

# Chapter 5

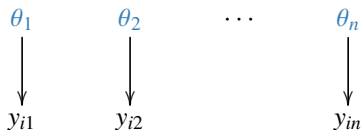
- 5.1 Lead-in to hierarchical models
- 5.2 Exchangeability (useful concept)
- 5.3 Bayesian analysis of hierarchical models (we use Stan/brms for computation)
- 5.4 Hierarchical normal model (we use Stan/brms for computation)
- 5.5 Example: parallel experiments in eight schools (useful discussion on benefits of hierarchical model)
- 5.6 Meta-analysis (can be skipped)
- 5.7 Weakly informative priors for hierarchical variance parameters

# Hierarchical model

- In simple model: posterior for the parameters
- In hierarchical model: posterior for the prior parameters

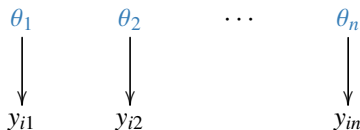
# Hierarchical model

- Example: CVD treatment effectiveness
  - in hospital  $j$  the survival probability is  $\theta_j$
  - observations  $y_{ij}$  tell whether patient  $i$  survived in hospital  $j$

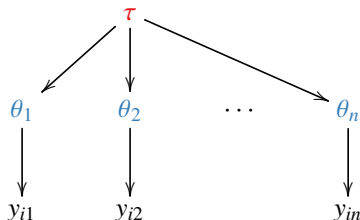


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- Example: CVD treatment effectiveness
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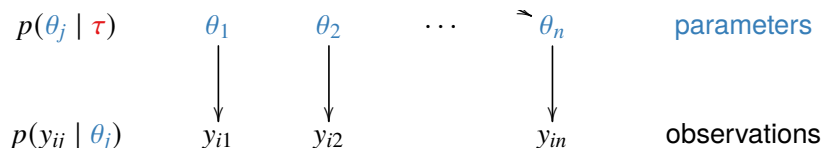
- sensible to assume that  $\theta_j$  are similar



- natural to think that  $\theta_j$  have common population distribution
- $\theta_j$  is not directly observed and the population distribution is unknown

# Hierarchical model: terms

Level 1: observations given parameters  $p(y_{ij} \mid \theta_j)$



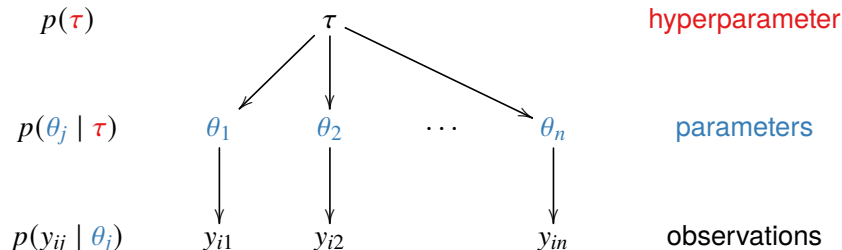
Joint posterior

$$\begin{aligned} p(\theta, \tau \mid y) &\propto p(y \mid \theta, \tau) p(\theta, \tau) \\ &\propto p(y \mid \theta) p(\theta \mid \tau) p(\tau) \end{aligned}$$

# Hierarchical model: terms

Level 1: observations given parameters  $p(y_{ij} \mid \theta_j)$

Level 2: parameters given hyperparameters  $p(\theta_j \mid \tau)$

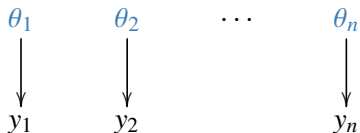


Joint posterior

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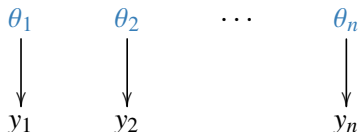
# Compare

- "Separate model" (model with separate/independent effects)

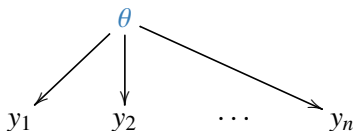


# Compare

- "Separate model" (model with separate/independent effects)



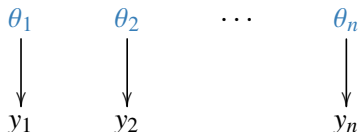
- "Joint model" (model with a common effect / pooled model)



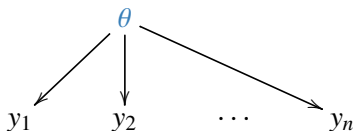


# Compare

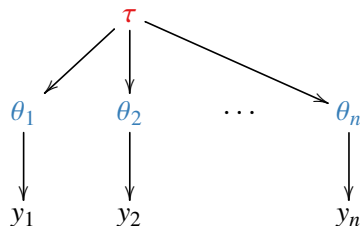
- "Separate model" (model with separate/independent effects)



- "Joint model" (model with a common effect / pooled model)



- Hierarchical model



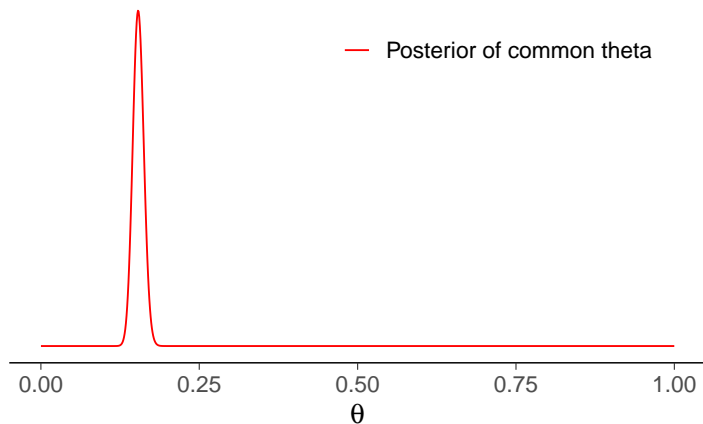
## Hierarchical binomial model: rats

- Medicine testing
- Type F344 female rats in control group given placebo
  - count how many get endometrial stromal polyps
  - familiar binomial model example



