Bayesian Linear Modeling: An introduction using brms and rstan

Lecture notes for MSc Cognitive Science, MSc Cognitive Systems, and MSc Linguistics, University of Potsdam, Germany

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1 Foundational ideas

1.1 Introduction

 The materials are available from:

- OSF
- github

Acknowledgments: A few things have been borrowed from the linear modeling and hierarchical linear modeling chapters in https://github.com/vasishth/FGME_Stan_2017. The course notes have benefitted a lot from the lectures and writings of Michael Betancourt. Other sources are acknowledged within the lecture notes.

1.1.1 Intended audience and prerequisites

This course is intended for **graduate students** in all relevant MSc programs related to Cognitive Science at the University of Potsdam, Germany. At the time of writing, this includes Cognitive Science and Linguistics.

The public course home page is here. The university-internal moodle forum for homework submissions and internal communications is here.

I assume here that the graduate student taking this course has elementary numeracy acquired usually at the class 10 level. Calculus and linear algebra are mentioned in the notes but I do not require the student to know these topics. Whenever calculus and linear algebra come up, I will explain what the equations or formulas mean just in time. No **active** ability in these areas is needed. What I do assume is basic (class 10) algebra, basic set theory, and arithmetic ability.

For example:

- $x^a * x^b = x^{a+b}$
- $\exp(\log(x)) = x$

Some very basic knowledge of R is assumed, but not much. If students don't know R, I will provide a quick introduction, although google is one's friend here.

1.1.2 Software needed

Before starting, please install

- R and RStudio
- The R package rstan:
  - Instructions for Windows
  - Instructions for Mac or Linux
- The R package brms

Please talk to the instructor if you have difficulties installing anything, although be warned that my knowledge of Windows is limited to knowing that it exists.

1.1.3 Motivation for course design

Because statistics inherently depends on mathematics, it is very important to get a reasonably formal introduction to the topic. Although an informal introduction can be good as a first course, stopping there is generally harmful and has been a failure in all Cognitive Science disciplines.

We see this in the way statistics is routinely abused in psycholinguistics, psychology, and linguistics, among other areas. Some examples from psycholinguistics are mentioned alongside each point:

- decide that an effect is "reliable" if $p < 0.05$ in a severely underpowered study; for examples, see Jäger, Engelmann, and Vasishth (2017), Vasishth et al. (2018).
- incorrectly argue that the null is true when $p > 0.05$, or arguing that the null is false when is a bit over $p > 0.05$, but the researcher wants desperately that p be less than 0.05; for discussion, see Vasishth and Nicenboim (2016), Nicenboim and Vasishth (2016).
- flexibly analyze data to get the result desired: analyze many dependent measures and choose whichever result you like, ignoring the rest; see Malsburg and Angele (2017).
- ignore model assumptions, focusing only on p-value; examples are discussed in Vasishth et al. (2013), Nicenboim, Roettger, and Vasishth (2018), Vasishth et al. (2017).
- flexibly change the research question, theory, or predictions after seeing the data; for discussion of the distinction between confirmatory vs exploratory testing, see Nicenboim et al. (2018).
- argue for a significant interaction after showing a significant effect in one pair of conditions and no significant effect in another pair (Nieuwenhuis, Forstmann, and Wagenmakers 2011).

Most people do not make these mistakes intentionally (that would be scientific misconduct!). The problem is ignorance about what statistics can and cannot give you.

In the past, I have made these mistakes too. For examples of mistakes listed above from my own work, see Vasishth and Lewis (2006), Vasishth (2003).

In a modest attempt to at least partly remedy this situation, the present course attempts to provide some understanding of the basic formal ideas behind statistical modeling.

If you find typos or outright errors in this document, please open an issue here. Alternatively, if you know how to, you can alternatively fork and make a pull request.

The central idea we will explore in this course is: given data, how to use Bayes' theorem to quantify uncertainty about a scientific question of interest. In order to understand the methodology, some passive understanding of the following topics needs to be in place:

- Basic probability theory:
  - sum and product rule
  - conditional probability
  - independence of events
  - Bayes' rule
- The theory of random variables
  - the distinction betweeen the probability density/mass function $f(x)$ vs cumulative distribution function $F(x)$
  - inverse CDF, $F^{-1}(x)$
  - expectation and variance of (transformations of) random variables
- Probability density/mass functions
  - Ten common distributions
  - Jointly distributed random variables
  - Sums of random variables
  - Marginal and conditional pdfs
  - Covariance, correlation, and the variance-covariance matrix
  - Multivariate normal distributions
- Maximum likelihood estimation
  - How to find MLEs analytically (some calculus needed here)
  - How to find MLEs using the R function optim
  - Visualization of the log likelihood

Without a clear understanding of these concepts, generalized confusion is an inevitable outcome. That is why it is so important to expend some energy in understanding these concepts.

But before we dive in, it may help to step back and get an overview of where we are going in this course.

1.1.4 Preview: Steps in Bayesian analysis

The way we will conduct data analysis is as follows.

- Given data, specify a *likelihood function*.
- Specify *prior distributions* for model parameters.
- Evaluate whether model makes sense, using *fake-data simulation*, *prior predictive* and *posterior predictive* checks, and (if you want to claim a discovery) calibrating *true* and *false discovery rates*.
- Using software, derive *marginal posterior distributions* for parameters given likelihood function and prior density. I.e., simulate parameters to get *samples from posterior distributions* of parameters using some *Markov Chain Monte Carlo (MCMC) sampling algorithm*, specifically, the Hamiltonian Monte Carlo method.
- Check that the model converged using *model convergence* diagnostics.
- Summarize *posterior distributions* of parameter samples and make your scientific decision.

The above is what you will learn in this course; all the terms introduced above will be explained in these notes and in class. We begin with basic probability theory.

1.2 Brief review of probability theory

The best reference textbooks I know for s first contact with probability theory are Kerns (2018) and Blitzstein and Hwang (2014). My notes below are a bit terse because I am assuming you will look at these if something is unclear.

1.2.1 Axioms of Probability

We assume here a basic knowledge of set theory. Let S be a set of events. For example, for a single coin toss, $S = \{A_1, A_2\}$, where A_1 is the event that we get a heads, and A_2 the event that we get a tails.

1. **Axiom 1** $\mathbb{P}(A) \geq 0$ for any event $A \subset S$.
2. **Axiom 2** $\mathbb{P}(S) = 1$.
3. **Axiom 3** If the events $A_1, A_2, A_3, \ldots$ are disjoint then

$$\mathbb{P}\left(\bigcup_{i=1}^{n} A_i\right) = \sum_{i=1}^{n} \mathbb{P}(A_i) \text{ for every } n, \tag{1}$$

and furthermore,

$$\mathbb{P}\left(\bigcup_{i=1}^{\infty} A_i\right) = \sum_{i=1}^{\infty} \mathbb{P}(A_i). \tag{2}$$

Three important propositions:

Proposition 1

Let $E \cup E^c = S$. Then,

$$1 = P(S) = P(E \cup E^c) = P(E) + P(E^c) \tag{3}$$

or:

$$P(E^c) = 1 - P(E) \tag{4}$$

Proposition 2

If $E \subset F$ then $P(E) \leq P(F)$.

Proposition 3

$$P(E \cup F) = P(E) + P(F) - P(EF) \tag{5}$$

1.2.2 Conditional Probability

This is a central concept in this course. The conditional probability of event B given event A, denoted $\mathbb{P}(B \mid A)$, is defined by

$$\mathbb{P}(B \mid A) = \frac{\mathbb{P}(A \cap B)}{\mathbb{P}(A)}, \quad \text{if } \mathbb{P}(A) > 0. \tag{6}$$

Theorem

For any fixed event A with $\mathbb{P}(A) > 0$,

1. $\mathbb{P}(B|A) \geq 0$, for all events $B \subset S$,
2. $\mathbb{P}(S|A) = 1$, and

3. If B_1, B_2, B_3,... are disjoint events,

then:

$$\mathbb{P}\left(\bigcup_{k=1}^{\infty} B_k \,\middle|\, A\right) = \sum_{k=1}^{\infty} \mathbb{P}(B_k|A). \tag{7}$$

In other words, $\mathbb{P}(\cdot|A)$ is a legitimate probability function. With this fact in mind, the following properties are immediate:

For any events A, B, and C with $\mathbb{P}(A) > 0$,

1. $\mathbb{P}(B^c|A) = 1 - \mathbb{P}(B|A)$.
2. If $B \subset C$ then $\mathbb{P}(B|A) \leq \mathbb{P}(C|A)$.
3. $\mathbb{P}[(B \cup C)|A] = \mathbb{P}(B|A) + \mathbb{P}(C|A) - \mathbb{P}[(B \cap C|A)]$.
4. The Multiplication Rule. For any two events A and B,

$$\mathbb{P}(A \cap B) = \mathbb{P}(A)\mathbb{P}(B|A). \tag{8}$$

And more generally, for events A_1, A_2, A_3,..., A_n,

$$\mathbb{P}(A_1 \cap A_2 \cap \cdots \cap A_n) = \mathbb{P}(A_1)\mathbb{P}(A_2|A_1)\cdots\mathbb{P}(A_n|A_1 \cap A_2 \cap \cdots \cap A_{n-1}). \tag{9}$$

1.2.3 Independence of events

(Taken nearly verbatim from Kerns 2018.)

Definition

Events A and B are said to be independent if

$$\mathbb{P}(A \cap B) = \mathbb{P}(A)\mathbb{P}(B). \tag{10}$$

Otherwise, the events are said to be dependent.

From the above definition of conditional probability, we know that when $\mathbb{P}(B) > 0$ we may write

$$\mathbb{P}(A|B) = \frac{\mathbb{P}(A \cap B)}{\mathbb{P}(B)}. \tag{11}$$

In the case that A and B are independent, the numerator of the fraction factors so that $\mathbb{P}(B)$ cancels, with the result:

$$\mathbb{P}(A|B) = \mathbb{P}(A) \text{ when } A, B \text{ are independent.} \tag{12}$$

Proposition 4

If E and F are independent events, then so are E and F^c, E^c and F, and E^c and F^c.

Proof:

Assume E and F are independent. Since $E = EF \cup EF^c$ and EF and EF^c are mutually exclusive,

$$\begin{aligned} P(E) =& P(EF) + P(EF^c) \\ =& P(E)P(F) + P(EF^c) \end{aligned} \tag{13}$$

Equivalently:

$$\begin{aligned} P(EF^c) =& P(E)[1 - P(F)] \\ =& P(E)P(F^c) \end{aligned} \tag{14}$$

1.2.4 Bayes' rule

(Quoted nearly verbatim from Kerns 2018.)

Theorem Bayes' Rule. Let $B_1, B_2, \ldots, B_n$ be mutually exclusive and exhaustive and let A be an event with $\mathbb{P}(A) > 0$. Then

$$\mathbb{P}(B_k|A) = \frac{\mathbb{P}(B_k)\mathbb{P}(A|B_k)}{\sum_{i=1}^{n} \mathbb{P}(B_i)\mathbb{P}(A|B_i)}, \quad k = 1, 2, \ldots, n. \tag{15}$$

The proof follows from looking at $\mathbb{P}(B_k \cap A)$ in two different ways. For simplicity, suppose that $P(B_k) > 0$ for all k. Then

$$\mathbb{P}(A)\mathbb{P}(B_k|A) = \mathbb{P}(B_k \cap A) = \mathbb{P}(B_k)\mathbb{P}(A|B_k). \tag{16}$$

Since $\mathbb{P}(A) > 0$ we may divide through to obtain

$$\mathbb{P}(B_k|A) = \frac{\mathbb{P}(B_k)\mathbb{P}(A|B_k)}{\mathbb{P}(A)}. \tag{17}$$

Now remembering that $\{B_k\}$ is a partition (i.e., mutually exclusive and exhaustive), the denominator of the last expression is

$$\mathbb{P}(A) = \sum_{k=1}^{n} \mathbb{P}(B_k \cap A) = \sum_{k=1}^{n} \mathbb{P}(B_k)\mathbb{P}(A|B_k). \tag{18}$$

1.3 Random variable theory

A random variable X is a function $X : S \to \mathbb{R}$ that associates to each outcome $\omega \in S$ exactly one number $X(\omega) = x$.

S_X is all the x's (all the possible values of X, the support of X). I.e., $x \in S_X$. We can also sloppily write $X \in S_X$.

Good example: number of coin tosses till H

- $X : \omega \to x$
- ω: H, TH, TTH,... (infinite)
- $x = 0, 1, 2, \ldots; x \in S_X$

Every discrete (continuous) random variable X has associated with it a **probability mass (distribution) function (pmf, pdf)**. I.e., PMF is used for discrete distributions and PDF for continuous. (I will sometimes use lower case for pdf and sometimes upper case. Some books use pdf for both discrete and continuous distributions.)

$$p_X : S_X \to [0, 1] \tag{19}$$

defined by

$$p_X(x) = P(X(\omega) = x), x \in S_X \tag{20}$$

[**Note**: Books sometimes abuse notation by overloading the meaning of X. They usually have: $p_X(x) = P(X = x), x \in S_X$]

Probability density functions (continuous case) or probability mass functions (discrete case) are functions that assign probabilities or relative frequencies to all events in a sample space.

The expression

$$X \sim f(\cdot) \tag{21}$$

means that the random variable X has pdf/pmf $g(\cdot)$. For example, if we say that $X \sim N(\mu, \sigma^2)$, we are assuming that the pdf is

$$f(x) = \frac{1}{\sqrt{2\pi\sigma^2}} \exp[-\frac{(x-\mu)^2}{2\sigma^2}] \tag{22}$$

We also need a **cumulative distribution function** or cdf because, in the continuous case, P(X=some point value) is zero and we need a way to talk about P(X in a specific range). cdfs serve that purpose.

In the continuous case, the cdf or distribution function is defined as:

$$P(X < x) = F(X < x) = \int_{-\infty}^{X} f(x)\, dx \tag{23}$$

1.3.1 The normalization constant in pdfs

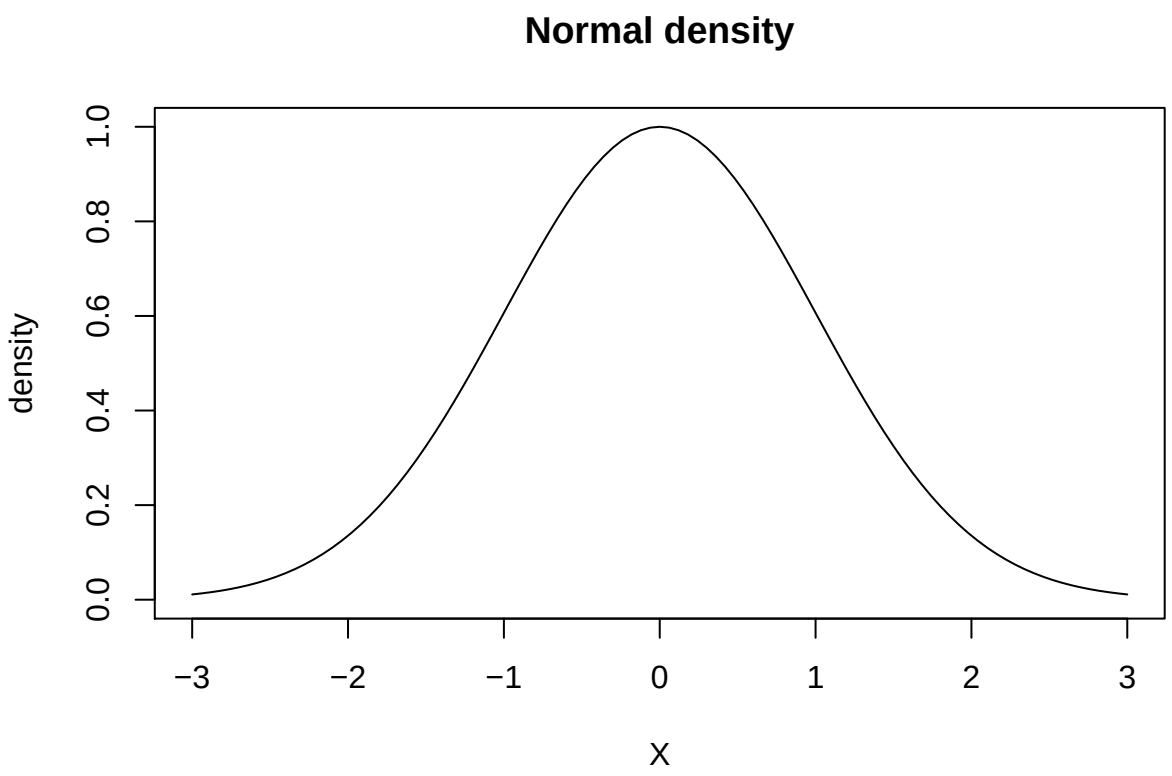
Almost any function can be a pdf as long as it sums to 1 over the sample space. Here is an example of a function that doesn't sum to 1:

$$f(x) = \exp[-\frac{(x-\mu)^2}{2\sigma^2}] \tag{24}$$

This is the "kernel" of the normal pdf, and it doesn't sum to 1:

```
normkernel<-function(x,mu=0,sigma=1){
  exp((-(x-mu)^2/(2*(sigma^2))))
}

x<-seq(-10,10,by=0.01)
```

```r
plot(function(x) normkernel(x), -3, 3,
      main = "Normal density",ylim=c(0,1),
              ylab="density",xlab="X")
```

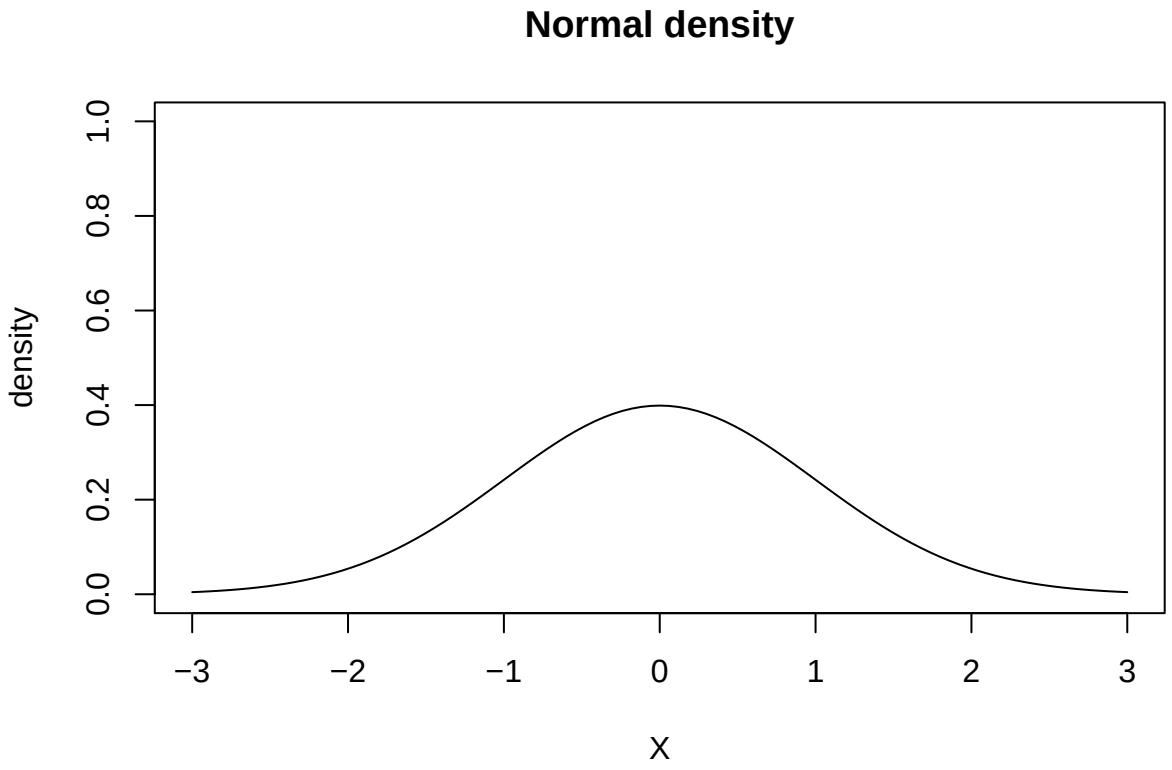



```r
### area under the curve is less than 1:
integrate(normkernel,lower=-Inf,upper=Inf)
```

```
## 2.51 with absolute error < 0.00023
```

Adding a normalizing constant makes the above kernel density a pdf.

```r
norm<-function(x,mu=0,sigma=1){
  (1/sqrt(2*pi*(sigma^2))) * exp((-(x-mu)^2/(2*(sigma^2))))
}

x<-seq(-10,10,by=0.01)

plot(function(x) norm(x), -3, 3,
      main = "Normal density",ylim=c(0,1),
              ylab="density",xlab="X")
```




```
### area under the curve sums to 1:
integrate(norm,lower=-Inf,upper=Inf)
```

```
## 1 with absolute error < 0.000094
```

1.3.2 The pdf f(x) and the cdf F(x)

Recall that a random variable X is a function $X : S \to \mathbb{R}$ that associates to each outcome $\omega \in S$ exactly one number $X(\omega) = x$. S_X is all the x's (all the possible values of X, the support of X). I.e., $x \in S_X$.

X is a continuous random variable if there is a non-negative function f defined for all real $x \in (-\infty, \infty)$ having the property that for any set B of real numbers,

$$P\{X \in B\} = \int_B f(x)\,dx \tag{25}$$

Kerns has the following to add about the above:

> Continuous random variables have supports that look like
>
> $$S_X = [a,b] \text{ or } (a,b), \tag{26}$$

or unions of intervals of the above form. Examples of random variables that are often taken to be continuous are:

- the height or weight of an individual,
- other physical measurements such as the length or size of an object, and
- durations of time (usually).

E.g., in psychology and linguistics we take as continous:

1. reading time: Here the random variable X has possible values ω ranging from 0 ms to some upper bound b ms, and the RV X maps each possible value ω to the corresponding number (0 to 0 ms, 1 to 1 ms, etc.).
2. acceptability ratings (technically not true; but people generally treat ratings as continuous, at least in psycholinguistics)
3. Event related potentials

Every continuous random variable X has a probability density function (PDF) denoted f_X associated with it that satisfies three basic properties:

1. $f_X(x) > 0$ for $x \in S_X$,
2. $\int_{x \in S_X} f_X(x)\,\mathrm{d}x = 1$, and
3. $\mathbb{P}(X \in A) = \int_{x \in A} f_X(x)\,\mathrm{d}x$, for an event $A \subset S_X$.

We can say the following about continuous random variables:

- Usually, the set A in condition 3 above takes the form of an interval, for example, $A = [c,d]$, in which case

$$\mathbb{P}(X \in A) = \int_c^d f_X(x)\,\mathrm{d}x. \tag{27}$$

- It follows that the probability that X falls in a given interval is simply the area under the curve of f_X over the interval.
- Since the area of a line $x = c$ in the plane is zero, $\mathbb{P}(X = c) = 0$ for any value c. In other words, the chance that X equals a particular value c is zero, and this is true for any number c. Moreover, when $a < b$ all of the following probabilities are the same:

$$\mathbb{P}(a \leq X \leq b) = \mathbb{P}(a < X \leq b) = \mathbb{P}(a \leq X < b) = \mathbb{P}(a < X < b). \tag{28}$$

$f(x)$ is the probability density function of the random variable X.

Since X must assume some value, f must satisfy

$$1 = P\{X \in (-\infty, \infty)\} = \int_{-\infty}^{\infty} f(x)\,dx \tag{29}$$

If $B = [a, b]$, then

$$P\{a \leq X \leq b\} = \int_{a}^{b} f(x)\,dx \tag{30}$$

If $a = b$, we get

$$P\{X = a\} = \int_{a}^{a} f(x)\,dx = 0 \tag{31}$$

Hence, for any continuous random variable,

$$P\{X < a\} = P\{X \leq a\} = F(a) = \int_{-\infty}^{a} f(x)\,dx \tag{32}$$

F is the **cumulative distribution function**. Differentiating both sides in the above equation:

$$\frac{dF(x)}{dx} = f(x) \tag{33}$$

Just to reiterate this: the density (PDF) is the derivative of the CDF. You can go back and forth between the pdf and the CDF by integrating or differentiating:

$$\int_{a}^{b} f(x)\,dx \Rightarrow F(a) \tag{34}$$

$$dF(x)/dx = f(x) \tag{35}$$

$F(x)$ will give you some probability u. The **inverse of the cdf**, $F^{-1}(u)$ gives us back the quantile x such that $F(x) = u$. *This fact will be of great relevance to us.*

1.3.3 Some basic results concerning random variables

1.
$$E[X] = \int_{-\infty}^{\infty} x f(x)\, dx \tag{36}$$

2.
$$E[g(X)] = \int_{-\infty}^{\infty} g(x) f(x)\, dx \tag{37}$$

3.
$$E[aX + b] = aE[X] + b \tag{38}$$

4.
$$Var[X] = E[(X - \mu)^2] = E[X^2] - (E[X])^2 \tag{39}$$

5.
$$Var(aX + b) = a^2 Var(X) \tag{40}$$

So far, we have learnt what a random variable is, and we know that by definition it has a pdf and a cdf associated with it. Why did we go through all this effort to learn all this? The payoff becomes apparent next.

1.3.4 What you can do with a pdf

You can:

1. Calculate the mean:

   Discrete case:

$$E[X] = \sum_{i=1}^{n} x_i p(x_i) \tag{41}$$

   Continuous case:

$$E[X] = \int_{-\infty}^{\infty} x f(x)\, dx \tag{42}$$

2. Calculate the variance:

$$Var(X) = E[X^2] - (E[X])^2 \tag{43}$$

3. Compute quartiles: e.g., for some pdf f(x):

$$\int_{-\infty}^{Q} f(x)\,dx \tag{44}$$

For example, take $f(x)$ to be the normal distribution with mean 0 and sd 1. Suppose we want to know:

$$\int_{0}^{1} f(x)\,dx \tag{45}$$

We can do this in R as follows:[1]

```
pnorm(1)-pnorm(0)
```

Why are we going through these basic results? As Betancourt puts it (see here, at minute 9:55): "Bayesian computations reduce to (computing) expectations and, consequently, to integration." We will be computing expectations a lot in this course, using software. We will never have to do this by hand because we will be working in high-dimensional spaces and will have no choice but to use numerical approximations.

1.4 Ten important distributions

These distributions are generally used quite frequently in Bayesian data analyses, especially in psychology and linguistics applications. For the first few distributions, we show the pdf and cdf. The Binomial and Poisson are discrete distributions, the rest are continuous.

You should install the following add-in into RStudio:

```
if ( !('devtools' %in% installed.packages()) ) install.packages("devtools")

devtools::install_github("bearloga/tinydensR")
```

Then, run

```
library(tinydensR)
univariate_discrete_addin()
```

or

[1] This is a very important piece of R code here. Make sure you understand the relationship between the integral and the R functions used here.

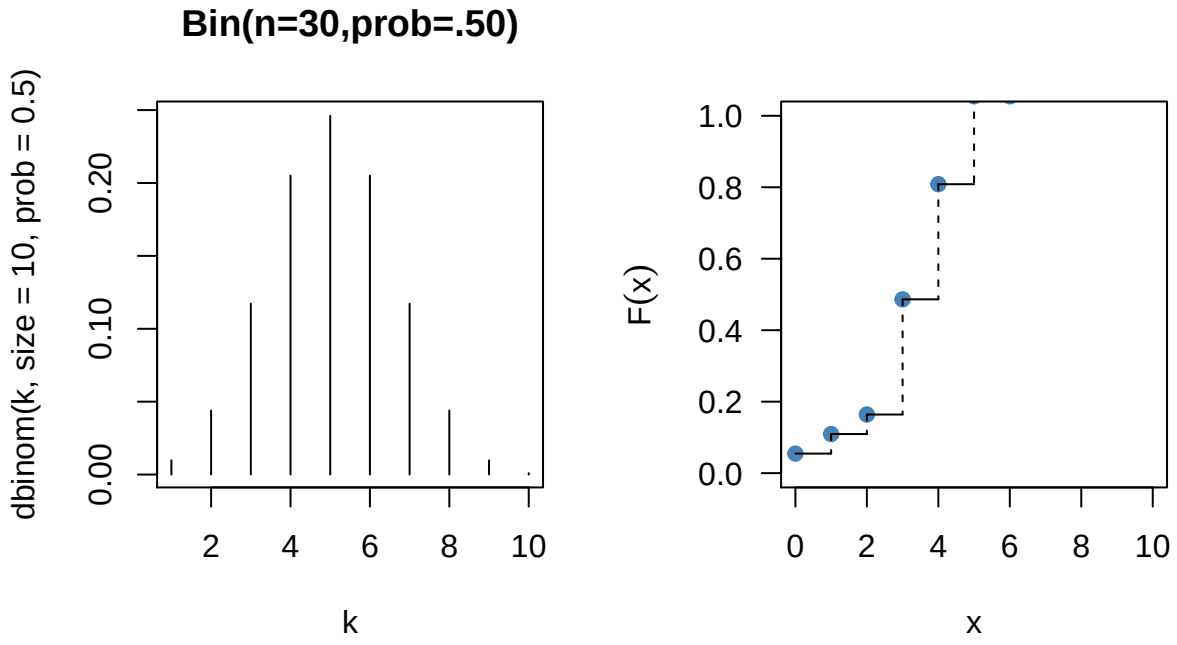


Figure 1: Example of the pmf Bin(n=10,prob=.50).

```
univariate_continuous_addin()
```

to visualize the distributions under different parameterizations. Note that RStudio may occasionally crash when this command is run. Just restart RStudio if this happens.

1.4.1 Binomial

Examples: coin tosses, question-response accuracy

Probability mass function:

If we have x successes in n trials, given a success probability p for each trial. If $x \sim Bin(n, p)$.

$$P(x \mid n, p) = \binom{n}{k} p^k (1-p)^{n-k} \tag{46}$$

[Recall that: $\binom{n}{k} = \frac{n!}{(n-r)!r!}$. Hence, given x and n, this term will be a constant.]

Figure 1 shows the pmf and cdf.

Expectation and variance:

The mean is np and the variance $np(1-p)$.

When $n = 1$ we have the Bernoulli distribution.

Relevant functions in R

```
###pmf:
dbinom(x, size, prob, log = FALSE)
### cdf:
pbinom(q, size, prob, lower.tail = TRUE, log.p = FALSE)
### inverse cdf:
qbinom(p, size, prob, lower.tail = TRUE, log.p = FALSE)
### pseudo-random generation of samples:
rbinom(n, size, prob)
```

Notational conventions: A binomial distribution, n trials each with probability θ of occurring, is written $Bin(\theta, n)$. Given a random variable with this distribution, we can write $R \mid \theta, n \sim Bin(\theta, n)$ or $p(r \mid \theta, n) = Bin(\theta, n)$, where r is the realization of R. We can drop the conditioning in $R \mid \theta, n$, so that we can write: given $R \sim Bin(\theta, n)$, what is $Pr(\theta_1 < \theta < \theta_2 \mid r, n)$.

1.4.2 Poisson

Examples: traffic accidents, typing errors, customers arriving in a bank, number of fixations in reading.

Probability density function

Let λ be the average number of events in the time interval $[0, 1]$. Let the random variable X count the number of events occurring in the interval. Then:

$$f_X(x) = \mathbb{P}(X = x) = \mathrm{e}^{-\lambda} \frac{\lambda^x}{x!}, \quad x = 0, 1, 2, \ldots \tag{47}$$

Expectation and variance

$$E[X] = \lambda \tag{48}$$

$$Var(X) = \lambda \tag{49}$$

Relevant functions in R

```
dpois(x, lambda)
ppois(q, lambda, lower.tail = TRUE)
```

```
qpois(p, lambda, lower.tail = TRUE)
rpois(n, lambda)
```

1.4.3 Uniform

Example: All outcomes have equal probability.

Probability density function:

A random variable (X) with the continuous uniform distribution on the interval (α, β) has PDF

$$f_X(x) = \begin{cases} \frac{1}{\beta-\alpha}, & \alpha < x < \beta, \\ 0, & \text{otherwise} \end{cases} \tag{50}$$

The associated R function is $\mathsf{dunif}(\texttt{min} = a, \texttt{max} = b)$. We write $X \sim \mathsf{unif}(\texttt{min} = a, \texttt{max} = b)$. Due to the particularly simple form of this PDF we can also write down explicitly a formula for the CDF F_X:

$$F_X(a) = \begin{cases} 0, & a < 0, \\ \frac{a-\alpha}{\beta-\alpha}, & \alpha \le t < \beta, \\ 1, & a \ge \beta. \end{cases} \tag{51}$$

The pdf and cdf are show in Figure 2.

Expectation and variance:

$$E[X] = \frac{\beta + \alpha}{2} \tag{52}$$

$$Var(X) = \frac{(\beta - \alpha)^2}{12} \tag{53}$$

Relevant functions in R

```
dunif(x, min = 0, max = 1, log = FALSE)
punif(q, min = 0, max = 1, lower.tail = TRUE, log.p = FALSE)
qunif(p, min = 0, max = 1, lower.tail = TRUE, log.p = FALSE)
runif(n, min = 0, max = 1)
```

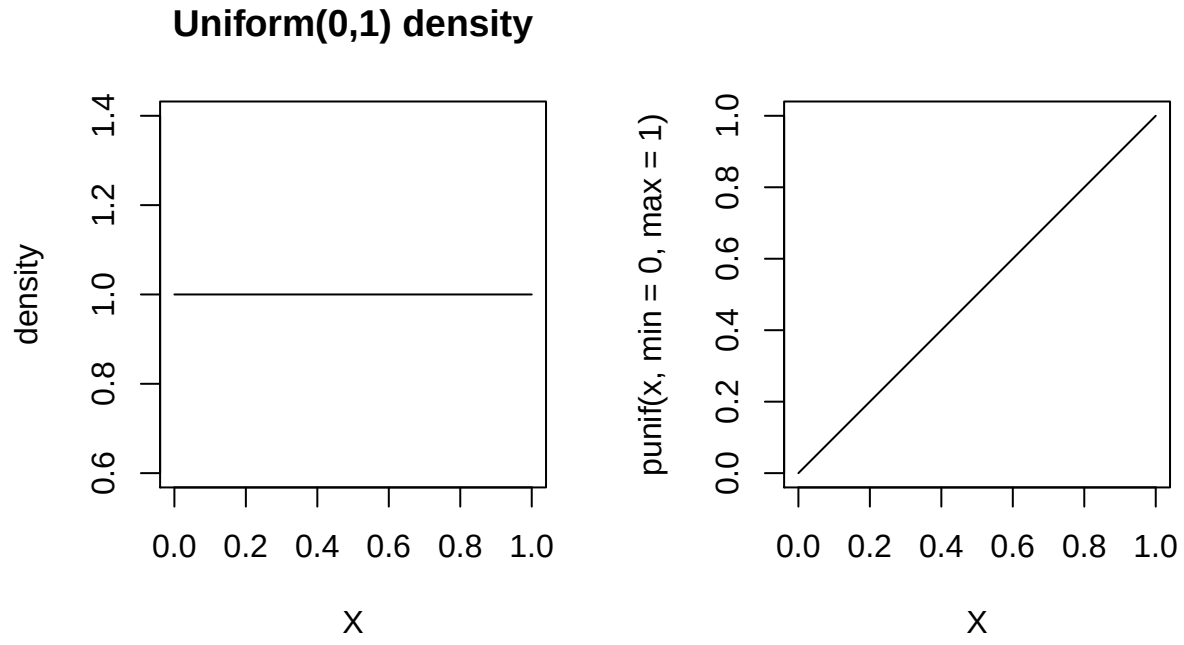


Figure 2: Uniform(0,1) distribution, pdf and cdf.

1.4.4 Normal

Examples: heights, weights of people

Probability density function

$$f_X(x) = \frac{1}{\sigma\sqrt{2\pi}} e^{\frac{-(x-\mu)^2}{2\sigma^2}}, \quad -\infty < x < \infty. \tag{54}$$

We write $X \sim \mathsf{norm}(\texttt{mean} = \mu, \texttt{sd} = \sigma)$, and the associated R function is `dnorm(x, mean = 0, sd = 1)`.

If X is normally distributed with parameters μ and σ^2, then $Y = aX + b$ is normally distributed with parameters $a\mu + b$ and $a^2\sigma^2$.

Special case: Standard or unit normal random variable

If X is normally distributed with parameters μ and σ^2, then $Z = (X - \mu)/\sigma$ is normally distributed with parameters $0, 1$.

We conventionally write $\Phi(x)$ for the CDF:

$$\Phi(x) = \frac{1}{\sqrt{2\pi}} \int_{-\infty}^{x} e^{\frac{-y^2}{2}} dy \quad \text{where } y = (x-\mu)/\sigma \tag{55}$$

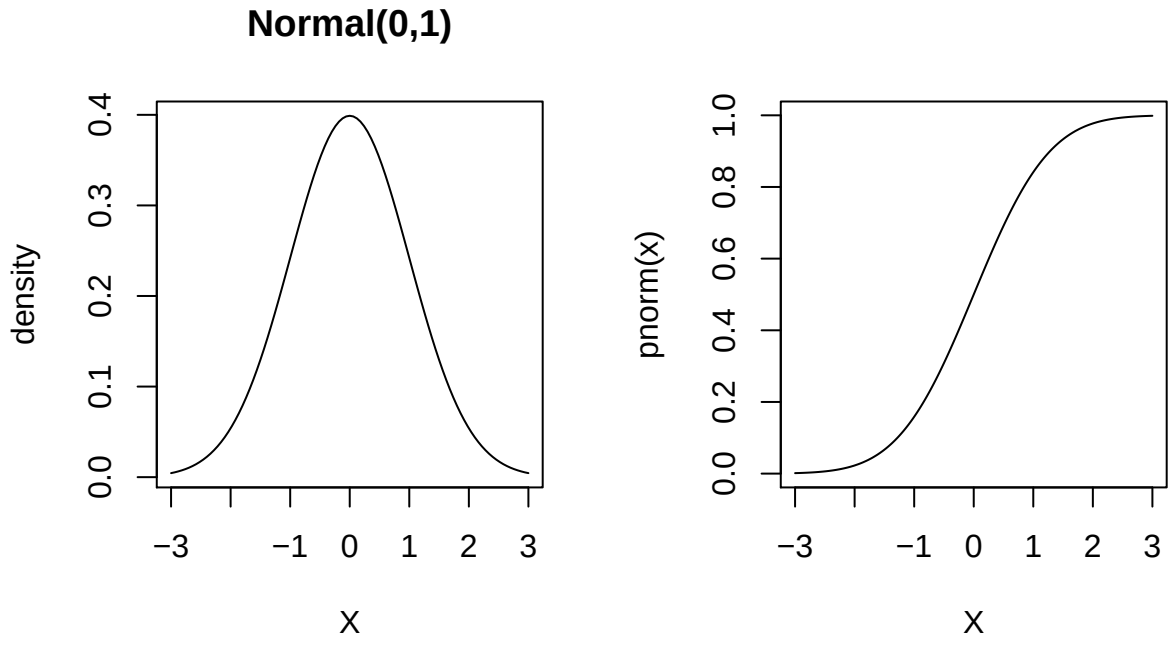


Figure 3: Normal distribution.

Old-style (pre-computer era) printed tables give the values for positive x; for negative x we do:

$$\Phi(-x) = 1 - \Phi(x), \quad -\infty < x < \infty \tag{56}$$

If Z is a standard normal random variable (SNRV) then

$$p\{Z \leq -x\} = P\{Z > x\}, \quad -\infty < x < \infty \tag{57}$$

Since $Z = ((X-\mu)/\sigma)$ is an SNRV whenever X is normally distributed with parameters μ and σ^2, then the CDF of X can be expressed as:

$$F_X(a) = P\{X \leq a\} = P\left(\frac{X-\mu}{\sigma} \leq \frac{a-\mu}{\sigma}\right) = \Phi\left(\frac{a-\mu}{\sigma}\right) \tag{58}$$

The standardized version of a normal random variable X is used to compute specific probabilities relating to X (it is also easier to compute probabilities from different CDFs so that the two computations are comparable).

Expectation and variance

$$E[X] = \mu \tag{59}$$

$$Var(X) = \sigma^2 \tag{60}$$

Relevant functions in R

```
dnorm(x, mean = 0, sd = 1, log = FALSE)
pnorm(q, mean = 0, sd = 1, lower.tail = TRUE, log.p = FALSE)
qnorm(p, mean = 0, sd = 1, lower.tail = TRUE, log.p = FALSE)
rnorm(n, mean = 0, sd = 1)
```

1.4.5 Log-Normal

Examples: reaction time, reading time

Probability density function

$$f_X(x) = \frac{1}{x\sigma\sqrt{2\pi}} e^{\frac{-(\log x-\mu)^2}{2\sigma^2}}, \quad 0 < x < \infty. \tag{61}$$

```
op<-par(mfrow=c(1,2),pty="s")
plot(function(x) dlnorm(x), 0, 4,
      main = "LogNormal(0,1)",
              ylab="density",xlab="X")
x<-seq(0,4,by=0.001)
plot(x,plnorm(x),main="",type="l",xlab="X")
```

Note:

-μ, σ are on the log scale. -If $X \sim LogNormal(\mu, \sigma)$, this is the same as saying that $\log(X)$ is normally distributed.

Expectation and variance

$$E[X] = \exp(\mu + \sigma^2/2) \tag{62}$$

$$Var(X) = E[X]\exp(\sigma^2 - 1) \tag{63}$$

Relevant functions in R

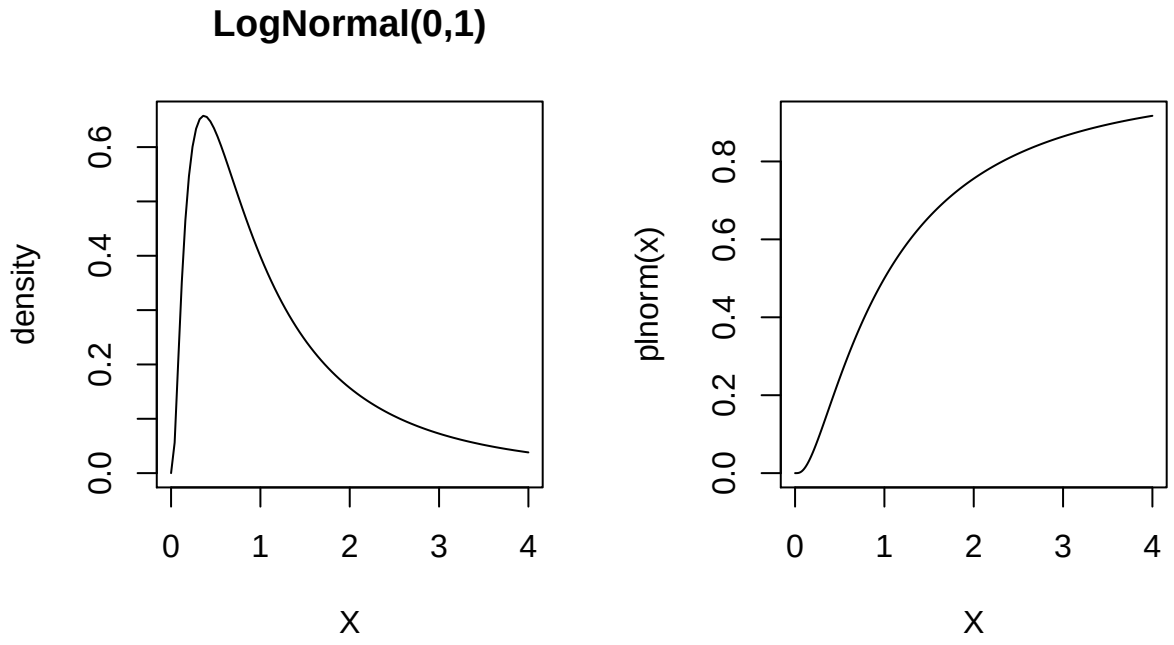


Figure 4: LogNormal(0,1) distribution.

```
dlnorm(x, meanlog = 0, sdlog = 1)
plnorm(q, meanlog = 0, sdlog = 1, lower.tail = TRUE)
qlnorm(p, meanlog = 0, sdlog = 1, lower.tail = TRUE)
rlnorm(n, meanlog = 0, sdlog = 1)
```

1.4.6 Beta

Example: Distribution of probability of success.

Probability density function

This is a generalization of the continuous uniform distribution. Think of parameter a as number of successes, and parameter b as number of failures.

$$f(x) = \begin{cases} \frac{1}{B(a,b)} x^{a-1}(1-x)^{b-1} & \text{if } 0 < x < 1 \\ 0 & \text{otherwise} \end{cases}$$

where

$$Beta(a,b) = \int_0^1 x^{a-1}(1-x)^{b-1}\,dx$$

We write $X \sim \texttt{beta}(\texttt{shape1} = a, \texttt{shape2} = b)$.

Expectation and variance

$$E[X] = \frac{a}{a+b} \text{ and } Var(X) = \frac{ab}{(a+b)^2(a+b+1)}. \tag{64}$$

Relevant functions in R

```
dbeta(x, shape1, shape2)
pbeta(q, shape1, shape2)
qbeta(p, shape1, shape2)
rbeta(n, shape1, shape2)
```

1.4.7 Exponential

Examples: Waiting time for an arrival from a Poisson process (e.g., reading times)

Probability density function

For some $\lambda > 0$,

$$f(x) = \begin{cases} \lambda e^{-\lambda x} & \text{if } x \geq 0 \\ 0 & \text{if } x < 0. \end{cases}$$

Expectation and variance

$$E[X] = \frac{1}{\lambda} \tag{65}$$

$$Var(X) = \frac{1}{\lambda^2} \tag{66}$$

Relevant functions in R

```
dexp(x, rate=1)
pexp(q, rate=1)
qexp(p, rate=1)
rexp(n, rate=1)
```

1.4.8 Gamma

Examples: reading times, distribution of inverse of variance.

