www.nr.no

Space-time modeling of the spread of a disease between marine fish farms

Magne Aldrin, Norwegian Computing Center and the University of Oslo
Ragnar Bang Huseby, Norwegian Computing Center
in collaboration with the National Veterinary Institute
and with A. Frigessi and others at the University of Oslo

INFER March 2011

Similar ideas used in work on

- Foot-and-mouth disease
- Swine fever virus
- Hospital infections

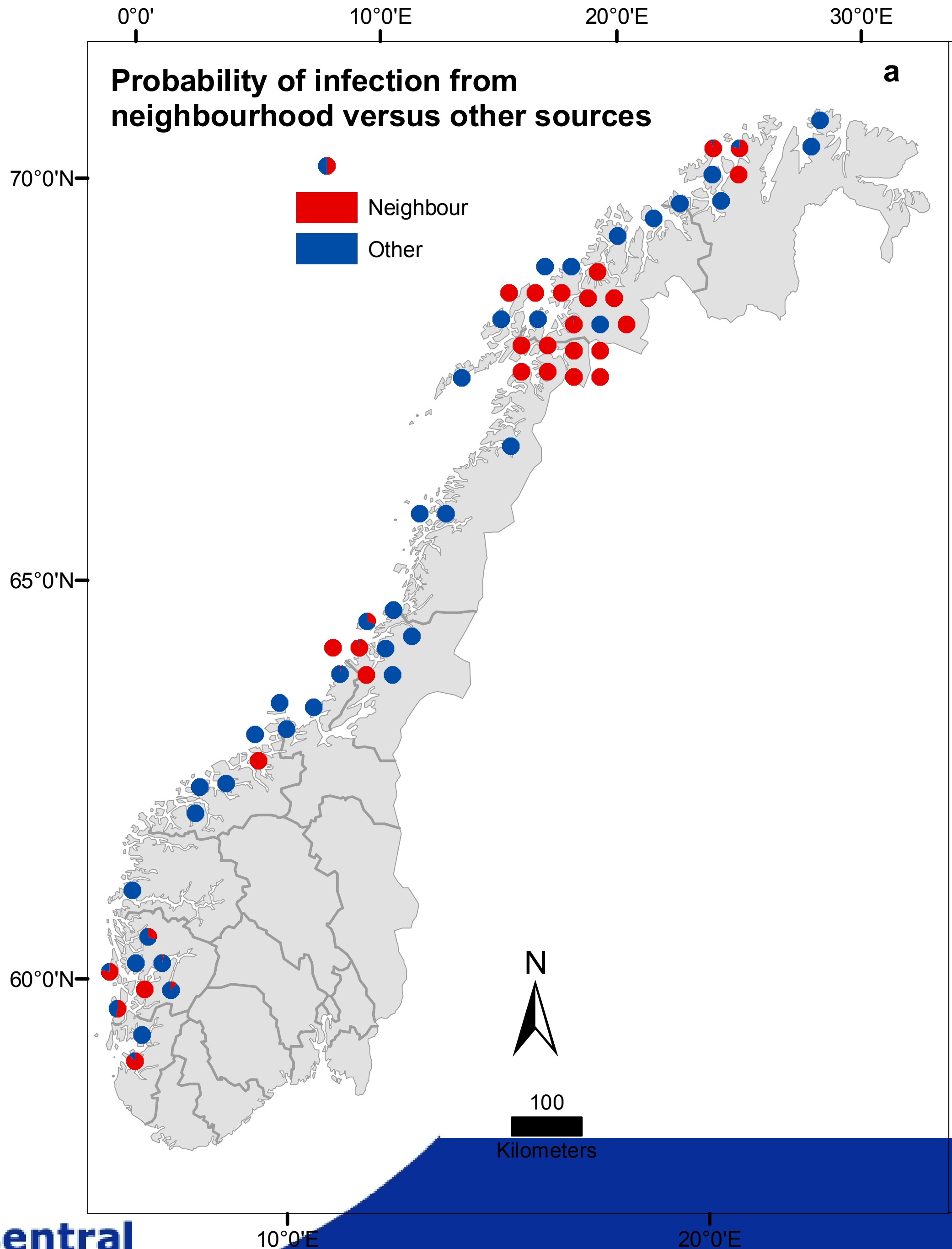
The aquaculture industry

- In Norway:
  Export value of farmed fish $>$ export value of wild fish!
- 1200 fish farms in Norway, spread along the coast, mostly producing salmon

