

Bayesian analysis of a dynamical model for the epidemiology of the USUTU virus

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The disease

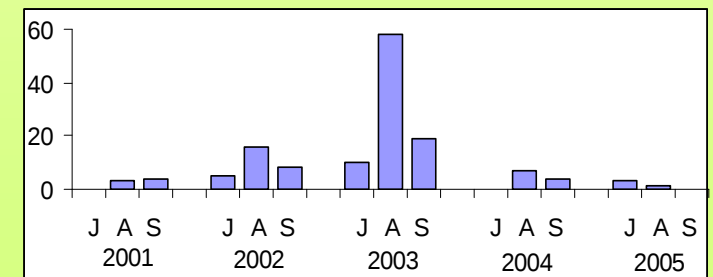
USUTU-Virus:

- a relative of the West Nile Virus
- transferred by mosquitos
- affects blackbirds
- appeared in Austria in 2001



Data used in the analysis:

- Monitoring in Eastern Austria
- 2001 to 2005
July, Aug, Sep
- Total: 138
infected birds



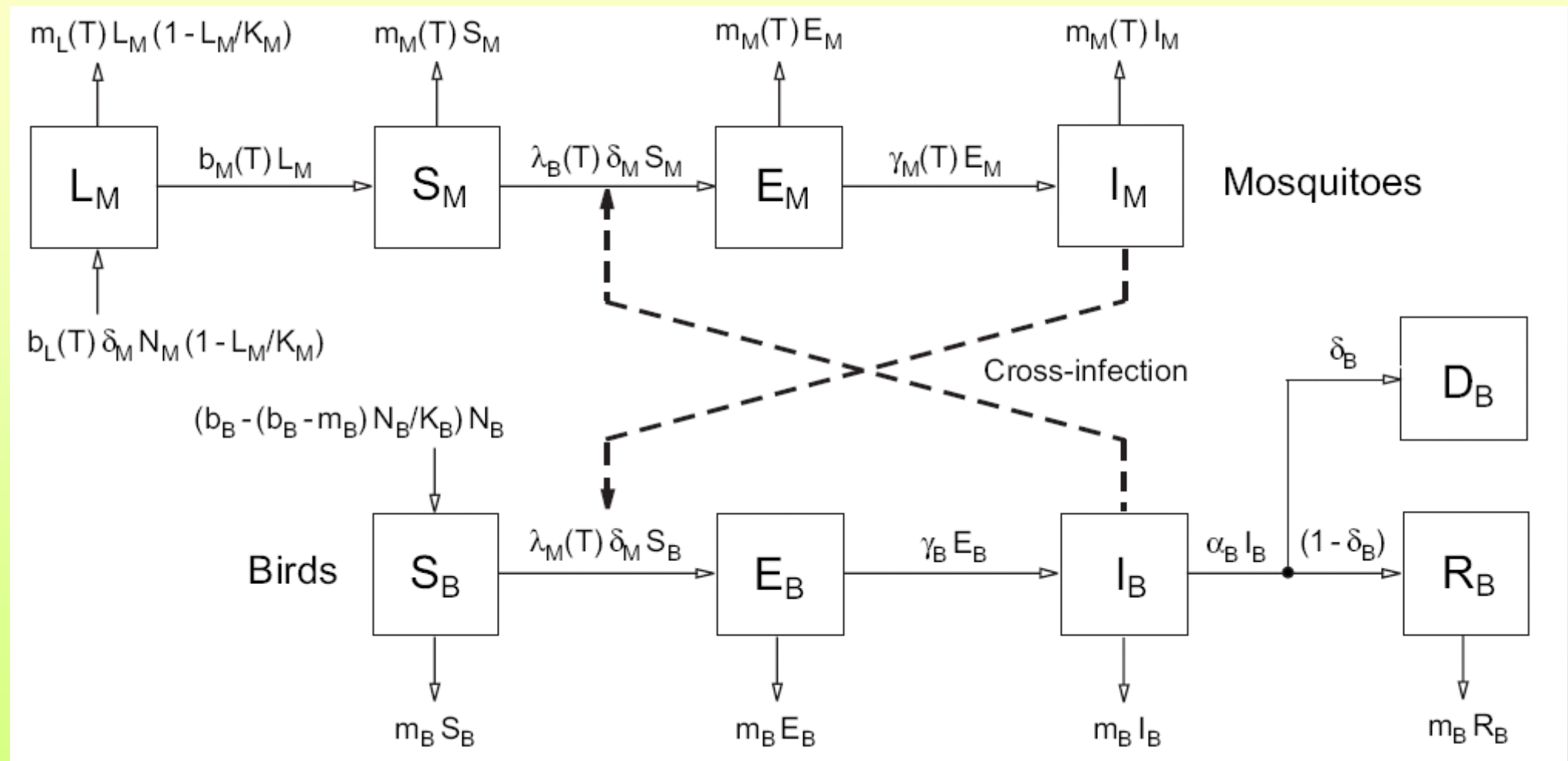
The initial dynamical model

- Rubel et al. (2007)* developed an arbovirus model to explain the spread dynamics of the West Nile virus (WNV) and the USUTU virus (USUV).

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- The model is a SEIR (*Susceptible-Infected-Infectious-Recovered*) model with 9 compartments (4 for mosquitos and 5 for birds).
- According to this, the model consists of a system of 9 differential equations.

Diagram of the model



The values of the model parameters are taken from the literature (rates: per day and per capita)

birth rate of birds	seasonal (depends on the calendar day)
birth rate of mosquito larvae	temperature-dependent
USUV mortality rate of birds	0.3
mortality rate of birds, other causes	0.0012
incubation time of the virus in birds	1.5 day
incubation time of the virus in mosquitos	temperature-dependent
and so on...	

Motivation to develop a stochastic model

1. Parameters of a deterministic model are fixed values, but the epidemiological **process has inherently stochastic components**:
 - the number of infected birds found
 - daily temperature values
 - model parameters, e.g. birth rates, mortality rates, etc. (bird and mosquito populations are heterogeneous, consisting of subpopulations)
2. Results from a deterministic model are also fixed values, but **one would like to know about the reliability and stability of results**: SD, confidence intervals, etc. for the parameter estimates as well as for the predictions.

The extended stochastic model

Based on the above dynamic model, we have developed a **hierarchical Bayes model**: on each level of the model we have introduced some stochastic components:

- some model parameters are randomised,
- temperatur data are randomised,
- the number of observed infected birds is modeled by a random variable with Poisson distribution, so that its parameter comes from the model.

(details will be given later)

Bayesian analysis of a stochastic model

In a Bayes model **the parameters to analyse are regarded as random variables**, characterised by their probability distributions.

- We have an idea about the parameter **before the observation of the data**: this is incorporated in the ***prior distribution***.
- **The observation of data can modify this idea**: the modified idea is mirrored by the ***posterior distribution***.

