Solutions Manual (Complete)

for

Doing Bayesian Data Analysis: A Tutorial with R and BUGS

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Chapter 2.

Exercise 2.1. [Purpose: To get you to think about what beliefs can be altered by inference from data.] Suppose I believe that exactly 47 angels can dance on my head. (These angels cannot be seen or felt in any way.) Can you provide any evidence that would change my belief?

No. By assumption, the belief has no observable consequences, and therefore no observable data can affect the belief.

Suppose I believe that exactly 47 anglers can dance on the floor of the bait shop. Is there any evidence you could provide that would change my belief?

Yes. Because dancing anglers and bait–shop floors have measurable spatial extents, data from observed anglers and floors can influence the belief.

Exercise 2.2. [Purpose: To get you to actively manipulate mathematical models of probabilities. Notice, however, that these models have no parameters.] Suppose we have a four–sided die from a board game. (On a tetrahedral die, each face is an equilateral triangle. When you roll the die, it lands with one face down and the other three visible as the faces of a three–sided pyramid. To read the value of the roll, you pick up the die and see what landed face down.) One side has one dot, the second side has two dots, the third side has three dots, and the fourth side has four dots. Denote the value of the bottom face as x. Consider the following three mathematical descriptions of the probabilities of x. Model A: p(x)=1/4. Model B: p(x)=x/10. Model C: p(x)=12/(25x). For each model, determine the value of p(x) for each value of x. Describe in words what kind of bias (or lack of bias) is expressed by each model.

Model A: $p(x=1) = 1/4$, $p(x=2) = 1/4$, $p(x=3) = 1/4$, $p(x=4) = 1/4$. This model is unbiased, in that every value has the same probability.
Model B: $p(x=1) = 1/10$, $p(x=2) = 2/10$, $p(x=3) = 3/10$, $p(x=4) = 4/10$. This model is biased toward higher values of x.
Model C: $p(x=1) = 12/25$, $p(x=2) = 12/50$, $p(x=3) = 12/75$, $p(x=4) = 12/100$. (Notice that the probabilities sum to 1.) This model is biased toward lower values of x.

Exercise 2.3. [Purpose: To get you to think actively about how data cause beliefs to shift.] Suppose we have the tetrahedral die introduced in the previous exercise, along with the three candidate models of the die's probabilities. Suppose that initially we are not sure what to believe about the die. On the one hand, the die might be fair, with each face landing with the same probability. On the other hand, the die might be biased, with the faces that have more dots landing down more often (because the dots are created by embedding heavy jewels in the die, so that the sides with more dots are more likely to land on the bottom). On yet another hand, the die might be biased such that more dots on a face make it less likely to land down (because maybe the dots are bouncy rubber or protrude from the

surface). So, initially, our beliefs about the three models can be described as p(A) = p(B) = p(C) = 1/3. Now we roll the die 100 times and find these results: #1's D 25, #2's = 25, #3's = 25, and #4's = 25. Do these data change our beliefs about the models? Which model now seems most likely?

The data are consistent with Model A, which predicts equal numbers of each outcome. Therefore, after observing the data, we should re–allocate belief toward Model A and away from Model B and Model C. Model A seems most likely.

Suppose when we rolled the die 100 times, we found these results: #1's = 48, #2's = 24, #3's = 16, and #4's = 12. Now which model seems most likely?

The data are most consistent with Model C. Therefore, after observing the data, we should re–allocate belief toward Model C and away from Model A and Model B. Model C seems most likely.

Exercise 2.4. [Purpose: To actually do Bayesian statistics, eventually, and the next exercises, immediately.] Install R on your computer. (And if that's not exercise, I don't know what is.)

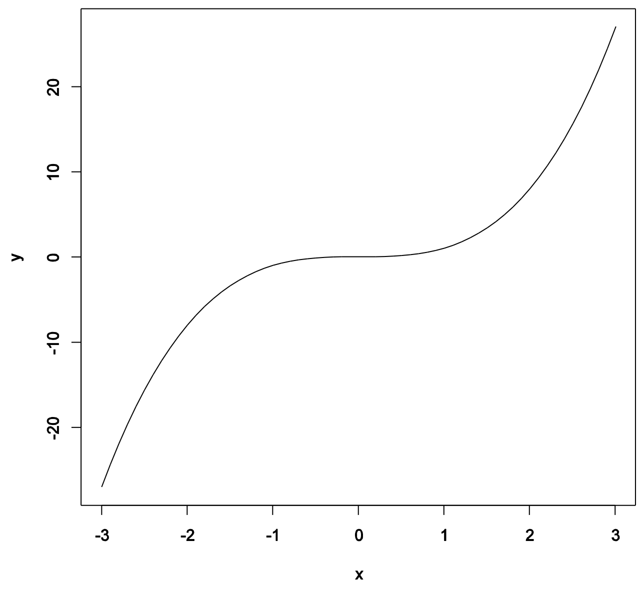
No written answer needed.

Exercise 2.5. [Purpose: To be able to record and communicate the results of your analyses.] Run the code named SimpleGraph.R. The last line of the code saves the graph to a file in a format called "encapsulated PostScript" (abbreviated as eps), which your favorite word processor might be able to import. If your favorite word processor does not import eps files, then read the R documentation and find some other format that your word processor likes better; try help('dev.copy2eps'). You may find that you can just copy and paste the displayed graph directly into your document, but it can be useful to save the graph as a stand–alone file for future reference. Include the code listing and the resulting graph in a document that you compose using a word processor of your choice.

The answer depends on individual software preferences. EPS files can be imported into many typesetting programs, and so no modification to the code is necessary. Some people may find that storing the file in PDF format is more desirable, in which case the command dev.copy2pdf is useful instead of dev.copy2eps.

Exercise 2.6. [Purpose: To gain experience with the details of the command syntax within R.] Adapt the code of SimpleGraph.R so that it plots a cubic function ($y = x^3$) over the interval x in [–3,+3]. Save the graph in a file format of your choice. Include a listing of your code, commented, and the resulting graph.

```
x = seq( from = -3 , to = 3 , by = 0.1 ) # Specify vector of x values.
y = x^3                                  # Specify corresponding y values.
plot( x , y , type = "l" )               # Make a graph of the x,y points.
dev.copy2eps( file = "CubicGraph.eps" )  # Save the plot to an EPS file.
```

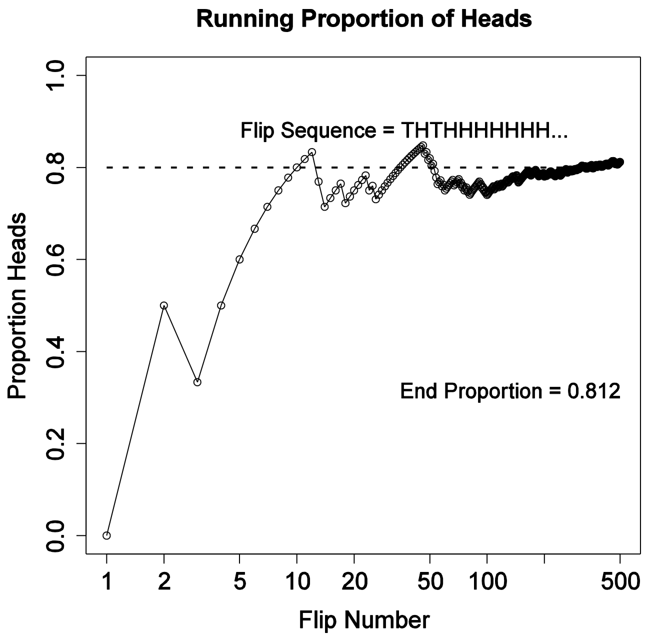


Chapter 3.

Exercise 3.1. [Purpose: To give you some experience with random number generation in R.] Modify the coin–flipping program in Section Subsection 3.5.1 (RunningProportion.R) to simulate a biased coin that has p(H) = 0.8. Change the height of the reference line in the plot to match p(H). Comment your code. Hint: Read the help for sample.

```
# Goal: Toss a coin N times and compute the running proportion of heads.
N = 500     # Specify the total number of flips, denoted N.
# Generate a random sample of N flips for a fair coin (heads=1, tails=0);
# the function "sample" is part of R:
#set.seed(47405) # Uncomment to set the "seed" for random number generator.
flipsequence = sample( x=c(0,1) , prob=c(.2,.8) , size=N , replace=TRUE )
# Compute the running proportion of heads:
r = cumsum( flipsequence ) # The function "cumsum" is built in to R.
n = 1:N                    # n is a vector.
runprop = r / n            # component by component division.
# Graph the running proportion:
# To learn about the parameters of the plot function,
# type help('par') at the R command prompt.
# Note that "c" is a function in R.
plot( n , runprop , type="o" , log="x" ,
        xlim=c(1,N) , ylim=c(0.0,1.0) , cex.axis=1.5 ,
        xlab="Flip Number" , ylab="Proportion Heads" , cex.lab=1.5 ,
        main="Running Proportion of Heads" , cex.main=1.5 )
# Plot a dotted horizontal line at y=.8, just as a reference line:
lines( c(1,N) , c(.8,.8) , lty=2 , lwd=2 )
# Display the beginning of the flip sequence. These string and character
# manipulations may seem mysterious, but you can de-mystify by unpacking
# the commands starting with the innermost parentheses or brackets and
# moving to the outermost.
flipletters = paste( c("T","H")[ flipsequence[ 1:10 ] + 1 ] , collapse="" )
displaystring = paste( "Flip Sequence = " , flipletters , "..." , sep="" )
text( 5 , .9 , displaystring , adj=c(0,1) , cex=1.3 )
# Display the relative frequency at the end of the sequence.
text( N , .3 , paste("End Proportion =",runprop[N]) , adj=c(1,0) , cex=1.3 )
# Save the plot to an EPS file.
dev.copy2eps( file = "Exercise3.1.eps" )
```

Below is an exemplary graph; displays will differ across runs because the flip sequence is random.