Industry threatened by infectious diseases

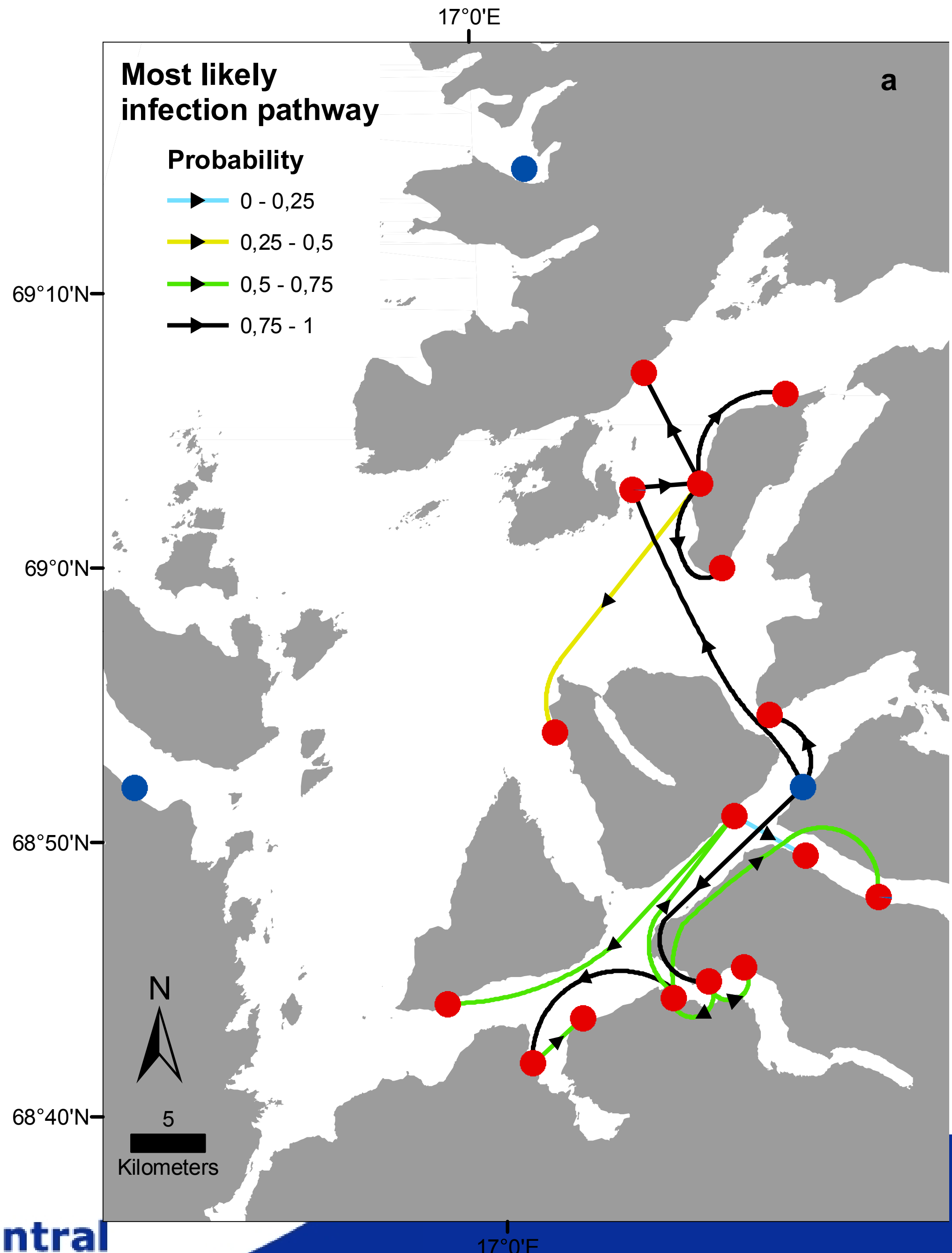
- Infectious Salmon Anaemia (ISA) epidemics:
  - ⋆ Scotland 1999: cost 100 million £
  - ⋆ Shetland 2009: cost 40 million £
  - ⋆ Chile 2008: 7000 jobs lost

Norway: 70 ISA outbreaks 2003-2009



Norsk Regnesentral
NORWEGIAN COMPUTING CENTER

ISA outbreaks in Troms 2007-2009



Norsk Regnesentral
NORWEGIAN COMPUTING CENTER

Data

- Monthly data 2003-2009
- Information on all farms active in this period
  - ⋆ Biomass of fish, tells when a farm is active
  - ⋆ Sea distances between all farms
  - ⋆ Local contact networks between all farms (same ownership, may share staff and equipment)