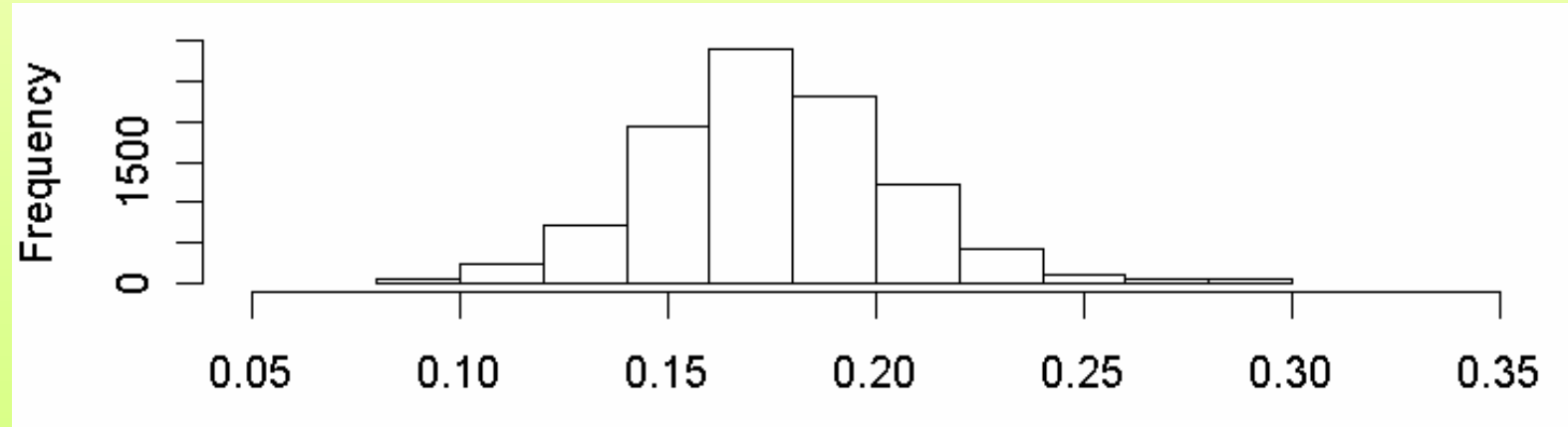
An example of the prior and posterior distributions

Parameter: infection probability bird $\rightarrow$ mosquito
(if a susceptible mosquito bites an infectious bird)

Prior distribution: uniform distribution in $[0,1]$

Estimated posterior distribution:

(Histogram based on 10.000 simulations)



Interpretation: the information in the observed data has reduced the uncertainty concerning the parameter!

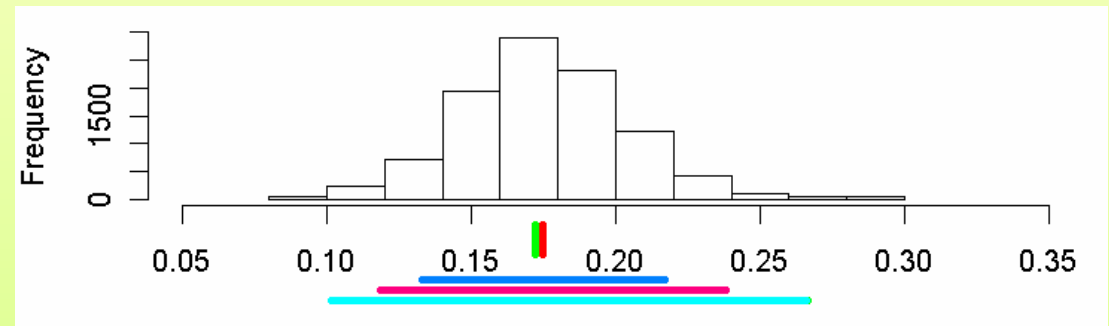
Bayesian point and interval estimates

- posterior mean
- posterior median
- 90, 95%, 99% posterior interval (credible interval)

In the last example:

