Lesson 2: Simulation of stochastic dynamic models

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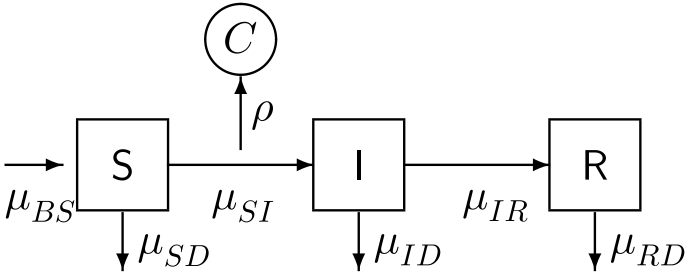
Objectives

This tutorial develops some classes of dynamic models relevant to biological systems, especially for epidemiology.

1. Dynamic systems can often be represented in terms of *flows* between *compartments*.
2. We develop the concept of a *compartment model* for which we specify *rates* for the flows between compartments.
3. We show how deterministic and stochastic versions of a compartment model are derived and related.
4. We introduce Euler's method to simulate from dynamic models.
5. We specify deterministic and stochastic compartment models in pomp using Euler method simulation.

A basic compartment model: The SIR model I

- We develop deterministic and stochastic representations of a susceptible-infected-recovered (SIR) system, a fundamental class of models for disease transmission dynamics.
- We set up notation applicable to general compartment models (Bretó et al. 2009).



S : susceptible	I : infected and infectious
R : recovered and/or removed	C : reported cases

A basic compartment model: The SIR model II

- We suppose that each arrow has an associated rate, so here there is a rate $\mu_{SI}(t)$ at which individuals in S transition to I, and μ_{IR} at which individuals in I transition to R.
- To account for demography (births/deaths/migration) we allow the possibility of a source and sink compartment, which is not usually represented on the flow diagram. We write μ_{BS} for a rate of births into S, and denote mortality rates by μ_{SD}, μ_{ID}, μ_{RD}.
- The rates may be either constant or time-varying.
- For the simplest SIR model, ignoring demography, we set

$$\mu_{BS} = \mu_{SD} = \mu_{ID} = \mu_{RD} = 0.$$

General notation for compartment models I

To develop a systematic notation, it turns out to be convenient to keep track of the flows between compartments as well as the number of individuals in each compartment:

- $N_{SI}(t)$: the number of individuals who have transitioned from S to I **by** time t. We say that $N_{SI}(t)$ is a *counting process*.
- $N_{IR}(t)$: the number of individuals transitioning from I to R **by** time t.

To include demography, we could keep track of birth and death events by the counting processes:

- $N_{BS}(t)$: the number of newborns into S **by** time t.
- $N_{SD}(t)$, $N_{ID}(t)$, $N_{RD}(t)$: the number of deaths from S, I, and R compartments **by** time t, respectively.

General notation for compartment models II

- For discrete population compartment models, the flow counting processes are non-decreasing and integer valued.
- For continuous population compartment models, the flow counting processes are non-decreasing and real valued.

Compartment model from counting processes

- The numbers of people in each compartment can be computed via these counting processes. Ignoring demography, we have:

$$\begin{aligned} S(t) &= S(0) - N_{SI}(t) && \\ I(t) &= I(0) + N_{SI}(t) && -N_{IR}(t) \\ R(t) &= R(0) && +N_{IR}(t) \end{aligned}$$

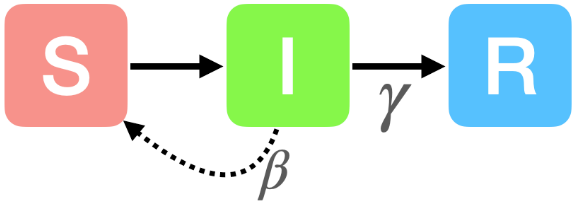
- These equations represent *conservation of individuals* or *what goes in must come out*.

Ordinary differential equation interpretation

Together with initial conditions specifying $S(0)$, $I(0)$ and $R(0)$, we just need to write down ordinary differential equations (ODEs) for the flow counting processes. These are:

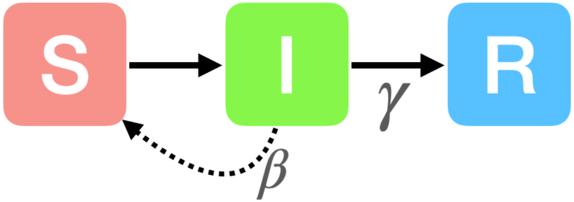
$$\frac{\mathrm{d}N_{SI}}{\mathrm{d}t} = \mu_{SI}(t)\,S(t)$$
$$\frac{\mathrm{d}N_{IR}}{\mathrm{d}t} = \mu_{IR}\,I(t)$$

