Lab assignment 3: Probabilistic models

Deadline: 24.1., individual assignments: 28.1.

1 General lab information

We will follow the system in assignments that should be now familiar to you from Lab assignment 1 and Lab assignment 2. There are group assignments (Questions 1-5) and individual assignments (Questions 6 and 7). Group assignments should be shown to your teacher and get graded directly *during the lab meeting*. Answers to individual questions should be submitted to Blackboard via a Blackboard quiz (in a similar way as in previous assignments).

You can get up to 11 points (you can earn one bonus point on the assignment).

More details on the whole procedure (the following description is taken from Lab assignment 1 and slightly adapted to this assignment - please read it through):

You work in groups of 4 on these exercises, with help from a single teacher who is assigned to your group. We expect you to work on these exercises in class time so you can work with your group and teacher. It is not acceptable to miss these classes without agreement from your group, or to repeatedly miss classes. Then you will fail the assignment, which leads to failing the course. If your group members miss lab classes without agreement from your group, please inform your teacher.

We suggest all group members doing these exercises on their individual computers simultaneously: this improves (student) learning and also makes it easier to find mistakes. Don't rely on other group members' answers if you don't understand why they are correct: this is meant to be an interactive collaboration with your group, so ask your group members to explain. If your group gets stuck on a question or different group members can't agree on an answer, ask for help from your teacher. Please share your video if bandwidth and circumstances allow. This makes for a more personal conversation.

When your group is happy with your answer, work together to finalize your answer in a document shared with the whole group. Google docs is an excellent platform for working together on a shared document. Show these answers to your teacher as you work. You can share this document with the teacher too. Your teacher will grade you as you work to monitor your progress and address problems. But we need a record of all your answers, submitted at the end of the assignment (via Blackboard).

In group questions, it is generally best to start by asking every group member's opinion. Then work on a written answer together. Then explain your answer to your teacher. You can also ask your teacher to read what you wrote, but they will often ask questions. It is likely you will then have to update this answer after talking with your teacher. Please tell your teacher what changes you made next time you talk and show them what you wrote.

Many questions build on previous questions being completed correctly, so you should be confident of your answer before using it in further questions: ask for help if you are unsure. If you get stuck and the teacher can't get help immediately, you can move on to the next topic until your teacher can help.

Teachers are only available during scheduled class hours.

2 Introduction

The goal of this assignment is to develop a model of how (some) adjectives are interpreted and to optimize the model on experimental data. Along the way, you will learn to construct Bayesian models, both as cognitive models and as data models.

The model is part of Probabilistic pragmatics, in particular, the Rational Speech Act Theory (RSA; not to be confused with the Representational similarity analysis that you learned in Lab Assignment 2). The

RSA that we will study here is discussed in **?** but we do not make use of the whole power of those cognitive models. The implementation you work on has been discussed in **?**.[1] Even though you can probably finish the task without checking **?**, I strongly recommend you to take a look at the paper, as it will make more sense of what you are programming on the theoretical/conceptual level (the paper is 6 pages long and the model is discussed on pages 1-3).

3 What will you need?

You will need this file, which also includes snippets of the R code and the description of the task. The R code is also condensed in a separate file in this zip folder. You can take that R file and directly build on that. Finally, you will need data, which are included as a csv file 'adjective-data.csv' in the same zip folder.

The file requires a few R packages. Obviously, you need to install them to make everything work. The most difficult one can be the package BayesianTools: this is a package for Bayesian inference. It is a small, lightweight package, currently maintained. However, it is developed just by one person and it is not much known in the community so it could be that not every issue with installation is ironed out. I will say a bit more about the package below.

4 Model specification

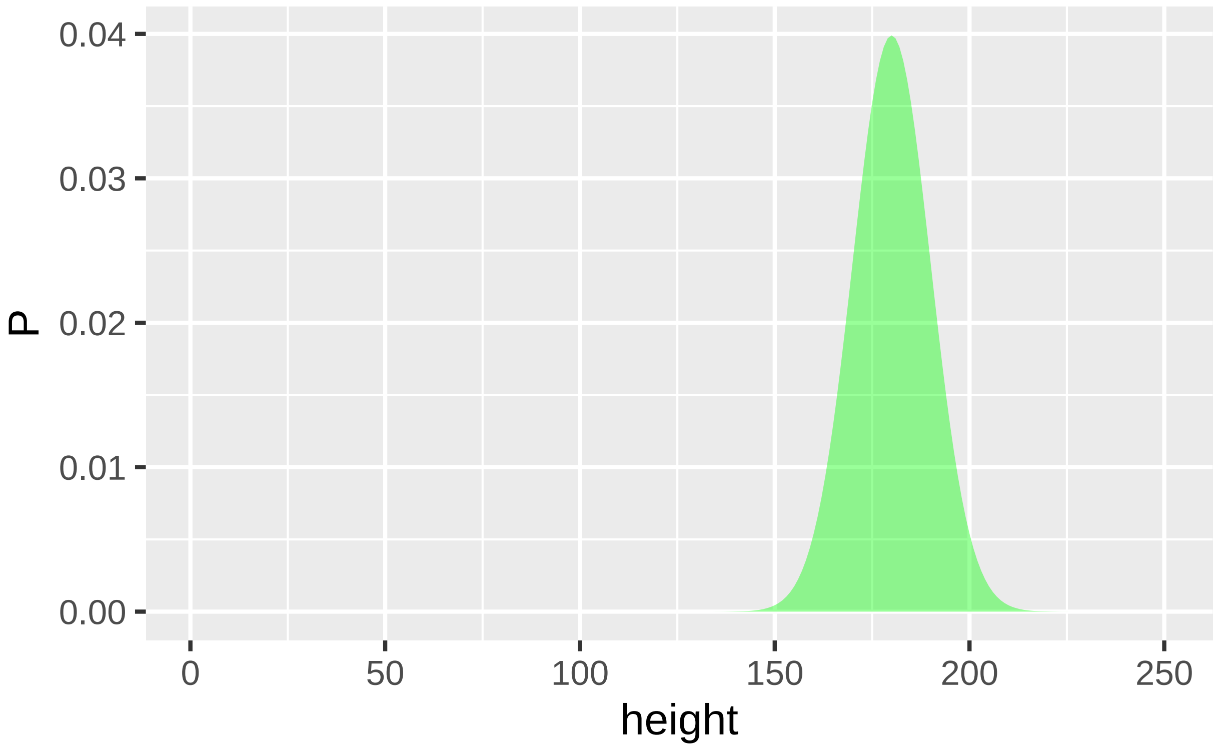
We will develop a model of the interpretation of adjectives. Basically, we are interested in the production of sentences like 'x is tall'. When would it make sense to say a sentence like that?