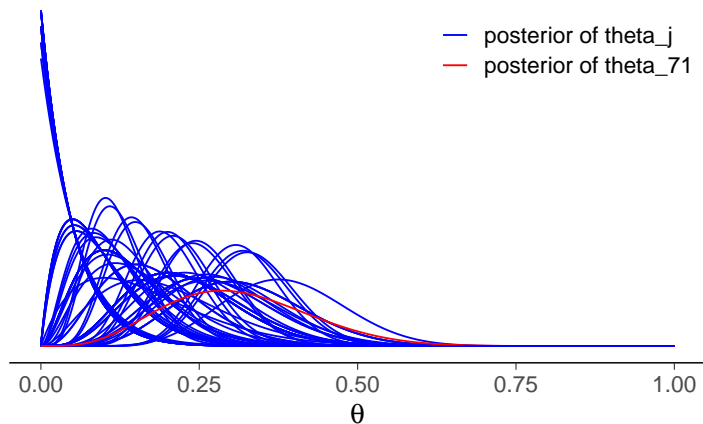
# Hierarchical binomial model: rats

Pooled model



# Hierarchical binomial model: rats

Separate model



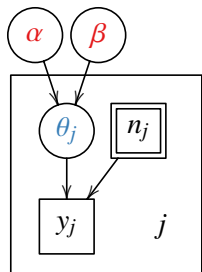
# Hierarchical binomial model: rats

- Hierarchical binomial model for rats  
prior parameters  $\alpha$  and  $\beta$  are unknown

$$\theta_j \mid \alpha, \beta \sim \text{Beta}(\theta_j \mid \alpha, \beta)$$

$$y_j \mid n_j, \theta_j \sim \text{Bin}(y_j \mid n_j, \theta_j)$$

- Joint posterior  $p(\theta_1, \dots, \theta_J, \alpha, \beta \mid y)$ 
  - multiple parameters

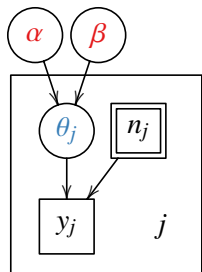


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- Joint posterior  $p(\theta_1, \dots, \theta_J, \alpha, \beta \mid y)$ 
  - multiple parameters
  - factorize  $\prod_{j=1}^J p(\theta_j \mid \alpha, \beta, y) p(\alpha, \beta \mid y)$

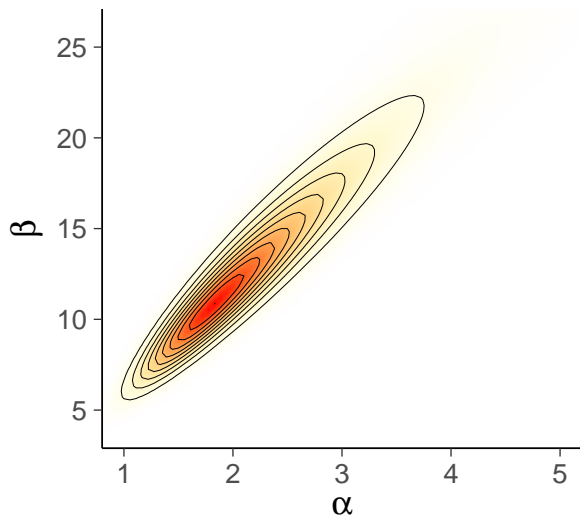
# Hierarchical binomial model: rats

- Population prior  $\text{Beta}(\theta_j \mid \alpha, \beta)$
- Hyperprior  $p(\alpha, \beta)$ ?
  - $\alpha, \beta$  both affect the location and scale
  - BDA3 has  $p(\alpha, \beta) \propto (\alpha + \beta)^{-5/2}$ 
    - diffuse prior for location and scale (BDA3 p. 110)
- demo5\_1