Exercise 3.2. [Purpose: To have you work through an example of the logic presented in Section 3.2.1.2.] Determine the exact probability of drawing a 10 from a shuffled pinochle deck. (A pinochle deck has 48 cards. There are six values: 9, 10, jack, queen, king, and ace. There are two copies of each value in each of the standard four suits: hearts, diamonds, clubs, and spades.)
(A) What is the probability of getting a 10?

There are 8 10's in 48 cards, hence p(10) = 8/48.

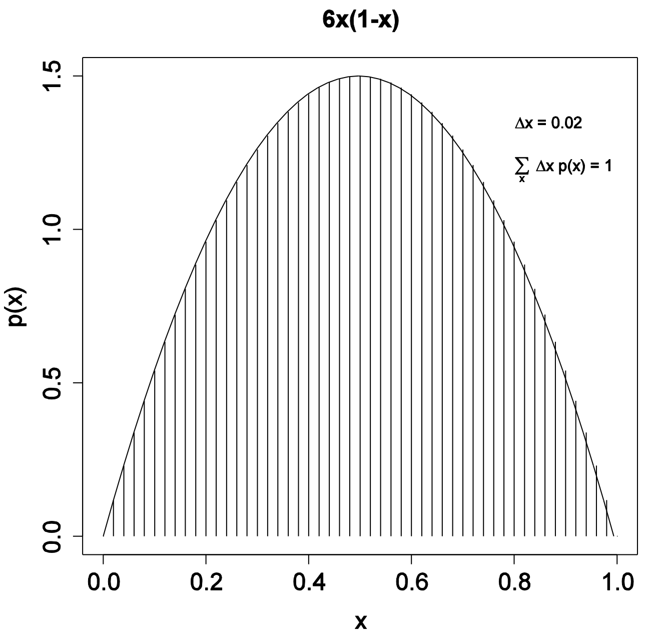
(B) What is the probability of getting a 10 or jack?

There are 8 10's and 8 jacks and they are mutually exclusive. Hence p(10 or jack) = (8+8)/48.

Exercise 3.3. [Purpose: To give you hands–on experience with a simple probability density function, in R and in calculus, and to reemphasize that density functions can have values larger than 1.] Consider a spinner with a [0,1] scale on its circumference. Suppose that the spinner is slanted or magnetized or bent in some way such that it is biased, and its probability density function is p(x) = 6x(1–x) over the interval x in [0, 1].

(A) Adapt the code from Section Subsection 3.5.2 (IntegralOfDensity.R) to plot this density function and approximate its integral. Comment your code. Be careful to consider values of x only in the interval [0, 1]. Hint: You can omit the first couple lines regarding meanval and sdval, because those parameter values pertain only to the normal distribution. Then set xlow=0 and xhigh=1.

```
# Graph of normal probability density function, with comb of intervals.
xlow  = 0 # Specify low end of x-axis.
xhigh = 1 # Specify high end of x-axis.
dx = 0.02                 # Specify interval width on x-axis
# Specify comb points along the x axis:
x = seq( from = xlow , to = xhigh , by = dx )
# Compute y values, i.e., probability density at each value of x:
y = 6 * x * ( 1 - x )
# Plot the function. "plot" draws the intervals. "lines" draws the curve.
plot( x , y , type="h" , lwd=1 , cex.axis=1.5
      , xlab="x" , ylab="p(x)" , cex.lab=1.5
      , main="6x(1-x)" , cex.main=1.5 )
lines( x , y )
# Approximate the integral as the sum of width * height for each interval.
area = sum( dx * y )
# Display info in the graph.
text( 0.8 , .9*max(y) , bquote( paste(Delta , "x = " ,.(dx)) )
      , adj=c(0,.5) )
text( 0.8 , .8*max(y) ,
      bquote(
        paste( sum(,x,) , " " , Delta , "x p(x) = " , .(signif(area,3)) )
      ) , adj=c(0,.5) )
# Save the plot to an EPS file.
dev.copy2eps( file = "Exercise3.3.eps" )
```



(B) Derive the exact integral using calculus. Hint: See the example, Equation 3.7.

$$\int_0^1 dx(6x(1-x)) = 6\int_0^1 dx(x-x^2) = 6\left[\tfrac{1}{2}x^2 - \tfrac{1}{3}x^3\right]_0^1 = 6\left(\left[\tfrac{1}{2}1^2 - \tfrac{1}{3}1^3\right] - \left[\tfrac{1}{2}0^2 - \tfrac{1}{3}0^3\right]\right) = 1$$

(C) Does this function satisfy Equation 3.3?

Yes, the integral of the function across its domain is 1, just as it should be for a probability density function.

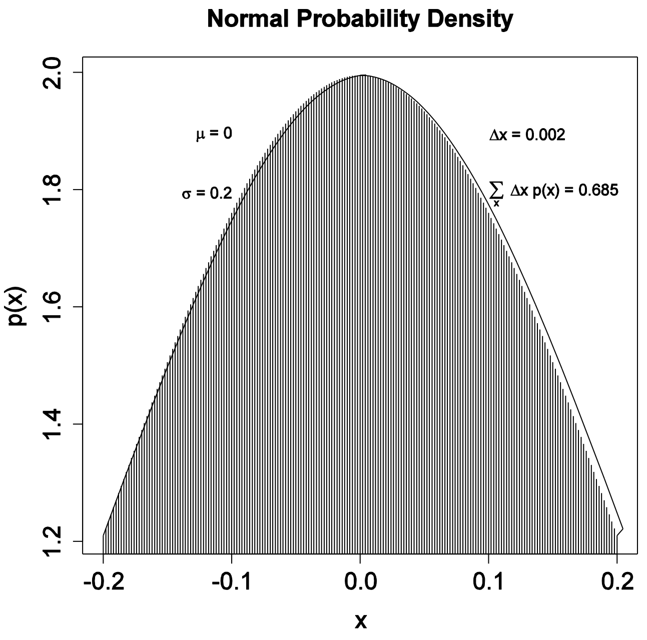
(D) From inspecting the graph, what is the maximal value of p(x)?

Visual inspection of the graph suggests that p(x) is maximal at x=0.5. This is also the mean, because the distribution is symmetric.

Exercise 3.4. [Purpose: To have you use a normal curve to describe beliefs. It's also handy to know the area under the normal curve between μ and σ.]

(A) Adapt the code from Section Subsection 3.5.2 (IntegralOfDensity.R) to determine (approximately) the probability mass under the normal curve from x = μ – σ to x = μ + σ. Comment your code. Hint: Just change xlow and xhigh appropriately, and change the text location so that the area still appears within the plot.

```
# Graph of normal probability density function, with comb of intervals.
meanval = 0.0              # Specify mean of distribution.
sdval = 0.2                # Specify standard deviation of distribution.
xlow  = meanval - 1*sdval # Specify low end of x-axis.
xhigh = meanval + 1*sdval # Specify high end of x-axis.
dx = 0.002                 # Specify interval width on x-axis
# Specify comb points along the x axis:
x = seq( from = xlow , to = xhigh , by = dx )
# Compute y values, i.e., probability density at each value of x:
y = ( 1/(sdval*sqrt(2*pi)) ) * exp( -.5 * ((x-meanval)/sdval)^2 )
# Plot the function. "plot" draws the intervals. "lines" draws the bell
curve.
plot( x , y , type="h" , lwd=1 , cex.axis=1.5
      , xlab="x" , ylab="p(x)" , cex.lab=1.5
      , main="Normal Probability Density" , cex.main=1.5 )
lines( x , y )
# Approximate the integral as the sum of width * height for each interval.
area = sum( dx * y )
# Display info in the graph.
text( -0.5*sdval , .95*max(y) , bquote( paste(mu ," = " ,.(meanval)) )
      , adj=c(1,.5) )
text( -0.5*sdval , .9*max(y) , bquote( paste(sigma ," = " ,.(sdval)) )
      , adj=c(1,.5) )
text( 0.5*sdval , .95*max(y) , bquote( paste(Delta , "x = " ,.(dx)) )
      , adj=c(0,.5) )
text( 0.5*sdval , .9*max(y) ,
      bquote(
        paste( sum(,x,) , " " , Delta , "x p(x) = " , .(signif(area,3)) )
      ) , adj=c(0,.5) )
# Save the plot to an EPS file.
dev.copy2eps( file = "Exercise3.4.eps" )
```



The graph indicates that the area under the normal curve between μ and σ is about 34%.

(B) Now use the normal curve to describe the following belief. Suppose you believe that women's heights follow a bell–shaped distribution, centered at 162 cm with about two–thirds of all women having heights between 147 cm and 177 cm.

The previous part indicates that about two–thirds of the normal distribution falls between μ – σ and μ + σ. Therefore we can describe the belief as a normal distribution with mean at 162 and standard deviation of 177–162=15 (which is the same as 162–147).