Connection to Poisson: if X measures the length of time until the first event occurs in a Poisson process with rate λ then $X \sim \texttt{exp}(\texttt{rate} = \lambda)$. If we let Y measure the length of time until the α^{th} event occurs then $Y \sim \texttt{gamma}(\texttt{shape} = \alpha, \texttt{rate} = \lambda)$. When α is an integer this distribution is also known as the **Erlang** distribution.

The Chi-squared distribution is the Gamma distribution with $\lambda = 1/2$ and $\alpha = n/2$, where n is an integer:

Probability density function

This is a generalization of the exponential distribution. We say that X has a Gamma distribution and write $X \sim \texttt{gamma}(\texttt{shape} = \alpha, \texttt{rate} = \lambda)$, where $\alpha > 0$ (called shape) and $\lambda > 0$ (called rate). It has PDF

$$f(x) = \begin{cases} \frac{\lambda e^{-\lambda x}(\lambda x)^{\alpha-1}}{\Gamma(\alpha)} & \text{if } x \geq 0 \\ 0 & \text{if } x < 0. \end{cases}$$

$\Gamma(\alpha)$ is called the gamma **function** (note: it's lower case gamma, and it's a function, not a distribution):

$$\Gamma(\alpha) = \int_0^\infty e^{-y} y^{\alpha-1}\, dy = (\alpha-1)\Gamma(\alpha-1)$$

Note that for integral values of n, $\Gamma(n) = (n-1)!$ (follows from above equation).

Expectation and variance

$$E[X] = \alpha/\lambda \tag{67}$$

$$Var(X) = \alpha/\lambda^2 \tag{68}$$

Relevant functions in R

```
dgamma(x, rate, scale = 1/rate)
pgamma(q, rate, scale = 1/rate)
qgamma(p, rate, scale = 1/rate)
```

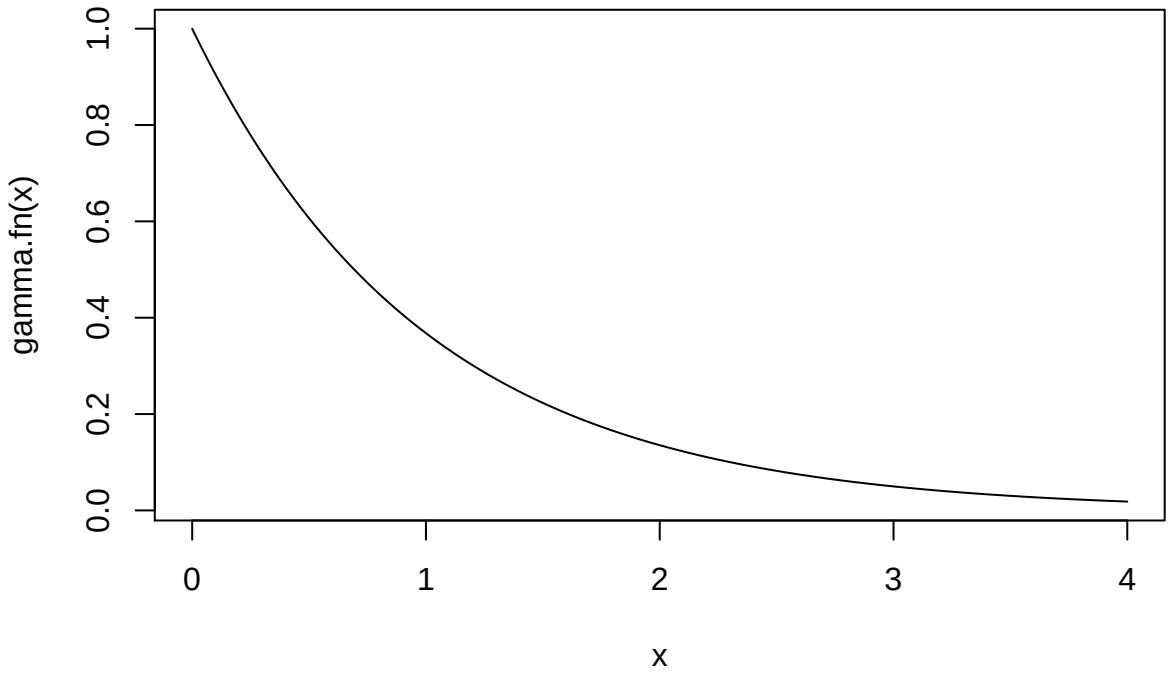


Figure 5: The Gamma distribution.

```
rgamma(n, rate, scale = 1/rate)
```

```
x<-seq(0,4,by=.01)
plot(x,gamma.fn(x),type="l")
```

```
x<-seq(0,100,by=.01)
plot(x,gamma.fn(x),type="l")
```

1.4.9 Student's t

Examples: reading times.

Probability density function

A random variable X with PDF

$$f_X(x) = \frac{\Gamma[(r+1)/2]}{\sqrt{r\pi}\,\Gamma(r/2)} \left(1+\frac{x^2}{r}\right)^{-(r+1)/2}, \quad -\infty < x < \infty \tag{69}$$

is said to have Student's t distribution with r degrees of freedom, and we write $X \sim \mathtt{t}(\mathtt{df} = r)$.

We will write $X \sim t(\mu, \sigma^2, r)$, where r is the degrees of freedom $(n-1)$, where n is sample size.

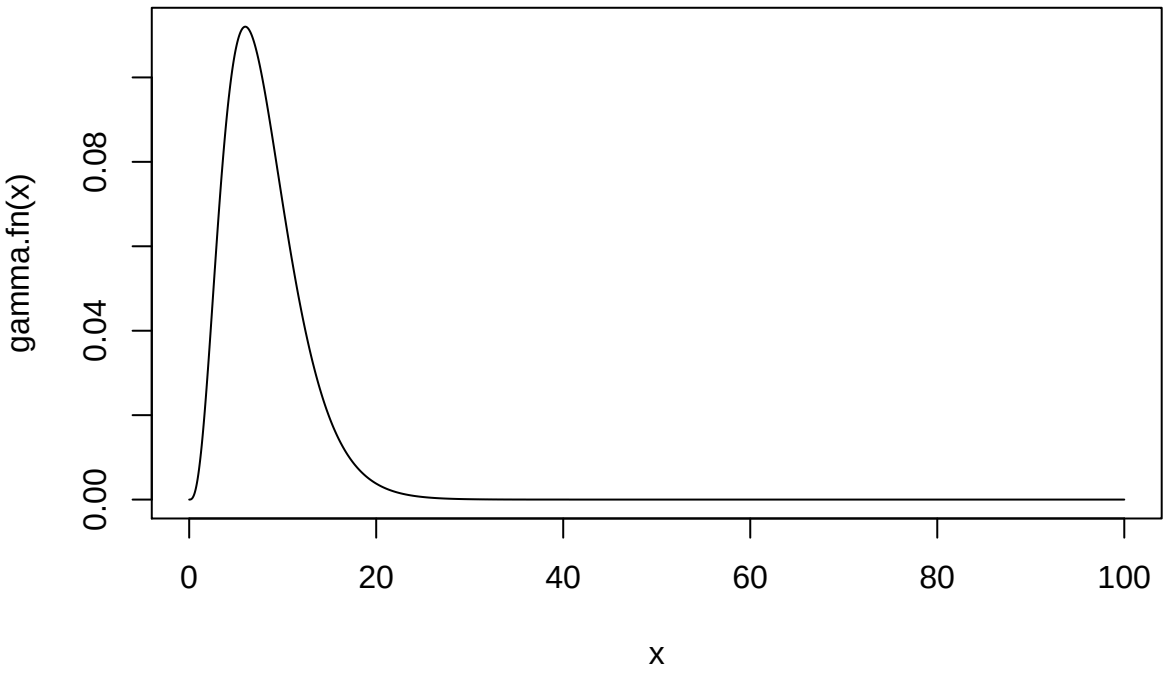


Figure 6: The chi-squared distribution.

Expectation and variance

$$E[X] = 0 \text{ if } n > 1 \text{ otherwise undefined} \tag{70}$$

$$Var(X) = \frac{n}{n-2}, \text{ when } n > 2 \text{ otherwise undefined} \tag{71}$$

Relevant functions in R

```
dt(x, df)
pt(q, df)
qt(p, df)
rt(n, df)
```

1.4.10 Summary of distributions

Distribution	PMF/PDF and Support	Expected Value	Variance
Binomial $Bin(n,p)$	$P(X=k)=\binom{n}{k}p^k q^{n-k}$ $k \in \{0,1,2,\ldots n\}$	np	npq
Poisson $Pois(\lambda)$	$P(X=k)=\frac{e^{-\lambda}\lambda^k}{k!}$ $k \in \{0,1,2,\ldots\}$	λ	λ
Uniform $Unif(a,b)$	$f(x)=\frac{1}{b-a}$ $x \in (a,b)$	$\frac{a+b}{2}$	$\frac{(b-a)^2}{12}$
Normal $Normal(\mu,\sigma)$	$f(x)=\frac{1}{\sigma\sqrt{2\pi}}e^{-(x-\mu)^2/(2\sigma^2)}$ $x \in (-\infty,\infty)$	μ	
Log-Normal $LogNormal(\mu,\sigma)$	$\frac{1}{x\sigma\sqrt{2\pi}}e^{-(\log x-\mu)^2/(2\sigma^2)}$ $x \in (0,\infty)$	$\theta=e^{\mu+\sigma^2/2}$	$\theta^2(e^{\sigma^2}-1)$
Beta Beta(a,b)	$f(x)=\frac{\Gamma(a+b)}{\Gamma(a)\Gamma(b)}x^{a-1}(1-x)^{b-1}$ $x \in (0,1)$	$\mu=\frac{a}{a+b}$	$\frac{\mu(1-\mu)}{(a+b+1)}$
Exponential $Exp(\lambda)$	$f(x)=\lambda e^{-\lambda x}$ $x \in (0,\infty)$	$\frac{1}{\lambda}$	$\frac{1}{\lambda^2}$
Gamma $Gamma(a,\lambda)$	$f(x)=\frac{1}{\Gamma(a)}(\lambda x)^a e^{-\lambda x}\frac{1}{x}$ $x \in (0,\infty)$	$\frac{a}{\lambda}$	$\frac{a}{\lambda^2}$
Student-t $t(n)$	$\frac{\Gamma((n+1)/2)}{\sqrt{n\pi}\Gamma(n/2)}(1+x^2/n)^{-(n+1)/2}$ $x \in (-\infty,\infty)$	0 if $n>1$	$\frac{n}{n-2}$ if $n>2$

The above table is adapted from https://github.com/wzchen/probability_cheatsheet.

1.5 Jointly distributed random variables

1.5.1 Discrete case

[This section is an extract from Kerns.]

Consider two discrete random variables X and Y with PMFs f_X and f_Y that are supported on the sample spaces S_X and S_Y, respectively. Let $S_{X,Y}$ denote the set of all possible observed **pairs** (x,y), called the **joint support set** of X and Y. Then the **joint probability mass function** of X and Y is the function $f_{X,Y}$ defined by

$$f_{X,Y}(x,y) = \mathbb{P}(X = x, Y = y), \quad \text{for } (x,y) \in S_{X,Y}. \tag{72}$$

Every joint PMF satisfies

$$f_{X,Y}(x,y) > 0 \text{ for all } (x,y) \in S_{X,Y}, \tag{73}$$

and

$$\sum_{(x,y)\in S_{X,Y}} f_{X,Y}(x,y) = 1. \tag{74}$$

It is customary to extend the function $f_{X,Y}$ to be defined on all of $\mathbb{R}^2$ by setting $f_{X,Y}(x,y) = 0$ for $(x,y) \notin S_{X,Y}$.

In the context of this chapter, the PMFs f_X and f_Y are called the **marginal PMFs** of X and Y, respectively. If we are given only the joint PMF then we may recover each of the marginal PMFs by using the Theorem of Total Probability: observe

$$\begin{aligned} f_X(x) &= \mathbb{P}(X = x), & (75)\\ &= \sum_{y\in S_Y} \mathbb{P}(X = x, Y = y), & (76)\\ &= \sum_{y\in S_Y} f_{X,Y}(x,y). & (77) \end{aligned}$$

By interchanging the roles of X and Y it is clear that

$$f_Y(y) = \sum_{x\in S_X} f_{X,Y}(x,y). \tag{78}$$

Given the joint PMF we may recover the marginal PMFs, but the converse is not true. Even if we have **both** marginal distributions they are not sufficient to determine the joint PMF; more information is needed.

Associated with the joint PMF is the **joint cumulative distribution function** $F_{X,Y}$ defined by

$$F_{X,Y}(x,y) = \mathbb{P}(X \le x, Y \le y), \quad \text{for } (x,y) \in \mathbb{R}^2.$$

The bivariate joint CDF is not quite as tractable as the univariate CDFs, but in principle we could calculate it by adding up quantities of the form in Equation~72. The joint CDF is typically not used in practice due to its inconvenient form; one can usually get by with the joint PMF alone.

Example:

Roll a fair die twice. Let X be the face shown on the first roll, and let Y be the face shown on the second roll. For this example, it suffices to define

$$f_{X,Y}(x,y) = \frac{1}{36}, \quad x = 1,\ldots,6,\ y = 1,\ldots,6.$$

The marginal PMFs are given by $f_X(x) = 1/6$, $x = 1,2,\ldots,6$, and $f_Y(y) = 1/6$, $y = 1,2,\ldots,6$, since

$$f_X(x) = \sum_{y=1}^{6} \frac{1}{36} = \frac{1}{6}, \quad x = 1,\ldots,6,$$

and the same computation with the letters switched works for Y.

Here, and in many other ones, the joint support can be written as a product set of the support of X "times" the support of Y, that is, it may be represented as a cartesian product set, or rectangle, $S_{X,Y} = S_X \times S_Y$ where $S_X \times S_Y = \{(x,y) :\ x \in S_X, y \in S_Y\}$. This form is a necessary condition for X and Y to be **independent** (or alternatively **exchangeable** when $S_X = S_Y$). But please note that in general it is not required for $S_{X,Y}$ to be of rectangle form.

1.5.2 Continuous case

For random variables X and y, the **joint cumulative pdf** is

$$F(a,b) = P(X \le a, Y \le b) \quad -\infty < a,b < \infty \tag{79}$$

The **marginal distributions** of F_X and F_Y are the CDFs of each of the associated RVs:

1. The CDF of X:

$$F_X(a) = P(X \le a) = F_X(a,\infty) \tag{80}$$

2. The CDF of Y:

$$F_Y(a) = P(Y \le b) = F_Y(\infty,b) \tag{81}$$

Definition 1. ***Jointly continuous****: Two RVs X and Y are jointly continuous if there exists a function $f(x,y)$ defined for all real x and y, such that for every set C:*

$$P((X,Y) \in C) = \iint\limits_{(x,y)\in C} f(x,y)\,dx\,dy \tag{82}$$

*$f(x,y)$ is the **joint PDF** of X and Y.*

Every joint PDF satisfies

$$f(x,y) \geq 0 \text{ for all } (x,y) \in S_{X,Y}, \tag{83}$$

and

$$\iint\limits_{S_{X,Y}} f(x,y)\,\mathrm{d}x\,\mathrm{d}y = 1. \tag{84}$$

For any sets of real numbers A and B, and if $C = \{(x,y) : x \in A, y \in B\}$, it follows from equation~82 that

$$P((X \in A, Y \in B) \in C) = \int_B \int_A f(x,y)\,dx\,dy \tag{85}$$

Note that

$$F(a,b) = P(X \in (-\infty,a]), Y \in (-\infty,b])) = \int_{-\infty}^{b} \int_{-\infty}^{a} f(x,y)\,dx\,dy \tag{86}$$

Differentiating, we get the joint pdf:

$$f(a,b) = \frac{\partial^2}{\partial a \partial b} F(a,b) \tag{87}$$

One way to understand the joint PDF:

$$P(a < X < a+da, b < Y < b+db) = \int_b^{d+db} \int_a^{a+da} f(x,y)\,dx\,dy \approx f(a,b)dadb \tag{88}$$

Hence, $f(x,y)$ is a measure of how probable it is that the random vector (X,Y) will be near (a,b).

1.5.3 Marginal probability distribution functions

If X and Y are jointly continuous, they are individually continuous, and their PDFs are:

$$\begin{aligned} P(X \in A) =& P(X \in A, Y \in (-\infty, \infty)) \\ &= \int_A \int_{-\infty}^{\infty} f(x,y)\, dy\, dx \\ &= \int_A f_X(x)\, dx \end{aligned} \tag{89}$$

where

$$f_X(x) = \int_{-\infty}^{\infty} f(x,y)\, dy \tag{90}$$

Similarly:

$$f_Y(y) = \int_{-\infty}^{\infty} f(x,y)\, dx \tag{91}$$

1.5.4 Independent random variables

Random variables X and Y are independent iff, for any two sets of real numbers A and B:

$$P(X \in A, Y \in B) = P(X \in A) P(Y \in B) \tag{92}$$

In the jointly continuous case:

$$f(x,y) = f_X(x) f_Y(y) \quad \text{for all } x, y \tag{93}$$

A necessary and sufficient condition for the random variables X and Y to be independent is for their joint probability density function (or joint probability mass function in the discrete case) $f(x,y)$ to factor into two terms, one depending only on x and the other depending only on y. %This can be stated as a proposition:

Example from Kerns:
Let the joint PDF of (X,Y) be given by

$$f_{X,Y}(x,y) = \frac{6}{5}\left(x + y^2\right), \quad 0 < x < 1,\ 0 < y < 1.$$

The marginal PDF of X is

$$\begin{aligned} f_X(x) &= \int_0^1 \frac{6}{5}\left(x+y^2\right)\,\mathrm{d}y, \\ &= \frac{6}{5}\left(xy+\frac{y^3}{3}\right)\Big|_{y=0}^{1}, \\ &= \frac{6}{5}\left(x+\frac{1}{3}\right), \end{aligned}$$

for $0 < x < 1$, and the marginal PDF of Y is

$$\begin{aligned} f_Y(y) &= \int_0^1 \frac{6}{5}\left(x+y^2\right)\,\mathrm{d}x, \\ &= \frac{6}{5}\left(\frac{x^2}{2}+xy^2\right)\Big|_{x=0}^{1}, \\ &= \frac{6}{5}\left(\frac{1}{2}+y^2\right), \end{aligned}$$

for $0 < y < 1$.

In this example the joint support set was a rectangle $[0,1]\times[0,1]$, but it turns out that X and Y are not independent. This is because $\frac{6}{5}\left(x+y^2\right)$ cannot be stated as a product of two terms ($f_X(x)f_Y(y)$).

1.5.5 Sums of independent random variables

(Taken nearly verbatim from Ross 2002.)

Suppose that X and Y are independent, continuous random variables having probability density functions f_X and f_Y. The cumulative distribution function of $X+Y$ is obtained as follows:

$$\begin{aligned} F_{X+Y}(a) =& P(X+Y \le a) \\ &= \iint\limits_{x+y\le a} f_{XY}(x,y)\,dx\,dy \\ &= \iint\limits_{x+y\le a} f_X(x)f_Y(y)\,dx\,dy \\ &= \int_{-\infty}^{\infty}\int_{-\infty}^{a-y} f_X(x)f_Y(y)\,dx\,dy \\ &= \int_{-\infty}^{\infty}\int_{-\infty}^{a-y} f_X(x)\,dx f_Y(y)\,dy \\ &= \int_{-\infty}^{\infty} F_X(a-y)f_Y(y)\,dy \end{aligned} \tag{94}$$

The CDF F_{X+Y} is the **convolution** of the distributions F_X and F_Y.

If we differentiate the above equation, we get the pdf f_{X+Y}:

$$\begin{aligned} f_{X+Y} &= \frac{d}{dx}\int_{-\infty}^{\infty} F_X(a-y)f_Y(y)\,dy \\ &= \int_{-\infty}^{\infty} \frac{d}{dx}F_X(a-y)f_Y(y)\,dy \\ &= \int_{-\infty}^{\infty} f_X(a-y)f_Y(y)\,dy \end{aligned} \tag{95}$$

1.5.6 Conditional distributions

1.5.6.1 Discrete case

Recall that the conditional probability of B given A, denoted $\mathbb{P}(B \mid A)$, is defined by

$$\mathbb{P}(B \mid A) = \frac{\mathbb{P}(A \cap B)}{\mathbb{P}(A)}, \quad \text{if } \mathbb{P}(A) > 0. \tag{96}$$

If X and Y are discrete random variables, then we can define the conditional PMF of X given that $Y = y$ as follows:

$$\begin{aligned} p_{X|Y}(x \mid y) &= P(X = x \mid Y = y) \\ &= \frac{P(X = x, Y = y)}{P(Y = y)} \\ &= \frac{p(x,y)}{p_Y(y)} \end{aligned} \tag{97}$$

for all values of y where $p_Y(y) = P(Y = y) > 0$.

The **conditional cumulative distribution function** of X given $Y = y$ is defined, for all y such that $p_Y(y) > 0$, as follows:

$$\begin{aligned} F_{X|Y} &= P(X \leq x \mid Y = y) \\ &= \sum_{a \leq x} p_{X|Y}(a \mid y) \end{aligned} \tag{98}$$

If X and Y are independent then

$$p_{X|Y}(x \mid y) = P(X = x) = p_X(x) \tag{99}$$

See the examples starting p. 264 of Ross (2002).

1.5.6.2 Continuous case

(Taken almost verbatim from Ross 2002.)

If X and Y have a joint probability density function $f(x,y)$, then the conditional probability density function of X given that $Y = y$ is defined, for all values of y such that $f_Y(y) > 0$,by

$$f_{X|Y}(x \mid y) = \frac{f(x,y)}{f_Y(y)} \tag{100}$$

We can understand this definition by considering what $f_{X|Y}(x \mid y)\,dx$ amounts to:

$$\begin{aligned} f_{X|Y}(x \mid y)\,dx =& \frac{f(x,y)}{f_Y(y)}\frac{dxdy}{dy} \\ =& \frac{f(x,y)dxdy}{f_Y(y)dy} \\ =& \frac{P(x < X < x+dx, y < Y < y+dy)}{y < P < y+dy} \end{aligned} \tag{101}$$

1.5.7 Covariance and correlation

There are two very special cases of joint expectation: the **covariance** and the **correlation**. These are measures which help us quantify the dependence between X and Y.
Definition 2. *The **covariance** of X and Y is*

$$Cov(X,Y) = \mathbb{E}(X - \mathbb{E}X)(Y - \mathbb{E}Y). \tag{102}$$

Shortcut formula for covariance:

$$\mathrm{Cov}(X,Y) = \mathbb{E}(XY) - (\mathbb{E}X)(\mathbb{E}Y). \tag{103}$$

The Pearson product moment correlation between X and Y is the covariance between X and Y rescaled to fall in the interval $[-1,1]$. It is formally defined by

$$\mathrm{Corr}(X,Y) = \frac{\mathrm{Cov}(X,Y)}{\sigma_X \sigma_Y}. \tag{104}$$

The correlation is usually denoted by $\rho_{X,Y}$ or simply ρ if the random variables are clear from context. There are some important facts about the correlation coefficient:

1. The range of correlation is $-1 \leq \rho_{X,Y} \leq 1$.
2. Equality holds above ($\rho_{X,Y} = \pm 1$) if and only if Y is a linear function of X with probability one.

1.5.7.1 Variance-covariance matrices

The variances in a multivariate distribution will be composed of

- variances for each random variable
- covariances between pairs of random variables, which includes some correlation ρ between pairs of random variables

E.g., for a bivariate distribution with random variables u_0 and u_1, this information is expressed in a so-called variance-covariance matrix.

$$\Sigma = \begin{pmatrix} \sigma_{u0}^2 & \rho\,\sigma_{u0}\sigma_{u1} \\ \rho\,\sigma_{u0}\sigma_{u1} & \sigma_{u1}^2 \end{pmatrix} \tag{105}$$

the covariance $Cov(X,Y)$ between two variables X and Y is defined as the product of their correlation ρ and their standard deviations σ_X and σ_Y, such that, $Cov(X,Y) = \rho\,\sigma_X\sigma_Y$.

$$\Sigma_u = \begin{pmatrix} \sigma_{u_0}^2 & \rho_u\sigma_{u_0}\sigma_{u_1} \\ \rho_u\sigma_{u_0}\sigma_{u_1} & \sigma_{u_1}^2 \end{pmatrix} \tag{106}$$

The covariance matrix can be decomposed into a matrix of standard deviations and a correlation matrix. The correlation matrix looks like this:

$$\rho_u = \begin{pmatrix} 1 & \rho \\ \rho & 1 \end{pmatrix} \tag{107}$$

This means that we can decompose the covariance matrix into three parts:

$$\Sigma = \begin{pmatrix} \sigma_{u_0} & 0 \\ 0 & \sigma_{u_1} \end{pmatrix} \begin{pmatrix} 1 & \rho_u \\ \rho_u & 1 \end{pmatrix} \begin{pmatrix} \sigma_{u_0} & 0 \\ 0 & \sigma_{u_1} \end{pmatrix} \tag{108}$$

1.5.7.2 The Cholesky decomposition

Assume that we have an $n \times n$ correlation matrix ρ_u. We can obtain a square root of this matrix, which is called the lower triangular matrix $\mathbf{L_u}$. If we multiply $\mathbf{L_u}$ with its transpose, we get the correlation matrix:

$\mathbf{L_u}\mathbf{L_u}^T = \rho_u$.

The matrix $\mathbf{L_u}$ is called the Cholesky factor of $\rho_\mathbf{u}$:

$$\mathbf{L_u} = \begin{pmatrix} l_{11} & 0 \\ l_{21} & l_{22} \end{pmatrix} \tag{109}$$

As an example, let's assume a correlation of 0.8.

```r
rho <- 0.8
#Correlation matrix
rho_u <- matrix(c(1,rho,rho,1),ncol=2)

# Cholesky factor:
L_u <- t(chol(rho_u))
# Verify that we recover rho_u, %*%
# indicates matrix multiplication (=! element-wise multiplication)
L_u %*% t(L_u)
```

```
##      [,1] [,2]
## [1,]  1.0  0.8
## [2,]  0.8  1.0
```

What is the Cholesky factor useful for? We can use the Cholesky factor to generate correlated random variables in the following way.

Step 1. We generate uncorrelated values that will be associated with random variable u from a $Normal(0,1)$. In our case we have u_0 and u_1, so we will generate:

$$z_{u_0} \sim Normal(0,1)$$
$$z_{u_1} \sim Normal(0,1)$$

For example, assuming only 10 data points:

```r
N_subj <- 10
z_u0 <- rnorm(N_subj,0,1)
z_u1 <- rnorm(N_subj,0,1)
```

Step 2. By multiplying the Cholesky factor by our z's we generate a matrix of correlated variables (with standard deviation 1).

A very informal explanation of why this works is that we are making the variable that corresponds to the slope to be a function of a scaled version of the intercept.

For example:

```r
# matrix z_u
z_u <- matrix(c(z_u0,z_u1),ncol=N_subj,byrow=TRUE)

L_u %*% z_u
```

```
##         [,1]   [,2]   [,3]   [,4]   [,5]  [,6]   [,7] [,8]   [,9]  [,10]
## [1,]  0.4419  0.242 -0.528 -0.334 -0.489 1.500  0.125 2.17 -0.272 -1.721
## [2,] -0.0822 -1.030 -0.146 -0.542 -0.711 0.815 -0.117 1.37  0.851 -0.875
```

Step 3. The last step is to scale the previous matrix to the desired standard deviation. We define the diagonalized matrix as before:

$$\begin{pmatrix} \tau_{u_0} & 0 \\ 0 & \tau_{u_1} \end{pmatrix}$$

For example:

```
tau_u0 <- .2
tau_u1 <- .01
(diag_matrix_tau <- matrix(c(tau_u0,0,0,tau_u1),ncol=2))
```

```
##      [,1] [,2]
## [1,]  0.2 0.00
## [2,]  0.0 0.01
```

We pre-multiply it by the correlated variables with SD of 1 from before:

For example:

```
u <- diag_matrix_tau %*% L_u %*% z_u

# We should find that the rows have approx. correlation 0.8
cor(u[1,],u[2,])
```

```
## [1] 0.731
```

```
# We should be able to recover the tau's as well:
sd(u[1,])
```

```
## [1] 0.219
```

```
sd(u[2,])
```

```
## [1] 0.00811
```

This process of generating correlated random variables will be useful when we start fitting hierarchical linear models: we will define a prior on the Cholesky factor of the correlation matrix, and then assemble the variance-covariance matrix as shown above, and then generate correlated random variables (varying intercepts and slopes).

1.5.8 Multivariate normal distributions

This is a very important distribution that we will need in linear mixed models.

Consider the bivariate case first. Suppose we have two univariate random variables $U0 \sim Normal(\mu_0, \sigma_{u0})$ and $U1 \sim Normal(\mu_1, \sigma_{u1})$ that have covariance $\rho\sigma_{u0}\sigma_{u1}$. We write this as:

$$\begin{pmatrix} U_0 \\ U_1 \end{pmatrix} \sim \mathcal{N}\left(\begin{pmatrix} \mu_0 \\ \mu_1 \end{pmatrix}, \Sigma\right) \tag{110}$$

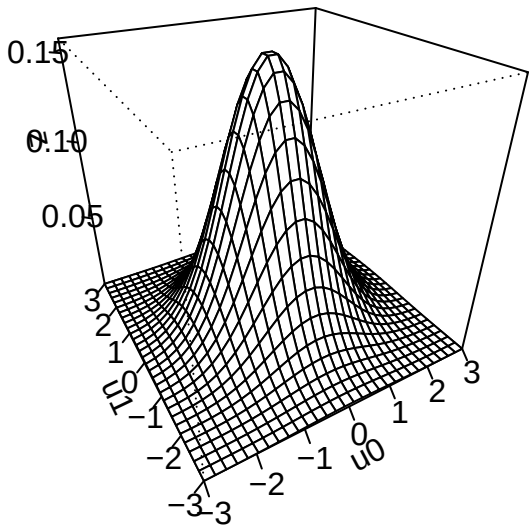


Figure 7: Visualization of two uncorrelated random variables.

The variances and covariances between the two random variables are described by a 2×2 variance-covariance matrix. The diagonals have the variances, and the off-diagonals have the covariance between the two random variables.

$$\Sigma = \begin{pmatrix} \sigma_{u0}^2 & \rho\sigma_{u0}\sigma_{u1} \\ \rho\sigma_{u0}\sigma_{u1} & \sigma_{u1}^2 \end{pmatrix} \tag{111}$$

We develop some graphical intuition about bivariate distributions next.

1.5.8.1 Graphical intuition for the bivariate case

If we have two independent random variables U0, U1, and we examine their joint distribution, we can plot a 3-d plot which shows, u0, u1, and f(u0,u1).

Bivariate distribution with no correlation (independent random variables): E.g., $u0 \sim N(0,1)$ and $u1 \sim N(0,1)$, with two independent random variables. See Figure 7.

```
library(mvtnorm)
u0 <- u1 <- seq(from = -3, to = 3, length.out = 30)
Sigma1<-diag(2)
f <- function(u0, u1) dmvnorm(cbind(u0, u1), mean = c(0, 0),sigma = Sigma1)
z <- outer(u0, u1, FUN = f)
```

```
persp(u0, u1, z, theta = -30, phi = 30, ticktype = "detailed")
```

Bivariate distribution with positive correlation: see Figure 8.

```
Sigma2<-matrix(c(1,.6,.6,1),byrow=FALSE,ncol=2)
f <- function(u0, u1) dmvnorm(cbind(u0, u1), mean = c(0, 0),sigma = Sigma2)
z <- outer(u0, u1, FUN = f)
```

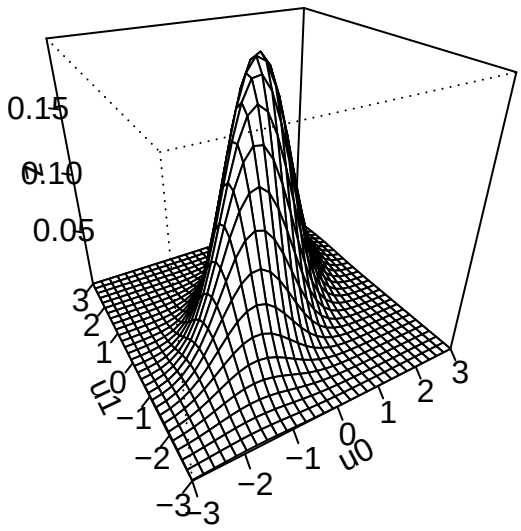


Figure 8: Visualization of two positively correlated random variables.

```
persp(u0, u1, z, theta = -30, phi = 30, ticktype = "detailed")
```

Bivariate distribution with negative correlation: see Figure 9.

```
Sigma3<-matrix(c(1,-.6,-.6,1),byrow=FALSE,ncol=2)
f <- function(u0, u1) dmvnorm(cbind(u0, u1), mean = c(0, 0),sigma = Sigma3)
z <- outer(u0, u1, FUN = f)
```

```
persp(u0, u1, z, theta = -30, phi = 30, ticktype = "detailed")
```

1.5.8.2 Visualizing conditional distributions in a bivariate

You can run the following code to get a visualization of what a conditional distribution looks like when we take "slices" from the conditioning random variable:

```
bivn<-mvrnorm(1000,mu=c(0,1),Sigma=matrix(c(1,0,0,2),2))
bivn.kde<-kde2d(bivn[,1],bivn[,2],n=50)

for(i in 1:50){
  plot(bivn.kde$z[i,1:50],type="l",ylim=c(0,0.1))
  Sys.sleep(.5)
}
```

If you run this code, you will see "slices" from the bivariate distribution.

1.5.8.3 Formal definition of the multivariate normal

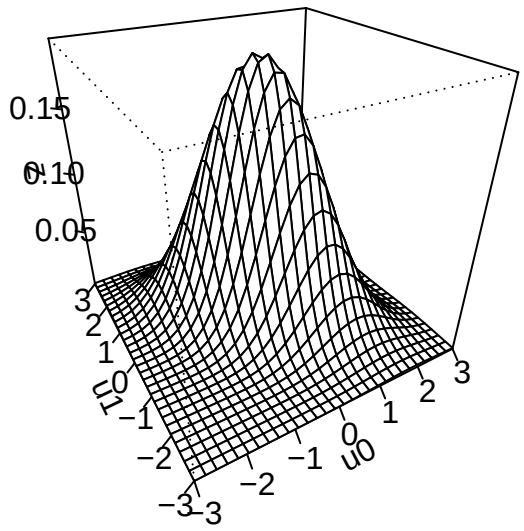


Figure 9: Visualization of two negatively correlated random variables.

Having acquired a graphical intuition, we turn to the formal definitions. Recall that in the univariate normal distribution:

$$f(x) = \frac{1}{\sqrt{2\pi\sigma^2}} e\{-\frac{(\frac{(x-\mu)}{\sigma})^2}{2}\} \quad -\infty < x < \infty \tag{112}$$

We can write the power of the exponential as:

$$\left(\frac{(x-\mu)}{\sigma}\right)^2 = (x-\mu)(x-\mu)(\sigma^2)^{-1} = (x-\mu)(\sigma^2)^{-1}(x-\mu) = Q \tag{113}$$

Generalizing this to the multivariate case:

$$Q = (x-\mu)'\Sigma^{-1}(x-\mu) \tag{114}$$

Σ is a variance-covariance matrix, and Σ^{-1} is its inverse.

So, for the multivariate case:

$$f(x) = \frac{1}{\sqrt{2\pi det(\Sigma)}} e\{-Q/2\} \quad -\infty < x_i < \infty, i = 1, \ldots, n \tag{115}$$

$det(\Sigma)$ is the determinant of the matrix.

Properties of the multivariate normal (MVN) X:

- Linear combinations of X are normal distributions.
- All subsets of X's components have a normal distribution.

- Zero covariance implies independent distributions.
- Conditional distributions are normal.

1.6 Maximum likelihood estimation

1.6.1 Discrete case

Suppose the observed independent sample values are $x_1, x_2, \ldots, x_n$ from some random variable with pmf $P(\cdot)$ that has a parameter θ. The probability of getting these particular values is

$$P(X_1 = x_1, X_2 = x_2, \ldots, X_n = x_n) = f(X_1 = x_1, X_2 = x_2, \ldots, X_n = x_n; \theta) \tag{116}$$

i.e., the function f is the value of the joint probability **distribution** of the random variables $X_1, \ldots, X_n$ at $X_1 = x_1, \ldots, X_n = x_n$. Since the sample values have been observed and are fixed, $f(x_1, \ldots, x_n; \theta)$ is a function of θ. The function f is called a **likelihood function**.

1.6.2 Continuous case

Here, f is the joint probability **density**, the rest is the same as above.
Definition 3. *If $x_1, x_2, \ldots, x_n$ are the values of a random sample from a population with parameter θ, the **likelihood function** of the sample is given by*

$$L(\theta) = f(x_1, x_2, \ldots, x_n; \theta) \tag{117}$$

for values of θ within a given domain. Here, $f(X_1 = x_1, X_2 = x_2, \ldots, X_n = x_n; \theta) = f(x_1; \theta) \cdot f(x_2; \theta) \ldots f(x_n; \theta)$ is the joint likelihood of the random variables $X_1, \ldots, X_n$ at $X_1 = x_1, \ldots, X_n = x_n$.

So, the method of maximum likelihood consists of maximizing the likelihood function with respect to θ. The value of θ that maximizes the likelihood function is the **MLE** (maximum likelihood estimate) of θ.

1.6.3 Finding maximum likelihood estimates for different distributions

Example 1

Let X_i, $i = 1, \ldots, n$ be a random variable with PDF $f(x; \sigma) = \frac{1}{2\sigma} exp(-\frac{|x|}{\sigma})$. Find $\hat{\sigma}$, the MLE of σ.

$$L(\sigma) = \prod f(x_i; \sigma) = \frac{1}{(2\sigma)^n} exp(-\sum \frac{|\, x_i \,|}{\sigma}) \tag{118}$$

Let ℓ be log likelihood (log lik). The log likelihood is much easier to work with, because products become sums. Then:

$$\ell(x;\sigma) = \sum \left[-\log 2 - \log \sigma - \frac{|\, x_i \,|}{\sigma} \right] \tag{119}$$

Differentiating and equating to zero to find maximum:

$$\ell'(\sigma) = \sum \left[-\frac{1}{\sigma} + \frac{|\, x_i \,|}{\sigma^2} \right] = -\frac{n}{\sigma} + \frac{|\, x_i \,|}{\sigma^2} = 0 \tag{120}$$

Rearranging the above, the MLE for σ is:

$$\hat{\sigma} = \frac{\sum |\, x_i \,|}{n} \tag{121}$$

Example 2: Poisson

$$L(\mu;x) = \prod \frac{\exp^{-\mu} \mu^{x_i}}{x_i!} \tag{122}$$

$$= \exp^{-\mu} \mu^{\sum x_i} \frac{1}{\prod x_i!} \tag{123}$$

Log lik:

$$\ell(\mu;x) = -n\mu + \sum x_i \log \mu - \sum \log y! \tag{124}$$

Differentiating:

$$\ell'(\mu) = -n + \frac{\sum x_i}{\mu} = 0 \tag{125}$$

Therefore:

$$\hat{\lambda} = \frac{\sum x_i}{n} \tag{126}$$

Example 3: Binomial

$$L(\theta) = \binom{n}{x} \theta^x (1-\theta)^{n-x} \tag{127}$$

Log lik:

$$\ell(\theta) = \log \binom{n}{x} + x \log \theta + (n-x) \log(1-\theta) \tag{128}$$

Differentiating:

$$\ell'(\theta) = \frac{x}{\theta} - \frac{n-x}{1-\theta} = 0 \tag{129}$$

Thus:

$$\hat{\theta} = \frac{x}{n} \tag{130}$$

Example 4: Normal

Let $X_1, \ldots, X_n$ constitute a random variable of size n from a normal population with mean μ and variance σ^2, find joint maximum likelihood estimates of these two parameters.

$$L(\mu;\sigma^2) = \prod N(x_i;\mu,\sigma) \tag{131}$$

$$= (\tfrac{1}{2\pi\sigma^2})^{n/2} \exp(-\tfrac{1}{2\sigma^2}\sum(x_i-\mu)^2) \tag{132}$$

$$\tag{133}$$

Taking logs and differentiating with respect to μ and σ^2, we get:

$$\hat{\mu} = \frac{1}{n}\sum x_i = \bar{x} \tag{134}$$

and

$$\hat{\sigma}^2 = \frac{1}{n}\sum (x_i - \bar{x})^2 \tag{135}$$

1.6.4 Visualizing likelihood and maximum log likelihood for normal

For simplicity consider the case where $N(\mu = 0, \sigma^2 = 1)$.

```
op<-par(mfrow=c(1,2),pty="s")
plot(function(x) dnorm(x,log=FALSE), -3, 3,
      main = "Normal density",
              ylab="density",xlab="X")
abline(h=0.4)
plot(function(x) dnorm(x,log=TRUE), -3, 3,
      main = "Normal density (log)",
              ylab="density",xlab="X")
abline(h=log(0.4))
```

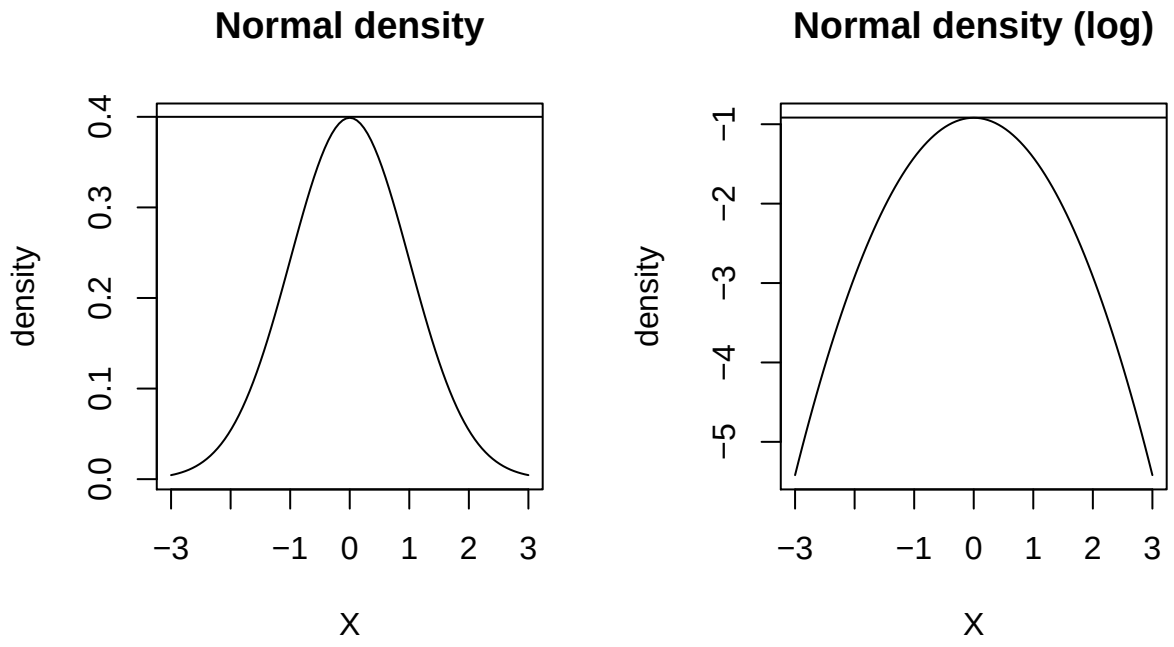


Figure 10: Maximum likelihood and log likelihood.

1.6.5 MLE using R

1.6.5.1 One-parameter case

Estimating θ for the binomial distribution: Let's assume we have the result of 10 coin tosses. We know that the MLE is the number of successes divided by the sample size:

```
x<-rbinom(10,1,prob=0.5)
sum(x)/length(x)
```

```
## [1] 0.7
```

We will now get this number using MLE. We do it numerically to illustrate the principle. First, we define a negative log likelihood function for the binomial. Negative because the function we will use to optimize does minimization by default, so we just flip the sign on the log likelihood to convert the maximum to a minimum.

```
negllbinom <- function(p, x){
  -sum(dbinom(x, size = 1, prob = p,log=T))
}
```

Then we run the optimization function:

```
optimize(negllbinom,
         interval = c(0, 1),
         x = x)
```

```
## $minimum
```

```
## [1] 0.7
##
## $objective
## [1] 6.11
```

1.6.5.2 Two-parameter case

Here is an example of MLE using R. Note that in this example, we could have analytically figured out the MLEs. Instead, we are doing this numerically. The advantage of the numerical approach becomes obvious when the analytical way is closed to us.

Assume that you have some data that was generated from a normal distribution, with mean 500, and standard deviation 50. Let's say you have 100 data points.

```
data<-rnorm(100,mean=500,sd=50)
```

Let's assume we don't know what the mean and standard deviation are. Now, of course you know how to estimate these using the standard formulas. But right now we are going to estimate them using MLE.