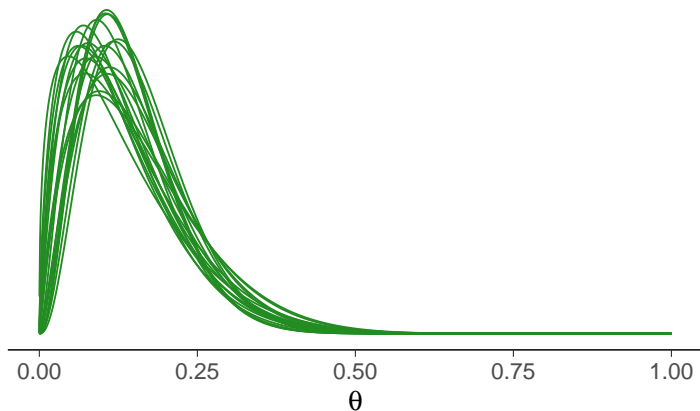
## Hierarchical binomial model: rats

The marginal of  $\alpha$  and  $\beta$



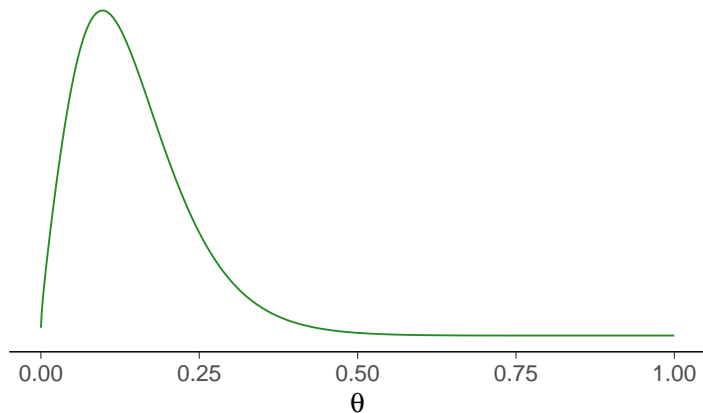
## Hierarchical binomial model: rats

Beta( $\alpha, \beta$ ) given posterior draws of  $\alpha$  and  $\beta$



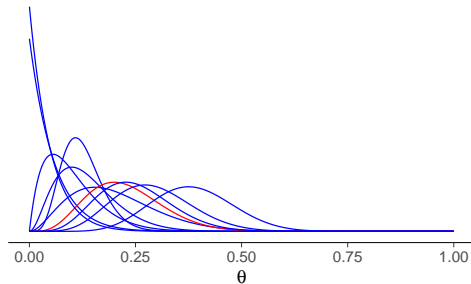
## Hierarchical binomial model: rats

Population distribution (prior) for  $\theta_j$



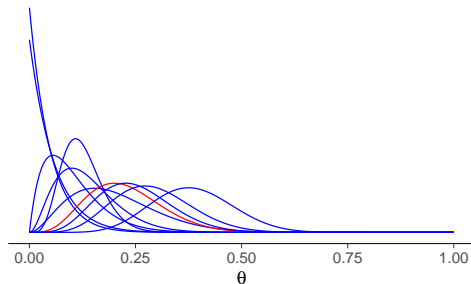
# Hierarchical binomial model: rats

Separate model

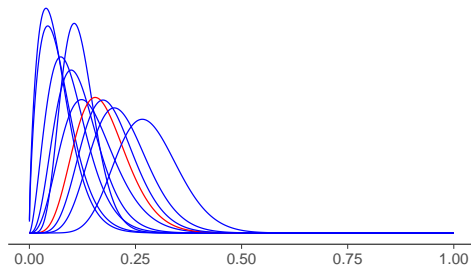


# Hierarchical binomial model: rats

Separate model

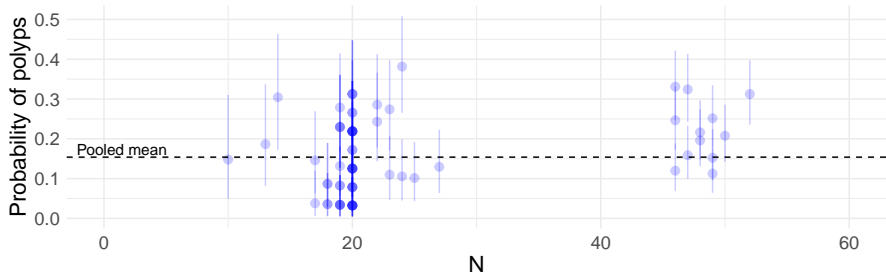


Hierarchical model

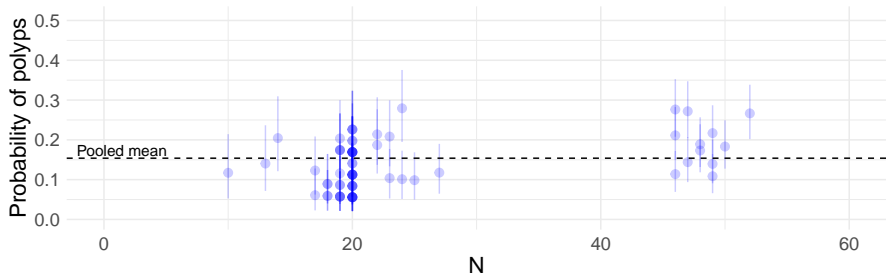


# Hierarchical model and group size: Rats

## Separate

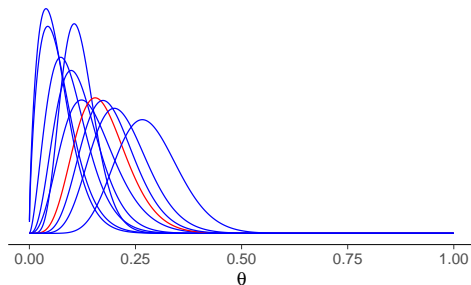


## Hierarchical

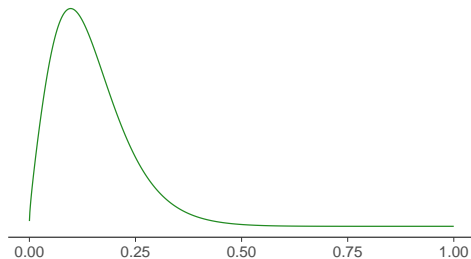


# Hierarchical binomial model: rats

Hierarchical model



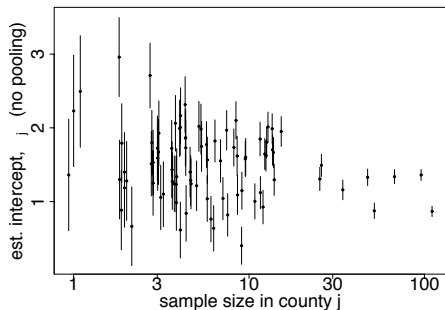
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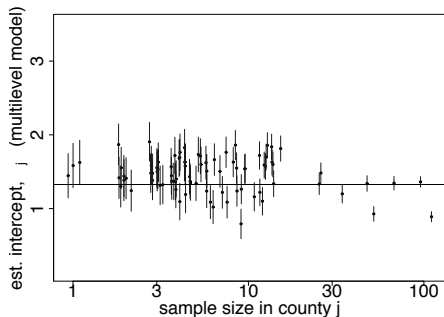
# Hierarchical model and group size: Radon

919 home radon levels in 85 counties in Minnesota:

Separate



Hierarchical





# Diet effect on chicken weights (at age 12 days)

- A typical treatment effect analysis
- Models
  - a separate model, in which each diet is modeled individually
  - a pooled model, in which all measurements are combined and there is no distinction between diets
  - a hierarchical model

## Stan vs brms

[illegible]

## Stan vs brms

```
model {  
  // Priors  
  for (diet in 1:N_diets) {  
    mean_diet[diet] ~ normal(0, 10);  
    sd_diet[diet] ~ exponential(1);  
  }  
  
  // Observation model / likelihood  
  for (obs in 1:N_observations) {  
    weight[obs] ~ normal(mean_diet[diet_idx[obs]],  
                          sd_diet[diet_idx[obs]]);  
  }  
  // Best practice would be to write the likelihood  
  // without the for loop as  
  // weight ~ normal(mean_diet[diet_idx],  
  //                  sd_diet[diet_idx]);  
}
```

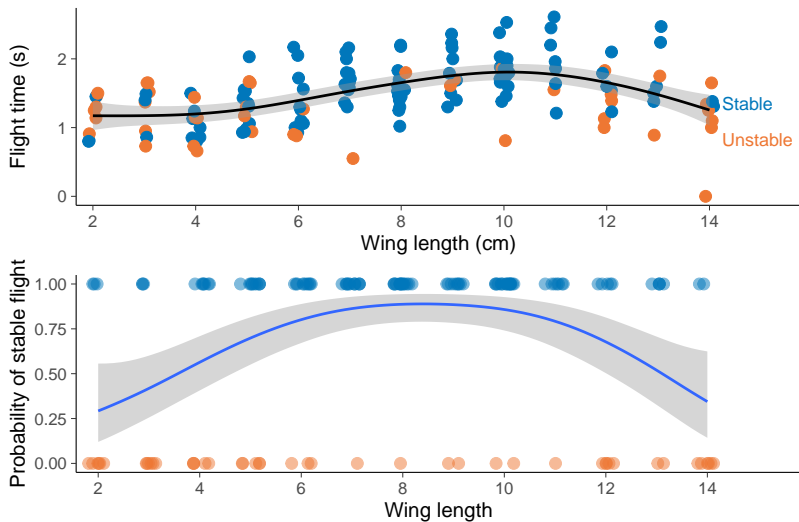
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  }  
}  
  
