

From BRMS to Stan

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BRMS: Bayesian Regression and Multilevel modeling in Stan

Recap from last week

- BRMS extended formula syntax for multi-level regressions

`response ~ pterms + (gterms | group)`

- pterms* define *population-level* effects; same for all observations.
- gterms* define *group-level* effects; vary across *group* variable.
- The intercept term is 1 or 0 for no intercept; if unspecified, default is 1.

```
fit1 <- brm(Reaction ~ Days + (Days | Subject), data = sleepstudy)
```

equivalent to

```
fit1 <- brm(Reaction ~ 1 + Days + (1 + Days | Subject), data = sleepstudy)
```

Stan Program File (review)

A Stan program consists of one or more named program blocks, strictly ordered

```
functions {  
  // declare, define functions  
} data {  
  // declare input data  
} transformed data {  
  // transform inputs, define program data  
} parameters {  
  // declare (continuous) parameters  
} transformed parameters {  
  // define derived parameters  
} model {  
  // compute the log joint distribution  
} generated quantities {  
  // define quantities of interest  
}
```

Stan Program Blocks - Execution During Sampling (review)

- data, transformed data blocks - executed once on startup
- parameters -
 - on startup: initialize parameters
 - at every step of inference algorithm: validate constraints
- transformed parameters, model blocks - executed every *step* of the sampler
- generated quantities - executed every *iteration* of the sampler
- After every sampler iteration, program outputs current values of all variables in parameters, transformed parameters, and generated quantities blocks.

From BRMS to Stan

- BRMS: specify arguments to the `brm` function: formula, data, family, prior.
 - BRMS generates Stan model code.
 - BRMS code is not quite human-readable, but efficiently coded.
- Stan: specify a model using elements of the Stan probabilistic programming language.
 - `data` block defines `y`, as well as all unmodeled data inputs.
 - `parameters` block defines all distributional parameters.
 - `model` block specifies the likelihood and priors.
- *Goal: make Stan code equally efficient.*

Stepwise Model Development: Hello, World!

- A "Hello, World!" program is the name given to the first, simplest possible program written when learning a new programming language.
 - **Pro tip: always start with “Hello, World!”**
- End goal is a efficient and maintainable multi-level model
 $\text{Reaction} \sim \text{Days} + (\text{Days} | \text{Subject})$
- Initial goal is a simple linear model - complete pooling across subjects
 $\text{Reaction} \sim \text{Days}$
($\text{Reaction} \sim 1 + \text{Days}$ - by default, model includes global intercept.)
- Carry over BRMS efficiencies to Stan model

Stan Model sleep_simple.stan

```
data {  
  int<lower=0> N;    vector[N] day;    vector[N] y;    // reaction time  
}  
  
transformed data {  
  real day_mean = mean(day);  
  vector[N] day_centered = day - day_mean;  
}  
  
parameters {  
  real alpha;  real b_day;    // intercept, slope  
  real<lower=0> sigma; // residual standard deviation  
}  
  
model {  
  y ~ normal(alpha + day_centered * b_day, sigma);  
  alpha ~ normal(250, 50);    // informed prior for human reaction times in ms  
  b_day ~ normal(10, 10);    // weakly informed prior for per-day effect  
  sigma ~ normal(0, 10);    // very weakly informative prior  
}  
  
generated quantities {  
  real b_intercept = alpha - b_day * day_mean;  
  array[N] real y_rep = normal_rng(alpha + day_centered * b_day, sigma);  
}
```

Notebook - Stan, BRMS complete pooling model

```
sleep_data = list(  
  N = nrow(sleepstudy), J = length(unique(sleepstudy$Subject)),  
  subj = as.integer(sleepstudy$Subject), day = sleepstudy$Days,  
  y = as.double(sleepstudy$Reaction)  
)  
  
sleep_simple = cmdstan_model("stan/sleep_simple.stan")  
sleep_simple_stanfit = sleep_simple$sample(data = sleep_data)  
as.data.frame(sleep_simple_stanfit$summary(variables = c('b_intercept', 'b_day', 'sigma')))  
  
priors <- c(set_prior("normal(250, 50)", class = "Intercept"),  
  set_prior("normal(10, 10)", class = "b"),  
  set_prior("normal(0, 10)", class = "sigma"))  
  
sleep_simple_brmsfit = brm(Reaction ~ Days, data = sleepstudy, prior = priors)  
sleep_simple_brmsfit
```


Multilevel models

- Capture the structure in the data
- Sleep study: reaction time varies by subject
 - BRMS formula: `Reaction ~ 1 + Days + (1 + Days|Subject)`
- Expand Stan model - why not just:
 - Add per-subject parameter vector[J] `beta_subject`
 - Add hyperparameters `mu_subj, sigma_subj,`
`beta_subject ~ normal(mu_subj, sigma_subj)`
 - ???
- Nope, not that easy.