Common notation for a deterministic SIR model



- β: transmission rate, encompasses the frequency of contacts and transmission probability between individuals
- γ: recovery rate, rate that infected individuals become "uninfectious"
  - Duration of infectiousness on average is $\frac{1}{\gamma}$
- $S + I + R = N$

Common notation for a deterministic SIR model - equations



$$
\begin{aligned}
\frac{\mathrm{d}S}{\mathrm{d}t} &= -\beta S \frac{I}{N} \\
\frac{\mathrm{d}I}{\mathrm{d}t} &= \beta S \frac{I}{N} - \gamma * I \\
\frac{\mathrm{d}R}{\mathrm{d}t} &= \gamma I
\end{aligned}
$$

Stochastic Differential Equations (SDEs)

- By including randomness in the ODE system, we can have the stochastic differential equation (SDE) system.
- For example, for the ODE $\frac{\mathrm{d}x}{\mathrm{d}t} = h(x)$, a natural way to add stochastic variation is

$$\frac{\mathrm{d}X}{\mathrm{d}t} = h(X) + \sigma \frac{\mathrm{d}B}{\mathrm{d}t}$$

where $\{B(t)\}$ is Brownian motion and so dB/dt is Brownian noise.

The simple counting process and the reactions I

- A deterministic SIR model has a fixed trajectory, indicating that the number of each compartment at any time is fixed with given parameters and intial states; thus the transitions between compartments are fixed at any time.
- A stochastic SIR model, in the contrary, the trajectory and the transitions between compartments at any time are stochastic.
- Recall $N_{SI}(t)$ and $N_{IR}(t)$ are counting processes, indicating the number of total individuals transitioned from S to I and I to R by time t, respectively.
- A *simple counting process* is one which cannot count more than one event at a time.

The simple counting process and the reactions II

- We then can relate the counting process to the common SIR reactions with the corresponding probabilities.
- Note that we are using *little o notation* and we write $h(\delta) = o(\delta)$ to mean $\lim_{\delta \to 0} \frac{h(\delta)}{\delta} = 0$.

Table 1: Relationship between the counting processes, the reactions, and the probabilities.

Counting	Reaction	Probability
$N_{SI}(t+\delta) = N_{SI}(t) + 1$	$S \to S - 1$ $I \to I + 1$	$\beta S(t) I(t) \delta / N + o(\delta)$
$N_{SI}(t+\delta) = N_{SI}(t)$		$1 - \beta S(t) I(t) \delta / N + o(\delta)$
$N_{IR}(t+\delta) = N_{IR}(t) + 1$	$I \to I - 1$ $R \to R + 1$	$\gamma I(t) \delta + o(\delta)$
$N_{IR}(t+\delta) = N_{IR}(t)$		$1 - \gamma I(t) \delta + o(\delta)$

The Euler's method I

- When referring the counting and its corresponding probability in Table 1, it is obvious that we can derive a continuous time Markov chain (CTMC) for the SIR model:

$$\begin{aligned}
\mathbb{P}\left[N_{SI}(t+\delta)=N_{SI}(t)+1\right] &= \beta\, S(t)\, I(t)/N\,\delta + o(\delta), \\
\mathbb{P}\left[N_{IR}(t+\delta)=N_{IR}(t)+1\right] &= \gamma\, I(t)\delta + o(\delta).
\end{aligned}$$

- For $k = 1, 2, \ldots$, by discretizing this CTMC with small time step δ, we can derive a numerical solution with the state variables $\tilde{S}(k\delta)$, $\tilde{I}(k\delta)$, $\tilde{R}(k\delta)$:

$$\begin{aligned}
\tilde{S}(k\delta) &= S(0) - \tilde{N}_{SI}(k\delta) \\
\tilde{I}(k\delta) &= I(0) + \tilde{N}_{SI}(k\delta) - \tilde{N}_{IR}(k\delta) \\
\tilde{R}(k\delta) &= R(0) + \tilde{N}_{IR}(k\delta)
\end{aligned}$$

- $\tilde{N}_{SI}(t)$ and $\tilde{N}_{IR}(t)$: the numerical solutions for $N_{SI}(t)$ and $N_{IR}(t)$

The Euler's method II

- Let current $t = k\delta$, consider the small time interval $t \le \tau \le t + \delta$.
- Assume that the gradients $\frac{\mathrm{d}N_{SI}}{\mathrm{d}t} = \mu_{SI}(t)\, S(t)$ and $\frac{\mathrm{d}N_{IR}}{\mathrm{d}t} = \mu_{IR}\, I(t)$ are approximately constant
- We can have $\tilde{N}_{SI}(t+\delta)$ and $\tilde{N}_{IR}(t+\delta)$ as:

$$
\begin{aligned}
\tilde{N}_{SI}(t+\delta) &= \tilde{N}_{SI}(t) + \delta\, \beta\, S(t)\, I(t)\,/N \\
\tilde{N}_{IR}(t+\delta) &= \tilde{N}_{IR}(t) + \delta\, \gamma\, I(t)
\end{aligned}
$$

The Euler's method III

Now we can include stochastic variation in the Euler's method.

