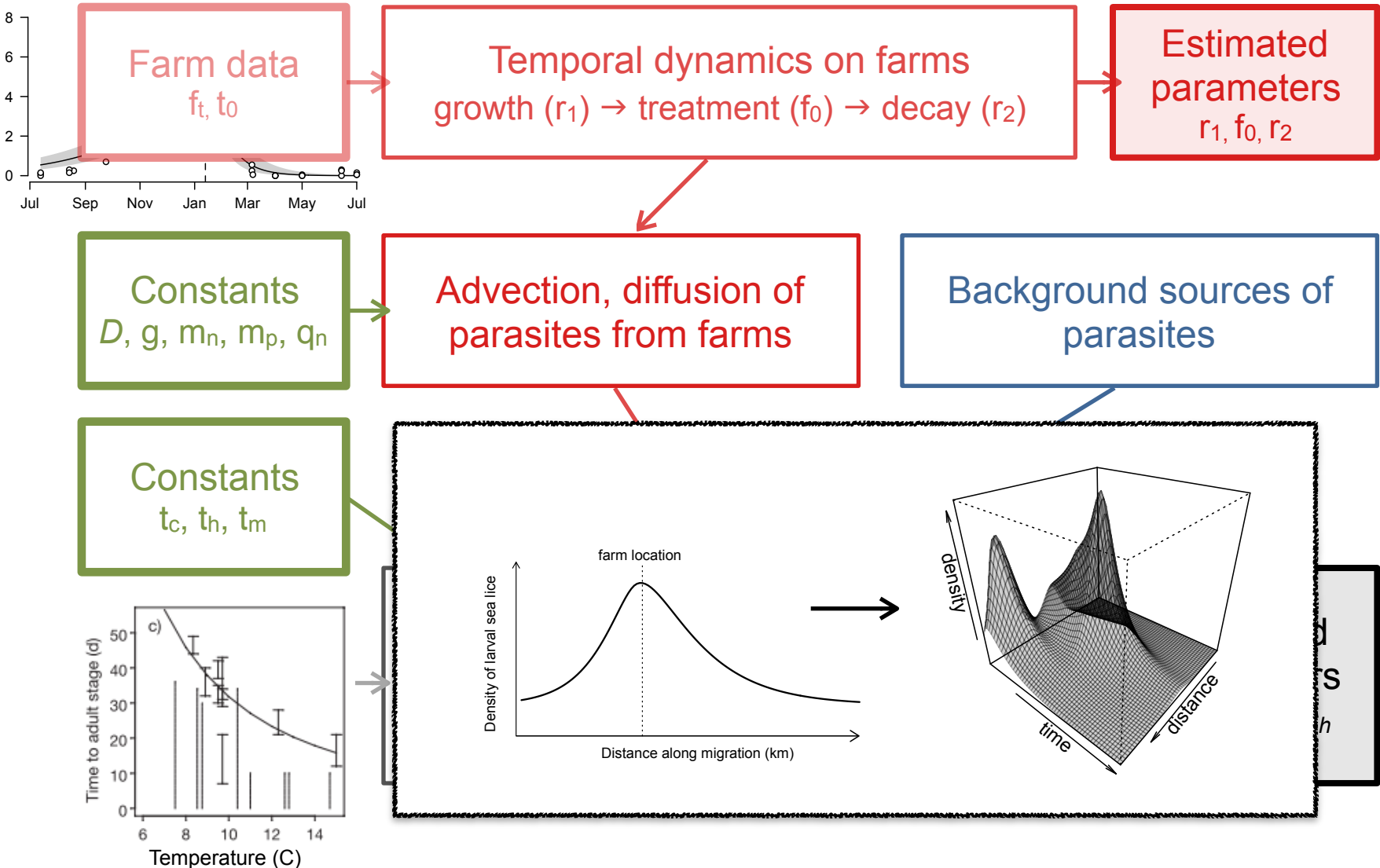


- Assumed to be a constant source through time
 - steady-state solution to advection-diffusion-decay equations