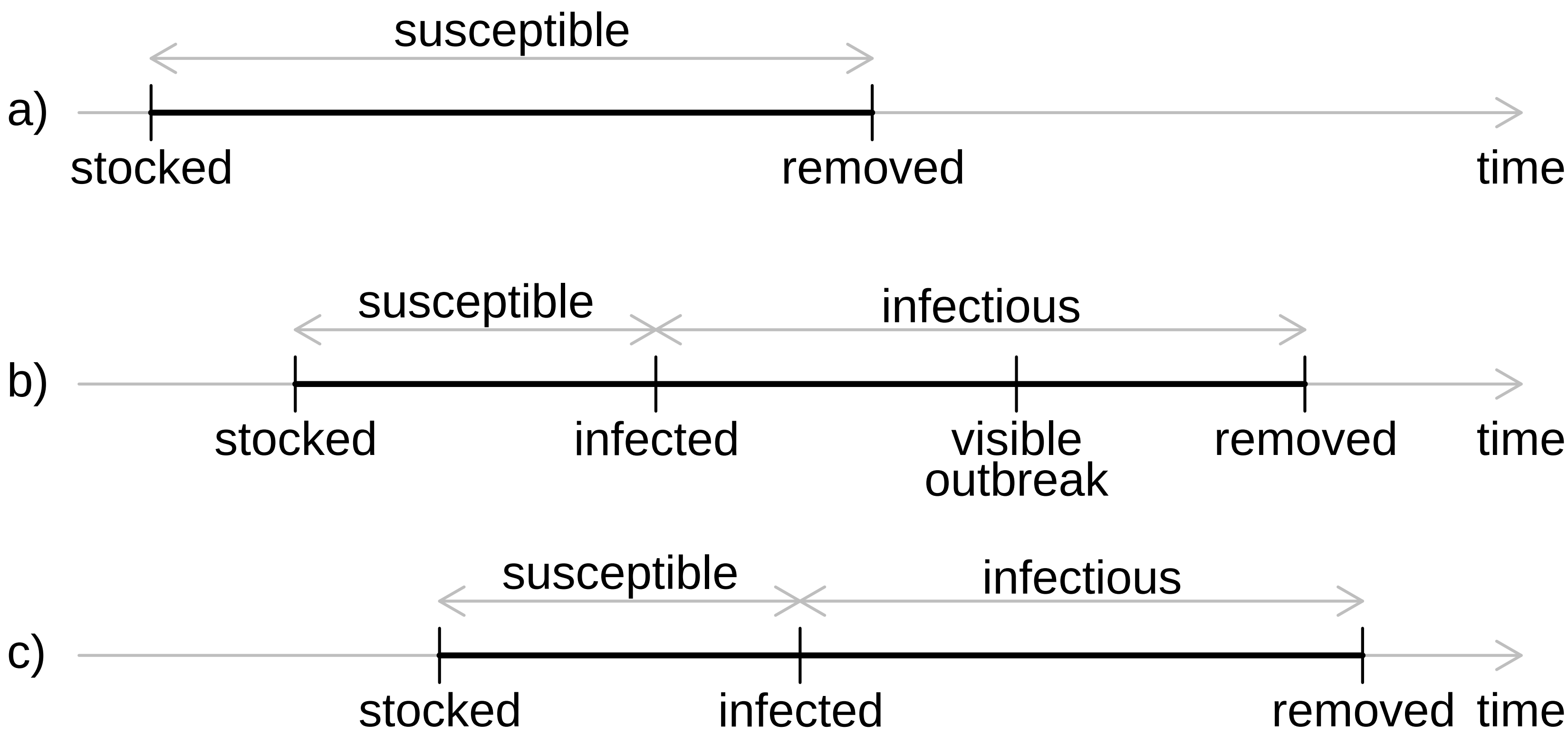
Three diseases

- Information on outbreaks of three diseases
  - ⋆ When and where
  - ⋆ 500 HSMI
  - ⋆ 300 PD
  - ⋆ 70 ISA
- No information on infection time, except infection time $<$ outbreak time

Basic data unit in our modeling

- Fish cohort: A group of fish at a fish farm
- Stocked at some time and slaugthered/removed 2-3 years later
- Only one cohort at a fish farm at a time
- During some years a farm have several subsequent cohorts
- Note: we do not consider individual fish

