Bayesian data analysis 3

MODIFIED BAYES' THEOREM:

$$P(H|X) = P(H) \times \left(1 + P(C) \times \left(\frac{P(X|H)}{P(X)} - 1\right)\right)$$

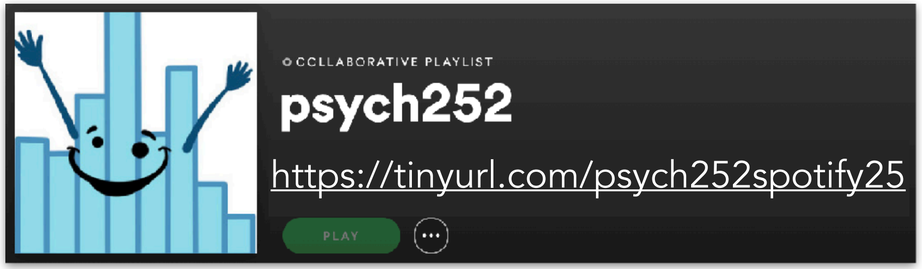
H: HYPOTHESIS

X: OBSERVATION

P(H): PRIOR PROBABILITY THAT H IS TRUE

P(X): PRIOR PROBABILITY OF OBSERVING X

P(C): PROBABILITY THAT YOU'RE USING BAYESIAN STATISTICS CORRECTLY



03/07/2025

Logistics

Homework 7 (the last one, yay)

submission is optional

My name goes here

The names of the people I have worked w

2022-03-03 22:20:30

1 Instructions

This homework is due by **Thursday, March 10th, 8:00pm**.

As per usual, please upload your rendered pdf on Canvas.

Note:

- Some code chunks contain some skeleton code. The code chunk opt
so that knitting the RMarkdown document doesn't throw any erro
`eval=T` when you knit your homework, so that your calculations
- Make sure to show the results of your calculations in the knitted pd
function at the end of a code chunk.
- Some questions ask for a short written response as indicated by t

Good luck with the homework! If you have any questions, make sure t
Thursday and/or post your questions on EdStem.

1.1 Load data

For the logistic regression question, we will use a data set which has inf
transplant patients.

```
data(heart_transplant, package = "openintro")
df.heart = heart_transplant %>%
  mutate(survived = ifelse(survived == "dead", 0, 1))
```

Here is a description of the data set:

> The Stanford University Heart Transplant Study was conducted
> perimental heart transplant program increased lifespan. Each pat
> designated officially a heart transplant candidate, meaning that
> would most likely benefit from a new heart. Then the actual hear
> few weeks to several months depending on the availability of a don
> this waiting period show improvement and get deselected as a hear
> the purposes of this experiment those patients were kept in the da

1.2 Part 1: Logistic regression (3 points)

Question 1.1: (1 point)

Fit a logistic regression where you predict whether or not a person `sur`
the model summary.

1

```
### YOUR CODE HERE ###

######################
```

Question 1.2: (1 point)

Use inverse logit to transform the log odds of the model coefficients into a probability of s
interpretable, and describe these results from the model.

```
### YOUR CODE HERE ###

######################
```

Your answer:

Question 1.3: (1 point)

Visualize the results of the logistic regression model that you've fitted in Question 2. Th
describe the relationship between age and the probability of survival.

```
### YOUR CODE HERE ###

######################
```

Your answer:

1.3 Part 2: Bayesian inference "by hand" (8 points)

This homework is from "PSYCH 10: Introduction to Statistical Methods" which is taugh
You may find taking a look at this online chapter useful: Doing Bayesian Estimation

Question 2.1: (2 points)

Let's say that we are interested in the probability that a new drug called Bayesium w
disease of frequentitis. For our purposes we are happy to estimate this variable (which we
the nearest of 0.1.

Create a data frame called bayesium that includes the following variables:

- `theta`: a vector containing values of theta ranging from 0.0 to 1.0 in steps of 0.1
- `flat_prior`: a vector representing a flat, uniform prior across all possible values o
the same prior value for each level of theta). This should be a probability distributio
sum to one.
- `bayes_prior`: a vector containing a prior based on a binomial distribution with a
reflecting the prior of a Bayesian who strongly believes that the treatment will have
be obtained using the command: `dbinom(seq(0,10), 10, p = 0.9)`
- `freq_prior`: a vector containing a prior based on a binomial distribution with a
reflecting the prior of a frequentist who strongly believes that the treatment will h
- `dogmatic_prior`: a vector containing a prior with all of its density on theta = 0
other values of theta, reflecting the prior of an very dogmatic Bayesian with very s

```
### YOUR CODE HERE ###

######################
```

Question 2.2: (2 points)

Let's say that we perform a clinical trial of the new drug in 20 people and we find that 10
are saved by the drug. Create a variable within the bayesium data frame called `likeli`
the binomial likelihood for these data given each value of theta. (Hint: use an R function

2

function of the binomial distribution to calculate the number of 'successes' or saved lives in a certain number of trials or participants).

Then compute the posterior probabilities for each different prior and add them to the bayesium data frame within the following variables:

- `posterior_flat`: posterior given `flat_prior`
- `posterior_bayes`: posterior given `bayes_prior`
- `posterior_freq`: posterior given `freq_prior`
- `posterior_dogmatic`: posterior given `dogmatic_prior`

Each of these should be normalized so that they are probabilities (i.e. they sum to one).

```
df.bayesium = df.bayesium %>%
  ### YOUR CODE HERE ###
  mutate(likelihood =    ) %>%

  # compute posterior probabilities for each type of prior, and add to df

  ######################
```

Question 2.3: (4 points)

For each of the four priors, make a separate figure in which you plot the prior across all values of theta, and include the following: the prior with a black dotted line, the likelihood as a red dashed line, and the posterior with a solid line in blue. Add a title to the plot that includes the name of the prior. You can combine the figures into one using the "patchwork" or "cowplot" library (take a look at notes from the class `03_visualization2`). Alternatively, you can also just create one figure and make figure panels using the `facet_wrap()` or `facet_grid()` function.

```
### YOUR CODE HERE ###

# plot priors, likelihood, and posteriors

######################
```

Then, in your own words, describe how the different priors affect the respective maximum posterior estimates.

Your answer:

1.4 Part 3: Bayesian data analysis (4 points)

Question 3.1: (1 point)

Build a bayesian model from the `df.heart` data similar to the frequentist model in Question 1.1. Call this model `fit.brm`

```
### YOUR CODE HERE ###
fit.brm = brm(formula =
              family =
              data =
              file = "cache/brm",
              seed = 1)
######################
```

Question 3.2: (1 point)

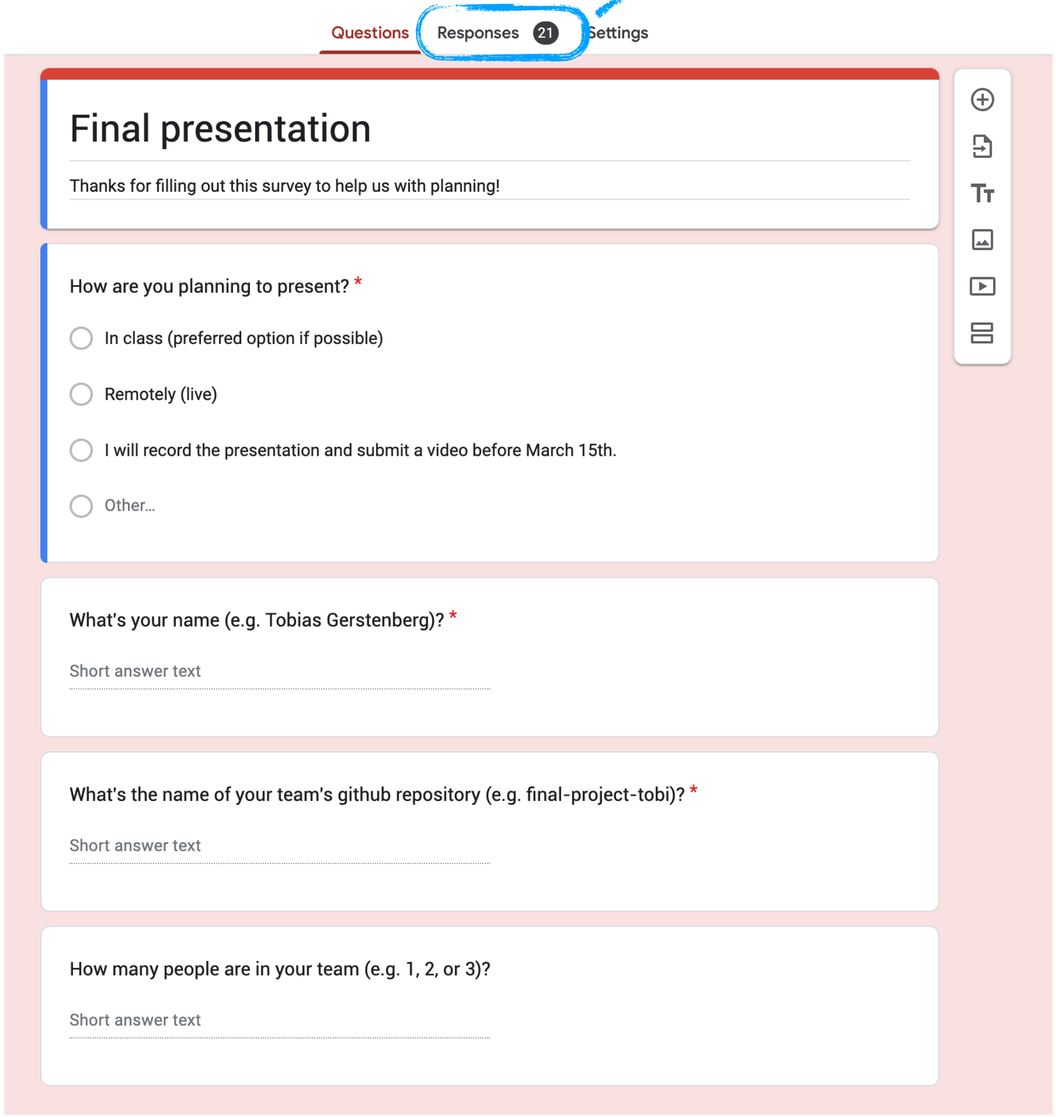
Print the summary of this model and interpret its coefficients. Compare these to the coefficients from the frequentist model you built in Question 1.1.

3

the best 6 of your homeworks count

Final presentation survey

goal: everyone!



https://tinyurl.com/psych252presentation25

Plan for today

- Quick recap
- Doing Bayesian data analysis **with BRMS**
  - Testing hypotheses
  - Model evaluation
  - Reporting results
- Some more examples
  - Sleep data
  - Titanic data
- Going beyond

Quick recap

Quick recap: What affects the posterior?

What affects the posterior?

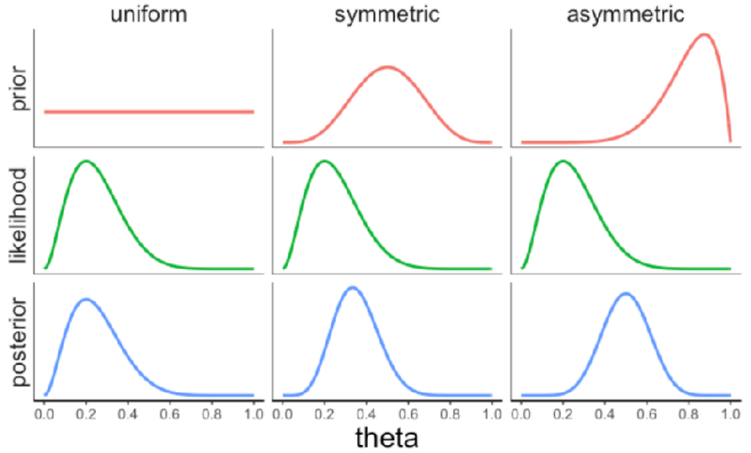
1. the prior over hypotheses
2. the likelihood of the data given each hypothesis

$$\underbrace{p(H \mid D)}_{\text{Posterior}} = \frac{\overbrace{p(D \mid H)}^{\text{Likelihood}} \cdot \overbrace{p(H)}^{\text{Prior}}}{\underbrace{p(D)}_{\text{Normalizing constant}}}$$

45

The effect of the **prior**

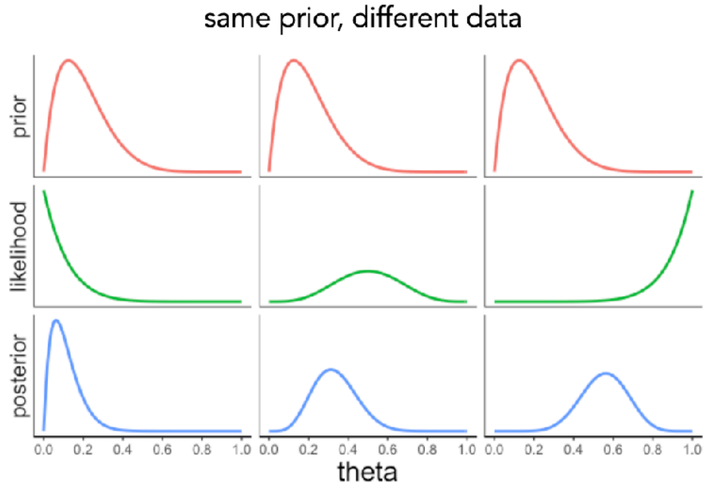
same data, different priors



46

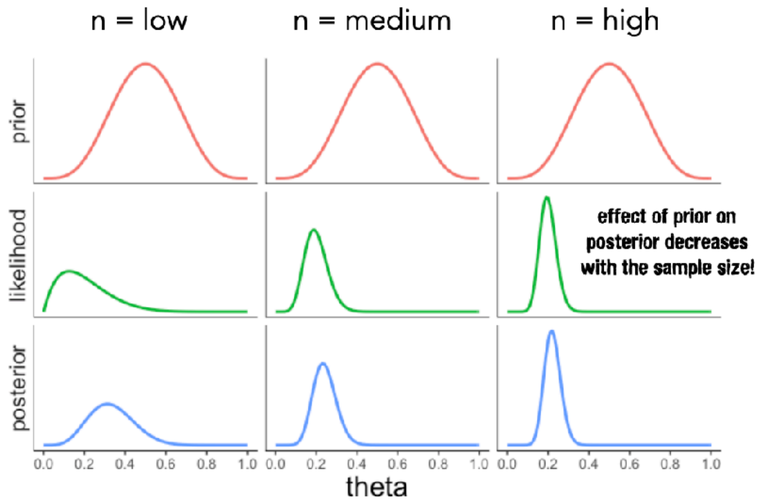
The effect of the **likelihood**

same prior, different data



47

The effect of **sample size**



48

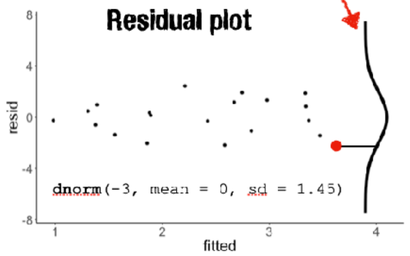
Quick recap: **likelihood**, prior, inference

Likelihood

Gaussian distribution

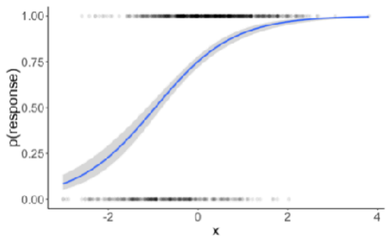
$$Y_i = b_0 + b_1 \cdot x_i + e_i$$

$$e_i \sim \mathcal{N}(0, \sigma)$$



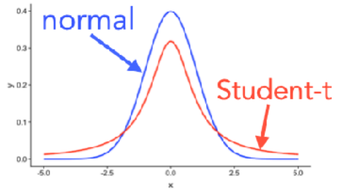
Binomial distribution

```
fit.glm = glm(formula = survived ~ 1 + fare,
              family = "binomial",
              data = df.titanic)
```



53

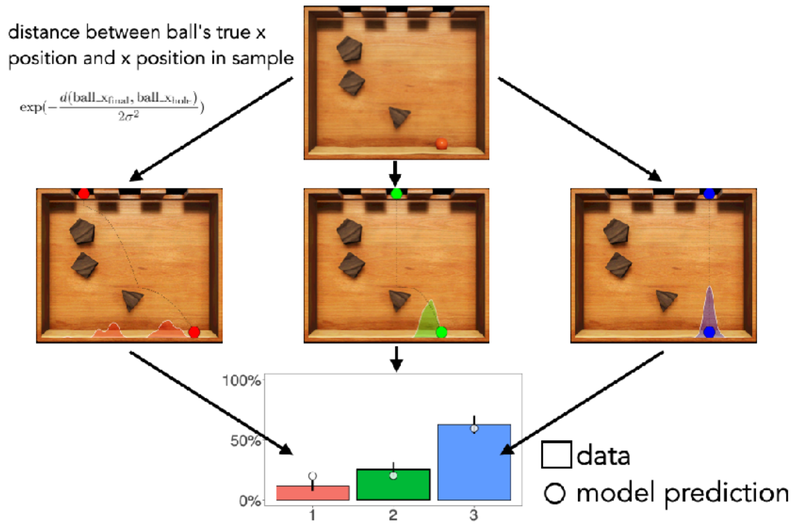
Likelihood



- **Bernoulli:**
  - binary data
  - a single trial
- **Poisson**: count of discrete events
- **Beta-binomial**: like binomial but probability of success may change across trials
- **Student-t:**
  - same as Normal
  - handles greater variability in the data (distribution has **fat tails**)

- ...

54

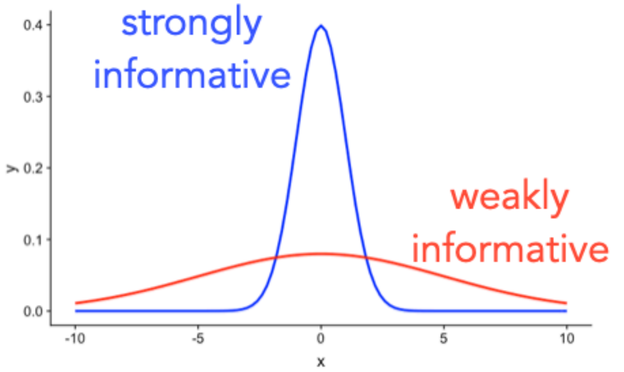


Quick recap: likelihood, **prior**, inference

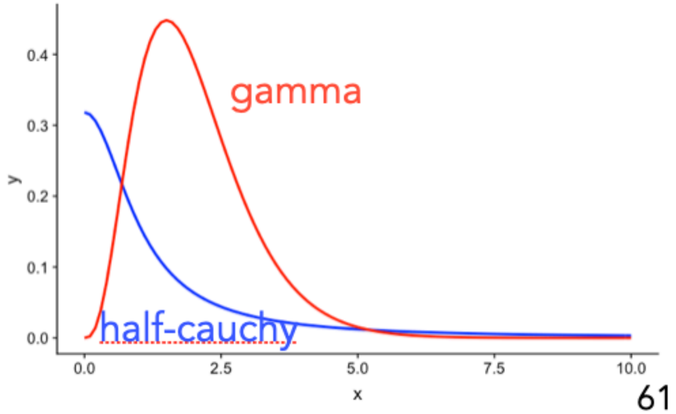
Prior

- **uniform**:
  - continuous or discrete
  - bounded between minimum and maximum
- **gaussian:**
  - sd determines how informative the prior is
- **gamma, half-cauchy**:
  - for parameters we know are positive

for **beta coefficients** in a regression



for **standard deviation** of the Gaussian



61

Quick recap: likelihood, prior, **inference**

Likelihood Prior

Posterior

$$p(H \mid D) = \frac{p(D \mid H) \cdot p(H)}{p(D)}$$

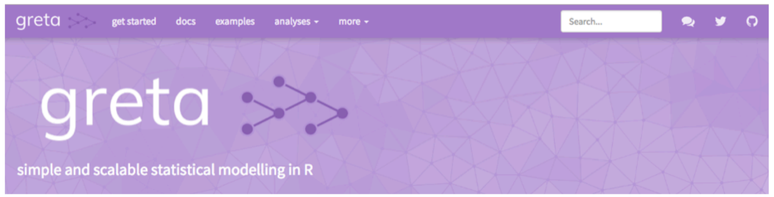
Normalizing constant

the devil is in the denominator …

Quick recap: Doing Bayesian data analysis

Software packages

```
library("greta")
```



- let's us write Bayesian models directly in R with a simple syntax
- uses Tensorflow to implement Hamiltonian Monte Carlo sampling (a fast inference algorithm ...)

16

Model specification

```
1  library("greta")
2  library("tidybayes")
3
4  # variables & priors
5  b0 = normal(0, 10)
6  b1 = normal(0, 10)
7  sd = cauchy(0, 3, truncation = c(0, Inf))
8
9  # linear predictor
10 mu = b0 + b1 * attitude$complaints
11
12 # observation model (likelihood)
13 distribution(attitude$rating) = normal(mu, sd)
14
15 # define the model
16 m = model(b0, b1, sd)
```

priors

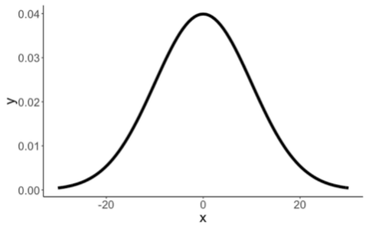
linear combination

Gaussian likelihood

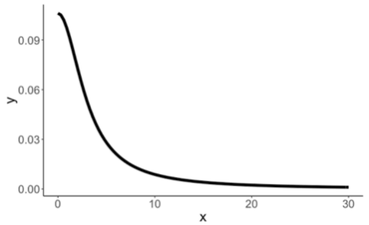
build the model

22

Priors



Gaussian prior on intercept and coefficient



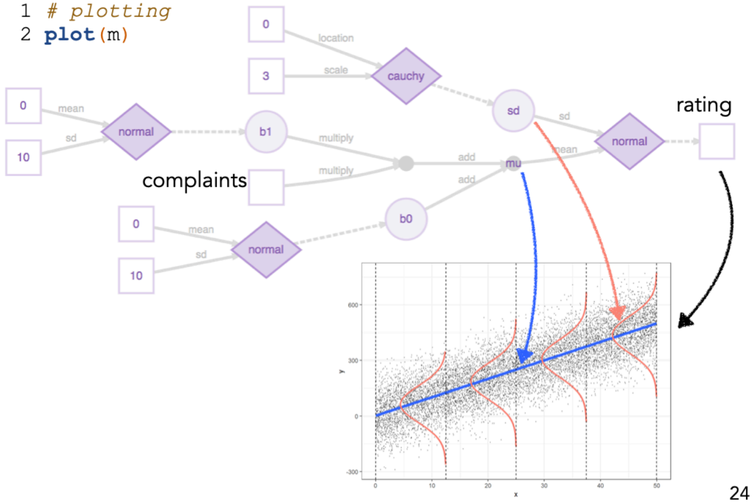
Truncated Cauchy prior on the standard deviation

weakly informative priors (allow for a wide range of possible values)

23

Graphical representation of the model

```
1 # plotting
2 plot(m)
```



24

Inference via sampling

Markov Chain Monte Carlo inference

```
1 # sampling
2 draws = mcmc(m, n_samples = 1000)
3
4 # tidy up the draws
5 df.draws = tidy_draws(draws) %>%
6   clean_names()
```