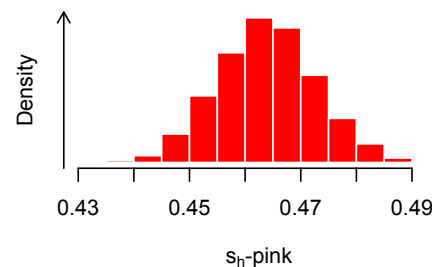
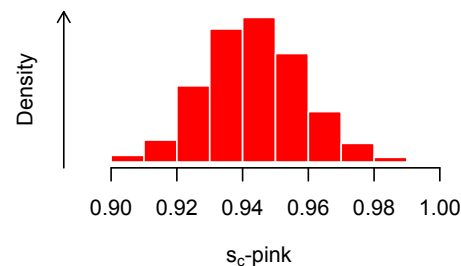
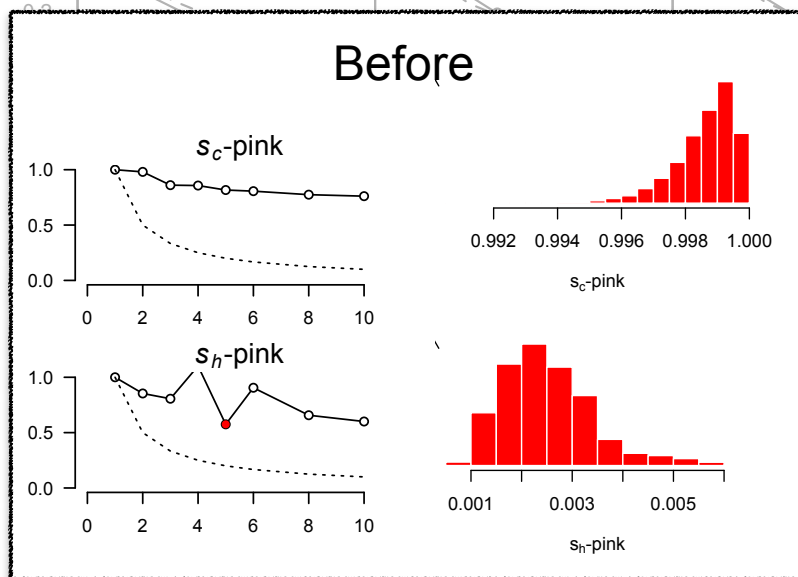
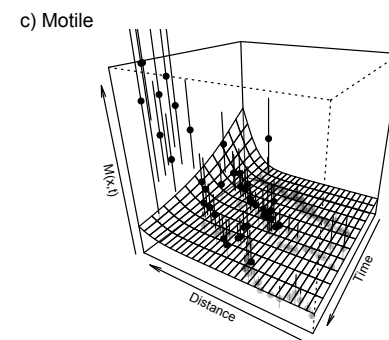
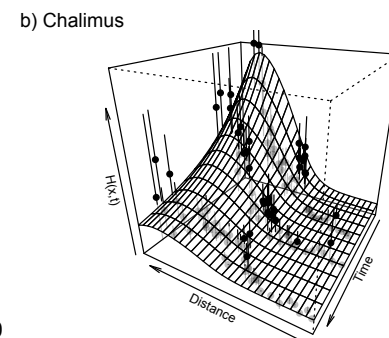
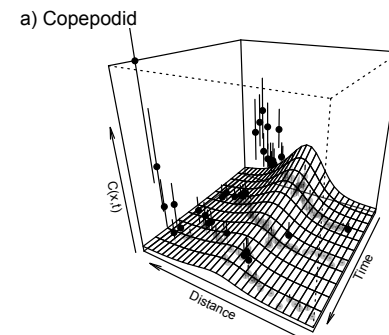
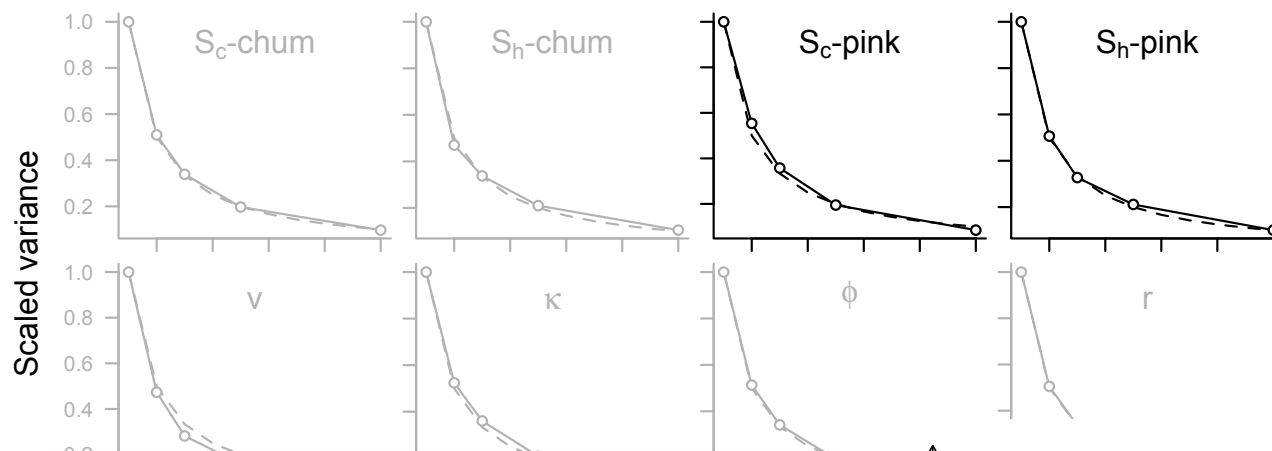