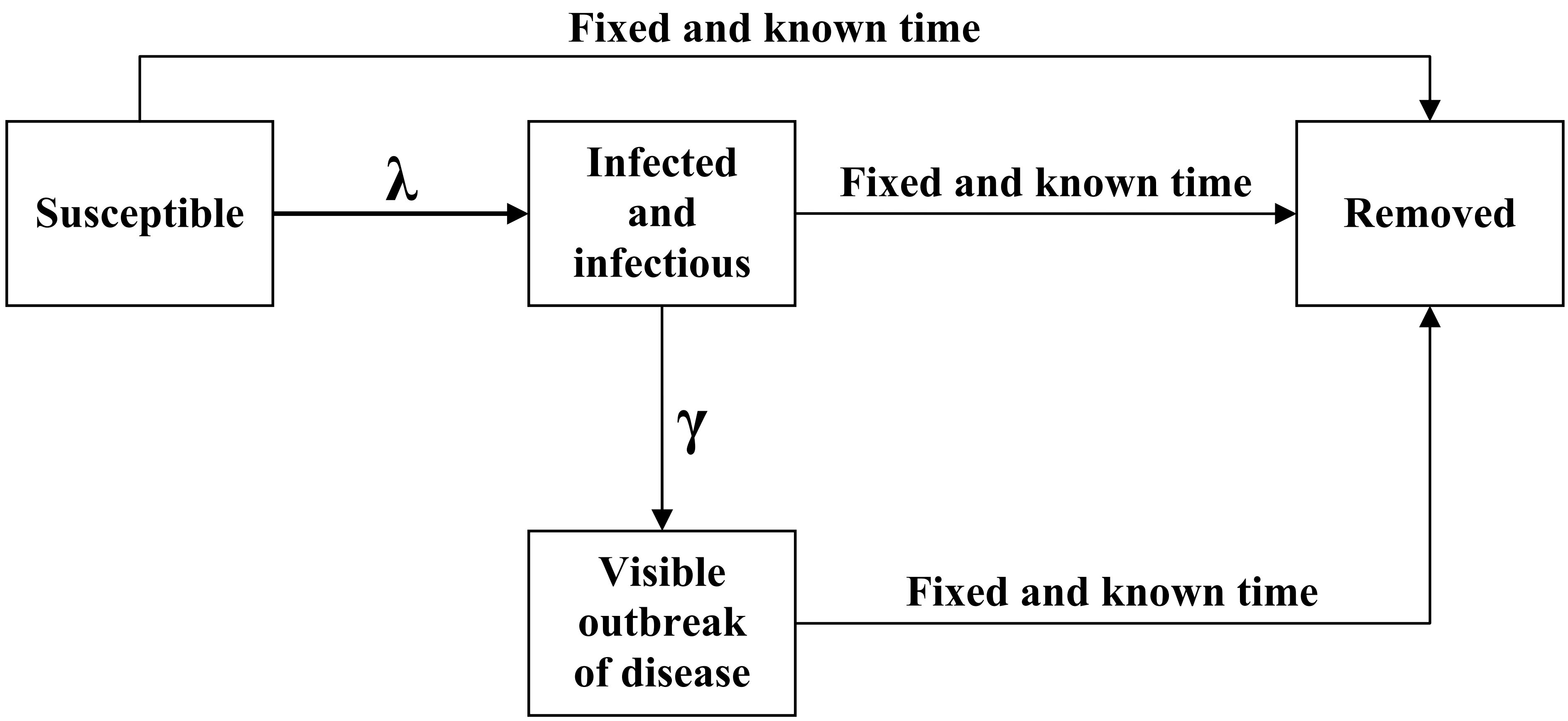
Susceptible and infectious cohorts



Two sub-models

- Infection process - but infection time unobserved
  - ⋆ Infection rate λ
- Outbreak process - outbreak time observed
  - ⋆ Outbreak rate γ

Model overwiev



Infection model

Additive-multiplicative model for the total infection rate (intensity) for fish cohort i at time t

$$\lambda_i(t) = S_i(t) \cdot \kappa_i^s(t) \cdot [\lambda_i^d(t) + \lambda_i^c(t) + \lambda_i^p(t) + \lambda_i^o(t)]$$

Multiplicative terms

- $S_i(t)$ is an at-risk indicator, which
  is 1 when fish cohort i is susceptible and 0 otherwise

- $\kappa_i^s(t)$ is a factor proportional to
  the susceptibility of fish cohort i, dependent on
  ⋆ size of the fish cohort (number of fish)
  ⋆ sea temperature
  ⋆ season

Four transmission pathways

- $\lambda_i^d(t)$ - Transmission from
infected fish cohorts at neighbouring farms,
dependent on seaway *distance* to infected fish cohorts

