

## Epidemic Models Practical 3: Stochastic epidemiological models

Accompanying R codes: *Deterministic vs Stochastic SIR.R* with auxiliary files *SIR.R*, *stochastic SIR model.R*

### Outline:

In this practical you will run and analyse stochastic epidemiological models and compare them with their deterministic counterpart.

**Open the R-script *Deterministic vs Stochastic SIR.R* and the auxiliary files *SIR.R*, *stochastic SIR model.R***

The code represents the SIR model in a homogeneous (and also potentially heterogeneous) populations with parameters  $\beta = 0.83$  infections per day,  $\gamma = 1/8.2$  per day in a population of  $N=1000$  individuals, where 1 infectious individual is introduced into a population of 999 non-infected individuals. The auxiliary file *SIR.R* codes the equations for the deterministic model, whereas the auxiliary file *stochastic SIR model.R* implements Gillespie's direct algorithm for the stochastic model. Note that the file *stochastic SIR model.R* codes also models with genetic variation in susceptibility and infectivity, but we only use it here for homogeneous populations

- 1. Take some time to familiarize yourself with the code in *Deterministic vs Stochastic SIR.R*. Then use the code to generate a graph that shows the proportion of susceptible, infected and recovered individuals over time for 10 realizations of the same epidemics. How do the individual profiles relate to the profile of the equivalent deterministic model?**
- 2. Use the command `head(testData1[[1]]$SIRts, 20)` and `tail(testData1[[1]]$SIRts, 20)` to trace the first and last 20 events of the last realization of the epidemic, respectively. What do you notice with regards to sequence of events and the time steps between consecutive events?**
- 3. Now change the code to produce the SIR profiles for a population consisting of 10 individuals only. What impact does a small population have on the predicted epidemics?**