Exercise 3.5. [Purpose: To recognize and work with the fact that Equation 3.11 can be solved for the conjoint probability, which will be crucial for developing Bayes' theorem.] School children were surveyed regarding their favorite foods. Of the total sample, 20% were 1st graders, 20% were 6th graders, and 60% were 11th graders. For each grade, the following table shows the proportion of respondents that chose each of three foods as their favorite:

	Ice Cream	**Fruit**	**French Fries**
1st graders	**0.3**	**0.6**	**0.1**
6th graders	**0.6**	**0.3**	**0.1**
11th graders	**0.3**	**0.1**	**0.6**

From that information, construct a table of conjoint probabilities of grade and favorite food. Also, say whether grade and favorite food are independent and how you ascertained the answer. Hint: You are given p(grade) and p(food|grade). You need to determine p(grade, food).

By definition, p(food|grade) = p(grade,food)/p(grade). Therefore p(grade,food) = p(food|grade)*p(grade). Therefore we multiply each row of the table by its corresponding marginal distribution to get the conjoint probabilities:

	Ice Cream	Fruit	French Fries
1st graders	0.3*0.2=0.06	0.6*0.2=0.12	0.1*0.2=0.02
6th graders	0.6*0.2=0.12	0.3*0.2=0.06	0.1*0.2=0.02
11th graders	0.3*0.6=0.18	0.1*0.6=0.06	0.6*0.6=0.36

If the attributes were independent, then we could multiply the marginal probabilities to get the conjoint probabilities. Any cell that violates that equality indicates lack of independence. Consider, for example, the top left cell. Its conjoint probability is p(1stGrade,IceCream) = 0.06. On the other hand, the product of the marginals is p(1stGrade) * p(IceCream) = 0.20 * 0.36 = 0.072, which does not equal the conjoint probability.

Chapter 4.

Exercise 4.1. [Purpose: Application of Bayes' rule to disease diagnosis, to see the important role of prior probabilities.] Suppose that in the general population, the probability of having a particular rare disease is 1 in a 1000. We denote the true presence or absence of the disease as the value of a parameter, θ, that can have the value θ = ☹ if disease is present, or the value θ = ☺ if the disease is absent. The base rate of the disease is therefore denoted p(θ = ☹) = 0.001. This is our prior belief that a person selected at random has the disease.

Suppose that there is a test for the disease that has a 99% hit rate, which means that if a person has the disease, then the test result is positive 99% of the time. We denote a positive test result as D = + and a negative test result as D = –. The observed test result is a bit of data that we will use to modify our belief about the value of the underlying disease parameter. The hit rate is expressed as p(D = + | θ = ☹) = 0.99. The test also has a false alarm rate of 5%. This means that 5% of the time when the disease is not present, the test falsely indicates that the disease is present. We denote the false alarm rate as p(D = + | θ = ☺) = 0.05.

Suppose we sample a person at random from the population, administer the test, and it comes up positive. What is the posterior probability that the person has the disease? Mathematically expressed, we are asking, what is p(θ = ☹ | D = +)? Before determining the answer from Bayes' rule, generate an intuitive answer and see if your intuition matches the Bayesian answer. Most people have an intuition that the probability of having the disease is near the hit rate of the test (which in this case is 0.99).

Hint: The following table of conjoint probabilities might help you understand the possible combinations of events. (The following table is a specific case of Table 4.2, p. 57.) The prior probabilities of the disease are on the bottom marginal. When we know that the test result is positive, we restrict our attention the row marked D = +.

[The table is not reproduced here.]

By Bayes' rule,
p(θ = ☹ | D = +) = p(D = + | θ = ☹) p(θ = ☹) / p(D = +)
= p(D = + | θ = ☹) p(θ = ☹) / [p(D=+|θ=☹) p(θ=☹) + p(D=+|θ=☺) p(θ=☺)]
= 0.99 * 0.001 / [0.99 * 0.001 + 0.05 * 0.999]
= 0.0194 (rounded to three significant digits)
Thus, despite the high hit rate of the test, the small prior and non–negligible false–alarm rate make the posterior probability less than 2%. (This analysis assumes that there were no other symptoms and that the person was selected at random so that the prior is applicable.)

Exercise 4.2. [Purpose: Iterative application of Bayes' rule, to see how posterior probabilities change with inclusion of more data.] Continuing from the previous exercise, suppose that the same randomly selected person as in the previous exercise is retested after the first test comes back positive, and on the retest the result is negative. Now what is the probability that the person has the disease? Hint: For the prior probability of the retest, use the posterior computed from the previous exercise. Also notice that p(D = – | θ = ☹) = 1 – p(D = + | θ = ☹) and p(D = – | θ = ☺) = 1 – p(D = + | θ = ☺).

To avoid rounding error, it is important to retain many significant digits for the prior. From the previous exercise, p(θ = ☹) = 0.0194346289753. Then, by Bayes' rule,
p(θ = ☹ | D = –) = p(D = – | θ = ☹) p(θ = ☹) / p(D = –)
= p(D = – | θ = ☹) p(θ = ☹) / [p(D=–|θ=☹) p(θ=☹) + p(D=–|θ=☺) p(θ=☺)]
where p(θ = ☹) is the posterior from the previous exercise. Hence
p(θ = ☹ | D = –) = (1–0.99)*0.0194… / [(1–0.99)*0.0194… + (1–.05)*(1–0.0194…)]
= 0.000209 (rounded to three significant digits)

Exercise 4.3. [Purpose: To get an intuition for the previous results by using "natural frequency" and "Markov" representations.]

(A) Suppose that the population consists of 100,000 people. Compute how many people should fall into each cell of the table in the hint shown in Exercise 4.1. To compute the expected frequency of people in a cell, just multiply the cell probability by the size of the population. To get you started, a few of the cells of the frequency table are filled in [below]. … Your job for this part of the exercise is to fill in the frequencies of the remaining cells of the table.

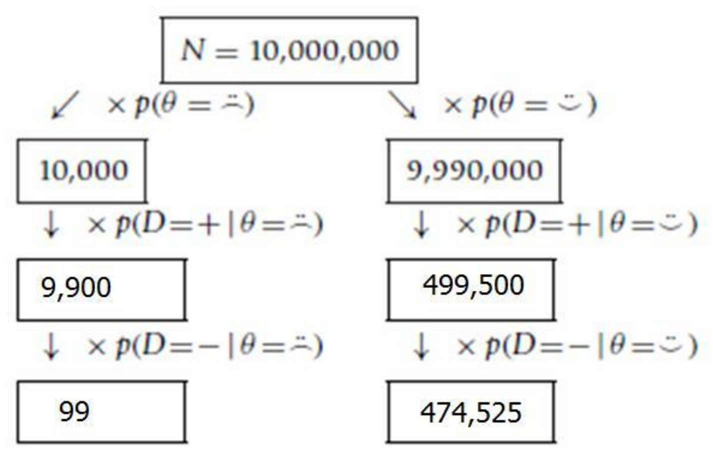
	θ = ☹	θ = ☺	
D = +	freq(D = + , θ = ☹) = p(D = + , θ = ☹) N = p(D = + | θ = ☹) p(θ = ☹) N = .99 * .001 * 100000 = 99	freq(D = + , θ = ☺) = p(D = + , θ = ☺) N = p(D = + | θ = ☺) p(θ = ☺) N = .05 * (1-.001) * 100000 = 4,995	5,094
D = –	freq(D = – , θ = ☹) = p(D = – , θ = ☹) N = p(D = – | θ = ☹) p(θ = ☹) N = (1-.99) * .001 * 100000 = 1	freq(D = – , θ = ☺) = p(D = – , θ = ☺) N = p(D = – | θ = ☺) p(θ = ☺) N = (1-.05) * (1-.001) * 100000 = 94,905	94,906
	100	99,900	N=100,000

(B) Take a good look at the frequencies in the table you just computed for the previous part. These are the so-called "natural frequencies" of the events, as opposed to the somewhat unintuitive expression in terms of conditional probabilities (Gigerenzer & Hoffrage, 1995). From the cell frequencies alone, determine the proportion of people who have the disease, given that their test result is positive. Before computing the exact answer

arithmetically, first give a rough intuitive answer merely by looking at the relative frequencies in the row D = +. Does your intuitive answer match the intuitive answer you provided back in Exercise 4.1? Probably not. Your intuitive answer here is probably much closer to the correct answer. Now compute the exact answer arithmetically. It should match the result from applying Bayes' rule in Exercise 4.1.

The result is positive, so we focus attention on the row D = +, which has a total of 5,094 people of whom 99 have the disease. Hence
p(θ = ☹ | D = +) = 99 / 5094 = 0.01943463
This exactly matches the result of Exercise 4.1.

(C) Now we'll consider a related representation of the probabilities in terms of natural frequencies, which is especially useful when we accumulate more data. Krauss, Martignon, & Hoffrage (1999) called this type of representation a "Markov" representation. Suppose now we start with a population of N D 10,000,000 people. We expect 99.9% of them (i.e., 9,990,000) not to have the disease, and just 0.1% (i.e., 10,000) to have the disease. Now consider how many people we expect to test positive. Of the 10,000 people who have the disease, 99% (i.e., 9900), will be expected to test positive. Of the 9,990,000 people who do not have the disease, 5%, (i.e., 499,500) will be expected to test positive. Now consider retesting everyone who has tested positive on the first test. How many of them are expected to show a negative result on the retest? Use this diagram to compute your answer:



(D) Use the diagram in the previous part to answer this question: What proportion of people who test positive at first and then negative on retest actually have the disease? In other words, of the total number of people at the bottom of the diagram in the previous part (those are the people who tested positive then negative), what proportion of them are in the left branch of the tree? How does the result compare with your answer to Exercise 4.2?