Posterior mean = 0.178 █

Posterior median = 0.175 █



90% posterior interval: (0.137, 0.227) —

95% (0.119, 0.236) —

99% (0.103, 0.266) —

Analysis by simulation: the MCMC (Markov Chain Monte Carlo) method

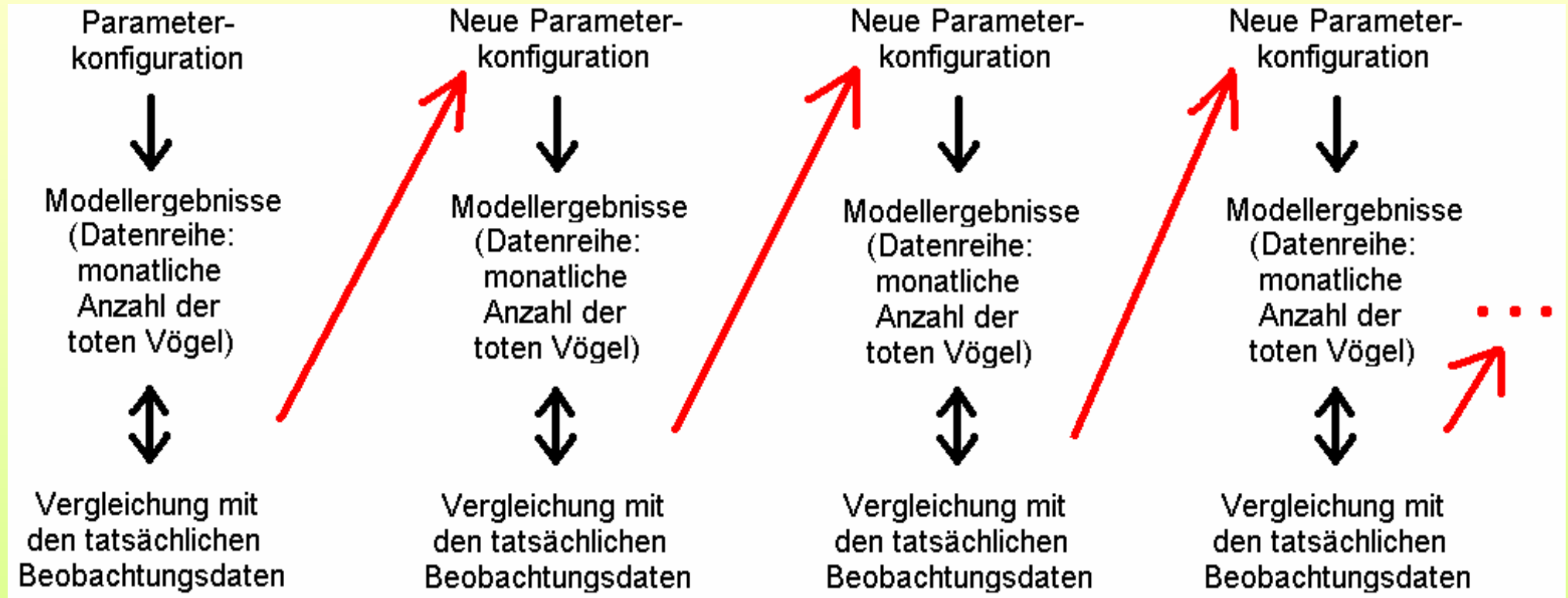
If the model is too complex, it is too difficult to determine the posterior distribution analytically.

Solution: simulation using the computer.

Main idea of the MCMC:

- We find a Markov chain having the posterior distribution as its stationary distribution (there are various methods to do this) and generate a long sequence of states
- After an initial transient period, the states will follow the posterior distribution

What is the Markov chain in our case?



We made 100 000 steps and took the last 10 000 parameter configurations to represent the posterior distribution.

The extended stochastic model: more details

- We selected **four model parameters** for analysis with **uniform prior distributions** in a certain range

Parameter	Range
Infektion rate bird $\rightarrow$ mosquito	(0.05, 0.5)
Infektion rate mosquito $\rightarrow$ bird	(0.5, 1)
Minimal number of mosquitos surviving winter (per bird)	(0.5, 2)
Maximal number of mosquitos (carrying capacity of the environment) per bird	(5,150)

- Other parameters were held fixed (values taken from the literature)

- **Birth rate of birds was randomised** by multiplication with a uniform random variable between 0.9 and 1.1 ($\pm 10\%$).
- **Temperature data were randomised** by addition of Gaussian random variable ($\mu=0$, $\sigma=1.25$, σ estimated from temperature data of 12 meteorological stations).
- **MCMC method** was applied with 100 000 steps. Results are based on the last 10 000 steps. (Convergence was checked by visual comparison of the posterior distributions from the last three blocks consisting of 10 000 steps each.)
- The model was implemented in **FORTRAN** while the analysis was made with **R**.

