

LadyBug – a software environment for stochastic epidemic models

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LadyBug

A program for *simulation* and *parameter estimation* in stochastic epidemic models.



Characteristics

- Susceptible-Exposed-Infected-Recovered compartment models
- spatial dimension of population: lattice layout.
- modeling of infectious diseases for small populations
- application areas: analysis of (small-scale) disease dynamics for infectious diseases in humans and animals

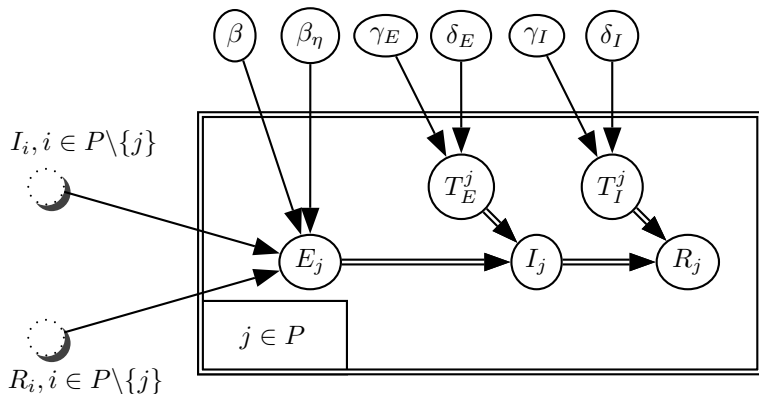
Stochastic epidemic models (1)

- A closed population P hosted in k units. P is divided into susceptible, exposed, infected, and recovered.
- The k units are arranged in a $k = k_1 \times k_2$ lattice.
- $S(0) = n$, $E(0) = m$.
- At time t , an individual j in unit u_j meets infectious at rate

$$\beta I_{u_j}(t) + \beta_\eta \sum_{u \in N(u_j)} I_u(t)$$

- If a susceptible meets an infected it becomes exposed.

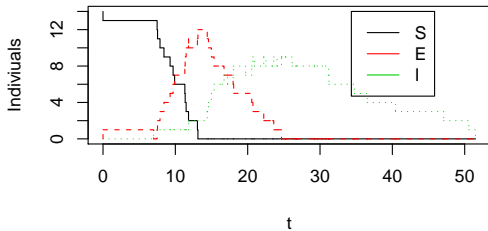
Stochastic epidemic models (2)



$$I_j = E_j + T_E^j, \quad R_j = I_j + T_I^j$$
$$T_X^j \sim \mathcal{Ga}(\gamma_X, \delta_X), \quad X \in \{E, I\}$$

Features of LadyBug – Simulation

- Simulate epidemic trajectories, i.e. $S(t)$, $E(t)$, $I(t)$ and $R(t)$.



- Simulate the final size, Z , of the epidemic.
- Calculate $E(Z)$ through Monte-Carlo Integration.
- Study the effect of control measures, e.g. vaccination.