We first write down the negation of the log likelihood function. We take the negation because the optimization function we will be using (see below) does minimization by default, so to get the maximum with the default setting, we just change the sign.

The function `nllh.normal` takes a vector `theta` of parameter values, and a data frame `data`.

```
nllh.normal<-function(theta,data){
  ## decompose the parameter vector to
  ## its two parameters:
  m<-theta[1]
  s<-theta[2]
  ## read in data
  x <- data
  n<-length(x)
  ## log likelihood:
  logl<- sum(dnorm(x,mean=m,sd=s,log=TRUE))
  ## return negative log likelihood:
  -logl
  }
```

Here is the negative log lik for mean = 40, sd 4, and for mean = 800 and sd 4:

```
nllh.normal(theta=c(40,4),data)
```

```
## [1] 657725
```

```
nllh.normal(theta=c(800,4),data)
```

```
## [1] 296427
```

As we would expect, the negative log lik for mean 500 and sd 50 is much smaller (due to the sign change) than the two log liks above:

```
nllh.normal(theta=c(500,50),data)
```

```
## [1] 532
```

Basically, you could sit here forever, playing with combinations of values for mean and sd to find the combination that gives the optimal log likelihood. R has an optimization function that does this for you. We have to specify some sensible starting values:

```
opt.vals.default<-optim(theta<-c(700,40),
                        nllh.normal,
      data=data,
      hessian=TRUE)
```

Finally, we print out the estimated parameter values that maximize the likelihood:

```
opt.vals.default$par
```

```
## [1] 496  49
```

Knowledge of maximum likelihood estimation will be needed in the next chapter.

2 Introduction to Bayesian data analysis

Recall Bayes' rule:

Theorem 1. ***Bayes' Rule***. *Let B_1, B_2, ..., B_n be mutually exclusive and exhaustive and let A be an event with $\mathbb{P}(A) > 0$. Then*

$$\mathbb{P}(B_k|A) = \frac{\mathbb{P}(B_k)\mathbb{P}(A|B_k)}{\sum_{i=1}^{n} \mathbb{P}(B_i)\mathbb{P}(A|B_i)}, \quad k = 1, 2, \ldots, n. \tag{136}$$

When A and B are observable events, we can state the rule as follows:

$$p(A \mid B) = \frac{p(B \mid A)p(A)}{p(B)} \tag{137}$$

Note that $p(\cdot)$ is the probability of an event.

When looking at probability distributions, we will encounter the rule in the following form.

$$f(\theta \mid \text{data}) = \frac{f(\text{data} \mid \theta)f(\theta)}{f(y)} \tag{138}$$

Here, $f(\cdot)$ is a probability density, not the probability of a single event. $f(y)$ is called a "normalizing constant", which makes the left-hand side a probability distribution.

$$f(y) = \int f(x, \theta)\, d\theta = \int f(y \mid \theta) f(\theta)\, d\theta \tag{139}$$

If θ is a discrete random variable taking one value from the set $\{\theta_1, \ldots, \theta_n\}$, then

$$f(y) = \sum_{i=1}^{n} f(y \mid \theta_i) P(\theta = \theta_i) \tag{140}$$

Without the normalizing constant, we have the relationship:

$$f(\theta \mid \text{data}) \propto f(\text{data} \mid \theta) f(\theta) \tag{141}$$

Note that the likelihood $L(\theta; \text{data})$ (our data is fixed) is proportional to $f(\text{data} \mid \theta)$, and that's why we can refer to $f(\text{data} \mid \theta)$ as the likelihood in the following Bayesian incantation:

$$\text{Posterior} \propto \text{Likelihood} \times \text{Prior} \tag{142}$$

Our central goal is going to be to derive the posterior distribution and then summarize its properties (mean, median, 95% credible interval, etc.).

Usually, we don't need the normalizing constant to understand the properties of the posterior distribution. That's why Bayes' theorem is often stated in terms of the proportionality shown above.

Incidentally, this is supposed to be the moment of great divide between frequentists and Bayesians: the latter assign a probability distribution to the parameter, the former treat the parameter as a point value.

Two examples will clarify how we can use Bayes' rule to obtain the posterior. Both examples involve so-called conjugate priors, which are defined as follows:

> Given the likelihood $f(x \mid \theta)$, if the prior $f(\theta)$ results in a posterior $f(\theta \mid x)$ that has the same form as $f(\theta)$, then we call $f(\theta)$ a conjugate prior.

2.1 Example 1: Binomial Likelihood, Beta prior, Beta posterior

This is a contrived example, just meant to provide us with a smooth entry into Bayesian data analysis. Suppose that an individual with aphasia answered 46 out of 100 questions correctly in a particular sentence comprehension task. The research question is, what is the probability that their average response is greater than 0.5, i.e., above chance.

The likelihood function will tell us $P(\text{data} \mid \theta)$:

```
dbinom(46, 100, 0.5)
```

```
## [1] 0.058
```

Note that

$$P(\text{data} \mid \theta) \propto \theta^{46}(1-\theta)^{54} \tag{143}$$

So, to get the posterior, we just need to work out a prior distribution $f(\theta)$.

$$f(\theta \mid \text{data}) \propto f(\text{data} \mid \theta) f(\theta) \tag{144}$$

For the prior, we need a distribution that can represent our uncertainty about the probabiliy θ of success. The Beta distribution is commonly used as prior for proportions. We say that the Beta distribution is conjugate to the binomial density; i.e., the two densities have similar functional forms.

The pdf is

$$f(x) = \begin{cases} \frac{1}{B(a,b)} x^{a-1}(1-x)^{b-1} & \text{if } 0 < x < 1 \\ 0 & \text{otherwise} \end{cases}$$

where

$$B(a,b) = \int_0^1 x^{a-1}(1-x)^{b-1}\,dx$$

In R, we write $X \sim \texttt{beta}(\texttt{shape1} = \alpha, \texttt{shape2} = \beta)$. The associated R function is $\texttt{dbeta}(\texttt{x}, \texttt{shape1}, \texttt{shape2})$.

The mean and variance are

$$E[X] = \frac{a}{a+b} \text{ and } Var(X) = \frac{ab}{(a+b)^2(a+b+1)}. \tag{145}$$

The Beta distribution's parameters a and b can be interpreted as (our beliefs about) prior successes and failures, and are called **hyperparameters**. Once we choose values for a and b, we can plot the Beta pdf. Here, we show the Beta pdf for three sets of values of a,b:

```
plot(function(x)
  dbeta(x,shape1=1,shape2=1), 0,1,
      main = "Beta density",
              ylab="density",xlab="X",ylim=c(0,3))

text(.5,1.1,"a=1,b=1")

plot(function(x)
  dbeta(x,shape1=3,shape2=3),0,1,add=T)
text(.5,1.6,"a=3,b=3")


plot(function(x)
  dbeta(x,shape1=6,shape2=6),0,1,add=T)
text(.5,2.6,"a=6,b=6")
```

As Figure 11 shows, as the a,b values are increased, the spread decreases.

If we don't have much prior information, we could use a=b=1; this gives us a uniform prior; this is called an uninformative prior or non-informative prior (although having no prior knowledge is, strictly speaking, not uninformative). If we have a lot of prior knowledge and/or a strong belief that θ has a particular value, we can use a larger a,b to reflect our greater certainty about the parameter. Notice that the larger our parameters a and b, the narrower the spread of the distribution; this makes sense because a larger sample size (a greater number of successes a, and a greater number of failures b) will lead to more precise estimates.

The central point is that the Beta distribution can be used to define the prior distribution of θ.

Just for the sake of illustration, let's take four different beta priors, each reflecting increasing certainty.

1. Beta(a=2,b=2)

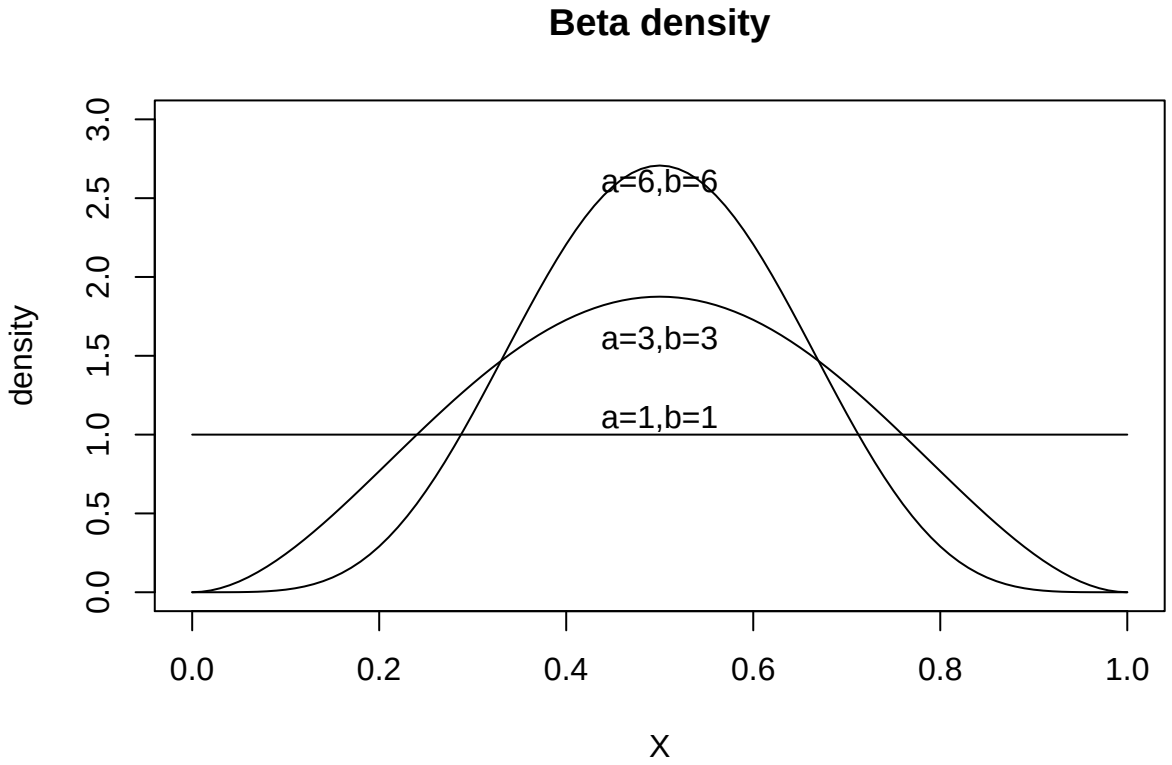


Figure 11: Examples of the beta distribution with different parameter values.

2. Beta(a=3,b=3)
3. Beta(a=6,b=6)
4. Beta(a=21,b=21)

Each reflects a belief that $\theta = 0.5$, with varying degrees of (un)certainty. Now we just need to plug in the likelihood and the prior:

$$f(\theta \mid \text{data}) \propto f(\text{data} \mid \theta) f(\theta) \tag{146}$$

The four corresponding posterior distributios would be:

$$f(\theta \mid \text{data}) \propto [\theta^{46}(1-\theta)^{54}][\theta^{2-1}(1-\theta)^{2-1}] = \theta^{47}(1-\theta)^{55} \tag{147}$$

$$f(\theta \mid \text{data}) \propto [p^{46}(1-p)^{54}][p^{3-1}(1-p)^{3-1}] = p^{48}(1-p)^{56} \tag{148}$$

$$f(\theta \mid \text{data}) \propto [\theta^{46}(1-\theta)^{54}][\theta^{6-1}(1-\theta)^{6-1}] = \theta^{51}(1-\theta)^{59} \tag{149}$$

$$f(\theta \mid \text{data}) \propto [\theta^{46}(1-\theta)^{54}][\theta^{21-1}(1-\theta)^{21-1}] = \theta^{66}(1-\theta)^{74} \tag{150}$$

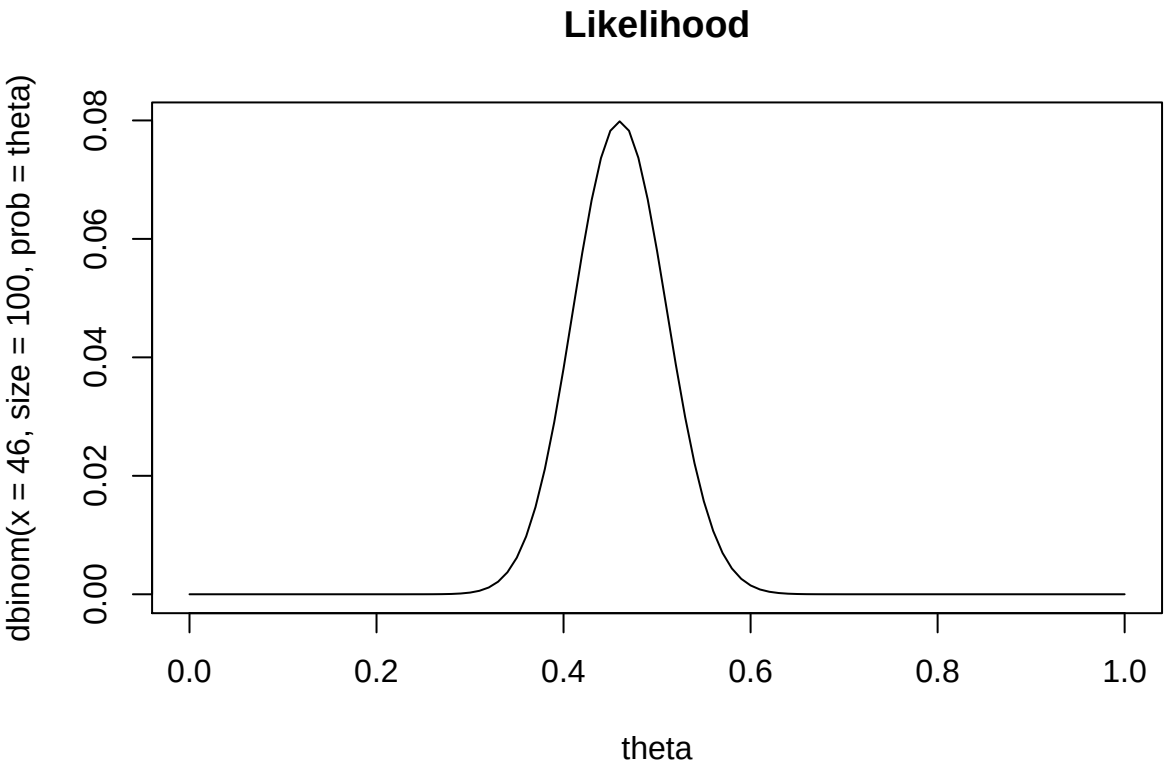


Figure 12: Binomial likelihood function.

We can now visualize each of these triplets of priors, likelihoods and posteriors. Note that I use the beta to model the likelihood because this allows me to visualize all three (prior, lik., posterior) in the same plot. The likelihood function is actually as shown in Figure 12:

```
theta=seq(0,1,by=0.01)

plot(theta,dbinom(x=46,size=100,prob=theta),
     type="l",main="Likelihood")
```

We can represent the likelihood in terms of the Beta as well, as shown in Figure 13:

```
plot(function(x)
  dbeta(x,shape1=46,shape2=54),0,1,
              ylab="",xlab="X")
```

2.2 Example 2: Poisson Likelihood, Gamma prior, Gamma posterior

This is also a contrived example. Suppose we are modeling the number of times that a speaker says the word "the" per day.

The number of times x that the word is uttered in one day can be modeled by a Poisson distribution:

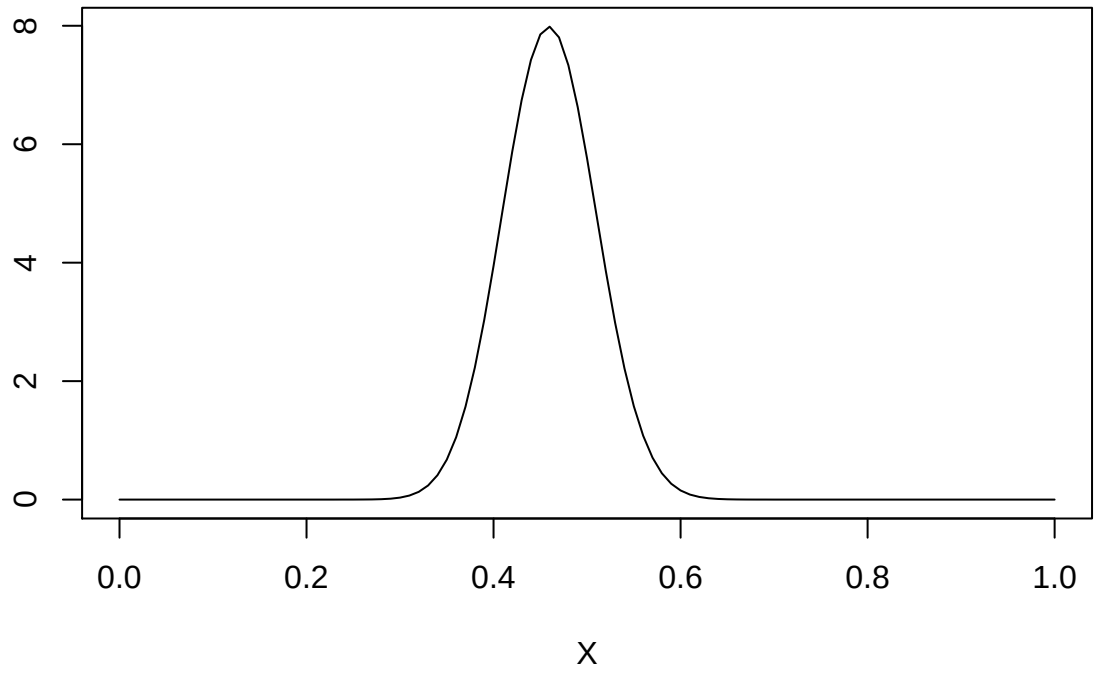


Figure 13: Using the beta distribution to represent a binomial.

$$f(x \mid \theta) = \frac{\exp(-\theta)\theta^x}{x!} \tag{151}$$

where the rate θ is unknown, and the numbers of utterances of the target word on each day are independent given θ.

We are told that the prior mean of θ is 100 and prior variance for θ is 225. This information could be based on the results of previous studies on the topic.

In order to visualize the prior, we first fit a Gamma density prior for θ based on the above information.

Note that we know that for a Gamma density with parameters a, b, the mean is $\frac{a}{b}$ and the variance is $\frac{a}{b^2}$. Since we are given values for the mean and variance, we can solve for a,b, which gives us the Gamma density.

If $\frac{a}{b} = 100$ and $\frac{a}{b^2} = 225$, it follows that $a = 100 \times b = 225 \times b^2$ or $100 = 225 \times b$, i.e., $b = \frac{100}{225}$.

This means that $a = \frac{100 \times 100}{225} = \frac{10000}{225}$. Therefore, the Gamma distribution for the prior is as shown below (also see Figure 14):

$$\theta \sim Gamma(\frac{10000}{225}, \frac{100}{225}) \tag{152}$$

```
x<-0:200
plot(x,dgamma(x,10000/225,100/225),type="l",lty=1,main="Gamma prior",ylab="density",cex.
```

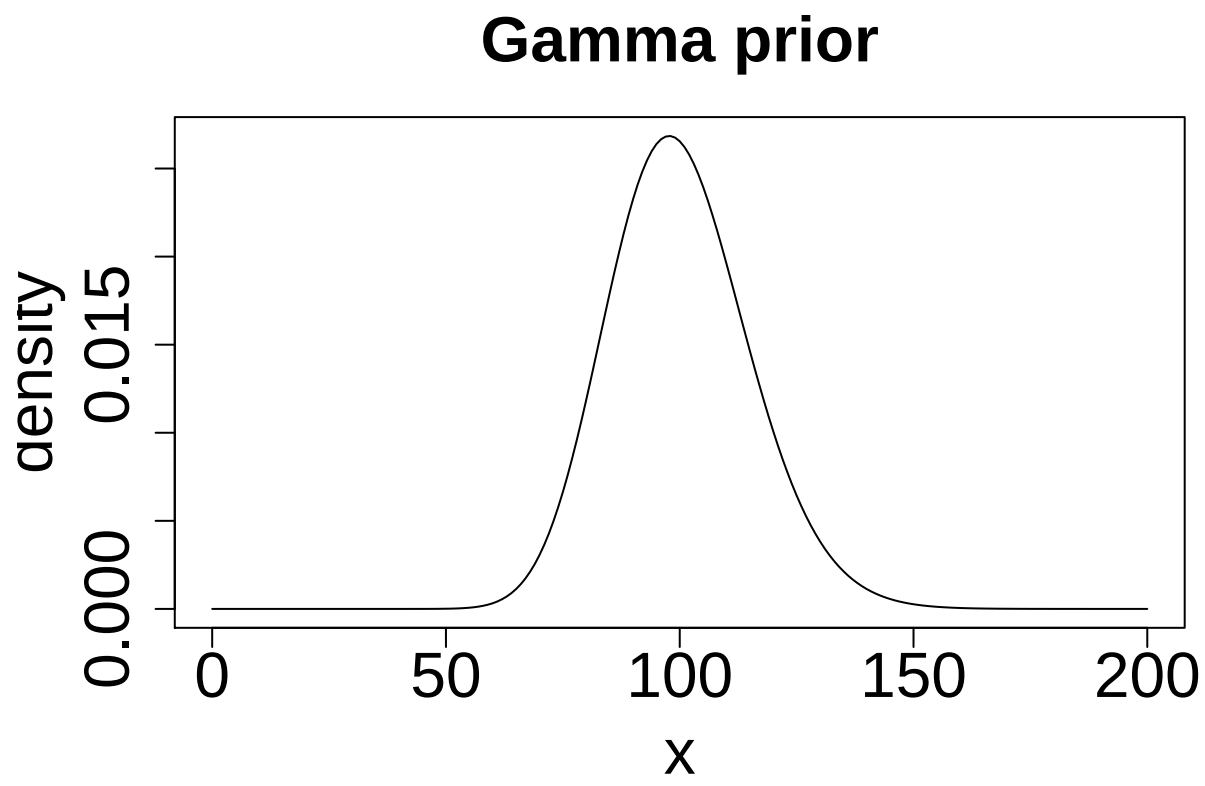


Figure 14: The Gamma prior for the parameter theta.

A distribution for a prior is **conjugate** if, multiplied by the likelihood, it yields a posterior that has the distribution of the same family as the prior.

It turns out that the Gamma distribution is a conjugate prior for the Poisson distribution. For the Gamma distribution to be a conjugate prior for the Poisson, the posterior needs to have the general form of a Gamma distribution. We derive this conjugacy result below. The proof just involves very simple algebra.

Given that

$$\text{Posterior} \propto \text{Prior Likelihood} \tag{153}$$

and given that the likelihood is:

$$\begin{aligned} L(\mathbf{x} \mid \theta) &= \prod_{i=1}^{n} \frac{\exp(-\theta)\theta^{x_i}}{x_i!} \\ &= \frac{\exp(-n\theta)\theta^{\Sigma_i^n x_i}}{\prod_{i=1}^{n} x_i!} \end{aligned} \tag{154}$$

we can compute the posterior as follows:

$$\text{Posterior} = \left[\frac{\exp(-n\theta)\theta^{\sum_i^n x_i}}{\prod_{i=1}^n x_i!}\right]\left[\frac{b^a\theta^{a-1}\exp(-b\theta)}{\Gamma(a)}\right] \tag{155}$$

We can disregard the terms $x!, \Gamma(a), b^a$, which do not involve θ, we have

$$\begin{aligned}\text{Posterior} \propto &\exp(-n\theta)\theta^{\sum_i^n x_i}\theta^{a-1}\exp(-b\theta)\\ =&\theta^{a-1+\sum_i^n x_i}\exp(-\theta(b+n))\end{aligned} \tag{156}$$

We can now figure out the parameters of the posterior distribution, and show that it will be a Gamma distribution.

First, note that the Gamma distribution in general is $Gamma(a,b) \propto \theta^{a-1}\exp(-\theta b)$. So it's enough to state the above as a Gamma distribution with some parameters a, b.

If we equate $a^* - 1 = a - 1 + \sum_i^n x_i$ and $b^* = b + n$, we can rewrite the above as:

$$\theta^{a^*-1}\exp(-\theta b^*) \tag{157}$$

This means that $a^* = a + \sum_i^n x_i$ and $b^* = b + n$. We can find a constant k such that the above is a proper probability density function, i.e.:

$$\int_{-\infty}^{\infty} k\theta^{a^*-1}\exp(-\theta b^*) = 1 \tag{158}$$

Thus, the posterior has the form of a Gamma distribution with parameters $a^* = a + \sum_i^n x_i, b^* = b + n$. Hence the Gamma distribution is a conjugate prior for the Poisson.

2.2.1 Concrete example given data

Suppose we know that the number of "the" utterances is $115, 97, 79, 131$. We can derive the posterior distribution as follows.

The prior is Gamma(a=10000/225,b=100/225). The data are as given; this means that $\sum_i^n x_i = 422$ and sample size $n = 4$. It follows that the posterior is

$$\begin{aligned}Gamma(a^* = a + \sum_i^n x_i, b^* = b + n) =&Gamma(10000/225 + 422, 4 + 100/225)\\ =&Gamma(466.44, 4.44)\end{aligned} \tag{159}$$

The mean and variance of this distribution can be computed using the fact that the mean is $\frac{a*}{b*} = 466.44/4.44 = 104.95$ and the variance is $\frac{a*}{b*^2} = 466.44/4.44^2 = 23.66$.

```r
### load data:
data<-c(115,97,79,131)

a.star<-function(a,data){
  return(a+sum(data))
}

b.star<-function(b,n){
  return(b+n)
}

new.a<-a.star(10000/225,data)
new.b<-b.star(100/225,length(data))

### post. mean
(post.mean<-new.a/new.b)
```

```
## [1] 105
```

```r
### post. var:
(post.var<-new.a/(new.b^2))
```

```
## [1] 23.6
```

Now suppose you get one new data point:

```r
new.data<-c(200)
```

We can compute the parameters of the posterior Gamma distributions using the function we wrote above:

```r
new.a.2<-a.star(new.a,new.data)
new.b.2<-b.star(new.b,length(new.data))

### new mean
(new.post.mean<-new.a.2/new.b.2)
```

```
## [1] 122
```

```r
### new var:
(new.post.var<-new.a.2/(new.b.2^2))
```

```
## [1] 22.5
```

Thus, new data can be used with the previous posterior distribution as prior, to compute the new posterior.

2.2.2 The posterior is a weighted mean of prior and likelihood

We can express the posterior mean as a weighted sum of the prior mean and the maximum likelihood estimate of θ.

The posterior mean is:

$$\frac{a*}{b*} = \frac{a + \sum x_i}{n + b} \tag{160}$$

This can be rewritten as

$$\frac{a*}{b*} = \frac{a + n\bar{x}}{n + b} \tag{161}$$

Dividing both the numerator and denominator by b:

$$\frac{a*}{b*} = \frac{(a + n\bar{x})/b}{(n + b)/b} = \frac{a/b + n\bar{x}/b}{1 + n/b} \tag{162}$$

Since a/b is the mean m of the prior, we can rewrite this as:

$$\frac{a/b + n\bar{x}/b}{1 + n/b} = \frac{m + \frac{n}{b}\bar{x}}{1 + \frac{n}{b}} \tag{163}$$

We can rewrite this as:

$$\frac{m + \frac{n}{b}\bar{x}}{1 + \frac{n}{b}} = \frac{m \times 1}{1 + \frac{n}{b}} + \frac{\frac{n}{b}\bar{x}}{1 + \frac{n}{b}} \tag{164}$$

This is a weighted average: setting $w_1 = 1$ and $w_2 = \frac{n}{b}$, we can write the above as:

$$m\frac{w_1}{w_1 + w_2} + \bar{x}\frac{w_2}{w_1 + w_2} \tag{165}$$

A n approaches infinity, the weight on the prior mean m will tend towards 0, making the posterior mean approach the maximum likelihood estimate of the sample.

In general, in a Bayesian analysis, as sample size increases, the likelihood will dominate in determining the posterior mean.

Regarding variance, since the variance of the posterior is:

$$\frac{a*}{b*^2} = \frac{(a + n\bar{x})}{(n + b)^2} \tag{166}$$

as n approaches infinity, the posterior variance will approach zero: more data will reduce variance (uncertainty).

2.3 Summary

We saw two examples where we can do the computations to derive the posterior using simple algebra. There are several other such simple cases. However, in realistic data analysis settings, we cannot specify the posterior distribution as a particular density. We can only specify the priors and the likelihood.

For such cases, we need to use MCMC sampling techniques so that we can sample from the posterior distributions of the parameters.

We will discuss three approaches for sampling:

- Gibbs sampling using inversion sampling
- Metropolis-Hasting
- Hamiltonian Monte Carlo

2.4 MCMC sampling

2.4.1 The inversion method for sampling

This method works when we know the closed form of the pdf we want to simulate from and can derive the inverse of that function.

Steps:

1. Sample one number u from $Unif(0,1)$. Let $u = F(z) = \int_L^z f(x)\,dx$ (here, L is the lower bound of the pdf f).
2. Then $z = F^{-1}(u)$ is a draw from $f(x)$.

2.4.1.1 Example 1: Samples from Standard Normal

Take a sample from the Uniform(0,1):

```
u<-runif(1,min=0,max=1)
```

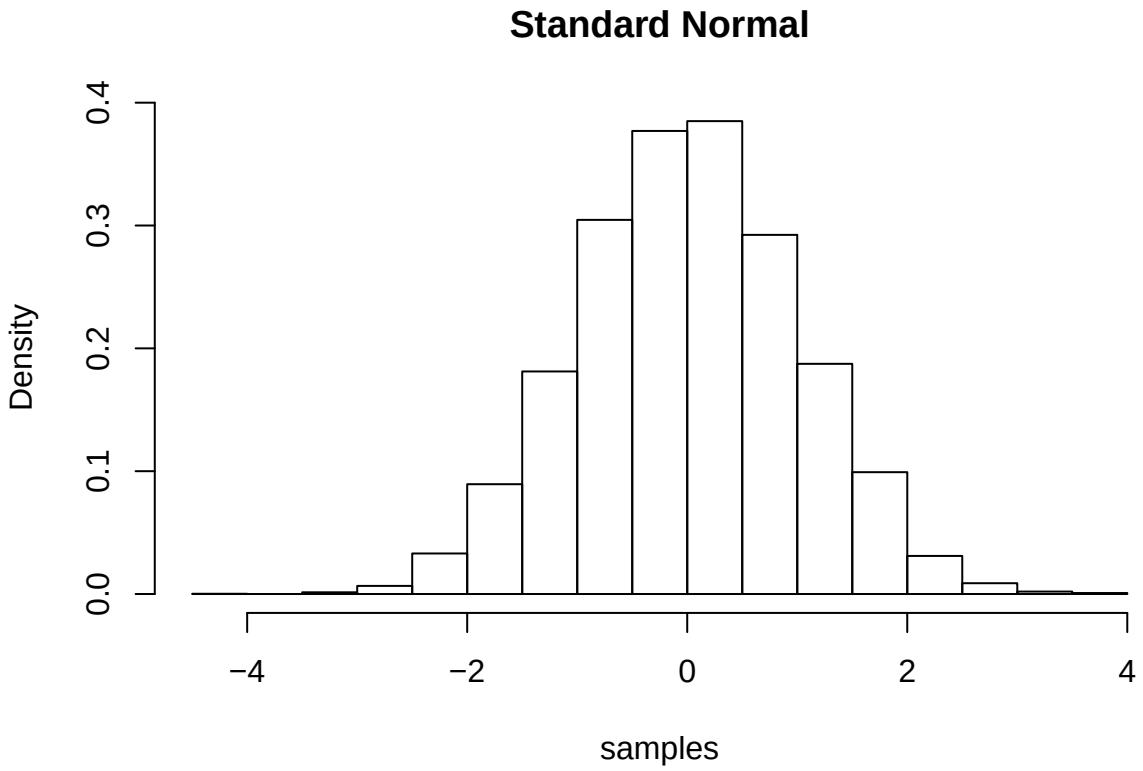
Let f(x) be a Normal density—we want to sample from this density. The inverse of the CDF in R is qnorm. It takes as input a probability and returns a quantile.

```
qnorm(u)
```

```
## [1] 2.11
```

If we do this repeatedly, we will get samples from the Normal distribution (here, the standard normal).

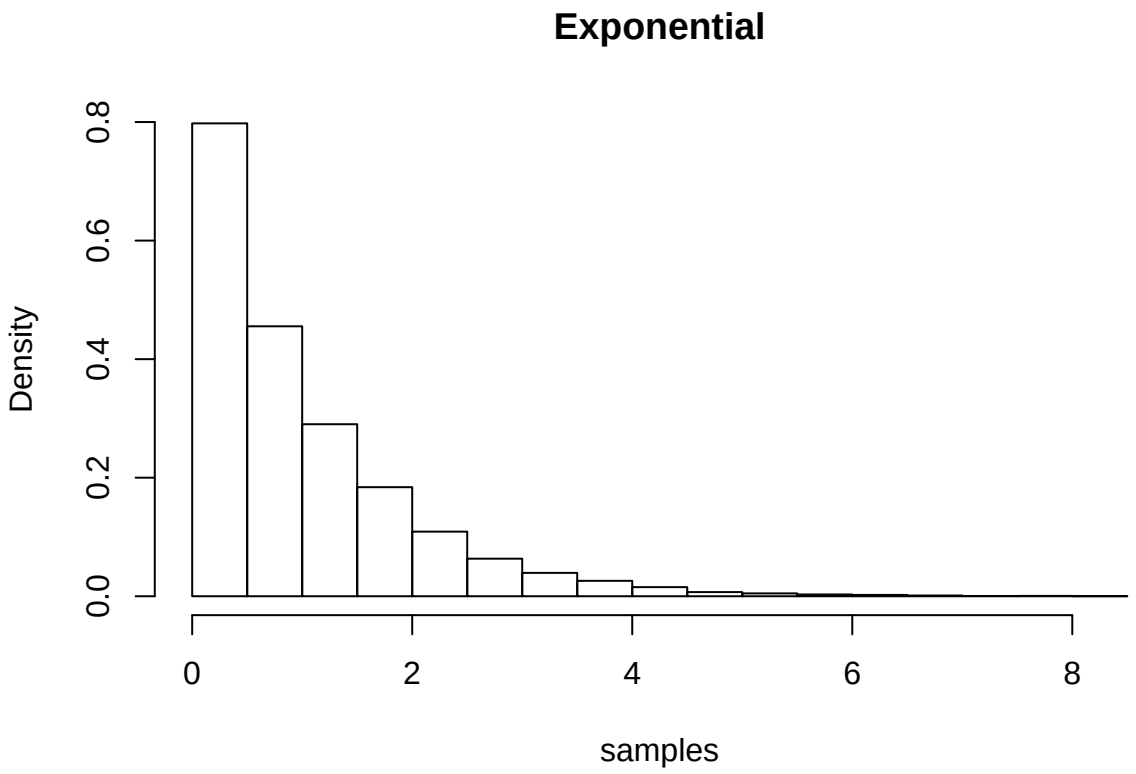
```
nsim<-10000
samples<-rep(NA,nsim)
for(i in 1:nsim){
  u <- runif(1,min=0,max=1)
  samples[i]<-qnorm(u)
}
hist(samples,freq=FALSE,main="Standard Normal")
```



2.4.1.2 Example 2: Samples from Exponential or Gamma

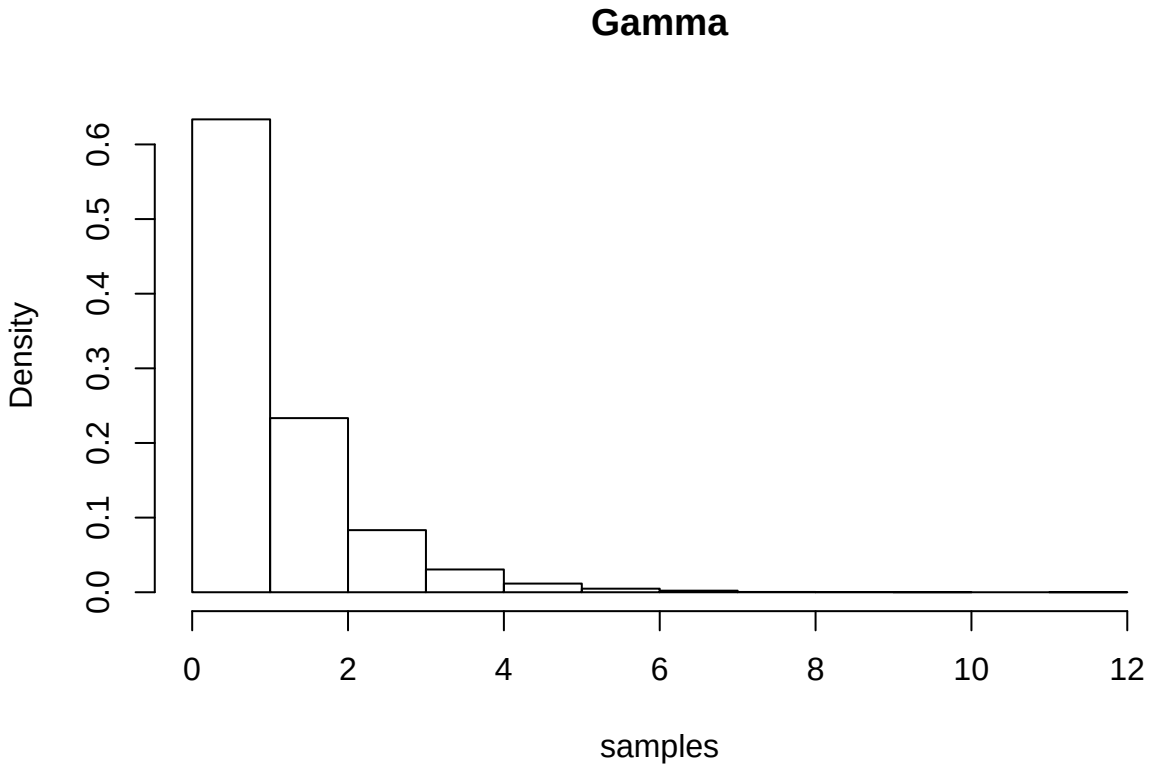
Now try this with the exponential with rate 1:

```
nsim<-10000
samples<-rep(NA,nsim)
for(i in 1:nsim){
  u <- runif(1,min=0,max=1)
  samples[i]<-qexp(u)
}
hist(samples,freq=FALSE,main="Exponential")
```



Or the Gamma with rate and shape 1:

```
nsim<-10000
samples<-rep(NA,nsim)
for(i in 1:nsim){
  u <- runif(1,min=0,max=1)
  samples[i]<-qgamma(u,rate=1,shape=1)
}
hist(samples,freq=FALSE,main="Gamma")
```



2.4.1.3 Example 3

Let $f(x) = \frac{1}{40}(2x+3)$, with $0 < x < 5$. Now, we can't just use the family of q functions in R, because this density is not defined in R.

We have to draw a number from the uniform distribution and then solve for z, which amounts to finding the inverse function:

$$u = \int_0^z \frac{1}{40}(2x+3) \tag{167}$$

```
u<-runif(1000,min=0,max=1)

z<-(1/2) * (-3 + sqrt(160*u +9))
```

This method can't be used if we can't find the inverse, and it can't be used with multivariate distributions.

2.4.2 Gibbs sampling

Gibbs sampling is a very commonly used method in Bayesian statistics. Here is how it works.

Let Θ be a vector of parameter values, let length of Θ be k. Let j index the j-th iteration.

Algorithm:

1. Assign some starting values to Θ:

   $\Theta^{j=0} \leftarrow S$

2. Set $j \leftarrow j+1$

3. 1. Sample $\theta_1^j \mid \theta_2^{j-1} \dots \theta_k^{j-1}$.

   2. Sample $\theta_2^j \mid \theta_1^j \theta_3^{j-1} \dots \theta_k^{j-1}$.

⋮

   k. Sample $\theta_k^j \mid \theta_1^j \dots \theta_{k-1}^j$.

4. Return to step 1.

2.4.2.1 Example: A simple bivariate distribution

Assume that our bivariate (joint) density is:

$$f(x,y) = \frac{1}{28}(2x+3y+2) \tag{168}$$

Using the methods discussed in the Foundations chapter, it is possible to analytically work out the conditional distributions from the joint distribution:

$$f(x \mid y) = \frac{f(x,y)}{f(y)} = \frac{(2x+3y+2)}{6y+8} \tag{169}$$

$$f(y \mid x) = \frac{f(x,y)}{f(x)} = \frac{(2x+3y+2)}{4y+10} \tag{170}$$

The Gibbs sampler algorithm is:

1. Set starting values for the two parameters $x = -5, y = -5$. Set j=0.

2. Sample x^{j+1} from $f(x \mid y)$ using inversion sampling. You need to work out the inverse of $f(x \mid y)$ and $f(y \mid x)$ first. To do this, for $f(x \mid u)$, we have find z_1:

   $$u = \int_0^{z_1} \frac{(2x+3y+2)}{6y+8}\, dx \tag{171}$$

   And for $f(y \mid x)$, we have to find z_2:

   $$u = \int_0^{z_2} \frac{(2x+3y+2)}{4y+10}\, dy \tag{172}$$

   It doesn't matter if you can't solve this integral; the solution is given in the code below.

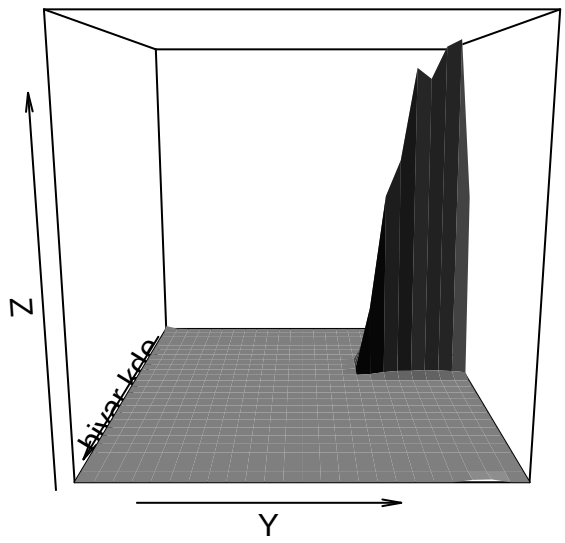


Figure 15: Example of posterior distribution of a bivariate distribution.

```
#R program for Gibbs sampling using inversion method
## program by Scott Lynch, modified by SV:
x<-rep(NA,2000)
y<-rep(NA,2000)
x[1]<- -5
y[1]<- -5

for(i in 2:2000)
{ #sample from x | y
  u<-runif(1,min=0, max=1)
  x[i]<-sqrt(u*(6*y[i-1]+8)+(1.5*y[i-1]+1)*(1.5*y[i-1]+1))-
    (1.5*y[i-1]+1)
  #sample from y | x
u<-runif(1,min=0,max=1)
y[i]<-sqrt((2*u*(4*x[i]+10))/3 +((2*x[i]+2)/3)*((2*x[i]+2)/3))-
    ((2*x[i]+2)/3)
}
```

You can run this code to visualize the simulated posterior distribution. See Figure 15.

```
library(MASS)
bivar.kde<-kde2d(x,y)
persp(bivar.kde,phi=10,theta=90,shade=0,border=NA,
      main="Simulated bivariate density using Gibbs sampling")
```

A central insight here is that knowledge of the conditional distributions is enough to simulate from the joint distribution, provided such a joint distribution exists.

2.5 Hamiltonian Monte Carlo

Instead of Gibbs sampling, Stan uses this more efficient sampling approach. HMC works well for the high-dimensional models we will fit (hierarchical models). Gibbs sampling faces difficulties with some of the complex hierarchical models we will be fitting later. HMC will always succeed for these complex models.

One limitation of HMC (which Gibbs sampling does not have) is that HMC only works with continuous parameters (not discrete parameters).

For our purposes, it is enough to know what sampling using MCMC is, and that HMC gives us posterior samples efficiently. A good reference explaining HMC is Neal and others (2011). However, this paper is technically very demanding. More intuitively accessible introductions are available via Michael Betancourt's home page: https://betanalpha.github.io/. In particular, this video is helpful: https://youtu.be/jUSZboSq1zg.

2.5.1 HMC demonstration

The HMC algorithm takes as input the log density and the gradient of the log density. In Stan, these will be computed internally; the user doesn't need to do any computations.

For example, suppose the log density is $f(\theta) = -\frac{\theta^2}{2}$. Its gradient is $f'(\theta) = -\theta$. Setting this gradient to 0, and solving for θ, we know that the maximum is at 0. We know it's a maximum because the second derivative, $f''(\theta) = -1$, is negative. See Figure 16.