Notice that the total of the bottom is 99 + 474,525 = 474,624 people who test positive and negative. The proportion of those who actually have the disease is 99 / 474,624 = 0.000209 (rounded to three significant digits). This matches the result from Exercise 4.2.

Exercise 4.4. [Purpose: To see a hands-on example of data-order invariance.] Consider again the disease and diagnostic test of the previous two exercises. Suppose that a person selected at random from the population gets the test and it comes back negative. Compute the probability that the person has the disease. The person then is retested, and on the second test the result is positive. Compute the probability that the person has the disease. How does the result compare with your answer to Exercise 4.2?

As noted in the answer to Exercise 4.2, retention of many significant digits is important to avoid rounding error.
After the first (negative) test,
p(θ = ☹ | D = –) = p(D = – | θ = ☹) p(θ = ☹) / p(D = –)
= p(D = – | θ = ☹) p(θ = ☹) / [p(D=–|θ=☹) p(θ=☹) + p(D=–|θ=☺) p(θ=☺)]
= (1–0.99)*0.001 / [(1–0.99)*0.001 + (1–.05)*(1–0.001)]
= 0.0000105367416180
After the second (positive) test,
p(θ = ☹ | D = +) = p(D = + | θ = ☹) p(θ = ☹) / p(D = +)
= p(D = + | θ = ☹) p(θ = ☹) / [p(D=+|θ=☹) p(θ=☹) + p(D=+|θ=☺) p(θ=☺)]
= 0.99 * 0.0000105… / [0.99 * 0.0000105… + 0.05 * (1-0.0000105…)]
= 0.000209 (rounded to three significant digits)
This result matches the previous exercises.

Exercise 4.5. [Purpose: An application of Bayes' rule to neuroscience, to infer cognitive function from brain activation.] Cognitive neuroscientists investigate which areas of the brain are active during particular mental tasks. In many situations, researchers observe that a certain region of the brain is active and infer that a particular cognitive function is therefore being carried out. Poldrack (2006) cautioned that such inferences are not necessarily firm and need to be made with Bayes' rule in mind. Poldrack (2006) reported the following frequency table of previous studies that involved any language-related task (specifically phonological and semantic processing) and whether or not a particular region of interest (ROI) in the brain was activated:

	Language Study	**Not Language Study**
Activated	**166**	**199**
Not activated	**703**	**2154**

Suppose that a new study is conducted and finds that the ROI is activated. If the prior probability that the task involves language processing is 0.5, what is the posterior probability, given that the ROI is activated? (Hint: Poldrack (2006) reports that it is 0.69. You job is to derive this number.)

p(Lang. | ROI Act.) = p(ROI Act. | Lang.) p(Lang.)
/ (p(ROI Act. | Lang.) p(Lang.) + p(ROI Act. | NotLang.) p(NotLang.))
= 166/(166+703)*0.5 / (166/(166+703)*0.5 + 199/(199+2154)*0.5)
= 0.693
Notice that the posterior probability of involving language is only a little higher than the prior.

Exercise 4.6. [Purpose: To make sure you really understand what is being shown in Figure 4.1.] Derive the posterior distribution in Figure 4.1 by hand. The prior has p(θ = .25) = .25, p(θ = .50) = .50, and p(θ = .75) = .25. The data consist of a specific sequence of flips with three heads and nine tails, so p(D|θ) = $\theta^3(1-\theta)^9$. Hint: Check that your posterior probabilities sum to 1.

p(θ=.25|D) = p(D|θ=.25) p(θ=.25)
/ [p(D|θ=.25) p(θ=.25) + p(D|θ=.50) p(θ=.50) + p(D|θ=.75) p(θ=.75) **]**
= $.25^3(1-.25)^9$*.25
/ [$.25^3(1-.25)^9$*.25 + $.50^3(1-.50)^9$*.50 + $.75^3(1-.75)^9$*.25]
= 0.705
Similarly, p(θ=.50|D) = 0.294 and p(θ=.75|D) = 0.001.
(For future reference, the denominator in the equation above is 0.0004158, rounded to four significant digits.)

Exercise 4.7. [Purpose: For you to see, hands on, that p(D) lives in the denominator of Bayes' rule.] Compute p(D) in Figure 4.1 by hand. Hint: Did you notice that you already computed p(D) in the previous exercise?

p(D) = p(D|θ=.25) p(θ=.25) + p(D|θ=.50) p(θ=.50) + p(D|θ=.75) p(θ=.75)
which is the denominator from the previous exercise, where we found that p(D)=0.0004158.

Chapter 5.

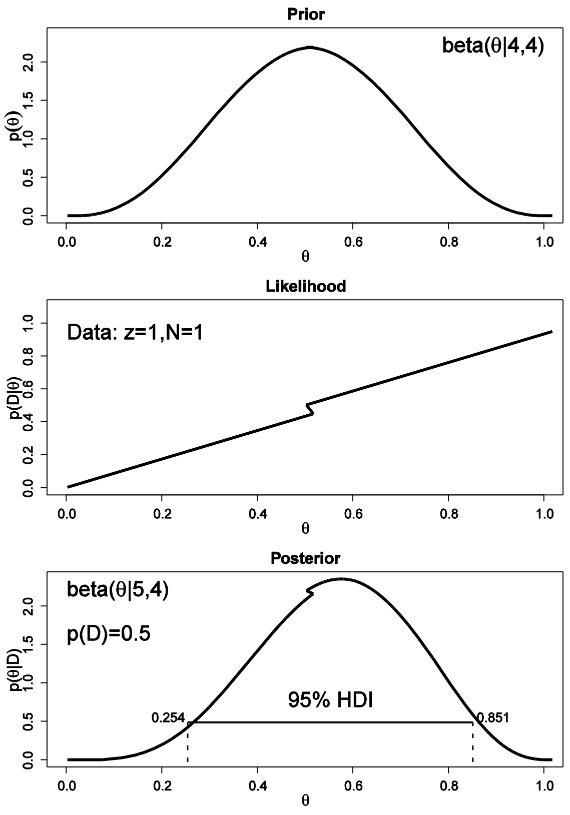
Exercise 5.1. [Purpose: To see the influence of the prior in each successive flip, and to see another demonstration that the posterior is invariant under reorderings of the data.] For this exercise, use the R function of Section 5.5.1 (BernBeta.R). (Read the comments at the top of the code for an example of how to use it, and don't forget to source the function before calling it.) Notice that the function returns the posterior beta values each time it is called, so you can use the returned values as the prior values for the next function call.

(A) Start with a prior distribution that expresses some uncertainty that a coin is fair: beta(θ|4, 4). Flip the coin once; suppose we get a head. What is the posterior distribution?

At the R command prompt, typing

```
post = BernBeta( c(4,4) , c(1) )
```

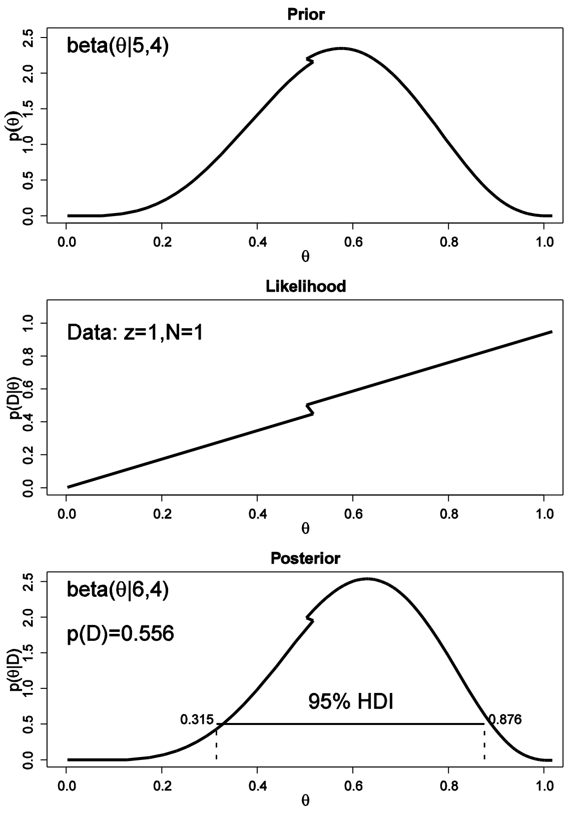
yields this figure:



(The jagged bits in the curve are artifacts of how Microsoft Word incorrectly renders EPS figures. The curves are actually smooth.)

(B) Use the posterior from the previous flip as the prior for the next flip. Suppose we flip again and get a head. Now what is the new posterior? (Hint: If you type post = BernBeta(c(4,4) , c(1)) for the first part, then you can type post = BernBeta(post , c(1)) for the next part.)