- $\lambda_i^c(t)$ - Transmission from infected fish cohorts at farms in the same local *contact network* (e.q. same workers)

- $\lambda_i^p(t)$ - Transmission from *previous* infected fish cohorts at the same fish farm i (e.g. remaining disease agent)

- $\lambda_i^o(t)$ - Transmission via *other*, non-specified, pathways

Neighbourhood transmission $\lambda_i^d(t)$

The sum over the individual contributions from all other fish cohorts

$$\lambda_i^d(t) = \sum_{j \neq i} \lambda_{ij}^d(t)$$

Contribution from fish cohort j

$$\lambda_{ij}^{d}(t) = I_j(t) \cdot \exp(-\phi \cdot d_{ij}) \cdot \kappa_j^i(t)$$

- $I_j(t)$: an indicator variable that is 1 if salmon farm j is infectious at time t, and 0 otherwise
- d_{ij}: the seaway distance between fish cohorts i and j, i.e. the distance between their farms
- ϕ: parameter - the effect of the seaway distance
- $\kappa_j^i(t)$: a factor proportional to the infectiousness of fish cohort j, dependent on
  - ⋆ the size of fish cohort j
  - ⋆ the time since it was infected, based on a SIR model

Norsk Regnesentral
NORWEGIAN COMPUTING CENTER

Outbreak model

The outbreak rate for fish cohort i at time t

$$\gamma_i(t) = I_i(t) \cdot \gamma_i^*(t)$$

- $I_i(t)$ is an at-risk indicator, which is 1 when fish farm i is infected and yet not slaughtered and 0 otherwise
- $\gamma_i^*(t)$ a smooth function of time since cohort i was infected, based on a SIR model

Norsk Regnesentral
NORWEGIAN COMPUTING CENTER

A Bayesian data augmentation approach

- Outbreak times are observed data, $\mathbf{D}^{obs}$
- Infection times are missing data, $\mathbf{D}^{mis}$
- Parameters $\boldsymbol{\theta}$

Posterior

$$p(\mathbf{D}^{mis}, \boldsymbol{\theta} | \mathbf{D}^{obs}) \propto p(\mathbf{D}^{obs}, \mathbf{D}^{mis} | \boldsymbol{\theta}) \cdot \pi(\boldsymbol{\theta})$$

Probability density $p(\mathbf{D}^{obs}, \mathbf{D}^{mis} | \boldsymbol{\theta})$

- Contributions from each infection process:

$$\lambda_i(t^*) \cdot \exp(-\int_{t_{start}}^{t^*} \lambda(t)\, dt) \text{ if infection occurs at } t = t^*$$

$$\exp(-\int_{t_{start}}^{t_{end}} \lambda(t)\, dt) \quad \text{if cohort } i \text{ is never infected}$$

- Similar contributions from the outbreak processes

Norsk Regnesentral
NORWEGIAN COMPUTING CENTER

Priors

- Mostly vague priors for the parameters, but some restricted to be non-negative
- For some parameters, the possibility of zero effect is of special interest
  - ⋆ E.g. prior for the distance parameter ϕ:
    - ∗ $P(\phi = 0) = 0.5$ - i.e. no effect of seaway distance between fish cohorts (farms)
    - ∗ $P(\phi > 0) = 0.5$ and then $\phi \sim$ Uniform(0,large number)