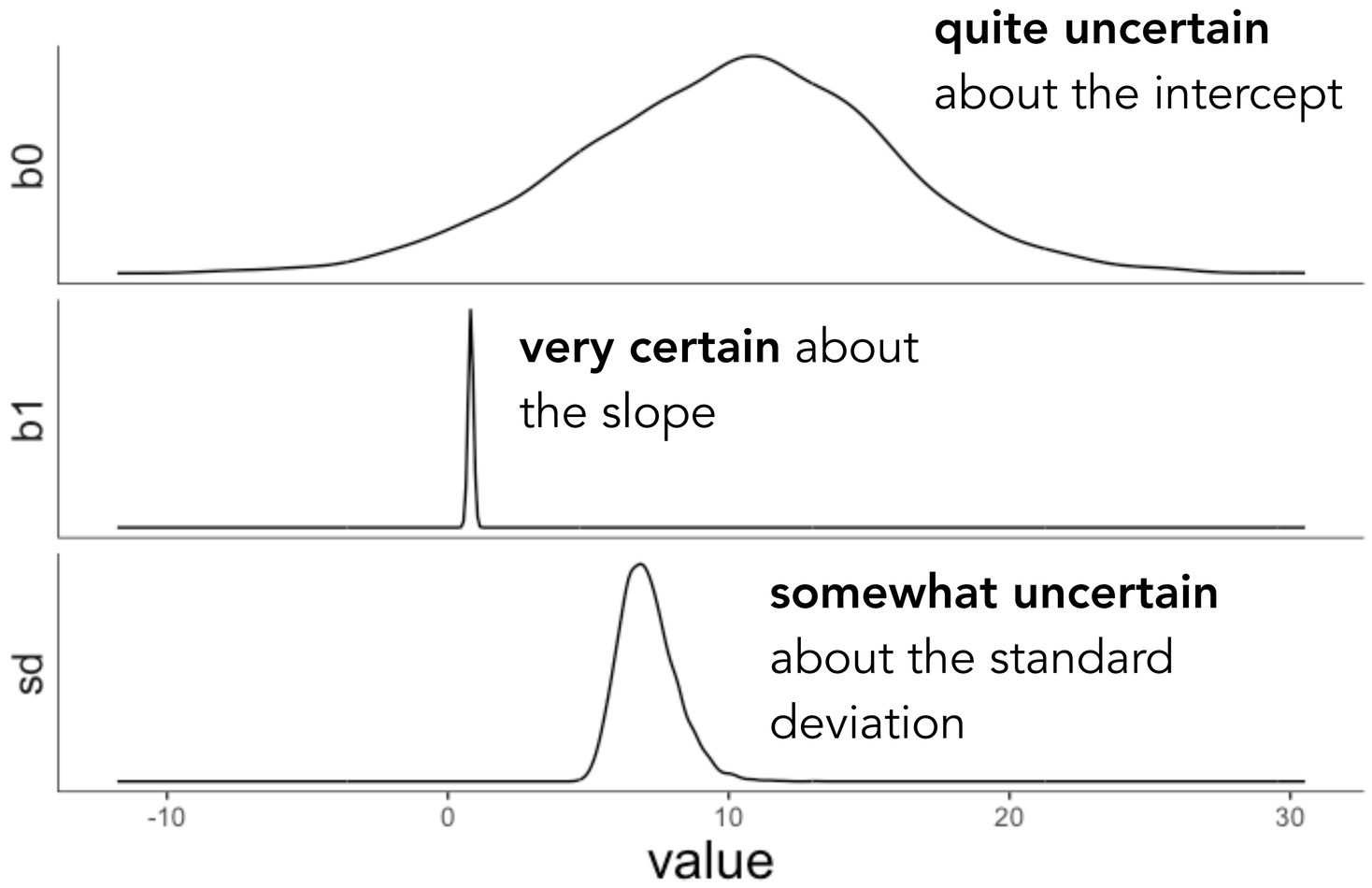
chain	iteration	draw	b0	b1	sd
1	1	1	6.08	0.87	7.60
1	2	2	1.12	0.95	7.66
1	3	3	-1.83	0.99	7.01
1	4	4	-4.23	1.02	6.64
1	5	5	3.26	0.87	7.96
1	6	6	-1.04	0.98	7.67
1	7	7	-0.83	0.97	10.12
1	8	8	-1.41	0.97	8.02
1	9	9	9.46	0.81	6.80
1	10	10	10.02	0.84	6.57

each of these is a solution for explaining the data

nice visualization of MCMC samplers

https://github.com/chi-feng/mcmc-demo

Visualize the posterior



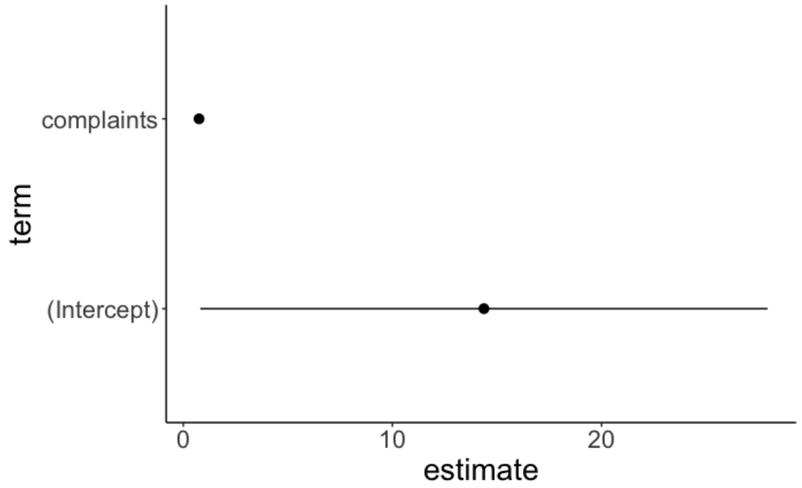
This is the solution of a Bayesian analysis.

A posterior distribution over each parameter in our model.

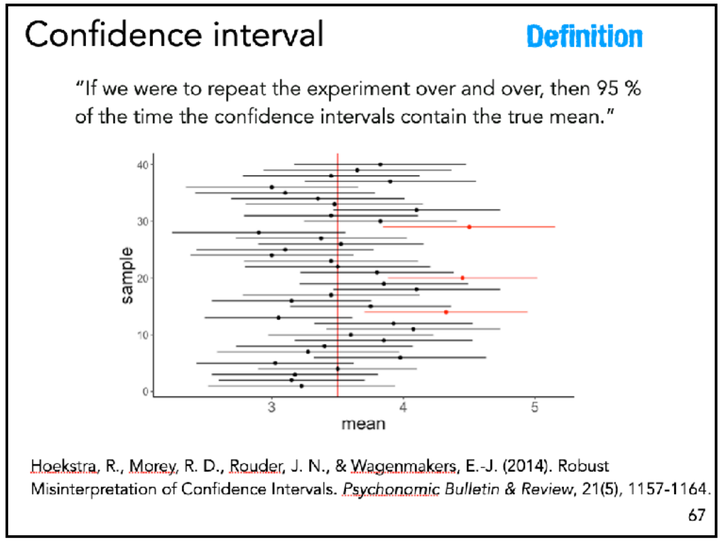
We can use this to visualize model predictions, and to test hypotheses.

Confidence interval

```
fit.lm = lm(formula = rating ~ 1 + complaints,
            data = df.attitude)
```

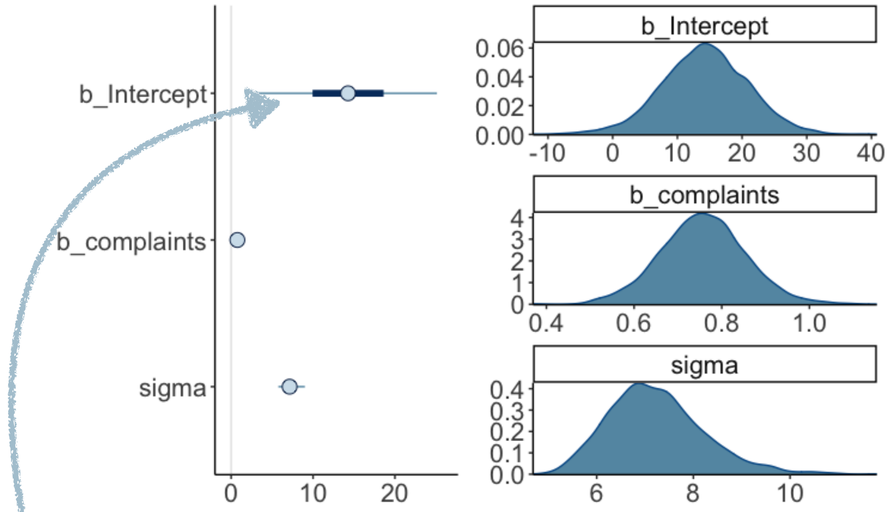


point estimate + confidence interval



Credible interval

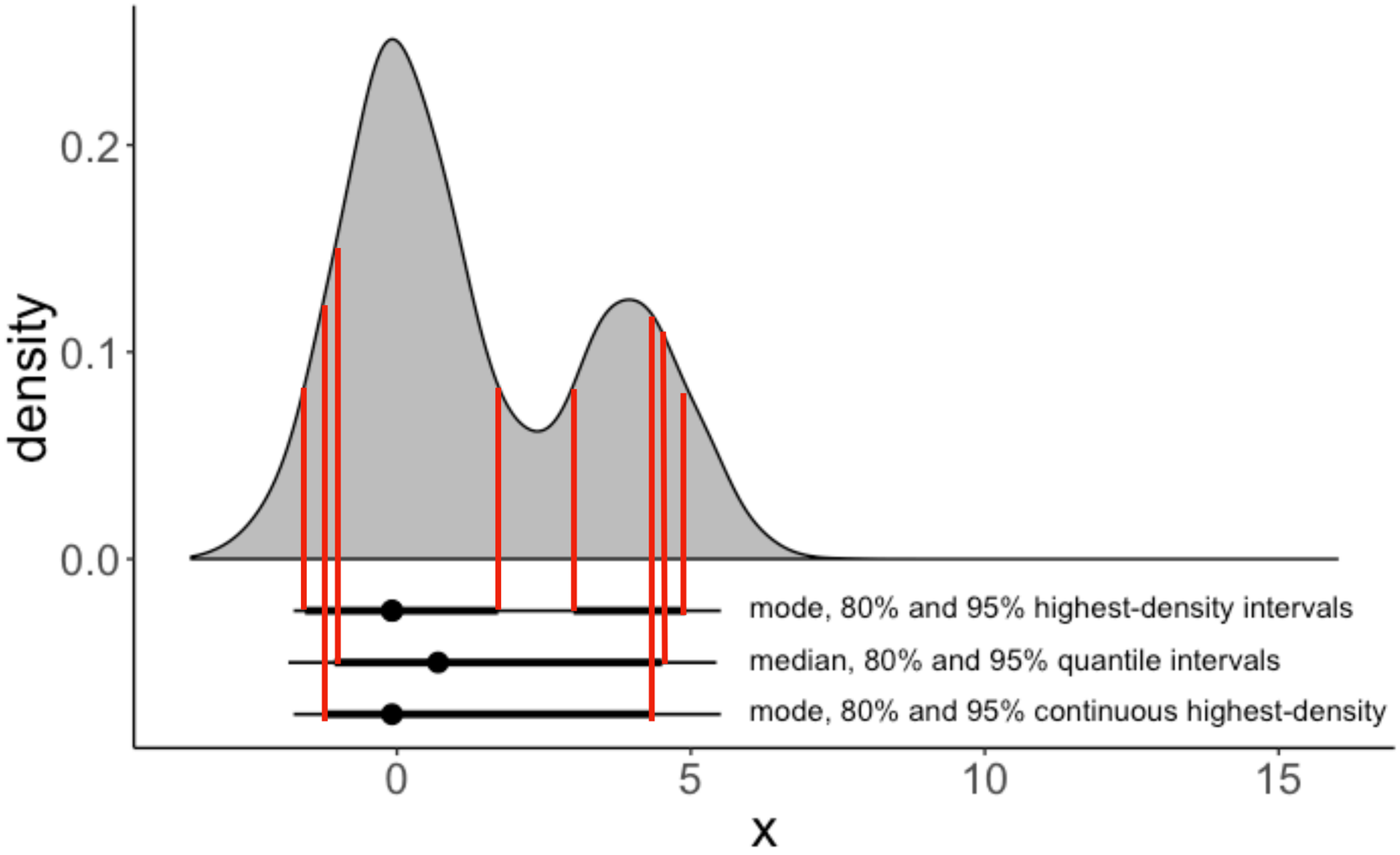
```
fit.brm = brm(formula = rating ~ 1 + complaints,
              data = df.attitude)
```



full posterior distribution over each parameter

with 90% the true parameter lies within this range

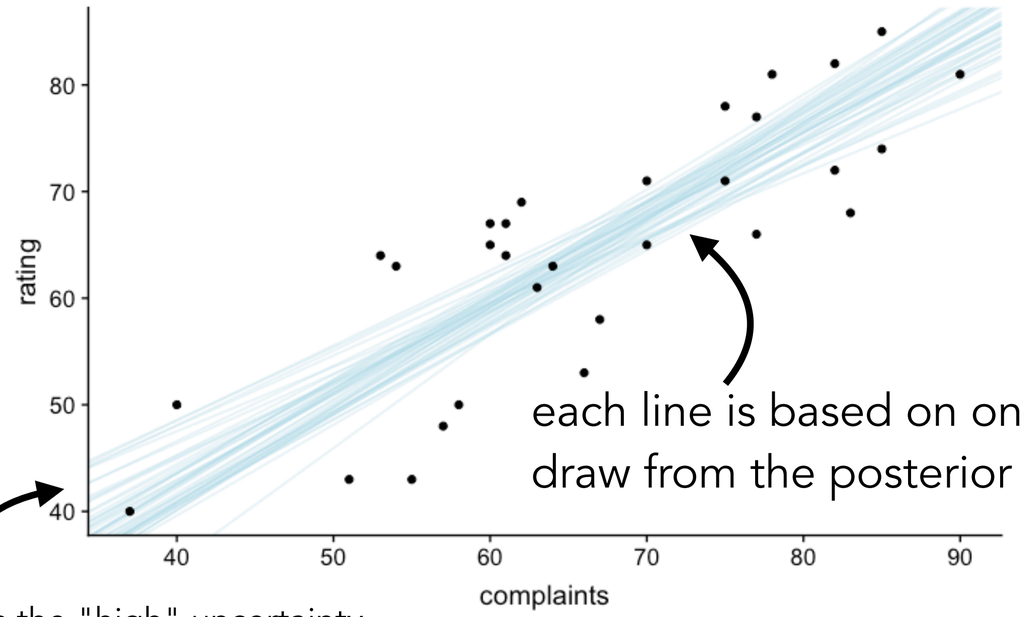
Different kinds of credible intervals



ways of summarizing the posterior distribution

Visualize the model predictions

```
ggplot(data = df.attitude,
       mapping = aes(x = complaints,
                     y = rating)) +
  geom_abline(data = df.draws %>%
                sample_n(size = 50),
              aes(intercept = b0,
                  slope = b1),
              alpha = 0.3,
              color = "lightblue") +
  geom_point()
```



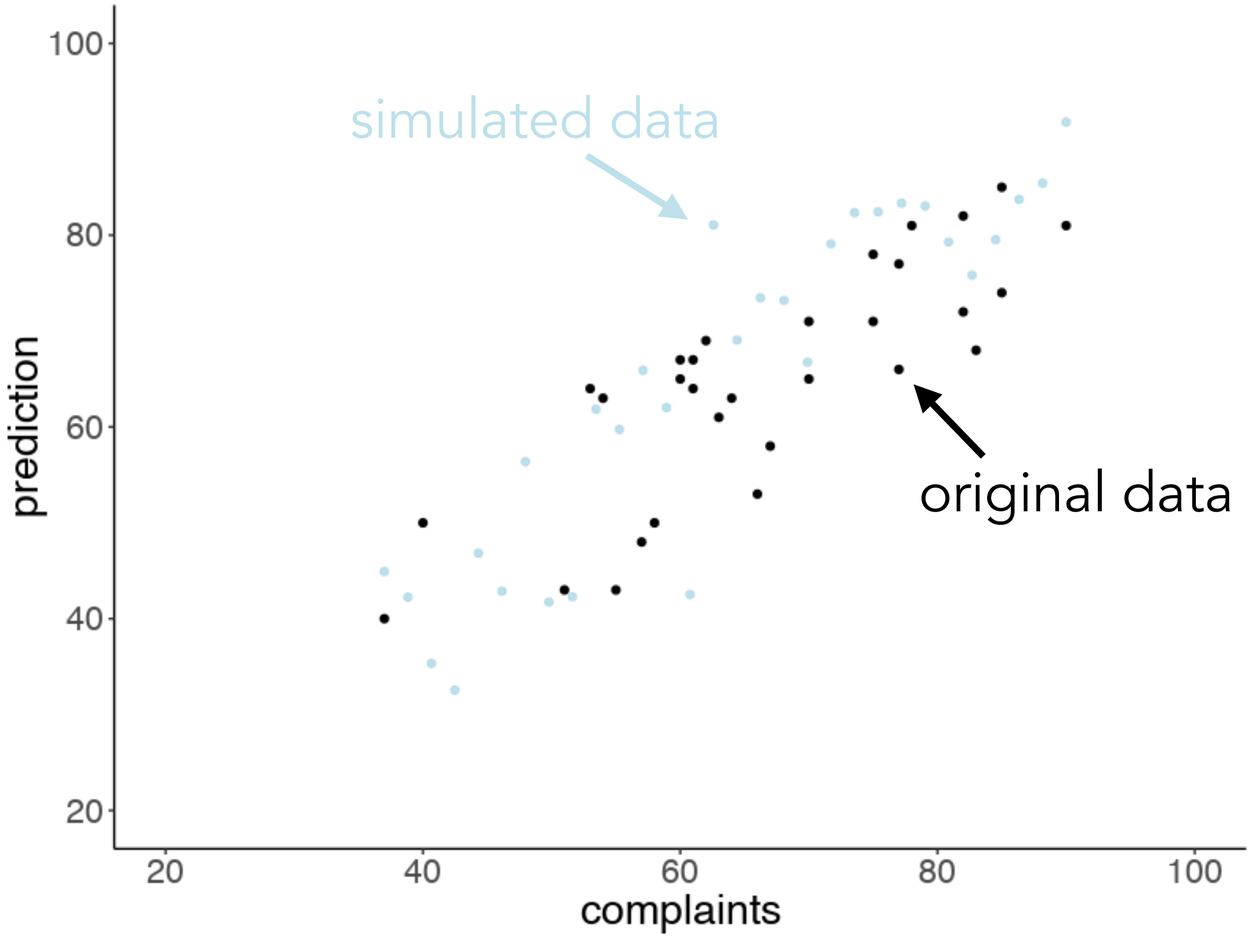
each line is based on one draw from the posterior

explains the "high" uncertainty about the intercept

chain	iteration	draw	b0	b1	sd
1	1	1	6.08	0.87	7.60
1	2	2	1.12	0.95	7.66
1	3	3	-1.83	0.99	7.01
1	4	4	-4.23	1.02	6.64
1	5	5	3.26	0.87	7.96
1	6	6	-1.04	0.98	7.67
1	7	7	-0.83	0.97	10.12
1	8	8	-1.41	0.97	8.02
1	9	9	9.46	0.81	6.30
1	10	10	10.02	0.84	6.57

Posterior predictive check

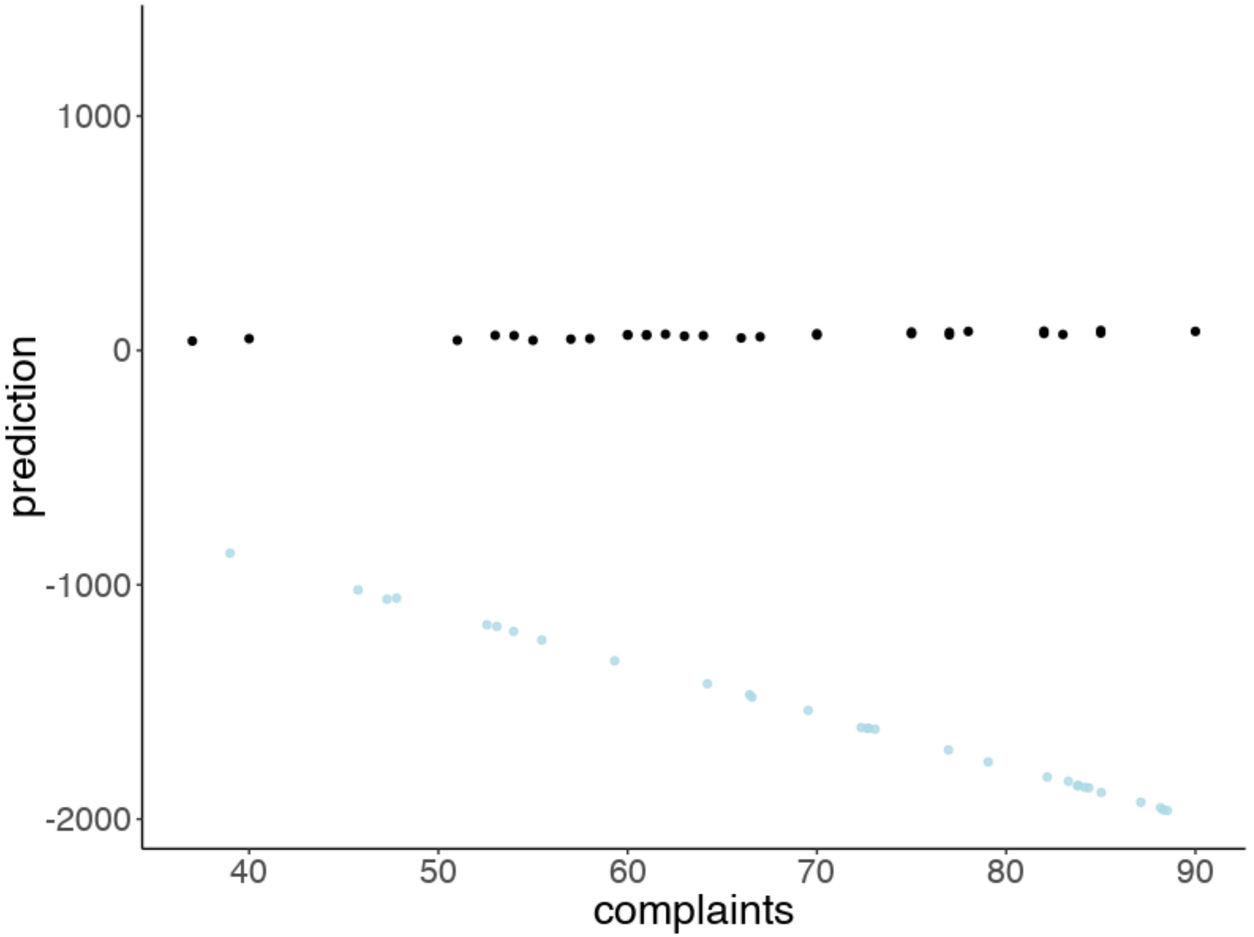
1. sample parameters from the **posterior distribution**
2. generate data using these parameters (using the likelihood function)



Hypothetical outcome plot

Prior predictive check

1. sample parameters from the **prior distribution**
2. generate data using these parameters (using the likelihood function)



Hypothetical outcome plot

Paul Bürkner

Doing Bayesian data analysis with BRMS

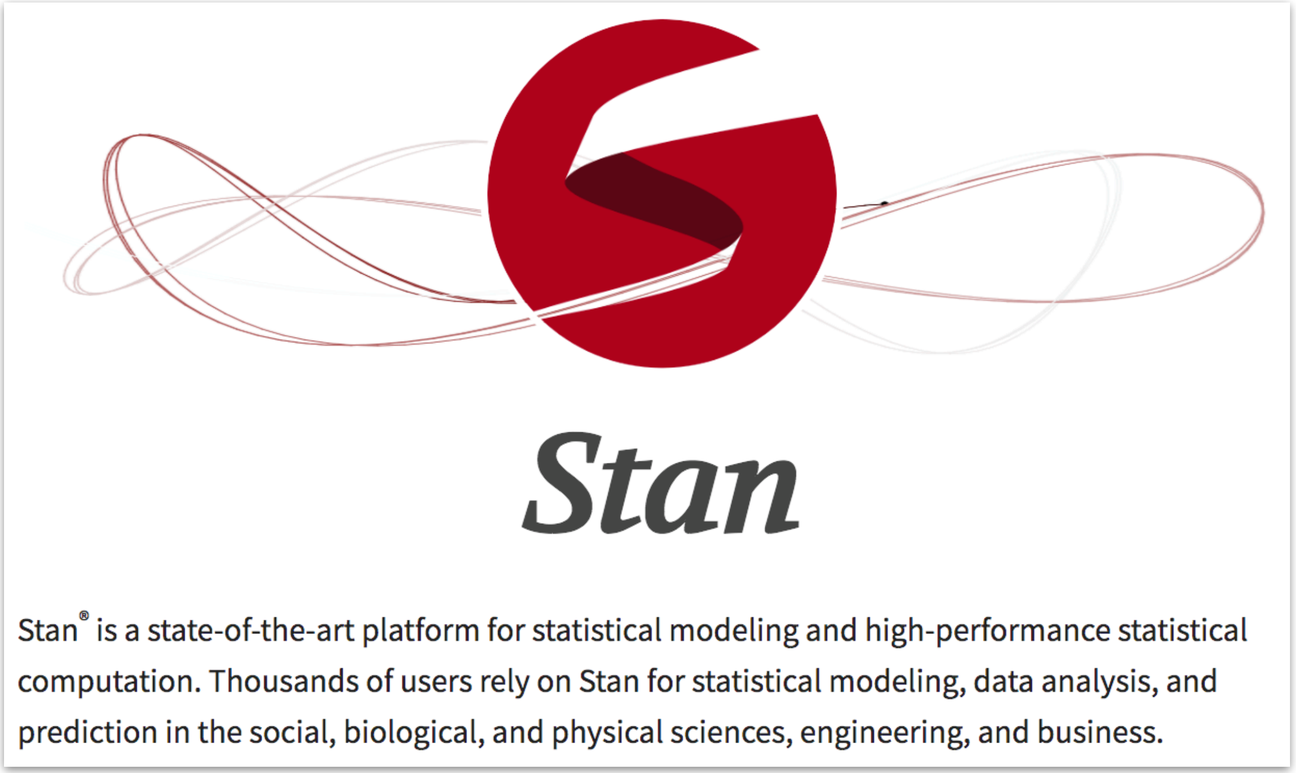
Software packages

```
library("brms")
```

Bayesian regression modeling with Stan

- very powerful package that makes it easy to run Bayesian regression models
- we specify models using the same syntax we've already learned based on **`lm()`**, **`glm()`**, and **`lmer()`**
- `brms` turns this into Stan code and fits the model
- we can then use `tidybayes` to investigate the posterior

