INTRODUCTION TO STAN

BAYESIAN STATISTICS FOR ECOLOGISTS

IGB 18. TO 26. NOVEMBER 2019

WHAT IS STAN?

- General purpose modelling and scientific programming language
- Imperative (like R, unlike BUGS) and probabilistic language
- Fully Bayesian inference using Hamiltonian Monte Carlo
 - Your model is compiled to a C++ program that is executed from within R
 - HMC converges faster and is more stable than Gibbs in many cases
 - Lower autocorrelation than Gibbs

WHY STAN?

- In many cases faster than Gibbs, even Gibbs in C++
- Much of the tuning, warmup, care and feeding is done automatically
- Model specification is very concise

VARIABLES

- Stan is strongly typed: all variables must be declared and used in their proper scope
 - real, int for single numbers
 - vector[i], matrix[i, j] for real-valued arrays to be used with linear algebra
 - arrays (for all other sequences)
- Stan supports variable constraints

```
real my_real;
int my_int;

vector [10] my_vector;
matrix [10, 20] my_matrix;

int my_int_array [10];
vector [10] array_of_vectors [5, 2];

real <lower=0, upper=1> constrained_real;
```

STRUCTURE OF A PROGRAM

- A Stan program consists of a series of optional **blocks** delimited by curly braces
- Order matters, and variables are visible from the top down (model can see variables declared in data, but not vice-versa!)
- Variable declarations must come first in each block
- data: only declares the data variables that will be passed to Stan
- parameters: only declares parameters that will be used in the model
- > model: defines the log probability of the model

```
functions {}

data {}

transformed data {}

parameters {}

transformed parameters {}

model {}

generated quantities {}
```

- Often helpful to work backwards, start with the model definition
- died is a data vector giving the number of trees that died
- ntrees is the vector of the total number of trees
- theta is the parameter to estimate
- To do:
 - Fill in the missing blocks
 - Add prior
 - ▶ Run the model in R

- Often helpful to work backwards, start with the model definition
- died is a data vector giving the number of trees that died
- ntrees is the vector of the total number of trees
- theta is the parameter to estimate
- To do:
 - Fill in the missing blocks
 - Add prior
 - Run the model in R

```
data {
    // fill in data declarations
}

parameters {
    // fill in parameters
}

model {
    died ~ binomial(ntrees, theta);
}
```

- It is helpful to include the number of data points as a data variable
- All data and parameters must be declared
- Data constraints serve as error checking, in this case checking for negative numbers
- Parameter constraints prevent the sampler from selecting impossible values
- All unobserved objects (e.g., theta) should appear on the left side of a statement:
 either = or ~
- Check carefully! It's not an error to forget this step

- It is helpful to include the number of data points as a data variable
- All data and parameters must be declared
- Data constraints serve as error checking, in this case checking for negative numbers
- Parameter constraints prevent the sampler from selecting impossible values
- All unobserved objects (e.g., theta) should appear on the left side of a statement:
 either = or ~
- Check carefully! It's not an error to forget this step

```
data {
    int<lower=0> n; // number of data points
    int<lower=0> died[n];
    int<lower=0> ntrees[n];
}
parameters {
    real<lower=0, upper=1> theta;
}
model {
    died ~ binomial(ntrees, theta);
    theta ~ ?????
}
```

- Running the model is simply a matter of pointing the stan() function at the .stan file you created
- Examine the summary of the model. Is the parameter estimate different from the MLE?
- You can use bayesplot to produce some useful diagnostics

- Running the model is simply a matter of pointing the stan() function at the .stan file you created
- Examine the summary of the model. Is the parameter estimate different from the MLE?
- You can use bayesplot to produce some useful diagnostics