Date (2005/2006)

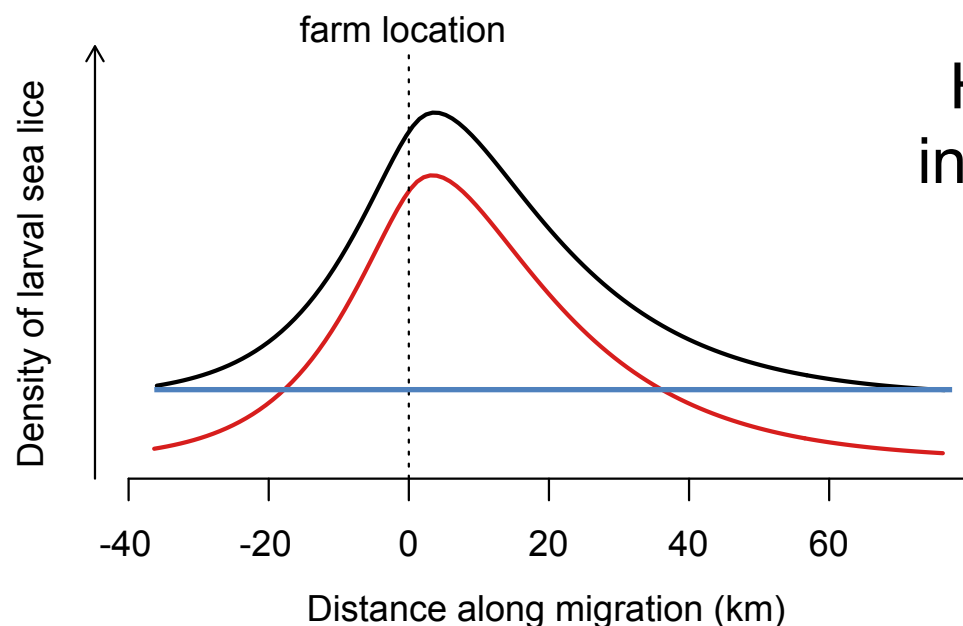
Revisiting model structure



Non-estimability of parameters



Revisiting our hypotheses



How did non-estimability influence our conclusions?