- Recall the SDE:

$$\frac{\mathrm{d}X}{\mathrm{d}t} = h(X) + \sigma\,\frac{\mathrm{d}B}{\mathrm{d}t}$$

where $\{B(t)\}$ is Brownian motion and so dB/dt is Brownian noise.

- An Euler approximation $\tilde{X}(t)$ within the small time interval $[t, t+\delta]$ and $t = k\delta$ for $k = 0, 1, 2, \ldots$ is

$$\tilde{X}(\,t+\delta\,) = \tilde{X}(t) + \delta\,h(\,\tilde{X}(t)\,) + \sigma\sqrt{\delta}\,Z_k$$

where $Z_1, Z_2, \ldots$ are independent standard normal random variables, i.e., $Z_k \sim \mathrm{Normal}\,(0,1)$.

- Although SDEs are often considered an advanced topic in probability, the Euler approximation doesn't demand much more than familiarity with the normal distribution.

The Euler's method IV

Now we can consider applying the Euler's method for a stochastic SIR model:

- A binomial approximation with exponential transition probabilities.

$$\begin{aligned}\tilde{N}_{SI}(t+\delta) &= \tilde{N}_{SI}(t) + \mathrm{Binomial}\big[\tilde{S}(t), 1 - \exp\big\{-\beta\,\tilde{I}(t)/N\,\delta\big\}\big],\\ \tilde{N}_{IR}(t+\delta) &= \tilde{N}_{IR}(t) + \mathrm{Binomial}\big[\tilde{I}(t), 1 - \exp\big\{-\delta\,\gamma\big\}\big],\end{aligned}$$

where $\mathrm{Binomial}(n,p)$ is a binomial random variable with mean np and variance $np(1-p)$. Here, $p = 1 - \exp\big\{-\beta\,\tilde{I}(t)/N\,\delta\big\}$ and $p = 1 - \exp\big\{-\delta\,\gamma\big\}$, respectively.

The Euler's method V

The following are two other ways for a stochastic SIR model with the Euler's approximation, what they are not as good as the previous one?

1. A Poisson approximation.

$$\tilde{N}_{SI}(t+\delta) = \tilde{N}_{SI}(t) + \mathrm{Poisson}\big[\beta\, \tilde{S}(t)\, \tilde{I}(t)/N\, \delta\big],$$

   where $\mathrm{Poisson}(\mu)$ is a Poisson random variable with mean $\mu = \beta\, \tilde{S}(t)\, \tilde{I}(t)/N\, \delta$.

2. A binomial approximation,

$$\tilde{N}_{SI}(t+\delta) = \tilde{N}_{SI}(t) + \mathrm{Binomial}\big[\tilde{S}(t), \beta\, \tilde{I}(t)/N\, \delta\big].$$

The Gillespie method I

- Numerical methods, such as the Euler's method, are approximations to the process by discretizing time using small time step δ
- However, the Gillespie method is the exact **Stochastic Simulation Method**, which leverages the Markov Property as well.
- In Table 1, by consider the reactions and the probabilities, we can derive the Gillespie algorithm for the stochastic SIR model.

The Gillespie method II

With initialization, $S(0)$, $I(0)$, and $R(0)$, at current time t:

1. Compute the total event rates: $\lambda_1 = \beta\, S(t)\, I(t)/N, \lambda_2 = \gamma\, I(t), \lambda = \lambda_1 + \lambda_2$
2. Compute the waiting time $\Delta t \sim \mathrm{Exponential}(\lambda)$
3. Select the reactions by sampling from probabilities $\left(\frac{\lambda_1}{\lambda}, \frac{\lambda_2}{\lambda}\right)$
4. Update the states from the selected reaction and update the time $t \to t + \Delta t$
5. Repeat 1-4 till the end of the simulation time

Even though the Gillespie is an exact stochastic simulation method, it has limitations such as:

- Computational Intensity: For complex systems with many reactions, the Gillespie method can become computationally expensive.
- Rare Events: For systems where some reactions are very rare, a large number of simulation steps may be needed to capture these events, making the method slow.

Euler vs. Gillespie

- Why and When would you prefer an implementation of Gillespie's algorithm to an Euler solution?

Worked solution to the Exercise

- Numerically, Gillespie's algorithm is often approximated using so-called tau-leaping methods. These are closely related to Euler's approach. In this context, the Euler method has sometimes been called tau-leaping.