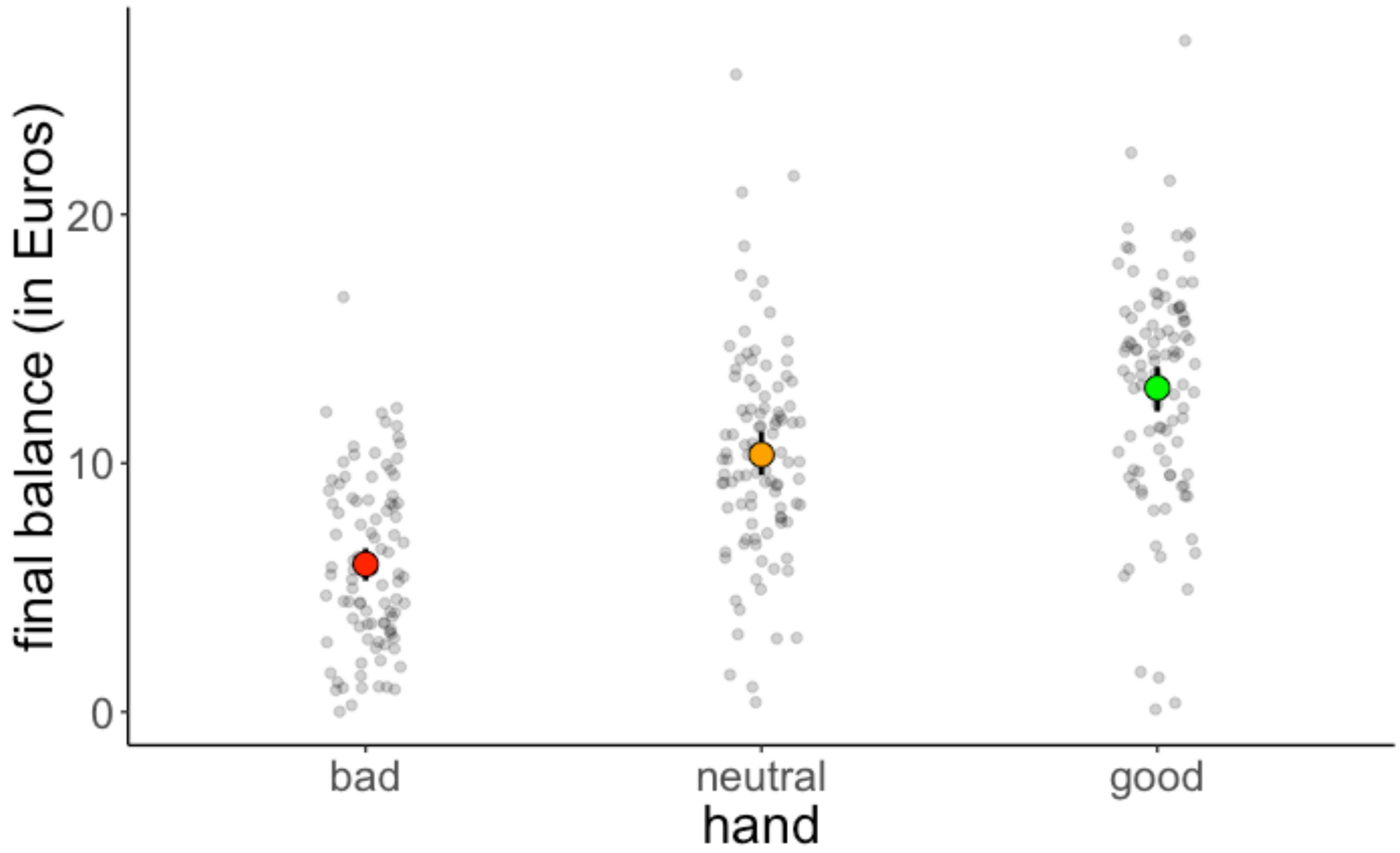
Software packages



https://mc-stan.org/

Poker data

Poker data



Using `lm()`

```
1 fit.lm_poker = lm(formula = balance ~ 1 + hand,
2                   data = df.poker)
3
4 fit.lm_poker %>% summary()
```

```
Call:
lm(formula = balance ~ 1 + hand, data = df.poker)

Residuals:
     Min       1Q   Median       3Q      Max
-12.9264  -2.5902  -0.0115   2.6573  15.2834

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   5.9415     0.4111  14.451  < 2e-16 ***
handneutral   4.4051     0.5815   7.576 4.55e-13 ***
handgood      7.0849     0.5815  12.185  < 2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 4.111 on 297 degrees of freedom
Multiple R-squared:  0.3377,   Adjusted R-squared:  0.3332
F-statistic:  75.7 on 2 and 297 DF,  p-value: < 2.2e-16
```

Using `brm()`


```
1 fit.brm_poker = brm(formula = balance ~ 1 + hand,
2                     data = df.poker)
3
4 fit.brm_poker %>% summary()
```

```
 Family: gaussian
  Links: mu = identity; sigma = identity
Formula: balance ~ 1 + hand
   Data: df.poker (Number of observations: 300)
Samples: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
         total post-warmup samples = 4000

Population-Level Effects:
            Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept       5.93      0.41     5.12     6.72 1.00     2986     2744
handneutral     4.41      0.58     3.30     5.55 1.00     3497     2903
handgood        7.10      0.58     5.99     8.29 1.00     3545     2932

Family Specific Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sigma     4.12      0.17     3.81     4.46 1.00     3650     2921

Samples were drawn using sampling(NUTS). For each parameter, Eff.Sample
is a crude measure of effective sample size, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).
```

Comparison between `lm()` and `brm()`

`lm()`

```
Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)    5.9415     0.4111  14.451  < 2e-16 ***
handneutral    4.4051     0.5815   7.576 4.55e-13 ***
handgood       7.0849     0.5815  12.185  < 2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

`brm()`

```
Population-Level Effects:
             Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept        5.93      0.41     5.12     6.72 1.00     2986     2744
handneutral      4.41      0.58     3.30     5.55 1.00     3497     2903
handgood         7.10      0.58     5.99     8.29 1.00     3545     2932
```

almost identical results!

What about the priors?

```
1 fit.brm_poker = brm(formula = balance ~ 1 + hand,
2                     data = df.poker)
```

By default, `brms` uses weakly informative priors for the model parameters.

There are quite a few other defaults, let's take a look under the hood ...

"Full" specification of the model

```
fit.brm_poker_full = brm(
  formula = balance ~ 1 + hand,
  family = "gaussian",
  data = df.poker,
  prior = c(
    prior(normal(0, 10), class = "b", coef = "handgood"),
    prior(normal(0, 10), class = "b", coef = "handneutral"),
    prior(student_t(3, 3, 10), class = "Intercept"),
    prior(student_t(3, 0, 10), class = "sigma")
  ),
  inits = list(
    list(Intercept = 0, sigma = 1, handgood = 5, handneutral = 5),
    list(Intercept = -5, sigma = 3, handgood = 2, handneutral = 2),
    list(Intercept = 2, sigma = 1, handgood = -1, handneutral = 1),
    list(Intercept = 1, sigma = 2, handgood = 2, handneutral = -2)
  ),
  iter = 4000,
  warmup = 1000,
  chains = 4,
  file = "cache/brm_poker_full",
  seed = 1
)
```

likelihood

priors

initialization

how many runs in the inference chain

how long for the warmup

how many chains

save the model result

make reproducible

fitting Bayesian models takes some time, so storing results is key

Turned into Stan code

```
// generated with brms 2.7.0
functions {
}
data {
  int<lower=1> N;  // total number of observations
  vector[N] Y;  // response variable
  int<lower=1> K;  // number of population-level effects
  matrix[N, K] X;  // population-level design matrix
  int prior_only;  // should the likelihood be ignored?
}
transformed data {
  int Kc = K - 1;
  matrix[N, K - 1] Xc;  // centered version of X
  vector[K - 1] means_X;  // column means of X before centering
  for (i in 2:K) {
    means_X[i - 1] = mean(X[, i]);
    Xc[, i - 1] = X[, i] - means_X[i - 1];
  }
}
parameters {
  vector[Kc] b;  // population-level effects
  real temp_Intercept;  // temporary intercept
  real<lower=0> sigma;  // residual SD
}
transformed parameters {
}
model {
  vector[N] mu = temp_Intercept + Xc * b;
  // priors including all constants
  target += normal_lpdf(b[1] | 0, 10);
  target += normal_lpdf(b[2] | 0, 10);
  target += student_t_lpdf(temp_Intercept | 3, 3, 10);
  target += student_t_lpdf(sigma | 3, 0, 10)
    - 1 * student_t_lccdf(0 | 3, 0, 10);
  // likelihood including all constants
  if (!prior_only) {
    target += normal_lpdf(Y | mu, sigma);
  }
}
generated quantities {
  // actual population-level intercept
  real b_Intercept = temp_Intercept - dot_product(means_X, b);
}
```

- probabilistic programming language
- flexible construction of Bayesian models
- ports have been written for R, Python, Julia, ...
- implements a fast inference algorithm

Results

posterior samples

b_Intercept	b_handneutral	b_handgood	sigma
5.97	4.27	7.48	3.94
5.11	5.25	7.40	3.91
7.03	3.78	5.80	4.48
5.72	4.18	7.25	4.00
6.01	4.44	6.15	4.57
5.94	4.69	6.72	4.36
6.39	3.84	6.40	3.92
5.24	5.15	7.69	4.16
6.12	4.51	7.20	4.14
6.43	3.71	6.37	4.13
5.85	5.01	7.32	4.00
6.51	3.58	6.62	3.95
5.85	4.45	7.62	4.17
5.80	5.45	6.36	4.10
5.48	5.51	7.22	3.99

⋮

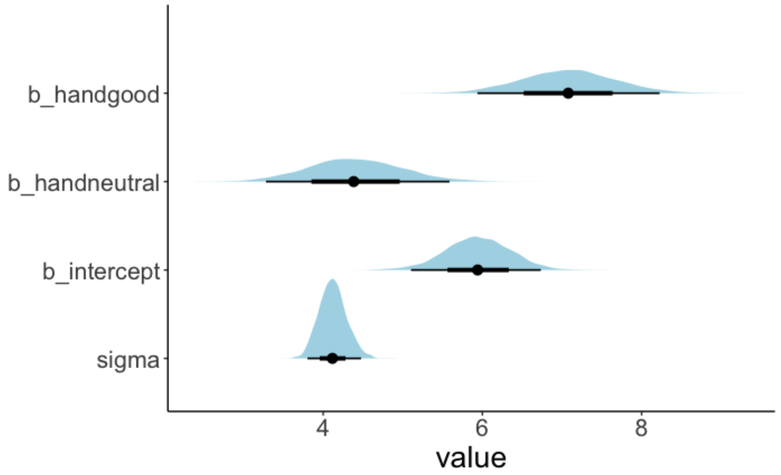
maximum a posteriori

summary of posterior

parameter	lower	mode	upper
b_handgood	5.97	7.07	8.27
b_handneutral	3.21	4.43	5.51
b_intercept	5.17	5.95	6.77
sigma	3.81	4.12	4.47

MAP estimate and 95% highest density interval

visualization



Testing hypotheses

Results

posterior samples

b_Intercept	b_handneutral	b_handgood	sigma
5.97	4.27	7.48	3.94
5.11	5.25	7.40	3.91
7.03	3.78	5.80	4.48
5.72	4.18	7.25	4.00
6.01	4.44	6.15	4.57
5.94	4.69	6.72	4.36
6.39	3.84	6.40	3.92
5.24	5.15	7.69	4.16
6.12	4.51	7.20	4.14
6.43	3.71	6.37	4.13
5.85	5.01	7.32	4.00
6.51	3.58	6.62	3.95
5.85	4.45	7.62	4.17
5.80	5.45	6.36	4.10
5.48	5.51	7.22	3.99

⋮

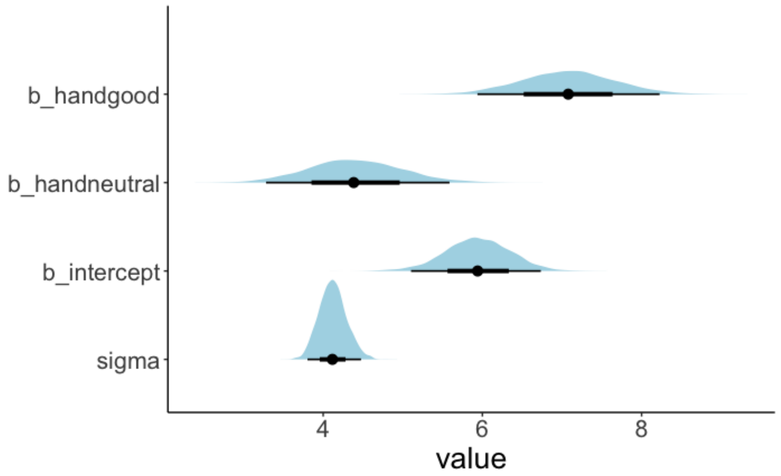
maximum a posteriori

summary of posterior

parameter	lower	mode	upper
b_handgood	5.97	7.07	8.27
b_handneutral	3.21	4.43	5.51
b_intercept	5.17	5.95	6.77
sigma	3.81	4.12	4.47

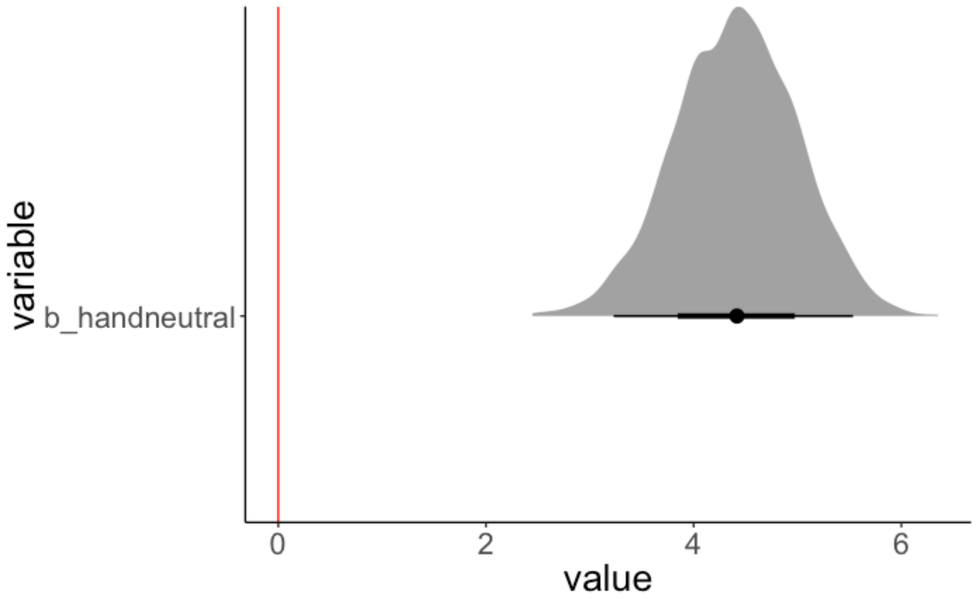
MAP estimate and 95% highest density interval

visualization



Asking questions based on the posterior

Do neutral hands earn more money than bad hands?



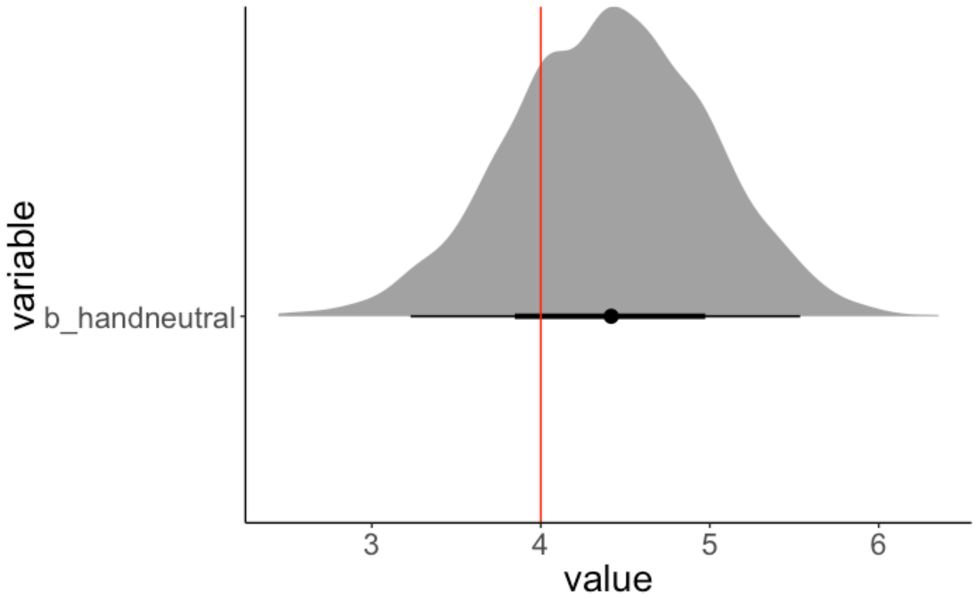
What's the probability that handneutral is less than 0?

```
1 hypothesis(fit.brm,
2            hypothesis = "handneutral < 0")
```

p = 0

Asking questions based on the posterior

Do neutral hands earn much more money than bad hands?



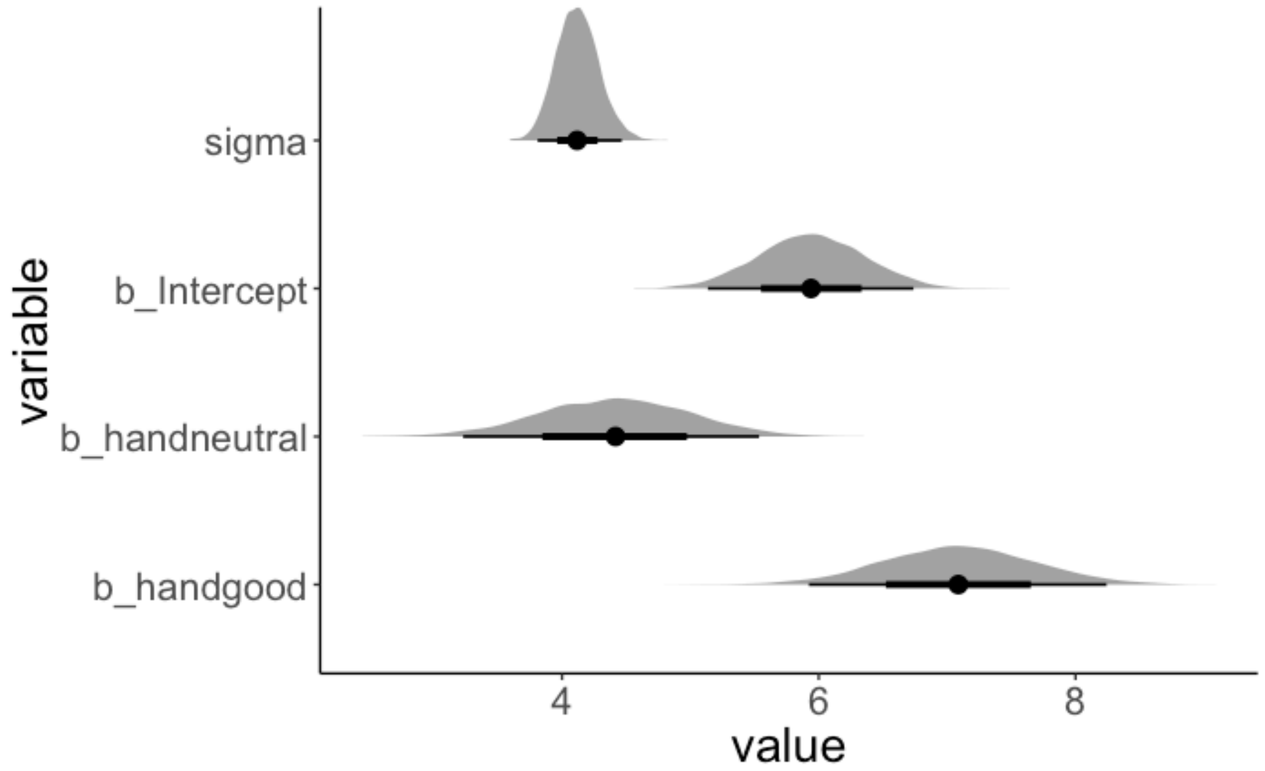
What's the probability that handneutral is **more than 4**?

```
1 hypothesis(fit.brm,
2            hypothesis = "handneutral > 4")
```

p = 0.75

Asking questions based on the posterior

Do good hands make twice as much as bad hands?

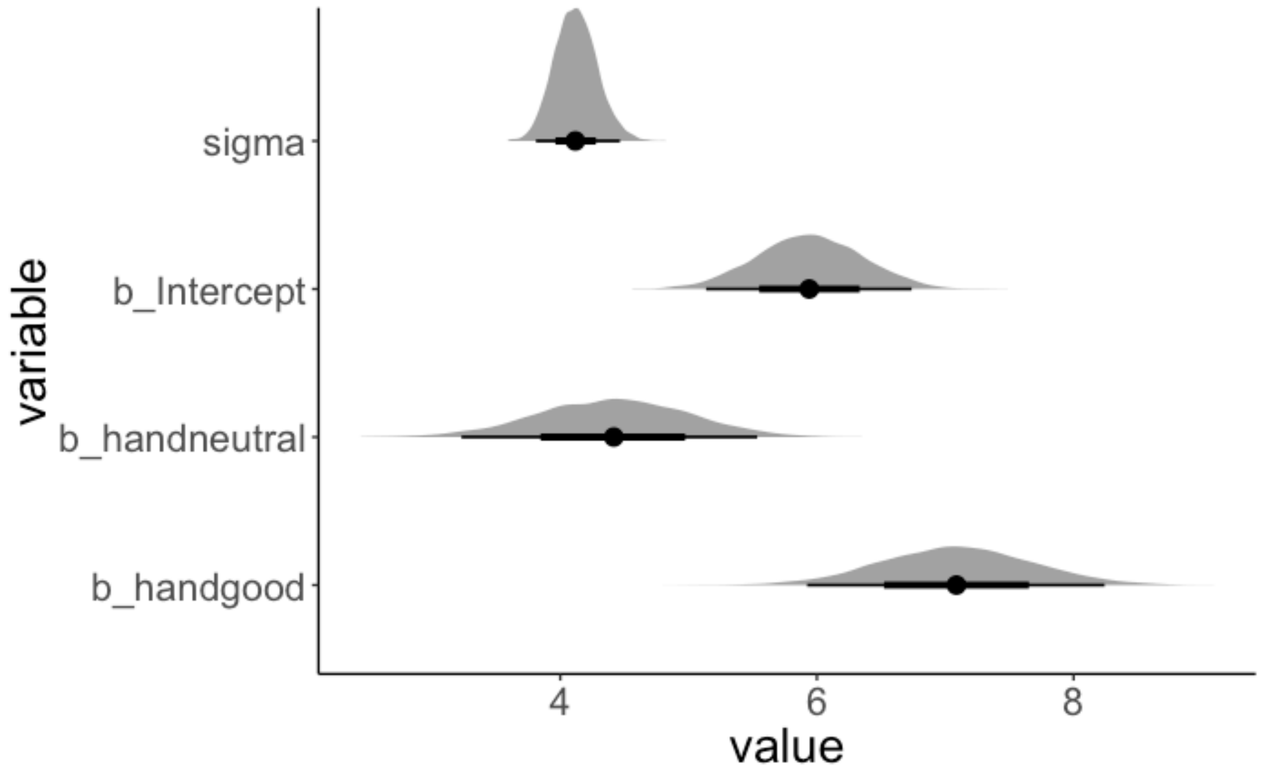



```
1 hypothesis(fit.brm,
2              hypothesis = "handgood + Intercept > 2 * Intercept")
```

p = 0.89

Asking questions based on the posterior

Are neutral hands worse than bad and good hands combined?




```
1 hypothesis(fit.brm,
2              hypothesis = "Intercept + handneutral < (Intercept + Intercept + handgood) / 2")
```

p = 0.04

Testing hypothesis

```
df.hypothesis = fit.brm %>%
  posterior_samples() %>%
  clean_names() %>%
  select(starts_with("b_")) %>%
  mutate(neutral = b_intercept + b_handneutral,
         bad_good_average = (b_intercept + b_intercept + b_handgood)/2,
         hypothesis = neutral < bad_good_average)
```

samples from the posterior

b_intercept	b_handneutral	b_handgood	neutral	bad_good_average	hypothesis
6.07	4.10	7.20	10.17	9.67	FALSE
6.06	4.44	6.95	10.49	9.53	FALSE
5.88	5.00	6.73	10.87	9.24	FALSE
5.85	4.78	6.18	10.63	8.94	FALSE
5.86	4.46	7.68	10.32	9.70	FALSE

```
df.hypothesis %>%
  summarize(p = sum(hypothesis)/n())
```

p = 0.04

Testing hypotheses

Having a posterior distribution allows us to ask questions about the data in a very flexible way!

The "emmeans" package is your friend!

