MACHINE LEARNING & GLOBAL HEALTH NETWORK

MRC Centre for Global Infectious Disease Analysis

Imperial College London

Introduction to Fitting an SIR model practical

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North-South-AIMS-Imperial: modern statistics and global health

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Fitting 2 different models: SIR model

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Fitting 2 different models: SIER model

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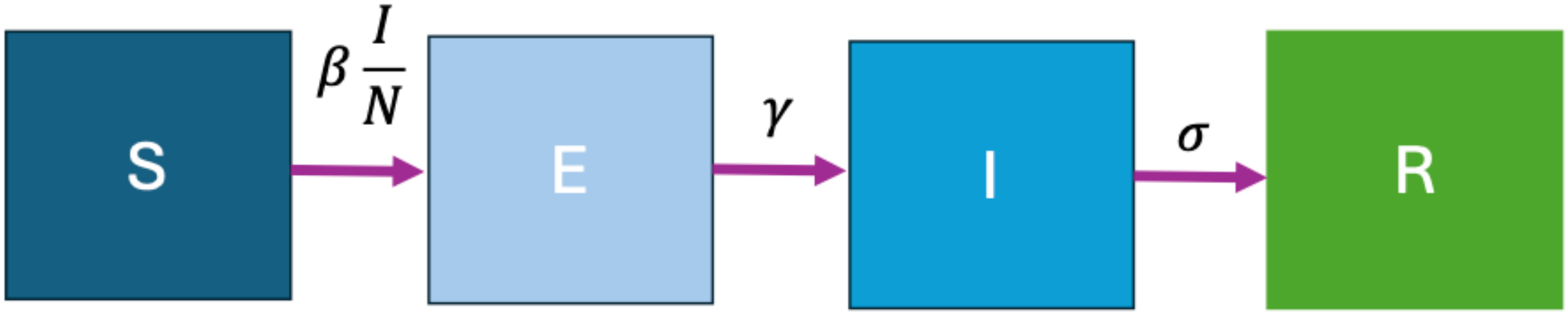

To 2 types of data: Prevalence

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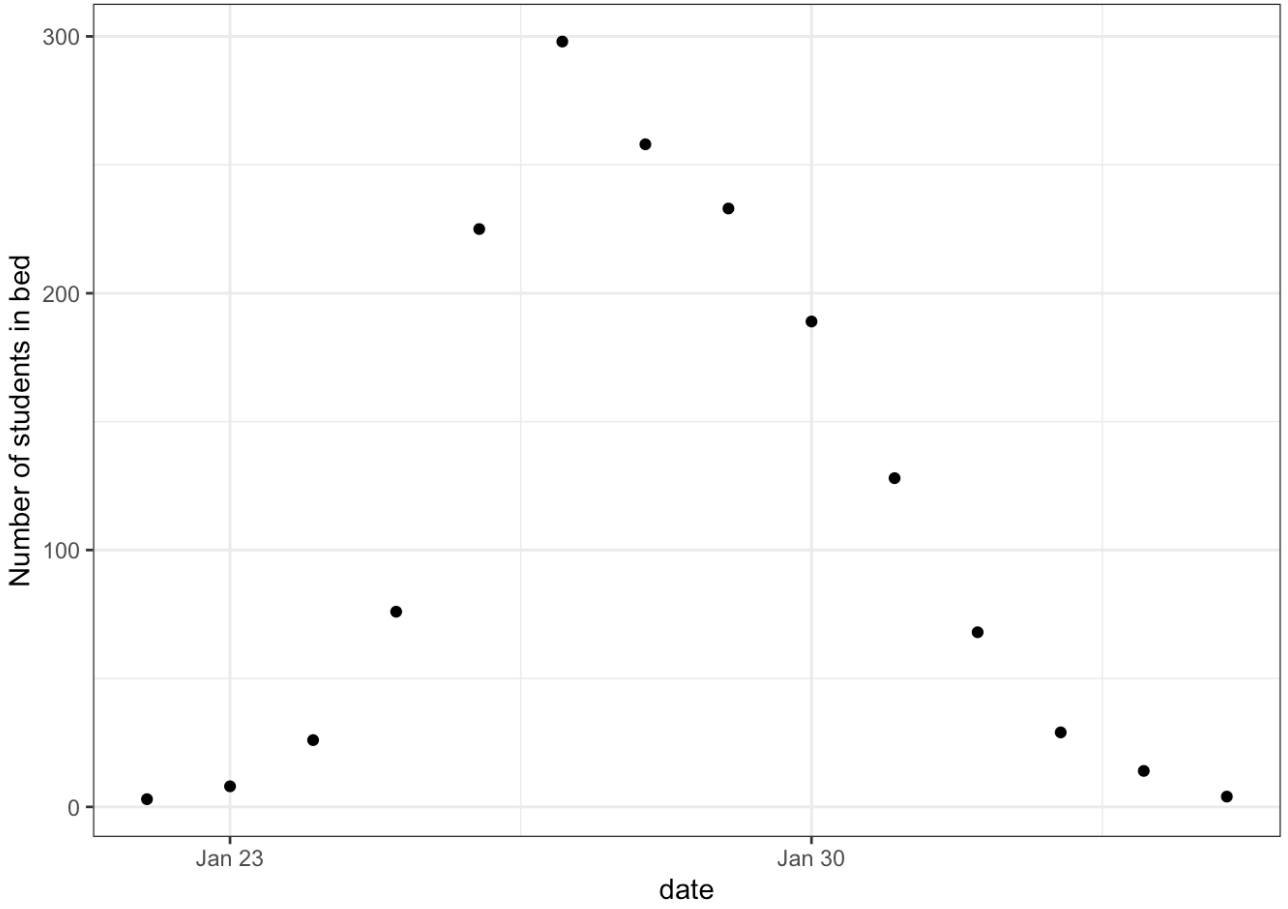
We examine an outbreak of influenza A (H1N1) in 1978 at a British boarding school. The data consists of the daily number of students in bed (prevalence data), spanning over a time interval of 14 days.



