

Stan Tutorial

STA 540 Case Study

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Outline for Section 1

- 1. Introduction to Stan
 - **1.1** Getting started
 - 1.2 Structure of a Stan program
 - 1.3 Integration with R
- Basic modeling
 - 2.1 Ordinary Linear Regression
 - 2.2 Generalized Linear Regression
 - 2.3 Hierarchical Models
- Advanced topics
 - 3.1 Log probability lp
 - 3.2 Latent variable models
 - 3.3 Auxiliary sampling

Loading Stan in R

```
library(rstan)
## Loading required package: StanHeaders
## rstan (Version 2.21.1, GitRev: 2e1f913d3ca3)
## For execution on a local, multicore CPU with
excess RAM we recommend calling
## options(mc.cores = parallel::detectCores()).
## To avoid recompilation of unchanged Stan programs,
we recommend calling
## rstan options(auto write = TRUE)
##
## Attaching package: 'rstan'
## The following object is masked from
'package:tidvr':
```

Stan program structure

A stan program involves the following blocks.

- functions
- data
- transformed data
- parameters
- transformed parameters
- model
- generated quantities

The blocks should be arranged in this given order.

Program block: data

The data block is for the declaration of variables that are read in as data.

Note that the data is only read in once.

Grammar:

```
[basic type]<range?> identifier[size];
```

```
data {
  int<lower=0> J;
  real y[J];
  real<lower=0> sigma[J];
}
```

Program block: parameters

The variables declared in the parameters program block correspond directly to the variables being sampled by Stan. The parameters defined in this block must be continuous. Grammar:

```
[basic type]<range?> identifier[size];
```

```
parameters {
   real mu;
   real<lower=0> tau;
   real eta[J];
}
```

Program block: model

The model program block consists of optional variable declarations followed by statements. The variables in the model block are local variables and are not written as part of the output.

Grammar:

identifier ~ distribution(args);

```
model {
  eta ~ normal(0, 1);
  y ~ normal(theta, sigma);
}
```

Try it out in R

Stan code: 8schools.stan

```
data {
  int<lower=0> J;
  // number of schools
  real y[J];
  // estimated treatment
      effects
  real<lower=0> sigma[J];
  // s.e. of effect estimates
parameters {
  real mu;
  real<lower=0> tau;
```

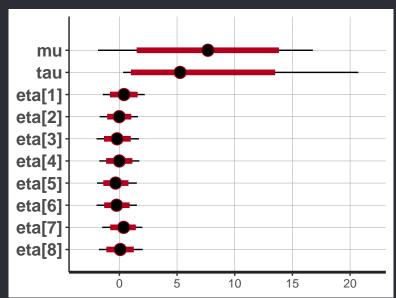
```
real eta[J];
transformed parameters {
  real theta[J];
  for (j in 1:J)
    theta[j] = mu + tau * eta[j
model {
 eta \sim normal(0, 1);
  y ~ normal(theta, sigma);
```

Try it out in R

R code:

```
set.seed(0)
schools dat <- list(</pre>
 J = 8,
  v = c(28, 8, -3, 7, -1, 1, 18, 12),
  sigma = c(15, 10, 16, 11, 9, 11, 10, 18)
fit <- stan(
  file = "8schools.stan", data = schools dat,
  iter = 1000, warmup = 100, chains = 4,
  [verbose = F, refresh = 0]
```

Try it out in R



Pre-compiling stan code

If the same model is to be fit on multiple datasets, it would be more efficient to pre-compile the stan model.

We can separate the compilation process from the sampling process.

• Compilation:

```
stan_m <- stan_model(file = ...)</pre>
```

Sampling:

```
fit <- sampling(stan_m, data = ...)</pre>
```

Pre-compiling stan code

If you are using RMarkdown, you can also add a stan chunk directly.

```
```{stan output.var = "model"}
 // some stan code
```
```

Behind the scenes, the RMarkdown chunk calls

```
model <- stan_model(model_code = the_code_text).</pre>
```

Therefore, you can do sampling in the next ordinary R chunk.

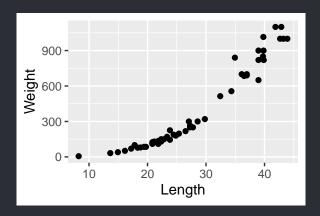
```
```{r}
 sampling(model, data = ...)
```
```

Outline for Section 2

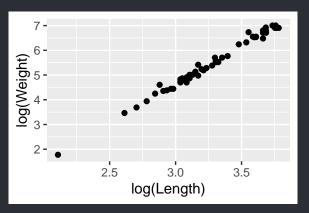
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The file Fish.csv contains the weight and body measurements of fish from seven species. Suppose we are interested in building a linear model to explain the association between weight and body measurements for perches.