Results

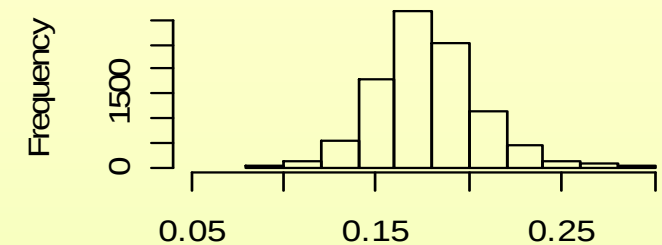
Parameter:

Infektion rate bird → mosquito

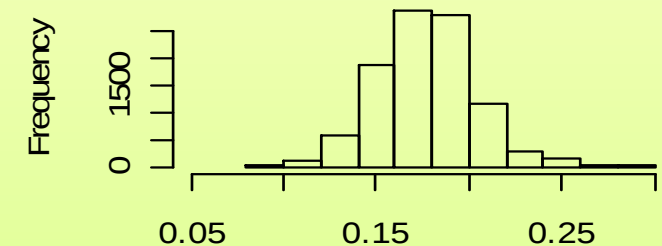
*(when a susceptible mosquito
bites an infectious bird)*

Value in the orig. model:	0.125
Range for the prior uniform distribution:	(0.05,0.5)
Posterior mean:	0.178
Posterior median:	0.175
95% post. interval:	(0.129,0.237)

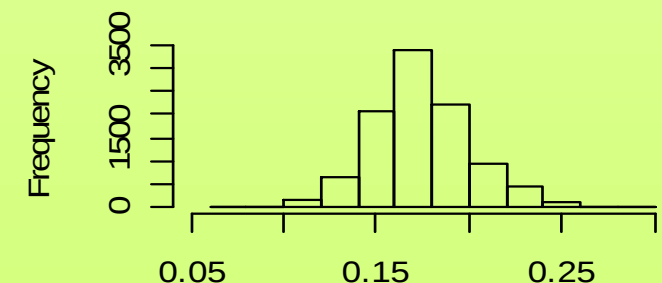
Letzte 10000



Vorletzte 10000



Vorvorletzte 10000



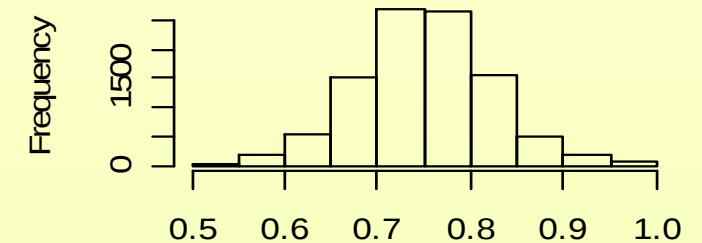
Parameter:

Infektion rate mosquito → bird

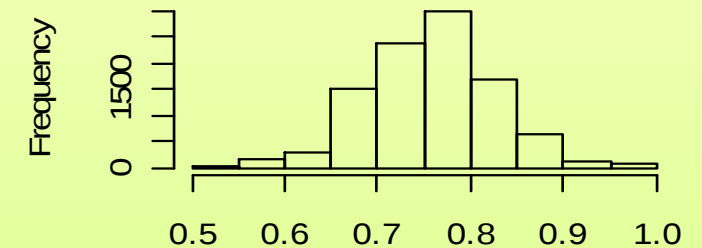
*(when an infectious mosquito
bits a susceptible bird)*

Value in the orig. model:	1
Range for the prior uniform distribution:	(0.5,1)
Posterior mean:	0.750
Posterior median:	0.750
95% post. interval:	(0.601,0.903)

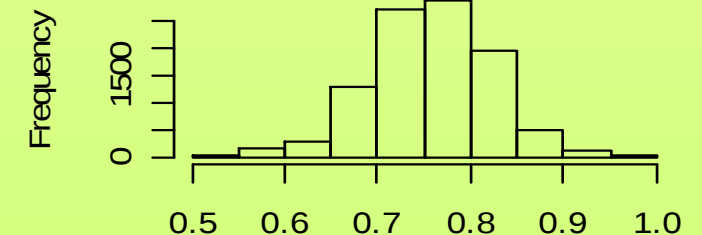
Letzte 10000



Vorletzte 10000



Vorvorletzte 10000



Parameter:

mosquitos surviving winter (per bird)