The common insight is that adjectives like 'tall' come with a threshold, Θ, which is a degree. Being tall is equivalent to being taller than the threshold.

Let's say we roughly know people's distribution of heights. Let's say, for the sake of the argument, that it is a normal distribution with mean 180 (cm) and st.d. 10. Let's plot it:

```r
library(ggplot2)

# we will work with points 1 to 250 (cm)
scale.points <- c(1:250)

# we create a dataframe for plotting
example.height <- data.frame(x = scale.points)

# we use sapply, which is a vectorized function application; see help if
# you don't understand it

# we add y, which is just the probability density function described above
# (normal distribution)
example.height$y <- sapply(example.height$x, function(x) {
    dnorm(x, mean = 180, sd = 10)
})

# this starts the plot creation
g1 <- ggplot(example.height, aes(x = x, y = y))

# we make the plot more pretty: we specify it should fill in area and add
# labels
g1 <- g1 + geom_area(fill = "green", alpha = 0.4) + xlab("height") + ylab("P") +
    theme_gray(20)
```

[1] https://pdfs.semanticscholar.org/7e72/6fe322f9cc4512f29ce14f8cd163bc52c794.pdf



What happens when a listener hears 'x is tall'? She should update the prior belief by assuming that x's height is above the threshold, i.e., she now knows that $d_A(x) > \Theta$, where A is in this case the adjective 'tall' and $d_A(x)$ is the height of x. The new belief of the listener, written as $\rho_0(d_A(x)|A;\Theta)$ is the conditional probability $P(d_A(x)|d_A(x) > \Theta)$, which updates the prior distribution as follows:

$$\rho_0(d_A(x)|A;\Theta) \quad = \quad \begin{cases} \frac{P(d_A(x))}{\int_\Theta^{max} P(d_A(x))dx} & d_A(x) \geq \Theta \\ 0 & d_A(x) < \Theta \end{cases}$$

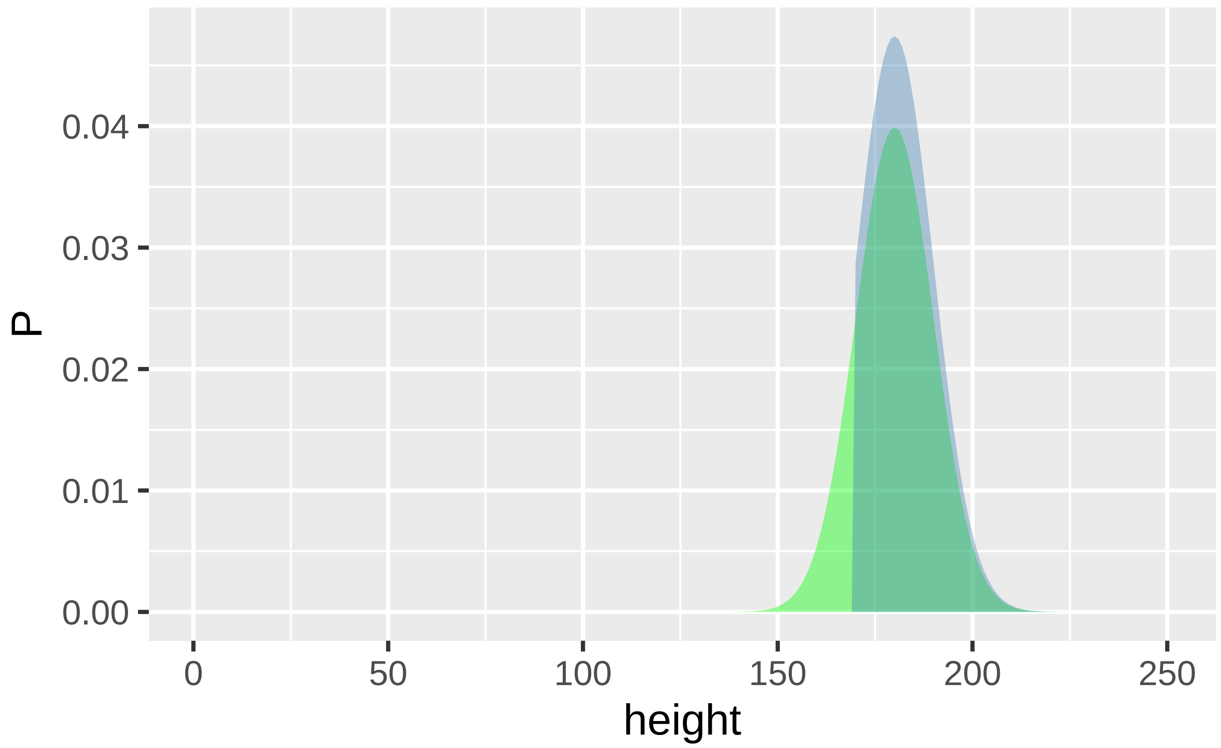
We will now build this function in R. Let's call the function literal.listener. The function is provided below:

```
literal.listener <- function(x, threshold, densityf, cumulativef) {

    ifelse(x >= threshold, densityf(x)/(1 - cumulativef(threshold)), 0)

}
```

Let us break this function down. It takes four arguments: the height x of an individual, threshold (Θ), and two functions: probability density function and cumulative distribution function. The first one is needed to calculate $P(d_A(x))$, the second one to calculate $\int_\Theta^{max} P(d_A(x))dx$. Take a look at the function, make sure you understand it.

Let's see how this function updates listener's beliefs, assuming that threshold is 170 (cm). Note what we fill in as densityf and cumulativef below: we work with the same normal distribution as for our listener's prior belief about heights, $N(180, 10)$.

```r
threshold <- 170

example.height$updated <- sapply(example.height$x, function(x) {
    literal.listener(x = x, threshold = threshold, densityf = function(x) {
        dnorm(x, 180, 10)
    }, cumulativef = function(x) {
        pnorm(x, 180, 10)
    })
})

# this starts the plot creation
g1 <- ggplot(example.height, aes(x = x, y = y))
g1 <- g1 + geom_area(fill = "green", alpha = 0.4)

# we add the result of updated belief
g1 <- g1 + geom_area(aes(y = updated), fill = "steelblue", alpha = 0.4)
g1 <- g1 + xlab("height") + ylab("P") + theme_gray(20)
```



What you can see in the graph is that the updated belief (in blue) cuts off probability at 170 and adds weight to degrees above 170, tracing the original distribution.