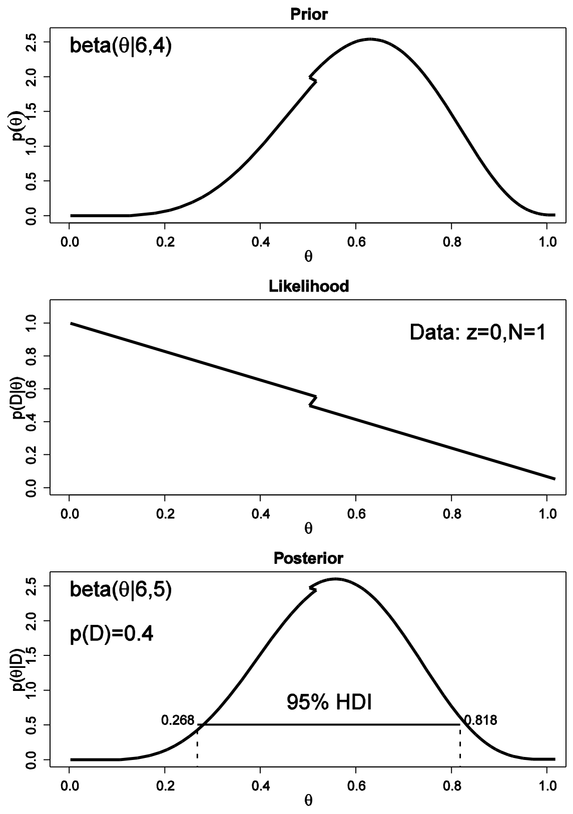
At the R command prompt, typing
post = BernBeta(post , c(1))
yields this figure:



(The jagged bits in the curve are artifacts of how Microsoft Word incorrectly renders EPS figures. The curves are actually smooth.)

(C) Using that posterior as the prior for the next flip, flip a third time and get T. Now what is the new posterior? (Hint: Type post = BernBeta(post , c(0)).)

At the R command prompt, typing
post = BernBeta(post , c(0))
yields this figure:



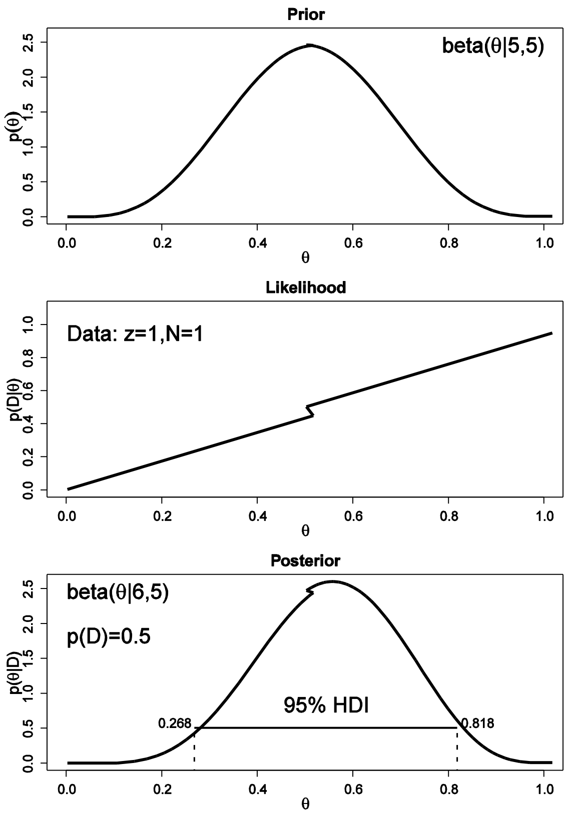
(The jagged bits in the curve are artifacts of how Microsoft Word incorrectly renders EPS figures. The curves are actually smooth.)

(D) Do the same three updates but in the order T, H, H instead of H, H, T. Is the final posterior distribution the same for both orderings of the flip results?

The sequence of commands is

```
post = BernBeta( c(4,4) , c(0) )
post = BernBeta( post , c(1) )
post = BernBeta( post , c(1) )
```

and the final graph looks like this:

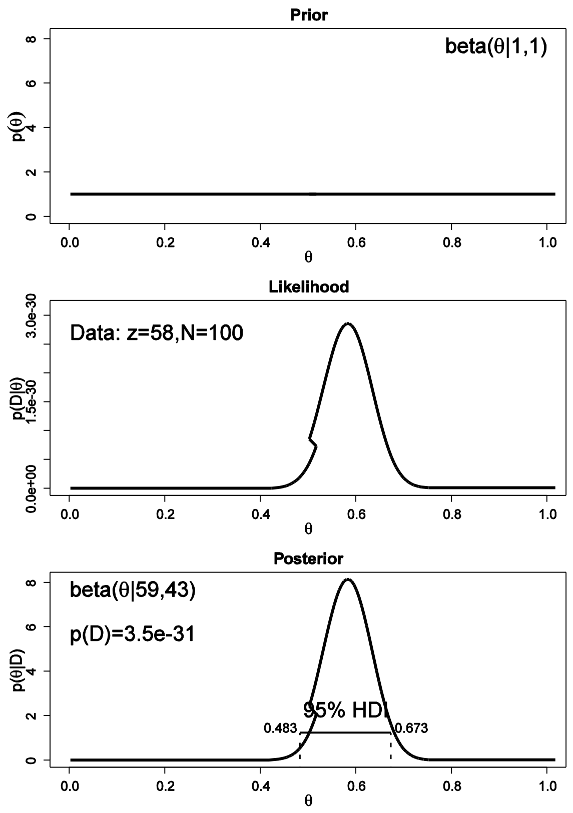


Notice that the ultimate posterior is the same as Part C, but the prior leading up to it is different because of the different sequence of updating. (The jagged bits in the curve are artifacts of how Microsoft Word incorrectly renders EPS figures. The curves are actually smooth.)

Exercise 5.2. [Purpose: To connect HDIs to the real world, with iterative data collection.] Suppose an election is approaching, and you are interested in knowing whether the general population prefers candidate A or candidate B. A just published poll in the newspaper states that of 100 randomly sampled people, 58 preferred candidate A and the remainder preferred candidate B.

(A) Suppose that before the newspaper poll, your prior belief was a uniform distribution. What is the 95% HDI on your beliefs after learning of the newspaper poll results?

The R command
post = BernBeta(c(1,1) , c(rep(1,58) , rep(0,42)))
yields



which has a 95% HDI from 0.483 to 0.673. (The jagged bits in the curve are artifacts of how Microsoft Word incorrectly renders EPS figures. The curves are actually smooth.)

(B) Based in the newspaper poll, is it credible to believe that the population is equally divided in its preferences among candidates?

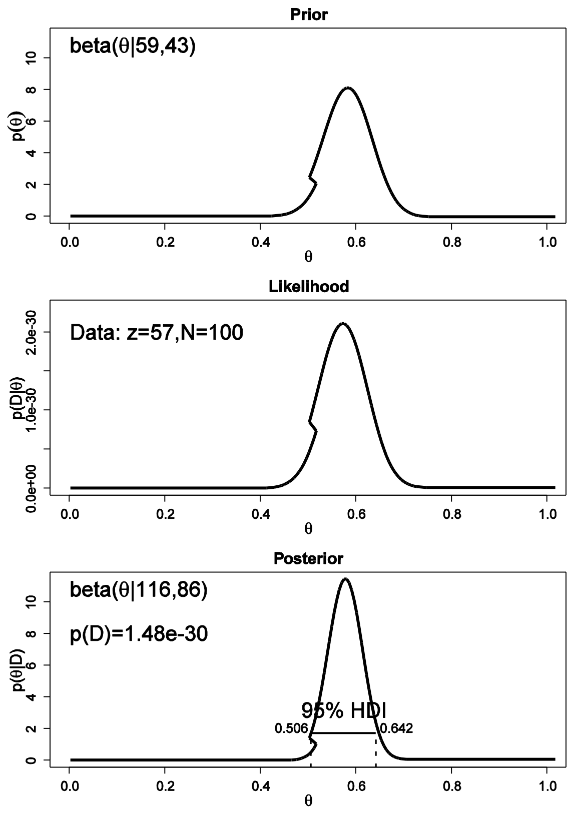
The HDI from Part A shows that θ=0.5 is among the credible values, hence it is credible to believe that the population is equally divided in its preferences.

(C) You want to conduct a follow-up poll to narrow down your estimate of the population's preference. In your follow-up poll, you randomly sample 100 people and find that 57 prefer candidate A and the remainder prefer candidate B. Assuming that peoples' opinions have not changed between polls, what is the 95% HDI on the posterior?

The R command

post = BernBeta(post , c(rep(1,57) , rep(0,43)))

yields



which has a 95% HDI from 0.506 to 0.642 (The jagged bits in the curve are artifacts of how Microsoft Word incorrectly renders EPS figures. The curves are actually smooth.)