Compartment models in pomp: The Consett Measles outbreaks I

Let's look at outbreak of measles in the town of Consett in England in 1948:

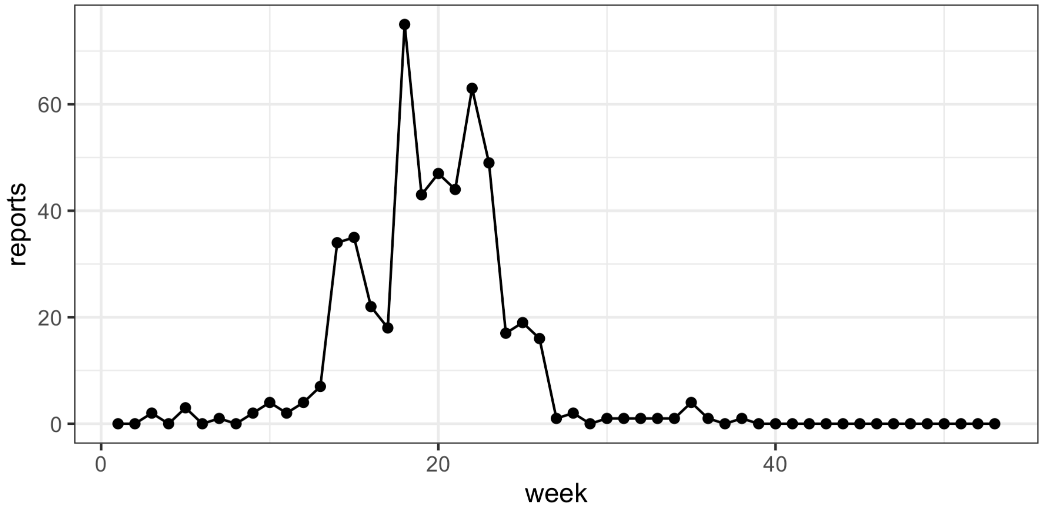
- the town had population of 38820,
- with 737 births over the course of the year.

```r
library(tidyverse)
read_csv("Measles_Consett_1948.csv") |>
  select(week,reports=cases) -> meas
meas |> as.data.frame() |> head(n=3)
```

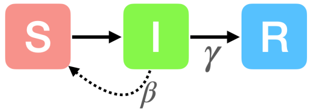
```
 week reports
    1       0
    2       0
    3       2
```

- `week`: time, indicates that the data are counted weekly
- `reports` variable: incidence, counts the number of reports of new measles cases each week

Compartment models in `pomp`: The Consett Measles outbreaks II



The SIR as a POMP model for measles I



- The **unobserved states**: $S(t)$, $I(t)$, $R(t)$, the numbers of individuals in the S, I, and R compartments, respectively.
- The constant population size: $N = S(t) + I(t) + R(t)$, as fixed at the known population size of 38,000.
- **Flows** move from one compartment to another over any particular time interval are modeled as *stochastic processes*.
- **Demographic stochasticity**: each individual in a compartment at any given time faces the same risk of exiting the compartment; the unavoidable randomness that arises from chance events occurring in a discrete and finite population.

The SIR as a POMP model for measles II

Recall the application of the Euler's method to a stochastic SIR model.

- ΔN_{SI} and ΔN_{IR}: the flows from S to I and from I to R over interval Δt, respectively:

$$\Delta N_{SI} \sim \mathrm{Binomial}\left(S, 1 - e^{-\beta \frac{I}{N} \Delta t}\right),$$
$$\Delta N_{IR} \sim \mathrm{Binomial}\left(I, 1 - e^{-\gamma \Delta t}\right).$$

The SIR as a POMP model for measles III

- Implement the dynamics in pomp as an R function:

```
sir_stoch <- function (S, I, R, N, Beta, Gamma, delta.t, ...) {
  dN_SI <- rbinom(n=1,size=S,prob=1-exp(-Beta*I/N*delta.t))
  dN_IR <- rbinom(n=1,size=I,prob=1-exp(-Gamma*delta.t))
  S <- S - dN_SI
  I <- I + dN_SI - dN_IR
  R <- R + dN_IR
  c(S = S, I = I, R = R)
}
```

- Note that, for a deterministic SIR model:

```
dN_SI <- Beta*S*I/N*delta.t
dN_IR <- Gamma*I*delta.t
```

The SIR as a POMP model for measles IV

We can implement the initialization function with the following assumptions:

- Assume the dynamics starts at week 0, $t0 = 0$.
- At $t0$, assume the initial number of infection is 1, that is $I = 1$.
- The initial number of susceptible is unknown, so we'll treat this fraction, η, as a parameter to be estimated.

```
sir_rinit <- function (N, Eta, ...) {
  c(S = round(N*Eta), I = 1, R = round(N*(1-Eta)))
}
```

The SIR as a POMP model for measles V

With the initialization function `sir_rinit` and the process function `sir_stoch`, we can build a `pomp` object with these two components and the data:

```
library(pomp)
meas |>
  pomp(
    times="week",t0=0,
    rprocess=euler(sir_stoch,delta.t=1/7),
    rinit=sir_rinit
  ) -> measSIR
```

- Question: what do `times="week"` and `delta.t=1/7` indicate?