For now, we only use one predictor: the average of three length measurements.



It looks like a log transform should be appropriate.



Thus, we use the following model.

$$\log(y_i) \sim \mathcal{N}(\alpha + \beta \log(x_i), \sigma^2).$$

Stan model:

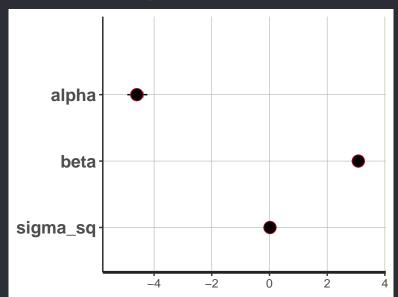
```
data {
  int<lower=0> N;
  real y[N];
  real x[N];
parameters {
  real alpha;
  real beta:
  real<lower=0> sigma sq;
```

```
model {
  alpha \sim normal(0, 1);
  beta \sim normal(0, 1);
  sigma sq \sim inv gamma(0.1,
       0.1);
  for (n in 1:N) {
    y[n] \sim normal(
      alpha + beta * x[n],
      sqrt(sigma sq)
```

More efficient:

```
data {
    int<lower=0> N;
    real y[N];
    real x[N];
    alpha
    beta sigma
parameters {
    real alpha;
    real lower=0> sigma_sq;
}
```

```
model {
   alpha ~ normal(0, 1);
   beta ~ normal(0, 1);
   sigma_sq ~ inv_gamma(0.1,
        0.1);
   y ~ normal(alpha + beta * x,
        sqrt(sigma_sq));
}
```



Now let's use all predictors

```
data {
  int<lower=0> N;
 int<lower=0> P;
  real y[N];
  matrix[N, P] X;
parameters {
  real alpha;
  real beta[P];
  real<lower=0> sigma_sq;
```

Generalized Linear Regression

 Advertisement.csv contains data of people's gender, age, estimated salary and whether they purchased the advertised product. The aim is to build a Bayesian model to predict the probability of purchase.

Generalized Linear Regression

- Advertisement.csv contains data of people's gender, age, estimated salary and whether they purchased the advertised product. The aim is to build a Bayesian model to predict the probability of purchase.
- awards.csv contains data of the number of awards some students achieved in college, with the type of program they are in (numbered 1, 2, 3) and their math scores. Considering only the math scores, build a Bayesian model for predicting the number of awards.

Hierarchical Models

Back to the Fish.csv data. This time, we would like to consider building a model on weight for all seven species, but only using the average body measurement as predictor.

- Species-specific intercepts
- Species-specific slopes

Data: Y (weight), X (measurement), G (species). Model:

$$Y_{ig} \sim \mathcal{N}(\alpha_g + x_{ig}\beta_g, \sigma^2),$$

where
$$\alpha_g \sim \mathcal{N}(0, \tau_\alpha^2)$$
, $\beta_g \sim \mathcal{N}(0, \tau_\beta^2)$.

Hierarchical Models

```
data {
  int<lower=0> N:
  real Y[N];
  real X[N];
  int<lower=1, upper=7> G[N];
parameters {
  real alpha[7];
  real beta[7];
  real<lower=0> sigma;
  real<lower=0> tau_alpha;
  real<lower=0> tau beta;
transformed parameters {
  vector[N] y hat;
```

```
for (i in 1:N) {
    y_hat[i] = alpha[G[i]] +
        beta[G[i]] * X[i];
model {
  sigma \sim inv gamma(0.1, 0.1);
  tau alpha \sim inv gamma(0.1,
      0.1);
  tau beta \sim inv gamma(0.1,
      0.1):
  alpha ~ normal(0, tau alpha);
  beta ~ normal(0, tau beta);
  y ~ normal(y hat, sigma);
```

Outline for Section 3

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- We've used (semi-)conjugate priors in order to sample from posterior distributions with ease.
- For Stan, there is no need to look for conjugacy.
- A posterior distribution is nothing other than its density function (recall that Stan only accepts continuous parameters), whose logarithm is often used instead in practice to avoid numerical issues.
- With this log posterior density function, Stan can sample from the posterior distribution using methods including HMC.