Norsk Regnesentral
NORWEGIAN COMPUTING CENTER

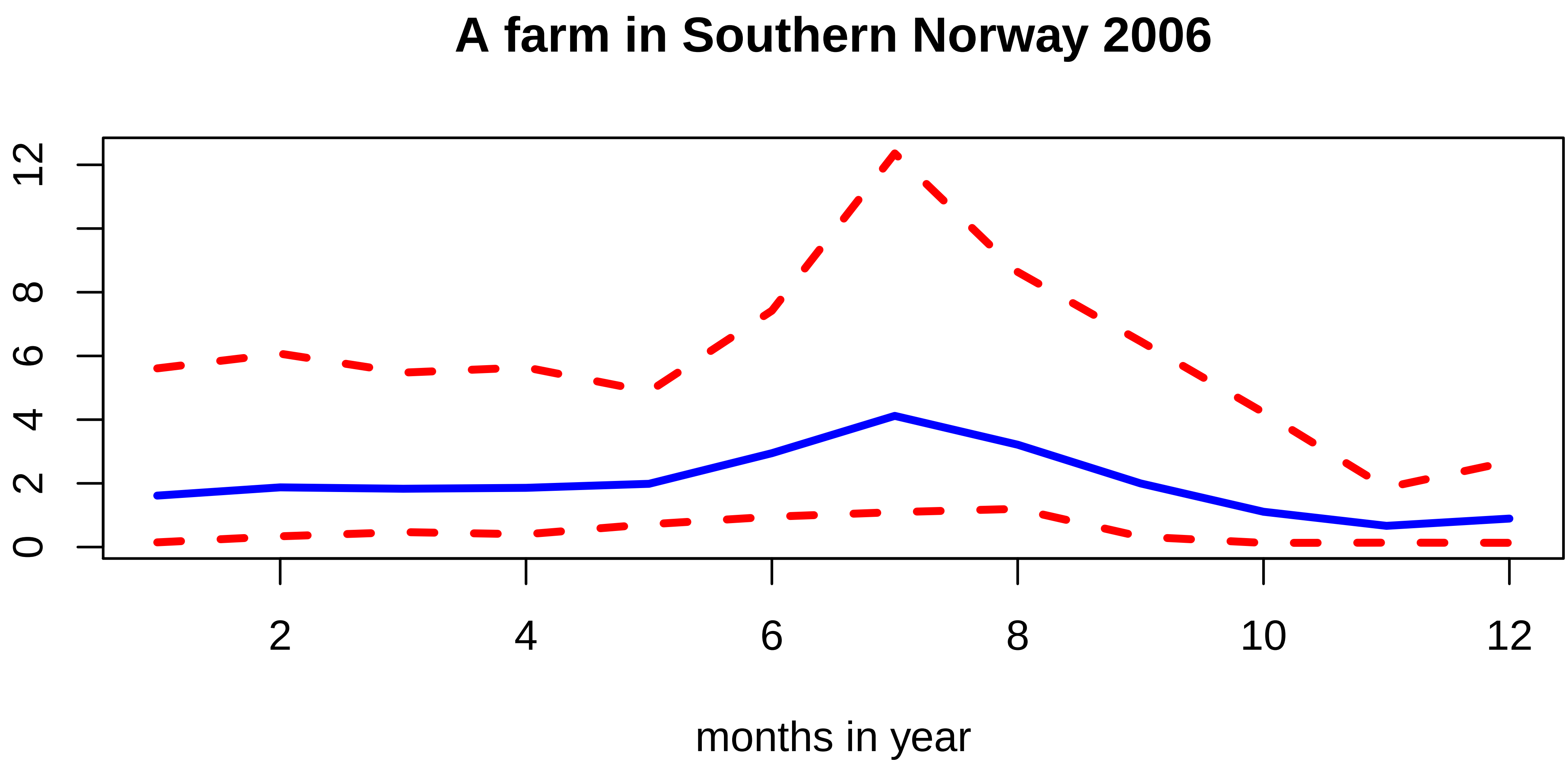
Estimation

- 15-30 parameters with priors
- More than 3000 cohorts with unknown infection times
- Markov Chain Monte Carlo techniques