```
1 fit.brm_poker %>%
2   emmeans(specs = consec ~ hand)
```

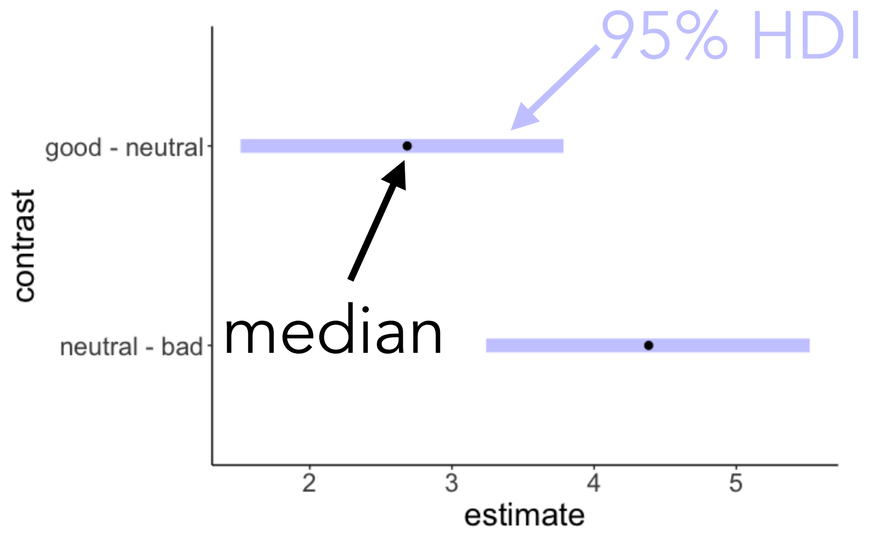
estimated mean for each group →

contrasts →

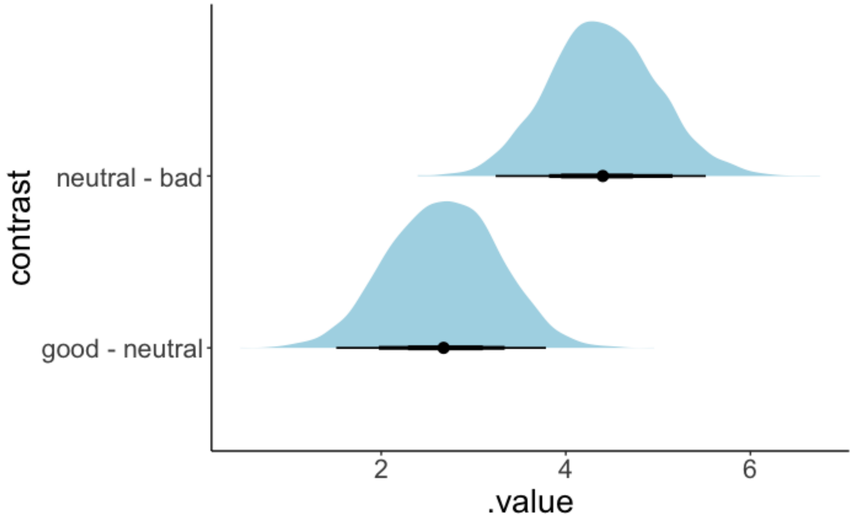
```
$emmeans
 hand    emmean lower.HPD upper.HPD
 bad       5.94      5.16      6.78
 neutral  10.34      9.55     11.15
 good     13.02     12.22     13.82

Point estimate displayed: median
HPD interval probability: 0.95

$contrasts
 contrast       estimate lower.HPD upper.HPD
 neutral - bad      4.38      3.24      5.52
 good - neutral     2.69      1.51      3.78

Point estimate displayed: median
HPD interval probability: 0.95
```

Visualizing the contrasts

```
fit.brm_poker %>%
  emmeans(specs = consec ~ hand) %>%
  pluck("contrasts") %>%
  plot()
```




```
fit.brm_poker %>%
  emmeans(specs = consec ~ hand) %>%
  pluck("contrasts") %>%
  gather_emmeans_draws() %>%
  ggplot(mapping = aes(y = contrast,
                       x = .value)) +
  stat_halfeye(fill = "lightblue",
               point_interval = mean_hdi,
               .width = c(0.5, 0.75, 0.95))
```



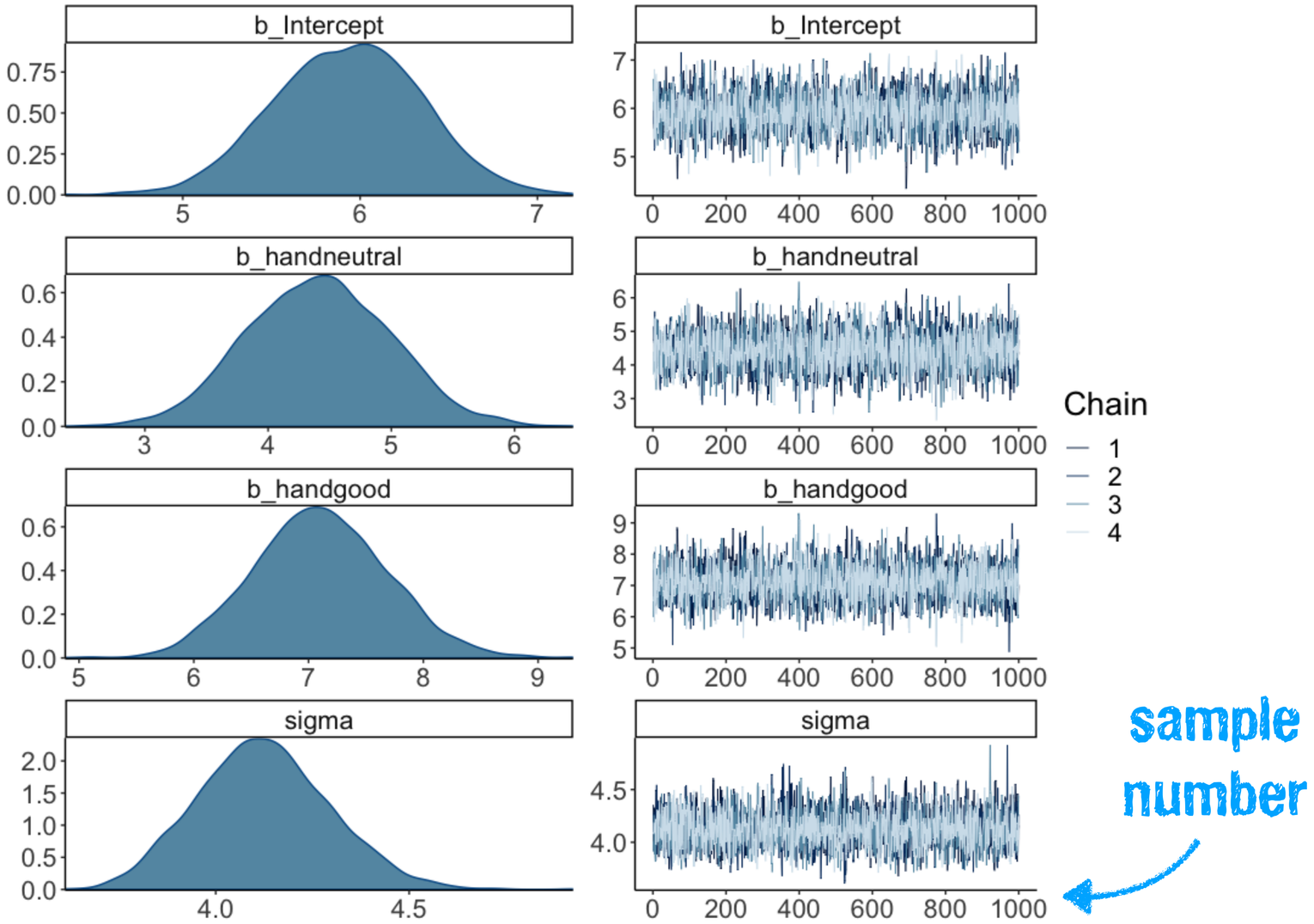
mean, 50% HDI, 75% HDI, 95% HDI

Model evaluation

1. Check whether inference worked

Can we trust the model results?

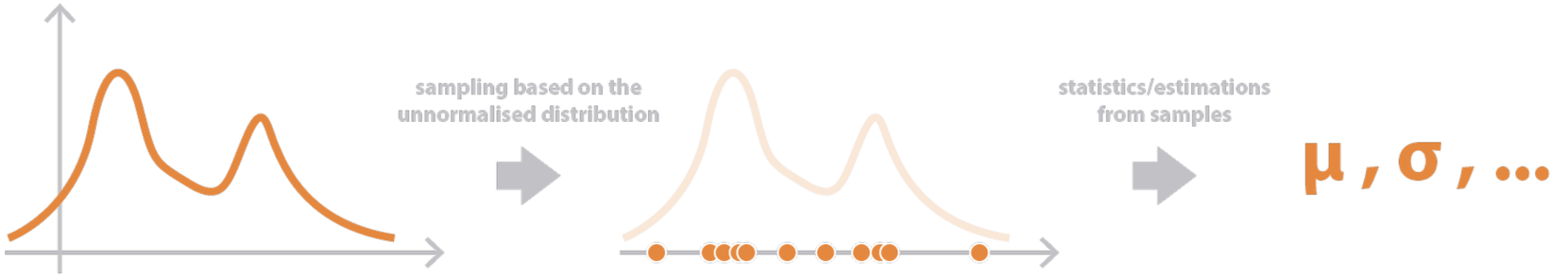
```
plot(fit.brm_poker)
```



https://chi-feng.github.io/mcmc-demo/

Can we trust the model results?

Inference via Markov Chain Monte Carlo (MCMC)

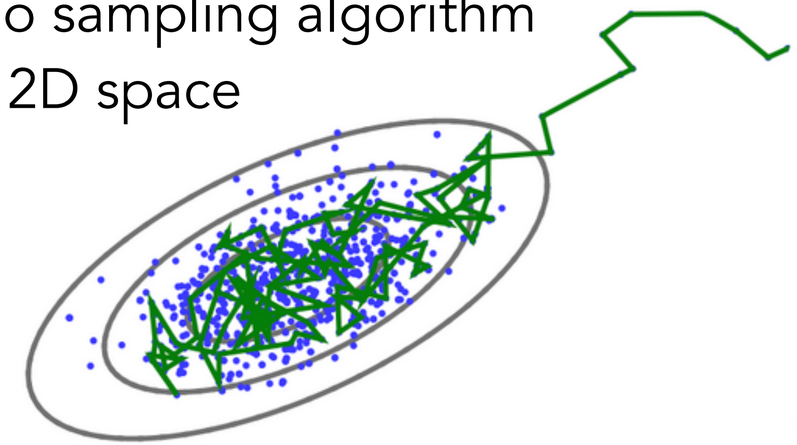


Unnormalised distribution
whose normalisation factor computation is intractable

Samples
that can be obtained with MCMC and without proceeding to the normalisation

Statistics or estimations
that can be computed based on the generated samples

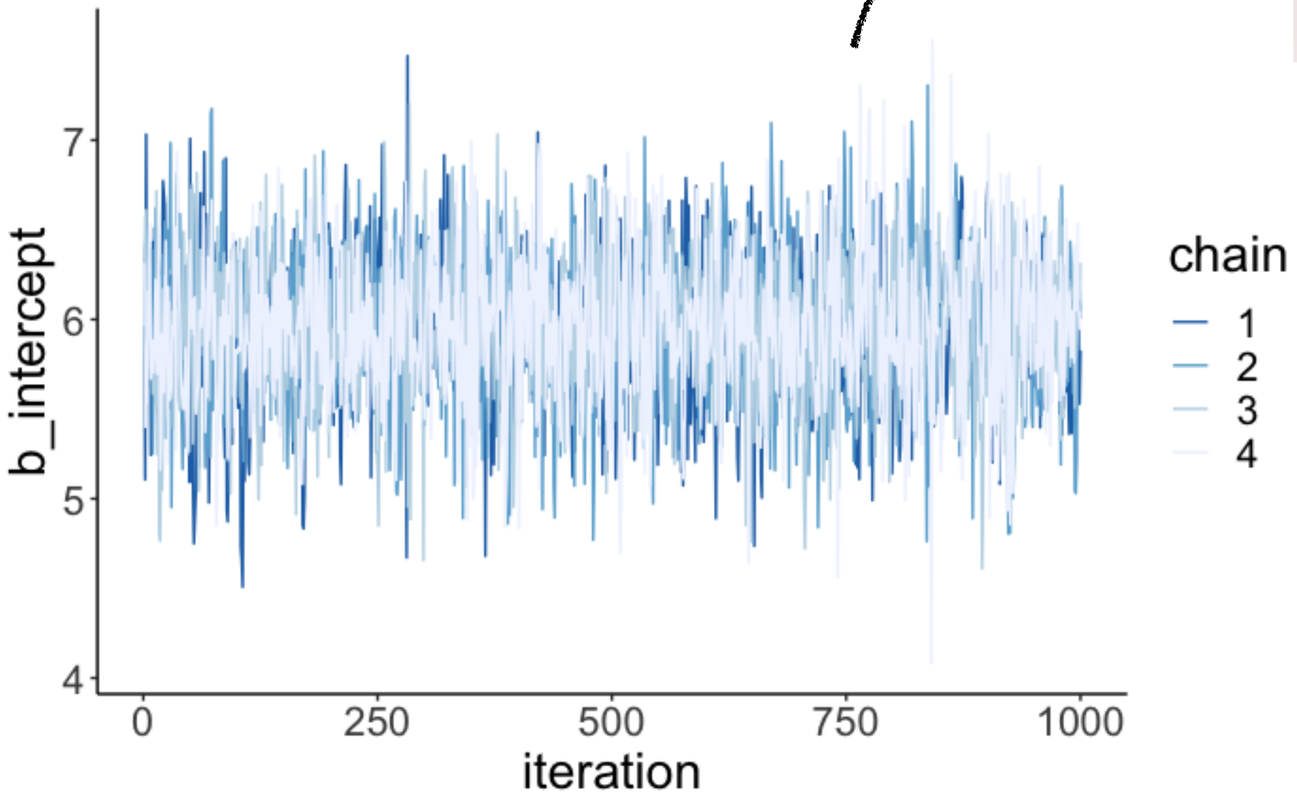
Markov Chain Monte Carlo sampling algorithm in a 2D space



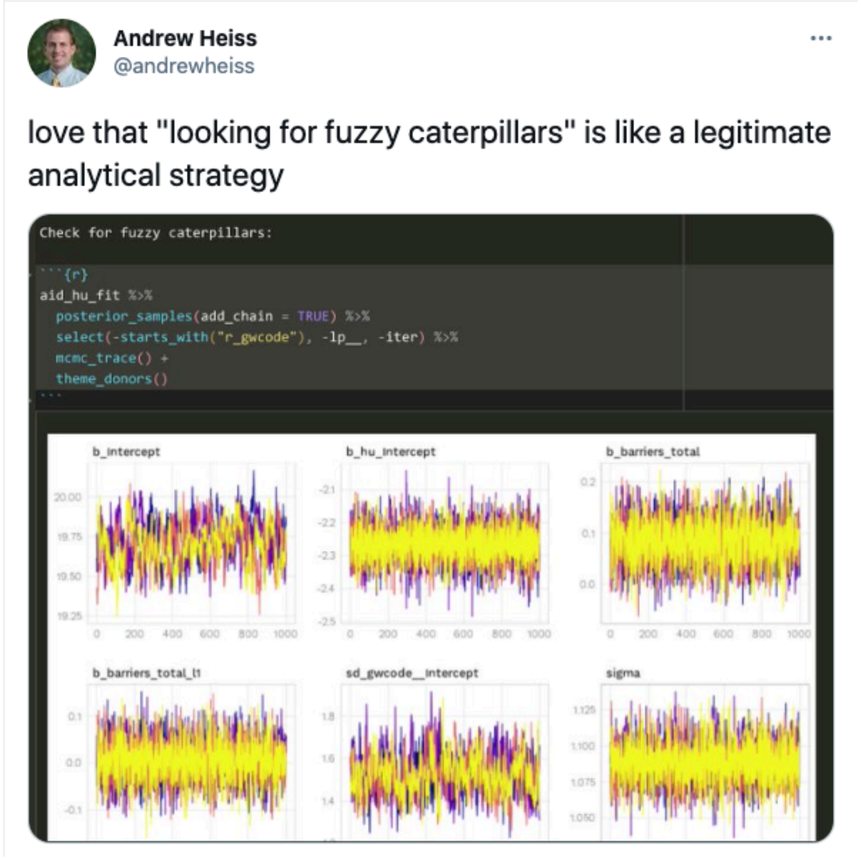
goal: draw **independent** samples from the posterior distribution

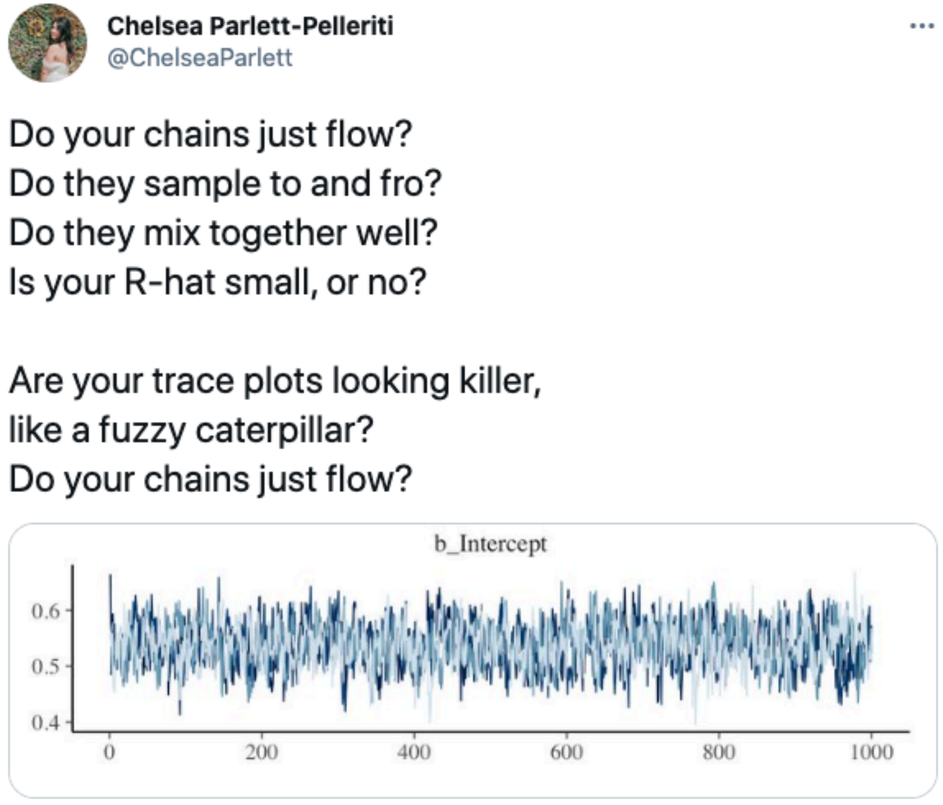
Can we trust the model results?

looks like a fuzzy caterpillar



Stats twitter chimes in ...





When things don't work out

only two data points!

incredibly wide uniform priors

10000000000

```
1  df.data = tibble(y = c(-1, 1))
2
3  fit.brm_wrong = brm(data = df.data,
4                      family = gaussian,
5                      formula = y ~ 1,
6                      prior = c(prior(uniform(-1e10, 1e10), class = Intercept),
7                                prior(uniform(0, 1e10), class = sigma)),
8                      inits = list(list(Intercept = 0, sigma = 1),
9                                   list(Intercept = 0, sigma = 1)),
10                     iter = 4000,
11                     warmup = 1000,
12                     chains = 2,
13                     file = "cache/brm_wrong")
```

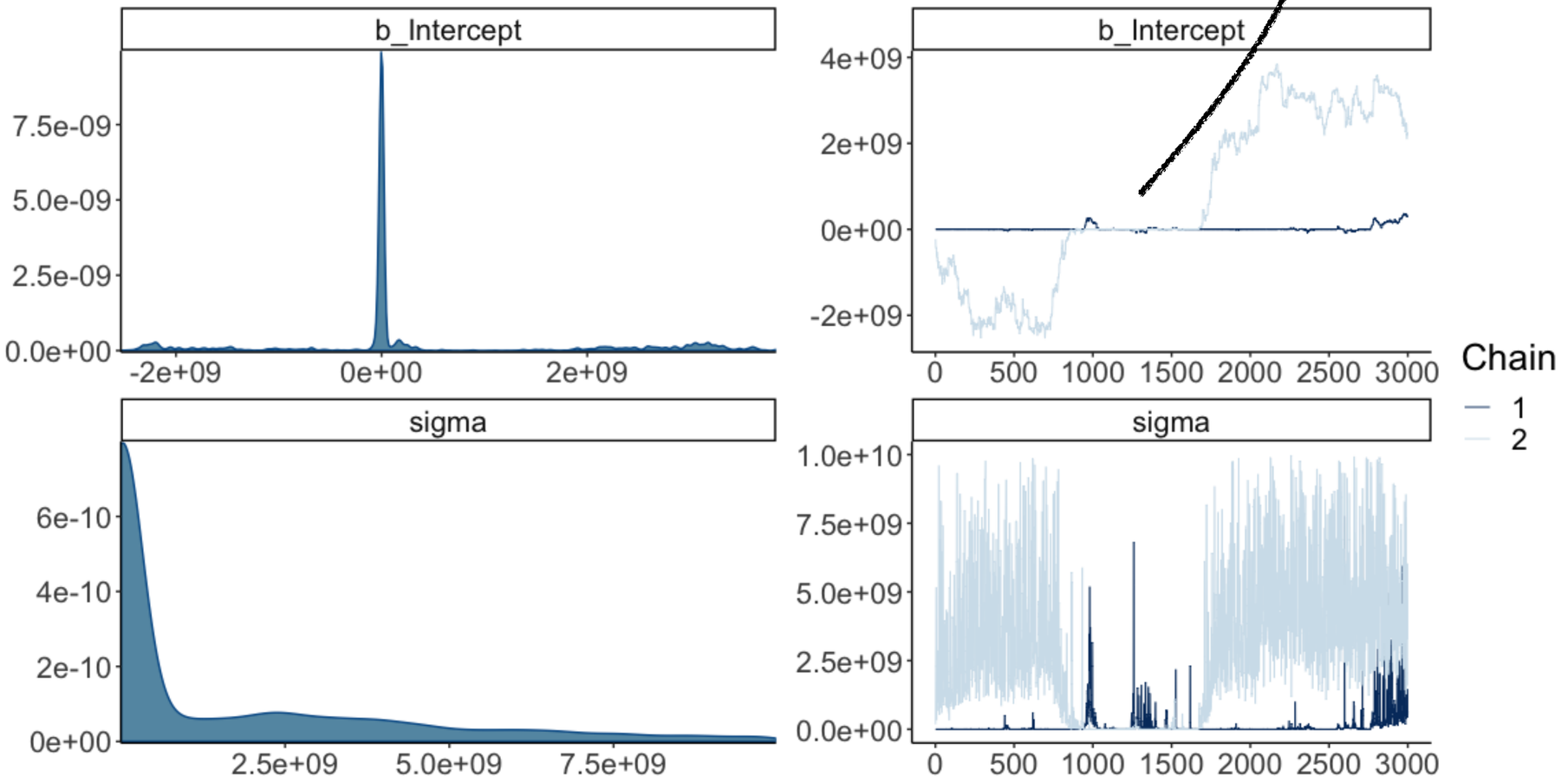
When things don't work out

```
summary(fit.brm_wrong)
```

```
The model has not converged (some Rhats are > 1.1). Do not analyse the results!
We recommend running more iterations and/or setting stronger priors.There were 1203 divergent
transitions after warmup. Increasing adapt_delta above 0.8 may help.
See http://mc-stan.org/misc/warnings.html#divergent-transitions-after-warmup Family: gaussian
  Links: mu = identity; sigma = identity
Formula: y ~ 1
   Data: df.data (Number of observations: 2)
Samples: 2 chains, each with iter = 4000; warmup = 1000; thin = 1;
         total post-warmup samples = 6000

Population-Level Effects:
             Estimate     Est.Error       l-95% CI      u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept 357550121.58 1416057299.71 -2244033111.47 3333594132.43 1.78        3       24

Family Specific Parameters:
           Estimate     Est.Error l-95% CI      u-95% CI Rhat Bulk_ESS Tail_ESS
sigma 1524412740.64 2392424321.98 21668.93 8317582240.06 1.40        4       41