This is the machinery we learnt in the foundations chapter (recall how we found MLEs in particular).

```
theta<-seq(-4,4,by=0.001)
plot(theta,-theta^2/2,type="l",main="Log density")
```

We first write down the Radford Neal algorithm for HMC; details can be ignored in the next piece of code below, which I got from Jarad Niemi's github repository.

```
## Radford Neal algorithm:
HMC_neal <- function(U, grad_U, e, L, current_theta) {
theta = current_theta
omega = rnorm(length(theta),0,1)
current_omega = omega
omega = omega - e * grad_U(theta) / 2
for (i in 1:L) {
theta = theta + e * omega
if (i!=L) omega = omega - e * grad_U(theta)
}
```

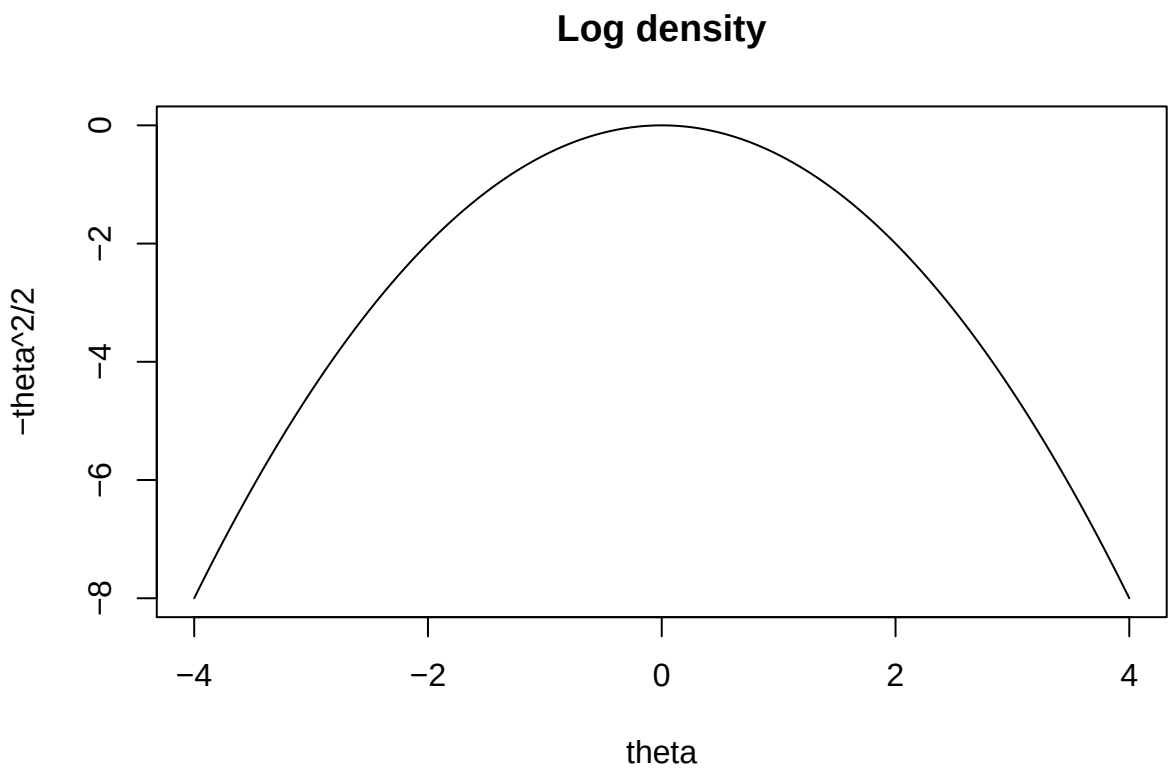


Figure 16: Example log density.

```
omega = omega - e * grad_U(theta) / 2
omega = -omega
current_U = U(current_theta)
current_K = sum(current_omega^2)/2
proposed_U = U(theta)
proposed_K = sum(omega^2)/2
if (runif(1) < exp(current_U-proposed_U+current_K-proposed_K))
{
return(theta)
}
else {
return(current_theta)
}
}

HMC <- function(n_reps, log_density, grad_log_density, tuning, initial) {
theta = rep(0, n_reps)
theta[1] = initial$theta
for (i in 2:n_reps) theta[i] = HMC_neal(U = function(x) -log_density(x),
grad_U = function(x) -grad_log_density(x),
e = tuning$e,
```

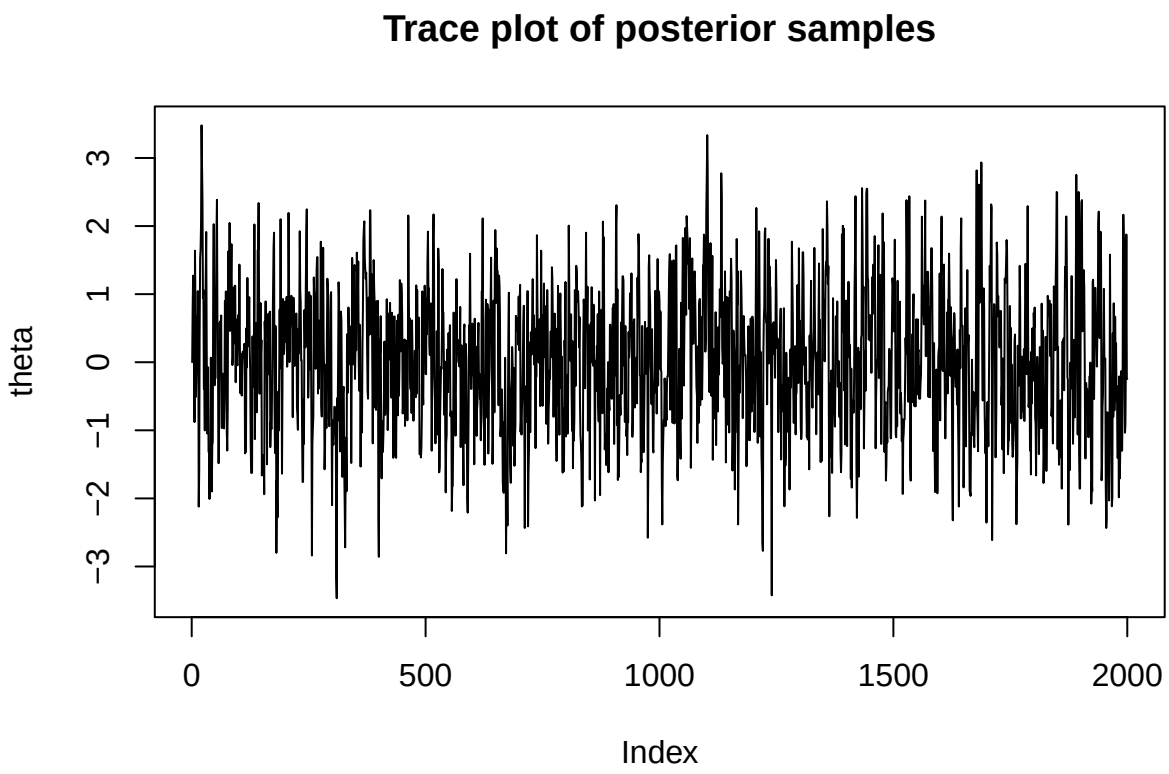


Figure 17: An example of a trace plot.

```
L = tuning$L,
theta[i-1])
theta
}
```

Then, we use the HMC function above to take 2000 samples from the posterior. We drop the first few (typically, the first half) samples, which are called warm-ups. The reason we drop them is that the initial samples may not yet be sampling from the posterior.

```
theta <- HMC(n_reps=2000,
             log_density=function(x) -x^2/2,
             grad_log_density=function(x) -x,
             tuning=list(e=1,L=1),
             initial=list(theta=0))
```

Figure 17 shows a **trace plot**, the trajectory of the samples over 2000 iterations. This is called a **chain**. When the sampler is correctly sampling from the posterior, we see a characteristic "fat hairy caterpillar" shape, and we say that the sampler has **converged**. You will see later what a failed convergence looks like.

```
plot(theta,type="l",main="Trace plot of posterior samples")
```

When we fit Bayesian models, we will always run four parallel chains. This is to make sure that

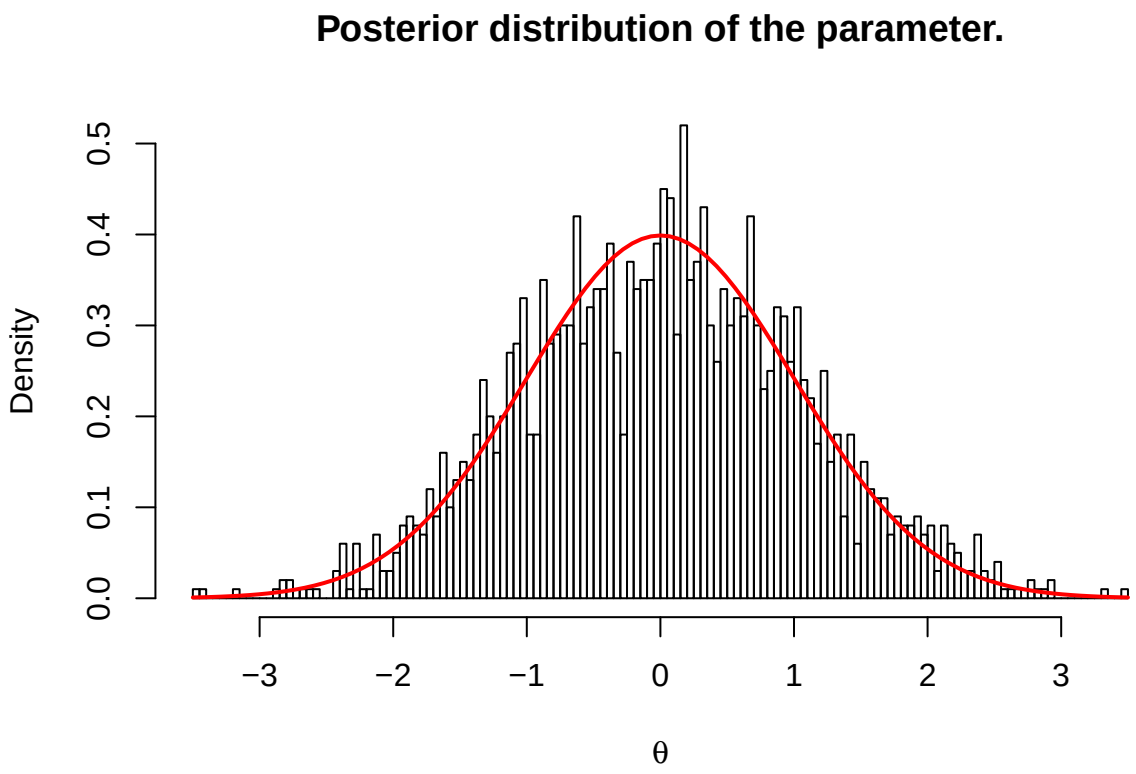


Figure 18: Sampling from the posterior using HMC. The red curve shows the distribution Normal(0,1).

even if we start with four different initial values chosen randomly, the chains all end up sampling from the same distribution. When this happens, we see that the chains overlap visually, and we say that the chains are **mixing**.

Figure 18 shows the posterior distribution of θ. We are not discarding samples here because the sampler converges quickly in this simple example.

```
hist(theta, freq=F, 100,

     main="Posterior distribution of the parameter.",
     xlab=expression(theta))
curve(dnorm, add=TRUE, col='red', lwd=2)
```

In the modeling we do in the following pages, the Stan software will do the sampling for us.

2.6 Further readings

Some good books introducing Bayesian data analysis methods are the following:

- McElreath, R. (2015). Statistical Rethinking. Texts in Statistical Science. This book is currently the best textbook in existence, and assumes no calculus or linear algebra knowledge.
- Kruschke, J. (2014). Doing Bayesian data analysis: A tutorial with R, JAGS, and Stan. Academic Press. This book is specifically designed for a psychology audience. I have only read parts of it and I find it very useful as a reference.
- Lynch, S. M. (2007). Introduction to applied Bayesian statistics and estimation for social scientists. Springer Science & Business Media. This book assumes knowledge of calculus and linear algebra. It gives a classical, statistician's introduction to Bayes. I highly recommend this book to people who know some (undergraduate math level) calculus and linear algebra.

2.7 Exercises

1. **Optional: if you know the basics of integration**. Suppose we are given that the pdf of θ, which ranges from 0 to 1, is proportional to θ^2. This means that there is some constant c (the constant of proportionality) such that $1 = c\int_0^1 \theta^2 d\theta$.
   (a) Find c.
   (b) Find the mean, median (hint: what is the median in terms of quantiles?) and variance of the above pdf.
   (c) Find the 95% credible interval, i.e., the lower and upper values in $P(lower < \theta < upper) = 0.95$.
2. Plot the priors, likelihoods, and posterior distributions in the four Beta-Binomial cases discussed in this chapter.
3. The French mathematician Pierre-Simon Laplace (1749-1827) was the first person to show definitively that the proportion of female births in the French population was less then 0.5, in the late 18th century, using a Bayesian analysis based on a uniform prior distribution). Suppose you were doing a similar analysis but you had more definite prior beliefs about the ratio of male to female births. In particular, if θ represents the proportion of female births in a given population, you are willing to place a Beta(100,100) prior distribution on θ.

   Show that this means you are more than 95% sure that θ is between 0.4 and 0.6, although you are ambivalent as to whether it is greater or less than 0.5.

   Now you observe that out of a random sample of $1,000$ births, 511 are boys. What is your posterior probability that $\theta > 0.5$?"
4. Consider normally distributed data with unknown mean but known variance σ^2. Before getting into the exercise, recall the idea of the *likelihood function*.

Suppose $X_1, \ldots, X_n$ is a random variable that comes from a normally distributed population with mean μ and variance σ^2. **In this exercise, we will talk about the Normal distribution in terms of the mean and variance, not standard deviation**. Suppose that the sample values $x_1, \ldots, x_n$ are independent.

Because these values are independent, the joint probability of getting these values is just the product of the individual probabilities:

$$\begin{aligned} P(X_1 = x_1, X_2 = x_2, \ldots, X_n = x_n) =& P(X_1 = x_1)P(X_2 = x_2)\ldots P(X_n = x_n) \\ =& f(X_1 = x_1, X_2 = x_2, \ldots, X_n = x_n; \theta) \end{aligned} \tag{173}$$

The last line $f(X_1 = x_1, X_2 = x_2, \ldots, X_n = x_n; \theta)$ means: "the joint probability of the values $x_1, \ldots, x_n$ given a specific value for the parameter(s) θ." Here, θ is the vector $< \mu >$. If σ were unknown, θ would be $< \mu, \sigma >$.

For different values of θ, we would get different values for the function $f(\cdot)$. In other words, we can talk about a function $L(\theta)$ given the data, that delivers different values for each value of θ. This is the *likelihood function*.

In other words:

$$L(x \mid \theta) = \prod N(x_i; \mu, \sigma^2) \tag{174}$$

$$= (\tfrac{1}{\sigma\sqrt{2\pi}})^n \exp(-\tfrac{1}{2\sigma^2}\textstyle\sum(x_i - \mu)^2) \tag{175}$$

$$\tag{176}$$

We assume that we already know σ^2. Given the likelihood function, we can ask: What is the value of μ that would maximize the probability of this data?

Taking logs and differentiating with respect to μ, we get:

$$\hat{\mu} = \frac{1}{n}\sum x_i = \bar{x} \tag{177}$$

Suppose that we have independent data as follows:

```
x<-c(15.7,14.7,16.1,16.2,15.1)
```

We typically start by calculating the mean (among other things):

Using this sample mean (and the given variance), we make a best guess as to the pdf that is assumed to have generated **each data point**:

$X \sim Normal(\bar{x}, \sigma^2)$

For n data points, we can characterize the sampling distribution of the sample means as:

$\bar{X} \sim N(\bar{x}, \sigma^2/n)$

More generally, the method of maximum likelihood consists of maximizing

So let us suppose we have independent and identically distributed data $x = \{x_1, \ldots, x_n\}$, where $X_i \sim Normal(\mu, \sigma^2)$. As mentioned above, assume that σ^2 is known as above, but μ is unknown.

It follows that the pdf for random variable representing any one data point is $Normal(\bar{x}, \sigma^2)$.

Now we make the big Bayesian move. Let our prior be that the sampling distribution of μ is $N(m, v)$. Note that this is the prior for the sampling distribution of the mean μ. It represents what we believe to be true about μ, including our degree of uncertainty about our belief.

Then, given Bayes' theorem

Posterior $\propto$ Prior $\times$ Likelihood

or

$$\text{Posterior} \propto \underset{\substack{\uparrow \\ prior}}{N(m, v)} \times \underset{\substack{\uparrow \\ likelihood}}{N(\bar{x}, \sigma^2/n)}$$

it is straightforward to derive analytically (proof omitted, but see @Lynch2007) that the posterior will be $Normal(m*, v*)$, where

$$v* = \frac{1}{\frac{1}{v} + \frac{n}{\sigma^2}} \tag{178}$$

$$m* = v* \left(\frac{m}{v} + \frac{n\bar{x}}{\sigma^2} \right) \tag{179}$$

Importantly, we can rewrite m* as a weighted mean of the prior and the sample mean:

$$m* = \frac{w_1}{w_1 + w_2} m + \frac{w_2}{w_1 + w_2} \bar{x} \tag{180}$$

where $w_1 = v^{-1}$ and $w_2 = (\frac{\sigma^2}{n})^{-1}$

Because of results like the one above, it is sometimes easier to talk about variance in terms of precision=1/variance.

Example of how we can use the above analytical result

Let the data be: 15.7,14.7,16.1,16.2,15.1. Variance (σ^2) is known to be 0.6. Let the prior be N(m=14,v=1). We will work out the posterior distribution using the formula.

```
derive.post<-function(n,x.bar,sigma2,m,v){
v.star<- 1/( (1/v) + n/sigma2 )
m.star<-v.star*(m/v + (n*x.bar/sigma2))
return(list(m.star,v.star))
}
```

```
data<-list(y=c(15.7,14.7,16.1,16.2,15.1))

post<-derive.post(n=length(data$y),
                  x.bar=mean(data$y),
                  sigma2=0.6,m=14,v=1)
```

You can now play with the weighting of the prior and data.

First, make the prior variance very low; this yields a shift of the posterior towards the prior, with low variance:

```
post<-derive.post(n=length(data$y),x.bar=mean(data$y),
                  sigma2=.6,m=14,v=0.0001)
```

Next, make the prior variance very high; this shifts the posterior towards the sample mean and variance:

```
post<-derive.post(n=length(data$y),
                  x.bar=mean(data$y),
                  sigma2=.6,m=14,v=100)
mean(data$y)
var(data$y)
```

This basically sums up a situation we will encounter in this course: we will use priors that express low certainty ("non-informative" priors), letting “the data speak for themselves.” But in cases where we do have prior information, we will use it! (This is impossible to do in frequentist settings) You will see how prior beliefs can be incorporated into your analysis.

Questions:

What role does sample size n play in the computation of the posterior? When sample size is increased in the above example, will the posterior lean towards the prior or the likelihood?

Visualize the prior, likelihood and posterior for v=0.001, v=100. Obtain the posterior distribution’s parameters using the formula.

3 Linear modeling

In this chapter, we will fit linear models of the following type. Suppose y is a vector of continuous responses; assume for now that it is coming from a normal distribution:

$y \sim Normal(\mu, \sigma)$

This is the simple linear model:

$y = \mu + \varepsilon$ where $\varepsilon \sim Normal(0, \sigma)$

There are two parameters, μ, σ, so we need priors on these. We expand on this simple model next.

Recall from the foundations chapter that the way we will conduct data analysis is as follows.

- Given data, specify a *likelihood function*.
- Specify *prior distributions* for model parameters.
- Evaluate whether model makes sense, using fake-data simulation, *prior predictive* and *posterior predictive* checks, and (if you want to claim a discovery) calibrating true and false discovery rates.
- Using software, derive *marginal posterior distributions* for parameters given likelihood function and prior density. I.e., simulate parameters to get *samples from posterior distributions* of parameters using some *Markov Chain Monte Carlo (MCMC) sampling algorithm*.
- Check that the model converged using *model convergence* diagnostics,
- Summarize *posterior distributions* of parameter samples and make your scientific decision.

We will now work through some specific examples to illustrate how the data analysis process works.

3.1 Example 1: A single subject pressing a button repeatedly

As a first example, we will fit a simple linear model to some reaction time data.

The file `button_press.dat` contains data of a subject pressing the space bar without reading in a self-paced reading experiment.

3.1.1 Preprocessing of the data

```
noreading_data <- read.table(header = F,"data/button_press.dat",
                             encoding="latin1")
noreading_data <- noreading_data[c("V2","V3","V5","V6","V8")]
colnames(noreading_data) <- c("type","item","wordn","word","y")
tail(noreading_data)
```

```
##       type item wordn           word   y
## 356 filler    3     0     Vielleicht 214
## 357 filler    3     1          haben 182
```

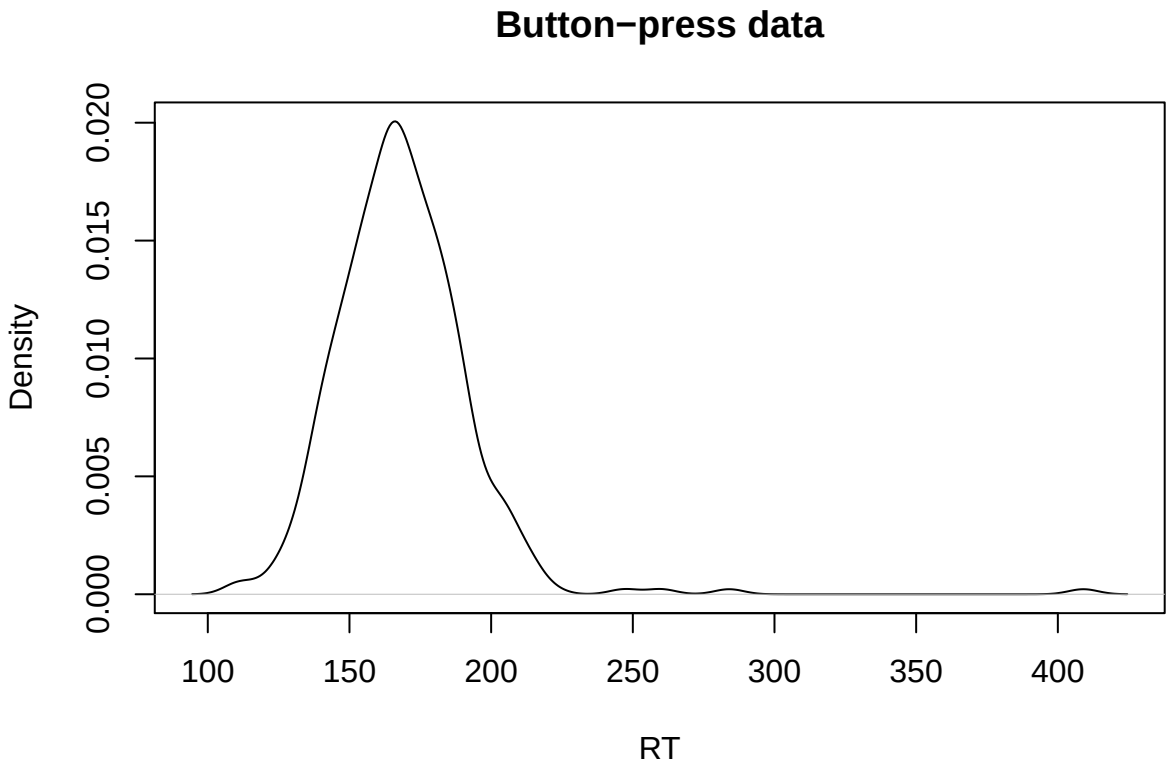


Figure 19: Visualizing the data.

```
## 358 filler    3     2 die_Zahnärztin 179
## 359 filler    3     3       aus_Bonn 177
## 360 filler    3     4  die_Patienten 183
## 361 filler    3     5      verklagt. 162
```

```
summary(noreading_data$y)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##     110     156     166     169     181     409
```

```
class(noreading_data)
```

```
## [1] "data.frame"
```

3.1.2 Visualizing the data

It is a good idea to look at the distribution of the data before doing anything else. See Figure 19.

```
plot(density(noreading_data$y),
     main="Button-press data",xlab="RT")
```

The data looks a bit skewed, but we ignore this for the moment.

3.1.3 Define the likelihood function

Let's model the data with the following assumptions:

- There is a true underlying time, μ, that the participant needs to press the space-bar.
- There is some noise in this process.
- The noise is normally distributed (this assumption is questionable given the skew but; we fix this assumption later).

This means that the likelihood for each observation i will be:

$$y_i \sim Normal(\mu, \sigma) \tag{181}$$

where $i = 1 \ldots N$.

This is just the simple linear model:

$$y = \mu + \varepsilon \text{ where } \varepsilon \sim Normal(0, \sigma) \tag{182}$$

3.1.4 Define the priors for the parameters

We are going to use the following priors for the two parameters in this model:

$$\begin{aligned} \mu &\sim Normal(0, 2000) \\ \sigma &\sim Normal(0, 500) \text{ truncated so that } \sigma > 0 \end{aligned} \tag{183}$$

In order to decide on a prior for the parameters, always visualize them first. See Figure 20.

```
op<-par(mfrow=c(1,2),pty="s")
x<-seq(-4000,4000,by=1)
plot(x,dnorm(x,mean=0,sd=2000),type="l",
     main=expression(paste("Prior for ",mu)),xlab=expression(mu))
x<-seq(0,4000,by=1)
plot(x,dnorm(x,mean=0,sd=500),type="l",
     main=expression(paste("Prior for ",sigma)),xlab=expression(sigma))
```

The prior for μ expresses the belief that the underlying mean button-pressing time could be both positive and negative, and given that the scale of the prior (in this case the standard deviation of the normal distribution) is 2000, we are $\approx 68\%$ certain that the true value would be between 2000 ms and -2000 ms and $\approx 95\%$ certain that it would be between -4000 ms and 4000 ms (two standard deviations away from zero). We know this because:

```
pnorm(2000,mean=0,sd=2000)-pnorm(-2000,mean=0,sd=2000)
```

```
## [1] 0.683
```

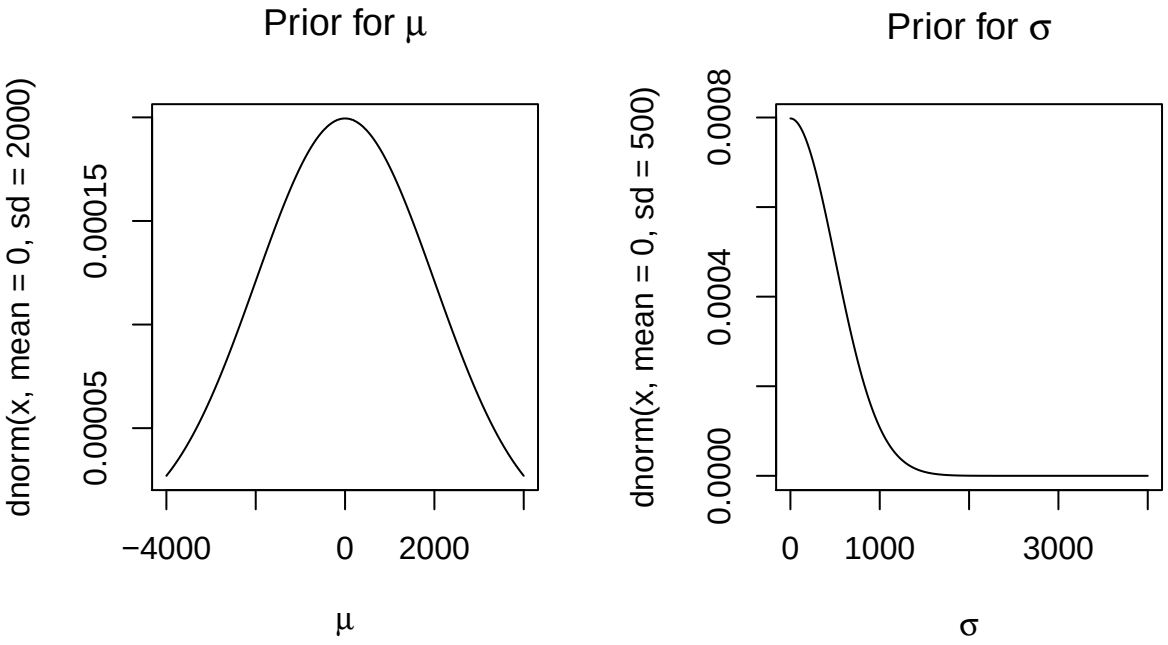


Figure 20: Visualizing the priors for example 1.

```
pnorm(4000,mean=0,sd=2000)-pnorm(-4000,mean=0,sd=2000)
```

```
## [1] 0.954
```

But we obviously know that button-pressing time can't be negative! So we have more prior information than what we are using for informing the model. We'll discuss this below.

Regarding the prior for σ: The values must be positive, and we are $\approx 68\%$ certain that the true value would be between 0 ms and 500 ms and $\approx 95\%$ certain that it would be between 0 ms and 1000 ms. **How would you check this using pnorm?**

3.1.5 Prior predictive checks

With these priors, we are going to generate something called the **prior predictive distribution**. This helps us check whether the priors make sense.

Formally, we want to know the density $f(\cdot)$ of data points $y_1, \ldots, n$, given a vector of priors Θ. In our example, $\Theta = \langle \mu, \sigma \rangle$. The prior predictive density is:

$$f(y_1, \ldots, y_n) = \int f(y_1) \cdot f(y_2) \cdots f(y_n) f(\Theta)\, d\Theta \tag{184}$$

In essence, we integrate out the parameters. Here is one way to do it in R:

- Take one sample from each of the priors
- Generate data using those samples

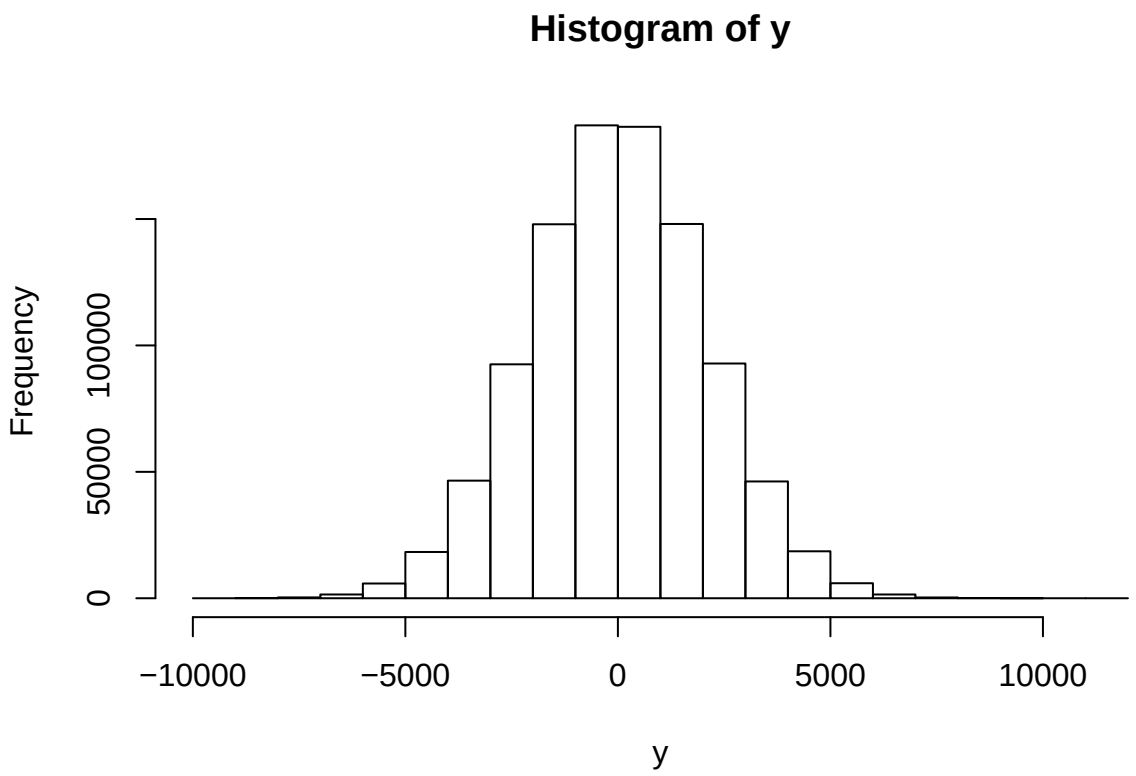


Figure 21: First attempt at prior predictive distribution of the data, model m1.

- Repeat until you have a substantial amount of data
- Plot the prior predictive density

```
nsim<-1000000
y<-rep(NA,nsim)
mu<-rnorm(nsim,mean=0,sd=2000)
sigma<-abs(rnorm(nsim,mean=0,sd=500))

for(i in 1:nsim){
y[i]<-rnorm(1,mean=mu[i],sd=sigma[i])
}

hist(y)
```

This prior predictive distribution in Figure 21 shows that the prior for μ is not realistic: how can button press time have negative values?

We can try to redefine the prior for μ to have only positive values, and then check again (Figure 22). We still get some negative values, but that is because we are assuming that

$y \sim Normal(\mu, \sigma)$

which will have negative values for small μ and large σ.

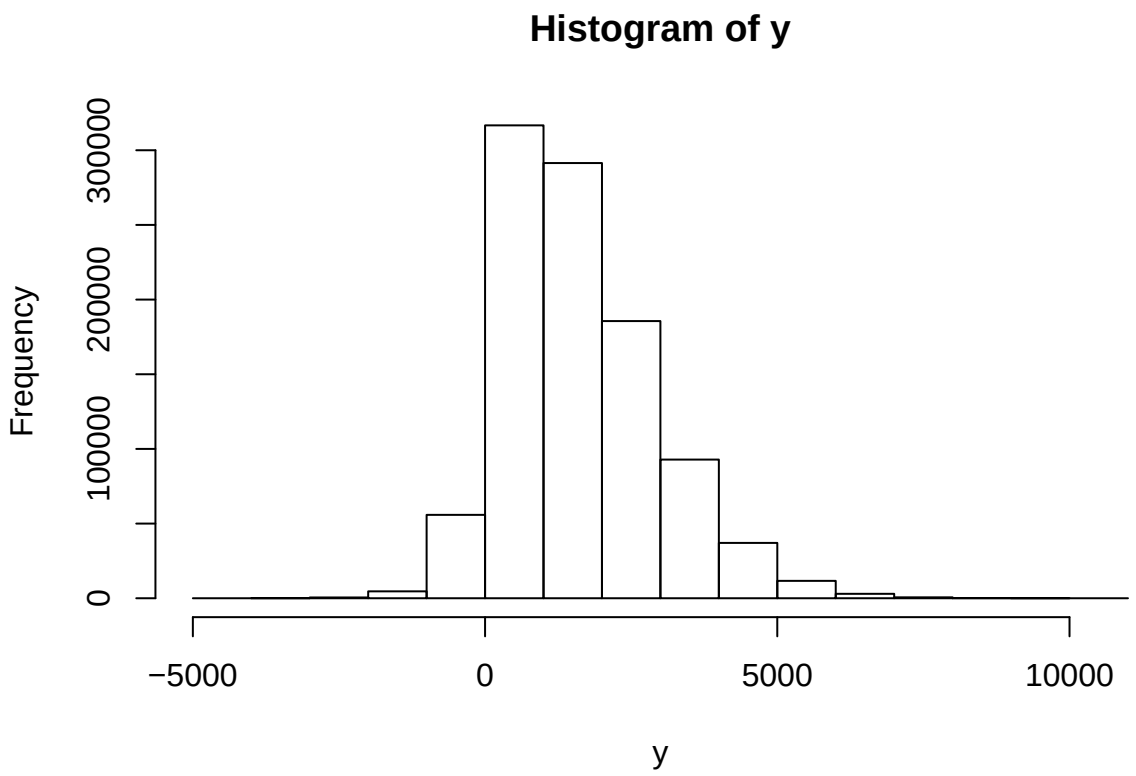


Figure 22: Second attempt at prior predictive distribution of the data, model m1.

```
nsim<-1000000
y<-rep(NA,nsim)
mu<-abs(rnorm(nsim,mean=0,sd=2000))
sigma<-abs(rnorm(nsim,mean=0,sd=500))

for(i in 1:nsim){
y[i]<-rnorm(1,mean=mu[i],sd=sigma[i])
}

hist(y)
```

This prior predictive distribution in Figure 22 looks reasonable for now.

Incidentally, we can generate a prior predictive distribution using Stan as follows.

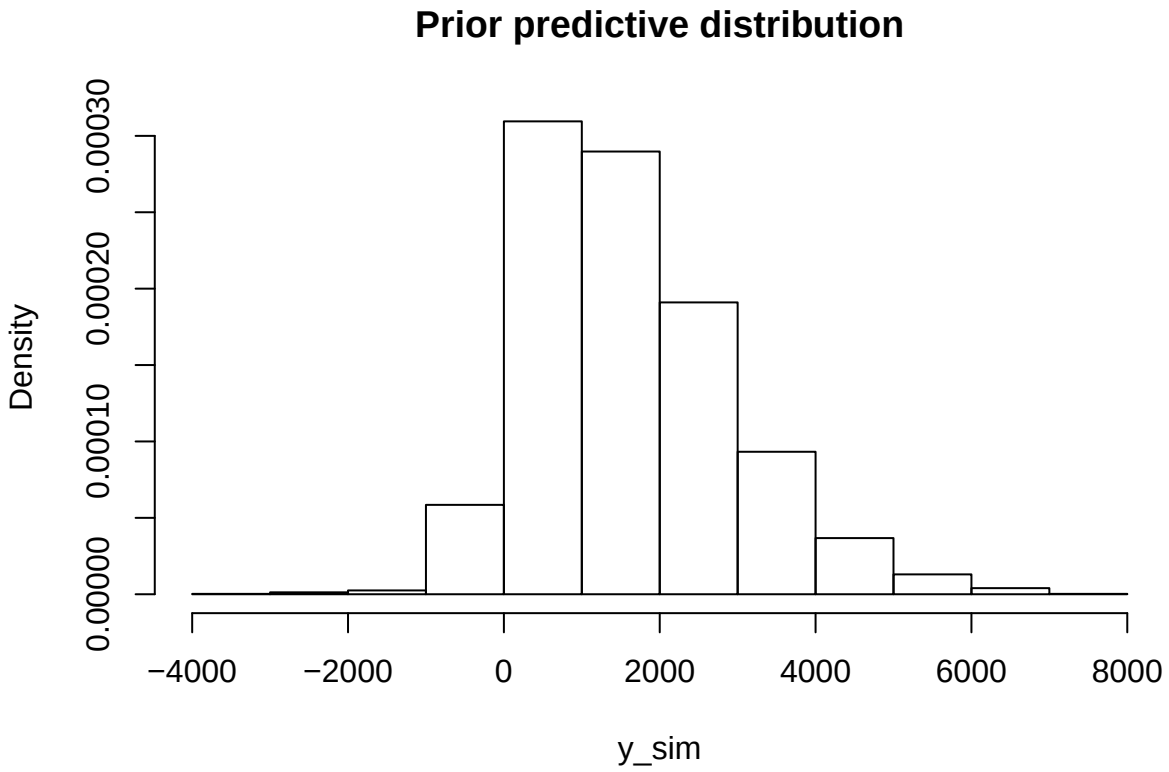
First, we define a Stan model that defines the priors and defines how the data are to be generated. The details of the code below will be explained in class. Documentation on Stan is available at mc-stan.org.

```
priorpred<-"data {
  int N;
}
parameters {
```

```
real<lower=0> mu;
real<lower=0> sigma;
}
model {
  // priors
    mu ~ normal(0,2000);
    sigma ~ normal(0,500);
}
generated quantities {
  vector[N] y_sim;
  // prior predictive
  for(i in 1:N) {
    y_sim[i] = normal_rng(mu,sigma);
  }
}
"
```

Then we generate the data:

```
## load rstan
library(rstan)
options(mc.cores = parallel::detectCores())

## generate 100 data sets
dat<-list(N=100)

## fit model:
m1priorpred<-stan(model_code=priorpred,
                  data=dat,
                  chains = 4,
                 iter = 2000)

## extract and plot one of the data-sets:
y_sim<-extract(m1priorpred,pars="y_sim")
hist(y_sim$y_sim[,1],
     main="Prior predictive distribution",
     xlab="y_sim",freq=FALSE)
```




```
##compare with real data:
#y_fake<-rnorm(100,mean=1543,sd=1291)
#hist(y_fake,col="red",add=TRUE,freq=FALSE)
## compare with mean:
#mn<-rep(NA,100)
#for(i in 1:100){
#mn[i]<-mean(y_sim$y_sim[,i])
#}
#hist(mn)
#abline(v=1550)
```

Having satisfied outselves that the priors mostly make sense, we now fit the model to fake data. The goal here is to ensure that the model recovers the true underlying parameters.

3.1.6 Fake-data simulation and modeling

Next, we write the Stan model, adding a likelihood in the model block:

```
m1<-"data {
  int N;
  real y[N]; // data
}
parameters {
real<lower=0> mu;
```

```
real<lower=0> sigma;
}
model {
// priors
mu ~ normal(0,2000);
sigma ~ normal(0,500);
// likelihood
y ~ normal(mu,sigma);
}
generated quantities {
  vector[N] y_sim;
 // posterior predictive
  for(i in 1:N) {
    y_sim[i] = normal_rng(mu,sigma);
  }
}
"
```

Then generate fake data with known parameter values (we decide what these are):

```
set.seed(123)
N <- 500
true_mu <- 400
true_sigma <- 125
y <- rnorm(N, true_mu, true_sigma)

y <- round(y)
fake_data <- data.frame(y=y)
dat<-list(y=y,N=N)
```

Finally, we fit the model:

```
## fit model:
m1rstan<-stan(model_code=m1,
                  data=dat,
                  chains = 4,
                iter = 2000)

## extract posteriors:
posteriors<-extract(m1rstan,pars=c("mu","sigma"))
```

Figure 23 shows that the true parameters that we defined when generating the fake data fall within the posterior distributions. This shows that the model can in principle recover the parameters. (One should do several fake data simulations to check that the model consistently recovers the true parameters.)

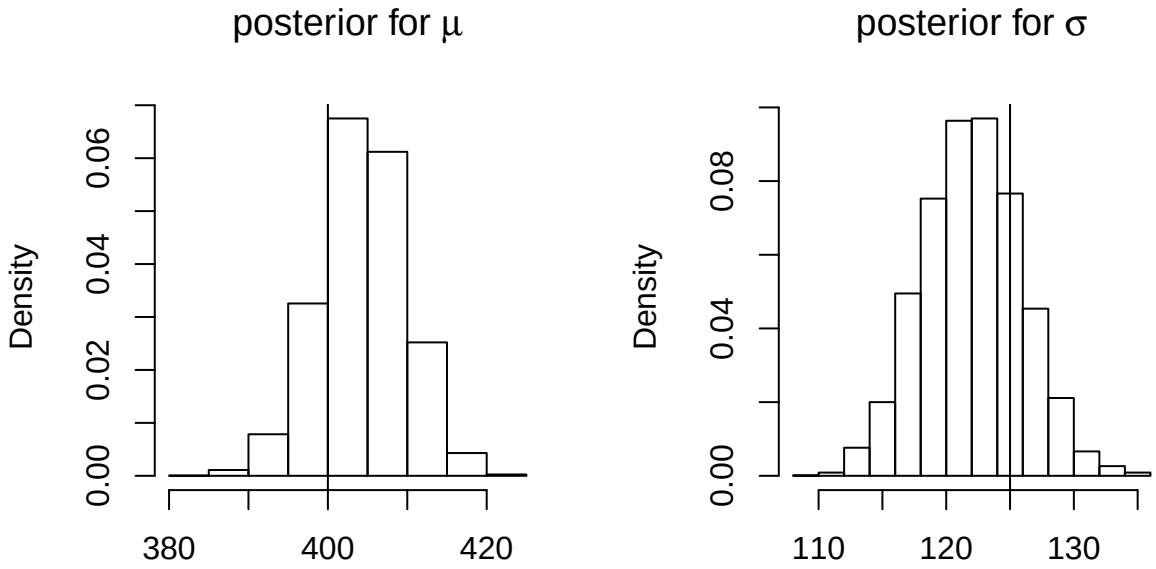


Figure 23: Posteriors from fake data, model m1. Vertical lines show the true values of the parameters.

```
op<-par(mfrow=c(1,2),pty="s")
hist(posteriors$mu,
     main=expression(paste("posterior for ",mu)),freq=FALSE,xlab="")
abline(v=400)
hist(posteriors$sigma,
     main=expression(paste("posterior for ",sigma)),freq=FALSE,xlab="")
abline(v=125)
```

3.1.7 Posterior predictive checks

Once we have the posterior distribution $f(\Theta \mid y)$, we can derive the predictions based on this posterior distribution:

$$p(y_{pred} \mid y) = \int p(y_{pred}, \Theta \mid y)\, d\Theta = \int p(y_{pred} \mid \Theta, y) p(\Theta \mid y)\, d\Theta \tag{185}$$

Assuming that past and future observations are conditionally independent given Θ, i.e., $p(y_{pred} \mid \Theta, y) = p(y_{pred} \mid \Theta)$, we can write:

$$p(y_{pred} \mid y) = \int p(y_{pred} \mid \Theta) p(\Theta \mid y)\, d\Theta \tag{186}$$

Note that we are conditioning y_{pred} only on y, we do not condition on what we don't know (Θ); **we integrate out the unknown parameters**.

This posterior predictive distribution is different from the frequentist approach, which gives only a predictive distribution of y_{pred} given our estimate of θ (a point value).

In the Stan code above, we have already generated the posterior predictive distribution, in the generated quantities block:

```
generated quantities {
  vector[N] y_sim;
 // posterior predictive
  for(i in 1:N) {
    y_sim[i] = normal_rng(mu,sigma);
  }
}
```

3.1.8 Implementing model in brms

An alternative to using rstan as we did above is the package brms. The advantage with using brms is that many of the details of model-specification are hidden from the user; the price paid is loss of transparency, and reduced flexibility in modeling. brms is a good software for fitting canned models, but for customized models you will always need Stan, so it is good to know both syntaxes. I personally do all my research using Stan almost exclusively.