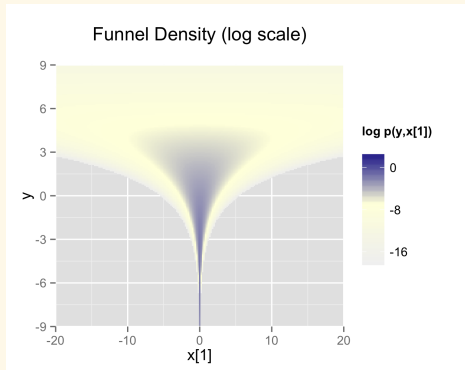
Multilevel models

- **Partial Pooling:** The hierarchical prior controls the pooling between levels:
 - Similar data across levels \rightarrow Low hierarchical variance \rightarrow Strong pooling
 - Dissimilar data across levels \rightarrow High hierarchical variance \rightarrow Weak pooling
- **Problem:** For low numbers of observations, MCMC sampler cannot resolve residual variance `sigma` and variance of hierarchical prior `sigma_subj`; many divergences
- **Solution:** Reparameterization, following code example in Stan User's Guide section [Hierarchical models and the non-centered parameterization](#)

Multilevel models and Neal's Funnel

- Neal's Funnel: extreme example of a challenging hierarchical model

$$p(y, x) = \text{normal}(y \mid 0, 3) \times \prod_{n=1}^9 \text{normal}(x_n \mid 0, \exp(y/2)).$$



Explore neck: need small stepsize on x -axis,
large stepsize on y -axis.

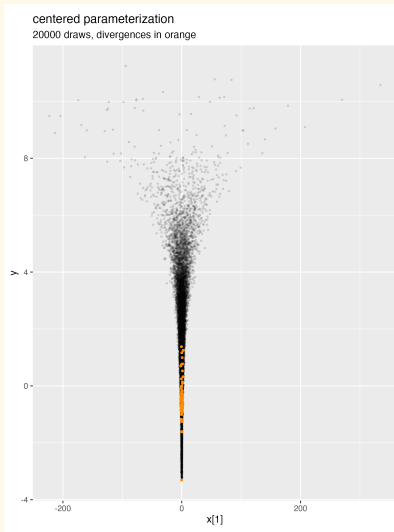
Explore mouth: need large stepsize on x -axis,
small stepsize on y -axis.

But stepsize is same for all axes; cannot
adequately sample either.

Funnel Example: Hierarchical Logistic Regression

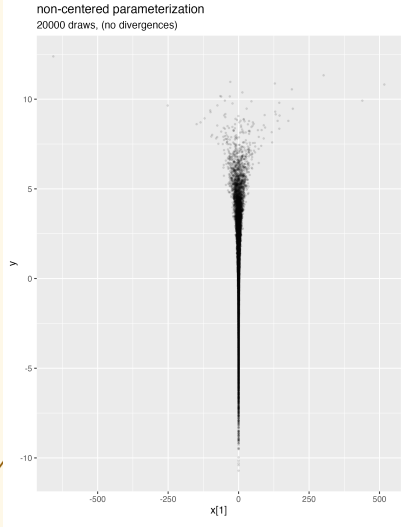
The natural parameterization is the “centered parameterization”

```
parameters {  
  real y;  
  vector[9] x;  
}  
model {  
  y ~ normal(0, 3);  
  x ~ normal(0, exp(y/2));  
}
```