Samples were drawn using sampling(NUTS). For each parameter, Eff.Sample
is a crude measure of effective sample size, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).
```

When things don't work out

doesn't look like a fuzzy caterpillar



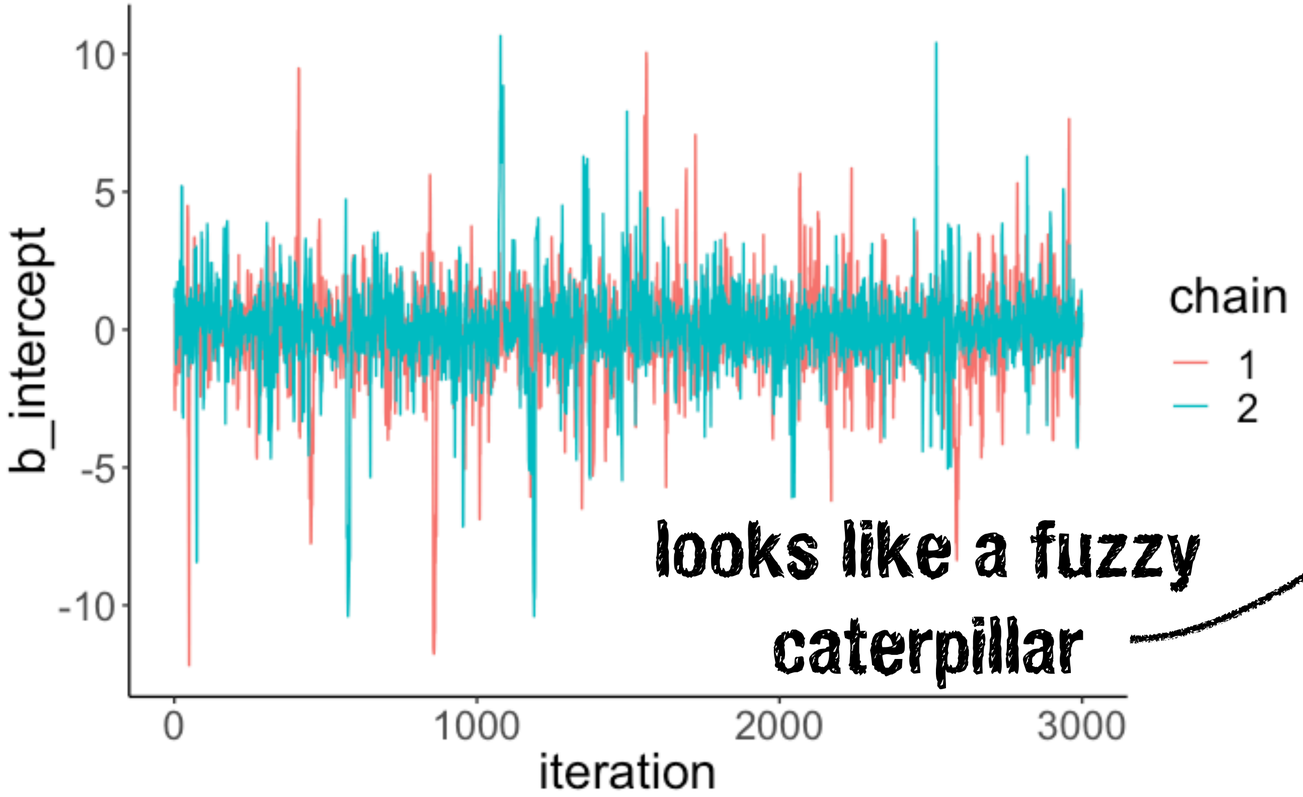
Having somewhat informative priors fixes things

```
1  fit.brm_right = brm(data = df.data,
2                      family = gaussian,
3                      formula = y ~ 1,
4                      prior = c(prior(normal(0, 10), class = Intercept), # more reasonable priors
5                                prior(cauchy(0, 1), class = sigma)),
6                      iter = 4000,
7                      warmup = 1000,
8                      chains = 2,
9                      seed = 1,
10                     file = "cache/brm_right")
```

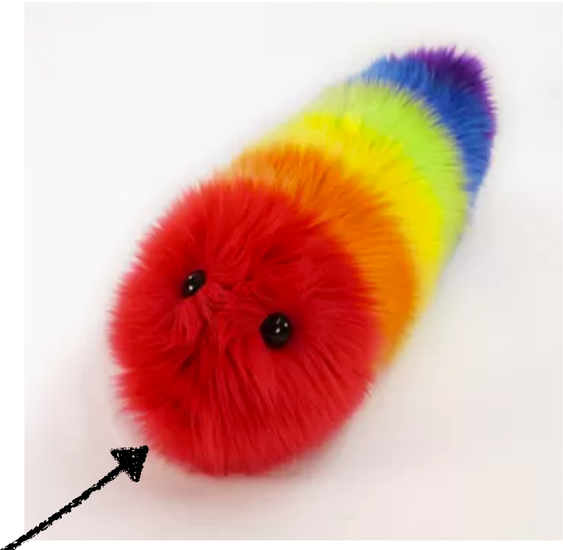
more reasonable priors

```
Family: gaussian
  Links: mu = identity; sigma = identity
Formula: y ~ 1
   Data: list(y = c(-1, 1)) (Number of observations: 2)
Samples: 2 chains, each with iter = 4000; warmup = 1000; thin = 1;
         total post-warmup samples = 6000

Population-Level Effects:
          Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat
Intercept    -0.06      1.72    -3.78     3.27       1033 1.00

Family Specific Parameters:
      Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat
sigma     2.21      6.99     0.61     6.92       1006 1.00

Samples were drawn using sampling(NUTS). For each parameter, Eff.Sample
is a crude measure of effective sample size, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).
```

Having somewhat informative priors fixes things



looks like a fuzzy caterpillar



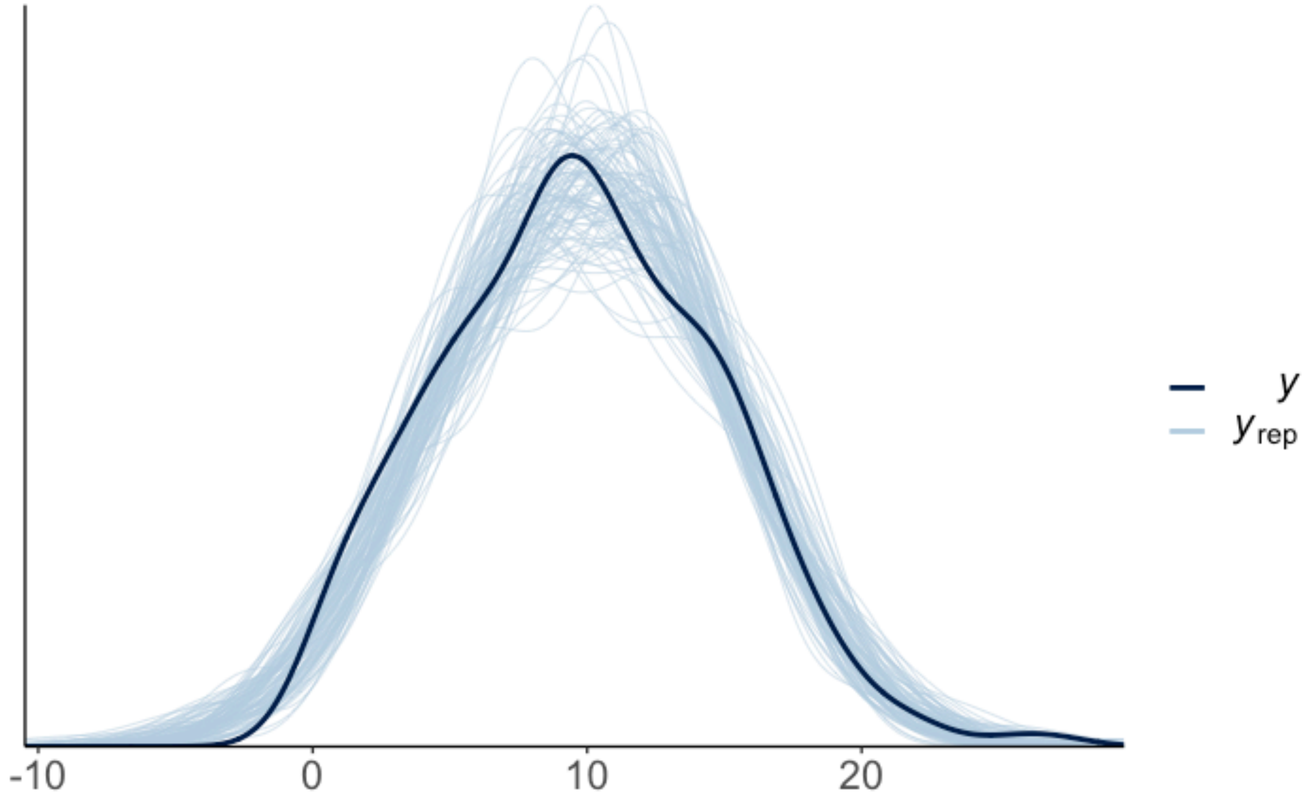
if things go wrong:

- set more informative priors
- run more warm-up samples
- adjust the sampling algorithm as suggested via the `control` argument

2. Visualize model predictions

Posterior predictive check

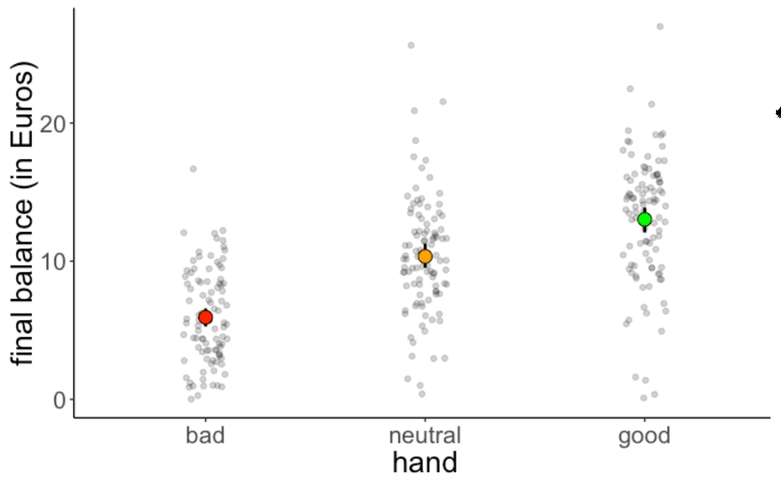
```
pp_check(fit.brm, nsamples = 100)
```



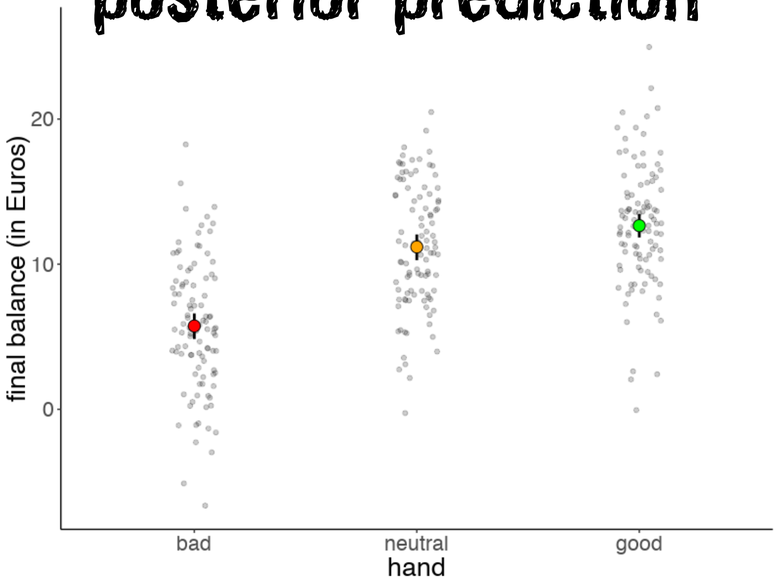
The model accurately captures the distribution of the response variable

Posterior predictive check

original data



posterior prediction

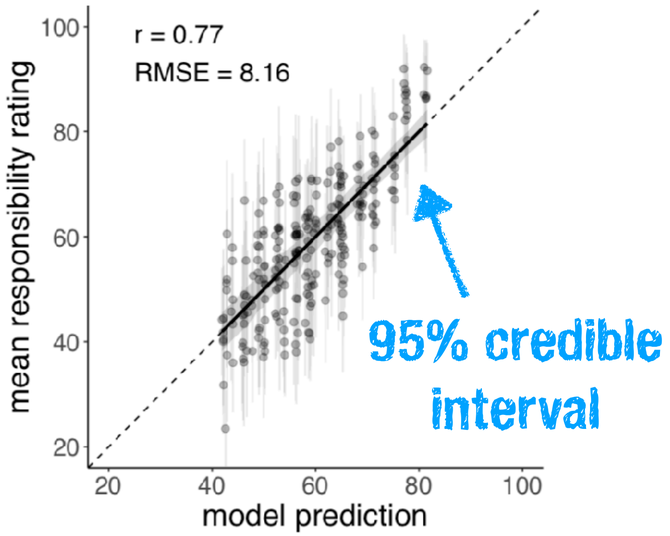


take a look at course notes for how to make these

Reporting results

Reporting results

Plots



Tables

Table 1

Estimates of the mean, standard error, and 95% HDIs of the different predictors in the Bayesian mixed effects model. Note: `n_causes` *= number of causes.*

```
responsibility ~ 1 + surprise + pivotality + n_causes + (1 + surprise + pivotality + n_causes | participant)
```

term	estimate	std.error	lower 95% HDI	upper 95% HDI
intercept	59.94	3.25	54.70	65.22
surprise	21.68	4.57	14.17	29.23
pivotality	13.52	1.82	10.47	16.53
n_causes	-5.72	0.50	-6.55	-4.90

model formula

parameter estimates

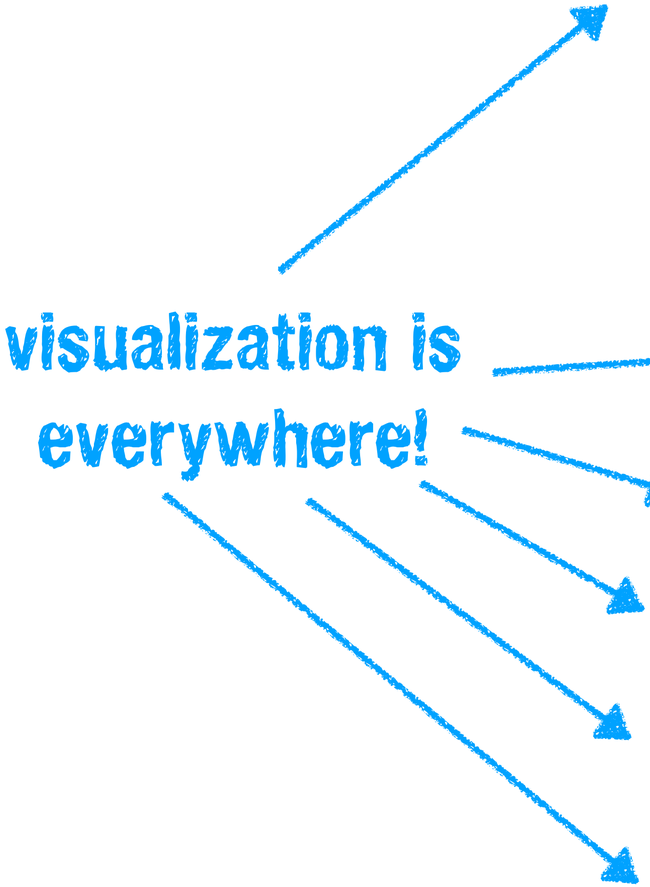
Text

We computed a Bayesian mixed effects model with random intercepts and slopes to predict participants' responsibility judgments (see Table 1). Figure 6b shows a scatter plot of the model predictions and participants' responsibility judgments for the full set of 170 scenarios (with 250 judgments). Overall, the model predicts participants' responsibility judgments well with r = .77 and RMSE = 8.16. Table 1 shows the estimates of the different predictors. As can be seen, none of the predictors' 95% HDIs overlap with 0.[1]

[1]For any statistical claim, we report the mean of the posterior distribution together with the 95% highest-density interval (HDI). All Bayesian models were written in Stan (Carpenter et al., 2017) and accessed with the brms package (Bürkner, 2017) in R (R Core Team, 2019).

Some more examples

Recipe for Bayesian analysis with `brms`

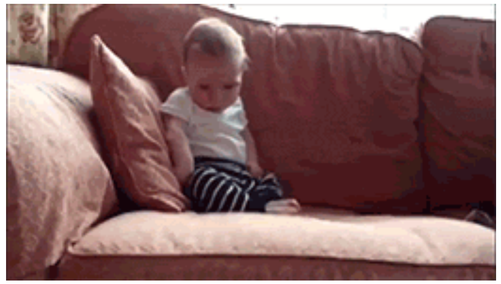


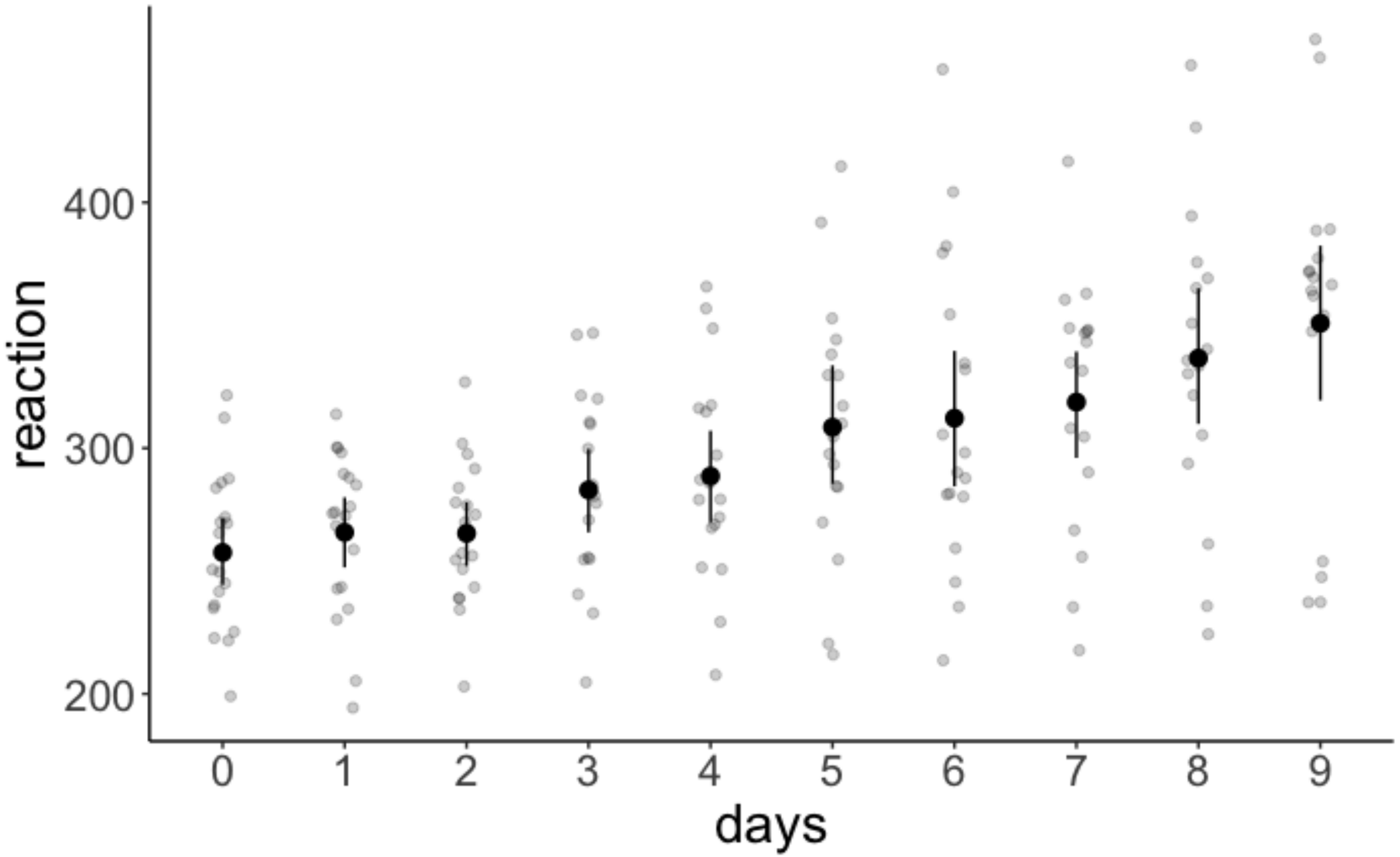
1. Visualize the data
2. Specify and fit the model
3. Model evaluation
   a) Did the inference work?
   b) Visualize model predictions
4. Interpret the model parameters
5. Test specific hypotheses
6. Report results

Sleep data

1. Visualize the data

Feeling sleepy?

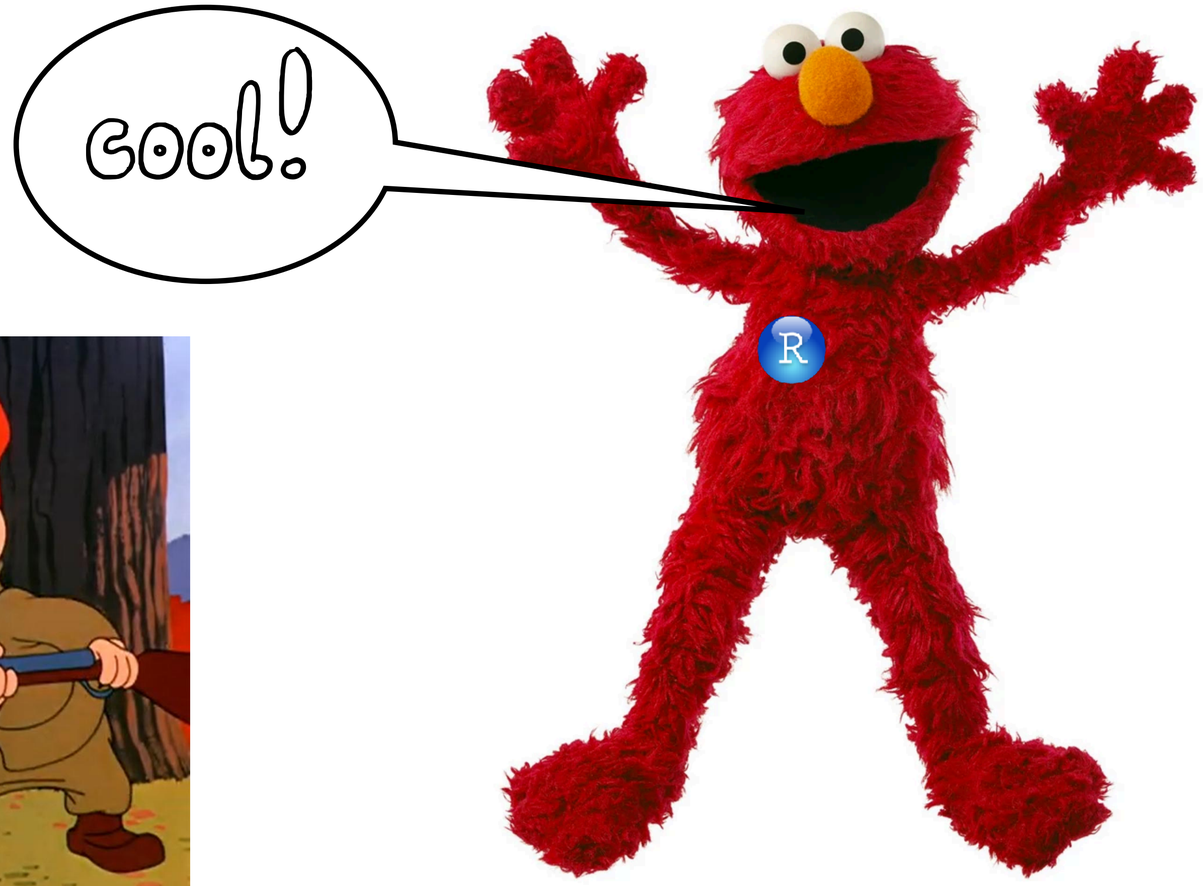




2. Specify and fit the model

1. Specify and fit the model

```
1 fit.brm_sleep = brm(formula = reaction ~ 1 + days + (1 + days | subject),
2                     data = df.sleep,
3                     seed = 1,
4                     file = "cache/brm_sleep")
```



3. Model evaluation

a) Did the inference work?