Of course, this is a simplistic example. We assumed that the threshold is 170. But normally, when we talk, how are we to know what the threshold is?

Qing and Franke take the value of Θ to arise through communicative efficiency. Details are in the paper. Let me just put in the formula for Expected Success (ES), which describes the expected chance of success to convey the height of someone by adopting a particular threshold ($\rho_0(d_A(x)|\emptyset;\Theta)$ is the probability of tallness of x after the speaker said nothing; it is equivalent to the prior distribution):

$$ES(\Theta) = \sum_{d_A(x)<\Theta} P(d_A(x)) \cdot \rho_0(d_A(x)|\emptyset;\Theta) + \sum_{d_A(x)\geq\Theta} P(d_A(x)) \cdot \rho_0(d_A(x)|A;\Theta)$$

This function is implemented below:

```
expected.success <- function(threshold, scale.points, densityf, cumulativef) {

    ifelse(threshold > min(scale.points), sum(sapply(scale.points[scale.points <
        threshold], function(x) {
        densityf(x) * densityf(x)
    })), 0) + sum(sapply(scale.points[scale.points >= threshold], function(x) {
        densityf(x) * literal.listener(x, threshold, densityf, cumulativef)
    }))

}
```

The function takes four arguments: the threshold, the scale points (because we sum discretized degress; for example, for tallness, we sum degrees per centimeter up to 250 cm) and densityf and cumulativef, which are passed onto literal.listener. Take a look at the function, make sure you understand it.

Three other functions need to be implemented in the model of adjective production. These are: (i) utility of threshold U; (ii) probability of using threshold; (iii) and given some degree d, how likely the speaker will use the adjective for d. These are defined as (where c and λ are free paramaters called *coverage parameter* and *lambda*, respectively):

$$U(\Theta; c) = ES(\Theta) + c \cdot \int_{[\Theta,max]} P(d_A(x))$$

$$P(\Theta;\lambda;c) = \frac{e^{\lambda\cdot U(\Theta;c)}}{\sum_t e^{\lambda\cdot U(t;c)}}$$

$$\sigma(A|d;\lambda;c) = \sum_{\Theta\leq d} P(\Theta;\lambda;c)$$

Question 1 (group, 2 pts) Start working individually. Compare interim outcomes in your group. When you agree on the final answer, write that in your online document. Once you completed the question, write it down and discuss your answer with your teacher. Of course, you can reach out to your teacher if anything is unclear.

First, implement the three functions. You should make use of the following code as your starting point, fill in the body of the functions.

```
utility <- function(threshold, scale.points, coverage.parameter, densityf,
    cumulativef) {
    ...
}


probability.threshold <- function(threshold, scale.points, lambda, coverage.parameter,
    densityf, cumulativef) {

    ...

}
```

```
use.adjective <- function(degree, scale.points, lambda, coverage.parameter,
    densityf, cumulativef) {

    ...

}
```

After you implement the functions, you can address the following question:

Given the distribution of height as described above (normal distribution, mean=180, st.d.=10), summarize the probability of using a threshold and how likely the speaker will use the adjective *tall*. For the summary, report at least two things. First, show two graphs: (i) what the probability of using threshold looks like on the scale $1 - 250$cm; (ii) the graph of the function σ on the same scale. Second, you should state which degree point has the highest probability of being used as a threshold, and on which degree point it is most likely the speaker will use the adjective *tall*. If the two values differ or are the same, say in a few words why you think this is so. For the task, use free parameters $\lambda = 50$ and $c = 0$.

Notes: It will help you to check the paper of Qing and Franke to understand what is going on. Furthermore, note that use.adjective can be slow if you repeatedly calculate the denominator in probability.threshold. Since this needs to be calculated only once, it is better to calculate the denominator directly in the body of the function use.adjective and plug that value in and not repeat calculation afterwards (this optimization trick is called memoization). Finally, in U, you can either use *max* value from scale.points (e.g., 250 cm), or, if you are going to work with predefined cumulative distribution function (e.g., cdf for normal distribution) it might be easier to just use the maximum value as present in that predefined function (i.e., infinity in case of normal distribution). The latter is easier to implement. You can also implement U using sum operation instead of cdf (but that's more work). In the two other functions, you need scale.points, because you will be summing up over them.

Further help: Here are a few tests that your implementation of the three functions should pass. If you do not pass these tests (they should give you TRUE), *do not continue*! Something is wrong with your code and you need to fix that before going on. Right now, we get Errors because the functions are not implemented.

```
# probability.threshold is a probability, so if you sum up all values it
# generates, the result should be 1
round(sum(sapply(1:10, function(x) {
    probability.threshold(x, 1:10, 50, 0, function(x) {
        dnorm(x, 5, 1)
    }, function(x) {
        pnorm(x, 5, 1)
    })
}))) == 1

## Error in probability.threshold(x, 1:10, 50, 0, function(x) {:  '...'  used in an incorrect
context

# for narrow normal distribution, prob. threshold should be max just one
# value above the average
which(sapply(1:10, function(x) {
    probability.threshold(x, 1:10, 50, 0, function(x) {
        dnorm(x, 5, 1)
    }, function(x) {
        pnorm(x, 5, 1)
    })
}) == max(sapply(1:10, function(x) {
    probability.threshold(x, 1:10, 50, 0, function(x) {
        dnorm(x, 5, 1)
    }, function(x) {
        pnorm(x, 5, 1)
    })
}))) == 6

## Error in probability.threshold(x, 1:10, 50, 0, function(x) {:  '...'  used in an incorrect
context

# use.adjective should be very unlikely on values 5 and smaller and very
# likely afterwards
round(sapply(1:10, function(x) {
    use.adjective(x, 1:10, 50, 0, function(x) {
        dnorm(x, 5, 1)
    }, function(x) {
        pnorm(x, 5, 1)
    })
})[5], 3) == 0.005

## Error in use.adjective(x, 1:10, 50, 0, function(x) {:  '...'  used in an incorrect context

round(sapply(1:10, function(x) {
    use.adjective(x, 1:10, 50, 0, function(x) {
        dnorm(x, 5, 1)
    }, function(x) {
        pnorm(x, 5, 1)
    })
})[6], 3) == 1

## Error in use.adjective(x, 1:10, 50, 0, function(x) {:  '...'  used in an incorrect context
```

Question 2 (group, 2 pts) Start working individually. Compare interim outcomes in your group. When you agree on the final answer, write that in your online document. Once you completed the question, write it down and discuss your answer with your teacher. Of course, you can reach out to your teacher if anything is unclear.