The SIR as a POMP model for measles VI

- Assume the **observations**, the `reports`, result from a process by which new infections are diagnosed in a hospital and reported with probability ρ.
- The diagnosed infections are immediately hospitalized, therefore, they have, presumably, a much lower transmission rate; let's assume each *week's* reports as being related to the number of individuals who have moved from I to R over the course of that week.
- We then define a new variable, H, that tracks these daily counts.

The SIR as a POMP model for measles VII

We now can modify the R functions to incorporate the new variable H:

```r
sir_stoch <- function (S, I, R, N, Beta, Gamma, delta.t, H, ...) {
  dN_SI <- rbinom(n=1,size=S,prob=1-exp(-Beta*I/N*delta.t))
  dN_IR <- rbinom(n=1,size=I,prob=1-exp(-Gamma*delta.t))
  S <- S - dN_SI
  I <- I + dN_SI - dN_IR
  R <- R + dN_IR
  H <- H + dN_IR
  c(S = S, I = I, R = R, H = H)
}

sir_rinit <- function (N, Eta, ...) {
  c(S = round(N*Eta), I = 1, R = round(N*(1-Eta)), H = 0)
}
```

The SIR as a POMP model for measles VIII

Note that, we are so far accounting for the *flows* between compartments by days, while the `reports` are weekly cases. Since we want H to tally only the incidence over the week, we'll need to reset it to zero at the beginning of each week. Thus, in pomp terminology, H is an **accumulator variable**. We accomplish this using the `accumvars` argument to pomp when build the object:

```r
measSIR |>
  pomp(
    rprocess=euler(sir_stoch,delta.t=1/7),
    rinit=sir_rinit,
    accumvars="H"
  ) -> measSIR
```

- Question: what does that mean by running a pomp function with the pomp object `measSIR`?

The SIR as a POMP model for measles IX

Last but not least, we need to define a **measurement model** to relate the **observations**, `reports`, to the **unobserved** accumulative state, H.

- We will model the data by a negative binomial variable,

$$\text{reports}_t \sim \text{NegBin}\left(\rho\, H(t), k\right).$$

  with mean $\rho\, H(t)$ and variance $\rho H(t) + \left(\rho H(t)\right)^2/k$. The binomial distribution does not have a separate variance parameter.

The SIR as a POMP model for measles X

- To include the observations in the model, we must write either a `dmeasure` or an `rmeasure` component, or both:

```r
sir_dmeas <- function (reports, H, Rho, k, log, ...) {
  dnbinom(x=reports, size=k, mu=Rho*H, log=log)
}

sir_rmeas <- function (H, Rho, k, ...) {
  c(reports=rnbinom(n=1, size=k, mu=Rho*H))
}
```

The SIR as a POMP model for measles XI

Eventually, we can add these two components to the previous `measSIR` object to update the `dmeasure` and `rmeasure` arguments:

```r
measSIR |>
  pomp(
    rmeasure=sir_rmeas,
    dmeasure=sir_dmeas
  ) -> measSIR
```

Specifying model components using C snippets I

- Although we can always specify basic model components using `R` functions, as above, we'll typically want the computational speed-up that we can obtain only by using compiled native code.
- pomp provides a facility for doing so with ease, using *C snippets*.
- C snippets are small pieces of C code used to specify basic model components.

Specifying model components using C snippets II

- For example, a C snippet encoding the rprocess for an `sir` model is as follows.

```
sir_stoch <- Csnippet("
  double dN_SI = rbinom(S,1-exp(-Beta*I/N*dt));
  double dN_IR = rbinom(I,1-exp(-Gamma*dt));
  S -= dN_SI;
  I += dN_SI - dN_IR;
  R += dN_IR;
  H += dN_IR;
")
```

Specifying model components using C snippets III

Note:

- It is necessary to define the data type for the real values `dN_SI` and `dN_IR` as `double`. The data type for states does not need to be defined at this stage and will be addressed later.
- `rbinom` is a built-in function used to generate random values from a binomial distribution. For additional built-in distributions in R, you can refer to this Rmath.h document.
- Remember to add a semicolon (`;`) after each line to ensure proper syntax.
- C snippets for the initializer and measurement model are:

Specifying model components using C snippets IV

```
sir_rinit <- Csnippet("
  S = nearbyint(Eta*N);
  I = 1;
  R = nearbyint((1-Eta)*N);
  H = 0;
")

sir_dmeas <- Csnippet("
  lik = dnbinom_mu(reports,k,Rho*H,give_log);
")

sir_rmeas <- Csnippet("
  reports = rnbinom_mu(k,Rho*H);
")
```

Specifying model components using C snippets V

- No need to define the type for likelihood `(lik)` here, as it is already predefined.
- `nearbyint` is a built-in function used to find the closest integer to a given value.
- `reports` is the variable name specified in your dataset.