brm(weight ~ 1 + (1 | Diet),
```

## Stan vs brms

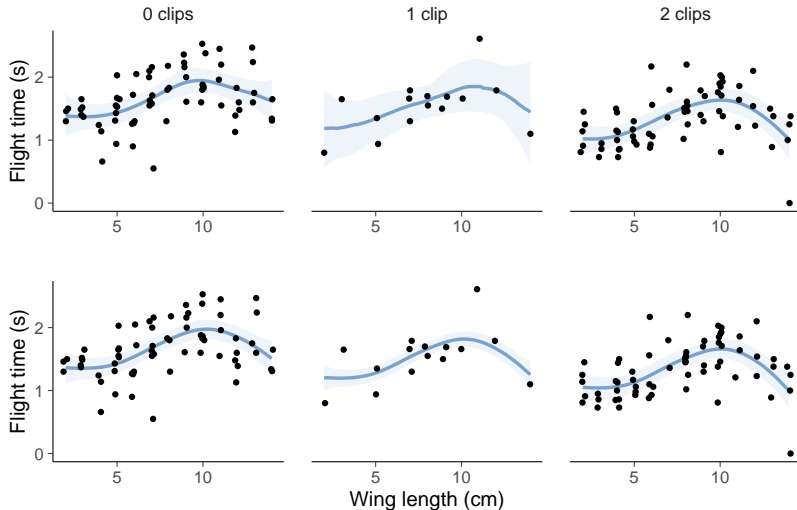
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  // Observation model / likelihood  
  for (obs in 1:N_observations) {  
    weight[obs] ~ normal(mean_diet[diet_idx[obs]],  
                          sd_diet[diet_idx[obs]]);  
  }  
}  
  
brm(weight ~ 1 + (1 | Diet), data=Chick12,  
     prior=c(prior(normal(0,1), class="Intercept"), # p(mu_0)  
             prior(normal(0,1), class="sigma"),     # p(sigma)  
             prior(normal(0,1), class="sd")),       # p(tau))
```

# Paper helicopters



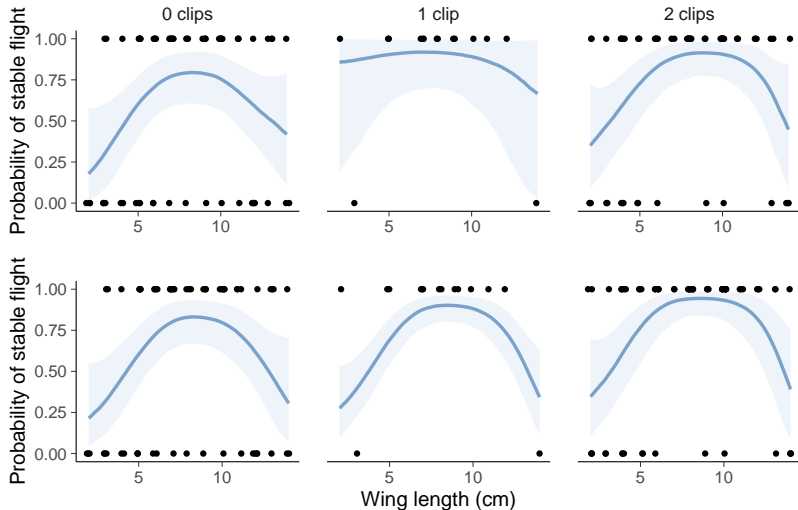
# Paper helicopters: flight time

Separate model vs. hierarchical model



# Paper helicopters: stability

Separate model vs. hierarchical model





## Paper helicopters: brms

Flight time

```
flight_time ~ s(wing_length) + s(wing_length, by = nclips)
```

## Paper helicopters: brms

Flight time

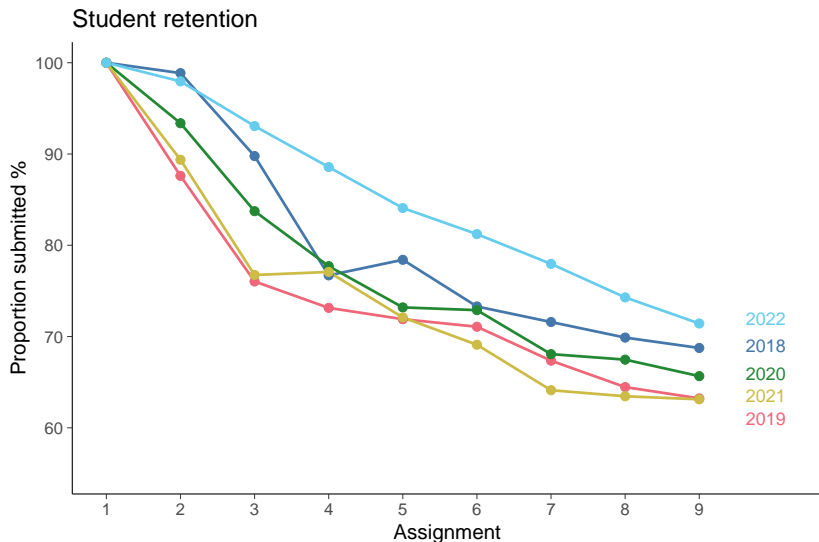
```
flight_time ~ s(wing_length) + s(wing_length, by = nclips)
```

Stability

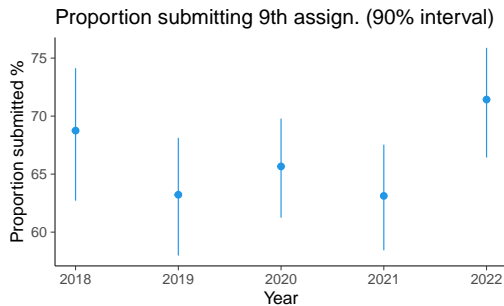
```
stable_flight ~ s(wing_length) + s(wing_length, by = nclips)  
family = bernoulli()
```

# Student retention

Was year 2022 better than earlier year?