Explore expected.success and use.adjective for various prior distribution functions. For this task, assume that coverage.parameter c is at 0 and lambda is at 50.

Above, we looked at heights, which are distributed normally. Let's consider two other cases. For each of those, calculate expected.success and use.adjective (the latter is implemented in Task 1). Then, plot the results, in the same way the results of function application are plotted in previous graphs. Furthermore, report which degree has the max value for expected.success in these two cases.

- IQ is claimed to be normally distributed, with mean 100 and roughly 95% of cases falling between 70-130 range. (Check normal distribution on wikipedia if you don't know it.) Specify the normal distribution and generate figures for expected.success and use.adjective using this distribution and report which degree has the highes expected.success. We assume that the relevant adjective in this case is 'smart' and we are interested in when it would make sense to express 'x is smart'. You should also adapt scale.points (there is no reason these points should go above 150).

- Waiting times have a gamma distribution. Specifics depend on situations and context, but it might be reasonable to say that waiting for buses is a gamma distribution with mean 2 and variance 2 (in minutes). (Check gamma distribution on wikipedia if you don't know it.) Specify the gamma distribution and generate figures for expected.success and use.adjective for this case (we assume that the relevant adjective is 'late', i.e., when would it make sense to say 'the bus is late'?) and report which degree has the highes expected.success. Again, you should adapt scale.points (it is enough if the scale goes up to 30).

5 Data

We now apply the constructed model to data from an experiment reported in Solt & Gotzner, Semantics and Linguistic Theory 22 (also in the zipped folder). In particular, we will look at experiment 1, section 3.1. The idea behind the experiment is that participants have to choose entities that they would classify using a given adjective. The grid of entities they are presented with represents the comparison class. The entities in this grid are distributed in various ways w.r.t. the property described by the adjective.

The experimental results are available in 'adjective-data.csv' (courtesy of the authors). For discussion of the experiment, you can also check Qing and Franke (who also replicate the experiment; their discussion is succint and clear).

```
data.adjective <- read.csv(file = "adjective-data.csv", header = TRUE)
```

There are four prior distributions for the adjectives. These are the labels and their description in Solt and Gotzner/Qing and Franke:[2]

```
gaussian.dist <- c(1, 2, 3, 4, 5, 6, 5, 4, 3, 2, 1, 0, 0, 0)
left.skew.dist <- c(2, 5, 6, 6, 5, 4, 3, 2, 1, 1, 1, 0, 0, 0)
moved.dist <- c(0, 0, 0, 1, 2, 3, 4, 5, 6, 5, 4, 3, 2, 1)
right.skew.dist <- c(1, 1, 1, 2, 3, 4, 5, 6, 6, 5, 2, 0, 0, 0)
```

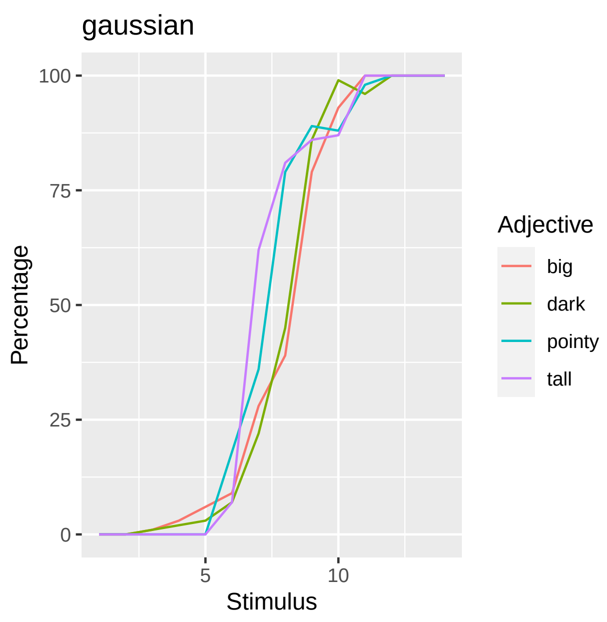
We will approximate them as follows:

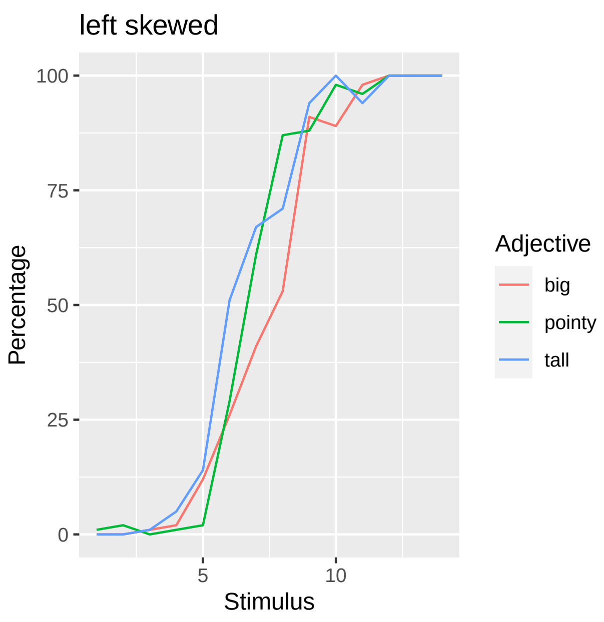
- gaussian.dist: normal distribution with 6 as mean and st.d. 2
- left skew: gamma distribution with shape 4 and scale 1.5
- moved dist: normal distribution with 9 as mean and st.d. 2
- right skew: this could be modeled as a combination of two normal distributions or, after transformation, as beta distribution; since it adds other complications, we will ignore this one in the rest of this exercise