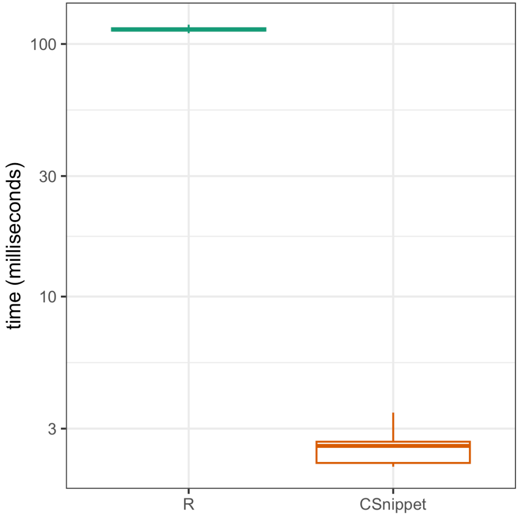
Specifying model components using C snippets VI

- A call to pomp replaces the basic model components with these, much faster, implementations:

```
measSIR |>
  pomp(
    rprocess=euler(sir_stoch,delta.t=1/7),
    rinit=sir_rinit,
    rmeasure=sir_rmeas,
    dmeasure=sir_dmeas,
    accumvars="H",
    statenames=c("S","I","R","H"),
    paramnames=c("Beta","Gamma","N","Eta","Rho","k")
  ) -> measSIR_C
```

Specifying model components using C snippets VII

- Note that, when using C snippets, one has to tell pomp which of the variables referenced in the C snippets are state variables and which are parameters. This is accomplished using the `statenames` and `paramnames` arguments.
- We can tell from the summary table that CSnippet is approximate 50 times faster than R.



Guessing plausible parameter values I

- To check the code is working properly, we simulate. This requires us to assign parameters. A little thought will get us some ballpark estimates.
- Recall that $\mathfrak{R}_0$ is the expected number of secondary infections resulting from one primary infection introduced into a fully susceptible population. For an SIR infection, one has that $\mathfrak{R}_0 \approx \frac{L}{A}$, where L is the lifespan of a host and A is the mean age of infection. Analysis of age-stratified serology data establish that the mean age of infection for measles during this period was around 4–5yr (Anderson and May 1991). Assuming a lifespan of 60–70yr, we have $\mathfrak{R}_0 \approx 15$.
- The basic theory of SIR epidemics gives the final-size equation,

$$\mathfrak{R}_0 = -\frac{\log(1-f)}{f},$$

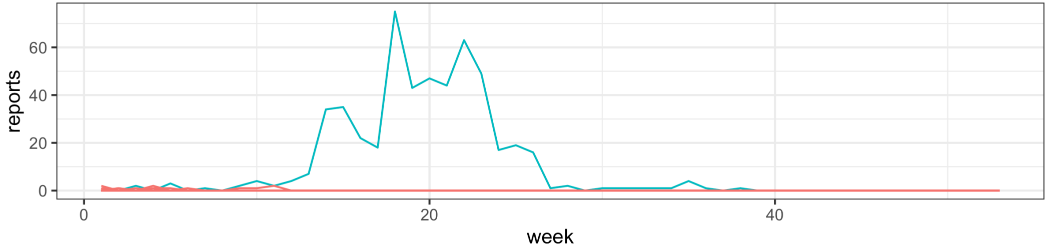
where f is the final size of the epidemic—the fraction of those susceptible at the beginning of the outbreak who ultimately become infected. For $\mathfrak{R}_0 > 5$, this equation predicts that $f > 0.99$.

Guessing plausible parameter values II

- In the data, it looks like there were a total of 521 infections. Assuming 50% reporting, we have that $S_0 \approx 1042$, so that $\eta = \frac{S_0}{N} \approx 0.027$.
- If the infectious period is roughly 2 weeks, then $1/\mu_{IR} \approx 2$ wk and $\beta = \mu_{IR}\mathfrak{R}_0 \approx 7.5\ \text{wk}^{-1}$.