To 2 types of data: Incidence

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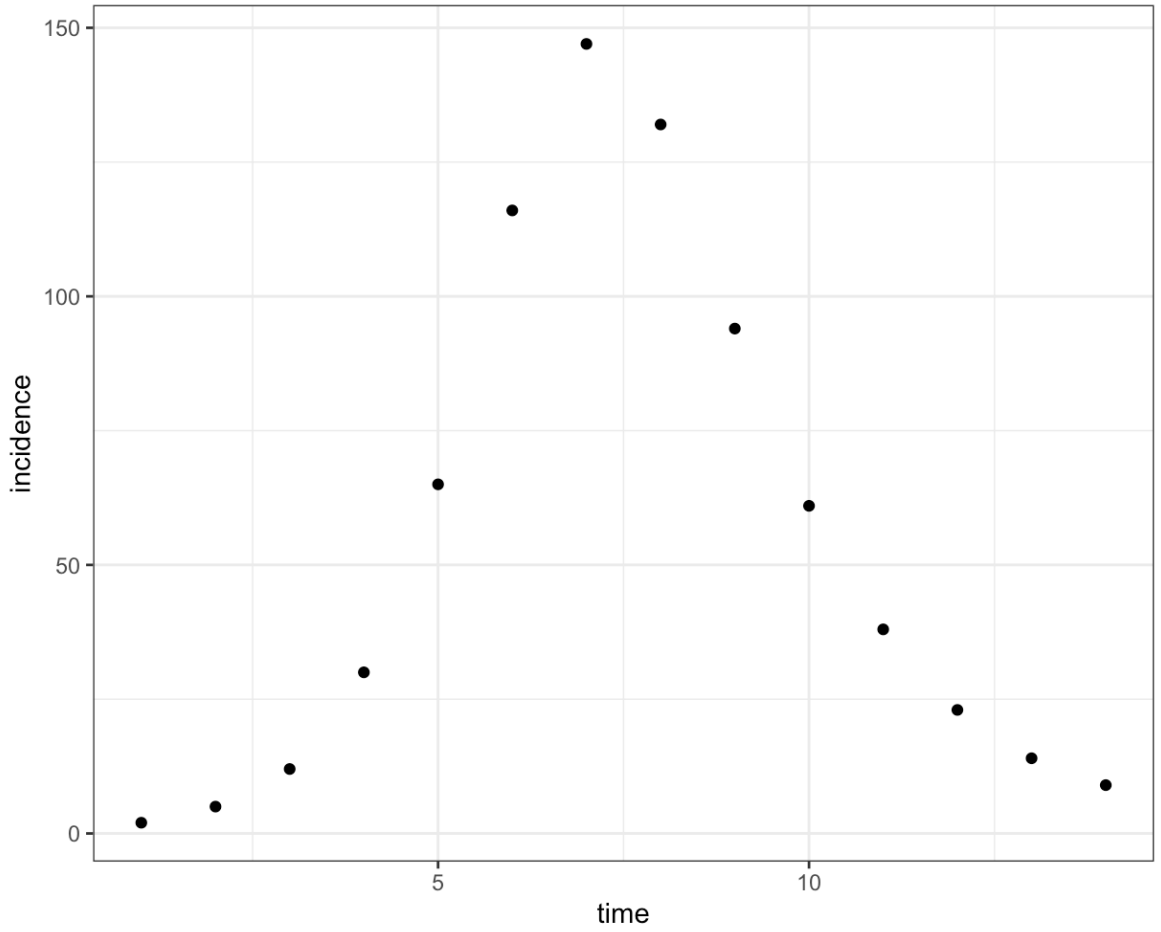
New cases of flu each day



Stan model file

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```
functions {
 real[] sir(real t, real[] y, real[] theta,
            real[] x_r,  int[] x_i) {
  }
}

data {
}

transformed data {
}

parameters {
}

transformed parameters{
}

model {
}

generated quantities {
}
```

Fitting the model in R

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```r
cases <- influenza_england_1978_school$in_bed

# total count
N <- 763;

# times
n_days <- length(cases)
t <- seq(1, n_days, by = 1)
t0 = 0

#initial conditions
i0 <- 1
s0 <- N - i0
e0 <- 0
r0 <- 0
y0 = c(S = s0, E = e0, I = i0, R = r0)

# data for Stan
data_seir <- list(n_days = n_days, y0 = y0, t0 = t0, ts = t, N = N, cases = cases)

# number of MCMC steps
niter <- 7500

model <- stan_model("stan_models/seir_prevalence.stan")

fit_seir_negbin <- sampling(model,
                data = data_seir,
                iter = niter,
                chains = 4,
                seed = 0)
```