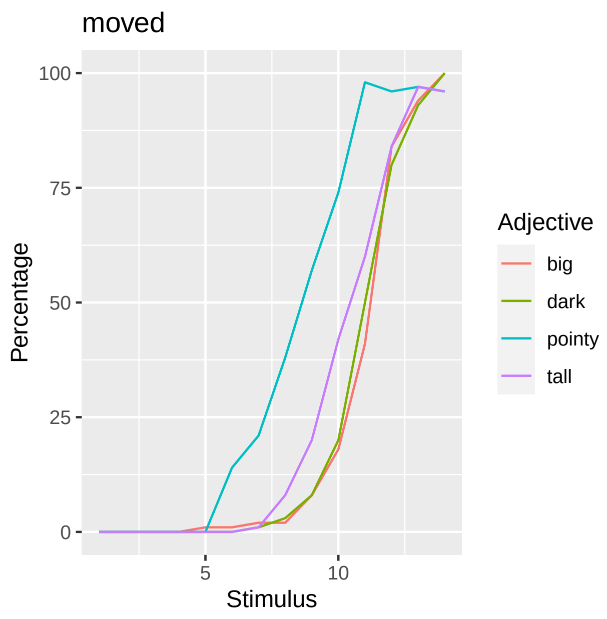
Here is a graphical summary of the relevant results. On the x-axis, we see the length on the scale of the adjective (e.g., 1 on the x-axis for tall means minimally tall, i.e., very short, 14 is the maximal height). On the y-axis, we see what percentage of stimuli of that type were chosen as representing the relevant adjective.

```
data.gaus <- data.adjective[data.adjective$Distribution == "gaussian", ]
data.left <- data.adjective[data.adjective$Distribution == "left", ]
data.moved <- data.adjective[data.adjective$Distribution == "moved", ]

library(ggplot2)
library(gridExtra)
p.g <- ggplot(data.gaus, aes(x = Stimulus, y = 100 * percentage, colour = Adjective)) +
    geom_line() + ylab("Percentage") + ggtitle("gaussian")
p.l <- ggplot(data.left, aes(x = Stimulus, y = 100 * percentage, colour = Adjective)) +
    geom_line() + ylab("Percentage") + ggtitle("left skewed")
p.m <- ggplot(data.moved, aes(x = Stimulus, y = 100 * percentage, colour = Adjective)) +
    geom_line() + ylab("Percentage") + ggtitle("moved")
```

[2]Note that Solt & Gotzner and Qing & Franke use the label left skew for what is normally called "right skew" in statistics and vice versa. Usually, "left skew" refers to the skew with a long tail on the left side, and "right skew" refers to the skew with a long tail on the right side.







Question 3 (group, 1 pt) Start working individually. Compare interim outcomes in your group. When you agree on the final answer, write that in your online document. Once you completed the question, write it down and discuss your answer with your teacher. Of course, you can reach out to your teacher if anything is unclear.

You will now check on a subset of the data how our model's predictions correlate with observations (more precisely: what is Pearson's correlation coefficient, r, between model's predictions and actual observations). You will also study what the role of prior belief is. You can use the R function *cor* in this task.

For the first check, let us consider predictions and observations with respect to the adjective 'big' in its three distributions. You should check the value of r between the data and the model three times, one per distribution. Furthermore, check the value of r with respect to three different parameters of the model (9 comparisons in total):

- lambda=40, coverage.parameter=0.1
- lambda=40, coverage.parameter=-0.1

- lambda=40, coverage.parameter=0

What coverage parameter gives us the best and the worst linear correlation? On which distribution do we get the best results?

After you are done with answering this, investigate what the role of prior distribution is. You can check this by hand on a small sample. Pick the coverage parameter that worked best in the previous subquestion. Then, select two distributions (e.g., left skew and moved) but in the model, flip their prior belief distributions (so, for example, gamma distribution is used on 'moved distribution' and normal distribution is used on 'left skewed distribution'). Report what prior distribution you used and report r. Answer these questions: Do we see that r is affected? Does the model suffer in having worse linear correlation with respect to the observed data? Say in a few words why this is the case.

6 Bayesian modeling

Finally, we are ready to do Bayesian modeling on the dataset. We will use the package BayesianTools for this. First, you have to install the package. Uncomment and use:

```r
# install.packages('BayesianTools')
```

After that, you can load the package:

```r
library(BayesianTools)
```

Notes about the installation: I saw (in discussion forums of the package) that having an older version of R than 3.5 could cause problems with the package. If you experience any, that is, if the installation ends with errors and the package fails to install, try to update your R software to a version of 3.5 or higher.

If you are going to work on Bayesian modeling more extensively in the future, I recommend that you use one of the popular and commonly used languages: STAN or JAGS. We do not do so here because these are languages independent of R and learning them would require much more energy and time. The advantage of BayesianTools is that the package is fully embedded in R, so using it is relatively easy, and furthermore, it can be combined with any function written in R. We will leverage this last point in this assignment.

We are going to build a model that will learn posterior distribution of the two free parameters, coverage.parameter and lambda. In a Bayesian model, we have to specify two things:

- prior distribution (NB. This is now the prior distribution for the parameters we want to study, i.e., coverage.parameter and lambda, this distribution is not related to prior distributions in the interpretation of adjectives!)
- likelihood

Let's try a simple example. Let's assume that we will want to find the posterior distribution of two parameters that should predict percentage of acceptance of data.gaus.big in each stimulus type (1-14). Let's call the two parameters $p1$ and $p2$. We will assume the following priors for $p1$ and $p2$:

- $p1 \sim Unif(0, 0.1)$, that is $p1$ is generated by Uniform distribution with the smallest possible value 0 and the largest possible value 0.1
- $p2 \sim Unif(0.1, 1)$, that is $p2$ is generated by Uniform distribution with the smallest possible value 0.1 and the largest possible value 1

We will assume that the likelihood is:

- data.gaus.big$percentage $\sim N(p1 + p2, 0.1)$

In words, we assume that percentage in data.gaus.big is generated by a normal distribution with standard deviation 0.1 and mean the sum of the two parameters, $p1$ and $p2$. We will now write everything in the model and see what the posterior distribution of the two parameters is.

Here is the prior:

```r
prior <- createUniformPrior(lower = c(0, 0.1), upper = c(0.1, 1), best = NULL)
```

Now, we are going to implement the likelihood (actually, BayesianTools uses log-likelihood, i.e., likelihood transformed by log). It is specified here (the first line just loads a subset of data that we will use):

```r
data.gaus.big <- subset(data.gaus, Adjective == "big")

likelihood <- function(param1) {

    collect <- 0

    for (i in 1:14) {
        collect <- collect + dnorm(data.gaus.big$percentage[i], mean = param1[1] +
            param1[2], sd = 0.1, log = TRUE)

    }

    return(collect)
}
```

We put everything in setup, specify the number of iterations and run sampling:

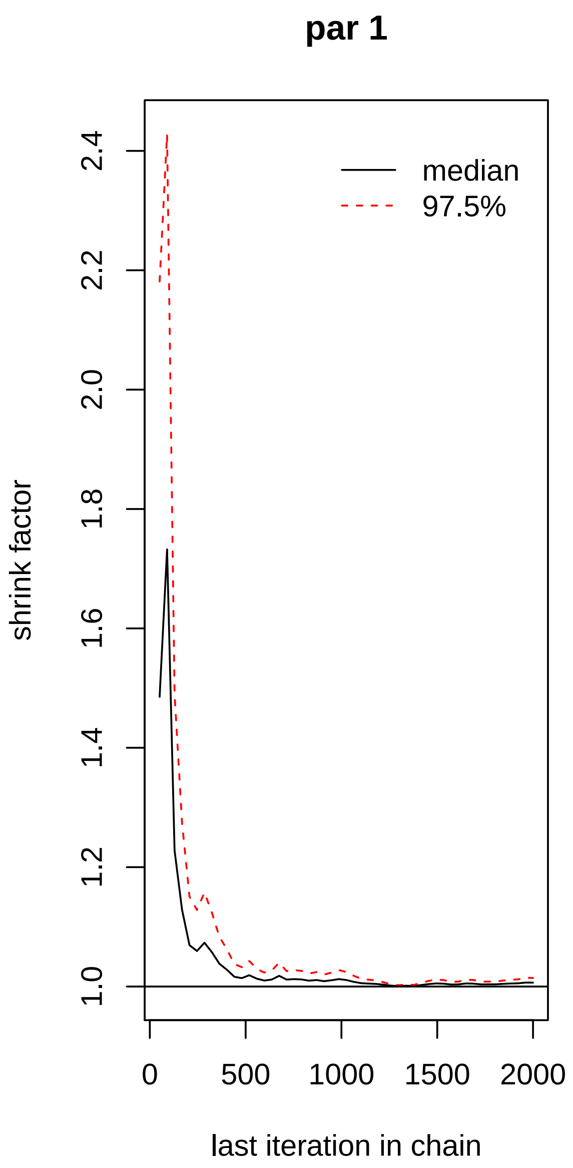
```r
bayesianSetup <- createBayesianSetup(likelihood = likelihood, prior = prior)

iter = 6000
settings = list(iterations = iter, nrChains = 3, message = FALSE)
out <- runMCMC(bayesianSetup = bayesianSetup, settings = settings)
```

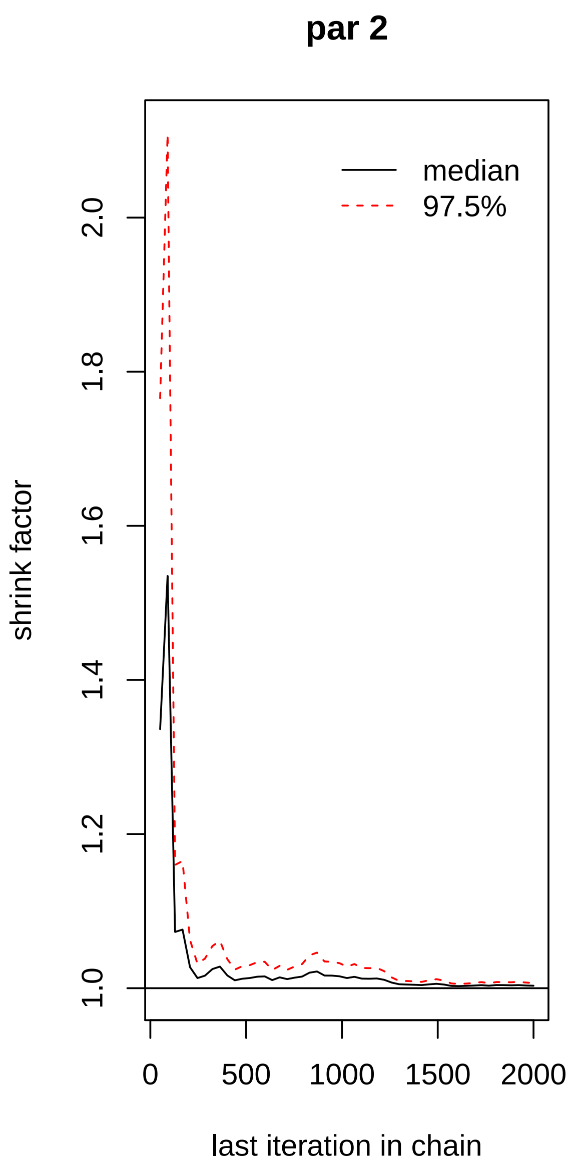
Sampling creates three chains and collects 2,000 draws per chain. The chains sample independently from each other. Ideally, the samples represent draws from the posterior distribution of the parameters (this is the distribution we care about).

Before we start going into any details of the model, we first need to check that chains converged. If they did not, we cannot be sure that we are looking at samples that are drawn from the posterior distribution.

We check convergence using the command gelmanDiagnostics.

```r
gelmanDiagnostics(out, plot = T)
```





```
## Potential scale reduction factors:
##
##       Point est. Upper C.I.
## par 1       1.01       1.01
## par 2       1.00       1.01
##
## Multivariate psrf
##
## 1.01
```

The output shows point estimates of potential scale reduction factors (psrf, also known as Rhat) per parameter. We also see plots showing the change in the value of psrf during sampling. As a rule of thumb, the point estimate of psrf cannot be higher than 1.1 for any parameter and ideally, it should be 1.05 or smaller. If this is not satisfied, we have to increase the number of iterations and run sampling again. If a significant increase of the number of iterations does not help, it is possible that something is wrong with either priors or likelihoods in the model and they should be changed.