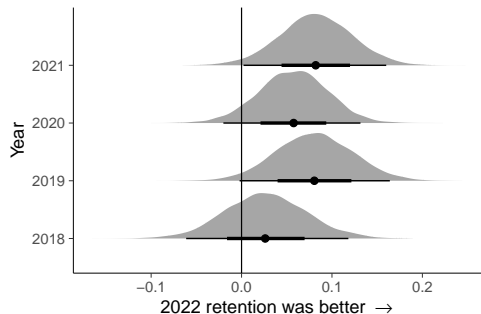
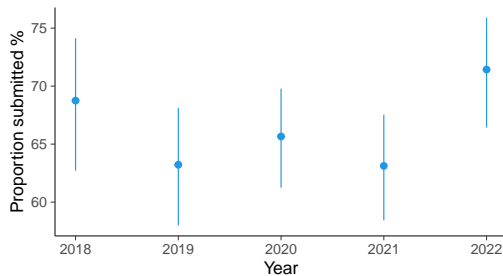


# Student retention separate model



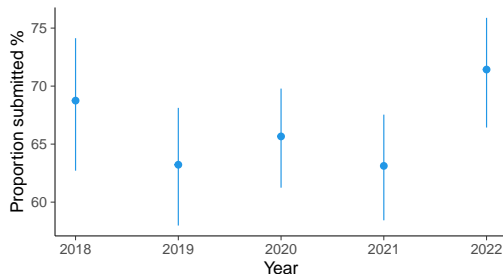
# Student retention separate model

Proportion submitting 9th assign. (90% interval)

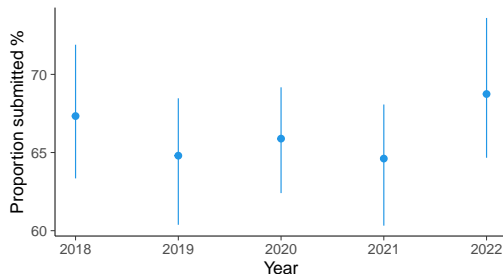


# Student retention separate vs hierarchical model

Proportion submitting 9th assign. (90% interval)

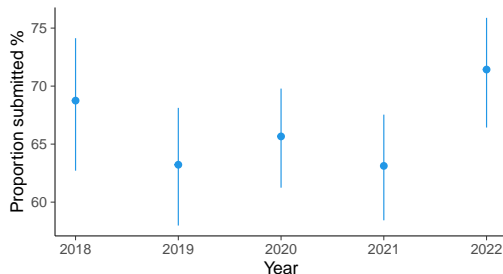


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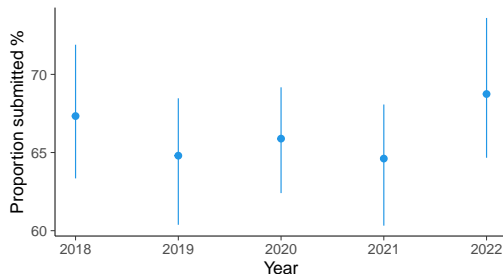


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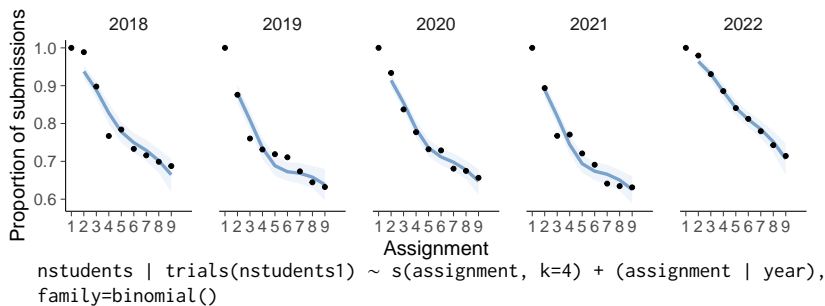


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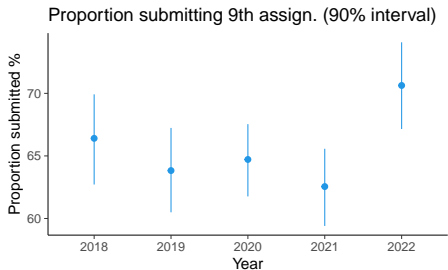
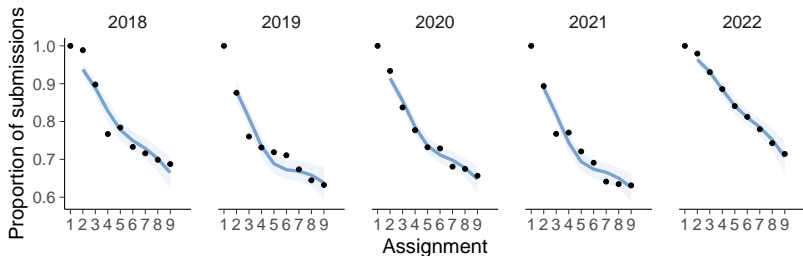
`nstudents | trials(nstudents1) ~ 1 + (1 | year), family=binomial()`

# Student retention latent spline model

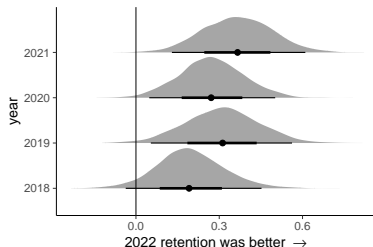
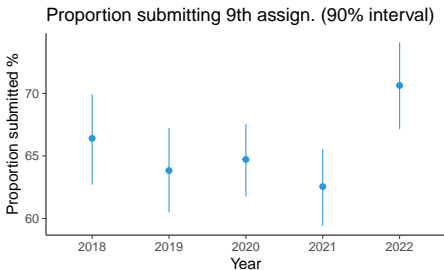
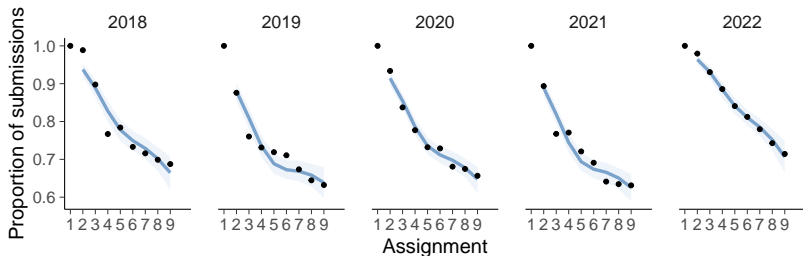