First, load the brms package; this packge runs Stan (Stan Development Team 2017) in the background. For an introduction to this package, see Bürkner (2017), and https://github.com/paul-buerkner/brms.

```
library(brms)
```

This model is expressed in brms in the following way. First, define the priors:

```
priors <- c(set_prior("normal(0, 2000)",
                      class = "Intercept"),
            set_prior("normal(0, 500)",
                      class = "sigma"))
```

Then, define the generative process assumed:

```
m1brms<-brm(y~1,noreading_data,prior = priors,
       iter = 2000,
       warmup = 1000,
       chains = 4,
       family = gaussian(),
       control = list(adapt_delta = 0.99))
```

1. The term `family = gaussian()` makes explicit the underlying likelihood function that is implicit in `lme4`. Other linking functions are possible, exactly as in the `glmer` function in `lme4`.

2. The term `prior` takes as argument the list of priors we defined earlier. Although this specification of priors is optional, the researcher should always explicitly specify each prior. Otherwise, `brms` will define a prior by default, which may or may not be appropriate.
3. The term `iter` refers to the number of iterations that the sampler makes to sample from the posterior distribution of each parameter (by default 2000). See the discussion on HMC earlier.
4. The term `warmup` refers to the number of iterations from the start of sampling that are eventually discarded (by default half of `iter`).
5. The term `chains` refers to the number of independent runs for sampling (by default four).
6. The term `control` refers to some optional control parameters for the sampler, such as `adapt_delta`, `max_treedepth`, and so forth, to be discussed later.

3.1.9 Summarizing the posteriors, and convergence diagnostics

The summary displayed below show summary statistics over the marginal posterior distributions of the parameters in the model. The summary shows posterior means, standard deviations (`sd`), quantiles, Monte Carlo standard errors (`se_mean`), split Rhats, and effective sample sizes (`n_eff`).

The summaries are computed after removing the warmup and merging together all chains. Notice that the `se_mean` is unrelated to the `se` of an estimate in the frequentist model, and we will ignore it in this course.

```
summary(m1brms)
```

```
##  Family: gaussian
##   Links: mu = identity; sigma = identity
## Formula: y ~ 1
##    Data: noreading_data (Number of observations: 361)
## 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 Eff.Sample Rhat
## Intercept   168.68      1.27   166.21   171.22       1825 1.00
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat
## sigma    24.97      0.91    23.27    26.80       2061 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).
```

A graphical summary of posterior distributions of model m1 is shown in Figure 24:

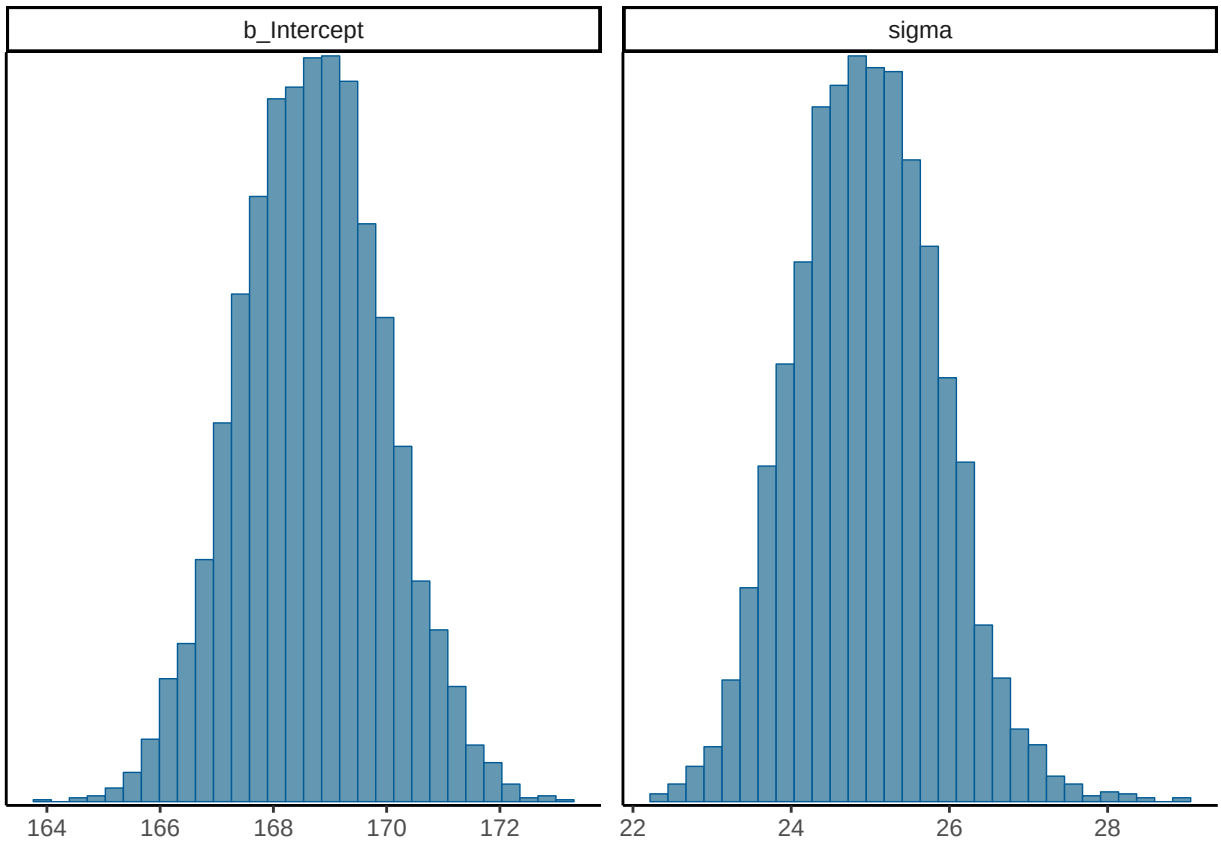


Figure 24: Posterior distributions of the parameters in model m1.

```
stanplot(m1brms,type="hist")
```

The trace plots in Figure 25 show how well the four chains are mixing:

```
stanplot(m1brms,type="trace")
```

An alternative way to plot is shown in Figure 26.

```
plot(m1brms)
```

3.1.10 MCMC diagnostics: Convergence problems and Stan warnings

Because we are using MCMC methods to sample from the posterior distributions, we need to make sure that the model has converged.

The most important checks or MCMC diagnostics are the following:

- The chains should look like a straight "fat hairy caterpillar": the chains should bounce around the same values and with the same variance.
- The R-hat statistic, $\hat{R}$s, of the parameters should be close to one (as a rule of thumb less than 1.1). This indicates that the chains have mixed and they are traversing the same distribution.

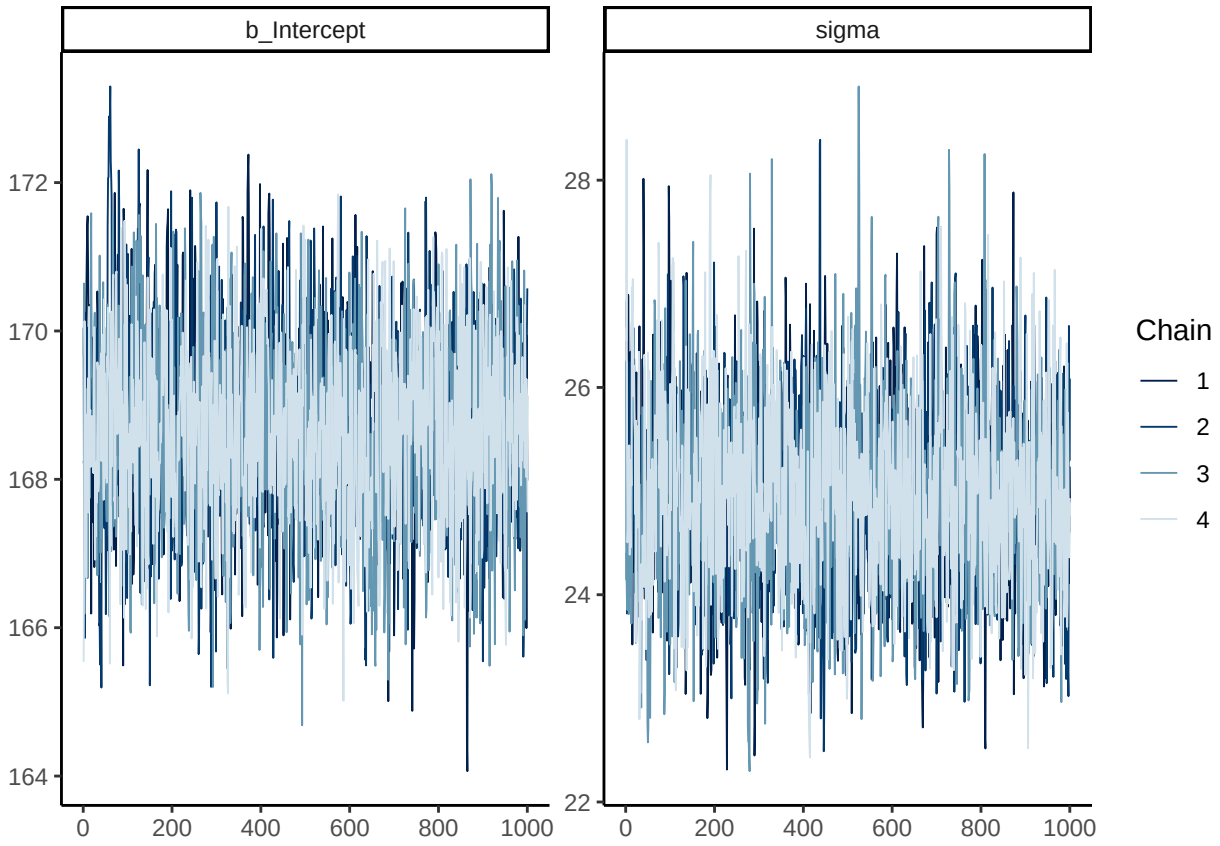


Figure 25: Trace plots in model m1.

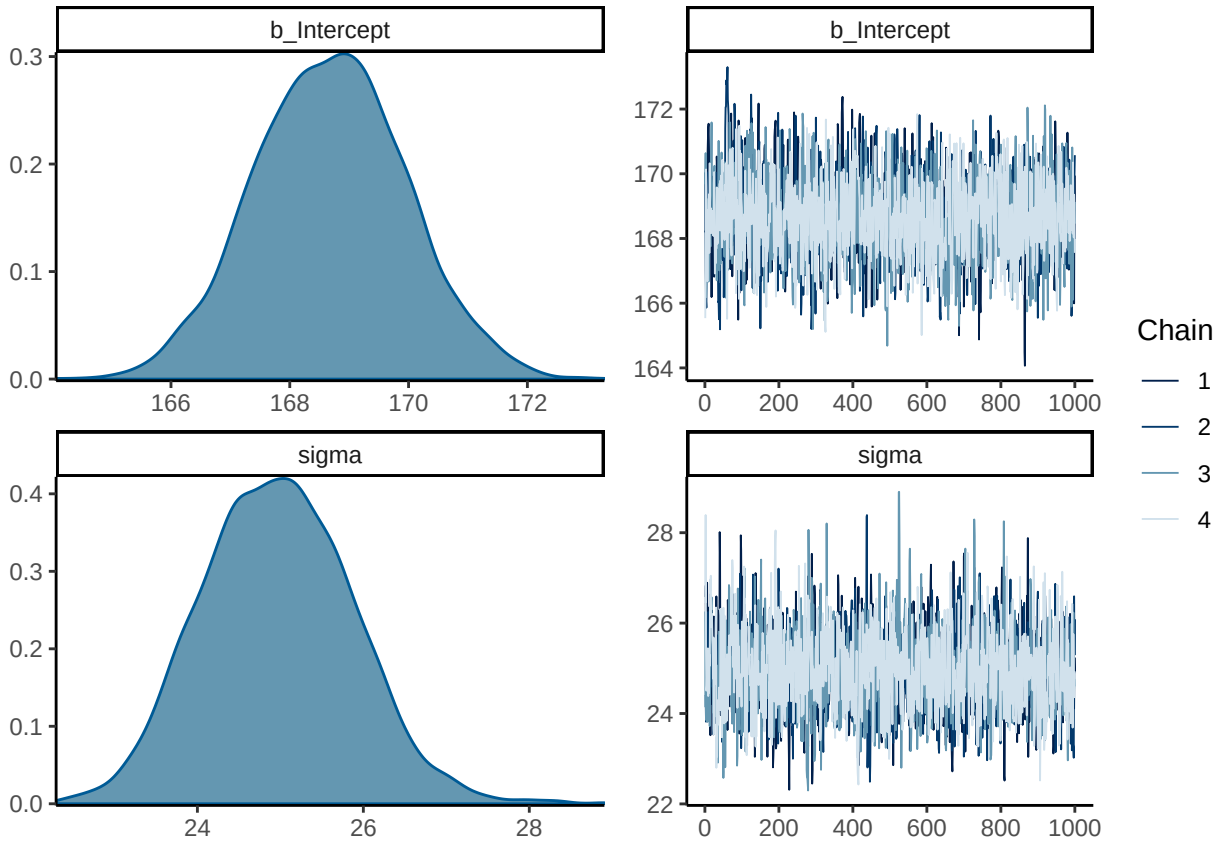


Figure 26: Posterior distributions and trace plots in model m1.

$\hat{R}$s are printed in the summary in the column `Rhat` (see section 11.4 of Gelman et al. 2014). These are the ratio of between to within chain variance.

- The effective sample size, n_{eff} should be large enough. The effective sample size is an estimate of the number of independent draws from the posterior distribution. Since the samples are not independent, n_{eff} will generally be smaller than the total number of samples, N. How large n_{eff} should be depends on the summary statistics that we want to use. But as a rule of thumb, $n_{eff}/N > 0.1$.
- Check that the software does not warnings such as divergent transitions, Bayesian fraction of missing information (BFMI) that was too low, etc. These warning may indicate that the sampler is not adequately exploring the parameter space. If you see these warnings, consult http://mc-stan.org/misc/warnings.html

For useful graphical checks see https://cran.r-project.org/web/packages/bayesplot/vignettes/MCMC-diagnostics.html

These issues **should not be ignored**! See the Appendix 3.4 for some troubleshooting ideas to solve them.

3.1.11 Summarizing the posterior distribution: posterior probabilities and the credible interval

We are assuming that there's a true underlying time it takes to press the space bar, μ, and there is normally distributed noise with distribution Normal(0,σ) that generates the different RTs. All this is encoded in our likelihood by assuming that RTs are distributed with an unknown true mean μ (and an unknown standard deviation σ).

The objective of the Bayesian model is to learn about the plausible values of μ, or in other words, to get a distribution that encodes what we know about the true mean of the distribution of RTs, and about the true standard deviation, σ, of the distribution of RTs.

Our model allows us to answer questions such as:

What is the probability that the underlying value of the mindless press of the space bar would be over, say 170 ms?

As an example, consider this model that we ran above:

```
priors <- c(set_prior("normal(0, 2000)",
                      class = "Intercept"),
            set_prior("normal(0, 500)",
                      class = "sigma"))

m1brms<-brm(y~1,noreading_data,prior = priors,
       iter = 2000,
       warmup = 1000,
       chains = 4,
```

```
       family = gaussian(),
       control = list(adapt_delta = 0.99))
```

```
## Compiling the C++ model
```

```
## recompiling to avoid crashing R session
```

```
## Start sampling
```

We now compute the posterior probability $Prob(\mu > 170)$:

```
mu_post<-posterior_samples(m1brms,pars=c("b_Intercept"))$b_Intercept
mean(mu_post>170)
```

```
## [1] 0.148
```

The credible interval

The 95% credible interval can be extracted for μ as follows:

```
posterior_interval(m1brms,pars=c("b_Intercept"))
```

```
##             2.5% 97.5%
## b_Intercept  166   171
```

This type of interval is also known as a *credible interval*. A credible interval demarcates the range within which we can be certain with a certain probability that the "true value" of a parameter lies given the data and the model. This is very different from the frequentist confidence interval! See for discussion, Hoekstra et al. (2014) and Morey et al. (2016).

The percentile interval is a type of credible interval (the most common one), where we assign equal probability mass to each tail. We generally report 95% credible intervals. But we can extract any interval, a 73% interval, for example, leaves 13.5% of the probability mass on each tail, and we can calculate it like this:

```
quantile(mu_post,prob=c(0.135,0.865))
```

```
## 13.5% 86.5%
##   167   170
```

3.1.11.1 Influence of priors and sensitivity analysis

Everything was normally distributed in our example (or truncated normal), but the fact that we assumed that RTs were normally distributed is completely unrelated to our (truncated) normally distributed priors. Let's try a uniform prior on μ with a low boundary of 0 and a high boundary of 5000. Here, we assume that every value between 0 and 5000 is equally likely. In general, this is a bad idea for two reasons: (i) it is computationally expensive (the sampler has a larger parameter space to search), and (ii) it is providing information that we know is not sensible (every value between 0 and 5000 cannot be equally likely). But in our very simple example these priors will give use the same posterior as with the normal priors.

$$\begin{aligned} \mu &\sim Uniform(0,5000) \\ \sigma &\sim Uniform(0,5000) \end{aligned} \tag{187}$$

```
priors <- c(set_prior("uniform(0, 5000)",
                      class = "Intercept"),
            set_prior("normal(0, 500)",
                      class = "sigma"))
```

```
m2<-brm(y~1,noreading_data,prior = priors,
       iter = 2000, chains = 4,family = gaussian(),
       control = list(adapt_delta = 0.99))
```

```
## Compiling the C++ model
```

```
## Start sampling
```

```
summary(m2)
```

```
##  Family: gaussian
##   Links: mu = identity; sigma = identity
## Formula: y ~ 1
##    Data: noreading_data (Number of observations: 361)
## 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 Eff.Sample Rhat
## Intercept   168.64      1.30   166.04   171.21       2184 1.00
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat
## sigma    25.02      0.93    23.30    26.95       1845 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).
```

In general, we don't want our priors to have too much influence on our posterior. This is unless we have *very* good reasons for having informative priors, such as a very small sample and a lot of prior information; an example would be if we have data from an impaired population, which makes it hard to increase our sample size.

We usually center the priors on 0 and we let the likelihood dominate in determining the posterior. This type of prior is called *weakly informative prior*. Notice that a uniform prior is not a weakly informative prior, it assumes that every value is equally likely, zero is as likely as 5000.

You should always do a *sensitivity analysis* to check how influential the prior is: try different priors

and verify that the posterior doesn't change drastically (for a published example, see Vasishth et al. 2013).

3.2 Example 2: Investigating adaptation effects

More realistically, we might have run the small experiment to find out whether the participant tended to speedup (practice effect) or slowdown (fatigue effect) while pressing the space bar.

3.2.1 Preprocessing the data

We need to have data about the number of times the space bar was pressed for each observation, and add it to our list. It's a good idea to center the number of presses (a covariate) to have a clearer interpretation of the intercept. In general, centering predictors is always a good idea, for interpretability and for computational reasons. See Schad et al. (2018) for details on this point.

```
# Create the new column in the data frame
noreading_data$presses <- 1:nrow(noreading_data)
# Center the column
noreading_data$c_presses <- noreading_data$presses - mean(noreading_data$presses)
```

3.2.2 Probability model

Our model changes, because we have a new parameter.

$$y_i \sim Normal(\alpha + presses_i \cdot \beta, \sigma) \tag{188}$$

where $i = 1 \ldots N$

And we are going to use the following priors:

$$\begin{aligned} \alpha &\sim Normal(0, 2000) \\ \beta &\sim Normal(0, 500) \\ \sigma &\sim Normal(0, 500) \text{ truncated so that } \sigma > 0 \end{aligned} \tag{189}$$

We are basically fitting a linear model, α represents the intercept (namely, the grand mean of the RTs), and β represents the slope. What information are the priors encoding? Do the priors make sense?

We'll write this in brms as follows.

```
priors <- c(set_prior("normal(0, 2000)",
                      class = "Intercept"),
            set_prior("normal(0, 500)",
```

```
                    class = "b",
                    coef="presses"),
          set_prior("normal(0, 500)",
                    class = "sigma"))
```

```
m2<-brm(y~1+presses,noreading_data,prior = priors,
       iter = 2000, chains = 4,family = gaussian(),
       control = list(adapt_delta = 0.99))
```

```
## Compiling the C++ model
```

```
## Start sampling
```

```
summary(m2)
```

```
##  Family: gaussian
##   Links: mu = identity; sigma = identity
## Formula: y ~ 1 + presses
##    Data: noreading_data (Number of observations: 361)
## 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 Eff.Sample Rhat
## Intercept   152.55      2.45   147.80   157.39       3203 1.00
## presses       0.09      0.01     0.07     0.11       3399 1.00
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat
## sigma    23.25      0.89    21.58    25.04       3003 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).
```

3.2.3 Summarizing the posterior and inference

How can we answer our research question? What is the effect of pressing the bar on the participant's reaction time?

We'll need to examine what happens with β. The summary gives us the relevant information:

```
m2_post_samp_b <- posterior_samples(m2, "^b")
beta_samples <- m2_post_samp_b$b_presses
beta_mean<-mean(beta_samples)
quantiles_beta <- quantile(beta_samples,prob=c(0.025,0.975))
```

```
beta_low<-quantiles_beta[1]
beta_high<-quantiles_beta[2]
```

We learn that the most likely values of β will be around the mean of the posterior 0.089, and we can be 95% certain that the true value of β *given the model and the data* lies between 0.066 and 0.111.

We see that as the number of times the space bar is pressed increases, the participant becomes slower. If we want to determine how likely it is that the participant was slower rather than faster, we can examine the proportion of samples above zero:

```
mean(beta_samples > 0)
```

```
## [1] 1
```

We would report this in a paper as $\hat{\beta} = 0.089$, 95% CrI = $[0.066, 0.111]$, $P(\beta > 0) \approx 1$. Plotting the posterior as a histogram is always a good idea.

Can we really conclude that there is a fatigue effect? It depends on how much we expect the fatigue to affect the RTs. Here we see that only after 100 button presses do we see a slowdown of 9 ms on average (0.09×100).

We need to consider whether the size of this effect has any scientific relevance by considering the previous literature. Sometimes this requires a meta-analysis. See Jäger, Engelmann, and Vasishth (2017), Nicenboim, Roettger, and Vasishth (2018) for examples. For examples of the use of this prior knowledge, see Nicenboim et al. (n.d.).

3.2.4 Posterior predictive checks

Let's say we know that our model is working as expected, since we already used fake data to test the recovery of the parameters (this will be a homework assignment).

We will now examine the *descriptive adequacy* of the models (Shiffrin et al. 2008; Gelman et al. 2014, Chapter 6): the observed data should look plausible under the *posterior predictive distribution*, as discussed above. The posterior predictive distribution is composed of one dataset for each sample from the posterior. (So it will generate as many datasets as iterations we have after the warm-up.) Achieving descriptive adequacy means that the current data could have been predicted by the model. Passing a test of descriptive adequacy is not strong evidence in favor of a model, but a major failure in descriptive adequacy can be interpreted as strong evidence against a model (Shiffrin et al. 2008).

To do posterior predictive checks for our last example, using brms, we need to do:

```
pp_check(m2, nsamples = 100)+
  theme(text = element_text(size=16),
        legend.text=element_text(size=16))
```

We'll use the values generated by our model to verify whether the general shape of the actual distribution matches the distributions from some of the generated datasets. Let's compare the real data against 100 of the predicted 4000 datasets.

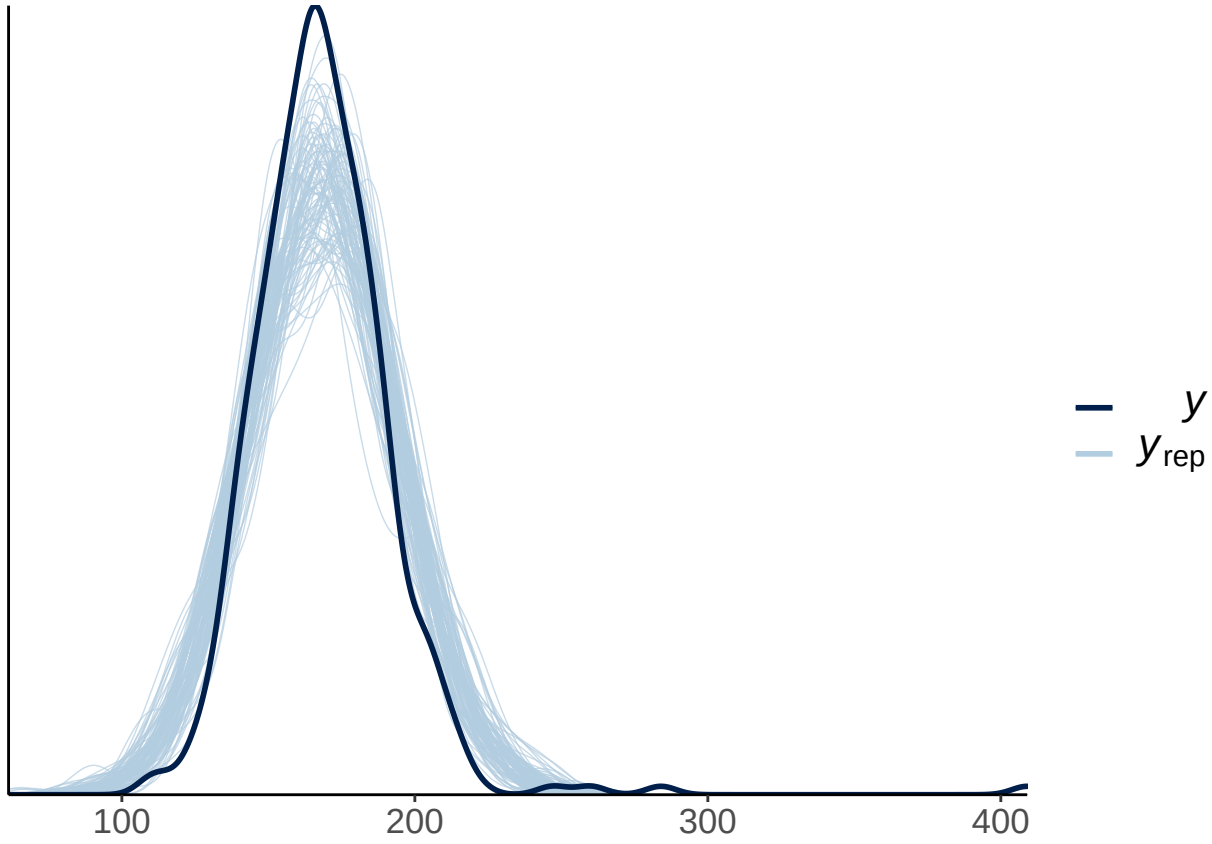


Figure 27: Posterior predictive check of model m2.

Are the posterior predicted data similar to the real data?

Figure 27 shows that our dataset seems to be more skewed to the right than our predicted datasets. This is not too surprising, we assumed that the likelihood was a normal distribution, but latencies are not very normal-like, they can't be negative and can be arbitrarily long.

3.2.5 Using the log-normal likelihood

Since we know that the latencies shouldn't be normally distributed, we can choose a more realistic distribution for the likelihood. A good candidate is the log-normal distribution since a variable (such as time) that is log-normally distributed takes only positive real values.

If Y is log-normally distributed, this means that $log(Y)$ is normally distributed.[2] Something important to notice is that the log-normal distribution is defined using again μ and σ, but this corresponds to the mean and standard deviation of the normally distributed logarithm $log(Y)$. Thus μ and σ are on a different scale than the variable that is log-normally distributed.

This also means that you can create a log-normal distribution by exponentiating the samples of a normal distribution. See Figure 28.

```
mu <- 6
sigma <- 0.5
N <- 100000
# Generate N random samples from a log-normal distribution
sl <- rlnorm(N, mu, sigma)
lognormal_plot <- ggplot(data.frame(samples=sl), aes(sl)) + geom_histogram() +
      ggtitle("Log-normal distribution\n") +
  ylim(0,25000) + xlim(0,2000)
# Generate N random samples from a normal distribution,
# and then exponentiate them
sn <- exp(rnorm(N, mu, sigma))
normalplot <- ggplot(data.frame(samples=sn), aes(sn)) + geom_histogram() +
      ggtitle("Exponentiated samples of\na normal distribution") + ylim(0,25000) + xlim

source("R/multiplot.R")
multiplot(lognormal_plot,normalplot,cols=)
```

3.2.6 Re-fit the model assuming a log-normal likelihood

If we assume that RTs are log-normally distributed, we'll need to change our model:

$$Y_i \sim LogNormal(\alpha + presses_i \cdot \beta, \sigma) \tag{190}$$

[2] In fact, $log_e(Y)$ or $ln(Y)$, but we'll write it as just $log()$

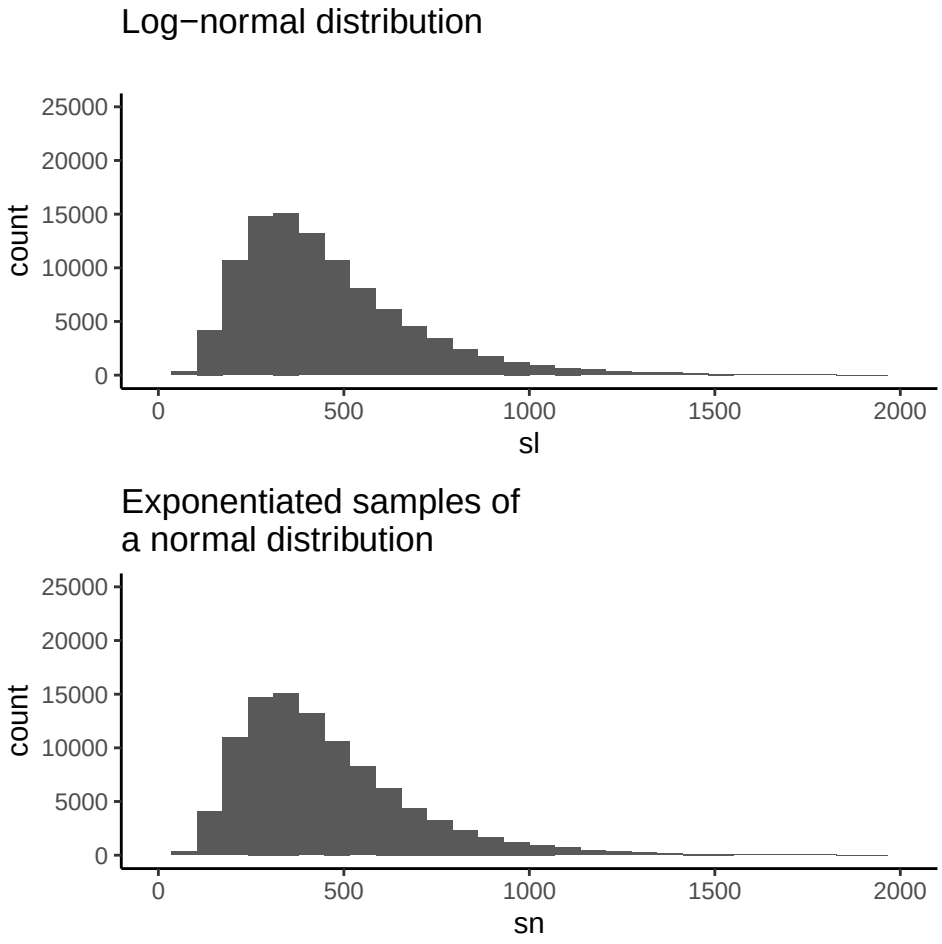


Figure 28: The log-normal distribution.

where $i = 1 \dots N$

But now the scale of our priors needs to change! They are no longer in milliseconds.

$$\begin{aligned} \alpha &\sim Normal(0, 10) \\ \beta &\sim Normal(0, 1) \\ \sigma &\sim Normal(0, 2) \text{ truncated so that } \sigma > 0 \end{aligned} \tag{191}$$

The interpretation of the parameters changes and it is more complex than if we were dealing with a linear model that assumes a normal likelihood:

- α. In our previous linear model, α represented the grand mean (or the grand median since in a normal distribution both coincide), and was equivalent to our previous μ (since β was multiplied by 0). But now, the grand mean needs to be calculated in the following way, $\exp(\alpha + \sigma^2/2)$. Interestingly, the grand median will just be $exp(\alpha)$,[3] and we could assume that this represents the underlying time it takes to press the space bar if there would be no noise, that is, if σ had no effect. This also means that the prior of α is not in milliseconds, but in log(milliseconds).
- β. In a linear model, β represents the slowdown for each time the space bar is pressed. Now β is the effect on the log-scale, and the effect in milliseconds depends on the intercept α: $\exp(\alpha + \beta) - \exp(\alpha)$. Notice that the log is not linear and the effect of β will have more impact on milliseconds as the intercept grows. For example, if we start with (i) $\exp(5) = 148$, and we add 0.1 in log-scale, $\exp(5 + 0.1) = 164$, we end up with a difference of 15 ms; if we start with (ii) $\exp(6) = 400$, and we add 0.1, $\exp(6 + 0.1) = 445$, we end up with a difference of 45 ms. You can also see this graphically below, in Figure 29.
- σ. This is the standard deviation of the normal distribution of $log(y)$.

3.2.7 What kind of information are the priors encoding?

- For α: We are 95% certain that the grand median of the RTs will be between ≈ 0 and 485165195 milliseconds. This is a (very-)weakly regularizing prior because it won't affect our results, but it will down-weight values for the grand median of the RTs that are extremely large, and won't allow the grand median to be negative. We calculate the previous range by back-transforming the values that lie between two standard deviations of the prior (2×10) to millisecond scale: $exp(-10 \times 2)$ and $exp(10 \times 2)$).
- For β: This is more complicated, because the effect on milliseconds will depend on the estimate of α. However, we can assume some value for α and it will be enough to be in the right order of magnitude. So let's assume 500 ms. That will mean that we are 95% certain that the effect of pressing the space bar will be between -491 and 26799 milliseconds. It is asymmetric because the log-scale is asymmetric. But the prior is weak enough so that if we assume 1000 or 100 instead of 500, the possible estimates of β will still be contained in the

[3] You can check in Wikipedia (https://en.wikipedia.org/wiki/Log-normal_distribution) why.

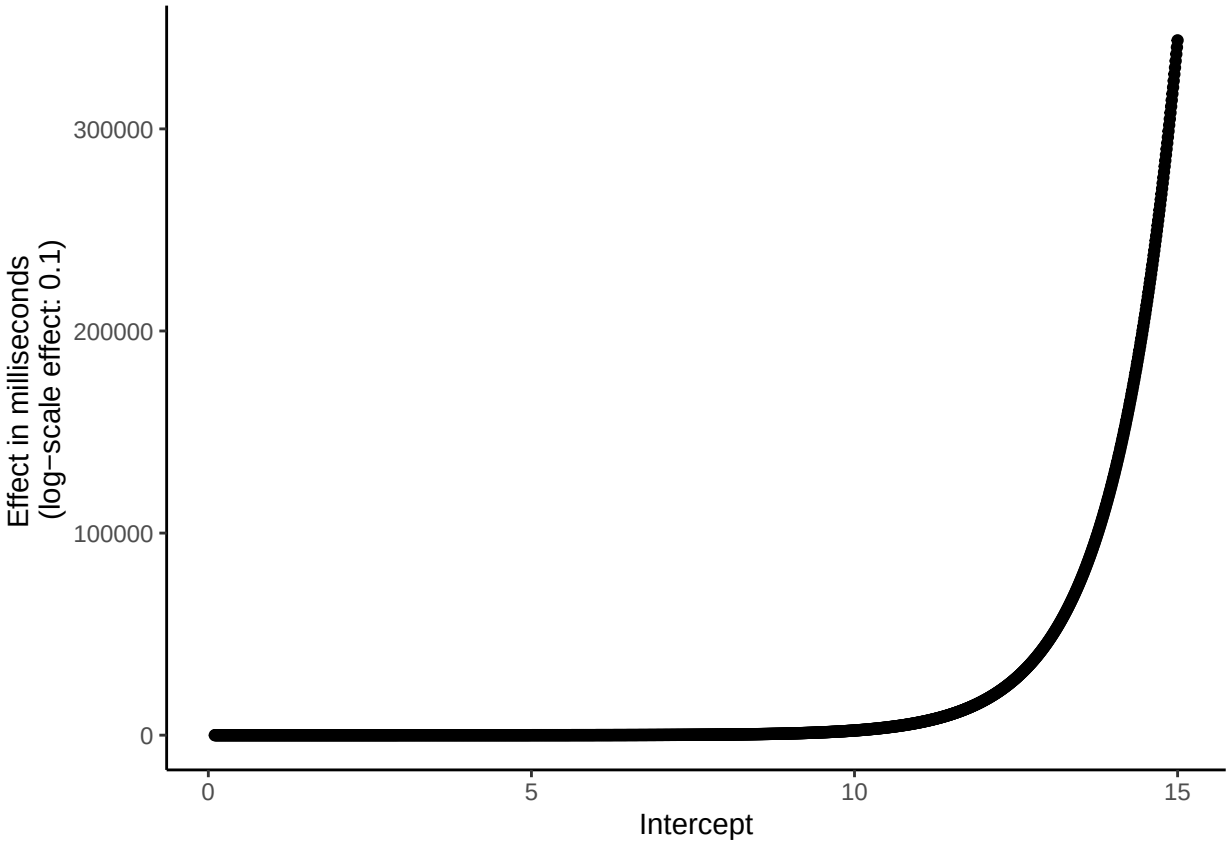


Figure 29: Back-transforming an effect of 0.1 log milliseconds to milliseconds.

prior distribution. We calculate this by first finding out the value in milliseconds when we are two standard deviations away in both directions: (2×2), that is $\exp(\log(500) - 2 \times 2)$ and $\exp(\log(500) + 2 \times 2)$, and we subtract from that the value of α that we assumed, 500: $\exp(\log(500) - 2 \times 2) - 500$ and $\exp(\log(500) + 2 \times 2) - 500$.

- For σ. This indicates that we are 95% certain that the standard deviation of $log(y)$ will be between 0 and 2. So 95% of the RTs will be between $\exp(\log(500) - 1 \times 2) = 68$ and $exp(log(500) + 1 \times 2) = 3695$.

What happens if we replace 500 by 100, and by 1000? What happens if it is 10 instead? Does it still makes sense?

We'll code the model as follows.

```
priors_log <- c(set_prior("normal(0, 10)",
                          class = "Intercept"),
                set_prior("normal(0, 1)",
                          class = "b",
                          coef="presses"),
                set_prior("normal(0, 2)",
                          class = "sigma"))
```

```
m2_logn<-brm(y~1+presses,noreading_data,prior = priors_log,
       iter = 2000, chains = 4,family = lognormal(),
       control = list(adapt_delta = 0.99,max_treedepth=15))
```

```
## Compiling the C++ model
```

```
## Start sampling
```

```
summary(m2_logn)
```

```
##  Family: lognormal
##   Links: mu = identity; sigma = identity
## Formula: y ~ 1 + presses
##    Data: noreading_data (Number of observations: 361)
## 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 Eff.Sample Rhat
## Intercept     5.02      0.01     5.00     5.05       1995 1.00
## presses       0.00      0.00     0.00     0.00       3603 1.00
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat
## sigma     0.12      0.00     0.11     0.13       1214 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).
```

We fit the model, and check its convergence as usual (this will be a homework assignment).

3.2.8 Summarizing the posterior and inference

Next, we turn to the question of what we can report as our results, and what we can conclude from the data.

We can summarize the posterior and do inference as discussed in Example 1. If we want to talk about the effect estimated by the model, we summarize the posterior of β in the following way: $\hat{\beta} = 0.001$, 95% CrI = $[0, 0.001]$.

But in most cases, the effect is easier to interpret in milliseconds. We generated the effect of 1 press in the generated quantities block, which is not the same as the linear model's β. Our generated estimate will tell us the estimate of the slowdown produced by pressing the space bar in the middle of the experiment once, assuming that the RTs are log-normally distributed: 0.079 ms, 95% CrI = $[0.063, 0.096]$. Coincidentally, it is close to the same value as before, but this is not always the case, and since it's not linear the effect won't be the same across the whole experiment.

3.2.9 Posterior predictive checks and distribution of summary statistics

We can now verify whether our predicted datasets look more similar to the real dataset. See Figure 30.

```
pp_check(m2_logn, nsamples = 100)+
  theme(text = element_text(size=16),legend.text=element_text(size=16))
```

Are the posterior predicted data now more similar to the real data?

It seems so, but it's not easy to tell. Another way to examine this would be to look at the *distribution of summary statistics*. The idea is to compare the distribution of representative summary statistics for the datasets generated by different models and compare them to the observed statistics. Since we suspect that the log-normal distribution may capture the long tail, we could use the maximum as a summary statistics. We could generate 100 posterior predictive data-sets, and then compute the maximum each time and plot the distribution of the maximum, comparing it with the maximum value (409) in the data.

```
m2_logn<-brm(y~1+presses,noreading_data,prior = priors_log,
       iter = 2000, chains = 4,
       family = lognormal(),
       control = list(adapt_delta = 0.99,max_treedepth=15))
```

```
## Compiling the C++ model
```

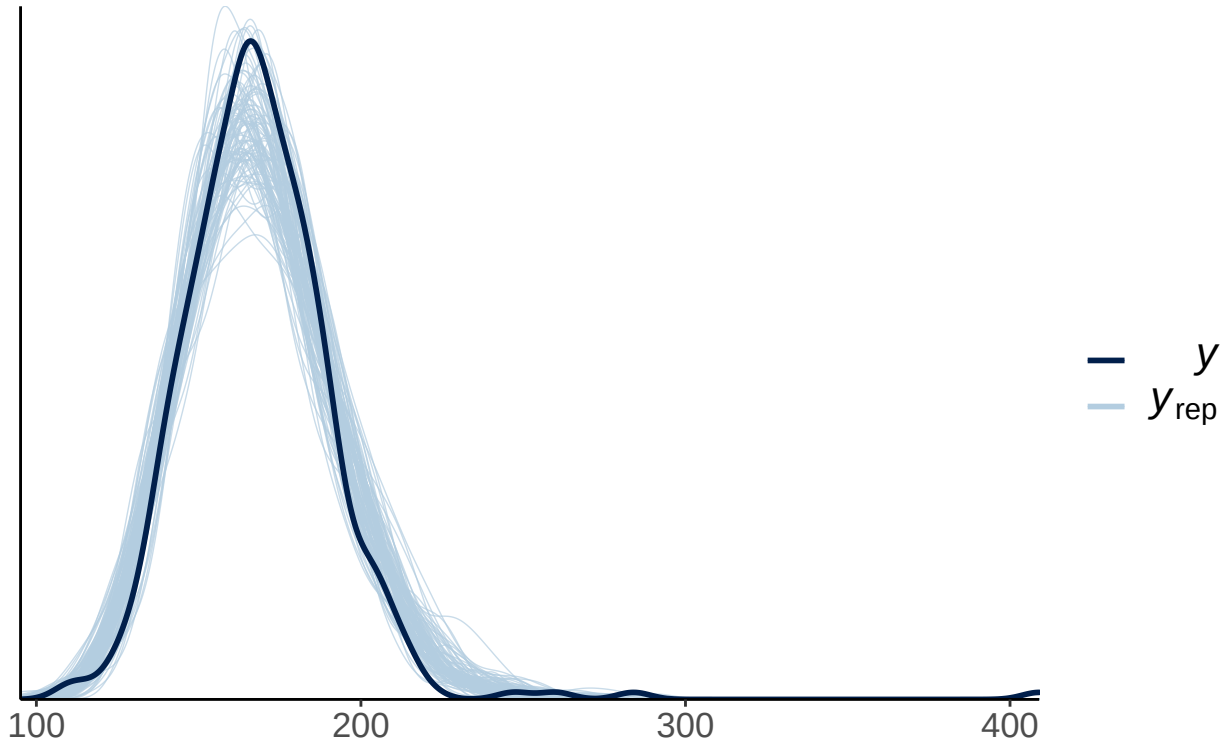


Figure 30: Posterior predictive check.

```
## recompiling to avoid crashing R session
```

```
## Start sampling
```

```
postsamp<-posterior_samples(m2_logn,"^b",add_chain=TRUE)

nsim<-100
maximum<-rep(NA,nsim)
for(i in 1:nsim){
ppm2_logn<-predict(m2_logn)
maximum[i]<-max(as.vector(ppm2_logn))
}
```

```
hist(maximum,main="Distribution of maximum values",freq=FALSE)
```

Figure 31 shows that we are unable to capture the maximum value of the observed data, so there's still room for improving the model. We will return to this question later in the course.

3.2.10 General workflow

This is the general workflow that we suggest when fitting a Bayesian model.