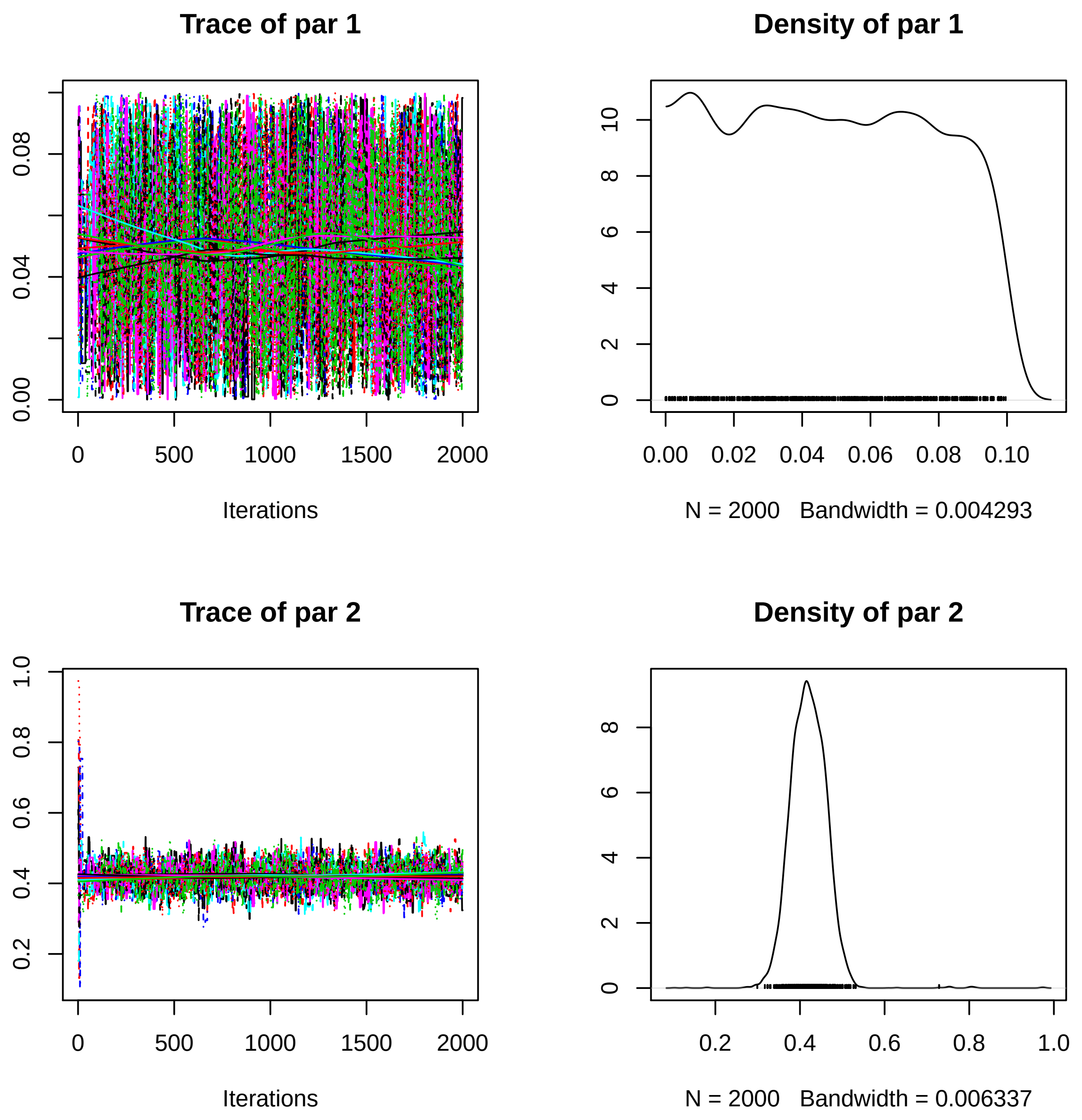
In our case, we see that the chains converged so we have no evidence that sampling failed. Thus, we can proceed to study the posterior distribution of the parameters. This is given here:

```
summary(out)

## # # # # # # # # # # # # # # # # # # # # # # # #
## ## MCMC chain summary ##
## # # # # # # # # # # # # # # # # # # # # # # # #
##
## # MCMC sampler:  DEzs
## # Nr. Chains:  9
## # Iterations per chain:  2000
## # Rejection rate:  0.681
## # Effective sample size:  1964
## # Runtime:  1.643  sec.
##
## # Parameters
##         psf   MAP  2.5% median 97.5%
## par 1 1.007 0.058 0.003  0.049 0.098
## par 2 1.003 0.412 0.343  0.419 0.498
##
## ## DIC:  228.373
## ## Convergence
##  Gelman Rubin multivariate psrf:  1.011
##
## ## Correlations
##        par 1  par 2
## par 1  1.000 -0.647
## par 2 -0.647  1.000
```

To read this, check MAP (maximum a posteriori estimation), which gives us point estimates – the mode of the distributions of the parameters. What we see is that $p1$ is kept low (since it cannot rise above 0.1, anyway) and the second parameter is around 0.4. This makes sense since most values are extreme (either 0 or 1) so having a mean of normal distribution around 0.4 minimizes the distance from those extreme values.

You can also plot the results:

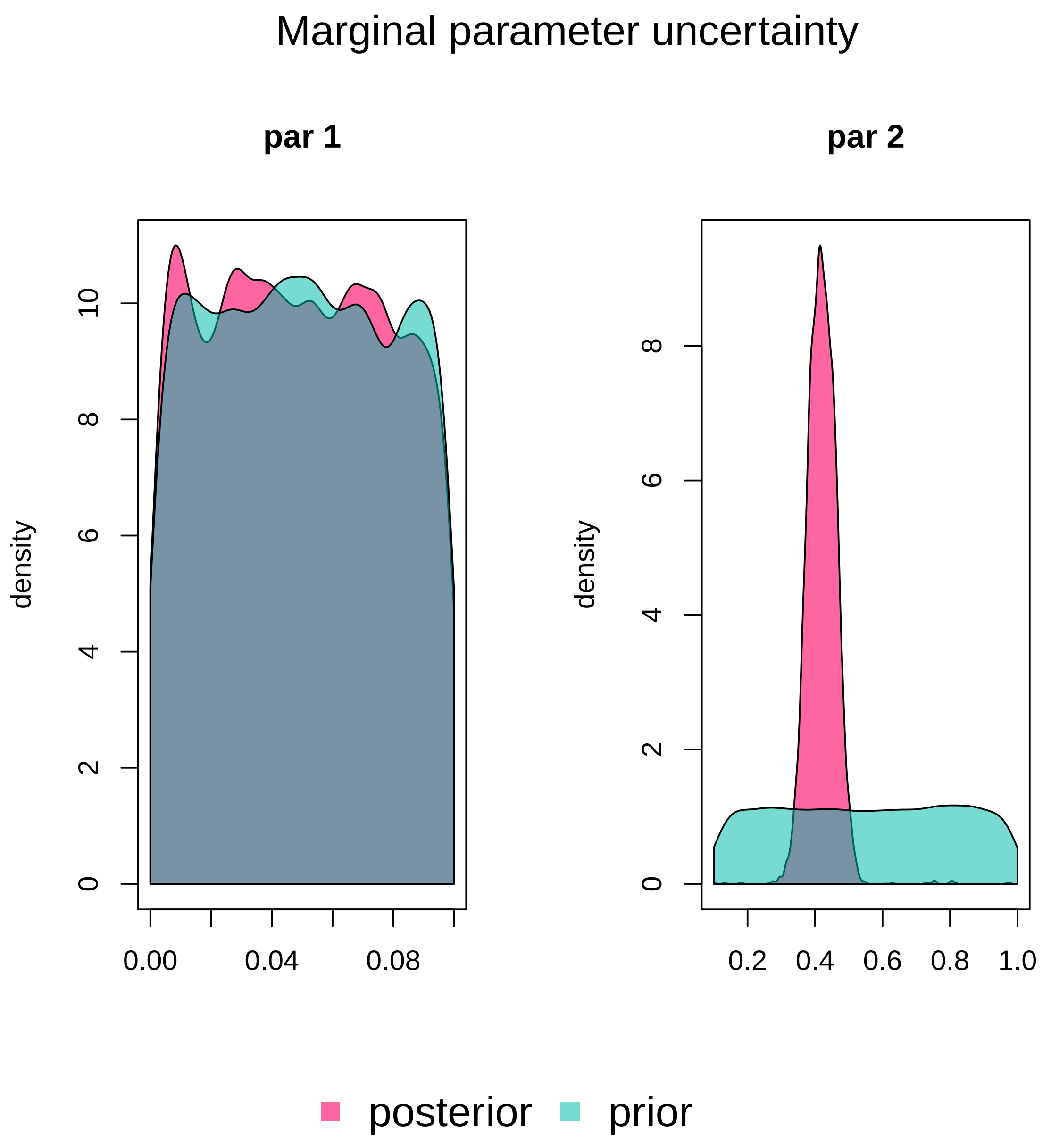
```
plot(out)
```



Trace plots show what values were sequentially sampled. Density plots show posterior probability density functions for the two parameters.

Finally, you can also plot marginal plots, which compares, per parameter, what prior and posterior distributions look like. We see that $p1$ was kept close to prior, while in $p2$ the model updated to a distribution much narrower than the prior.

```
marginalPlot(out)
```



You will now implement the parameter estimation for our model using the data from data.gaus.big (that is, we check only one adjective and only one distribution of that adjective).

I specify the prior distribution for you. The prior distribution for coverage.parameter is Uniform distribution Unif(-1,1) (that is, any value between -1 and 1 including -1 and 1 is equally likely, no other values are possible). The prior distribution for lambda is Unif(1, 50). This is how this is encoded:

```
prior <- createUniformPrior(lower = c(-1, 1), upper = c(1, 50), best = NULL)
```

Question 4 (group, 2 pts) Start working individually. Compare interim outcomes in your group. When you agree on the final answer, write that in your online document. Once you completed the question, write it down and discuss your answer with your teacher. Of course, you can reach out to your teacher if anything is unclear.

Finish the construction of the Bayesian model.

First, you have to specify likelihood. You should draw on the previous example. However, unlike in the previous example, the likelihood should be:

- data.gaus.big$percentage $\sim N(Model(coverage.parameter, lambda), 0.1)$

Where $Model$ is our model from Section 4. (In particular, you should make use of the function use.adjective in the new likelihood. Roughly, instead of adding up param1 and param2, you need to do something else.)

```
likelihood <- function(param1) {

    collect <- 0

    for (i in 1:14) {
        collect <- collect + dnorm(data.gaus.big$percentage[i], mean = ...,
            sd = 0.1, log = TRUE)

    }

    return(collect)
}
```

Now, you can run the model by uncommenting and executing the following code. Importantly, set.seed(123) should be executed before you start running the Bayesian model. This way, your answers should be replicable.

```
# set.seed(123) bayesianSetup <- createBayesianSetup(likelihood =
# likelihood, prior = prior)

# iter = 10000

# settings = list(iterations = iter, nrChains=3, message = FALSE)

# out <- runMCMC(bayesianSetup = bayesianSetup, settings = settings)
```

One thing to note in the commented-out code is that we increased iterations to 10,000. This is because we now deal with a more complex code than the first Bayesian model above, so 6,000 iterations might not be enough. However, this amount of iterations takes time and when you are debugging and testing the model, it is better to set iterations to some small number (say, a few hundreds). Use 10,000 iterations only when you think your model works.

After your model runs and successfully finishes:

- Check that chains converged.
- Explore the summary and plot of the variable out. This variable stores samples from posterior distributions of the parameters. If everything worked fine, out should carry posterior distributions of coverage parameter and lambda.

What do we see? What values have been found for lambda and coverage.parameter? Report summary statistics on lambda and coverage.parameter (MAP, median, 2.5percent to 97.5percent interval). Discuss briefly the summaries (i.e., are values in out widespread or very narrow? If so, why do you think this is the case and is it good/bad?)

Note: running the model with 10,000 iterations will take a while, probably around 15 minutes. If it does take significantly longer than that there is likely something wrong with your code. Try to run the Bayesian model on a small data subset (for example, not all 1:14 values) or with fewer iterations if your model takes too long.

Question 5 (group, 1 pt) Expand your model to construct the posterior distribution of the two parameters using three adjectives (*big*, *pointy*, *tall*) in all three distributions. Explore the distribution of the parameters in out. Plot the summary and report summary statistics on lambda and coverage.parameter.

Note: it will take a while to run the model, more so than the previous model. Still, sampling should be done in around 30-40 minutes. See also comments in Question 4.

Bonus question (group, 1 pt) We specified the likelihood using dnorm with sd=0.1. Is this sensible or not? Check what dnorm is and state what problems there might be with this particular function and with sd=0.1 for our data. Is there an alternative probability distribution that would make more sense? Do not worry if you cannot answer this question - it is a bonus point and requires good conceptual understanding of the Bayesian model and how it links to behavioral data.

Question 6 (individual, 1 pt) Draw the graphical representation of the model from Question 4 in the same way we did so in class (see, for example, slide 36 in the class Probabilistic models, 1st lecture): in the bottom you should signal what's the likelihood function (that connects it to data). Above that, you should specify the cognitive model, which has parameters that are fed to it from specific prior distributions. All the information can be read from the code and the modeling that you created in Question 4. Store this as a file (png, jpg, pdf). You can either draw your model in some drawing program or draw by hand and take a photo. Upload your graphical representation as your answer to this question on Blackboard quiz for assignment 3.

Question 7 (individual, 1 pt) Suppose there is a speaker who uses the adjective *big* as follows: she does not use the adjective at all for the lowest three values (values 1:3) and she always uses the adjective for any value higher than 3 (values 4:14). What would we predict for the coverage.parameter of this person? Should it be positive? Negative? Zero? (You can reason and/or adapt your Bayesian model to actually check your answer by computational simulation; you can assume the same prior distribution for lambda as in previous exercises, but you have to assume another prior for coverage.parameter and you have to construct a new dataset). Write your answer on Blackboard.