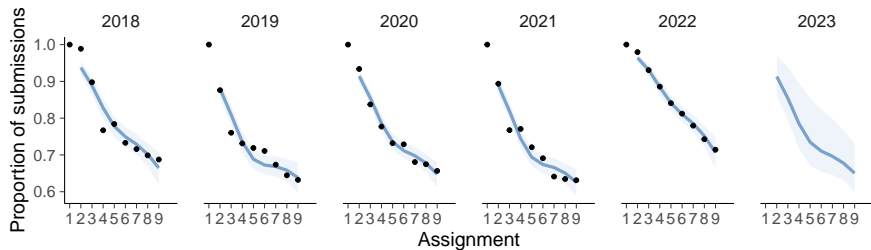
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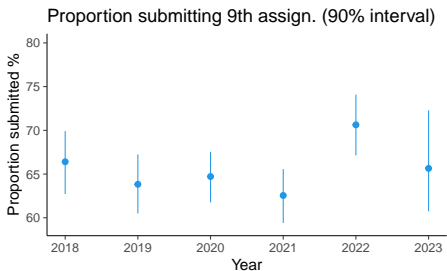
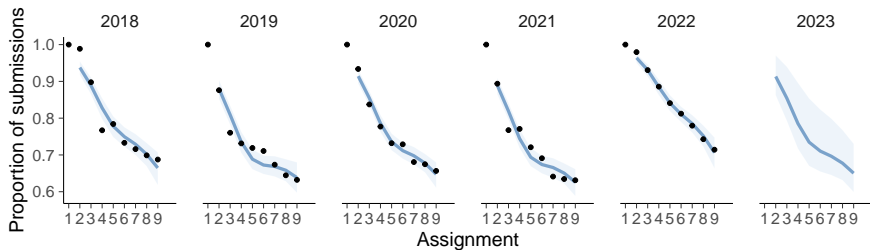
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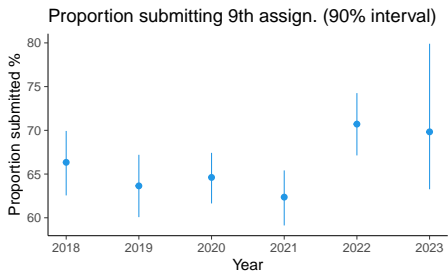
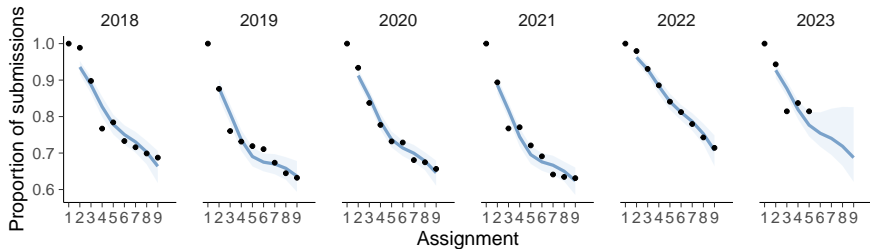
# Student retention latent spline model, year 2023?



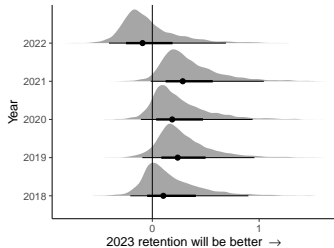
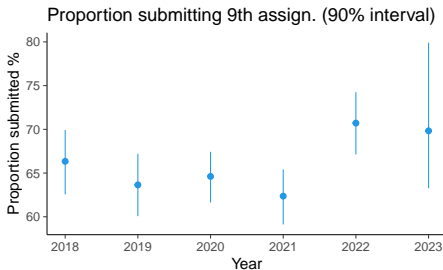
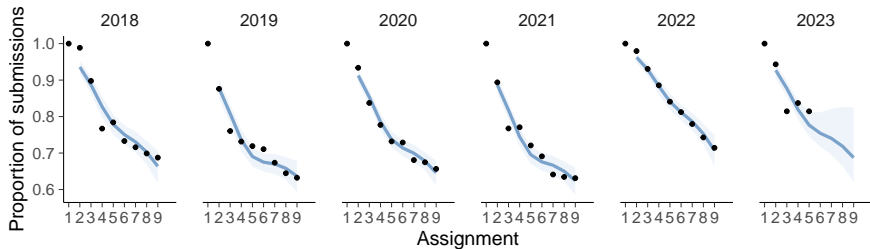
# Student retention latent spline model, year 2023?



# Student retention latent spline model, year 2023?



# Student retention latent spline model, year 2023?



## Centered vs non-centered parameterization

HMC divergences are more likely when using hierarchical models

## Centered vs non-centered parameterization

Hierarchical model code from the course demos

```
data {  
  int<lower=0> N; // number of observations  
  int<lower=0> K; // number of groups  
  array[N] int<lower=1, upper=K> x; // discrete group indicators  
  vector[N] y; // real valued observations  
}
```



## Centered vs non-centered parameterization

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  array[N] int<lower=1, upper=K> x; // discrete group indicators  
  vector[N] y; // real valued observations  
}  
  
parameters {  
  real mu0; // prior mean  
  real<lower=0> sigma0; // prior std constrained to be positive  
  vector[K] mu; // group means  
  real<lower=0> sigma; // common std constrained to be positive  
}
```

# Centered parameterization

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  real mu0; // prior mean  
  real<lower=0> sigma0; // prior std constrained to be positive  
  vector[K] mu; // group means  
  real<lower=0> sigma; // common std constrained to be positive  
}  
  
model {  
  mu0 ~ normal(10, 10); // weakly informative prior  
  sigma0 ~ normal(0, 10); // weakly informative prior  
  mu ~ normal(mu0, sigma0); // population prior with unknown param  
  sigma ~ lognormal(0, .5); // weakly informative prior  
  y ~ normal(mu[x], sigma); // observation model / likelihood  
}
```

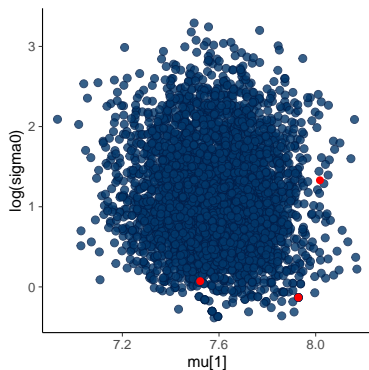
## Centered parameterization

First data with many observations per group: 3 summer months with each having 71 observations.

# Centered parameterization

First data with many observations per group: 3 summer months with each having 71 observations.

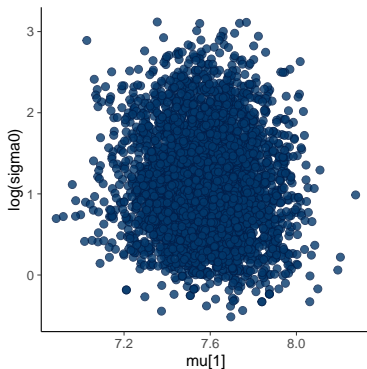
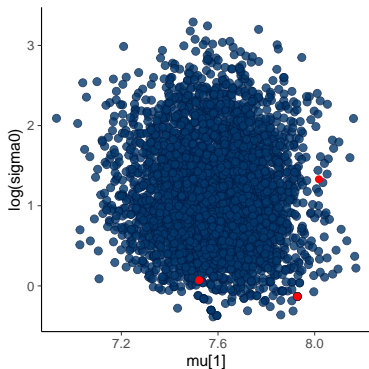
A few divergences that are not clustered.