```
1 fit.brm_sleep %>%
2   summary()
```

```
Family: gaussian
  Links: mu = identity; sigma = identity
Formula: reaction ~ 1 + days + (1 + days | subject)
   Data: df.sleep (Number of observations: 183)
Samples: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
         total post-warmup samples = 4000

Group-Level Effects:
~subject (Number of levels: 20)
                    Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)          26.18      6.25    15.65    40.54 1.00     1879     2463
sd(days)                6.59      1.53     4.14    10.13 1.00     1145     1625
cor(Intercept,days)     0.09      0.29    -0.46     0.67 1.00      993     1526

Population-Level Effects:
          Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept   252.18      6.86   238.47   265.42 1.00     1826     2766
days         10.46      1.69     7.13    13.78 1.00     1203     1782

Family Specific Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sigma    25.77      1.57    22.93    29.14 1.00     3864     2773

Samples were drawn using sampling(NUTS). For each parameter, Eff.Sample
is a crude measure of effective sample size, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).
```

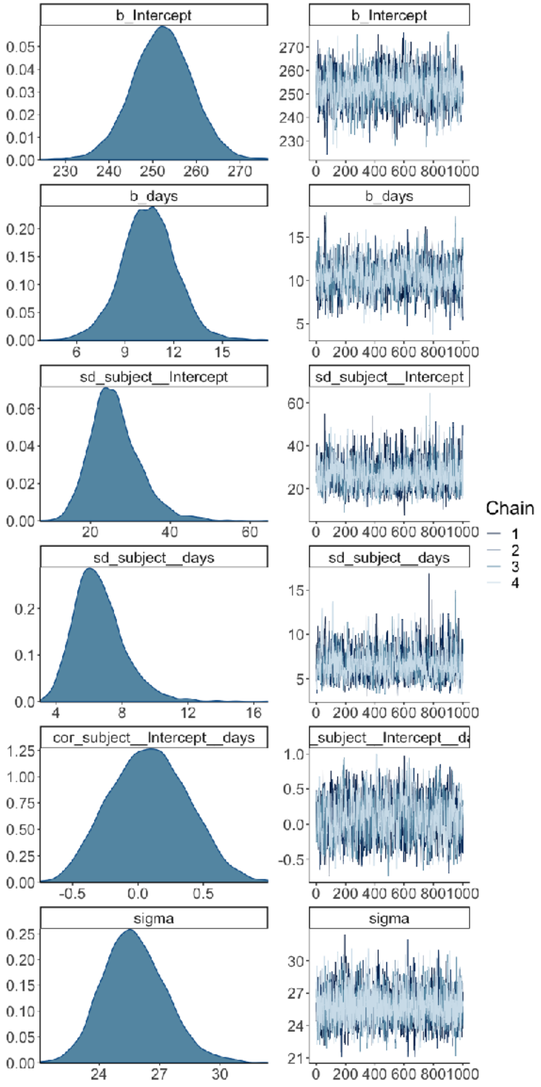
Rhat of 1.00 is good!

Roughly speaking, the effective sample size (**ESS**) of a quantity of interest captures how many independent draws contain the same amount of information as the dependent sample obtained by the MCMC algorithm.

https://mc-stan.org/misc/warnings.html

a) Did the inference work?

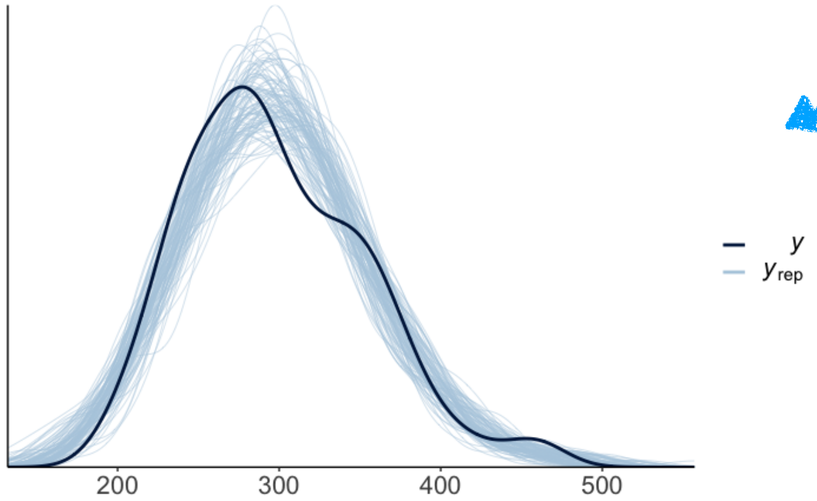
```
1 fit.brm_sleep %>%
2   plot(N = 6)
```



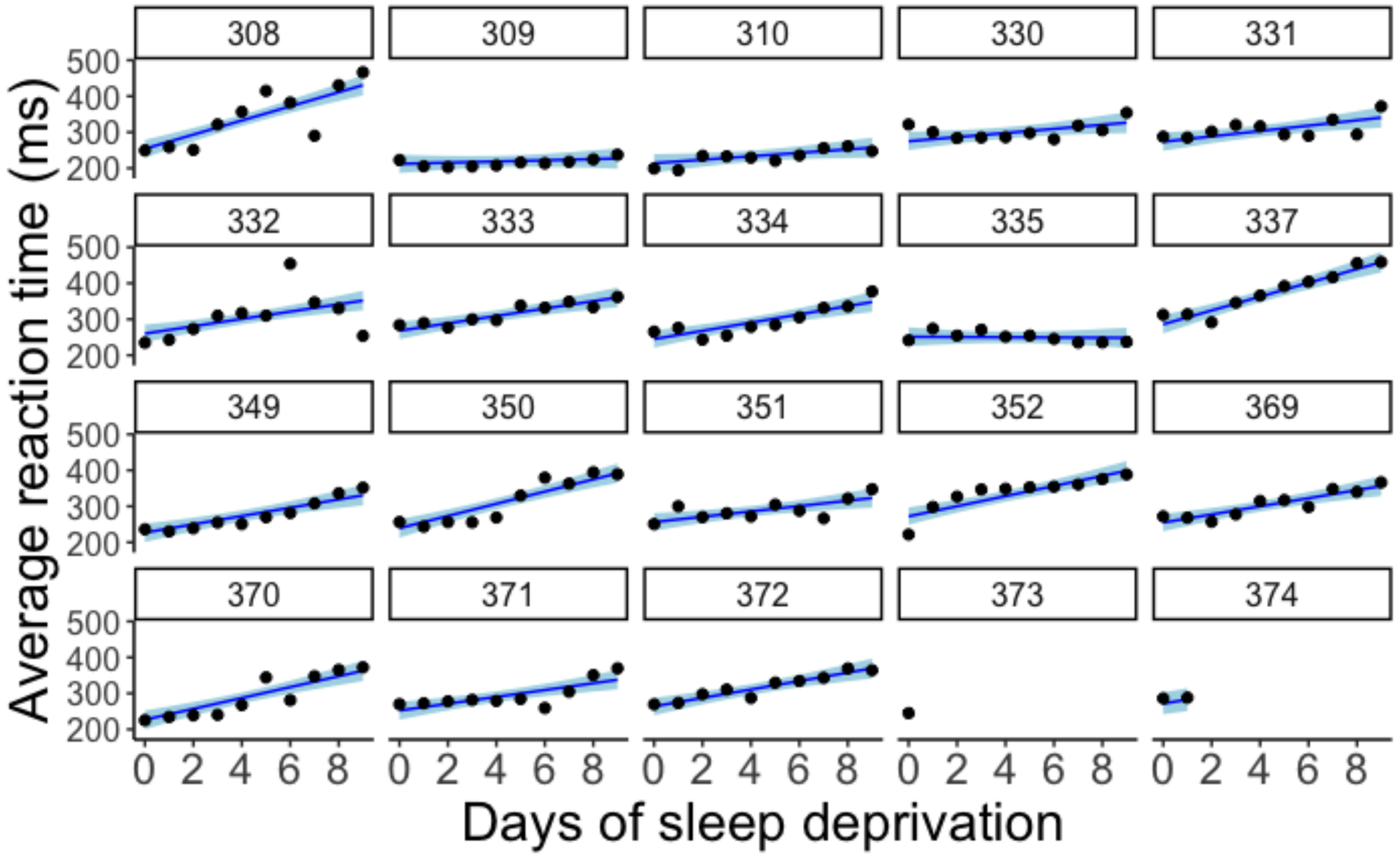
these look good!

also looks good!

```
1 pp_check(fit.brm_sleep,
2           nsamples = 100)
```

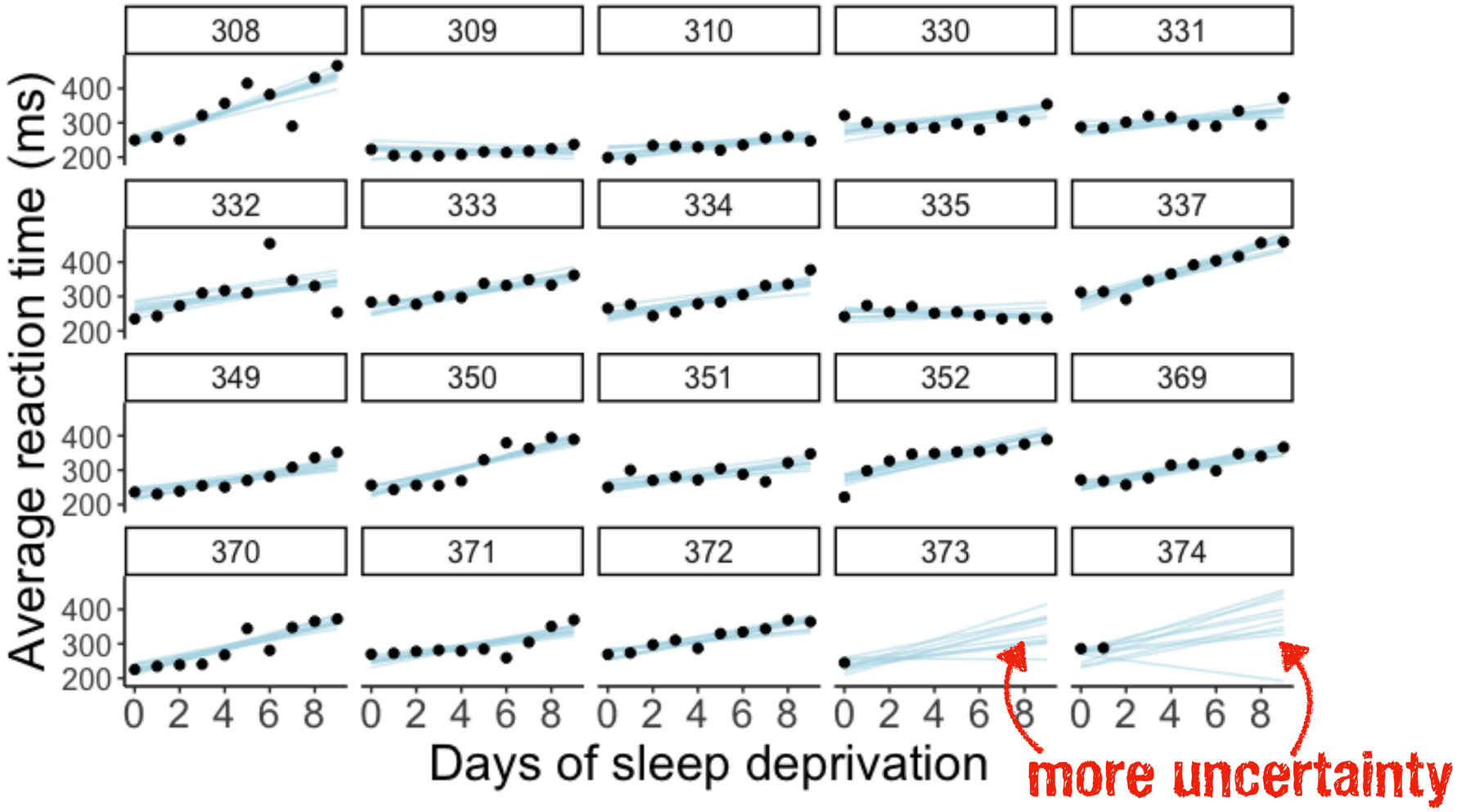


b) Visualize the model predictions



regression lines with 95% highest density intervals

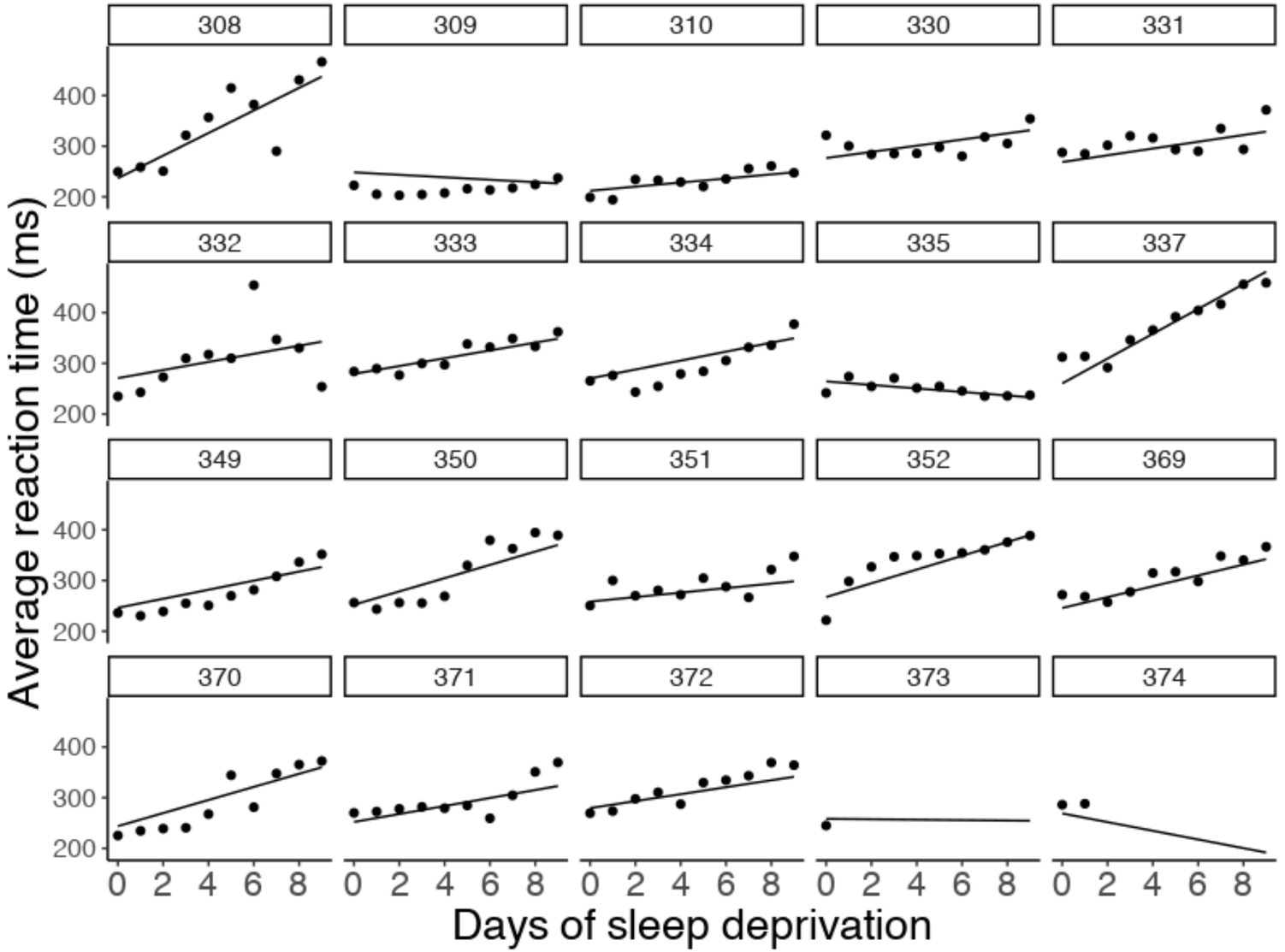
b) Visualize the model predictions



10 random samples from the posterior distribution

b) Visualize the model predictions

if you're feeling fancy



4. Interpret the model parameters

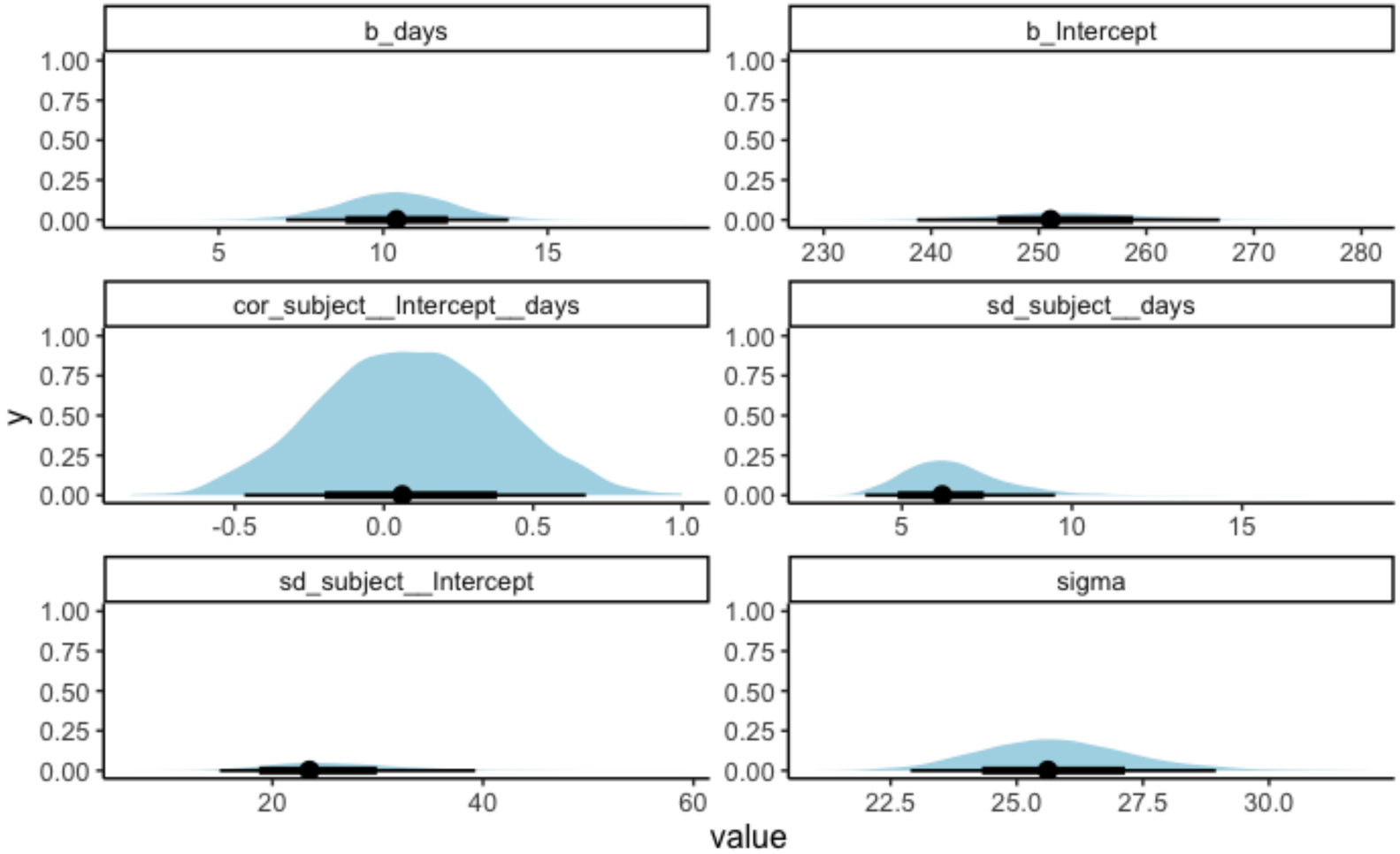
4. Interpret the model parameters

```
1 fit.brm_sleep %>%
2   tidy(conf.method = "HPDinterval")
```

95% highest density interval

effect	component	group	term	estimate	std.error	conf.low	conf.high
fixed	cond	NA	(Intercept)	252.39	7.00	238.69	266.82
fixed	cond	NA	days	10.34	1.72	7.05	13.81
ran_pars	cond	subject	sd__(Intercept)	26.14	6.37	15.00	39.27
ran_pars	cond	subject	sd__days	6.55	1.54	3.92	9.50
ran_pars	cond	subject	cor__(Intercept).days	0.09	0.30	-0.47	0.68
ran_pars	cond	Residual	sd__Observation	25.80	1.54	22.90	28.95

4. Interpret the model parameters



Posterior distribution for most parameters

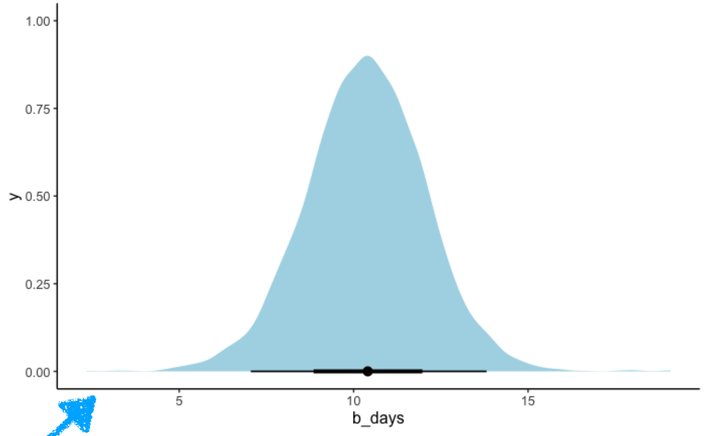
5. Test specific hypotheses

5. Test specific hypotheses

Did reaction times increase with the number of days of sleep deprivation?

```
1 fit.brm_sleep %>%
2    summary()
```

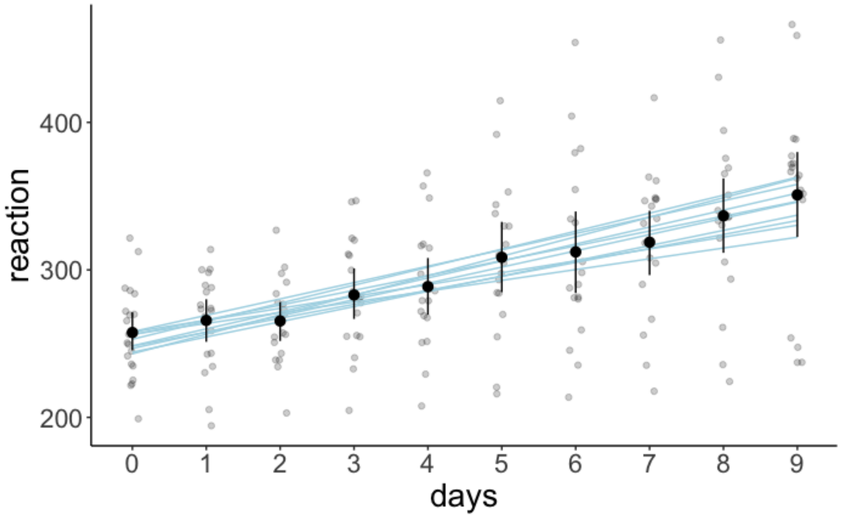
```
Family: gaussian
  Links: mu = identity; sigma = identity
Formula: reaction ~ 1 + days + (1 + days | subject)
   Data: df.sleep (Number of observations: 183)
Samples: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
         total post-warmup samples = 4000

Group-Level Effects:
~subject (Number of levels: 20)
                    Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)          26.18      6.25    15.65    40.54 1.00     1879     2463
sd(days)                6.59      1.53     4.14    10.13 1.00     1145     1625
cor(Intercept,days)     0.09      0.29    -0.46     0.67 1.00      993     1526

Population-Level Effects:
          Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept   252.18      6.86   238.47   265.42 1.00     1826     2766
days         10.46      1.69     7.13    13.78 1.00     1203     1782

Family Specific Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sigma    25.77      1.57    22.93    29.14 1.00     3864     2773