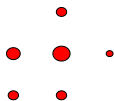
Example: Simulation in a 8x16 lattice

t= 0

 Exposed  Infected  Susceptible  Recovered

Example: Simulation in a 8x16 lattice

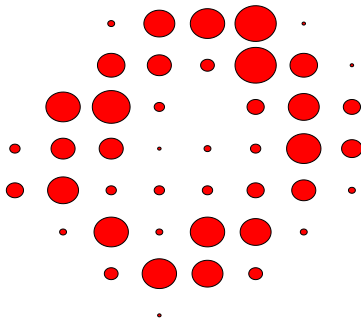
t= 26.5



Exposed Infected Susceptible Recovered

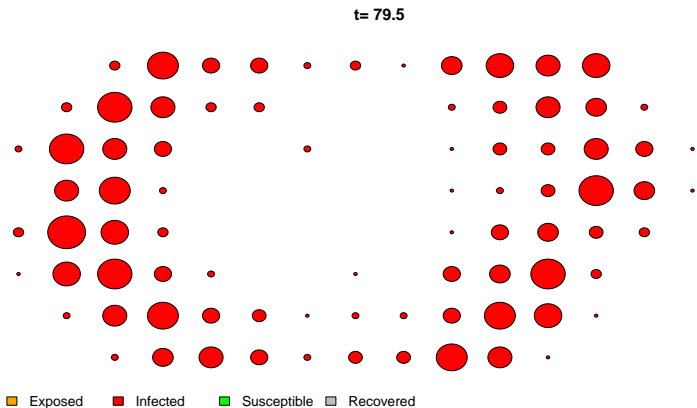
Example: Simulation in a 8x16 lattice

t= 53



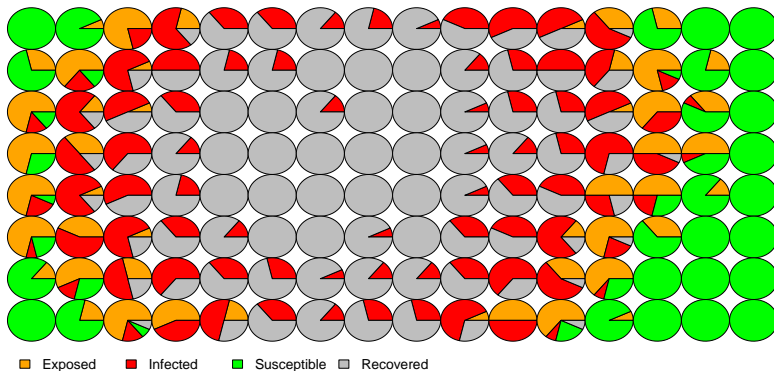
Exposed Infected Susceptible Recovered

Example: Simulation in a 8x16 lattice

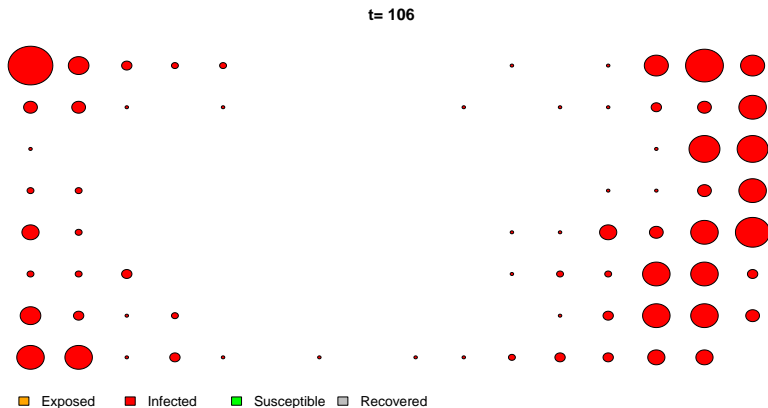


Example: Simulation in a 8x16 lattice

t = 79.5



Example: Simulation in a 8x16 lattice



Example: Simulation in a 8x16 lattice

t= 132.5



Example: Simulation in a 8x16 lattice

t= 159



 Exposed  Infected  Susceptible  Recovered

Example: Simulation in a 8x16 lattice

t= 185.4

 Exposed  Infected  Susceptible  Recovered

Features of LadyBug – Estimation

Full data, i.e. E, I, R -event times for all individuals

Likelihood or Bayesian inference for $\theta = (\beta, \beta_\eta, \gamma_E, \delta_E, \gamma_I, \delta_I)$.