## Centered parameterization

First data with many observations per group: 3 summer months with each having 71 observations.

And decreasing step size a little helps.



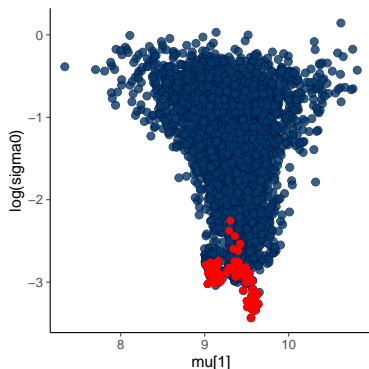
## Centered parameterization

Second data with a few observations per group: 71 years with each having 3 observations.

# Centered parameterization

Second data with a few observations per group: 71 years with each having 3 observations.

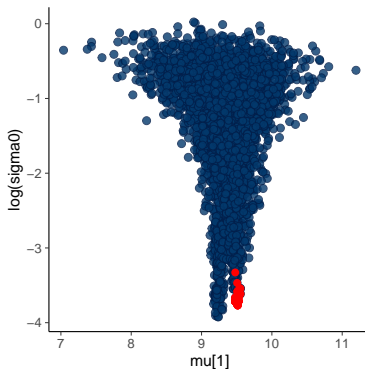
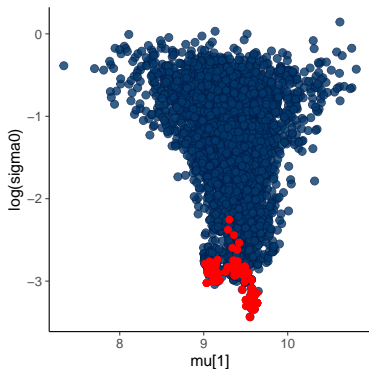
Many divergences that are clustered.



## Centered parameterization

Second data with a few observations per group: 71 years with each having 3 observations.

And decreasing step size doesn't remove the problem.





# Non-centered parameterization

## Transformation

```
parameters {  
  real mu0; // prior mean  
  real<lower=0> sigma0; // prior std constrained to be positive  
  vector[K] z; // latent variable  
  real<lower=0> sigma; // common std constrained to be positive  
}  
  
transformed parameters {  
  vector[K] mu = mu0 + sigma0 * z; // group means  
}  
  
model {  
  mu0 ~ normal(10, 10); // weakly informative prior  
  sigma0 ~ normal(0, 10); // weakly informative prior  
  z ~ normal(0, 1); // unit normal  
  sigma ~ lognormal(0, .5); // weakly informative prior  
  y ~ normal(mu[x], sigma); // observation model / likelihood  
}
```

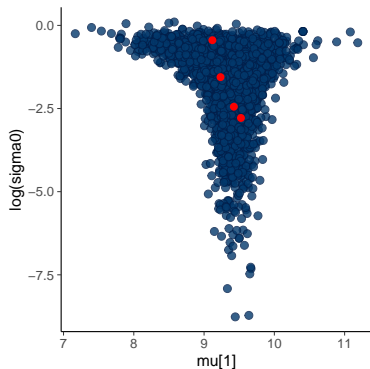
## Non-centered parameterization

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# Non-centered parameterization

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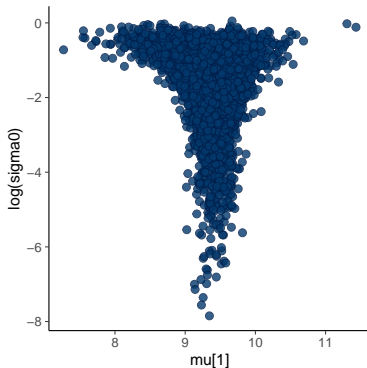
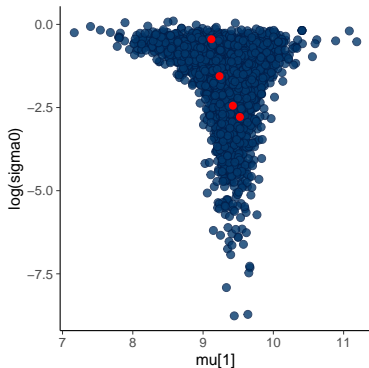
A few divergences that are not clustered.



## Non-centered parameterization

Second data with a few observations per group: 71 years with each having 3 observations.

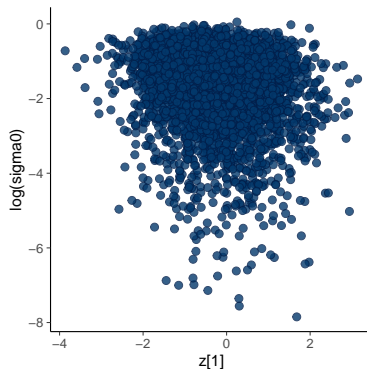
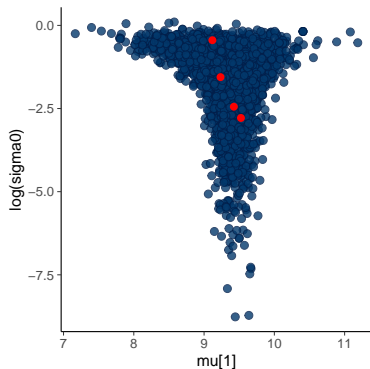
And decreasing step size a little helps.



# Non-centered parameterization

Second data with a few observations per group: 71 years with each having 3 observations.

Because we're actually sampling  $z$  and not  $\mu$



# Non-centered parameterization

No free lunch

- non-centered parameterization is good when likelihood is weak
- non-centered parameterization is bad when likelihood is strong

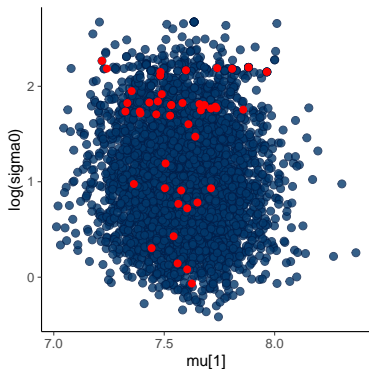
## Non-centered parameterization

First data with many observations per group: 3 summer months with each having 71 observations.

## Non-centered parameterization

First data with many observations per group: 3 summer months with each having 71 observations.

Many divergences that are not clustered.