1. Ambient sources - k
2. Farm sources - f
3. Both - k & f

Relative strength of farm vs. ambient sources of lice:

f / k

Original 2006 model (non-estimable)	29 - 16,165
Revised spatiotemporal 2006 model (estimable)	578
Published 2004 estimates	28 - 21,445

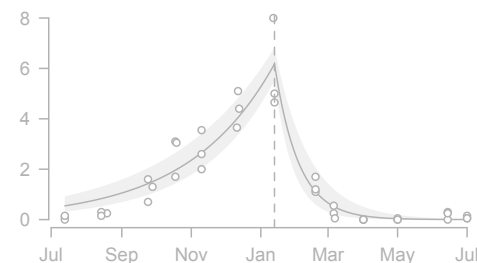
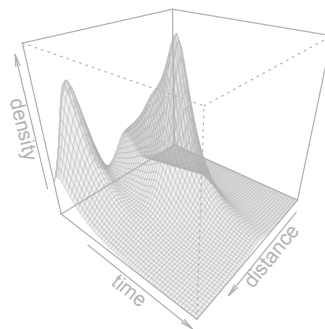
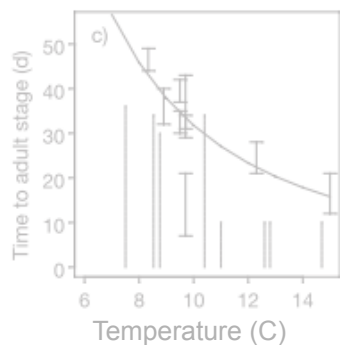
Case study: sea lice on juvenile salmon

1. How does one address problems of parameter non-estimability?

✓ Fixing parameters

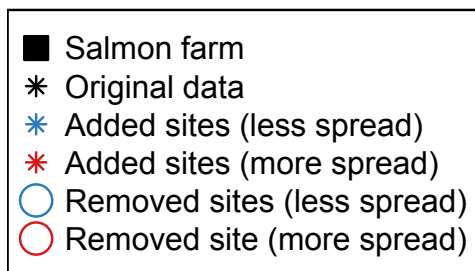
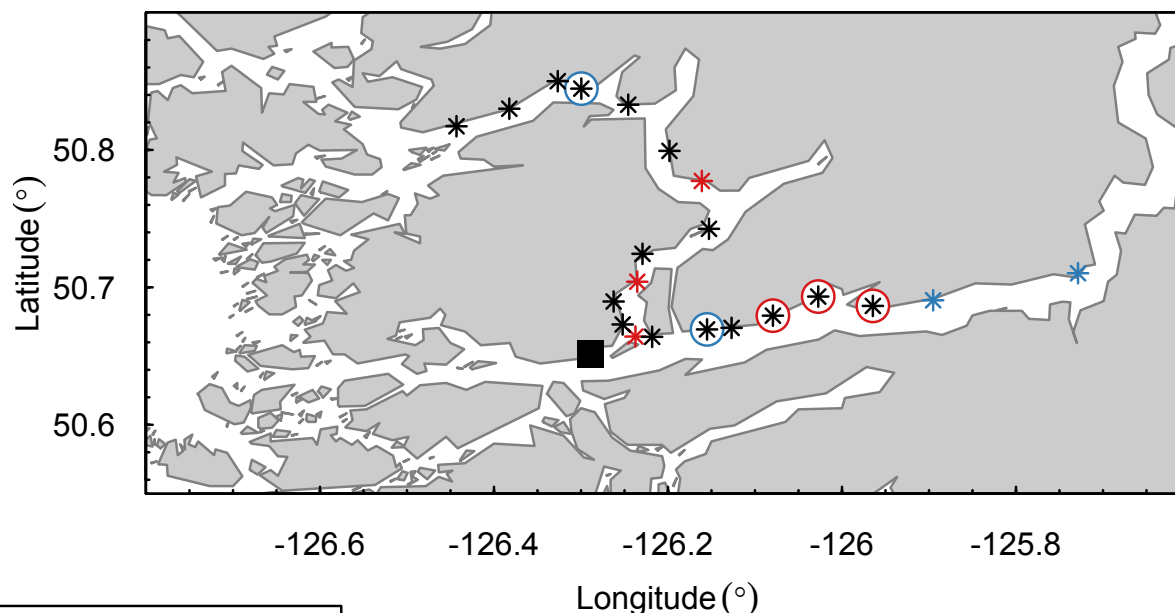
✓ Revisiting model