We have learned that

$$p(\theta \mid y) \propto p(\theta)p(y \mid \theta)$$

which is equivalent to

$$\log p(\theta \mid y) = \log p(\theta) + \log p(y \mid \theta),$$

up to an additive constant.

 Therefore, lp keeps updating itself with the sampling statements in the model block.

- Technically speaking, there is no real need to distinguish between statements for the prior distribution and for the conditional distribution.
- Both kinds of statements have the same effect of adding to lp the corresponding log probability.
- The sampling statement is just a short-hand notation for updating lp - no real sampling is done in this step.

• The sampling statement

```
alpha ~ N(0, 1);
```

is equivalent to directly updating lp by

```
target += normal_lpdf(alpha | 0, 1);
```

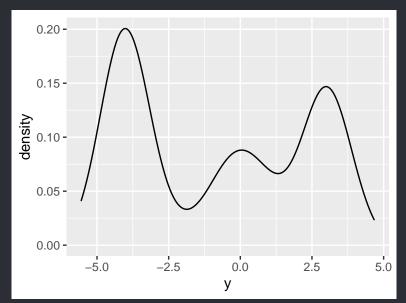
except that the sampling statement drops the normalizing constant.

Is it okay if one does not write any sampling statements on some parameters? If so, what prior is put on those parameters?

In this part, we use a simulated dataset where there are three groups of data points. Within group *j*, the outcome follows a normal distribution

$$Y_i \sim \mathcal{N}(\alpha_j, \sigma_j^2).$$

Unless in a hierarchical model, we do not observe the group each data point belongs to.



- Data: the outcome Y.
- Parameters: α_i , σ_i , and the group assignment g_i for data point i.
- Conditional distribution:

$$Y_i \mid \alpha_j, \sigma_j, g_i \sim \mathcal{N}(\alpha_{g_i}, \sigma_{g_i}^2).$$

• Is there a problem to convert it into Stan code?

- Data: the outcome Y.
- Parameters: α_i , σ_i , and the group assignment g_i for data point i.
- Conditional distribution:

$$Y_i \mid \alpha_j, \sigma_j, g_i \sim \mathcal{N}(\alpha_{g_i}, \sigma_{g_i}^2).$$

- Is there a problem to convert it into Stan code?
- Group assignment g_i is discrete!
- Solution: integrate (sum) out discrete parameters g_i.

- Suppose that $Pr(g_i = j) = \pi_i$.
- Then,

$$Y_i \mid \alpha_j, \sigma_j \sim \sum \pi_j \mathcal{N}(\alpha_j, \sigma_j^2).$$

- This is not a known distribution implemented in Stan, so we cannot use sampling statements for this conditional distribution.
- Instead, we have to update 1p manually.
- How to deal with summation under logarithm? log-sum-exp.

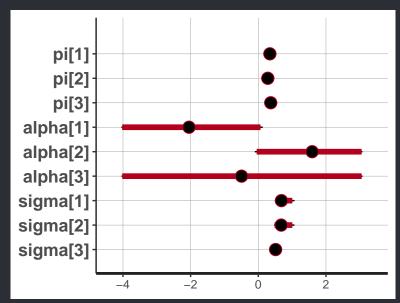
$$log-sum-exp(u, v) = log(exp(u) + exp(v)).$$

- $\pi = (\pi_1, \pi_2, \pi_3)$ is a parameter such that $\pi_j \in [0, 1], \sum \pi_j = 1$.
- This is called a simplex.

```
simplex[3] pi;
```

Updating lp:

```
vector[3] log_pi = log(pi);
for (i in 1:N) {
    vector[3] lps = log_pi;
    for (k in 1:3) {
        lps[k] += normal_lpdf(Y[i] | alpha[k], sigma[k]);
    }
    target += log_sum_exp(lps);
}
```



Auxiliary sampling

Sometimes, we might want to generate samples that are not parameters themselves.

- In the latent variable model, we might want to sample which group each point belongs to.
- For predicting the outcome given a new data point, we may want to sample the potential outcome given the posterior samples of parameters.
- To carry out posterior predictive checks, we need to sample data under the sampled parameters.

Auxiliary sampling

In Stan, this can be done within the generated quantities block. For example, if one is interested in sampling the group each data point belongs to, one can sample from the multinomial distribution with posterior samples of π .

```
generated quantities {
  int<lower=0> group[N, 3];
  for (i in 1:N) {
    group[i] = multinomial_rng(pi, 1);
  }
}
```