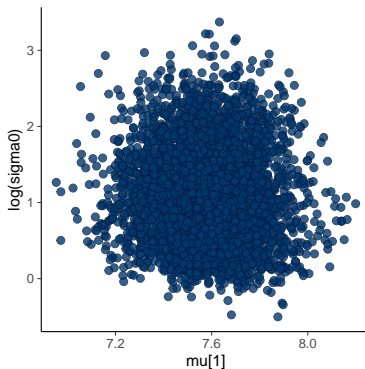
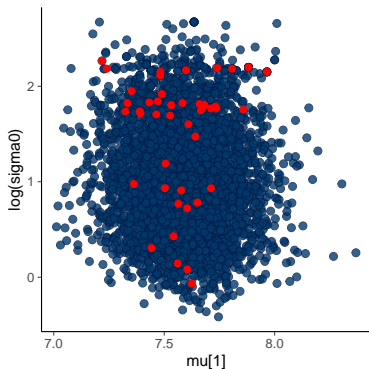




# Non-centered parameterization

First data with many observations per group: 3 summer months with each having 71 observations.

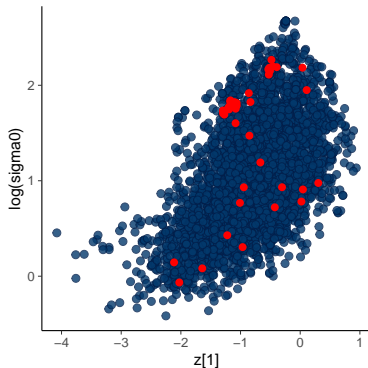
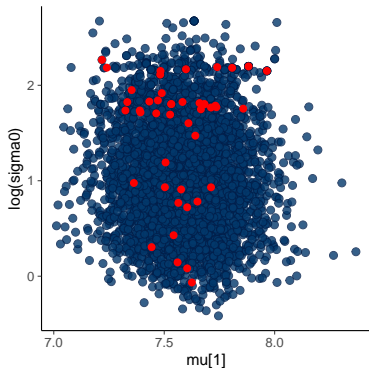
But decreasing step size a lot helps.



# Non-centered parameterization

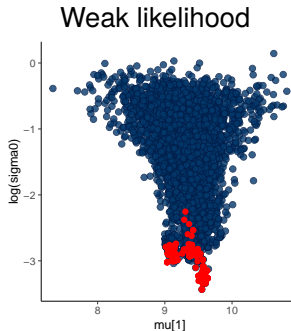
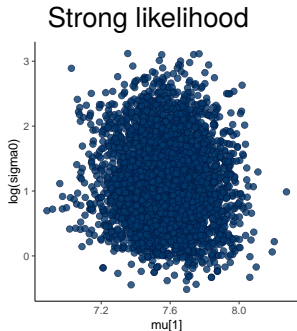
First data with many observations per group: 3 summer months with each having 71 observations.

Now the posterior for  $z$  is problematic.

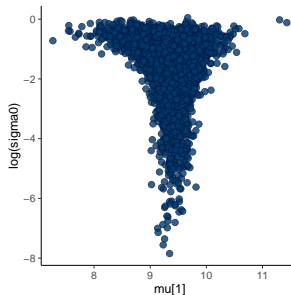
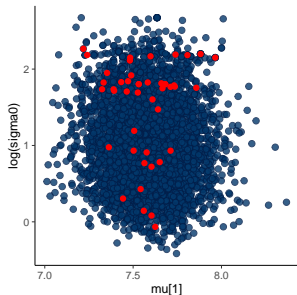


# Centered vs. non-centered parameterization

Centered param.



Non-centered param.



## brms and rstanarm

- brms and rstanarm use non-centered parameterization
  - as hierarchical models and Bayesian inference is most useful when likelihood is weak
- There can be need for both centered and non-centered parameterization in the same model
  - automation not easy, but research goes on

# Exchangeability

- Justifies why we can use
  - a joint model for data
  - a joint prior for a set of parameters
- Less strict than independence

# Exchangeability

- *Exchangeability*: Parameters  $\theta_1, \dots, \theta_J$  (or observations  $y_1, \dots, y_J$ ) are exchangeable if the joint distribution  $p$  is invariant to the permutation of indices  $(1, \dots, J)$
- e.g.

$$p(\theta_1, \theta_2, \theta_3) = p(\theta_2, \theta_3, \theta_1)$$

- Exchangeability implies symmetry: If there is no information which can be used *a priori* to separate  $\theta_j$  from each other, we can assume exchangeability. ("Ignorance implies exchangeability")

# Exchangeability

- Exchangeability does not mean that the results of the experiments could not be different
  - e.g. if we know that the experiments have been in two different laboratories, and we know that the other laboratory has better conditions for the rats, but we do not know which experiments have been made in which laboratory
  - a priori experiments are exchangeable
  - model could have unknown parameter for the laboratory with a conditional prior for rats assumed to come from the same place (clustering model)

# Exchangeability and additional information

- Example: bioassay
  - $y_i$  number of dead animals are not exchangeable alone



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- Example: bioassay
  - $y_i$  number of dead animals are not exchangeable alone
  - $x_i$  dose is additional information

# Exchangeability and additional information

- Example: bioassay
  - $y_i$  number of dead animals are not exchangeable alone
  - $x_i$  dose is additional information
  - $(x_i, y_i)$  exchangeable and logistic regression was used

$$p(\alpha, \beta \mid y, n, x) \propto \prod_{i=1}^n p(y_i \mid \alpha, \beta, n_i, x_i) p(\alpha, \beta)$$

# Hierarchical exchangeability

- Example: hierarchical rats example
  - all rats not exchangeable

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# Hierarchical exchangeability

- Example: hierarchical rats example
  - all rats not exchangeable
  - in a single laboratory rats exchangeable
  - laboratories exchangeable
  - → hierarchical model

## Partial or conditional exchangeability

- Conditional exchangeability
  - if  $y_i$  is connected to an additional information  $x_i$ , so that  $y_i$  are not exchangeable, but  $(y_i, x_i)$  exchangeable use joint model or conditional model  $(y_i \mid x_i)$ .

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- Conditional exchangeability
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- Partial exchangeability
  - if the observations can be grouped (a priori), then use hierarchical model



# Exchangeability

- The simplest form of the exchangeability (but not the only one) for the parameters  $\theta$  conditional independence

$$p(x_1, \dots, x_J \mid \theta) = \prod_{j=1}^J p(x_j \mid \theta)$$

## Exchangeability - Counter example

- A six sided die with probabilities  $\theta_1, \dots, \theta_6$ 
  - without additional knowledge  $\theta_1, \dots, \theta_6$  exchangeable
  - due to the constraint  $\sum_{j=1}^6 \theta_j$ , parameters are not independent and thus joint distribution can not be presented as iid

## Exchangeability

- See more examples in the BDA3 notes - Exchangeability vs. independence