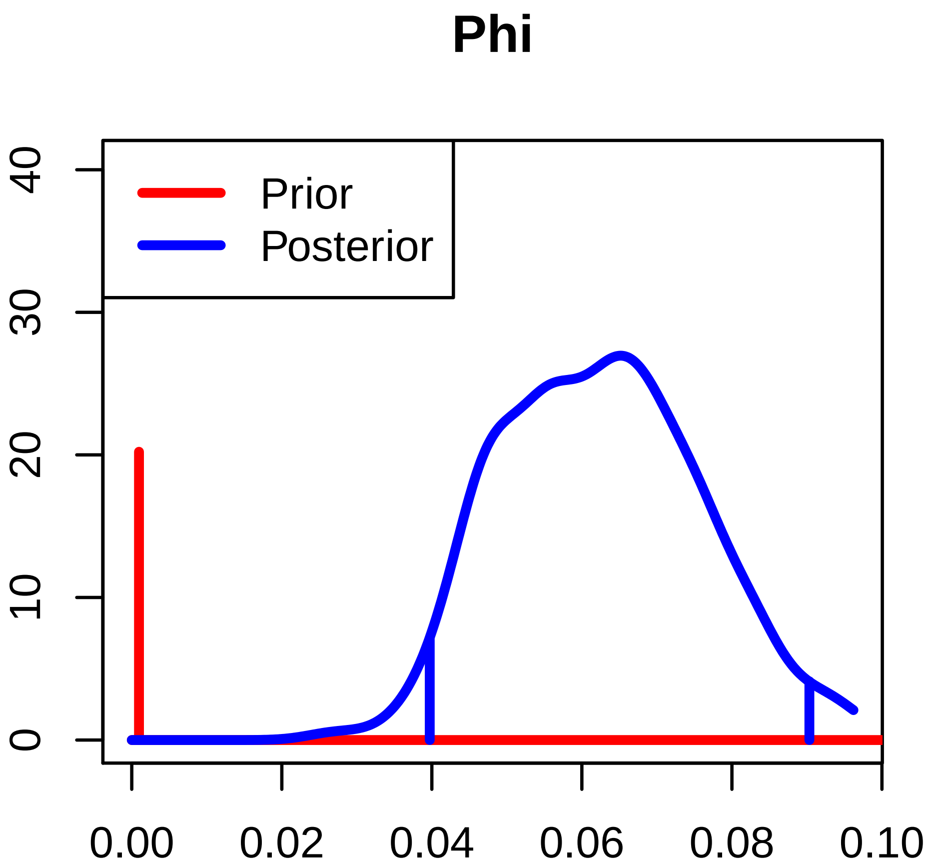
Results - Posteriors for HSMI

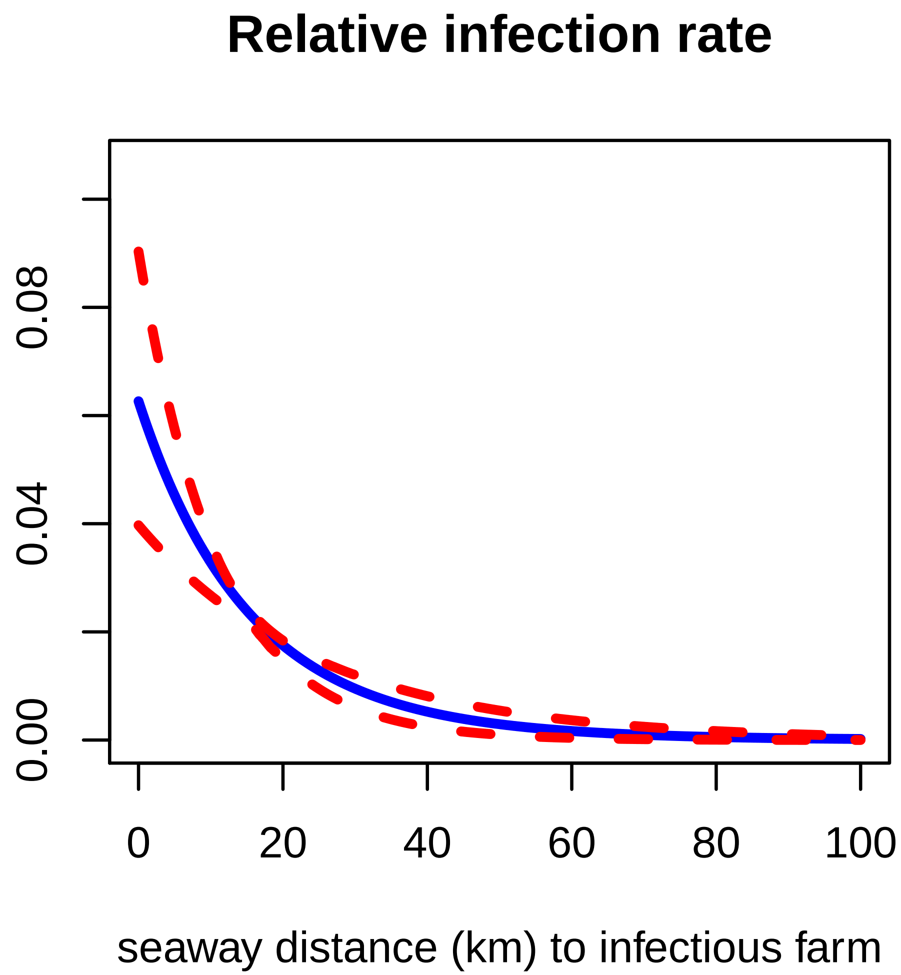
	Posterior mean	95 % cred.int. low	high
Mean time from infection to outbreak - given visible outbreak	2.7 months	2.1	3.4
% of cohorts infected	20	18	22
% of infected cohorts with outbreak	76	70	82