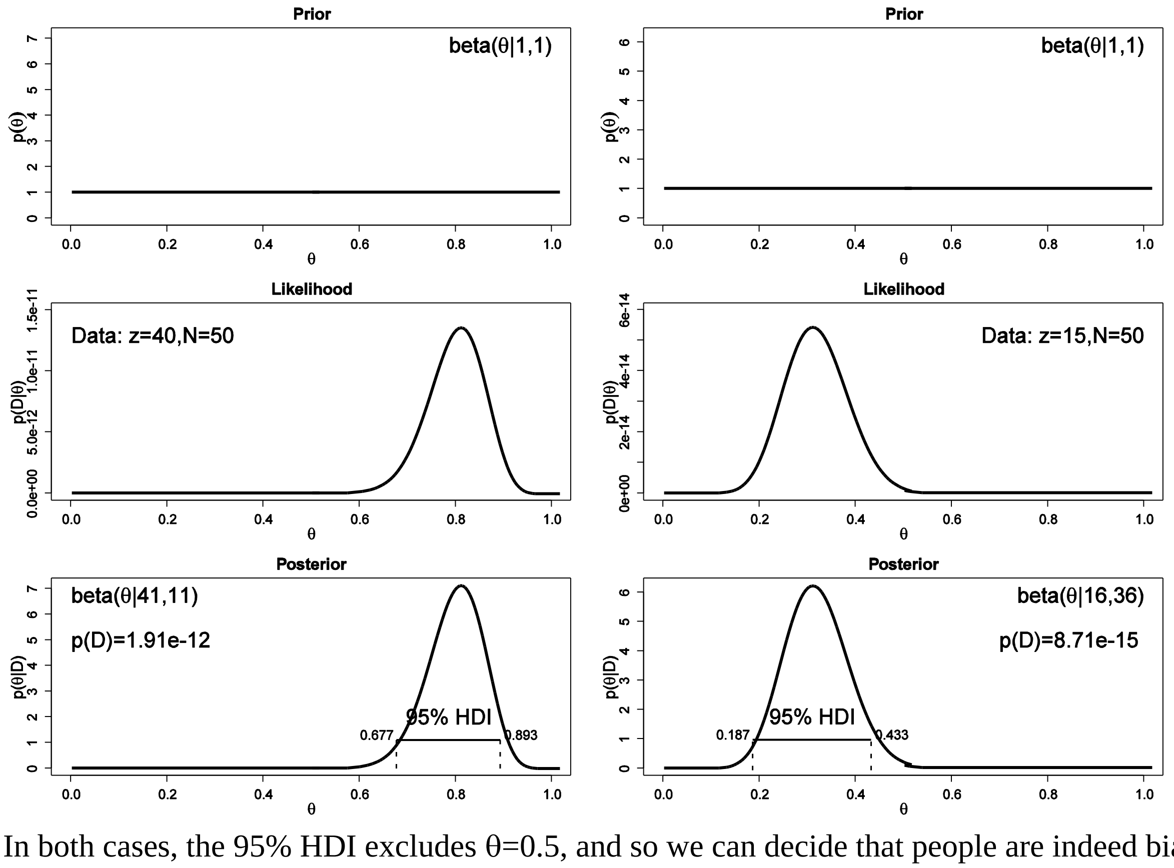
(D) Based on your follow-up poll, is it credible to believe that the population is equally divided in its preferences among candidates?

The HDI from Part C excludes θ=0.5, hence we could decide that the population is not equally divided (and prefers candidate A).

Exercise 5.3. [Purpose: To apply the Bayesian method to real data analysis. These data are representative of real data (Kruschke, 2009).] Suppose you train people in a simple learning experiment, as follows. When people see the two words "radio" and "ocean," on the computer screen, they should press the F key on the computer keyboard. They see several repetitions and learn the response well. Then you introduce another correspondence for them to learn: Whenever the words "radio" and "mountain" appear,

they should press the J key on the computer keyboard. You keep training them until they know both correspondences well. Now you probe what they've learned by asking them about two novel test items. For the first test, you show them the word "radio" by itself and instruct them to make the best response (F or J) based on what they learned before. For the second test, you show them the two words "ocean" and "mountain" and ask them to make the best response. You do this procedure with 50 people. Your data show that for "radio" by itself, 40 people chose F and 10 chose J. For the word combination "ocean" and "mountain," 15 chose F and 35 chose J. Are people biased toward F or toward J for either of the two probe types? To answer this question, assume a uniform prior, and use a 95% HDI to decide which biases can be declared to be credible.

The commands
post = BernBeta(c(1,1) , c(rep(1,40) , rep(0,10)))
post = BernBeta(c(1,1) , c(rep(1,15) , rep(0,35)))
yield these graphs:



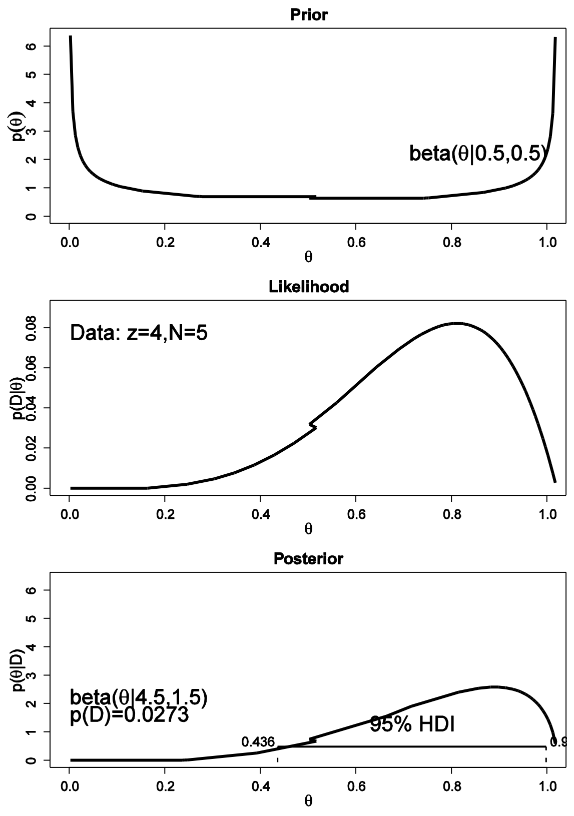
In both cases, the 95% HDI excludes θ=0.5, and so we can decide that people are indeed biased in their responses, toward F in the first case but toward J in the second case.

Exercise 5.4. [Purpose: To explore an unusual prior and learn about the beta distribution in the process.] Suppose we have a coin that we know comes from a magic-trick store, and therefore we believe that the coin is strongly biased either usually to come up heads or usually to come up tails, but we don't know which. Express this belief as a beta prior. (Hint: See Figure 5.1, upper-left panel.) Now we flip the coin five times and it comes up heads in four of the five flips. What is the posterior distribution? (Use the R function of Section 5.5.1 (BernBeta.R) to see graphs of the prior and posterior.)

The R command

```
post = BernBeta( c(.5,.5) , c(1,1,1,1,0) )
```

yields



(The jagged bits in the curve are artifacts of how Microsoft Word incorrectly renders EPS figures. The curves are actually smooth.)

Exercise 5.5. [Purpose: To get hands-on experience with the goal of predicting the next datum, and to see how the prior influences that prediction.]

(A) Suppose you have a coin that you know is minted by the federal government and has not been tampered with. Therefore, you have a strong prior belief that the coin is fair. You flip the coin 10 times and get 9 heads. What is your predicted probability of heads for the 11th flip? Explain your answer carefully; justify your choice of prior.

To justify a prior, we might say that our strength of fairness is equivalent to having previously seen the coin flipped 100 times and coming up heads in 50% of those flips. Hence the prior would be beta(θ|,50,50). (This is not the only correct answer; you might instead be more confident, and use a beta(θ|,500,500) if you suppose you've previously seen 1,000 flips with 50% heads.)

The posterior is beta(θ|,50+9,50+1), which has a mean of 59/(59+51) = 0.536. This is the predicted probability of heads for the next, i.e., 11th, flip.

(B) Now you have a different coin, this one made of some strange material and marked (in fine print) "Patent Pending, International Magic, Inc." You flip the coin 10 times and get 9 heads. What is your predicted probability of heads for the 11th flip? Explain your answer carefully; justify your choice of prior. Hint: Use the prior from Exercise 5.4.

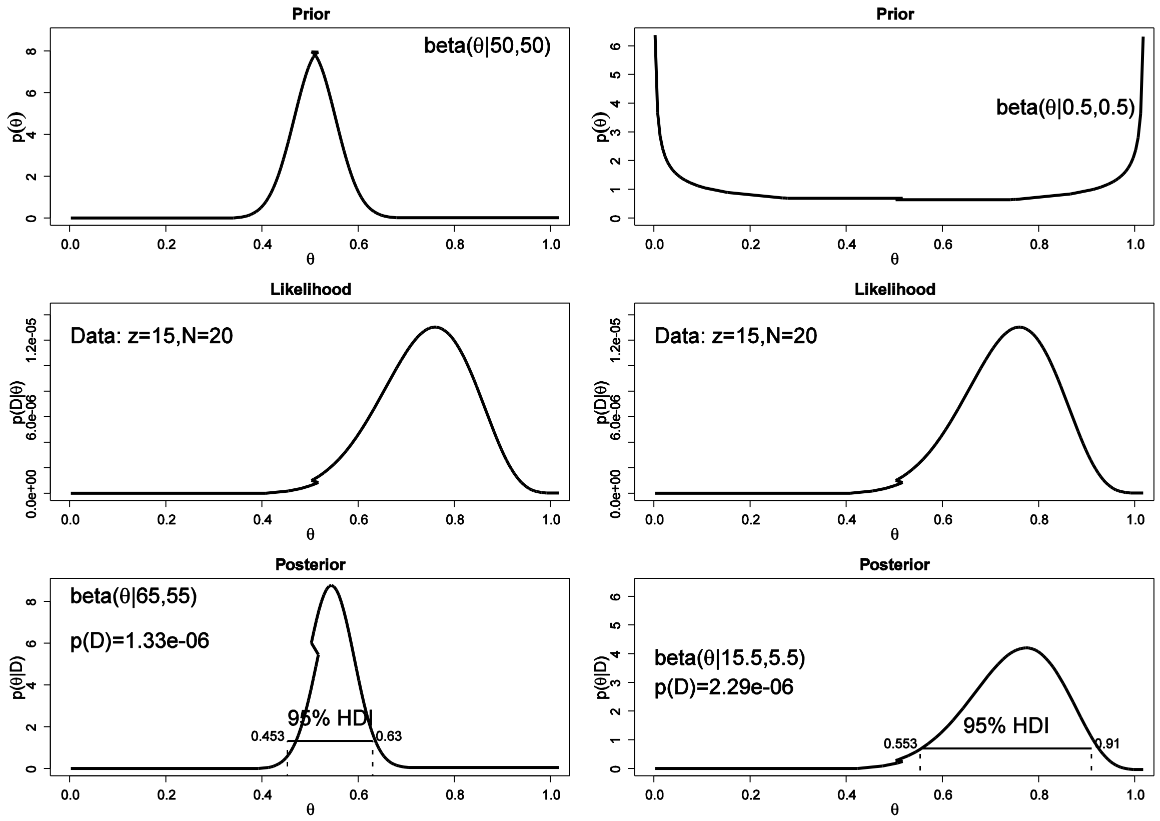
We use a beta(θ|0.5,0.5) prior, like Exercise 5.4, because it expresses a belief that the coin is either head biased or tail biased. The posterior is beta(θ|,0.5+9,0.5+1), which has a mean of 9.5/(9.5+1.5) = 0.863. This is the predicted probability of heads for the next, i.e., 11th, flip. Notice that it is quite different than the conclusion from Part A.