Samples were drawn using sampling(NUTS). For each parameter, Eff.Sample
is a crude measure of effective sample size, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).
```



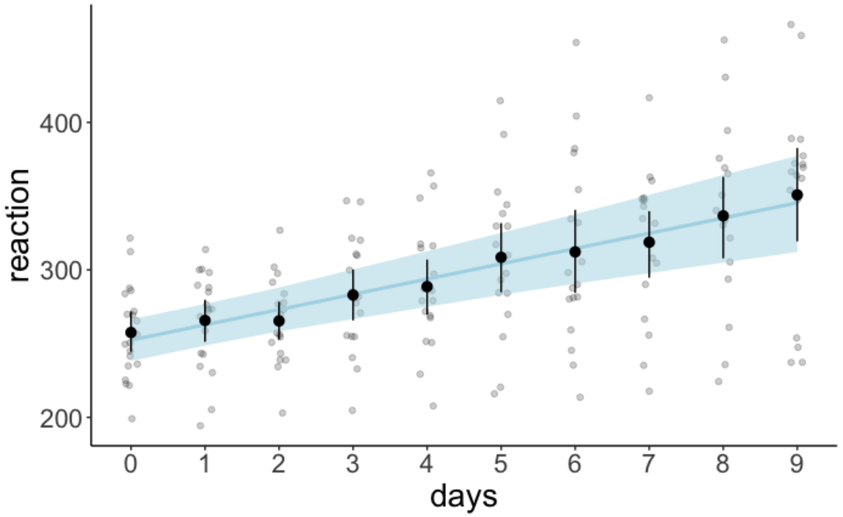
6. Report results

6. Report results

10 draws from the posterior



credible intervals



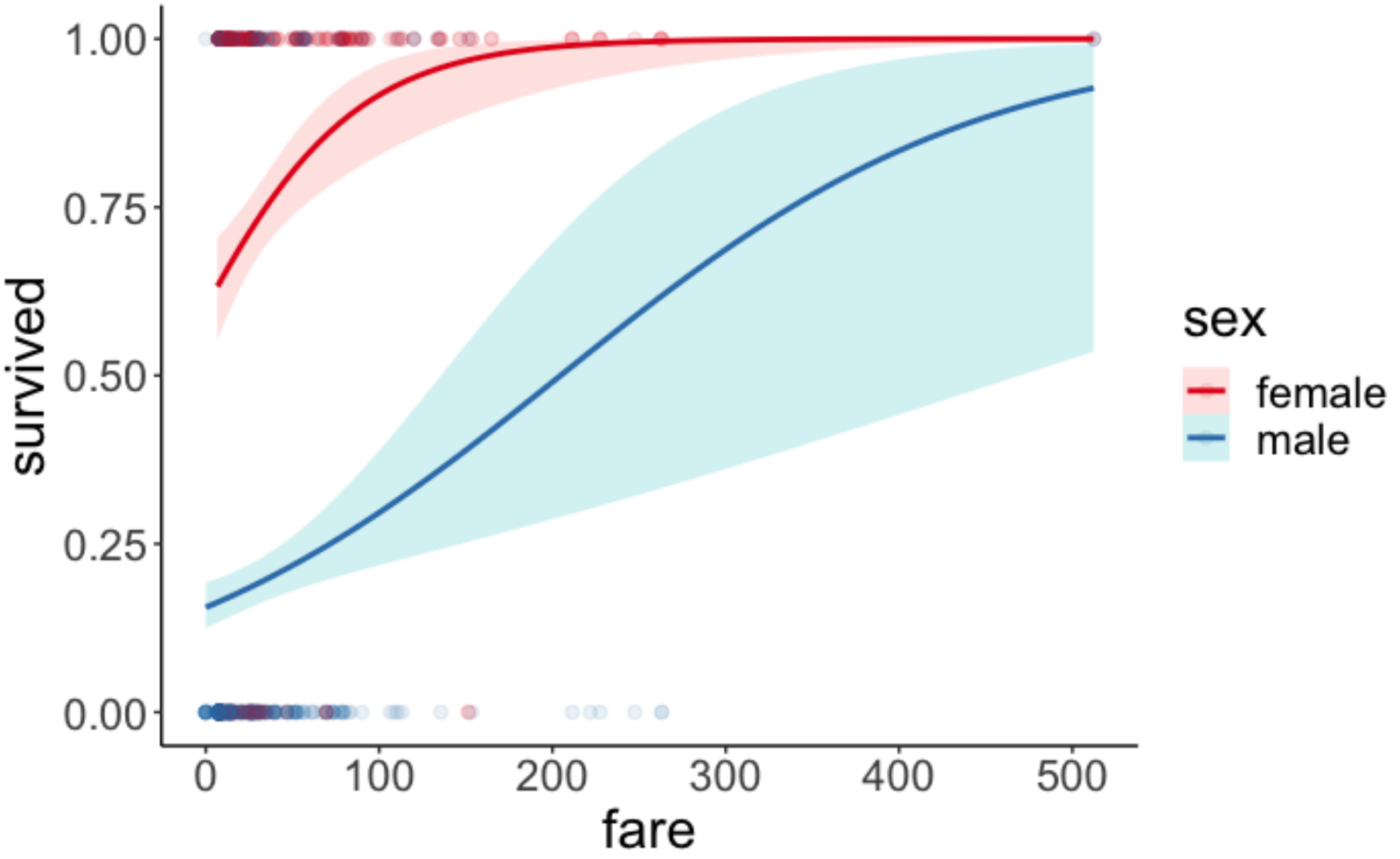
With each day of sleep deprivation, the reaction time increased by 10.5ms (95% HDI: 7.13, 13.78).

Recipe for Bayesian analysis with `brms`

1. Visualize the data
2. Specify and fit the model
3. Model evaluation
   a) Did the inference work?
   b) Visualize model predictions
4. Interpret the model parameters
5. Test specific hypotheses
6. Report results

Titanic data

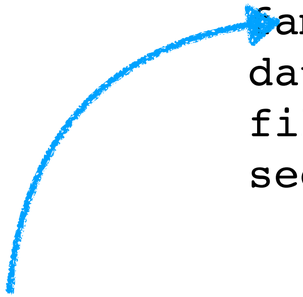
1. Visualize the data


1.00
0.75
0.50
0.25
0.00
survived
0
100
200
300
400
500
fare
sex
female
male

2. Specify and fit the model

1. Specify and fit the model

```
1 fit.brm_titanic = brm(formula = survived ~ 1 + fare * sex,
2                       family = "bernoulli",
3                       data = df.titanic,
4                       file = "cache/brm_titanic",
5                       seed = 1)
```



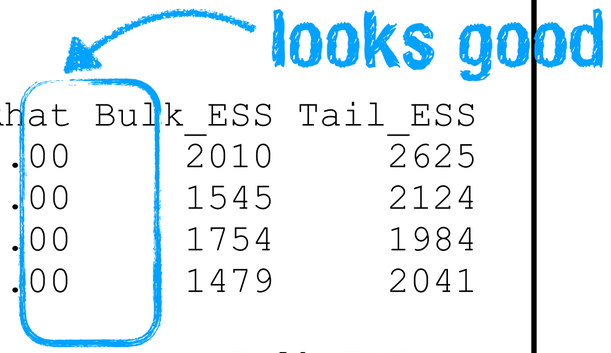
just need to
change the family

3. Model evaluation

a) Did the inference work?

```
1 fit.brm_titanic %>%
2    summary()
```

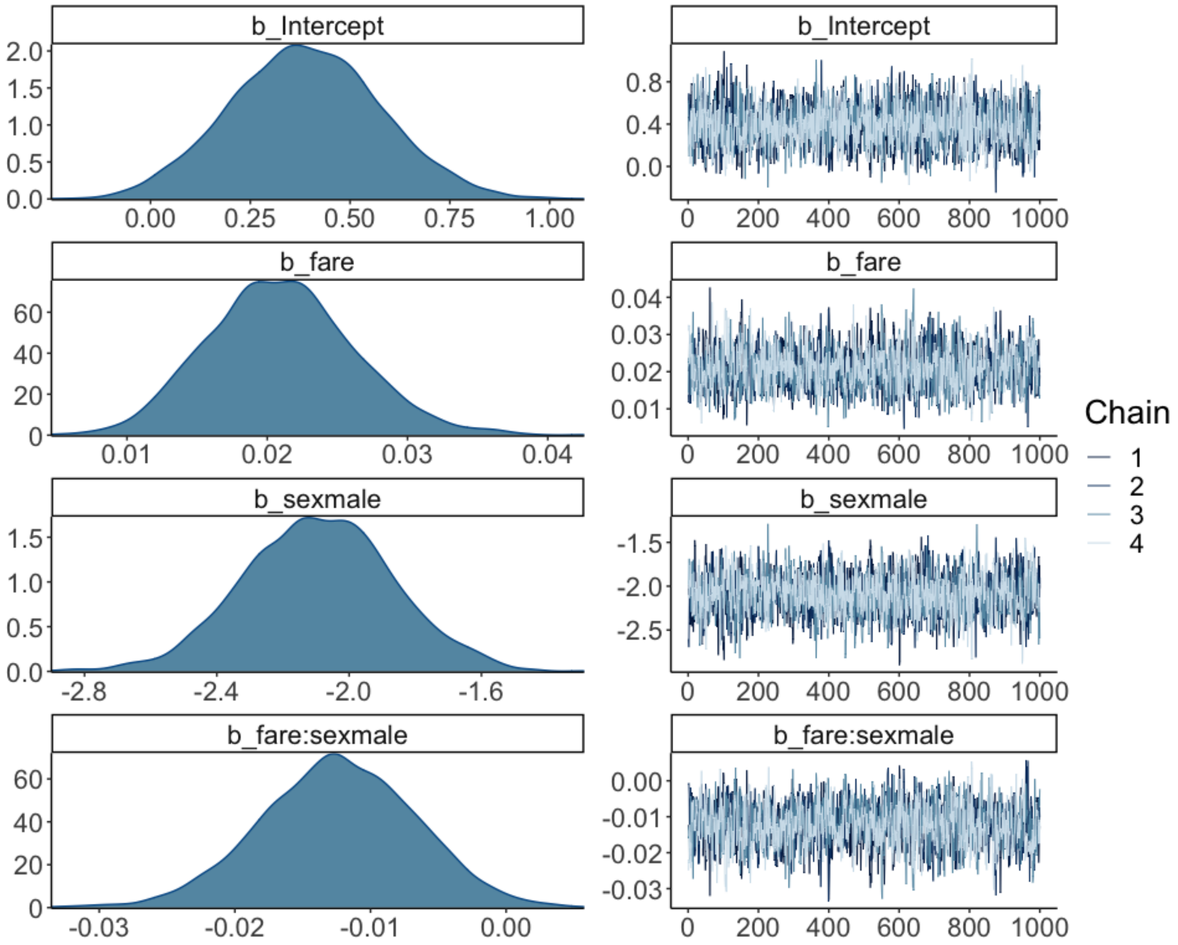
```
 Family: bernoulli
  Links: mu = logit
Formula: survived ~ 1 + fare * sex
   Data: df.titanic (Number of observations: 891)
Samples: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
         total post-warmup samples = 4000

Population-Level Effects:
             Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept        0.39      0.19     0.03     0.76 1.00     2010     2625
fare             0.02      0.01     0.01     0.03 1.00     1545     2124
sexmale         -2.09      0.23    -2.54    -1.65 1.00     1754     1984
fare:sexmale    -0.01      0.01    -0.02    -0.00 1.00     1479     2041

Samples were drawn using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).
```



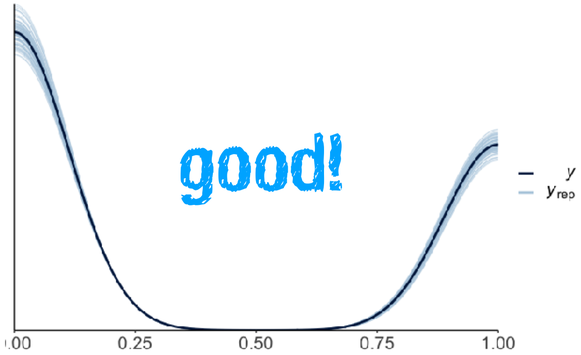
https://mc-stan.org/misc/warnings.html

a) Did the inference work?

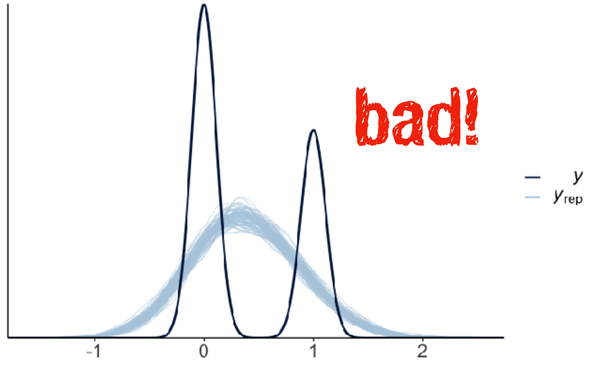
```
1 fit.brm_titanic %>%
2   plot()
```



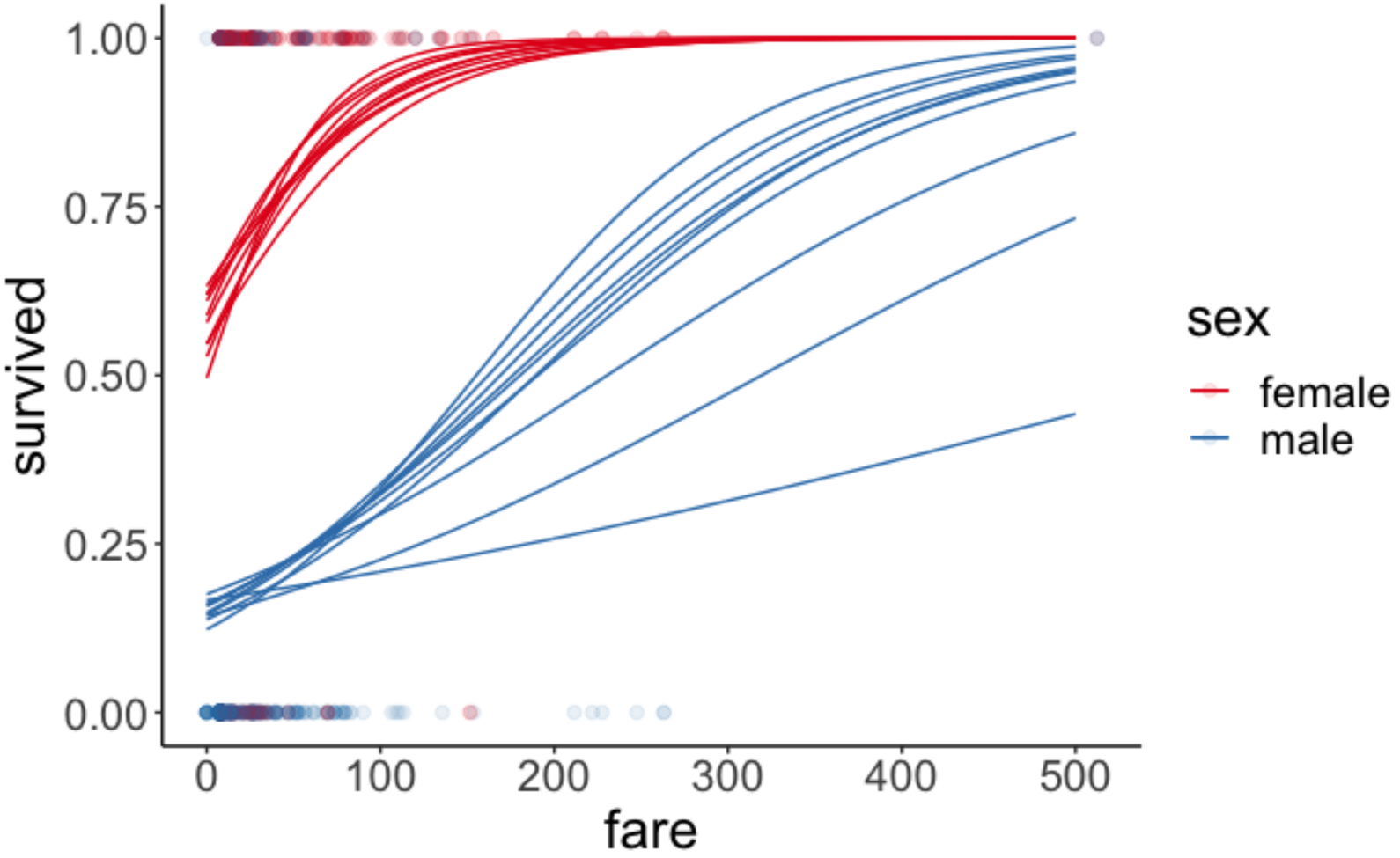

```
1 pp_check(fit.brm_titanic,
2            nsamples = 100)
```



model with Gaussian family



b) Visualize the model predictions



4. Interpret the model parameters

4. Interpret the model parameters

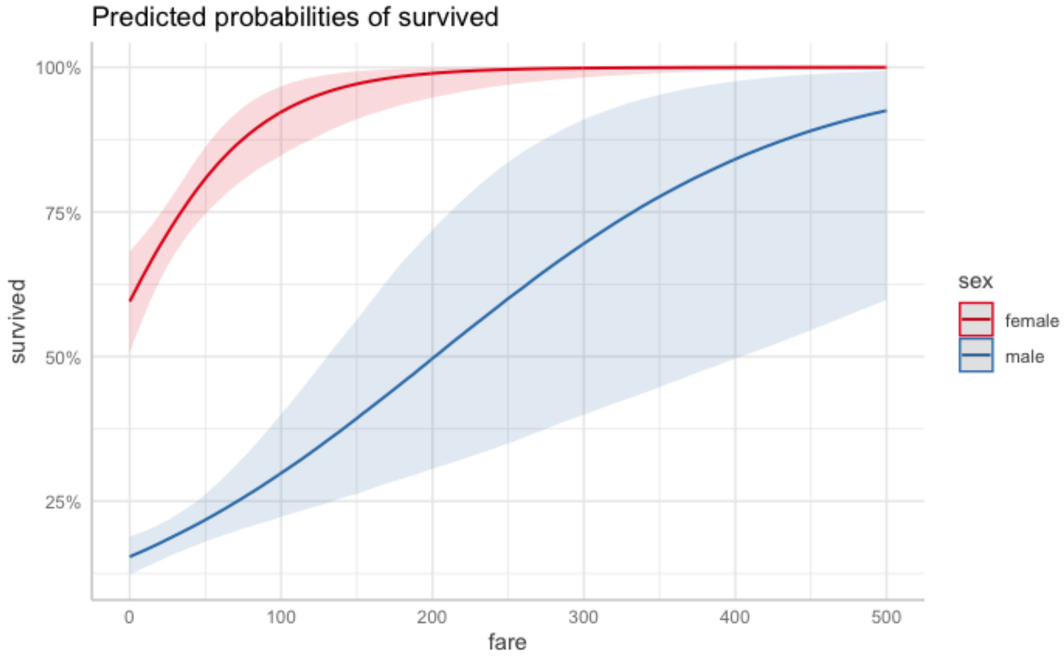
```
 Family: bernoulli
  Links: mu = logit
Formula: survived ~ 1 + fare * sex
   Data: df.titanic (Number of observations: 891)
Samples: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
         total post-warmup samples = 4000

Population-Level Effects:
             Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept        0.39      0.19     0.03     0.76 1.00     2010     2625
fare             0.02      0.01     0.01     0.03 1.00     1545     2124
sexmale         -2.09      0.23    -2.54    -1.65 1.00     1754     1984
fare:sexmale    -0.01      0.01    -0.02    -0.00 1.00     1479     2041

Samples were drawn using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).
```

log odds

4. Interpret the model parameters


```
1 fit.brm_titanic %>%
2   ggpredict(terms = c("fare [0:500]", "sex"))
```

```
# Predicted probabilities of survived
# x = fare

# sex = female

  x | Predicted |       95% CI
------------------------------
  0 |      0.60 | [0.51, 0.68]
 83 |      0.89 | [0.82, 0.95]
167 |      0.98 | [0.93, 1.00]
250 |      1.00 | [0.97, 1.00]
333 |      1.00 | [0.99, 1.00]
500 |      1.00 | [1.00, 1.00]

# sex = male

  x | Predicted |       95% CI
------------------------------
  0 |      0.15 | [0.12, 0.19]
 83 |      0.27 | [0.21, 0.35]
167 |      0.43 | [0.28, 0.62]
250 |      0.60 | [0.35, 0.84]
333 |      0.75 | [0.43, 0.94]
500 |      0.93 | [0.60, 0.99]
```



5. Test specific hypotheses

5. Test specific hypotheses

Were women more likely to survive than men?

```
1 fit.brm_titanic %>%
2   emmeans(specs = pairwise ~ sex,
3           type = "response")
```

$$\frac{(\frac{p_f}{1-p_f})}{(\frac{p_m}{1-p_m})}$$

```
NOTE: Results may be misleading due to involvement in interactions
$emmeans
 sex    response lower.HPD upper.HPD
 female    0.743      0.69     0.795
 male      0.194      0.16     0.225

Point estimate displayed: median
Results are back-transformed from the logit scale
HPD interval probability: 0.95

$contrasts
 contrast      odds.ratio lower.HPD upper.HPD
 female / male       12.1      8.39      16.6

Point estimate displayed: median
Results are back-transformed from the log odds ratio scale
HPD interval probability: 0.95
```

5. Test specific hypotheses

Was the effect of fare on survival different for men vs women?

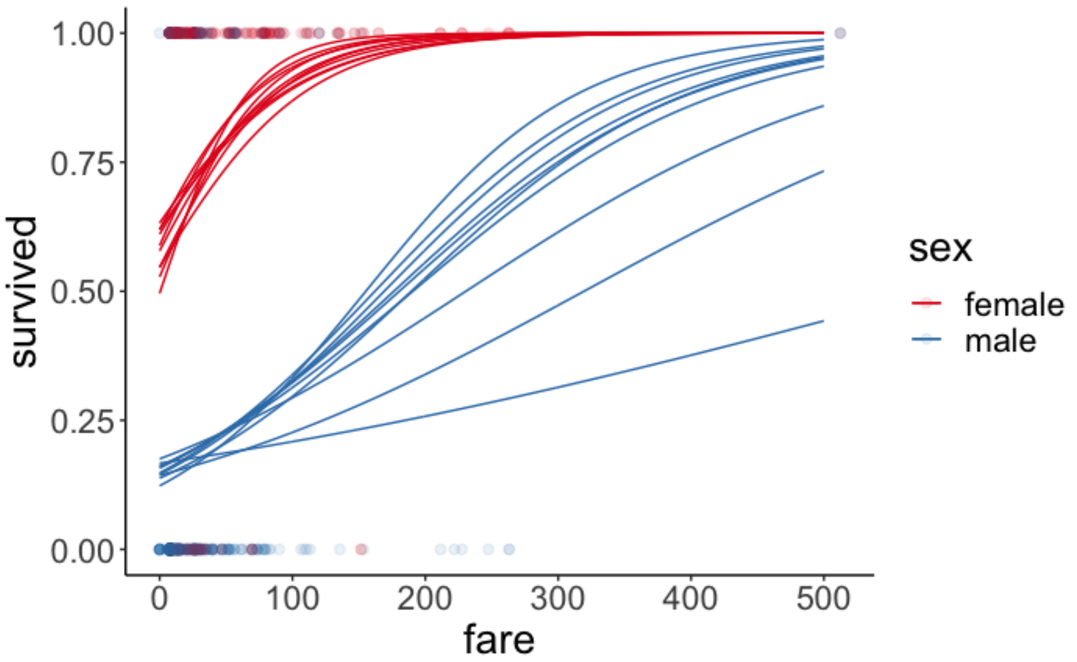
```
1 fit.brm_titanic %>%
2   emtrends(specs = pairwise ~ sex,
3            var = "fare")
```

```
$emtrends
 sex     fare.trend lower.HPD upper.HPD
 female     0.02083   0.01129     0.0316
 male       0.00845   0.00385     0.0135

Point estimate displayed: median
HPD interval probability: 0.95

$contrasts
 contrast       estimate lower.HPD upper.HPD
 female - male    0.0124  0.000884     0.0232

Point estimate displayed: median
HPD interval probability: 0.95
```

the chance of survival increased more with fare for female than male passengers

6. Report results

6. Report results



Female passengers were more likely to survive (74.3%) than male passengers (19.4%). The estimated odds ratio of survival for female vs. male passengers was 12.1 [8.4, 16.6].

The chance of survival increased more with fare for female compared to male passengers. The difference in slopes on the log odds scale was 0.01 [0, 0.02].

Going beyond

Evidence for the null hypothesis

Evidence for the null hypothesis

- There is nothing special about H_0 compared to H_1 in Bayesian inference
- We can get evidence of H_0 over H_1 (e.g. using the Bayes factor approach)

Rolling the dice

Four sided

Six sided

both dice are equally likely to be picked

p( ) = p( ) = 0.5

both dice are equal sided (uniform probability over the different numbers)

Which die do you think was rolled?

4 p(| data) = ?

4, 2, 1 p(| data) = 0.77

4, 2, 1, 3, 1 p(| data) = 0.88

4, 2, 1, 3, 1, 5 p(| data) = 0

Bayes factor

$$BF_{01} = \frac{p(D \mid H_0)}{p(D \mid H_1)}$$

probability of the data given H_0

probability of the data given H_1

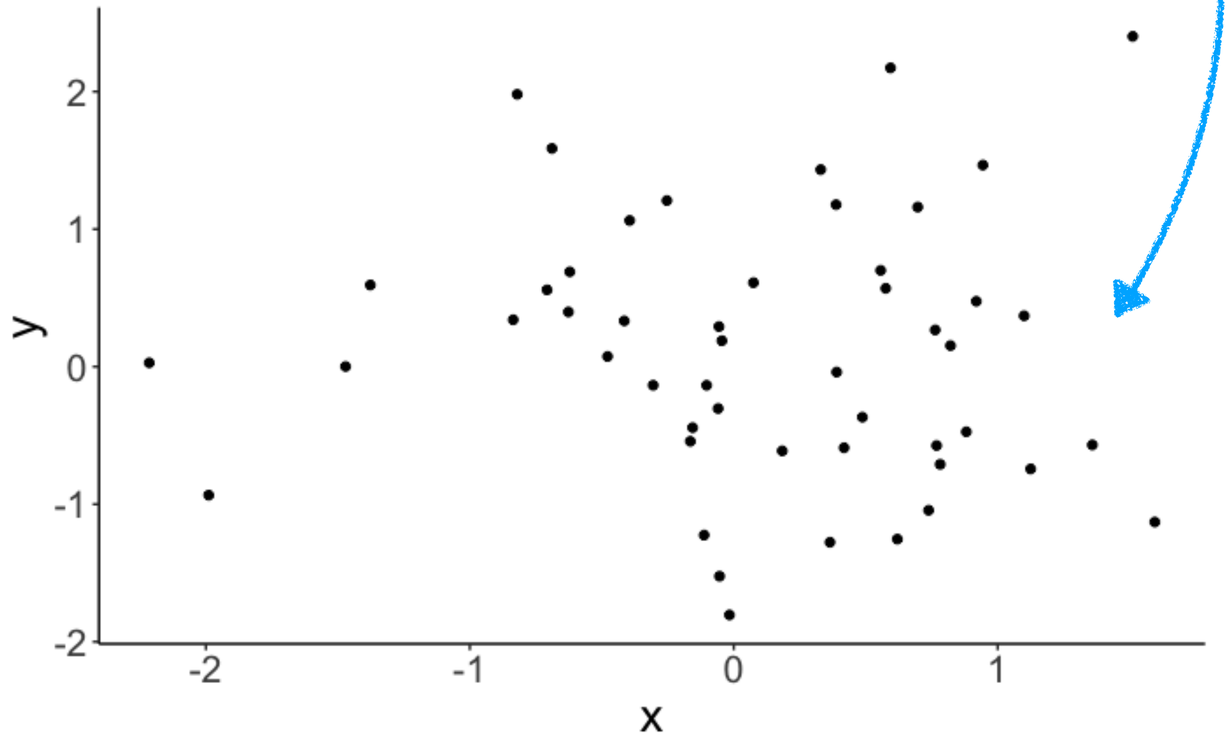
check this out

https://vuorre.netlify.com/post/2017/03/21/bayes-factors-with-brms/

Approximate LOO

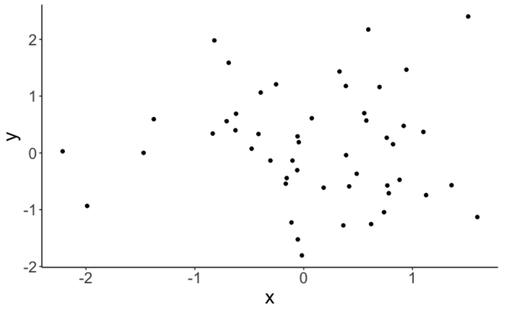
Evidence for the null hypothesis

```
1 set.seed(1)
2 df.loo = tibble(x = rnorm(n = 50),
3                 y = rnorm(n = 50))
4
5 ggplot(data = df.loo,
6        mapping = aes(x = x,
7                      y = y)) +
8   geom_point()
```



no relationship between x and y

Evidence for the null hypothesis

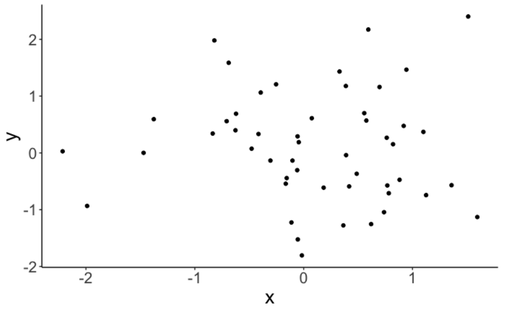



```
1 fit.lm_loo = lm(formula = y ~ 1 + x,
2                 data = df.loo)
3
4 fit.lm_loo %>%
5   summary()
```

```
Call:
lm(formula = y ~ 1 + x, data = df.loo)

Residuals:
    Min      1Q  Median      3Q     Max
-4.2185 -0.6735  0.0018  0.6734  4.2428

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)  0.0006437  0.0031639   0.203    0.839
x           -0.0019184  0.0031541  -0.608    0.543

Residual standard error: 1.001 on 99998 degrees of freedom
Multiple R-squared:  3.7e-06,  Adjusted R-squared:  -6.301e-06
F-statistic:  0.37 on 1 and 99998 DF,  p-value: 0.543
```

cannot reject the H_0 that the reduction in error due to x is what one would have expected by chance

Evidence for the null hypothesis




```
fit.brm_loo1 = brm(formula = y ~ 1, data = df.loo)

fit.brm_loo2 = brm(formula = y ~ 1 + x, data = df.loo)

fit.brm_loo1 = add_criterion(fit.brm_loo1, criterion = "loo")

fit.brm_loo2 = add_criterion(fit.brm_loo2, criterion = "loo")
```

approximate leave-one-out cross-validation

```
loo_compare(fit.brm_loo1, fit.brm_loo2)
```

```
             elpd_diff se_diff
fit.brm_loo1  0.0       0.0
fit.brm_loo2 -1.1       0.5
```

```
model_weights(fit.brm_loo1, fit.brm_loo2)
```

```
fit.brm_loo1 fit.brm_loo2
99.99999     0.00001
```

I want only positive coefficients!

I only want positive coefficients!