Effect of sea temperature and season



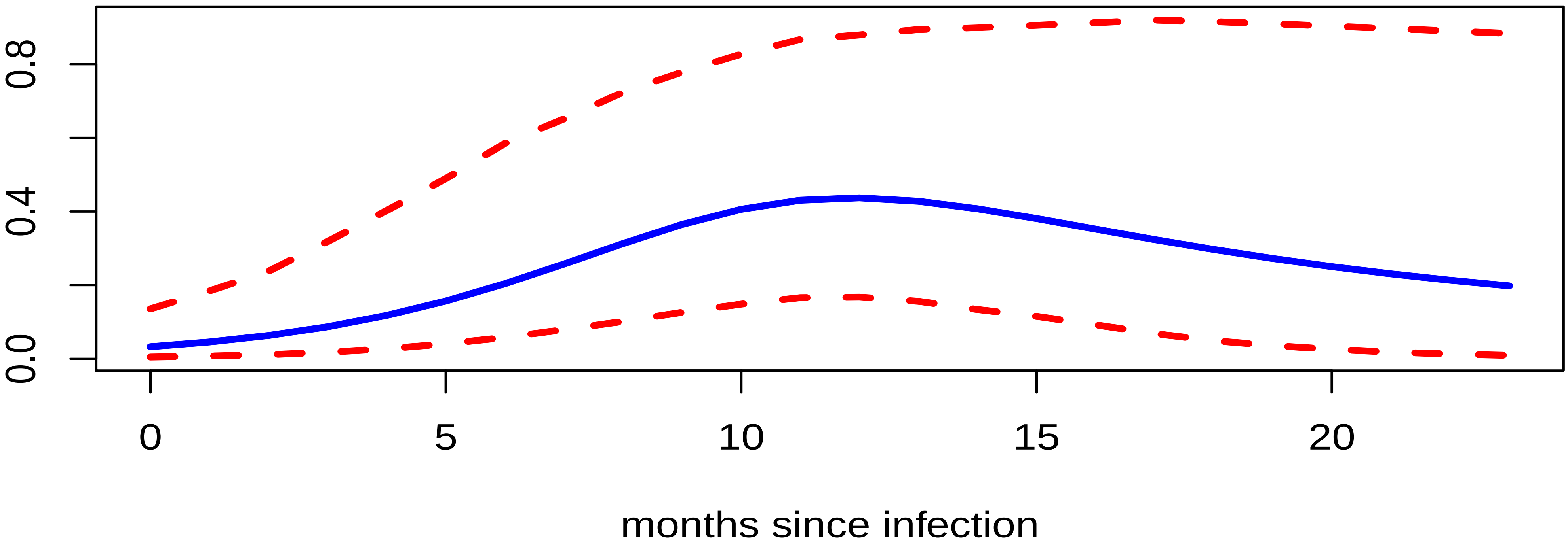
Effect of distance - ϕ





Effect of time since infection

on infectiousness in the infection process
and on the outbreak rate



Relative importance of transmission pathways

Proportion of infections related to neighbourhood transmission:
average the following expression over all infections

$$\lambda_i^d(t)/(\lambda_i^d(t) + \lambda_i^c(t) + \lambda_i^p(t) + \lambda_i^o(t))$$

Similar definitions for the other pathways

Relative importance in %

Pathway	
Neigbourhood	54
Contact network	18
Previous cohort	9
Other	19

Norsk Regnesentral
NORWEGIAN COMPUTING CENTER

Potential use of models for spread of diseases

- Better understanding of infection processes
- Tracing transmission routes
- Estimating the protective effect of vaccination, given data on vaccination
- Investigating the effects of potential interventions by scenario simulations - what-if
  - ⋆ the accumulated effects of vaccination on a network of fish farms for a specified effect of the vaccine
  - ⋆ the effect of re-locations of fish farms

References

- Aldrin, Lyngstad, Kristoffersen, Storvik, Borgan, Jansen (2011).
  Modelling the spread of infectious salmon anaemia (ISA) among salmon farms based on seaway distances between farms and genetic relationships between ISA virus isolates.
  To appear in the Journal of the Royal Society Interface.

- Aldrin, Storvik, Frigessi, Viljugrein, Jansen (2010).
  A stochastic model for the assessment of the transmission pathways of heart and skeleton muscle inflammation, pancreas disease and infectious salmon anaemia in marine fish farms in Norway.
  Preventive Veterinary Medicine, Vol. 93, p. 51-61.

- Scheel, Aldrin, Frigessi, Jansen (2007).
  A stochastic model for infectious salmon anemia (ISA) in Atlantic salmon farming.
  Journal of the Royal Society Interface, Vol. 4, p. 699-706.

Thanks for your attention!

Enjoy your lunch today!