Guessing plausible parameter values III

```
measSIR |>
  simulate(params=c(Beta=7.5,Gamma=0.5,Rho=0.5,k=10, Eta=0.03,N=38000),
    nsim=20,format="data.frame",include.data=TRUE) |>
  ggplot(aes(x=week,y=reports,group=.id,color=.id=="data")) +
  geom_line() + guides(color="none")
```



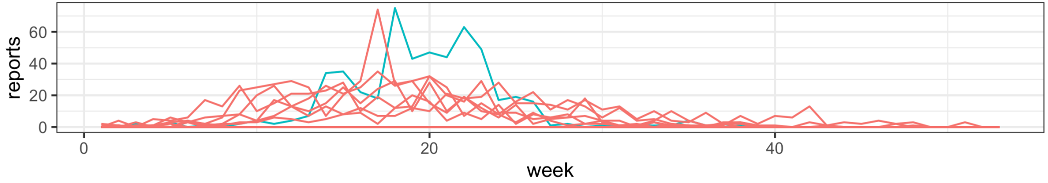
Exercise I: Explore the SIR model

Fiddle with the parameters to see if you can't find a model for which the data are a more plausible realization.

Worked solutions I: Explore the SIR model I

In the simulated outbreaks, the overall incidence is much too low, and the outbreak dies out immediately. We might try increasing the force of infection:

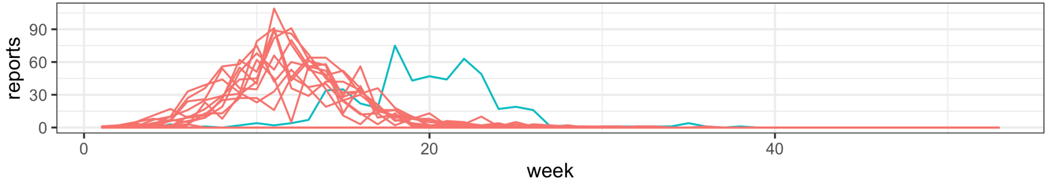
```r
measSIR |>
  simulate(params=c(Beta=25,Gamma=0.5,Rho=0.5,k=10,Eta=0.03,N=38000),
    nsim=20,format="data.frame",include.data=TRUE) |>
  ggplot(aes(x=week,y=reports,group=.id,color=.id=="data")) +
  geom_line() + guides(color="none")
```



Worked solutions I: Explore the SIR model II

Taking it farther...

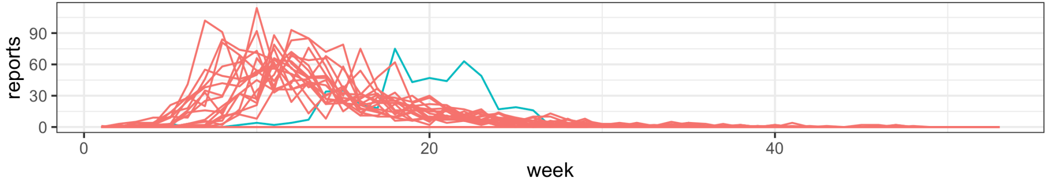
```
measSIR |>
  simulate(params=c(Beta=40,Gamma=0.5,Rho=0.5,k=10,Eta=0.03,N=38000),
    nsim=20,format="data.frame",include.data=TRUE) |>
  ggplot(aes(x=week,y=reports,group=.id,color=.id=="data")) +
  geom_line() + guides(color="none")
```



Worked solutions I: Explore the SIR model III

While this increases the overall incidence, the epidemic is now peaking too quickly. To counteract this, we might try reducing the recovery rate.

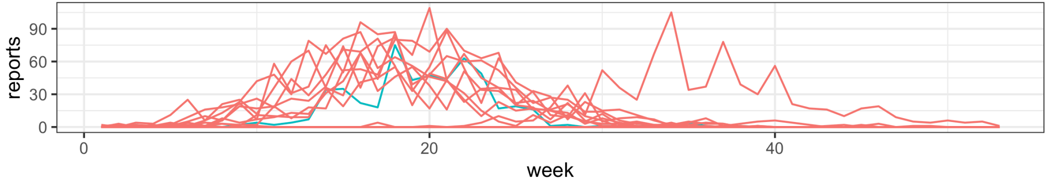
```r
measSIR |>
  simulate(params=c(Beta=40,Gamma=0.2,Rho=0.5,k=10,Eta=0.03,N=38000),
    nsim=20,format="data.frame",include.data=TRUE) |>
  ggplot(aes(x=week,y=reports,group=.id,color=.id=="data"))+
  geom_line() + guides(color="none")
```