1. Define the full probability model:
    a. Decide on the likelihood.

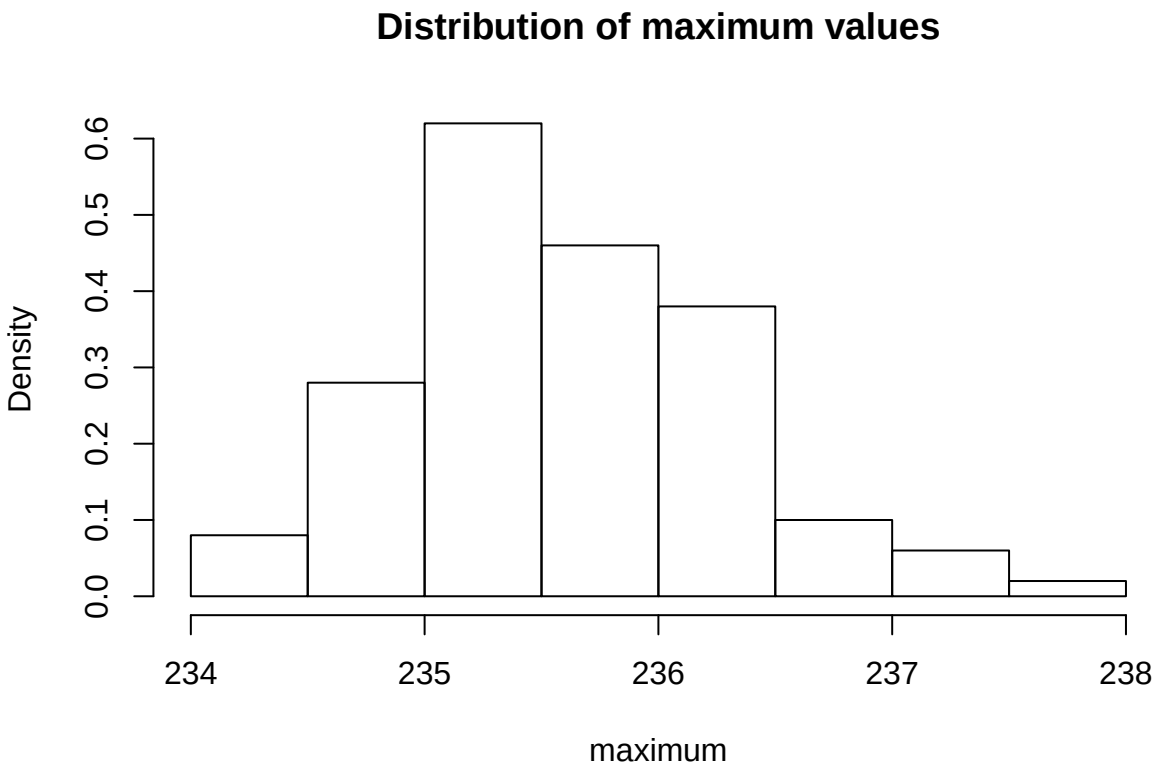


Figure 31: Distribution of maximum values in a posterior predictive check. The maximum in the data is 409 ms.

   b. Decide on the priors.
   c. Write the brms or Stan model.
2. Do prior predictive checks to determine if priors make sense.

3. Check model using fake data simulations:
   a. Simulate data with known values for the parameters.
   b. Fit the model and do MCMC diagnostics.
   c. Verify that it recovers the parameters from simulated data.
4. Fit the model with real data and do MCMC diagnostics.
5. Evaluate the model's fit (e.g., posterior predictive checks, distribution of summary statistics). This may send you back to 1.
6. Inference/prediction/decisions.
7. Conduct model comparison if there's an alternative model (to be discussed later).

3.3 Exercises

1. Load the data-set beauty.txt. This data-set shows beauty ratings and the teaching evaluation score of professors in a US university. The data are from Gelman and Hill (2007).

```
beauty<-read.table("data/beauty.txt",header=TRUE)
head(beauty)
```

```
##      beauty evaluation
## 1  0.201567        4.3
## 2 -0.826081        4.5
## 3 -0.660333        3.7
## 4 -0.766312        4.3
## 5  1.421445        4.4
## 6  0.500220        4.2
```

A beauty level of 0 means average beauty. Using a Bayesian linear model, carry out a full analysis to evaluate the question: does the physical attractiveness (beauty level) of the professor lead to a better teaching evaluation? - Plot the data and look at the distributions of the data. - Define a model in Stan to answer the question. - Do a fake-data simulation to check whether the model recovers the parameters. - Once satisfied with the model, fit the model and display the posteriors. - Carry out a posterior predictive check to determine whether the model makes reasonable predictions. - What would you conclude about the effect of beauty on evaluations?

2. The second or third most watched talk in the history of TED talks is by Amy Cuddy, some 49 million views. Watch the talk first (just google Amy Cuddy TED talk).

The claim is that adopting a high power for two minutes will increase your testosterone, improving your performance in, e.g., job interviews. We are going to evaluate this claim based on Cuddy's data.

The data are available from Harvard Dataverse:

https://dataverse.harvard.edu/dataset.xhtml?persistentId=doi:10.7910/DVN/FMEGS6

Incidentally, the first author of the Cuddy paper has disavowed the paper: see here.

```
## cleaned data
datc<-read.csv("data/ccy-clean-data.csv",
               header=TRUE)

## sanity check: one subject, one row
dim(datc)
```

```
## [1] 47 41
```

```
length(unique(datc$id))
```

```
## [1] 47
```

```
#drop ineligible and something else as in stata code:
datc<-subset(datc,inelig!="Ineligible (drop)" & anyoutv1!="Selected")
```

Then carry out the following exploration of the data. Examine male and female testosterone levels:

```
## subset males and females
males<-subset(datc,female=="Male")
females<-subset(datc,female=="Female")

## initial testosterone:
summary(males$testm1)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    31.0    47.8    60.6    70.5    90.4   143.6
```

```
summary(females$testm1)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    11.7    28.0    36.6    39.5    48.6    80.7
```

```
## after treatment:
summary(males$testm2)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    34.8    58.7    65.2    72.4    91.3   111.6
```

```
summary(females$testm2)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    2.15   23.70   38.77   38.82   48.27  105.48
```

Calculate mean post-treatment testosterone by gender, and ignoring gender:

```
round(with(datc,tapply(testm2,IND=list(female,hptreat),mean)))
```

```
##        High Low
## Female   45  33
## Male     65  82
```

```
round(with(datc,tapply(testm2,IND=list(hptreat),mean)))
```

```
## High  Low
##   52   48
```

By how much did testosterone increase after treatment? Means by gender:

```
## difference scores:
round(with(datc,tapply(testm2-testm1,IND=list(female,hptreat),mean)))
```

```
##        High Low
## Female    1  -2
```

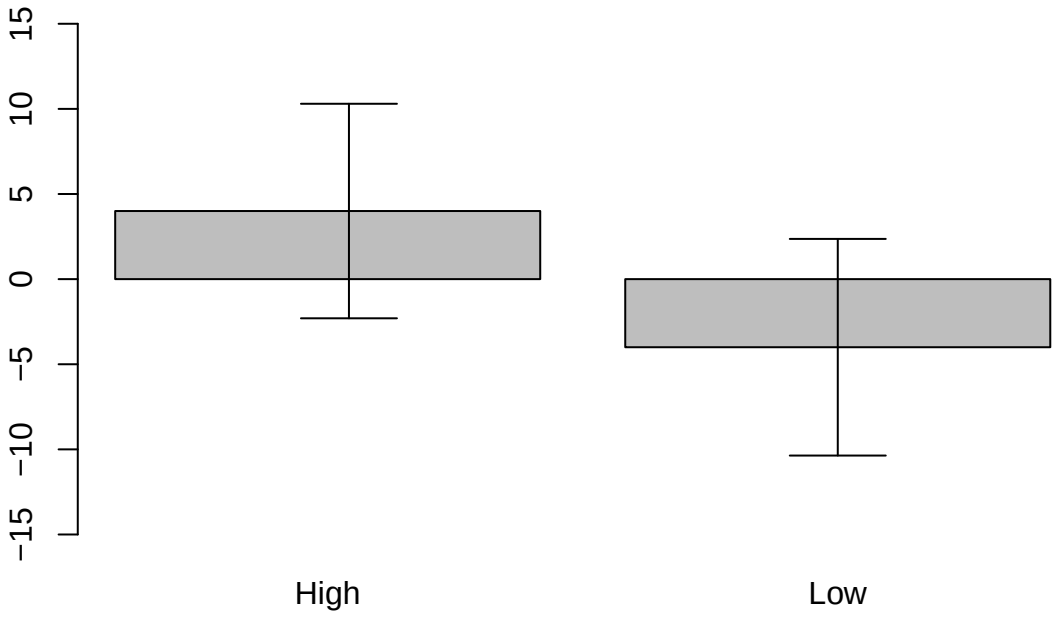


Figure 32: Recreation of Figure 3 in the Cuddy power posing study.

```
## Male     12 -10
```

Means ignoring gender: Figure 32 is the rough and ready version of fig 3 of the paper. The effects are a bit smaller in this data-set than the published result, probably because of the statistician's cleaning up of the data.

```
means<-round(with(datc,tapply(testm2-testm1,IND=hptreat,mean)))
sds<-with(datc,tapply(testm2-testm1,IND=hptreat,sd))
n<-length(datc$testm2)
ses<-sds/sqrt(n)

barplot(means,ylim=c(-15,15))
arrows(x0=.75,x1=.75,y0=means[1]-1.96*ses[1],y1=means[1]+1.96*ses[1],angle=90,code=3)
arrows(x0=1.9,x1=1.9,y0=means[2]-1.96*ses[2],y1=means[2]+1.96*ses[2],angle=90,code=3)
```

```
## calculate difference
diff<-datc$testm2-datc$testm1
## make data frame with differences as DV:
treatment<-datc$hptreat
diff_df<-data.frame(subj=1:length(treatment),
                    diff=diff,treatment=treatment)

## subset low and high pose subjects' data:
lowdiff<-subset(diff_df,treatment=="Low")
highdiff<-subset(diff_df,treatment=="High")
```

A typical approach would be to do a two-sample t-test:

```
## t-test, two sample:
t.test(highdiff$diff,lowdiff$diff)
```

```
##
##  Welch Two Sample t-test
##
## data:  highdiff$diff and lowdiff$diff
## t = 1.367, df = 36.86, p-value = 0.18
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -4.26404 21.93321
## sample estimates:
## mean of x mean of y
##   4.46800  -4.36658
```

There seems to be no evidence for power posing. Now, refit the model using various predictors:

- the initial testosterone value
- the initial and final cortisone (?) levels
- the gender of the subject.

The question we ask here is, is post-treatment testosterone higher for subjects exposed to high vs low power, controlling for these variables?

First, center all predictors:

```
## center all predictors
datc$ctestm1<-scale(datc$testm1,scale=FALSE)
datc$chptreat<-ifelse(datc$hptreat=="High",1,-1)
datc$cortm1<-scale(datc$cortm1,scale=FALSE)
datc$cortm2<-scale(datc$cortm2,scale=FALSE)
datc$female<-ifelse(datc$female=="Female",1,-1)
```

Fit the Bayesian version of model m0 below, using brms.

```
## This is the result that Fosse, Cuddy's statistician, found:
m0<-lm(testm2~ctestm1+chptreat+cortm1+
                 cortm2+female,datc)
```

Now, look at how gender affects the conclusions:

```
## with interaction with gender, the effect disappears:
m1<-lm(testm2~ctestm1+chptreat+cortm1+cortm2+female+chptreat:female,datc)
```

Fit the above model m1 using brms.

We could also have as dependent measure the **change** in testosterone in low vs high power subjects. This corresponds to the Fig 3 plot in the paper.

```
datc$change<-datc$testm2-datc$testm1
m2a<-lm(change~chptreat,datc)
```

Fit the above model in brms. Then take gender into account and check if gender has an effect:

```
## taking gender into account
m3a<-lm(change~chptreat+female,datc)
```

Fit m3a in brms.

Next, take the interaction between treatment and gender into account.

```
## taking interaction between treatment and gender into account
m4a<-lm(change~chptreat*female,datc)
```

Fit model 4a using brms.

What can we conclude from this data? Does power posing change testosterone levels?

3.4 Appendix - Troubleshooting problems of convergence

1. Rhat > 1.1 First of all check that there are no silly mistakes in the model. Forgetting to put parenthesis, multiplying the wrong parameters, using the wrong operation, etc. can create a model that can't converge. As our models grow in complexity there are more places where to make mistakes. Start simple, see if the model works, add complexity slowly, checking if the model converges at every step. In very rare occasions, when Rhat >1.1 and the model is correct, it may help to increase the number of iterations, but then it's usually a better idea to re-parametrize the model, see 3.
2. Stan gives a warning. The solution may also be point 1. But if the model is correctly specified, you should check Stan's website, there is a very good guide to solve problems in: http://mc-stan.org/misc/warnings.html. If this doesn't work, you may need to re-parametrize the model, see 3.
3. Some models have convergence issues because the sampler struggles to explore the parameters space. This is specially relevant in complex hierarchical models. In this case, the solution might be to re-parametrize the model. This is by no means trivial. However, the simplest parametrization trick to try is to have all the priors on the same rough scale, that is priors shouldn't have different orders of magnitude. You can find some suggestions in the chapter 21 of Stan manual (Stan Development Team 2017), and the following case study: http://mc-stan.org/users/documentation/case-studies/qr_regression.html.

4 Hierarchical linear modeling

4.1 Example 1: Reading time differences in subject vs object relatives in English

We begin with a classic question from the psycholinguistics literature: are subject relatives easier to process than object relatives? The data come from Experiment 1 in a paper by Grodner and Gibson (2005).

4.1.1 Scientific question: Is there a subject relative advantage in reading?

In two important papers, Gibson (2000) and Grodner and Gibson (2005) suggest that object relative clause sentences are more difficult to process than subject relative clause sentences because the distance between the relative clause verb *sent* and the head noun phrase of the relative clause, *reporter*, is longer in object vs subject relatives. Examples are shown below.

(1a) The *reporter* who the photographer *sent* to the editor was hoping for a good story. (object gap)

(1b) The *reporter* who *sent* the photographer to the editor was hoping for a good story. (subject gap)

The underlying explanation has to do with memory processes: shorter linguistic dependencies are easier to process due to either reduced interference or decay, or both. For implemented computational models that spell this point out, see Lewis and Vasishth (2005) and Engelmann, Jäger, and Vasishth (2018).

In the Grodner and Gibson data, the dependent measure is reading time at the relative clause verb, in milliseconds. We are expecting longer reading times in object gap sentences compared to subject gap.

4.1.2 Load data and reformat

```
library(dplyr)
gg05e1 <- read.table("data/GrodnerGibson2005E1.csv",sep=",", header=T)
gge1 <- gg05e1 %>% filter(item != 0)

gge1 <- gge1 %>% mutate(word_positionnew = ifelse(item != 15 &
                                                    word_position > 10,
                                                  word_position-1,
                                                  word_position))
#there is a mistake in the coding of word position,
#all items but 15 have regions 10 and higher coded
#as words 11 and higher

## get data from relative clause verb:
```

```
gge1crit <- subset(gge1, ( condition == "objgap" & word_position == 6 ) |
            ( condition == "subjgap" & word_position == 4 ))
```

4.1.3 Experiment design: Latin square and crossed subject and items

Two important properties of these data are worth noticing.

4.1.3.1 Latin-square design

First, the design is the classic repeated measure Latin square set-up. To see what this means, first look at the number of subjects and items, and the number of rows in the data frame:

```
length(unique(gge1crit$subject))
```

```
## [1] 42
```

```
length(unique(gge1crit$item))
```

```
## [1] 16
```

```
dim(gge1crit)[1]
```

```
## [1] 672
```

There are 42 subjects and 16 items. There are $42 \times 16 = 672$ rows in the data frame. Notice also that each subject sees exactly eight object gap and eight subject gap sentences:

```
head(xtabs(~subject+condition,gge1crit),n=4)
```

```
##         condition
## subject objgap subjgap
##       1      8       8
##       2      8       8
##       3      8       8
##       4      8       8
```

The researchers created 16 sets of subject and object relatives; one set is the pair of sentences shown in (1a) and (1b) above. In the data frame, both these two items have the same id 1, but no one subject will see both sentences in any one set. For example, item 1 is seen by subject 1 in the object gap condition (1a) and item 1 is seen by subject 2 in the subject gap condition (1b):

```
subset(gge1crit,item==1)[1:2,]
```

```
##     subject item condition word_position region_position rawRT residRT
## 6         1    1    objgap             6               3   320  -21.39
## 250       2    1   subjgap             4               3   357 -111.48
##     qcorrect experiment word_positionnew
## 6          0     tedrg3                6
```

```
## 250        1     tedrg2                4
```

Table 1: The Latin-square design in repeated measures experiments.

item id	group 1	group 2
1	objgap	subjgap
2	subjgap	objgap
3	objgap	subjgap
4	subjgap	objgap
⋮	⋮	⋮
16	subjgap	objgap

This is called a Latin-square design because of the following layout. See Table 1. Each subject is randomly assigned to Group 1 or 2, and one should have an even number of subjects in order to have a balanced data-set. Hence the 42 subjects in the Grodner and Gibson data: 21 in each group.

A useful way to ensure that you have balanced assignments of subjects to each group is to randomize the order of incoming participants in advance, such that pairs of subjects are assigned to group 1 and 2. Let order1 be such that the first subject gets group 1 and the second gets group 2, and order 2 that the first subject gets group 2 and the second group 1. Then just generate a random ordering to ensure that each pair of subjects lands in a balanced way across groups:

```
sample(rep(c("order1","order2"),11))
```

```
##  [1] "order1" "order1" "order2" "order1" "order2" "order1" "order2"
##  [8] "order2" "order1" "order1" "order2" "order2" "order2" "order2"
## [15] "order2" "order2" "order1" "order2" "order1" "order1" "order1"
## [22] "order1"
```

Latin square designs are used in psychology and linguistics (and other areas) because they are optimal in several ways.

Soon we will need to generate a fake data-frame with a repeated measures Latin square design. We can do this using R as follows (source: Vasishth et al. 2018):

```
library(MASS)
nitem <- 16
nsubj <- 42
## prepare data frame for two condition in a latin square design:
g1<-data.frame(item=1:nitem,
                 cond=rep(c("objgap","subjgap"),nitem/2))
g2<-data.frame(item=1:nitem,
                 cond=rep(c("objgap","subjgap"),nitem/2))

## assemble data frame in long format:
gp1<-g1[rep(seq_len(nrow(g1)),
              nsubj/2),]
gp2<-g2[rep(seq_len(nrow(g2)),
```

```
              nsubj/2),]

fakedat<-rbind(gp1,gp2)
## sanity check:
dim(fakedat)
```

```
## [1] 672   2
```

```
## add subjects:
fakedat$subj<-rep(1:nsubj,each=nitem)
fakedat<-fakedat[,c(3,1,2)]
fakedat$so<-ifelse(fakedat$cond=="objgap",1,-1)
```

For example, subject 1 sees the following conditions and items:

```
head(fakedat,n=16)
```

```
##    subj item    cond so
## 1     1    1  objgap  1
## 2     1    2 subjgap -1
## 3     1    3  objgap  1
## 4     1    4 subjgap -1
## 5     1    5  objgap  1
## 6     1    6 subjgap -1
## 7     1    7  objgap  1
## 8     1    8 subjgap -1
## 9     1    9  objgap  1
## 10    1   10 subjgap -1
## 11    1   11  objgap  1
## 12    1   12 subjgap -1
## 13    1   13  objgap  1
## 14    1   14 subjgap -1
## 15    1   15  objgap  1
## 16    1   16 subjgap -1
```

We will need this code later for fake data simulation.

4.1.3.2 Fully crossed subjects and items

In the data, because of the Latin square design, each subject sees exactly one item in one of the two conditions:

```
xtabs(~subject+item,gge1crit)
```

```
##         item
## subject 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16
##       1  1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
```

```
##       2  1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       3  1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       4  1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       5  1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       6  1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       7  1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       8  1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       9  1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       10 1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       11 1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       12 1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       13 1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       14 1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       15 1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       16 1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       17 1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       18 1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       19 1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       20 1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       21 1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       22 1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       23 1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       24 1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       25 1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       26 1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       27 1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       28 1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       29 1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       30 1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       31 1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       32 1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       33 1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       34 1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       35 1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       36 1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       37 1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       38 1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       39 1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       40 1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       41 1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
##       42 1 1 1 1 1 1 1 1 1  1  1  1  1  1  1  1
```

If there were some zeros in the above matrix, we would have an imbalance, and this would then be *partially crossed*. This kind of imbalance arises in data-sets due to missing data, where missingness can happen due to different reasons. E.g., in eyetracking, subjects sometimes skip the critical word

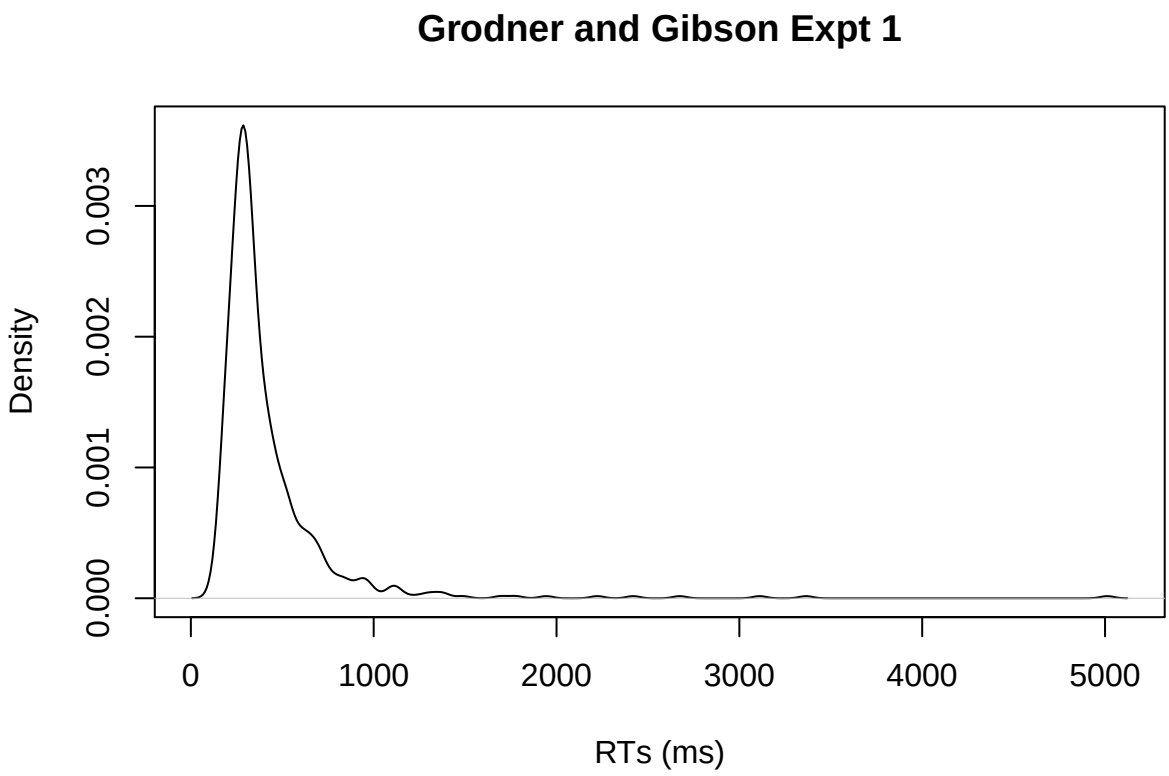


Figure 33: Distribution of reading times in the Grodner and Gibson Experiment 1 data, at the critical region.

entirely, or there is tracking loss; these events lead to a 0 ms reading time being recorded, and this could be treated as missing data (marked as NA). We return to this point in an advanced course on Bayesian modeling, to be offered at some later date.

4.1.4 The implied generative model

The above design implies a particular statistical model that takes us beyond the linear model.

To remind you, a simple linear model of the above data would be:

$$y = \alpha + \beta * x + \varepsilon \text{ where } \varepsilon \sim Normal(0, \sigma) \tag{192}$$

Here, object gaps are coded +1, subject gaps -1. See Schad et al. (2018) for an explanation of contrast coding.

```
gge1crit$so<-ifelse(gge1crit$condition=="objgap",1,-1)
```

As figure 33 shows, a Normal likelihood doesn't seem well motivated, so we will use the log-normal.

```
plot(density(gge1crit$rawRT),main="Grodner and Gibson Expt 1",xlab="RTs (ms)")
```

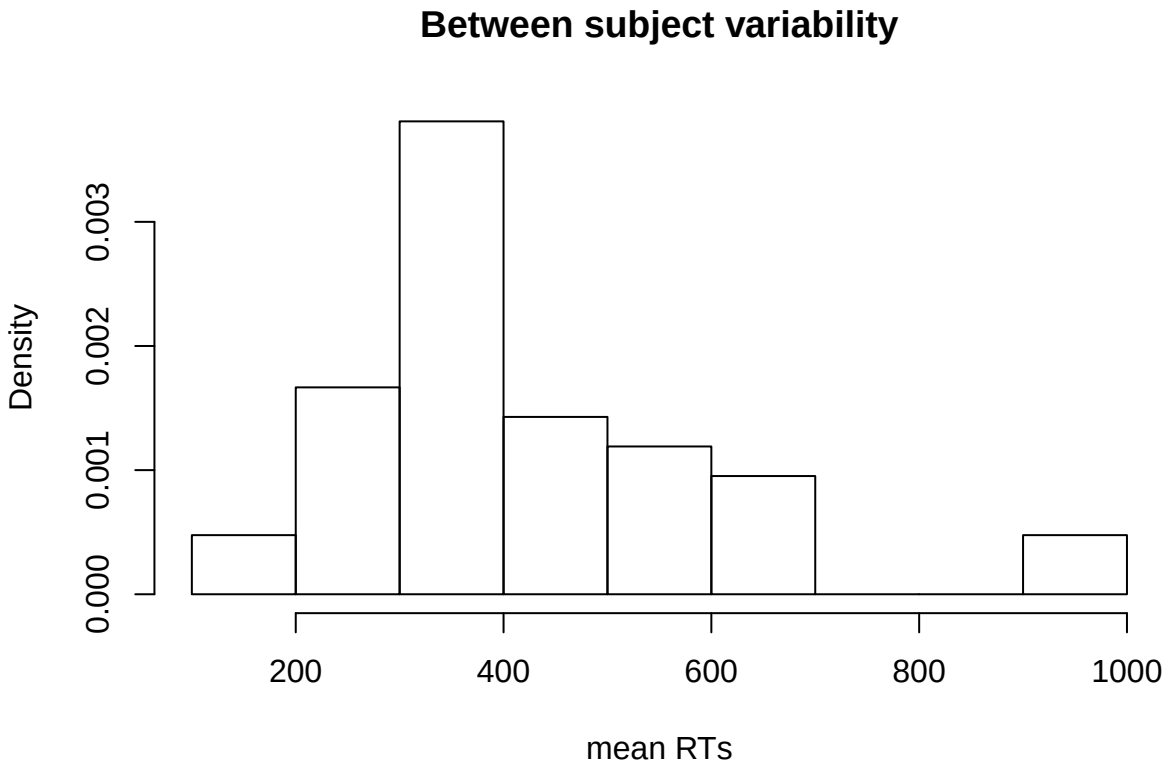


Figure 34: Between subject variability in mean reading times.

4.1.4.1 Between subject variability in mean reading time

The simple linear model above would ignore the fact that we have repeated measures from multiple subjects—the iid assumption is violated. Also, different subjects that may have different mean reading times (α differ for each subject) and different object gap processing costs (β differs for each subject). Some subjects will be slower and some faster, and some may suffer more with object gaps because of lower working memory capacity, lower attention, etc. (of course, we are speculating here, we have no measurements of these individual difference variables). See Figure 34 for a visualization of between subject variability in mean reading times.

```
hist(with(gge1crit,tapply(rawRT,subject,mean)),
     main="Between subject variability",
     xlab="mean RTs",freq=FALSE)
```

In the linear model, we can express the assumption that the grand mean intercept α needs an adjustment by subject, where subjects are indexed from $j = 1,\ldots,J$:

$$y_j = \alpha + u_{0j} + \beta * x_j + \varepsilon_j \tag{193}$$

where we now have two sources of variance:

- within subject variance, $\varepsilon_j \sim Normal(0,\sigma)$
- between subject variance in mean reading times, $u_{0j} \sim Normal(0,\sigma_{u0})$

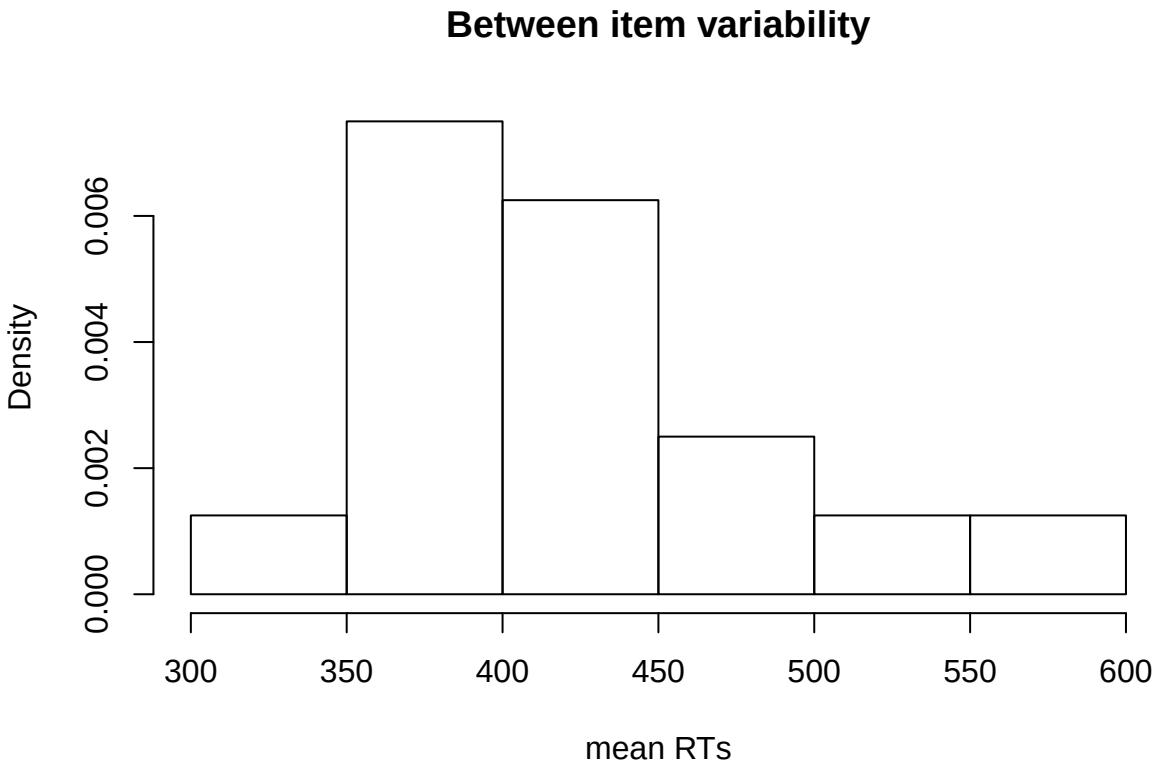


Figure 35: Between item variability in mean reading times.

In Bayes, the adjustment u_{0j} is a parameter. This is not the case in the frequentist paradigm (Bates et al. 2015).

4.1.4.2 Between item variability in mean reading time

We also see that items also differ, some would be read faster and some slower:

```
hist(with(gge1crit,tapply(rawRT,item,mean)),
     main="Between item variability",
     xlab="mean RTs",freq=FALSE)
```

For items ranging from $k = 1, \ldots, K$, we can add this assumption to the model:

$$y_{kj} = \alpha + u_{0j} + w_{0k} + \beta * x_{kj} + \varepsilon_{kj} \tag{194}$$

where there are now three variance components:

- $\varepsilon_{kj} \sim Normal(0, \sigma)$
- $u_{0j} \sim Normal(0, \sigma_{u0})$
- between item variability in mean reading time, $w_{0k} \sim Normal(0, \sigma_{w0})$

This model is called a *varying intercepts model* with crossed varying intercepts for subjects and for items.

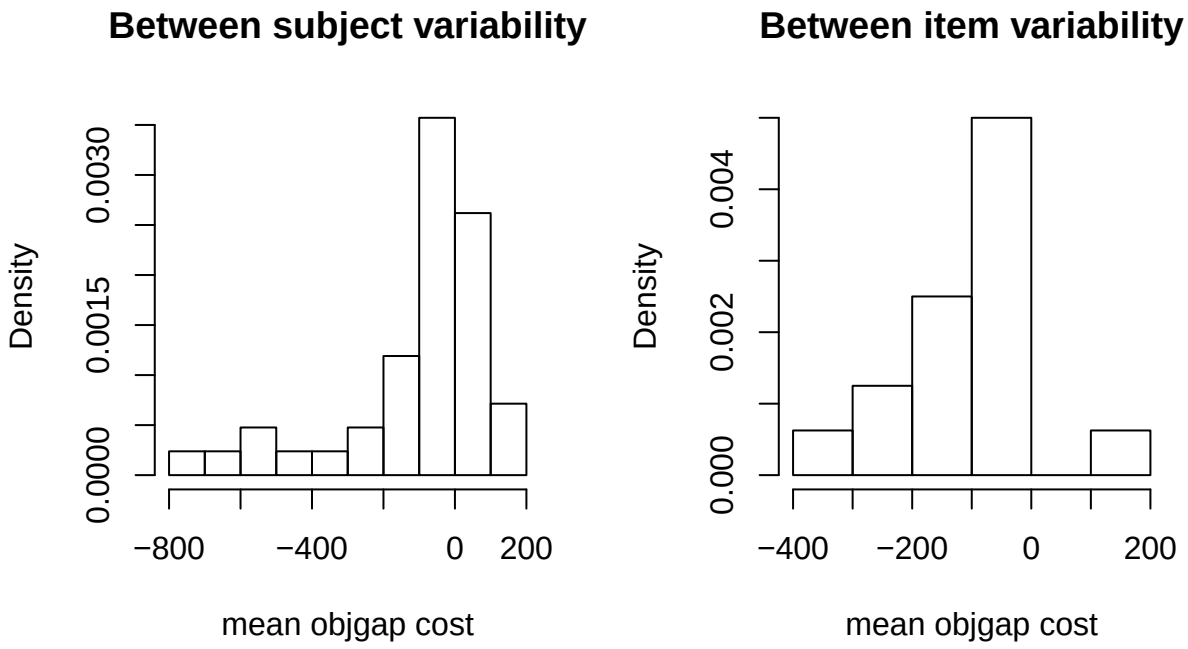


Figure 36: Between subject and item variability in object gap vs subject gap reading times.

4.1.4.3 Between subject and between item variability in objgap cost

The object gap cost can also vary by subject and by item. See Figure 36.

```
op<-par(mfrow=c(1,2),pty="s")
meanssubj<-with(gge1crit,
                tapply(rawRT,IND=list(subject,condition),mean))
diff<-meanssubj[,2]-meanssubj[,1]

hist(diff,
     main="Between subject variability",xlab="mean objgap cost",freq=FALSE)

meansitem<-with(gge1crit,tapply(rawRT,IND=list(item,condition),mean))
diff<-meansitem[,2]-meansitem[,1]

hist(diff,
     main="Between item variability",xlab="mean objgap cost",freq=FALSE)
```

We can incorporate this assumption into the model by adding adjustments to the β parameter:

$$y_{kj} = \alpha + u_{0j} + w_{0k} + (\beta + u_{1j} + w_{1k}) * x_{kj} + \varepsilon_{kj} \tag{195}$$

where

- $\varepsilon_{kj} \sim Normal(0, \sigma)$
- $u_{0j} \sim Normal(0, \sigma_{u0})$

- $u_{1j} \sim Normal(0, \sigma_{u1})$
- $w_{0k} \sim Normal(0, \sigma_{w0})$
- $w_{1k} \sim Normal(0, \sigma_{w1})$

This is called the *varying intercepts and slopes* model with *no correlation* between the intercepts and slopes.

4.1.5 The maximal model

There is one detail still missing in the model: the adjustments to the intercept and slope are correlated for subjects, and also for items. In other words, we have a bivariate distribution for the subject and item random effects:

$$y_{kj} = \alpha + u_{0j} + w_{0k} + (\beta + u_{1j} + w_{1k}) * x_{kj} + \varepsilon_{kj} \tag{196}$$

where $\varepsilon_{kj} \sim Normal(0, \sigma)$ and

$$\Sigma_u = \begin{pmatrix} \sigma^2_{u0} & \rho_u \sigma_{u0} \sigma_{u1} \\ \rho_u \sigma_{u0} \sigma_{u1} & \sigma^2_{u1} \end{pmatrix} \quad \Sigma_w = \begin{pmatrix} \sigma^2_{w0} & \rho_w \sigma_{w0} \sigma_{w1} \\ \rho_w \sigma_{w0} \sigma_{w1} & \sigma^2_{w1} \end{pmatrix} \tag{197}$$

$$\begin{pmatrix} u_0 \\ u_1 \end{pmatrix} \sim \mathcal{N}\left(\begin{pmatrix} 0 \\ 0 \end{pmatrix}, \Sigma_u \right), \quad \begin{pmatrix} w_0 \\ w_1 \end{pmatrix} \sim \mathcal{N}\left(\begin{pmatrix} 0 \\ 0 \end{pmatrix}, \Sigma_w \right) \tag{198}$$

This is a varying intercepts and slopes model with fully specified variance-covariance matrices for the subject and item random effects. It is sometimes called the **maximal model** (Barr et al. 2013).

4.1.6 Implementing the model

The above model is simple to implement in the Bayesian framework.

4.1.6.1 Specify and visualize priors

We define some priors first:

1. $\alpha \sim Normal(0, 10)$
2. $\beta \sim Normal(0, 1)$
3. Residual standard deviation: $\sigma \sim Normal_+(0, 1)$
4. All other standard deviations: $\sigma \sim Normal_+(0, 1)$
5. Correlation matrix: $\rho \sim LKJ(2)$.

The LKJ prior needs some explanation.

4.1.6.2 The LKJ prior on the correlation matrix

In this model, we assume that the vector $\mathbf{u} = \langle u_0, u_1 \rangle$ comes from a bivariate normal distribution with a variance-covariance matrix Σ_u. This matrix has the variances of the adjustment to the intercept and to the slope respectively along the diagonal, and the covariance on the off-diagonals.

Recall that the covariance $Cov(X,Y)$ between two variables X and Y is defined as the product of their correlation ρ and their standard deviations σ_X and σ_Y, such that, $Cov(X,Y) = \rho\sigma_X\sigma_Y$.

$$\Sigma_u = \begin{pmatrix} \sigma^2_{u_0} & \rho_u\sigma_{u_0}\sigma_{u_1} \\ \rho_u\sigma_{u_0}\sigma_{u_1} & \sigma^2_{u_1} \end{pmatrix} \tag{199}$$

The covariance matrix can be decomposed into a vector of standard deviations and a correlation matrix. The correlation matrix looks like this:

$$\begin{pmatrix} 1 & \rho_u \\ \rho_u & 1 \end{pmatrix} \tag{200}$$

In Stan, we write a matrix that has 0's on the off-diagonals as:

$$diag\_matrix(\sigma_{u_0}, \sigma_{u_1}) = \begin{pmatrix} \sigma_{u_0} & 0 \\ 0 & \sigma_{u_1} \end{pmatrix} \tag{201}$$

This means that we can decompose the covariance matrix into three parts:

$$\begin{aligned} \Sigma_u &= diag\_matrix(\sigma_{u_0}, \sigma_{u_1}) \cdot \rho_u \cdot diag\_matrix(\sigma_{u_0}, \sigma_{u_1}) \\ &= \begin{pmatrix} \sigma_{u_0} & 0 \\ 0 & \sigma_{u_1} \end{pmatrix} \begin{pmatrix} 1 & \rho_u \\ \rho_u & 1 \end{pmatrix} \begin{pmatrix} \sigma_{u_0} & 0 \\ 0 & \sigma_{u_1} \end{pmatrix} \end{aligned} \tag{202}$$

So we need priors for the σ_us and for ρ_u:

The basic idea of the LKJ prior is that its parameter (usually called *eta*, η, here it has value 2) increases, the prior increasingly concentrates around the unit correlation matrix (i.e., favors smaller correlation: ones in the diagonals and values close to zero in the lower and upper triangles). At $\eta = 1$, the LKJ correlation distribution is uninformative (similar to $Beta(1,1)$), at $\eta < 1$, it favors extreme correlations (similar to $Beta(a < 1, b < 1)$).

4.1.6.3 Visualize the priors

As always, it is a good idea to visualize these priors. See Figure 37.

```
priors_alpha <- c(0,10)
priors_beta <- c(0,1)
priors_sigma_e <- c(0,1)
priors_sigma_u <- c(0,1)
```

```
priors_sigma_w <- c(0,1)

## code for visualizing lkj priors:
fake_data <- list(x = rnorm(30,0,1),
                  N = 30, R = 2)

stancode <- "
data {
  int<lower=0> N;
  real x[N];
  int R;
  }
parameters {
  real mu;
  real<lower=0> sigma;
}
model {
  x ~ normal(mu,sigma);
}
generated quantities {
  corr_matrix[R] LKJ05;
  corr_matrix[R] LKJ1;
  corr_matrix[R] LKJ2;
  corr_matrix[R] LKJ4;
  LKJ05 = lkj_corr_rng(R,.5);
  LKJ1 = lkj_corr_rng(R,1);
  LKJ2 = lkj_corr_rng(R,2);
  LKJ4 = lkj_corr_rng(R,4);
}
"

fitfake <- stan(model_code = stancode, pars = c("LKJ05","LKJ1","LKJ2","LKJ4"),
                data = fake_data, chains = 4,
                iter = 2000)

corrs<-extract(fitfake,pars=c("LKJ05[1,2]","LKJ1[1,2]","LKJ2[1,2]","LKJ4[1,2]"))
```

```
op<-par(mfrow=c(2,3),pty="s")
par(oma = rep(0, 4),
    mar = c(2.7, 2.7, 0.1, 0.1),
    mgp = c(1.7, 0.4, 0))
b<-seq(-priors_alpha[2]*2,
       priors_alpha[2]*2,by=0.01)
plot(b,dnorm(b,mean=priors_beta[1],
```

```
              sd=priors_beta[2]),
     type="l",ylab="density",
     xlab=expression(alpha),ylim=c(0, 0.5))
plot(b,dnorm(b,mean=priors_beta[1],
              sd=priors_beta[2]),
     type="l",ylab="density",
     xlab=expression(beta),ylim=c(0, 0.5))
sig<-seq(0,priors_sigma_e[2]*3,by=0.01)
plot(sig,dnorm(sig,mean=priors_sigma_e[1],
               sd=priors_sigma_e[2]),type="l",ylab="density",
     xlab=expression(sigma[e]))
plot(sig,dnorm(sig,mean=priors_sigma_u[1],
               sd=priors_sigma_u[2]),type="l",ylab="density",
     xlab=expression(sigma[u[0]]))
plot(sig,dnorm(sig,mean=priors_sigma_u[1],
               sd=priors_sigma_u[2]),type="l",ylab="density",
     xlab=expression(sigma[w[0,1]]))
plot(density(corrs[[3]],bw=0.15),
     ylab="density",xlab=expression(rho),
     xlim=c(-1,1),main="")
```

We will return later to the question of whether these priors are appropriate and reasonable (short answer: no).