✓ Collecting more/
different data*



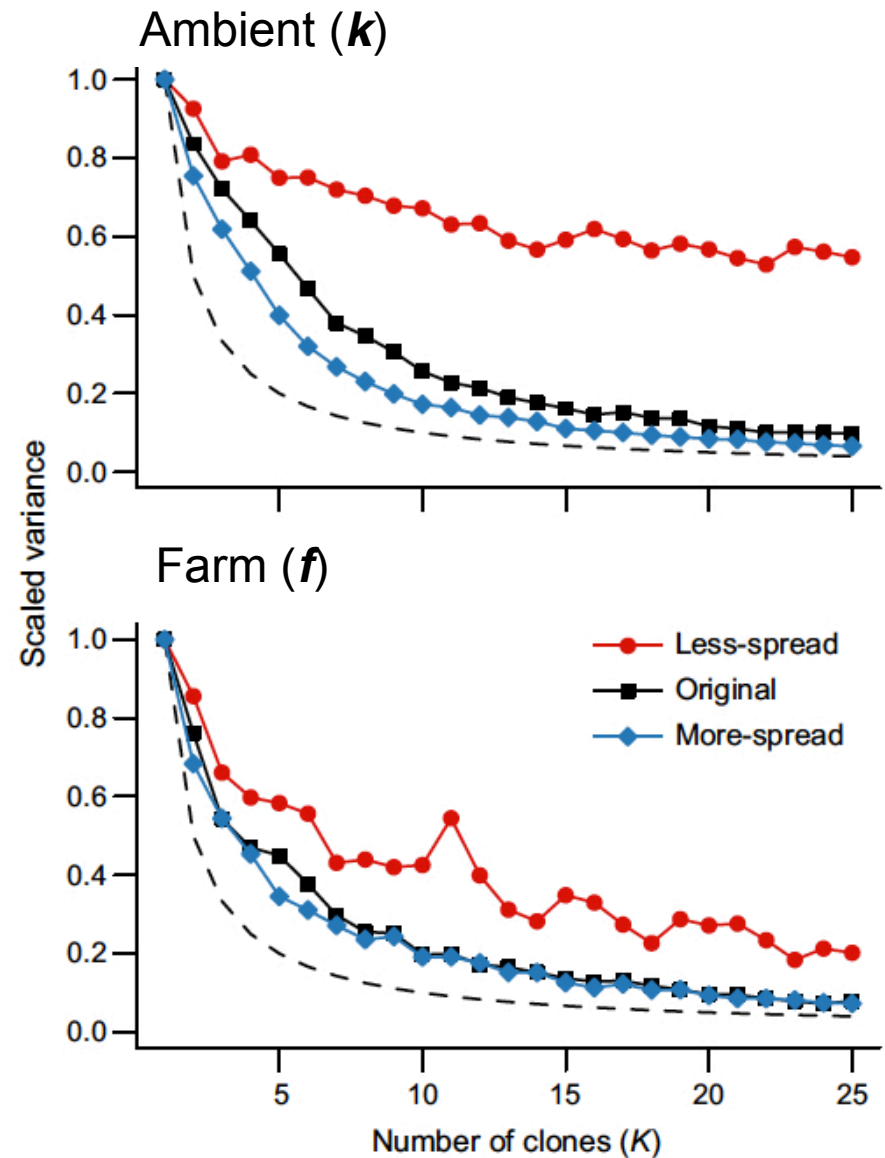
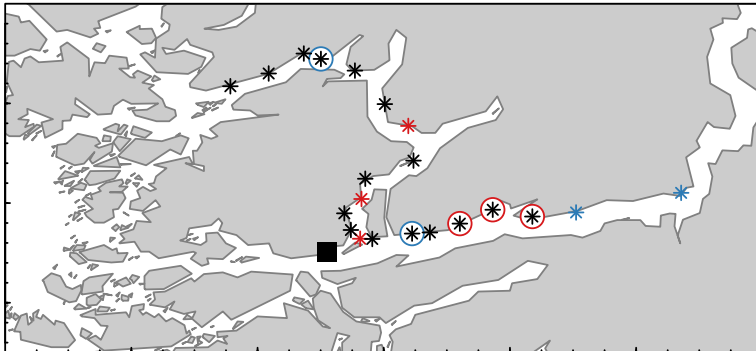
2. How does one avoid such problems to begin with!?