Worked solutions I: Explore the SIR model IV

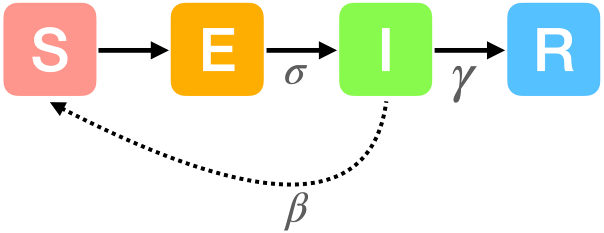
Additionally, we might have a look at the effects of changing the initial susceptible fraction, η:

```
measSIR |>
  simulate(params=c(Beta=15,Gamma=0.5,Rho=0.5,k=10,Eta=0.06,N=38000),
    nsim=20,format="data.frame",include.data=TRUE) |>
  ggplot(aes(x=week,y=reports,group=.id,color=.id=="data")) +
  geom_line() + guides(color="none")
```



Exercise II: Extend the SIR model to SEIR model

Below is a diagram of the so-called SEIR model. This differs from the SIR model in that infected individuals must pass a period of latency before becoming infectious.



Modify the codes above to construct a `pomp` object containing the Consett measles data and an SEIR model. Perform simulations as above and adjust parameters to get a sense of whether improvement is possible by including a latent period.

Worked solutions II: The SEIR model I

The existing code may be modified as follows:

```
seir_stoch <- Csnippet("
  double dN_SE = rbinom(S,1-exp(-Beta*I/N*dt));
  double dN_EI = rbinom(E,1-exp(-Sigma*dt));
  double dN_IR = rbinom(I,1-exp(-Gamma*dt));
  S -= dN_SE;
  E += dN_SE - dN_EI;
  I += dN_EI - dN_IR;
  R += dN_IR;
  H += dN_IR;
")
```

Worked solutions II: The SEIR model II

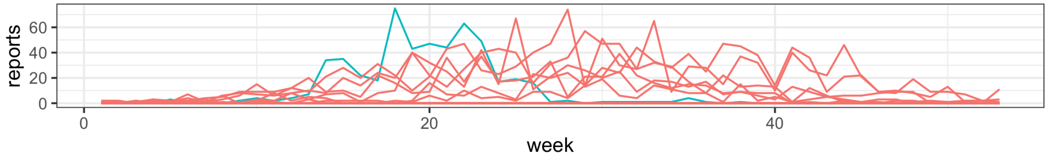
```r
seir_init <- Csnippet("
  S = nearbyint(Eta*N);
  E = 0; I = 1;
  R = nearbyint((1-Eta)*N);
  H = 0;
")

measSIR |>
  pomp(
    rprocess=euler(seir_stoch,delta.t=1/7),
    rinit=seir_init,
    paramnames=c("N","Beta","Sigma","Gamma","Rho","Eta","k"),
    statenames=c("S","E","I","R","H")
  ) -> measSEIR
```

Worked solutions II: The SEIR model III

Using the rough estimate that the latent period in measles is 8–10da, we take $\sigma \sim 0.8$wk^{-1} and $\gamma \sim 1.3$wk^{-1} (roughly the same generation time as before).

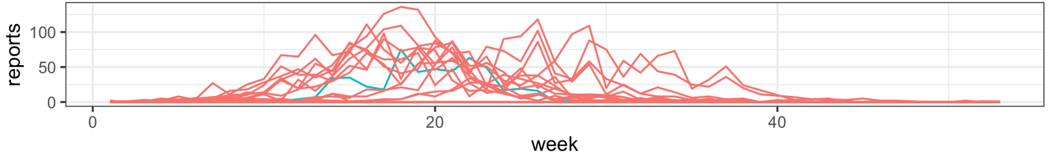
```
measSEIR |>
  simulate(params=c(Beta=30,Sigma=0.8,Gamma=1.3,
                    Rho=0.5,k=10,Eta=0.06,N=38000),
    nsim=20,format="data.frame",include.data=TRUE) |>
  ggplot(aes(x=week,y=reports,group=.id,color=.id=="data")) +
  geom_line() + guides(color="none")
```



Worked solutions II: The SEIR model IV

Again one can increase the force of infection:

```
measSEIR |>
  simulate(params=c(Beta=40,Sigma=0.8,Gamma=1.3,
                    Rho=0.5,k=10,Eta=0.06,N=38000),
    nsim=20,format="data.frame",include.data=TRUE) |>
  ggplot(aes(x=week,y=reports,group=.id,color=.id=="data")) +
  geom_line() + guides(color="none")
```



References

Anderson, R. M., and R. M. May. 1991. *Infectious Diseases of Humans*. Oxford: Oxford Univesity Press.

Bretó, Carles, Daihai He, Edward L. Ionides, and Aaron A. King. 2009. "Time Series Analysis via Mechanistic Models." *Ann Appl Stat* 3 (1): 319–48. https://doi.org/10.1214/08-AOAS201.

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- Compiled on 2024-07-24.

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`R` code for this lesson