4.1.7 Fit the model using brms

```
priors <- c(set_prior("normal(0, 10)", class = "Intercept"),
                      set_prior("normal(0, 1)", class = "b",
                                coef = "so"),
                      set_prior("normal(0, 1)", class = "sd"),
                      set_prior("normal(0, 1)", class = "sigma"),
                      set_prior("lkj(2)", class = "cor"))

m_gg<-brm(rawRT~so + (1+so|subject) + (1+so|item),gge1crit,family=lognormal(),
    prior=priors)
```

```
## Compiling the C++ model
```

```
## Start sampling
```

```
summary(m_gg)
```

```
##  Family: lognormal
##   Links: mu = identity; sigma = identity
## Formula: rawRT ~ so + (1 + so | subject) + (1 + so | item)
```

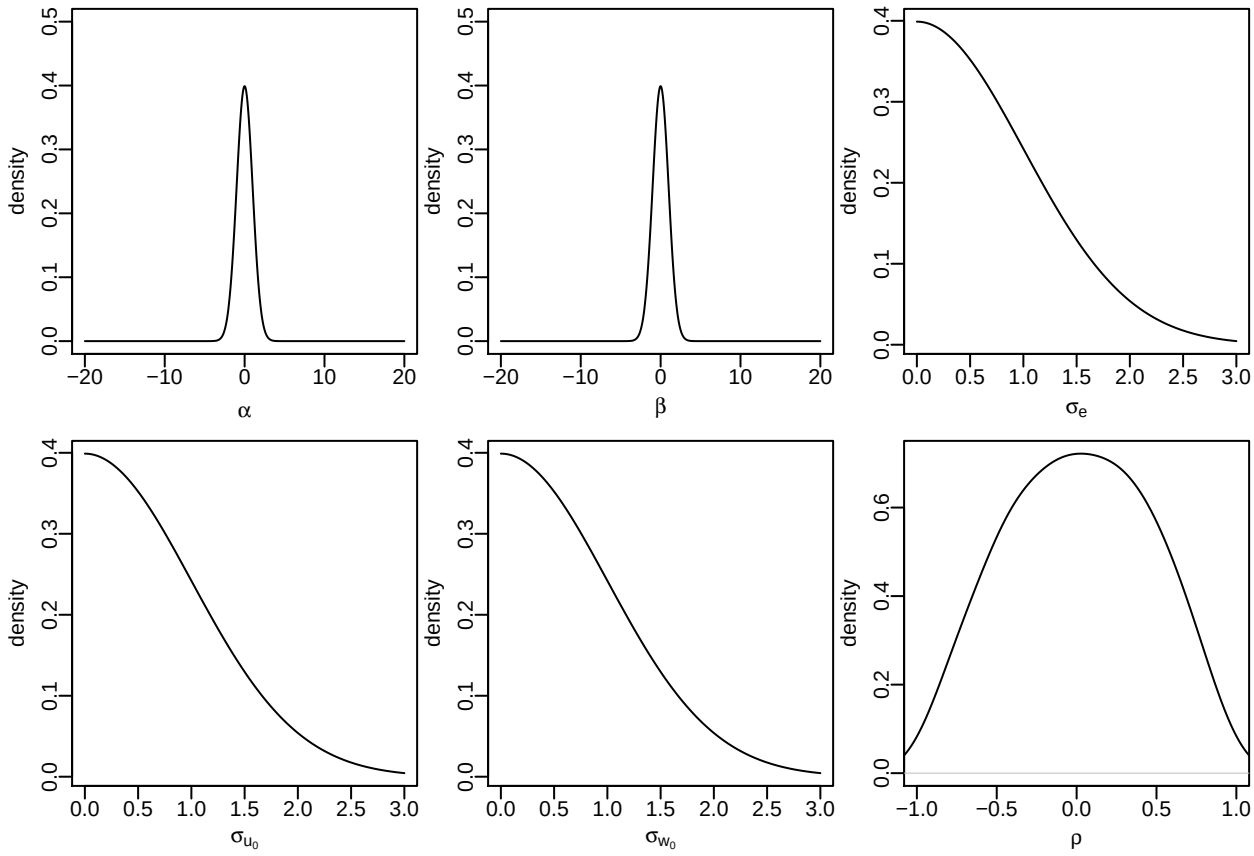


Figure 37: Priors for the Godner and Gibson data.

```
##    Data: gge1crit (Number of observations: 672)
## Samples: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
##          total post-warmup samples = 4000
##
## Group-Level Effects:
## ~item (Number of levels: 16)
##                   Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat
## sd(Intercept)         0.04      0.02     0.00     0.09       1359 1.00
## sd(so)                0.04      0.02     0.00     0.09       1513 1.00
## cor(Intercept,so)     0.29      0.41    -0.61     0.91       1825 1.00
##
## ~subject (Number of levels: 42)
##                   Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat
## sd(Intercept)         0.33      0.04     0.26     0.41        835 1.00
## sd(so)                0.11      0.02     0.07     0.16       1973 1.00
## cor(Intercept,so)     0.51      0.16     0.16     0.80       2082 1.00
##
## Population-Level Effects:
##           Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat
## Intercept     5.88      0.05     5.77     5.99        605 1.00
## so            0.06      0.03     0.01     0.11       1608 1.00
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat
## sigma     0.36      0.01     0.34     0.39       3343 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).
```

```
stanplot(m_gg,type="hist")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

Figure 38 shows the posterior distributions of the parameters on the log ms scale (for the coefficients and standard deviations). Notice that

- The object relative takes longer to read than the subject relative, as predicted. We know this because the parameter b_so is positive.
- The largest sources of variance are the subject intercepts, slopes, and the residual standard deviation. Look at the sd_subject parameters, and sigma.
- The by-item variance components are relatively small. Look at the sd_item parameters.
- The correlations have very wide uncertainty—the prior is dominating in determining the posteriors as there isn't that much data to obtain accurate estimates of these parameters. Look at the cor parameters.

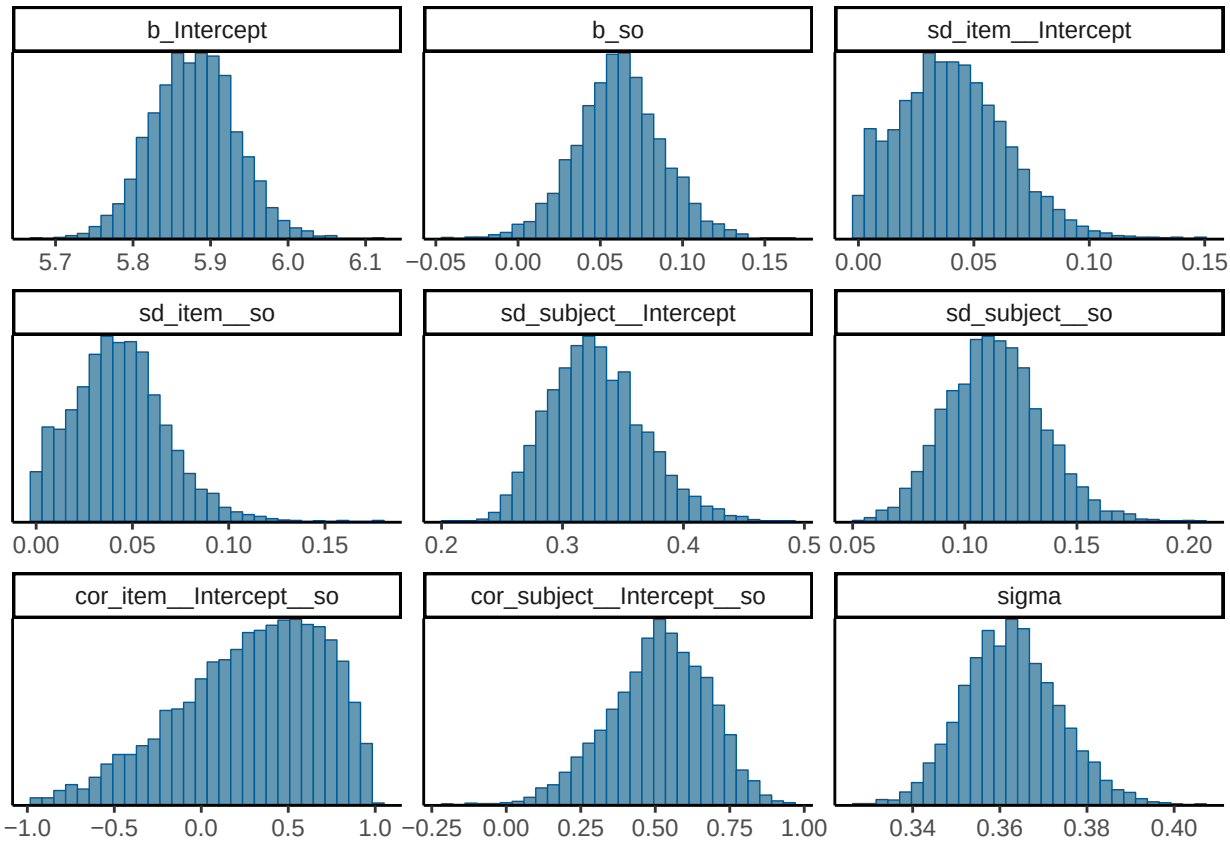


Figure 38: Posterior distributions of parameters in the Grodner and Gibson data.

4.1.8 Examine by subject random effects visually

First, extract the posterior samples of the parameters that we will need to compute individual differences.

```
library(bayesplot)
postgg<-posterior_samples(m_gg)
## extract variances:
alpha<-postgg$b_Intercept
beta<-postgg$b_so
cor<-posterior_samples(m_gg,"^cor")
sd<-posterior_samples(m_gg,"^sd")
sigma<-posterior_samples(m_gg,"sigma")

## item random effects won't be used below
item_re<-posterior_samples(m_gg,"^r_item")
subj_re<-posterior_samples(m_gg,"^r_subj")
```

4.1.8.1 By subject intercept adjustments

Figure 39 shows the adjustments to the intercept (α) by subject. This is on the log scale. Here, we are looking at the parameters u_0 in the model, which are assumed to be generated from $Normal(0, \sigma_{u0})$. The between subject variability is being captured here by this subject level parameter.

```
subjint<-subj_re[,1:42]
colnames(subjint)<-c(paste("u0,",1:42,sep=""))
intmns <- colMeans(subjint)
subjint<-subjint[,order(intmns)]
mcmc_areas(subjint)
```

4.1.8.2 By subject slope adjustments

Figure 40 shows the by-subject adjustments to the OR processing cost effect (β). Here, the assumption is that these adjustments are $u_1 \sim Normal(0, \sigma_{u_1})$.

```
subjslope<-subj_re[,(1:42)+42]
colnames(subjslope)<-c(paste("u1,",1:42,sep=""))
slopemns <- colMeans(subjslope)
subjslope<-subjslope[,order(slopemns)]
mcmc_areas(subjslope)
```

The correlation between u_0 and u_1 is represented by the correlation parameter ρ_u.

```
stanplot(m_gg,type="hist",
         pars="cor_subject__Intercept__so")
```

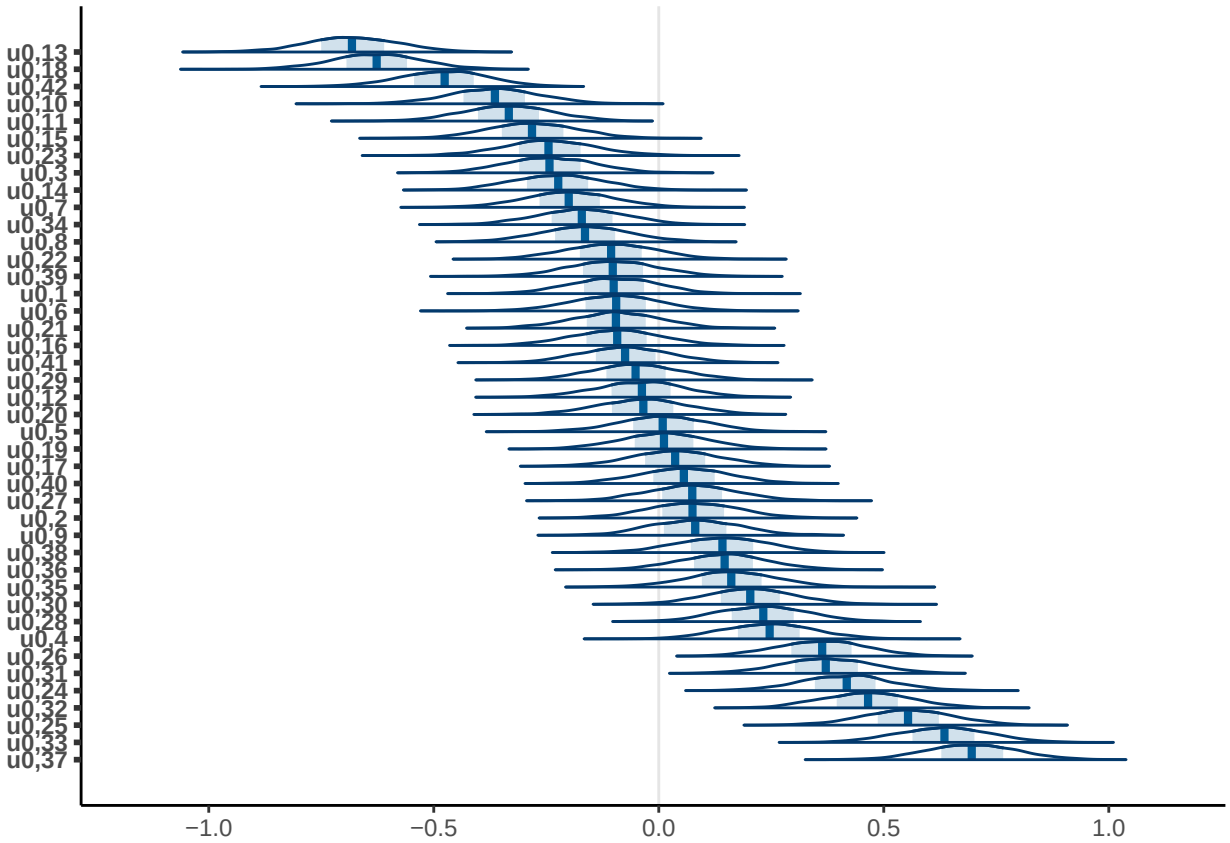


Figure 39: Variability in subject intercept adjustments in the Grodner and Gibson data.

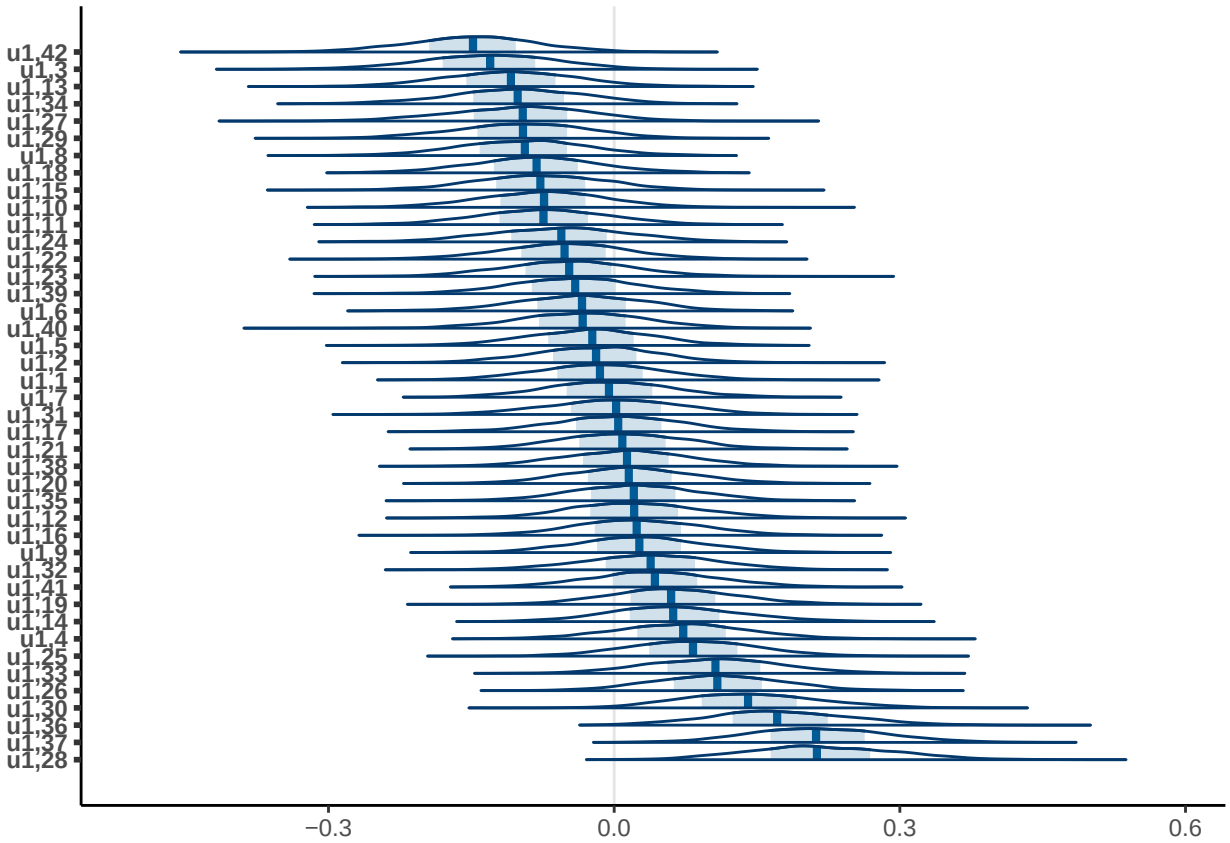


Figure 40: Variability in subject slope adjustments in the Grodner and Gibson data.

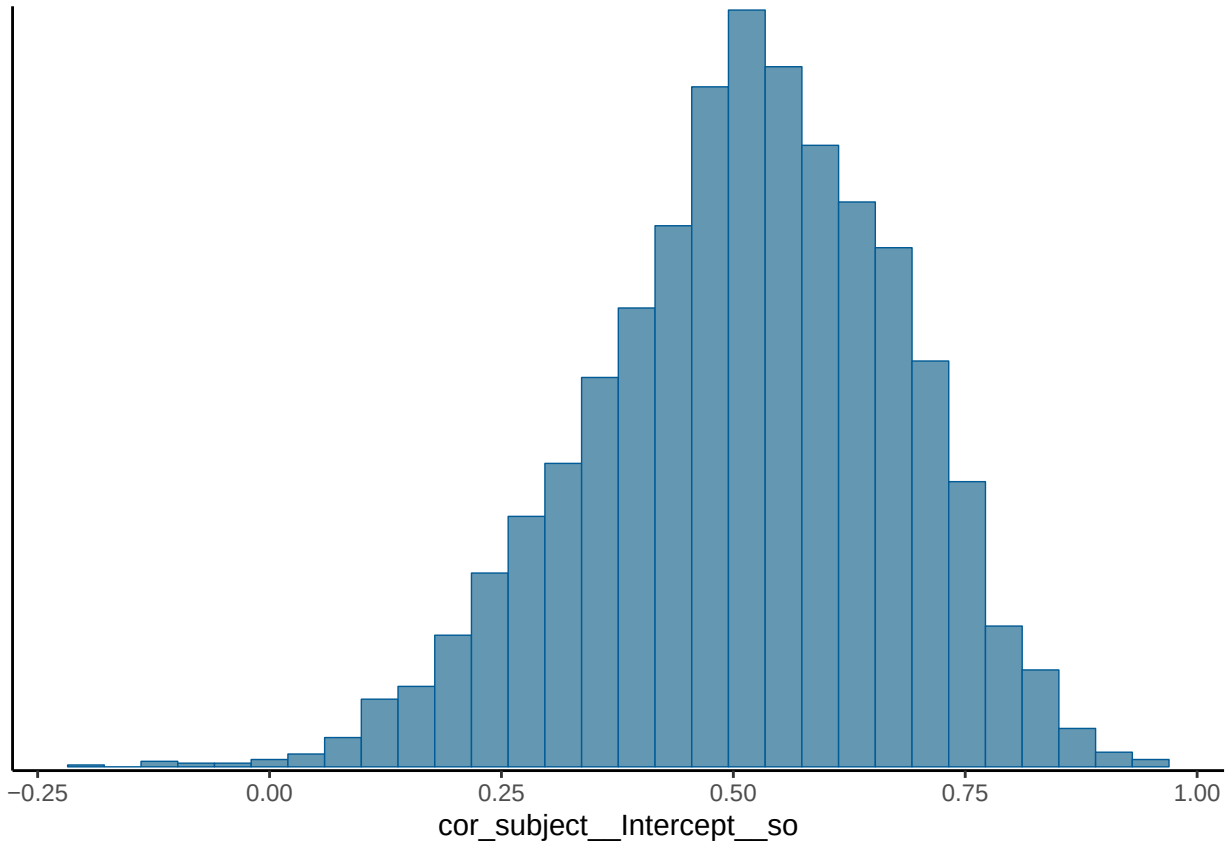


Figure 41: Posterior distributions of subject varying intercept and slope correlation parameter in the Grodner and Gibson data.

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

4.1.9 Examine mean and individual differences on the raw ms scale

It is useful to see the effects on the raw ms scale. The log ms scale is difficult to interpret.

4.1.9.1 Mean difference

In psychology and linguistics, undue emphasis is paid on reporting the overall mean effect. Figure 42 shows this—there seems to be a clear OR processing cost effect.

```
meandiff<- exp(alpha + beta) - exp(alpha - beta)
mean(meandiff)
```

```
## [1] 44.2876
```

```
round(quantile(meandiff,prob=c(0.025,0.975)),0)
```

```
##  2.5% 97.5%
```

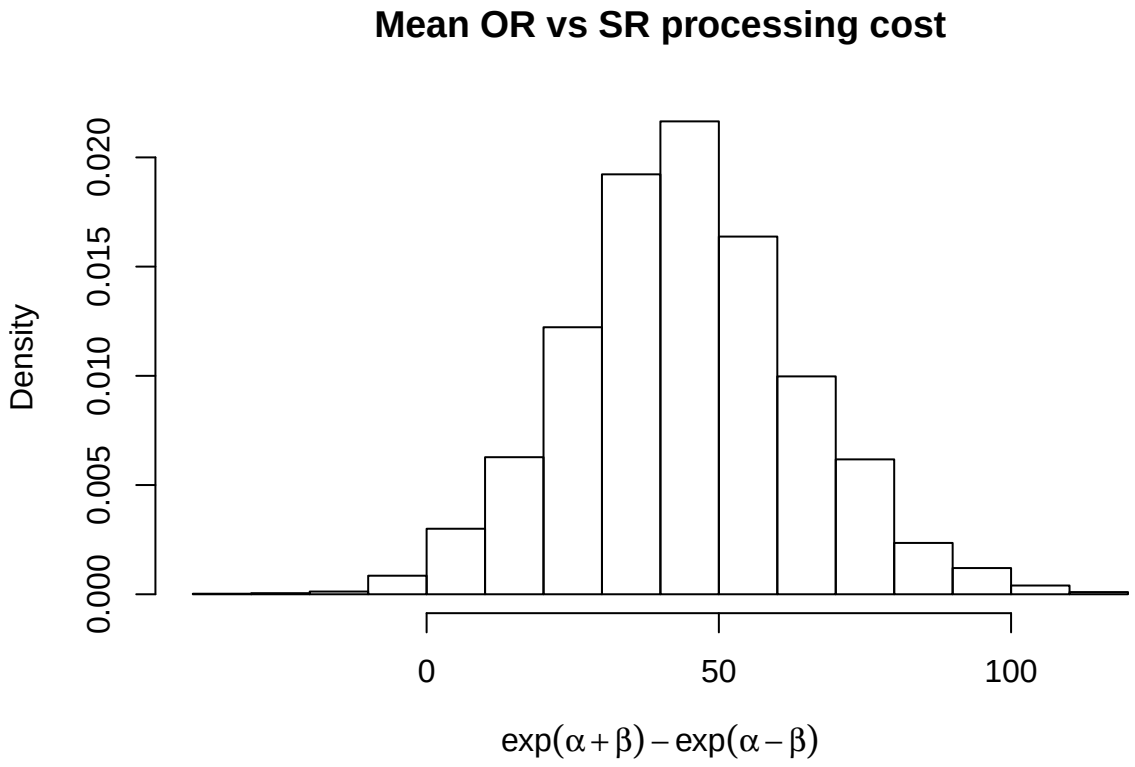


Figure 42: Mean OR processing cost effect in the Grodner and Gibson data.

```
##     7    85
```

Plot the histogram of the object relative processing cost in ms:

```
hist(meandiff,freq=FALSE,
     main="Mean OR vs SR processing cost",
     xlab=expression(exp(alpha + beta)- exp(alpha - beta)))
```

4.1.9.2 Individual effects of OR processing cost

However, only three out of 42 subjects show clear evidence for OR processing cost. See Figure 43.

```
subjdiff<-matrix(rep(NA,42*4000),nrow=42)
for(i in 1:42){
subjdiff[i,]<-exp(alpha + subj_re[,i]  + (beta+subj_re[,i+42])) -
  exp(alpha + subj_re[,i] -
        (beta+subj_re[,i+42]))
}

subjdiff<-t(subjdiff)

subjdiff<-as.data.frame(subjdiff)
colnames(subjdiff)<-paste("s",c(1:42),sep="")
```

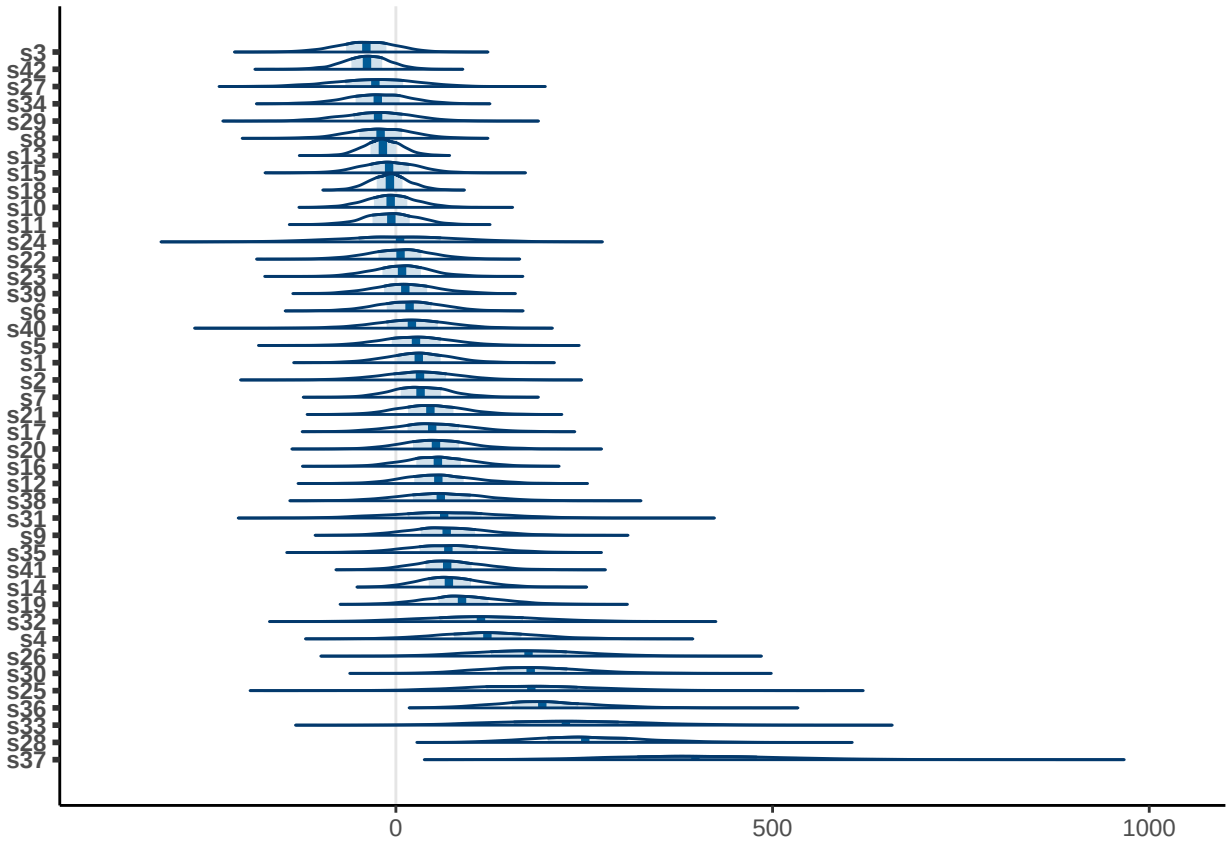


Figure 43: Variability in subject OR processing cost effect in the Grodner and Gibson data.

```
mns <- colMeans(subjdiff)
subjdiff<-subjdiff[,order(mns)]
mcmc_areas(subjdiff)
```

This illustrates a point that Blastland and Spiegelhalter (2014) make: "The average is an abstraction. The reality is variation." Any theory of sentence processing would have to be able to reproduce the pattern of individual differences observed, with only a few participants showing an OR processing cost and the majority showing equivocal conclusions. The average effect doesn't represent the behavior of many individuals in this sample.

4.1.10 To make discovery claims, calibrate the true and false discovery rate

Suppose that, based on these data and this model, we want to claim that there is a mean OR processing cost in English. In order to make a discovery claim, we need to understand the **true discovery rate** of this effect. In the frequentist world, this would be the *statistical power*, the probability of detecting an effect if there is in fact one.

First, we write a function to generate fake data:

```
library(MASS)
gen_fake_lnorm <- function(nitem=16,nsubj=42,
alpha=NULL,beta=NULL,
                           Sigma_u=NULL,Sigma_w=NULL,sigma_e=NULL){
  ## prepare data frame for two condition in a latin square design:
g1<-data.frame(item=1:nitem,
                 cond=rep(c("objgap","subjgap"),nitem/2))
g2<-data.frame(item=1:nitem,
                 cond=rep(c("objgap","subjgap"),nitem/2))

## assemble data frame in long format:
gp1<-g1[rep(seq_len(nrow(g1)),
              nsubj/2),]
gp2<-g2[rep(seq_len(nrow(g2)),
              nsubj/2),]

fakedat<-rbind(gp1,gp2)

## add subjects:
fakedat$subj<-rep(1:nsubj,each=nitem)
fakedat<-fakedat[,c(3,1,2)]
fakedat$so<-ifelse(fakedat$cond=="objgap",1,-1)

## subject random effects:
  u<-mvrnorm(n=length(unique(fakedat$subj)),
             mu=c(0,0),Sigma=Sigma_u)
  ## item random effects
  w<-mvrnorm(n=length(unique(fakedat$item)),
             mu=c(0,0),Sigma=Sigma_w)
  ## generate data row by row:
  N<-dim(fakedat)[1]
  rt<-rep(NA,N)
  for(i in 1:N){
    rt[i] <- rlnorm(1,alpha +
                      u[fakedat[i,]$subj,1] +
                      w[fakedat[i,]$item,1] +
                      (beta+u[fakedat[i,]$subj,2]+
                         w[fakedat[i,]$item,2])*fakedat$so[i],
                    sigma_e)}
  fakedat$rt<-rt
  fakedat$subj<-factor(fakedat$subj); fakedat$item<-factor(fakedat$item)
  fakedat}
```

Next, we extract the parameter means from the Bayesian model, and assemble the variance covari-

ance matrices for the subject and item random effects.

```
sds<-colMeans(sd)
cors<-colMeans(cor)
sig<-mean(sigma$sigma)
Sigma_u<-diag(sds[3:4]^2)
Sigma_u[1,2]<-Sigma_u[2,1]<-cors[2]*sds[3]*sds[4]
Sigma_w<-diag(sds[1:2]^2)
Sigma_w[1,2]<-Sigma_w[2,1]<-cors[1]*sds[1]*sds[2]
```

Then, we run 50 simulations, computing the 95% credible interval of the OR processing cost effect. Because this is a very time-consuming calculation, we are going to use previously computed values.

```
nsim<-50
betaquants<-matrix(rep(NA,nsim*2),ncol =2)
betameans<-matrix(rep(NA,nsim),ncol =2)

for(i in 1:nsim){
gg_fake<-gen_fake_lnorm(alpha=mean(alpha),
                        beta=mean(beta),
                Sigma_u=Sigma_u,Sigma_w=Sigma_w,
                sigma_e=sig)

m_gg_fake<-brm(rt~so + (1+so|subj) + (1+so|item),gg_fake,family=lognormal(),
    prior=priors,
    control = list(adapt_delta = 0.99,max_treedepth=15))
betapost<-posterior_samples(m_gg_fake)$b_so
betaquants[i,]<-quantile(betapost,prob=c(0.025,0.975))
betameans[i]<-mean(betapost)
}
save(betameans,
     file="data/truediscoverymeans.Rda")
save(betaquants,
     file="data/truediscoveryquants.Rda")
```

This simulation gives us an estimate of the proportion of times we would be able to detect an effect with 16 items and 42 subjects, assuming that the Grodner and Gibson data reflect a real difference between the two relative clause types.

Assuming that we are willing to declare an effect just in case 0 is not included in the 95% credible interval of the effect, the above simulation shows that we would detect the effect in only half of the repeated experiments.

```
> length(which(betaquants[,1]>0))/50
[1] 0.5
```

Thus, the true discovery rate is quite low. One would want the true discovery rate to be at least 80%.

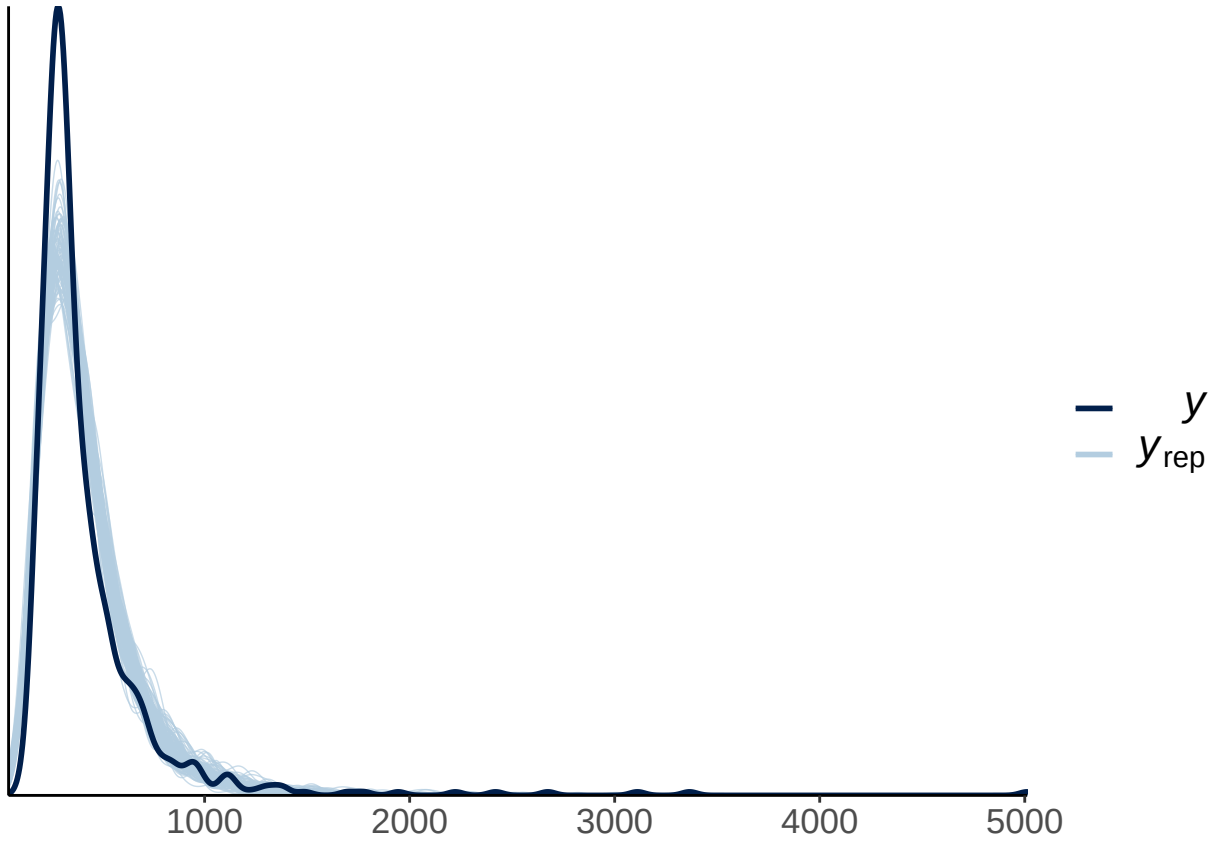


Figure 44: Posterior predictive check for the Grodner and Gibson data.

We can also investigate the false discovery rate—the proportion of times we would declare that we found an effect, when there is none. In frequentist statistics, this is called Type I error. The only change needed in the above simulation is to set β to 0, to reflect the assumption that there is no effect.

4.1.11 Posterior predictive checks

Figure 44 shows that we have reasonable coverage over the observed data.

```
pp_check(m_gg, nsamples = 100)+
  theme(text = element_text(size=16),
        legend.text=element_text(size=16))
```

4.2 Example 2: Question-response accuracies (Logistic regression)

The Grodner and Gibson (2005) data also has question-response accuracies: 1 if the response to a question following the sentence was correct, 0 otherwise. We show only the relevant columns below:

```
head(gge1crit[,c(1,2,3,8,11)])
```

```
##    subject item condition qcorrect so
## 6        1    1    objgap        0  1
## 19       1    2   subjgap        1 -1
## 34       1    3    objgap        0  1
## 49       1    4   subjgap        1 -1
## 68       1    5    objgap        1  1
## 80       1    6   subjgap        1 -1
```

One could aggregate the accuracy by item, and then just fit a hierarchical linear model:

```
meanp<-with(gge1crit,tapply(qcorrect,
                    IND=list(condition,subject),
                    mean))
q_df<-data.frame(subj=rep(c(1:42),2),
           so=rep(c(1,-1),each=42),
           p=c(meanp[1,],meanp[2,]))

head(q_df)
```

```
##   subj so     p
## 1    1  1 0.750
## 2    2  1 0.875
## 3    3  1 1.000
## 4    4  1 1.000
## 5    5  1 0.875
## 6    6  1 1.000
```

```
mqlmer<-lmer(p~so+(1|subj),q_df)
summary(mqlmer)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: p ~ so + (1 | subj)
##    Data: q_df
##
## REML criterion at convergence: -97.6
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.0372 -0.7770 -0.0706  0.9182  1.2008
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  subj     (Intercept) 0.000    0.000
##  Residual             0.016    0.126
```

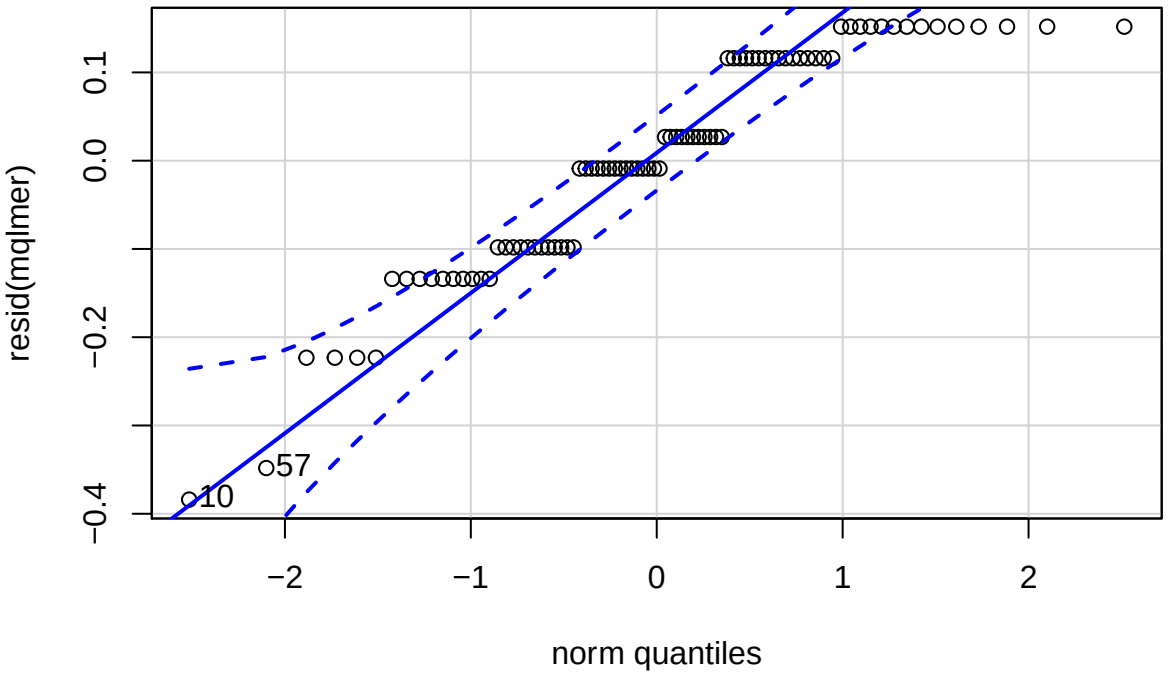


Figure 45: Residuals of the aggregated accuracy model for the question responses in the Grodner and Gibson data.

```
## Number of obs: 84, groups:  subj, 42
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)   0.8661     0.0138   62.79
## so            0.0179     0.0138    1.29
##
## Correlation of Fixed Effects:
##    (Intr)
## so 0.000
```

Figure 45 shows that the residuals don't really look particularly normal: the model assumption that $\varepsilon \sim Normal(0, \sigma)$ is difficult to defend.

```
library(car)
qqPlot(resid(mqlmer))
```

```
## [1] 10 57
```

Furthermore, think about the generative process; a 0,1 response is best seen as generated by a Bernoulli distribution with probability of success p: response $\sim Bernoulli(p)$.

One can therefore model each 0,1 response as being generated from a Bernoulli distribution, which is just a Binomial with a single trial. Thus, what is of interest is the probability of correct responses in subject vs object relatives:

```
round(100*with(gge1crit,
               tapply(qcorrect,condition,mean)))
```

```
##  objgap subjgap
##      88      85
```

We will transform the probability p of a correct response to a log-odds:

$$\log \frac{p}{1-p} \tag{203}$$

and assume that the log-odds of a correct response is affected by the relative clause type:

$$\log \frac{p}{1-p} = \alpha + \beta * so \tag{204}$$

This model is called a *logistic* regression because it uses the logistic or logit function to transform p to log odds space. Notice that there is no residual term in this model.

We can fit the above model easily using brms:

```
m_gg_q1<-brm(qcorrect~so,gge1crit,family=bernoulli(link="logit"))
```

```
## Compiling the C++ model
```

```
## Start sampling
```

```
summary(m_gg_q1)
```

Obviously, because the question-response data are also repeated measures, we must use a hierarchical linear model, with varying intercepts and slopes for subject and item, as in Example 1:

```
m_gg_q2<-brm(qcorrect~so+(1+so|subject) + (1+so|item),
             gge1crit,family=bernoulli(link="logit"))
```

```
## Compiling the C++ model
```

```
## Start sampling
```

```
summary(m_gg_q2)
```

This model is not especially good because many of the response accuracies are at ceiling. However, in principle this kind of model is appropriate for binary responses.

4.2.1 Convert posteriors back to probability space

What is theoretically important is the posterior distribution of the difference between object and subject relative response accuracy. That is on the probability scale. We can go from log-odds space

to probability space by solving this equation for p.

Using simple algebra, we can go from:

$$\log \frac{p}{1-p} = \alpha + \beta * so = \mu \tag{205}$$

to:

$$p = \exp(\mu)/(1+\exp(\mu)) \tag{206}$$

For object gap sentences, the factor *so* is coded as 1, so we have $\mu = \alpha + \beta$. For subject gap sentences, *so* is coded as -1, so we have $\mu = \alpha - \beta$. Therefore, we just need to plug in the expression for μ for object and subject relatives.

We can now straightforwardly plot the posterior distribution of the difference between object and subject relatives. See Figure 46. We see that there isn't any important difference between the two relative clause types.

```
postq<-posterior_samples(m_gg_q2)
alpha<-postq$b_Intercept
beta<-postq$b_so
mu_or<-alpha+beta
probor<-exp(mu_or)/(1+exp(mu_or))
mu_sr<-alpha-beta
probsr<-exp(mu_sr)/(1+exp(mu_sr))

hist(probor-probsr,freq=FALSE)
abline(v=0,lwd=2)
```

4.3 Exercises

1. Load the following two data-sets: gibsonwu2012data.txt, which is a data-set from Gibson and Wu (2013). This is self-paced reading data from Chinese relative clauses. The research question is whether Chinese is like English (does Chinese show an OR processing cost or not). The replication data, gibsonwu2012datarepeat.txt, is from Vasishth et al. (2013). This data uses the same items as in Gibson and Wu's study, but it has new subjects.

To load the data, run the following code:

```
## load first data-set:
gw<-read.table("data/gibsonwu2012data.txt",
                header=TRUE)
## code predictor:
gw$so <- ifelse(
  gw$type%in%c("subj-ext"),-1,1)
```

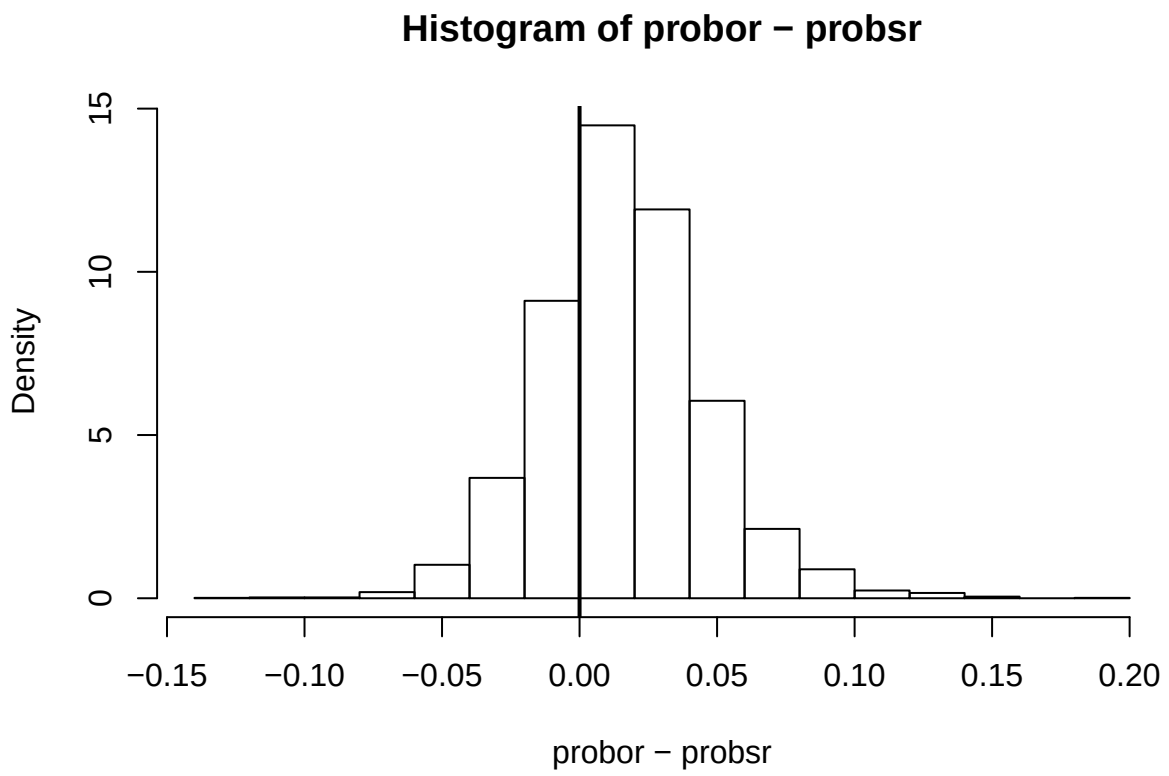


Figure 46: The difference in question-response accuracies between object and subject relatives.