Which sampling design should be adopted to ensure k and f are estimable?



1. Original sample locations (2004)
2. Less spatial spread
3. More spatial spread

Estimability of ambient and farm sources of sea lice





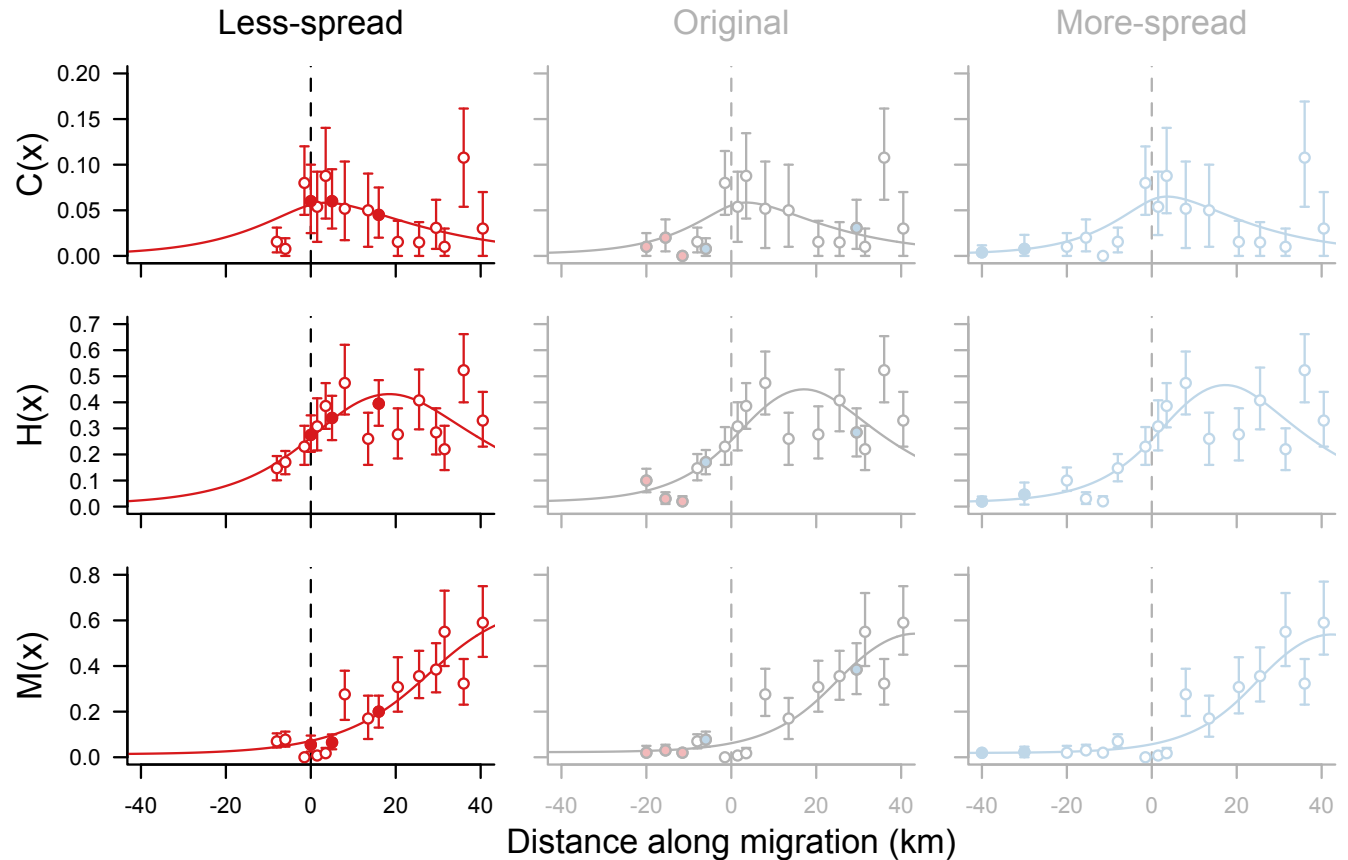
Fits to data



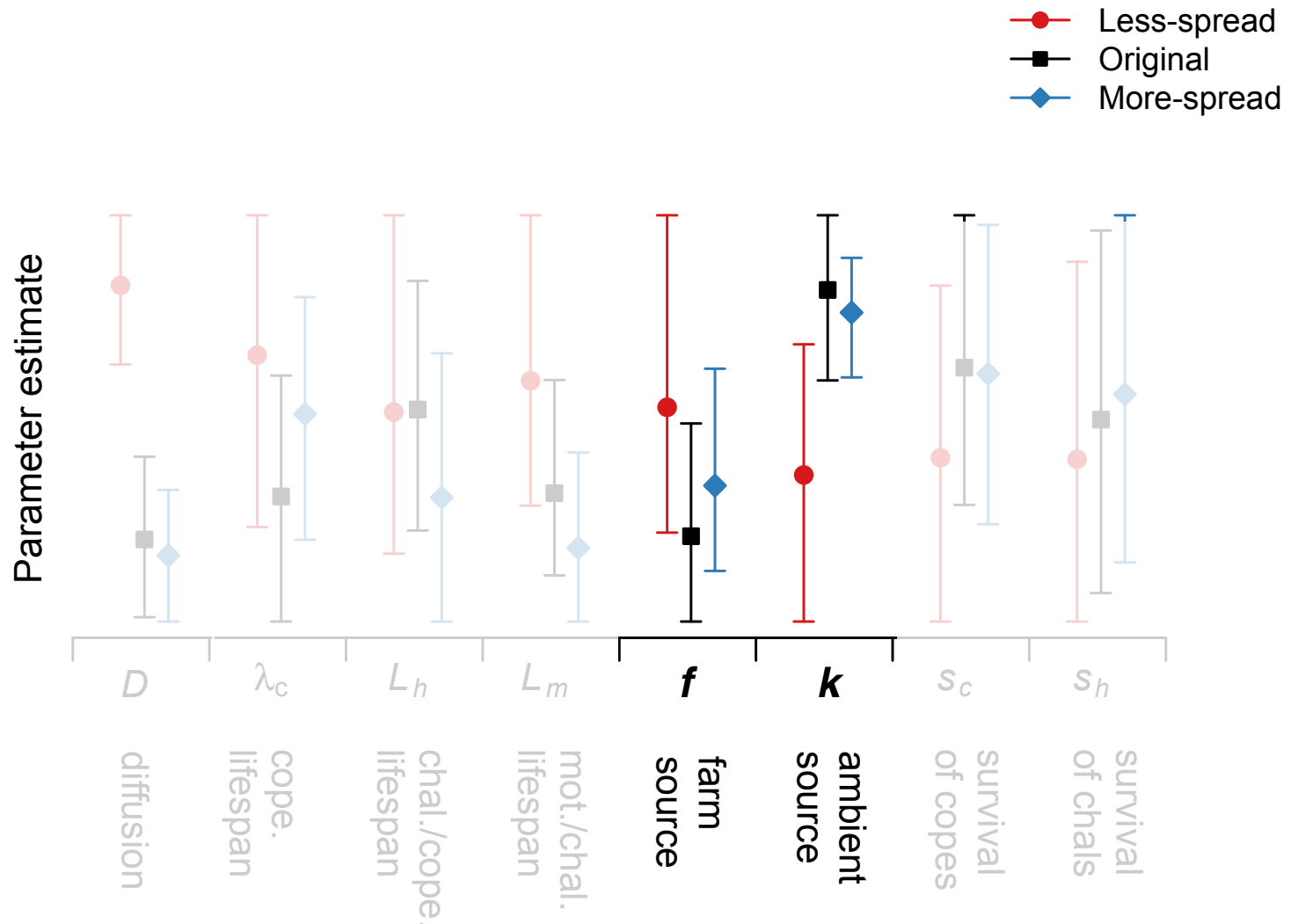
pattern 😊



process 😞

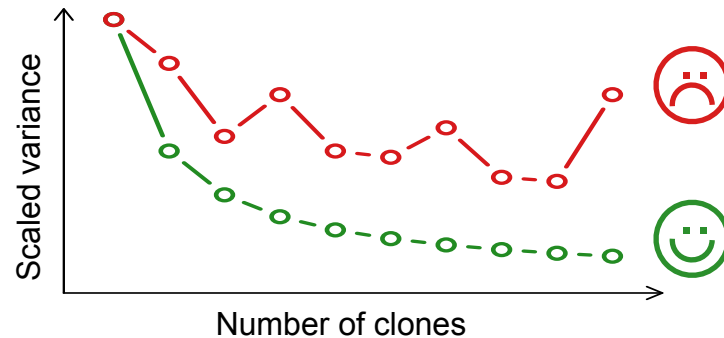


Parameter estimates



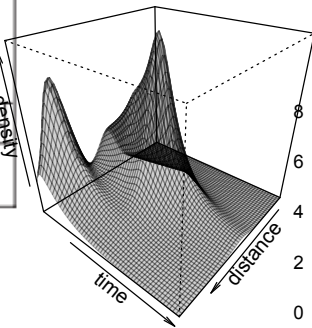
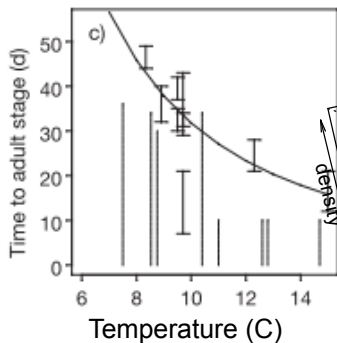
