Bayesian Modelling Using STAN

Statistical Modelling

- **Traditional methods**
  - Small number of well understood methods
  - Well-designed laboratory experiments with refutable hypothesis
  - Easily interpretable results
- **Real-world analysis**
  - Many interacting processes so experimental design is hard
  - Very expensive, reuse data as much as possible
  - Indirect interpretation of results
- **Statistical Modelling**
  - Generative model - mechanistic models of underlying processes (with unknown parameters)
  - Observation model - measurement uncertainty and biases (e.g. censoring)
  - Very complicated with no standard statistical tests

Stan for Bayesian Modelling

- **What is Stan?**
  - package for MCMC sampling
  - high-level language for describing Bayesian models
- **Why Stan?**
  - very fast development of new models
  - computationally and numerically efficient
  - integrated with R
  - well-documented and well-used with community support
- **State-space model**
  - hidden/latent variable models for time-series analysis
  - epidemiology model for estimating R(t)

https://github.com/BDI-pathogens/stan_epi_tutorial

State-Space Models

- State-space model (a.k.a. filters) are a class of model for analysing time-series data
- The original Kalman filter used to model measurement error

$$
\begin{aligned}
x_t &= y_t + \epsilon_t \quad \text{where} \quad \epsilon_t \sim N(0, \sigma_\epsilon^2) \quad \text{i.i.d.} \\
y_t &= y_{t-1} + \mu_t \quad \text{where} \quad \mu_t \sim N(0, \sigma_\mu^2) \quad \text{i.i.d.}
\end{aligned}
$$

- y_t is the hidden variable we are trying to measure
- x_t is the observed variable which contains noise
- Aim to decompose the observation in to change in the hidden variable and measurement error

Bayesian Modelling

- Bayes Theorem

$$P(A \mid B) = \frac{P(B \mid A)P(A)}{P(B)}$$

- Bayesian modelling

$$P(\text{model}|\text{data}) \propto P(\text{data}|\text{model})P(\text{model})$$

posterior distribution

Model

prior distribution

- Sample from the posterior distribution using Monte Carlo Markov Chain methods (MCMC)

Epidemiological Model

- Aim - to estimate the reproduction variable with time

- Hidden-variables
  - R_t - the reproduction number

$$R_t = R_{t-1} + \epsilon_t$$

$$\epsilon_t \sim \text{Normal}(0, \sigma_\epsilon)$$

  - I_t - the actual number of infections, model with renewal equation

$$I_t = R_t \sum_\tau I_{t-\tau} G_\tau$$

$$= R_t \sum_{\tau=t_1}^{t_2} \frac{I_{t-\tau}}{t_2 - t_1 + 1}$$

Epidemiological Model

- Observed-variables
  - C_t - the observed cases

$$C_t \sim \text{Poisson}(I_t)$$

- Priors
  - R_0 - the initial reproduction number

$$R_0 \sim \text{Uniform}(R_{0,\text{min}}, R_{0,\text{max}})$$

  - σ_ε - the size of daily change in R_t

$$\sigma_\epsilon \sim \text{Uniform}(0, \sigma_{\epsilon,\text{max}})$$

  - I_0 - the initial number infections

$$I_0 \sim \text{Uniform}(I_{0,\text{min}}, I_{0,\text{max}})$$

STAN 1.01

- Stan code is split in to blocks which are then interpreted by the Stan compiler to derive a model which can be sampled from. They key ones are:

  - data - list all variables which are passed to the model (e.g. t_{max}, t_1, $R_{0,min}$)

```
data {
 // In the data block all data and constants must be listed with data types
 // Examples

 // A real variable called r1
 real r1;

 // A integer variable called n1
 int<lower=0> n1;

 // An array called my_array of n1 intergers
 int my_array[n1];
}
```

STAN 1.01

- parameters - all parameters directly sampled by the model (e.g. R_0, ε_t)

```
parameters {
  // All parameters in the model which are sampled directly are listed here
  // Examples:

  // A real vairable called p1 which is between 0 and r1 in value
  real<lower=0,upper=r1> p1;

  // An array of reals called p_array of n1 values between 0 and r1
  real<lower=0,upper=r1> p_array[n1];
}
```

STAN 1.01

- transformed parameters - quantities derived from the directly sampled parameters (e.g. R_t, I_t)

```
transformed parameters {
  // Derived variables from the sampled parametrs
  // Examples - a simple randomw walk

  // An array of reals called walk and length n1
  real walk[n1];

  walk[1] = p1;
  for( idx in 2:n1 )
     walk[idx] = walk[idx-1] + p_array[idx];
}
```

STAN 1.01

- model - builds the likelihood of the model given the data (e.g. likelihood of C_t given I_t)

```
model {
  // Calculate the posterior liklihood of the model given the data

  // p_array is normall distributed with mean 0 and s.d. r1
  p_array ~ normal( 0, r1 );

  // observed is poisson distributed
  my_array ~ poisson( walk );
}
```

Initial Task

- Code the model in Stan and fit to data in R

  - download project from GitHub: **`BDI-pathogens/stan_epi_tutorial`**

  - install R packages: - **`hds_cdt/install.R`**

  - template Stan script: - **`hds_cdt/simple_model.stan`**

  - template R: - **`hds_cdt/simple_model.R`**

- Pointers
  - put ranges on all parameters (i.e. the priors)
  - need to have infections for t_2 days prior to the first observed point, set all to be I_0

Investigations

- Explore fitting the model to investigate

  - try the different simulated data files, what is the difference, do you need to change priors?

    - `hds_cdt/data/task1a.Rdata`
    - `hds_cdt/data/task1b.Rdata`
    - `hds_cdt/data/task1c.Rdata`

  - effect of the generation time on estimates of R(t)

  - censored data - how does the estimate of R(t) change depend upon the length of the data window

Working code is **`hds_cdt/task1.R`**, please try first, or just use it for hints