Missing or censored event times

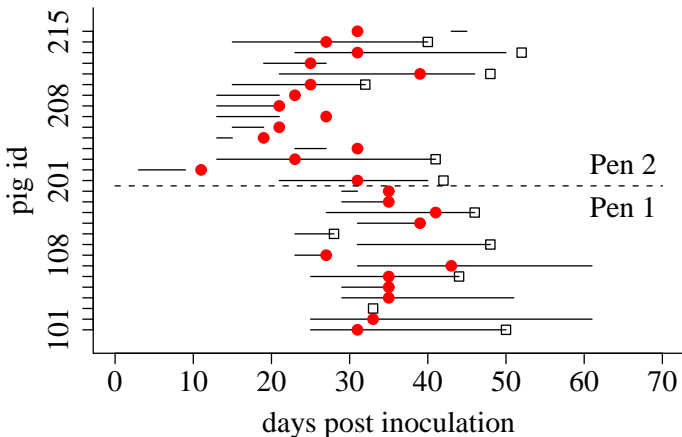
Impute missing/censored event times. Estimation through a Gibbs within Metropolis-Hastings MCMC algorithm.

Model Selection

Use *Akaike's information criterion* (likelihood) or the *deviance information criterion* (bayes) to investigate e.g. the spatial heterogeneity.

Example: CSFV Transmission Experiment (1)

- Population of 29 healthy pigs divided into two pens.
- Inoculate one pig with classical swine fever virus (CSFV).



Example: CSFV Transmission Experiment (2)

```
////////////////////////////////////  
// A subset of the experiment by Dewulf. et al., "An experimental  
// infection with classical swine fever in E2 sub-unit marker-vaccine  
// vaccinated and in non-vaccinated pigs", Vaccine 19, pp. 475-482.  
////////////////////////////////////  
unit 1 1 14 0  
unit 1 2 14 1  
beta 0.001 0.001 (0.4)  
betan 0.001 0.001 (0.005)  
incu 0.001 0.001 (1) 0.001 0.001 (1)  
inf 0.001 0.001 (1) 0.001 0.001 (0.110)  
diag 0.001 0.001 (8) 0.001 0.001 (0.8)  
//x      y      E      I      R      D  
1        1      19      25      50      31  
1        1      19      25      61      33  
1        1      (26)   (32)   33      CE  
1        1      23      29      51      35  
...  
1        2      15      21      40      31  
1        2      0       3       9       11  
1        2      7       13      41      23  
1        2      17      23      27      31  
...
```

Example: CSFV Transmission Experiment (3)

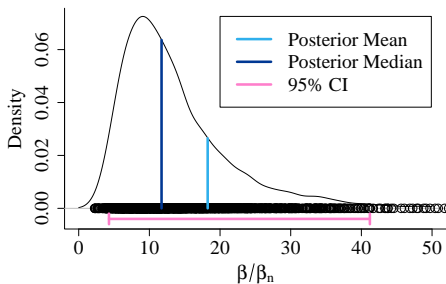
```
// Author:      Michael Höhle <hoehle@stat.uni-muenchen.de>
// Description: LadyBug configuration file to estimate parameters in CSFV
//              dataset using MCMC

(options
  seed=          1999    //fix seed value
  incuTimePDF=   gamma   //Distribution of incubation time.
  infTimePDF=    gamma   //Distribution of the infectious time
  diagTimePDF=   gamma   //Distribution of the seroconversion time
  meanVar=       false  //Mean variance representation of periods.
  ignoreE=       true
  ignoreI=       false  //ignore all inf times in the data file?
  ignoreD=       false  //ignore all sero times in the data file?
)

(method mcmc
  samples=2500
  thin=25
  burnin=25000
  ...
)
```

Example: CSFV Transmission Experiment (4)

- Quantify relationship between β and β_η for the CSFV experiment.



- Mean = 18.25, Median = 11.72, 95% CR = [4.3,41.2]
- The DIC_4 's are 664.76 (homogeneous model) and 633.35 (heterogeneous model).

LadyBug

A Java program for the *simulation* and *parameter estimation* in stochastic epidemic models.

Homepage

<http://www.stat.uni-muenchen.de/~hoehle/software/ladybug/>

Literature

Inference in disease transmission experiments using stochastic epidemic models, M. Höhle, E. Jørgensen, and P.D. O'Neill, Journal of the Royal Statistical Society, Series C, volume 54, part 2 (2005), pages 349-366.