(Minimal number of the mosquitos per bird that survive winter)

Value in the orig. model: 1

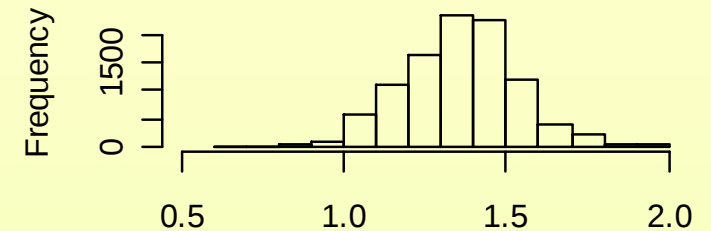
Range for the prior
uniform distribution: (0.5,2)

Posterior mean: 1.36

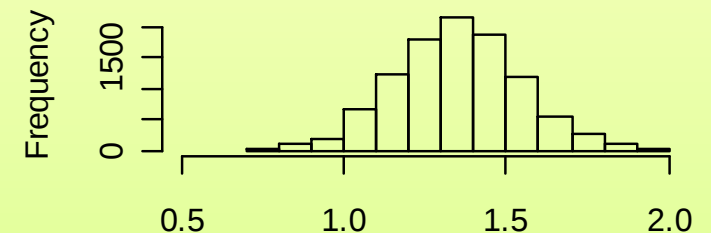
Posterior median: 1.37

95% post. interval: (1.03,1.73)

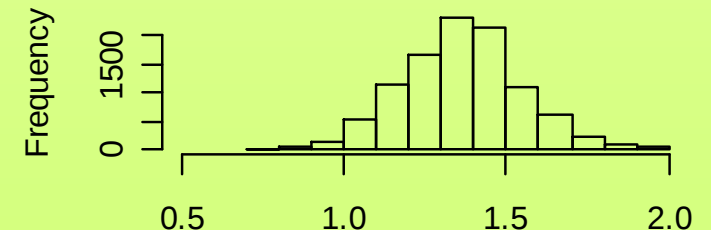
Letzte 10000



Vorletzte 10000



Vorvorletzte 10000



Parameter:

Maximal number of the larvae per bird

(Carrying capacity of the environment for mosquito larvae per bird)

Value in the orig. model: 100

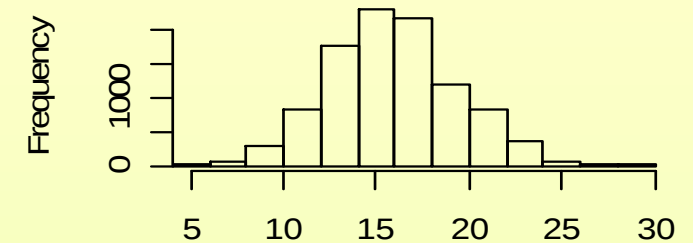
Range for the prior uniform distribution: (5,150)

Posterior mean: 15.9

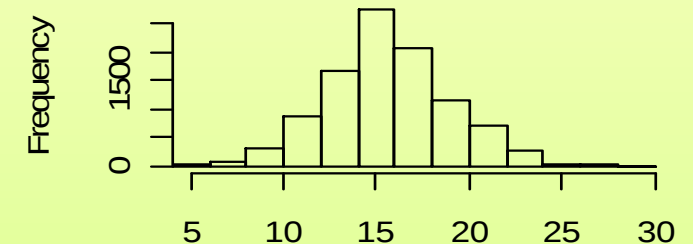
Posterior median: 15.6

95% post. interval: (9.4,22.9)