Non-centered reparameterization

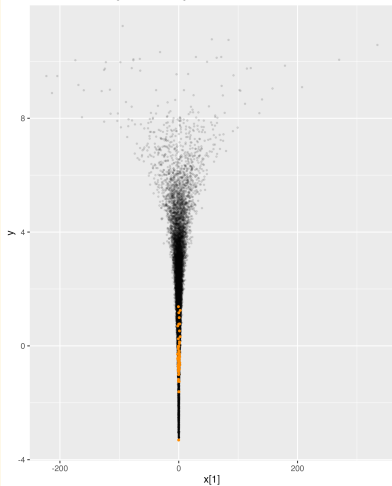
```
parameters {  
  real y_raw;  
  vector[9] x_raw;  
}  
  
transformed parameters {  
  real y;  
  vector[9] x;  
  
  y = 3.0 * y_raw;  
  x = exp(y/2) * x_raw;  
}  
  
model {  
  y_raw ~ std_normal(); // implies  $y \sim \text{normal}(0, 3)$   
  x_raw ~ std_normal(); // implies  $x \sim \text{normal}(0, \exp(y))$   
}
```



Compare Funnel Fits

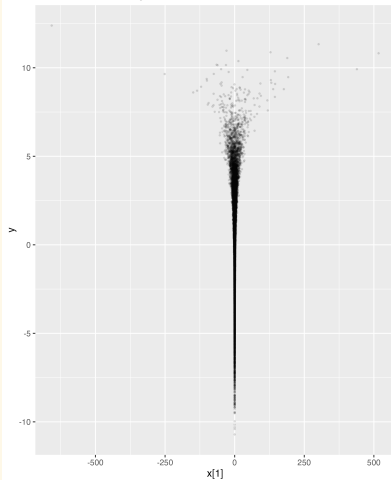
centered parameterization

20000 draws, divergences in orange



non-centered parameterization

20000 draws, (no divergences)



BRMS to Stan

- Recap: formula `Reaction ~ 1 + Days` becomes distribution statement:
`y ~ normal(alpha + day_centered * b_day, sigma);`
- Coding `Reaction ~ 1 + Days + (1 + Days | Subject)`
 - Global intercept and slope for Days
 - Subject-specific random intercepts and slopes
- Correlation between random effects: prior on subject effect is a multivariate normal with mean vector μ and covariance matrix Σ .
- Multivariate reparameterization

Multi-variate reparameterization

```
parameters {  
  vector[K] mu;  
  cov_matrix[K] Sigma;  
  vector[K] beta;  
  // ...  
}  
  
model {  
  beta ~ multi_normal(mu, Sigma);  
  // ...  
}
```


Efficient multi-variate reparameterization

- Following Stan User's Guide: [multivariate regression example](#)

```
parameters {  
  real b_intercept;  // global intercept  
  real b_day; // global day effect  
  real<lower=0> sigma;  
  
  // Subject-level effects - non-centered parameterization  
  matrix[2, J] z; // standardized random effects  
  cholesky_factor_corr[2] L_Omega; // Cholesky factor of correlation matrix  
  vector<lower=0>[2] tau; // scale of random effects  
}  
transformed parameters {  
  // random effects matrix [intercept, slope] by subject  
  matrix[2, J] r = diag_pre_multiply(tau, L_Omega) * z;  
}
```

Specifying the Likelihood

- $\text{Reaction} \sim 1 + \text{Day} + (1 + \text{Subject} \mid \text{Day})$

```
y ~ normal(r[1, subj]' + b_intercept + (r[2, subj]' + b_day) .* day,  
           sigma);
```

- Stan formula terms re-arranged for vectorization
 - `b_intercept` is population-level intercept
 - `r[1, subj]'` is vector of per-subject intercepts
 - `b_day` is population-level day effect
 - `r[2, subj]'` is vector of per-subject day effects

Recovering the Quantities of Interest

```
generated quantities {  
    // Reconstruct correlation matrix from Cholesky factor  
    matrix[2, 2] Omega;  
    Omega = multiply_lower_tri_self_transpose(L_Omega);  
  
    // Get random effect variances  
    vector[2] sd_r = tau;  
    real sd_intercept = sd_r[1];  
    real sd_day = sd_r[2];  
    real cor_intercept_day = Omega[1, 2];  
}
```

BRMS to Stan

- In BRMS, it's easy to specify varying intercept, varying slope effects.
- In Stan, it's not so easy, but it is well-documented.
- If you can code this, you can code most anything.

Notebook Demo

References

Stan User's Guide:

- Efficiency Tuning, [Hierarchical models and the non-centered parameterization](#)
- Efficiency Tuning, [Multivariate reparameterization](#)
- Regression, [Multivariate regression example](#)

Many Thanks!

Questions???