Exercise 5.6. [Purpose: To get hands-on experience with the goal of model comparison.] Suppose we have a coin, but we're not sure whether it's a fair coin or a trick coin. We flip it 20 times and get 15 heads. Is it more likely to be fair or trick? To answer this question, consider the value of the Bayes factor (i.e., the ratio of the evidences of the two models). When answering this question, justify your choice of priors to express the two hypotheses. Use the R function of Section 5.5.1 (BernBeta.R) to graph the priors and check that they reflect your beliefs; the R function will also determine the evidences from Equation 5.10.

For the fair coin, we'll use a beta(θ|50,50) prior to be consistent with Exercise 5.5(A), and for the trick coin we'll use a beta(θ|0.5,0.5) prior to be consistent with Exercise 5.4 (and both of those Exercises had justifications for those priors). Typing the R commands

```
post = BernBeta( c(50,50) , c( rep(1,15) , rep(0,5) ) )
post = BernBeta( c(0.5,0.5) , c( rep(1,15) , rep(0,5) ) )
```

yields



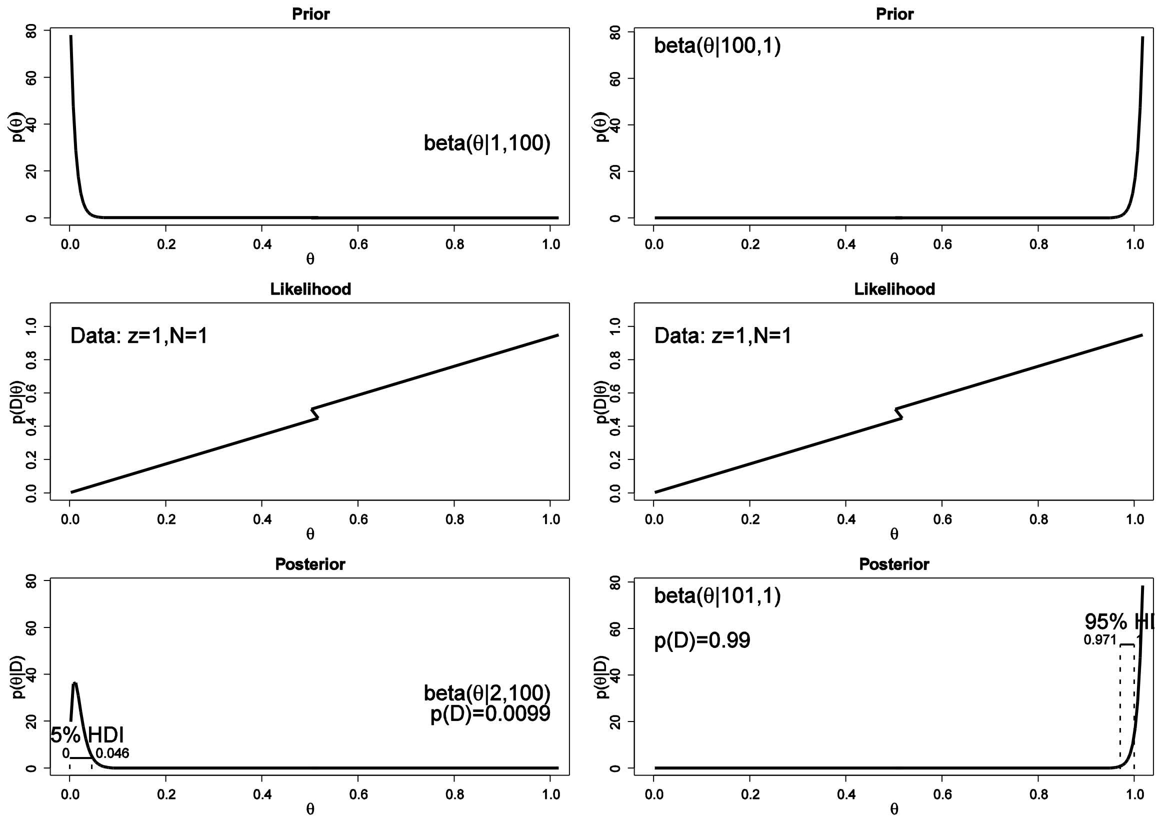
The posteriors show that p(D) is somewhat higher for the trick-coin prior than for the fair-coin prior. (Note: If the priors are different, the conclusion might be different!) (The jagged bits in the curve are artifacts of how Microsoft Word incorrectly renders EPS figures. The curves are actually smooth.)

Exercise 5.7. [Purpose: To see how very small data sets can give strong leverage in model comparison when the model predictions are very different.] Suppose we have a coin that we strongly believe is a trick coin, so it almost always comes up heads or it almost always comes up tails; we just don't know if the coin is the head-biased type or the tail-biased type. Thus, one model is a beta prior heavily biased toward tails, beta(θ|1,100), and the other model is a beta prior heavily biased toward heads, beta(θ|100,1). We flip the coin once and it comes up heads. Based on that single flip, what is the value of the Bayes factor (i.e., the ratio of the evidences of the two models)? Use the R function of Section 5.5.1 (BernBeta.R) to determine the evidences from Equation 5.10.

The R commands

```
post = BernBeta( c(1,100) , c(1) )
post = BernBeta( c(100,1) , c(1) )
```

yield the following graphs:



The head-biased prior is favored by a Bayes factor of 0.9900/0.0099 = 100, based on this single flip. (The jagged bits in the curve are artifacts of how Microsoft Word incorrectly renders EPS figures. The curves are actually smooth.)

Exercise 5.8. [Purpose: Hands-on learning about the method of posterior predictive checking.] Following the scenario of the previous exercise, suppose we flip the coin a total of N=12 times and it comes up heads in z=8 of those flips. Suppose we let a beta(θ|100,1) distribution describe the head-biased trick coin, and we let a beta(θ|1,100) distribution describe the tail-biased trick coin.

(A) What are the evidences for the two models, and what is the value of the Bayes factor?

Running BernBeta in R shows that for the 100,1 prior, p(D)=1.49e-07, and for the 1,100 prior, p(D)=2.02e-12. The Bayes factor is 1.49e-07 / 2.02e-12 = 73,800 (rounded). In other words, the head-biased prior is favored by a factor of more than 73,000 relative to the tail-biased prior!

Now for the new part, a posterior predictive check. Is the winning model actually a good model of the data? In other words, one model can be whoppingly better than the other, but that does not necessarily mean that the winning model is a good model; it might mean merely that the winning model is less bad than the losing model. One way to examine the veracity of the winning model is to simulate data sampled from the winning model and see if the simulated data "look like" the actual data. To simulate data generated by the winning model, we do the following: First, we will randomly generate a value of from the posterior distribution of the winning model. Second, using that value of , we will generate a sample of coin flips. Third, we will count the number of heads in the sample, as a summary of the sample. Finally, we determine whether the number of heads in a typical simulated sample is close to the number of heads in our actual sample. The following program carries out these steps. Study it, run it, and answer the questions that follow.

[program excluded to save space]

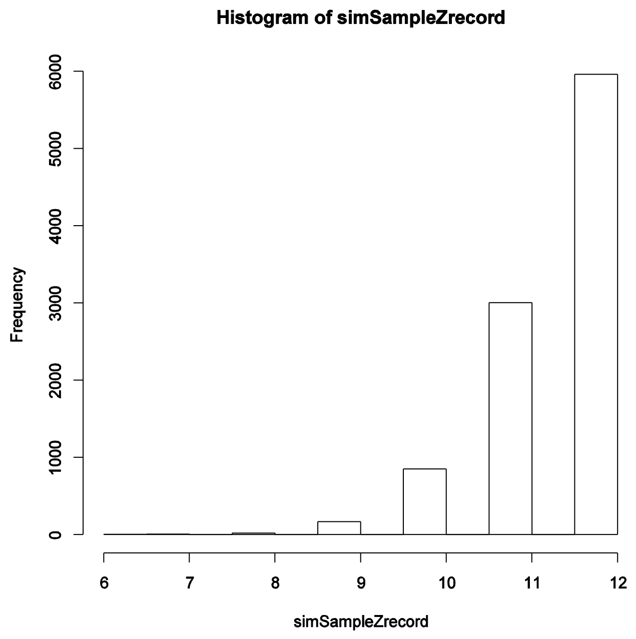
(B) How many samples (each of size N) were simulated?

The program line
nSimSamples = 10000
sets the number of simulated samples to 10000.