```
## subset critical region
gw1<-subset(gw,region=="headnoun")

gw2<-read.table("data/gibsonwu2012datarepeat.txt",
                header=TRUE)
```

For each of the two data-sets, do the following:

- Does the experiment have a Latin square design? Are the data balanced (equal number of cases for subject and object relatives from each subject)? Why or why not?
- Plot the distribution of the reading times. Is it skewed or normally distributed?
- First re-read 4.1.5. Write down in mathematical notation the maximal hierarchical linear model, with varying intercepts and slopes for subjects and items in order to investigate the effect of relative clause type on reading time. Assume a Log-Normal likelihood.
- Fit the model using brms. Use Normal(0,10) as a prior for the intercept, and Normal(0,1) priors for the other parameters. For correlations, use LKJ(2).
- Plot the posterior distributions of all parameters.
- Carry out diagnostic checks (trace plots, etc.) to make sure that the model converged.
- Carry out a posterior predictive check. Does the model's predicted data approximately match

the observed data?

- Plot individual subjects' effects. Do all subjects show consistent patterns?
- Now carry out the same steps as above for the replication of the Gibson and Wu study, published in .

Are the posterior distributions of the OR processing effect in the original Gibson and Wu data and the replication data similar in magnitude and in the width of the 95% credible interval?

2. Re-read section 4.1.10 first. Using the fake-data simulation method described in the notes, determine the *true discovery rates* and *false discovery rates* for the Gibson and Wu data and the replication data. For true discovery rate, assume a true OR processing effect of 0.04 on the log ms scale in both data-sets, and 30 subjects and 16 items (this computation will take some time, so do it overnight). The other parameters can be estimated from the respective data-set. False discovery rate refers to the proportion of times you would declare that an effect is present, in the case where there is no effect. Thus, the OR processing cost (the β parameter) would have to be assumed to be 0. As a criterion for declaring a discovery, assume that the 95% credible interval excludes zero.

3. The goal of this exercise is to become familiar with fitting models that have a more complex design than the simple two-condition experiments we have considered so far. Here we will fit a 2×2 repeated measures factorial design from Experiment 1 of Husain, Vasishth, and Srinivasan (2014). This was also a self-paced reading study on relative clauses. The dependent variable was the reading time *rt* of the relative clause verb, just like in the Grodner and Gibson (2005) study on English. The factors were relative clause type, which we code with the predictor *RCType* ($RCType = +1$ for object relatives and $RCType = -1$ for subject relatives) and distance between the head noun and the relative clause verb, which we code with the predictor *dist* ($dist = +1$ for long distance and $dist = -1$ for short distance). Their interaction is coded with the predictor *int*. The 60 subjects were speakers of Hindi, an Indo-Aryan language spoken primarily in India. The 24 items were presented in a standard Latin square design. This resulted in a total of 1440 data points. The first few lines from the data frame are shown below.

```
husain<-read.table("data/HusainEtAlexpt1data.txt",header=TRUE)
head(husain[,c(1,3,8,11,12,13)])
```

```
##     subj item   rt RCType dist int
## 103    1   14  438     -1   -1   1
## 121    1   16  531      1   -1  -1
## 154    1   15  422      1    1   1
## 171    1   18 1000     -1   -1   1
## 219    1    4  344      1   -1  -1
## 325    1   17  406     -1    1  -1
```

Our theoretical interest is in determining whether relative clause type and distance influence reading time, and whether there is an interaction between these two factors. We will use brms to determine the posterior probability distribution of the fixed effect β_1 for relative clause type, the fixed effect

β_2 for distance, and their interaction β_3.

Fit a varying intercepts, varying slopes model (maximal model) to this data-set. The model you should fit is:

```
m_husain <- brm(rt~ RCType + dist + int +
                  (1+RCType + dist + int|subj)+
                  (1+RCType + dist + int|item),
                husain,family=lognormal())
```

- First re-read 4.1.9. Extract the posteriors of the effect of RCType, dist, and int, and then transform them to the raw ms scale. Display the posterior distributions on the ms scale.

- Review the contrast coding mentioned above for the three predictors. What is the scientific interpretation of the posterior distributions computed above? Are object relatives easier or harder to process? What is the effect of distance on reading time? Is there any indication of an interaction between these two factors?

5 Model comparison and selection

5.1 Introduction

Bayes' rule can be written with reference to a specific statistical model M_1. D refers to the data. θ is the parameter, or vector of parameters.

$$P(\theta \mid D, M_1) = \frac{P(D \mid \theta, M_1) P(\theta \mid M_1)}{P(D \mid M_1)} \tag{207}$$

$P(D \mid M_1)$ is the likelihood, and is a single number that tells you the likelihood of the observed data D given the model M_1 (and only in the discrete case, it tells you the probability of the observed data D given the model). Obviously, you would prefer a model that gives a higher likelihood. For example, and speaking informally, if you have data that were generated from a Normal(0,1) distribution, then the likelihood of the data given that $\mu = 0$ will be higher than the likelihood given some other value like $\mu = 10$. The higher likelihood is telling us that the underlying model is more likely to have produced the data. So we would prefer the model with the higher likelihood: we would prefer Normal(0,1) over Normal(10,1) as the presumed distribution that generated the data.

```
x<-rnorm(100)
sum(dnorm(x,mean=0,sd=1,log=TRUE))
```

```
## [1] -129
```

```
sum(dnorm(x,mean=10,sd=1,log=TRUE))
```

```
## [1] -5233
```

One way to compare two models M_1 and M_2 is to use the Bayes factor:

$$BF_{12} = \frac{P(D \mid M_1)}{P(D \mid M_2)} \tag{208}$$

In essence, the Bayes factor is a likelihood ratio. (If you have studied frequentist linear modeling, you would have encountered the likelihood ratio test, otherwise known as the ANOVA.)

How to compute the likelihood? Consider the simple binomial case where we have a subject answer 10 questions, and they get 9 right. That's our data.

5.1.1 Discrete example

Assuming a binomial likelihood function, $Binomial(n, \theta)$, the two models we will compare are

- M_1, the parameter has a point value $\theta = 0.5$ with probability 1 (a very sharp prior), and
- M_2, the parameter has a vague prior $\theta \sim Beta(1,1)$. Recall that this $Beta(1,1)$ distribution is $Uniform(0,1)$.

The likelihood under M_1 is:

$$\binom{n}{k}\theta^9(1-\theta)^1 = \binom{10}{9}0.5^{10} \tag{209}$$

We already know how to compute this:

```
(probDataM1<-dbinom(9,p=0.5,size=10))
```

```
## [1] 0.00977
```

The marginal likelihood under M_2 involves solving the following integral:

$$P(D \mid M_2) = \int P(D \mid \theta, M_2) P(\theta \mid M_2)\, d\theta \tag{210}$$

The integral is simply integrating out ("summing over") all possible values of the parameter θ. To see what summing over all possible values means, first consider a discrete version of this: suppose we say that our θ can take on only these three values: $\theta_1 = 0, \theta_2 = 0.5, \theta_3 = 1$, and each has probability $1/3$. Then, the marginal likelihood of the data given this prior specification of θ would be:

$$\begin{aligned} P(D \mid M) =& P(\theta_1)P(D \mid \theta_1) + P(\theta_2)P(D \mid \theta_2) + P(\theta_3)P(D \mid \theta_3) \\ =& \sum P(D \mid \theta_i, M) P(\theta_i \mid M) \end{aligned} \tag{211}$$

In our discrete example, this evaluates to:

```
res<-(1/3)* (choose(10,9)* (0)^9 * (1-0)^1) + (1/3)*
  (choose(10,9)* (0.5)^9 * (1-0.5)^1) + (1/3)* (choose(10,9)* (1)^9 * (1-1)^1)
res
```

```
## [1] 0.00326
```

This may be easier to read in mathematical form:

$$\begin{aligned} P(D \mid M) =& P(\theta_1)P(D \mid \theta_1) + P(\theta_2)P(D \mid \theta_2) + P(\theta_3)P(D \mid \theta_3) \\ =& \frac{1}{3}\left(\binom{10}{9}0^9(1-0)^1\right) + \frac{1}{3}\left(\binom{10}{9}0.5^9(1-0.5)^1\right) + \frac{1}{3}\left(\binom{10}{9}1^9(1-1)^1\right) \\ =& 0.003 \end{aligned} \tag{212}$$

Essentially, we are computing the marginal likelihood $P(D \mid M)$ by averaging the likelihood across possible parameter values (here, only three possible values), with the prior probabilities for each parameter value serving as a weight.

The Bayes factor for Model 1 vs Model 2 would then be

```
0.0097/0.003
```

```
## [1] 3.23
```

Model 1, which assumes that θ has a point value 0.5, is approximately three times more likely than the Model 2 with the vague Beta(1,1) prior over θ.

5.1.2 Continuous example

The integral shown above does essentially the calculation we show above, but summing over the entire continuous space that is the range of possible values of θ:

$$P(D \mid M_2) = \int P(D \mid \theta, M_2)P(\theta \mid M_2)\, d\theta \tag{213}$$

Let's solve this integral analytically. We need to know only one small detail from integral calculus: $\int_a^b x^9\, dx = [\frac{x^{10}}{10}]_a^b$. Similarly: $\int_a^b x^{10}\, dx = [\frac{x^{11}}{11}]_a^b$. Having reminded ourselves of how to solve this simple integral, we proceed as follows.

Our prior for θ is $Beta(\alpha = 1, \beta = 1)$:

$$\begin{aligned} P(\theta \mid M_2) =& \frac{\Gamma(\alpha+\beta)}{\Gamma(\alpha)\Gamma(\beta)}\theta^{\alpha-1}\theta^{\beta-1} \\ =& \frac{\Gamma(2)}{\Gamma(1)\Gamma(1)}\theta^{1-1}\theta^{1-1} \\ =& 1 \end{aligned} \tag{214}$$

So, our integral simplifies to:

$$\begin{aligned} P(D \mid M_2) &= \int_0^1 P(D \mid \theta, M_2)\, d\theta \\ &= \int_0^1 \binom{10}{9} \theta^9 (1-\theta)^1 \, d\theta \\ &= \int_0^1 \binom{10}{9} (\theta^9 - \theta^{10}) \, d\theta \\ &= 10 \left[\frac{\theta^{10}}{10} - \frac{\theta^{11}}{11} \right]_0^1 \\ &= 10 \times \frac{1}{110} = \frac{1}{11} \end{aligned} \tag{215}$$

So, when Model 1 assumes that the θ parameter is 0.5, and Model 2 has a vague prior $Beta(1,1)$on the θ parameter, our Bayes factor will be:

$$BF_{12} = \frac{P(D \mid M_1)}{P(D \mid M_2)} = \frac{0.01}{1/11} = 0.107 \tag{216}$$

Thus, the model with the vague prior (M2) is about 9 times more likely than the model with $\theta = 0.5$:

$$\frac{1}{0.107} = 9.309 \tag{217}$$

We could conclude that we have some evidence against the guessing model M1 in this case. Jeffreys (1998) has suggested the following decision criterion using Bayes factors. Here, we are comparing two models, labeled 1 and 2.

- $BF_{12} > 100$: Decisive evidence
- $BF_{12} = 32 - 100$: Very strong
- $BF_{12} = 10 - 32$: Strong
- $BF_{12} = 3 - 10$: Substantial
- $BF_{12} = 2 - 3$: Not worth more than a bare mention

5.2 Prior sensitivity

The Bayes factor is sensitive to the choice of prior. It is therefore important to do a sensitivity analysis with different priors.

For the model M_2 above, consider the case where we have a prior on θ such that there are 10 possible values for θ, 0.1, 0.2, 0.3,...,1, and the probabilities of each value of θ are 1/10.

```r
theta<-seq(0.1,1,by=0.1)
w<-rep(1/10,10)

prob<-rep(NA,length(w))
for(i in 1:length(theta)){
prob[i]<-(1/w[i])*choose(10,9)*theta[i]^9*(1-theta[i]^1)
}
## Likelihood for model M2 with
## new prior on theta:
sum(prob)
```

```
## [1] 8.29
```

Now the Bayes factor for M1 compared to M2 is:

```r
0.0097/sum(prob)
```

```
## [1] 0.00117
```

Now, model M2 is decisively more likely compared to model M1:

```r
1/(0.0097/sum(prob))
```

```
## [1] 854
```

This toy example illustrates the effect of prior specification on the Bayes factor. It is therefore very important to display the Bayes factor under both uninformative and informative priors for the parameter that we are interested in.

One should never use a single 'default' prior and report a single Bayes factor.

5.3 The Bayes factor is the ratio of posterior to prior odds

The Bayes factor is really the ratio of posterior odds vs prior odds for any given pair of models:

$$BF = \frac{\text{posterior odds}}{\text{prior odds}}$$

In the context of our problem:

$$\underset{\substack{\uparrow \\ posterior\ odds}}{\frac{P(M_1 \mid D)}{P(M_2 \mid D)}} = \underset{\substack{\uparrow \\ BF_{12}}}{\frac{P(D \mid M_1)}{P(D \mid M_2)}} \underset{\substack{\uparrow \\ prior\ odds}}{\frac{P(M_1)}{P(M_2)}} \tag{218}$$

So, when the prior odds for M_1 vs M_2 are 1 (i.e., when both models are a priori equi-probable), then we are just interested in computing the posterior odds for the two models.

5.4 The Savage-Dickey method

This method consists of computing the Bayes factor by dividing the height of the posterior for the parameter of interest, θ, by the height of the prior for θ at the specific point corresponding to some null hypothesis value $\theta = \theta_0$. Because we call the baseline model the null model, we label it M_0.

The Savage-Dickey method is based on a theorem whose proof appears in several published works (Verdinelli and Wasserman 1995).

5.4.1 Savage-Dickey Density ratio

Suppose that M_1 is a model with parameters $\theta = (\phi, \omega)$, and M_0 is a model that is a restricted version of M_1 with $\omega = \omega_0$ and free parameter ϕ. Suppose that the priors in the two models satisfy

$$f(\phi \mid M_0) = f(\phi \mid \omega = \omega_0, M_1) \tag{219}$$

[The above holds if ϕ and ω are independent under M_1, that is, if $f(\phi, \omega \mid M_1) = f(\phi \mid M_1) f(\omega \mid M_1)$.]

Then, Bayes factor of M_0 can be written as

$$BF_{01} = \frac{f(\omega = \omega_0 \mid D, M_1)}{f(\omega = \omega_0 \mid M_1)} \tag{220}$$

5.5 Computing Bayes Factors using the Savage-Dickey method

This example is taken from Lee and Wagenmakers (2014). Suppose we have within-subjects data for two conditions. The data represent increase in recall performance in a memory task from the same subject, once in winter and once in summer. Suppose one theory says that increase in recall performance is higher in summer, but an alternative theory claims that there is no difference between the two seasons. We will test the null vs alternative hypotheses using Bayes factors.

```
# Read data:
Winter <- c(-0.05,0.41,0.17,-0.13,0.00,-0.05,0.00,0.17,0.29,0.04,0.21,0.08,0.37,
            0.17,0.08,-0.04,-0.04,0.04,-0.13,-0.12,0.04,0.21,0.17,0.17,0.17,
            0.33,0.04,0.04,0.04,0.00,0.21,0.13,0.25,-0.05,0.29,0.42,-0.05,0.12,
            0.04,0.25,0.12)

Summer <- c(0.00,0.38,-0.12,0.12,0.25,0.12,0.13,0.37,0.00,0.50,0.00,0.00,-0.13,
            -0.37,-0.25,-0.12,0.50,0.25,0.13,0.25,0.25,0.38,0.25,0.12,0.00,0.00,
            0.00,0.00,0.25,0.13,-0.25,-0.38,-0.13,-0.25,0.00,0.00,-0.12,0.25,
            0.00,0.50,0.00)
```

Let's say we want to compare the evidence for two hypotheses: the difference between the two conditions (Winter and Summer) is

$H_0 : \delta = 0$ and $H_0 : \delta \neq 0$.

Normally, we would do a paired t-test. We get a non-significant result:

```
## not significant:
t.test(Winter,Summer,paired=TRUE)
```

```
##
##  Paired t-test
##
## data:  Winter and Summer
## t = 0.8, df = 40, p-value = 0.4
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.0536  0.1219
## sample estimates:
## mean of the differences
##                  0.0341
```

Equivalently, one can do a one sample test after taking the pairwise differences in scores:

```
d <- Winter - Summer

nsubj<-length(Winter)


t.test(d)
```

```
##
##  One Sample t-test
##
## data:  d
## t = 0.8, df = 40, p-value = 0.4
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##  -0.0536  0.1219
## sample estimates:
## mean of x
##    0.0341
```

We will now compute the Bayes factor, using the Savage-Dickey method. This will allow us to test the null against the alternative hypothesis.

5.6 Example 1

Prepare data:

```
d <- d / sd(d)        # standardize the paired difference of scores
ndata <- length(d)  # number of subjects

data <- list(x=d, ndata=ndata)  # to be passed on to Stan
```

We will now compute, using Stan, the Bayes Factor for the two hypotheses $H_0 : \delta = 0$ and $H_1 : \delta \neq 0$.

The model is:

- $\delta \sim Cauchy(0, 1)$
- $\sigma \sim Cauchy(0, 1)_{I(0,\infty)}$
- $\mu \leftarrow \delta\sigma$
- $x_i \sim Normal(\mu, \sigma^2)$

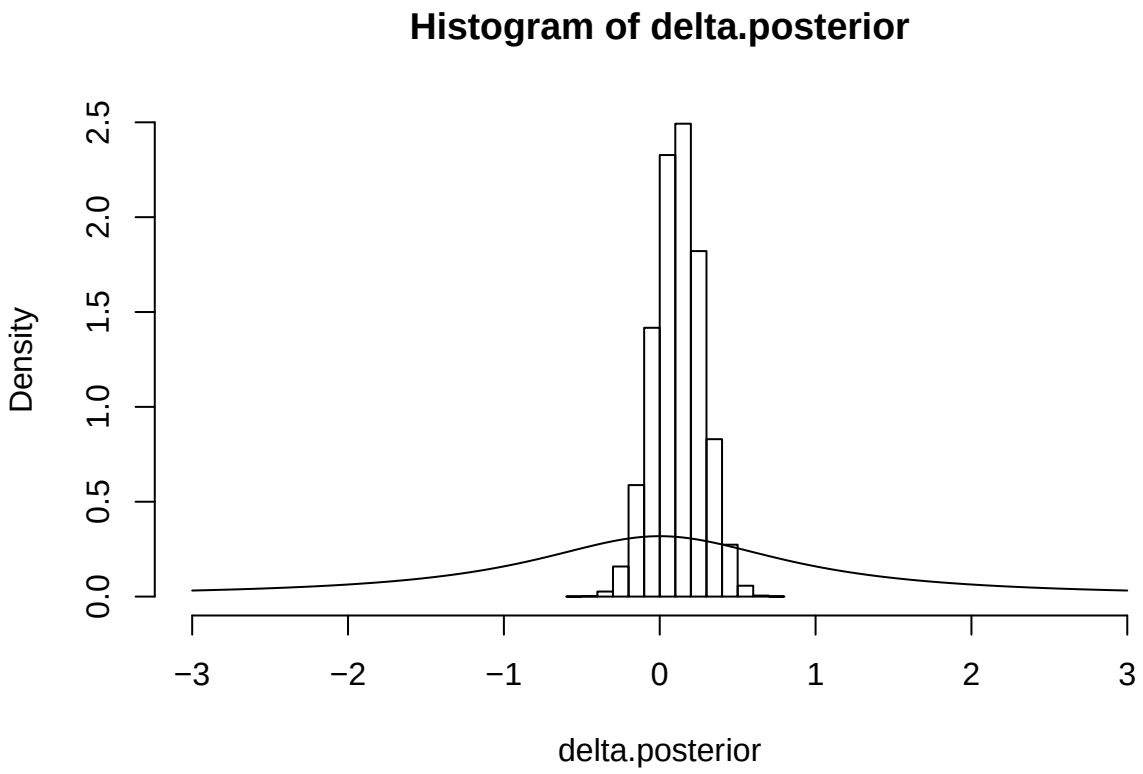
Define the model in Stan:

```
model_example1 <- "
// One-Sample Comparison of Means
data {
  int<lower=0> ndata;
  vector[ndata] x;
}
parameters {
  real sigmatmp;
  real delta;
}
transformed parameters {
  real mu;
  real<lower=0> sigma;
  sigma = fabs(sigmatmp);
  mu = delta * sigma;
}
model {
// delta and sigma come from (half) Cauchy Distributions
  sigmatmp ~ cauchy(0, 1);
  delta ~ cauchy(0, 1);
  // Data
  x ~ normal(mu, sigma);
}"
```

```
library(rstan)
# Parameters to be monitored
parameters <- c("delta")
```

```
samples <- stan(model_code=model_example1,
                data=data,
                iter=20000,
                chains=4)

# Collect posterior samples across all chains:
delta.posterior <- extract(samples,pars=parameters)$delta
```

```
hist(delta.posterior,freq=FALSE,xlim=c(-3,3))
x<-seq(-3,3,by=0.01)
lines(x,dcauchy(x))
```




```
#BFs based on logspline fit
library(polspline)
fit.posterior <- logspline(delta.posterior)

# 95% confidence interval:
x0 <- qlogspline(0.025,fit.posterior)
x1 <- qlogspline(0.975,fit.posterior)

posterior <- dlogspline(0, fit.posterior) # this gives the pdf at point delta = 0
prior     <- dcauchy(0)          # height of order-restricted prior at delta = 0
(BF01      <- posterior/prior)
```

```
## [1] 6.09
```

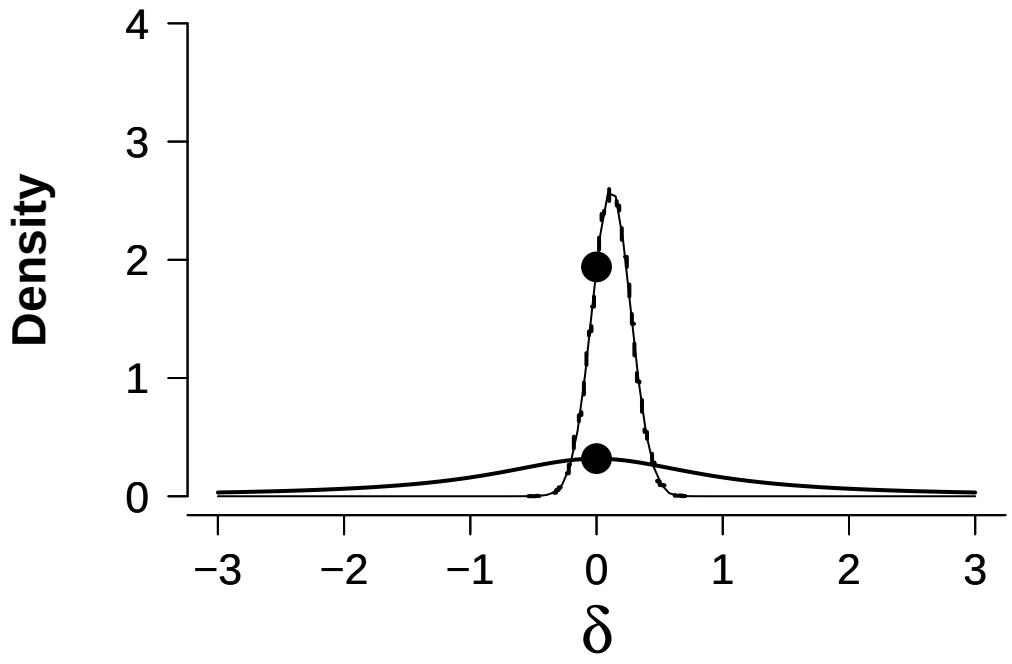


Figure 47: Shown are the prior and posterior densities on delta. The null hypothesis was that delta is 0, and we see that delta=0 has a value 6 times larger under the posterior compared to the prior. This means that the evidence for the null hypothesis that delta=0 is 6 times more than the alternative.

The odds of H_0 being true compared to H_1 are $6:1$.

5.6.1 Two methods for computing Bayes factors with brms

First, set up data as a data-frame:

```
library(brms)
y<-c(Winter,Summer)
#length(Winter)
n<-length(Summer)

cond<-factor(c(rep("winter",n),
        rep("summer",n)))
subject<-rep(rep(1:n),2)
dat<-data.frame(y,cond,subject)
head(dat)
```

```
##       y   cond subject
## 1 -0.05 winter       1
## 2  0.41 winter       2
## 3  0.17 winter       3
## 4 -0.13 winter       4
```

```
## 5  0.00 winter       5
## 6 -0.05 winter       6
```

Set priors:

```
priors0 <- c(set_prior("cauchy(0, 1)", class = "Intercept"),
                       set_prior("cauchy(0, 1)",
                                 class = "sd"),
                       set_prior("cauchy(0, 1)",
                                 class = "sigma"))

priors <- c(set_prior("cauchy(0, 1)", class = "Intercept"),
                       set_prior("cauchy(0, 1)",
                                 class = "b"),
                       set_prior("cauchy(0, 1)",
                                 class = "sd"),
                       set_prior("cauchy(0, 1)",
                                 class = "sigma"))
```

Using Savage-Dickey method (the hypothesis function in brms):

```
m_full <- brm(y ~ cond + (1|subject),
              data = dat,
              prior = priors,
              sample_prior = TRUE,
              iter = 10000,
        control=list(adapt_delta=0.99))
```

```
## Compiling the C++ model
```

```
## Start sampling
```

```
summary(m_full)
```

```
##  Family: gaussian
##   Links: mu = identity; sigma = identity
## Formula: y ~ cond + (1 | subject)
##    Data: dat (Number of observations: 82)
## Samples: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
##          total post-warmup samples = 20000
##
## Group-Level Effects:
## ~subject (Number of levels: 41)
##               Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat
## sd(Intercept)     0.04      0.03     0.00     0.10       7613 1.00
##
## Population-Level Effects:
##            Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat
```

```
## Intercept      0.07      0.03     0.01     0.13      27677 1.00
## condwinter     0.03      0.04    -0.05     0.12      32323 1.00
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat
## sigma     0.19      0.02     0.16     0.22      19473 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).
```

```
# H0: No effect of cond
BF_brms_m <- brms::hypothesis(m_full,
                        "condwinter = 0")
## Evidence for NULL model vs FULL model:
BF_brms_m$hypothesis
```

```
##         Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio
## 1 (condwinter) = 0   0.0339     0.042  -0.0482    0.116       6.38
##   Post.Prob Star
## 1     0.865
```

Using the bayes_factor function in brms:

```
m0<-brm(y~1+(1|subject),
        dat,prior=priors0,
        warmup=1000,
        iter=10000,
        save_all_pars = TRUE,
        control=list(adapt_delta=0.99))
```

```
## Compiling the C++ model
```

```
## Start sampling
```

```
m1<-brm(y~cond+(1|subject),
        dat,prior=priors,
        warmup=1000,
        save_all_pars = TRUE,
        iter=10000,
        control=list(adapt_delta=0.99))
```

```
## Compiling the C++ model
## Start sampling
```

```
bayes_factor(m0,m1)
```

```
## Iteration: 1
## Iteration: 2
```

```
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 6
## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
```

```
## Estimated Bayes factor in favor of bridge1 over bridge2: 22.00043
```

Notice that if you flip the order of the models in the function, the evidence is for the first model:

```
bayes_factor(m1,m0)
```

```
## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
```

```
## Estimated Bayes factor in favor of bridge1 over bridge2: 0.04535
```

5.7 Example 2

We will now compute, using Stan, the Bayes Factor for the two hypotheses $H_0 : \delta = 0$ and $H_1 : \delta \sim Cauchy(0,1)_{I(-\infty,0)}$.

The Bayesian model is:

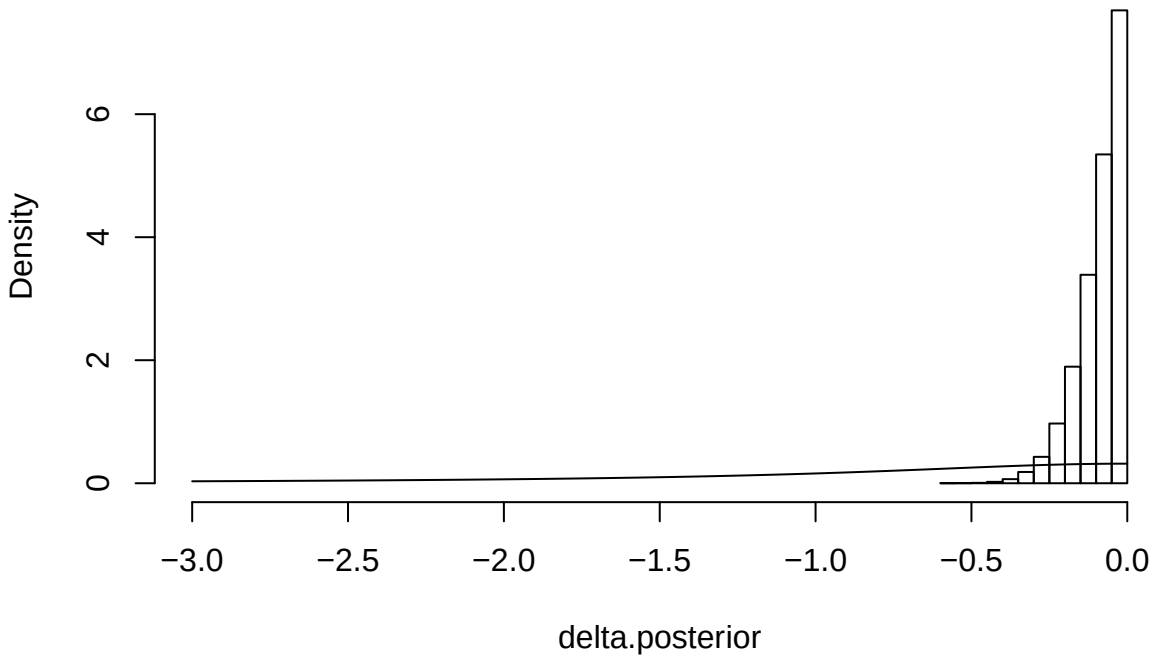
- $\delta \sim Cauchy(0,1)_{I(-\infty,0)}$
- $\sigma \sim Cauchy(0,1)_{I(0,\infty)}$
- $\mu \leftarrow \delta\sigma$
- $x_i \sim Normal(\mu, \sigma^2)$

```
## You could define initial values, but we
## will let Stan do this:
#myinits <- list(
#  list(delta=-abs(rnorm(1,0,1)), deltaprior=-abs(rnorm(1,0,1)), sigmatmp=.1),
#  list(delta=-abs(rnorm(1,0,1)), deltaprior=-abs(rnorm(1,0,1)), sigmatmp=.2),
#  list(delta=-abs(rnorm(1,0,1)), deltaprior=-abs(rnorm(1,0,1)), sigmatmp=.3))
```

```
# Parameters to be monitored
parameters <- c("delta")

model_example2 <- "
// One-Sample Comparison of Means
data {
  int<lower=0> ndata;
  vector[ndata] x;
}
parameters {
  real sigmatmp;
  real<upper=0> delta;
}
transformed parameters {
  real<lower=0> sigma;
  real mu;
  sigma = fabs(sigmatmp);
  mu = delta * sigma;
}
model {
  // Delta and sigma Come From (Half) Cauchy Distributions
  sigmatmp ~ cauchy(0, 1);
  delta ~ cauchy(0, 1);
  // Data
  x ~ normal(mu, sigma);
}"
```

```
## samples from model:
samples <- stan(model_code=model_example2,
                data=data,
                #init=myinits,
                pars=parameters,
                iter=30000,
                chains=4,
                control = list(adapt_delta = 0.99,max_treedepth=15))

# Collect posterior samples across all chains:
delta.posterior <- extract(samples)$delta
```

```
hist(delta.posterior,freq=FALSE,
     xlim=c(-3,0),main="Posterior distribution \n and prior (line)")
x<-seq(-3,0,by=0.001)
lines(x,dcauchy(x))
```



Now we compute the Bayes Factor, comparing the two hypotheses.

```
fit.posterior <- logspline(delta.posterior)

fit.posterior <- logspline(delta.posterior,ubound=0) # NB. note the bound

# 95% confidence interval:
x0 <- qlogspline(0.025,fit.posterior)
x1 <- qlogspline(0.975,fit.posterior)

posterior <- dlogspline(0, fit.posterior) # this gives the pdf at point delta = 0
prior     <- 2*dcauchy(0)       # height of order--restricted prior at delta = 0
(BF01      <- posterior/prior)
```

```
## [1] 15.5
```

According to this analysis, the null hypothesis $H_0 : \delta = 0$ being true is 15 times more likely than $H_1 : \delta \sim Cauchy(0,1)_{I(-\infty,0)}$.

```
#============ Plot Prior and Posterior  ============================
par(cex.main = 1.5, mar = c(5, 6, 4, 5) + 0.1, mgp = c(3.5, 1, 0), cex.lab = 1.5,
    font.lab = 2, cex.axis = 1.3, bty = "n", las=1)
xlow  <- -3
xhigh <- 0
yhigh <- 12
```

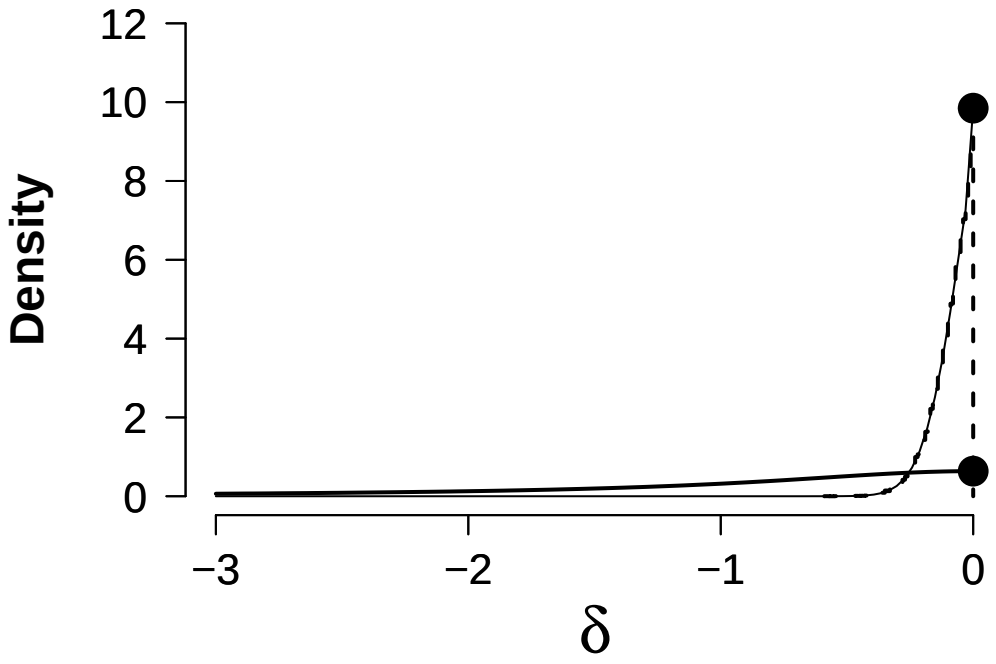


Figure 48: The prior and posterior densities.

```
Nbreaks <- 80
y       <- hist(delta.posterior, Nbreaks, plot=F)
plot(c(y$breaks, max(y$breaks)), c(0,y$density,0), type="S", lwd=2, lty=2,
     xlim=c(xlow,xhigh), ylim=c(0,yhigh), xlab=" ", ylab="Density", axes=F)
axis(1, at = c(-3,-2,-1,0), lab=c("-3","-2","-1","0"))
axis(2)
mtext(expression(delta), side=1, line = 2.8, cex=2)
#now bring in log spline density estimation:
par(new=T)
plot(fit.posterior, ylim=c(0,yhigh), xlim=c(xlow,xhigh), lty=1, lwd=1, axes=F)
points(0, dlogspline(0, fit.posterior),pch=19, cex=2)
# plot the prior:
par(new=T)
plot ( function( x ) 2*dcauchy( x, 0, 1 ), xlow, xhigh, ylim=c(0,yhigh),
       xlim=c(xlow,xhigh), lwd=2, lty=1, ylab=" ", xlab = " ", axes=F)
axis(1, at = c(-3,-2,-1,0), lab=c("-3","-2","-1","0"))
axis(2)
points(0, 2*dcauchy(0), pch=19, cex=2)
```

5.7.1 Try this out at home

Refit examples 1 and 2 with a different prior for σ. Does the Bayes Factor change in either case?

What happens when the prior for δ is changed to a suitable normal distribution?

5.7.2 Try this out at home

Estimate the Bayes factor for the hypotheses: $H_0 : \delta = 0$, and $H_1 : \delta \sim Cauchy(0,1)_{I(0,\infty)}$.

5.8 Example 3

Here is an example of a two-sample test.

The data:

```
x <- c(70,80,79,83,77,75,84,78,75,75,78,82,74,81,72,70,75,72,76,77)
y <- c(56,80,63,62,67,71,68,76,79,67,76,74,67,70,62,65,72,72,69,71)

n1 <- length(x)
n2 <- length(y)

# Rescale
y <- y - mean(x)
y <- y / sd(x)
x <- (x - mean(x)) / sd(x);

data <- list(x=x, y=y,
             n1=n1, n2=n2)
```

We could do an unpaired two-sample t-test:

```
t.test(x,y)
```

We see strong evidence against the null hypothesis.

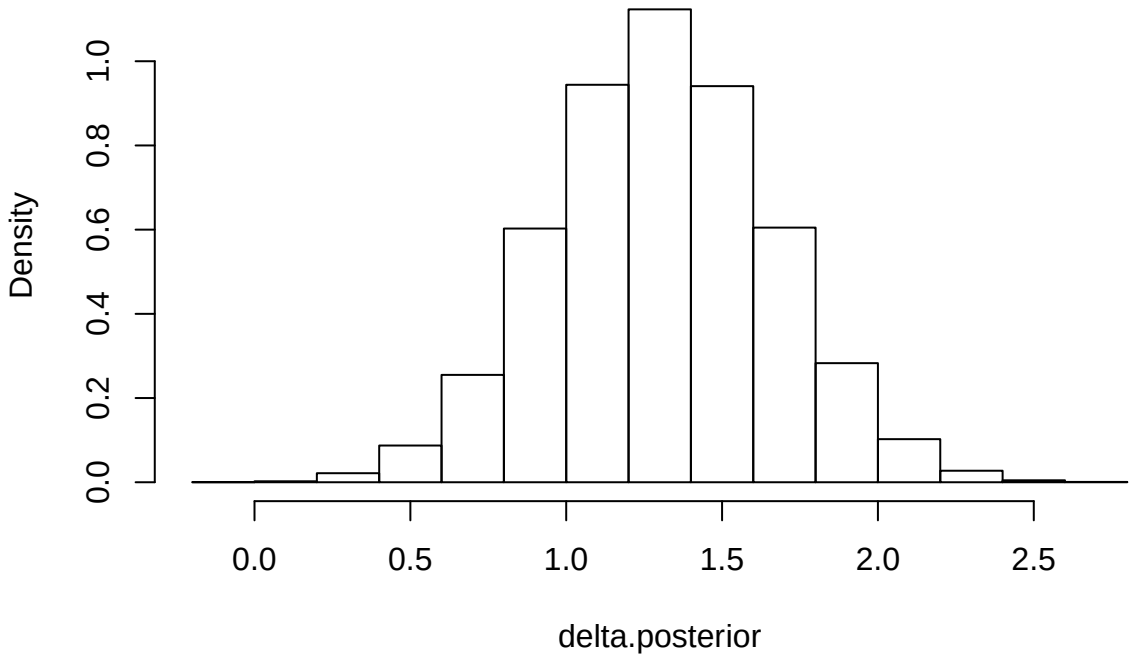
The Stan model:

```
model_example3 <- "
// Two-sample Comparison of Means
data {
  int<lower=1> n1;
  int<lower=1> n2;
  vector[n1] x;
  vector[n2] y;
}
parameters {
  real mu;
  real sigmatmp;
  real delta;
```

```
}
transformed parameters {
  real<lower=0> sigma;
  real alpha;
  sigma = fabs(sigmatmp);
  alpha = delta * sigma;
}
model {
  // Delta, mu, and sigma Come From (Half) Cauchy Distribution
  mu ~ cauchy(0, 1);
  sigmatmp ~ cauchy(0, 1);
  delta ~ cauchy(0, 1);
  // Data
  x ~ normal(mu + alpha / 2, sigma);
  y ~ normal(mu - alpha / 2, sigma);
}"
```

```
# Parameters to be monitored
parameters <- c("delta")

# The following command calls Stan with specific options.
# For a detailed description type "?rstan".
samples <- stan(model_code=model_example3,
                data=data,
                iter=20000,
                chains=4)

# Collect posterior samples across all chains:
delta.posterior <- extract(samples,pars=parameters)$delta
```

```
hist(delta.posterior,freq=FALSE)
```



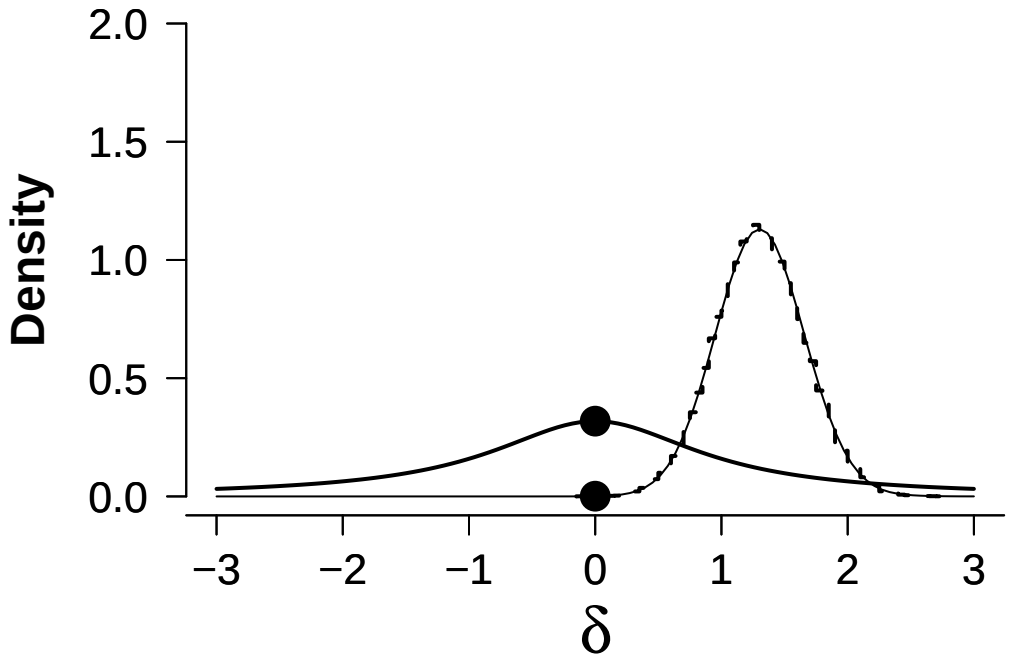

```
#============ BFs based on logspline fit ============================
library(polspline) # this package can be installed from within R
fit.posterior <- logspline(delta.posterior)

# 95% confidence interval:
x0 <- qlogspline(0.025,fit.posterior)
x1 <- qlogspline(0.975,fit.posterior)

posterior <- dlogspline(0, fit.posterior) # this gives the pdf at point delta = 0
prior     <- dcauchy(0)         # height of  prior at delta = 0
(BF01 <- posterior/prior)
```

```
## [1] 0.00322
```

The odds in favor of the alternative are 311 : 1. (The Lee and Wagenmakers book has a higher number, in the 400s.)

```
#============ Plot Prior and Posterior  ============================
par(cex.main = 1.5, mar = c(5, 6, 4, 5) + 0.1, mgp = c(3.5, 1, 0), cex.lab = 1.5,
    font.lab = 2, cex.axis = 1.3, bty = "n", las=1)
xlow  <- -3
xhigh <- 3
yhigh <- 2
Nbreaks <- 80
y       <- hist(delta.posterior, Nbreaks, plot=F)
plot(c(y$breaks, max(y$breaks)), c(0,y$density,0), type="S", lwd=2, lty=2,
```

```
     xlim=c(xlow,xhigh), ylim=c(0,yhigh), xlab=" ", ylab="Density", axes=F)
axis(1, at = c(-4,-3,-2,-1,0,1,2,3,4), lab=c("-4","-3","-2","-1","0",
                                              "1", "2", "3", "4"))
axis(2)
mtext(expression(delta), side=1, line = 2.8, cex=2)
#now bring in log spline density estimation:
par(new=T)
plot(fit.posterior, ylim=c(0,yhigh), xlim=c(xlow,xhigh), lty=1, lwd=1, axes=F)
points(0, dlogspline(0, fit.posterior),pch=19, cex=2)
# plot the prior:
par(new=T)
plot ( function( x ) dcauchy( x, 0, 1 ), xlow, xhigh, ylim=c(0,yhigh),
       xlim=c(xlow,xhigh), lwd=2, lty=1, ylab=" ", xlab = " ", axes=F)
axis(1, at = c(-4,-3,-2,-1,0,1,2,3,4), lab=c("-4","-3","-2","-1","0",
                                              "1", "2", "3", "4"))
axis(2)
points(0, dcauchy(0), pch=19, cex=2)
```



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