```
brm(formula = how_much_i_love_stats ~ 1 + tobi + ari + beth + satchel + shawn,
    data = df.stats_love)
```

coefficients in the model

```
# priors
priors = c(set_prior("normal(0,10)", class = "b", lb = 0))
```

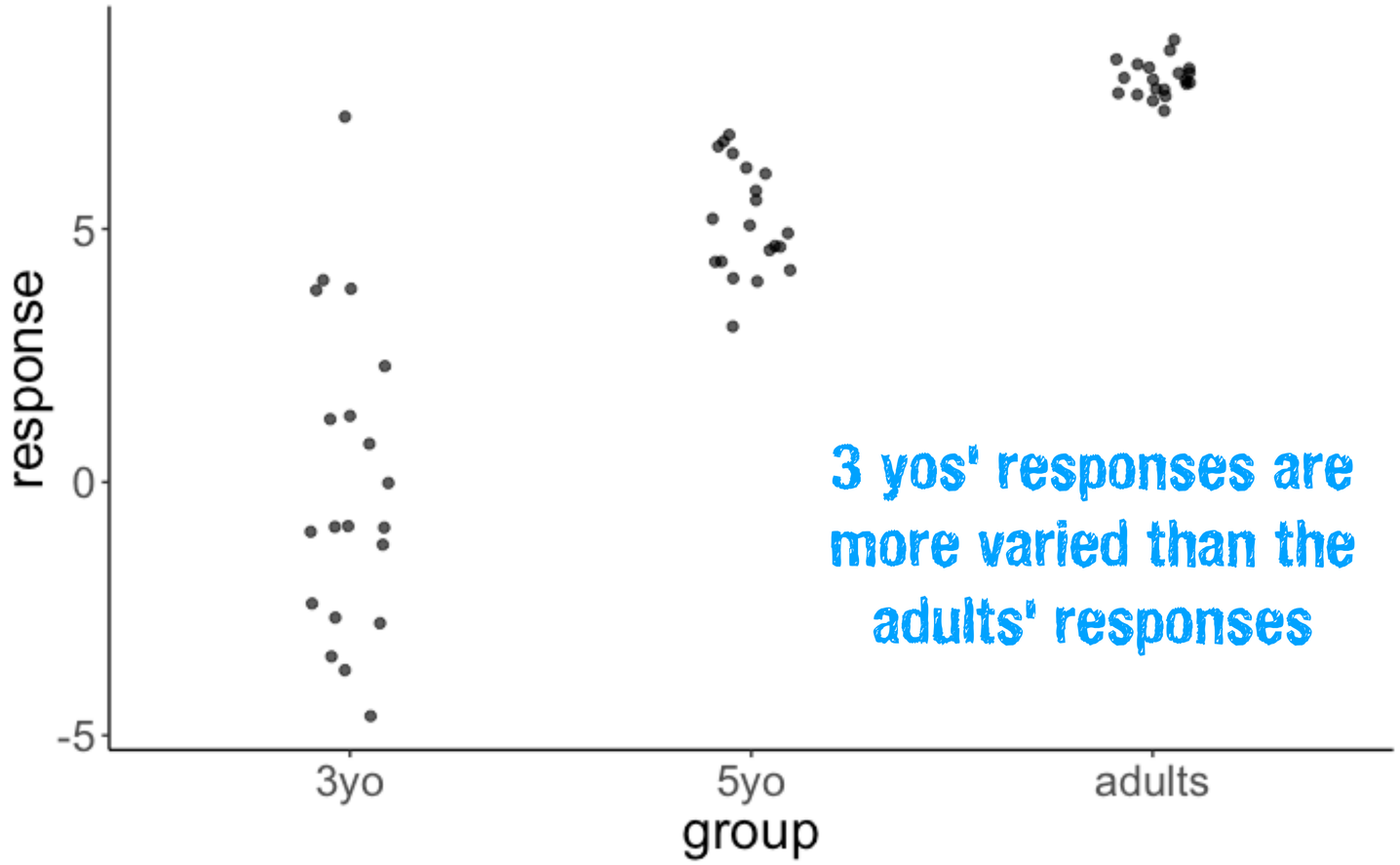
lower bound = 0

```
brm(formula = how_much_i_love_stats ~ 1 + tobi + ari + beth + satchel + shawn,
    prior = priors,
    data = df.stats_love)
```

Dealing with unequal variance

Unequal variance aka heteroscedasticity

```
df.variance = tibble(group = rep(c("3yo", "5yo", "adults"), each = 20),
                     response = rnorm(n = 60,
                                      mean = rep(c(0, 5, 8), each = 20),
                                      sd = rep(c(3, 1.5, 0.3), each = 20)))
```



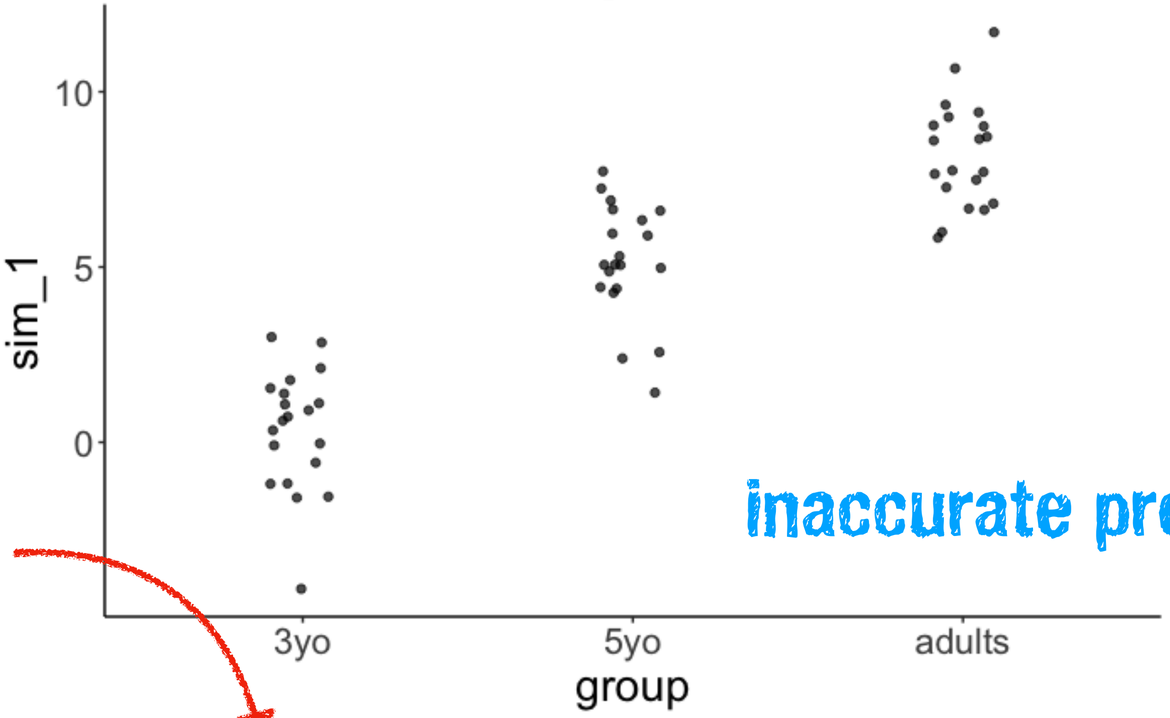
Unequal variance aka heteroscedasticity

```r
fit.lm1 = lm(formula = response ~ 1 + group,
             data = df.variance)

fit.lm1 %>%
  summary()
```

```
Call:
lm(formula = response ~ 1 + group, data = df.variance)

Residuals:
    Min      1Q  Median      3Q     Max
-4.6145 -0.8288 -0.0879  0.6315  7.2193

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.005336   0.421618  -0.013     0.99
group5yo     5.172810   0.596258   8.675 5.25e-12 ***
groupadults  7.970655   0.596258  13.368  < 2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 1.886 on 57 degrees of freedom
Multiple R-squared:  0.7635,   Adjusted R-squared:  0.7552
F-statistic: 91.99 on 2 and 57 DF,  p-value: < 2.2e-16
```

Unequal variance aka heteroscedasticity

```
1 fit.lm1 %>%
2   simulate() %>%
3   bind_cols(df.variance) %>%
4   ggplot(aes(x = group, y = sim_1)) +
5   geom_jitter(height = 0,
6               width = 0.1,
7               alpha = 0.7)
```



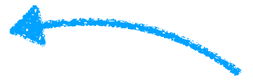
only one standard deviation fitted

inaccurate predictions ...

r.squared	adj.r.squared	sigma	statistic	p.value	df	logLik	AIC	BIC	deviance	df.residual
0.76	0.76	1.89	91.99	0	3	-121.65	251.3	259.68	202.65	57

Unequal variance aka heteroscedasticity

```
1 fit.brm1 = brm(formula = bf(response ~ group,
2                              sigma ~ group),
3                data = df.variance,
4                file = "cache/brm1",
5                seed = 1)
```



modeling both the means and variances

```
 Family: gaussian
  Links: mu = identity; sigma = log
Formula: response ~ group
         sigma ~ group
   Data: df.variance (Number of observations: 60)
Samples: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
         total post-warmup samples = 4000

Population-Level Effects:
                 Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept           -0.01      0.73    -1.41     1.51 1.01     1107     1072
sigma_Intercept      1.15      0.17     0.85     1.51 1.00     1991     1922
group5yo             5.18      0.77     3.60     6.65 1.00     1252     1327
groupadults          7.98      0.74     6.47     9.37 1.01     1110     1079
sigma_group5yo      -1.05      0.24    -1.51    -0.57 1.00     2249     2420
sigma_groupadults   -2.19      0.24    -2.66    -1.74 1.00     2171     2427

Samples were drawn using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).
```

Unequal variance aka heteroscedasticity

```
 Family: gaussian
  Links: mu = identity; sigma = log
Formula: response ~ group
         sigma ~ group
   Data: df.variance (Number of observations: 60)
Samples: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
         total post-warmup samples = 4000

Population-Level Effects:
                 Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept           -0.01      0.73    -1.41     1.51 1.01     1107     1072
sigma_Intercept      1.15      0.17     0.85     1.51 1.00     1991     1922
group5yo             5.18      0.77     3.60     6.65 1.00     1252     1327
groupadults          7.98      0.74     6.47     9.37 1.01     1110     1079
sigma_group5yo      -1.05      0.24    -1.51    -0.57 1.00     2249     2420
sigma_groupadults   -2.19      0.24    -2.66    -1.74 1.00     2171     2427

Samples were drawn using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).
```

on a log scale!

```
mean = c(0, 5, 8)
sd = c(3, 1.5, 0.3)
```

pretty good!

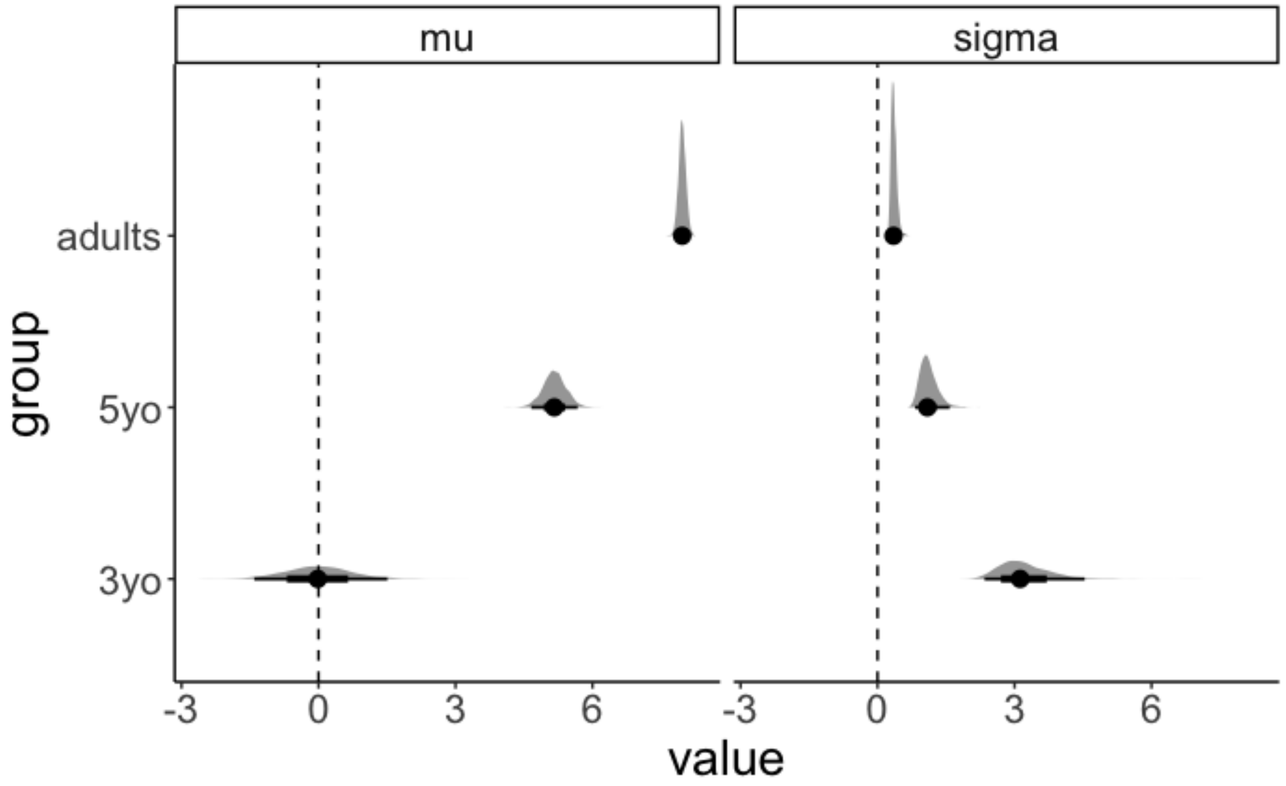
3 year olds $e^{1.15} = 3.16$

5 year olds $e^{1.15+(-1.05)} = 1.10$

adults $e^{1.15+(-2.19)} = 0.35$

Unequal variance aka heteroscedasticity

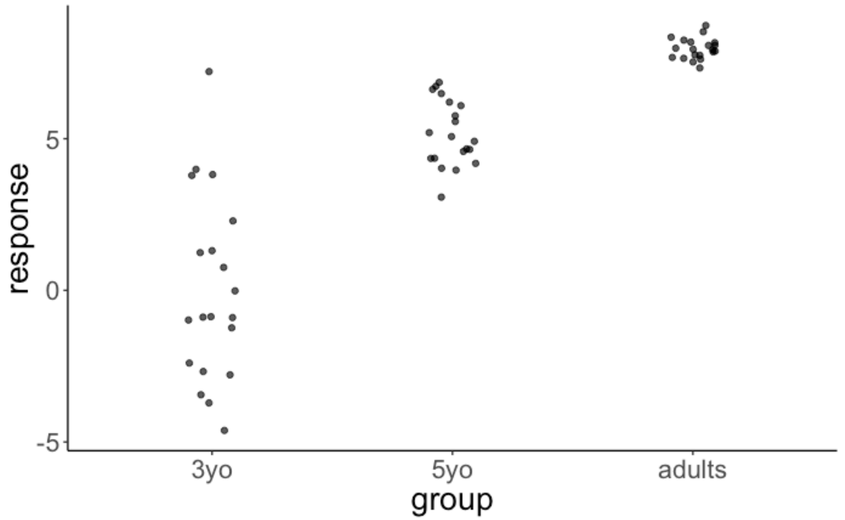
```
df.variance %>%
  expand(group) %>%
  add_fitted_draws(fit.brm1, dpar = TRUE) %>%
  select(group, .row, .draw, posterior = .value, mu, sigma) %>%
  pivot_longer(cols = c(mu, sigma),
               names_to = "index",
               values_to = "value") %>%
  ggplot(aes(x = value, y = group)) +
  geom_halfeyeh() +
  geom_vline(xintercept = 0, linetype = "dashed") +
  facet_grid(cols = vars(index))
```



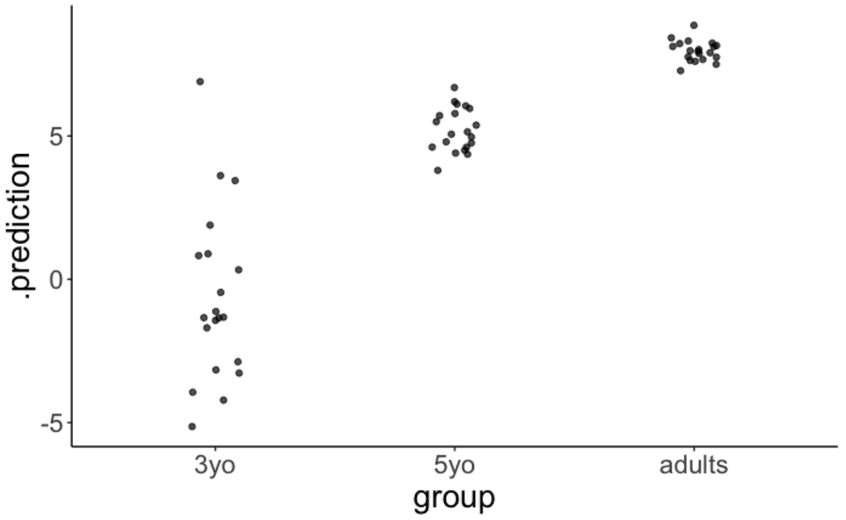
Unequal variance aka heteroscedasticity

```
df.variance %>%
  add_predicted_draws(model = fit.brm1,
                      n = 1) %>%
  ggplot(aes(x = group, y = .prediction)) +
  geom_jitter(height = 0,
              width = 0.1,
              alpha = 0.7)
```

original data



predicted data



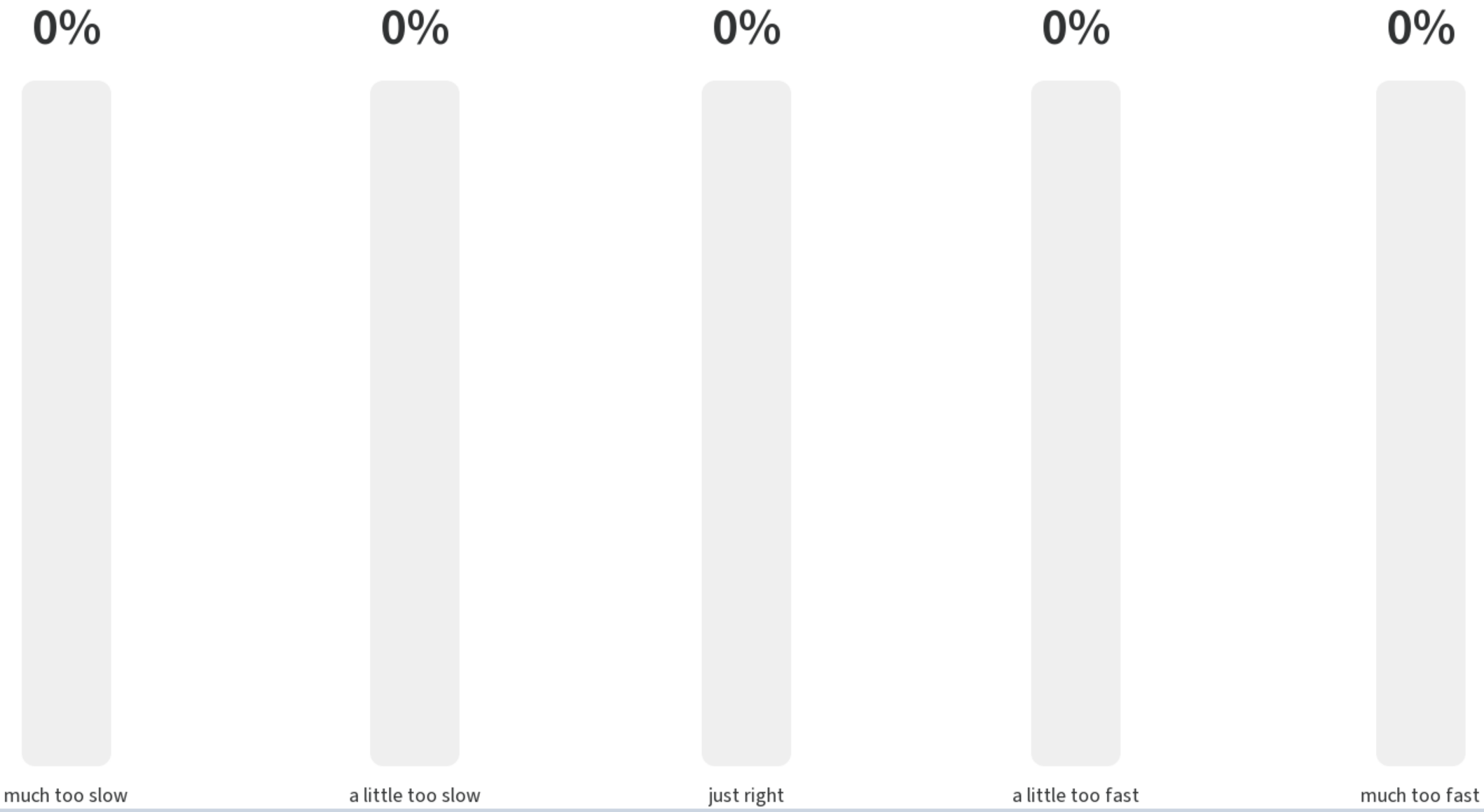
these predictions look good!

Plan for today

- Quick recap
- Doing Bayesian data analysis **with BRMS**
  - Testing hypotheses
  - Model evaluation
  - Reporting results
- Some more examples
  - Sleep data
  - Titanic data
- Going beyond

Feedback N

0



Thanks