Assignment 7

Fitting models to data

Juan Carlos Villaseñor-Derbez

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```
# Load packages
suppressPackageStartupMessages({
   library(deSolve)
   library(cowplot)
   library(bbmle)
   library(tidyverse)
})
```

Code up an SIR model in which the measurement error follows a Poisson distribution

```
data_flu <- read.csv("../../Labs/Lab7/boarding_school_flu.csv") %>%
  rename(time = day)
# define a SIRv.model function to pass to Isoda
SIR.model <- function (t, x, params) {</pre>
  S \leftarrow x[1]
  I <- x[2]
  R < -x[3]
  beta <- params[1]</pre>
  gamma <- params[2]</pre>
  N < -763
  dSdt <- -beta*S*I/N
  dIdt <- beta*S*I/N - gamma*I
  dRdt <- gamma*I
  return(list(c(dSdt,dIdt,dRdt)))
}
SO <- 762 # Initial number of susceptibles
IO <- 1 # Initial number of infecteds
RO <- 0 # Initial number of recovered
initial_values <- c(S=S0,I=I0,R=R0)</pre>
beta <- 2 # per host per week
gamma <- 0.5 # per week
params <- c(beta, gamma)</pre>
times \leftarrow seq(0, 15, by=0.1)
```

```
lsoda(initial_values, times, SIR.model, params) %>%
  as.data.frame() %>%
  left_join(data_flu, by = "time") %>%
  gather(group, count, -c(time, flu)) %>%
  mutate(count_error = rpois(length(count), count)) %>%
  ggplot(aes(x = time, color = group)) +
  geom_line(aes(y = count), size = 1) +
  geom_point(aes(y = count_error)) +
  geom_point(aes(y = flu), color = "black", size = 2) +
  scale_color_brewer(palette = "Set1")
```

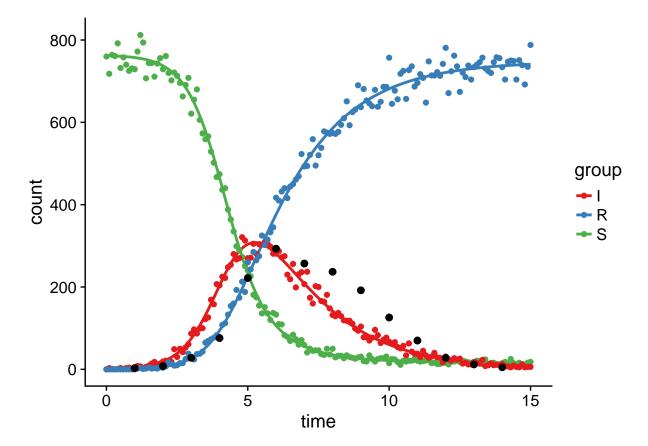


Figure 1: Simulation of a SIR model with $\beta=2$ and $\gamma=0.5$. Dots represent a random measurement error following a Poisson distribution. Black dots represent the 'flu' variable (beded kids) from the flu dataset.

Assume that the boys confined to bed corresponds to the infected class of the SIR model and fit the model using maximum likelihood

```
sir_nll <- function(beta, gamma){</pre>
  times <- c(0, data_flu$time)</pre>
  params <- c(beta, gamma)</pre>
  initial_values <- c(S = 762, I = 1, R = 0)
  results <- lsoda(func = SIR.model,
                    y = initial_values,
                    times = times,
                    parms = params) %>%
    as.data.frame()
  nll = -1*sum(dpois(data_flu$flu, results$I[2:15], log=TRUE))
  return(nll)
fit_sir <- mle2(sir_nll,</pre>
                 start = list(beta = 2,
                            gamma = 1),
                 method = "L-BFGS-B",
                 lower = c(0, 0),
                 upper = c(Inf, Inf))
```

Using the default values of $\beta = 2$ and $\gamma = 0.5$, we obtain a NLL = 240.66. The best fit is obtained with $\beta = 1.69$ and $\gamma = 0.48$, achieving a NLL = 76.57 Figure 2.

```
beta = coef(fit_sir)[1] # per host per week
gamma = coef(fit_sir)[2] # per week
parameters = c(beta, gamma)

times = seq(0, 15, by=0.1)

set.seed(43)

lsoda(initial_values, times, SIR.model, parameters) %>%
    as.data.frame() %>%
    left_join(data_flu, by = "time") %>%
    gather(group, count, -c(time, flu)) %>%
    mutate(count_error = rpois(length(count), count)) %>%
    ggplot(aes(x = time, color = group)) +
    geom_line(aes(y = count), size = 1) +
    geom_point(aes(y = count_error)) +
    geom_point(aes(y = flu), color = "black", size = 2) +
    scale_color_brewer(palette = "Set1")
```

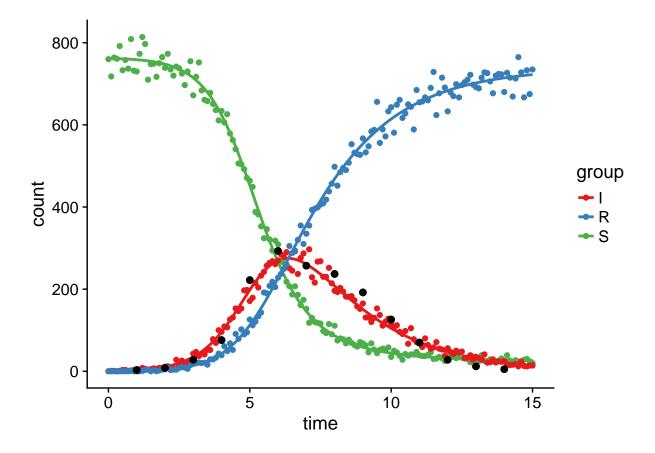


Figure 2: Simulation of a SIR model with optimized $\beta=1.69$ and $\gamma=0.48$. Dots represent a random measurement error following a Poisson distribution. Black dots represent the 'flu' variable (beded kids) from the flu dataset.

Compute the AIC of the SIR model and compare it to the SIRB model. Which model does AIC indicate is preferable?

The SIR model is more parsimonious than the SBIR model (AIC = 158.22 vs. AIC = 185.27).

Table 1: Corrected Akaike Information Criterion (AICc) for the SIR and SBIR models.

Model	k	N	AICc
SIR	2 3	14	158.2259
SBIR		14	185.2788