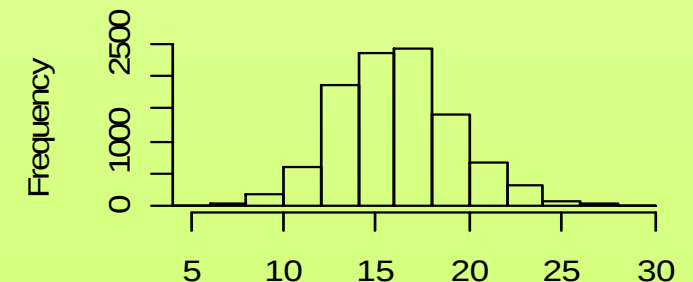
Letzte 10000



Vorletzte 10000



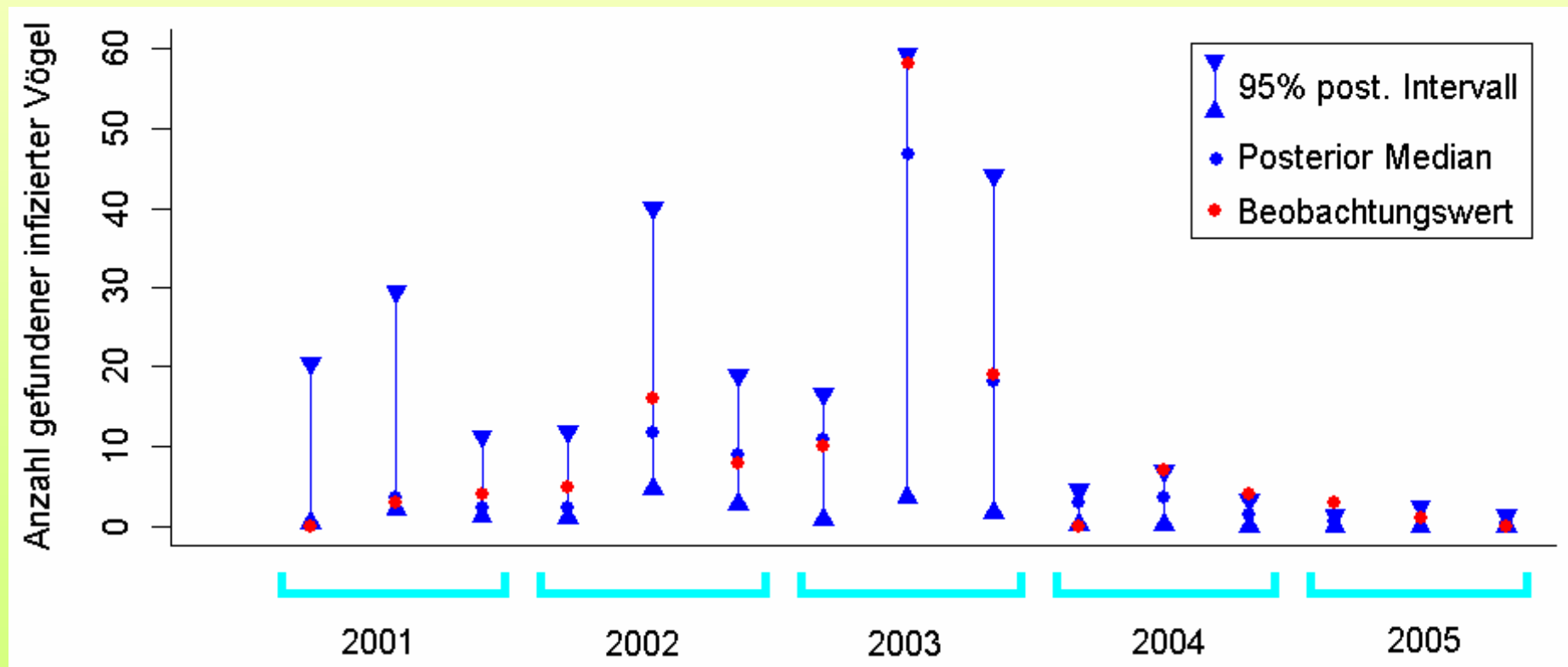
Vorvorletzte 10000



Estimation of stability of predictions

By simulation from the posterior distribution, it is possible to estimate the variability of the results (predictions).

(Graph based on 10 000 simulations)



Further tasks:

- Similar analyses for other model parameters
- Applying refined methods to check convergence of the MCMC method
- Applying same methodology for WNV data

Thanks for your attention!