Lousy lessons learned

Check parameter estimability!

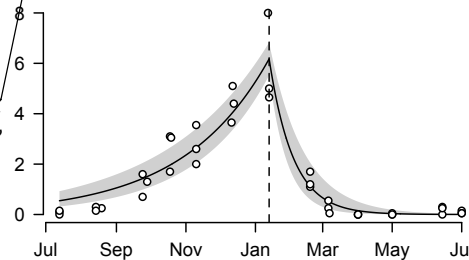


In our case estimability was fixable by:

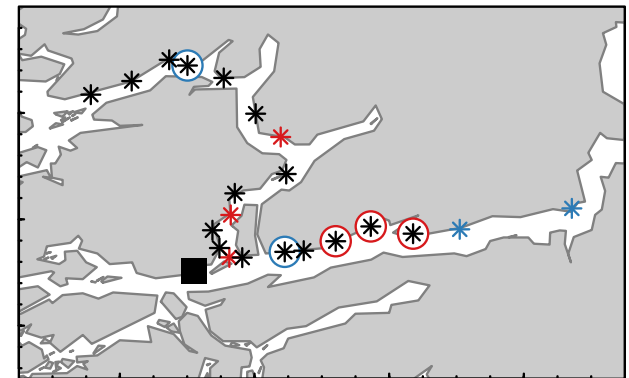
- ✓ Fixing parameters
- ✓ Revisiting model structure



- ✓ Collecting more/ different data*



OR **avoided** by investigating different spatial/temporal designs





Coauthors: Stephanie Peacock (Calgary), Subhash Lele (Alberta), Martin Krkosek (Toronto), Andrew Bateman (Uvic)



Max Wyman - Term Assistant Professor - Statistics, University of Alberta

The Department of Mathematical and Statistical Sciences at the University of Alberta invites applications for a Max Wyman Term Assistant Professorship in the area of Statistics. This is a non-tenure-track, three-year fixed-term position. The position offers a stimulating research and teaching environment with a reduced teaching load.

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