(C) Was the same value of used for every simulated sample, or were different values of used in different samples? Why?

The program line
sampleTheta = rbeta(1 , postA , postB)
randomly generates a different value for theta in every sample. This is because the various theta values are representative of the entire posterior distribution.

(D) Based on the simulation results, does the winning model seem to be a good model? Why or why not?



The program creates the histogram shown above, in which we can see that the model almost never generates simulated data in which z=8. The reason is that the head-biased model is extremely head-biased, but the result, 8 heads out of 12 flips, is only moderately head biased.

Thus, despite the fact that the extremely head-biased model is far better than the extremely tail-biased model, the extremely head-biased model is a poor model of the actual data.

Chapter 6.

Exercise 6.1. [Purpose: To understand the discretization used for the priors in the R functions of Section 6.7.1 (BernGrid.R) and throughout this chapter.] Consider this R code for discretizing a beta(θ|8,4) distribution:

```
nIntervals = 10
width = 1 / nIntervals
Theta = seq( from = width/2 , to = 1-width/2 , by = width )
approxMass = dbeta( Theta , 8 , 4 ) * width
pTheta = approxMass / sum( approxMass )
```

(A) What is the value of sum(approxMass)? Why is it not exactly 1?

0.9991421. This is not exactly 1.0 because this is, after all, a discrete approximation. We are lucky, in fact, that the sum is so close to 1.0 when using such wide intervals. As the width of the bins gets smaller, the sum will tend to get closer to 1.0.

(B) Suppose we use instead the following code to define the grid of points:

```
Theta = seq( from = 0 , to = 1 , by = width )
```

Why is this not appropriate? (Hint: Consider exactly what intervals are represented by the first and last values in Theta. Do those first and last intervals have the same widths as the other intervals? If they do, do they fall entirely within the domain of the beta distribution?)

This definition of intervals is infelicitous because the first and last intervals are centered at the end points of the domain, and therefore half of those intervals refer to values of theta that are invalid. In the limit, as the bin width goes toward zero, this problem becomes negligible. Another problem is that sometimes --- in particular for beta distributions with shape parameters less than 1 --- the density of the distribution at 0 or 1 can be infinite. We will stick to the method of Part A to be sure to avoid these problems.

Exercise 6.2. [Purpose: To practice specifying a nonbeta prior.] Suppose we have a coin that has a head on one side and a tail on the other. We think it might be fair, or it might be a trick coin that is heavily biased toward heads or tails. We want to express this prior belief with a single prior over . Therefore, the prior needs to have three peaks: one near zero, one around 0.5, and near 1.0. But these peaks are not just isolated spikes, because we have uncertainty about the actual value of .

(A) Express your prior belief as a list of probability masses over a fairly dense grid of θ values. Remember to set a gradual decline around the three peaks. Briefly justify your choice. Hint: You can specify the peaks however you want, but one simple way is something like this:

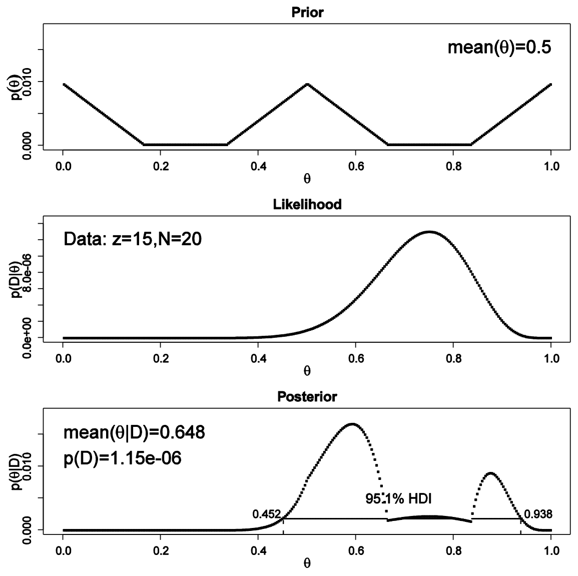
```
pTheta = c( 50:1 , rep(1,50) , 1:50 , 50:1 , ...
pTheta = pTheta / sum( pTheta )
width = 1 / length(pTheta)
```

```
Theta = seq( from = width/2 , to = 1-width/2 , by = width )
```

The exercise does not demand one specific answer. One reasonable answer completes the code in the Hint above, and is illustrated in the graph of Part B below.

(B) Suppose you flip the coin 20 times and get 15 heads. Use the R function of Section 6.7.1 (BernGrid.R) to display the posterior beliefs. Include the R code you used to specify the prior values.

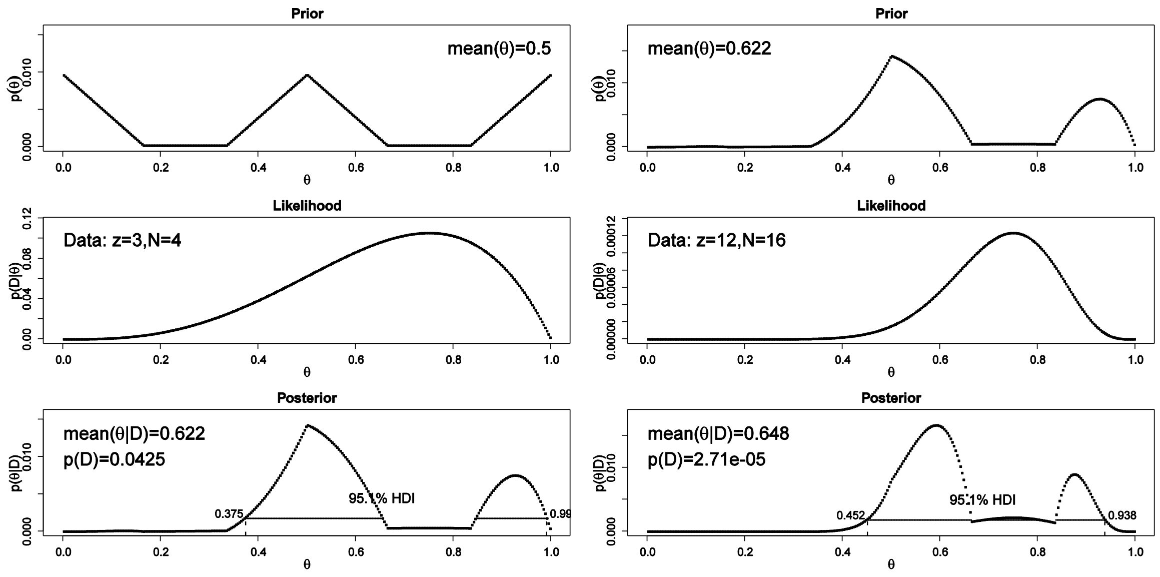
pTheta = c(50:1 , rep(1,50) , 1:50 , 50:1 , rep(1,50) , 1:50)
pTheta = pTheta / sum(pTheta)
width = 1 / length(pTheta)
Theta = seq(from = width/2 , to = 1-width/2 , by = width)
post = BernGrid(Theta , pTheta , c(rep(1,15),rep(0,5)))



Exercise 6.3. [Purpose: To use the function of Section 6.7.1 (BernGrid.R) for sequential updating (i.e., use output of one function call as the prior for the next function call). Observe that data ordering does not matter]
(A) Using the same prior that you used for the previous exercise, suppose you flip the coin just 4 times and get 3 heads. Use the R function of Section 6.7.1 (BernGrid.R) to display the posterior.
(B) Suppose we flip the coin an additional 16 times and get 12 heads. Now what is the posterior distribution? To answer this question, use the posterior distribution that is output by the function in the previous part as the prior for this part. Show the R commands you used to call the function. (Hint: The final posterior should match the posterior of Exercise 6.2, except that the graph of the prior should look like the posterior from the previous part. Figure 6.5 shows an example.)

pTheta = c(50:1 , rep(1,50) , 1:50 , 50:1 , rep(1,50) , 1:50)
pTheta = pTheta / sum(pTheta)

```
width = 1 / length(pTheta)
Theta = seq( from = width/2 , to = 1-width/2 , by = width )
post = BernGrid( Theta , pTheta , c(rep(1,3),rep(0,1)) )
post = BernGrid( Theta , post , c(rep(1,12),rep(0,4)) )
# Notice that post from the first call to BernGrid was used as the prior for
# the second call to BernGrid.
```

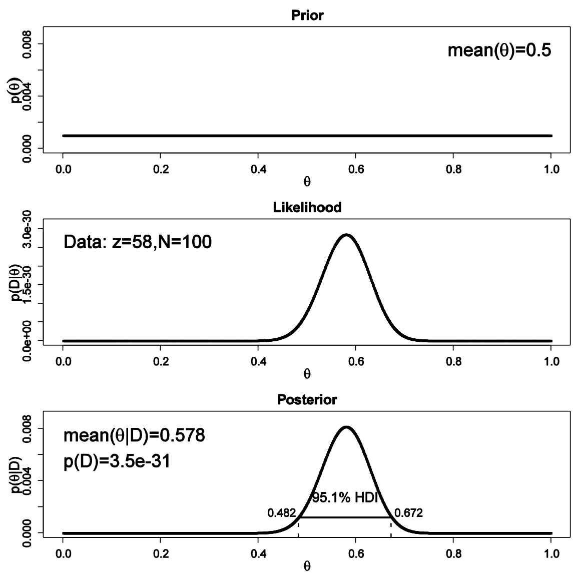


Notice that the ultimate posterior matches the one from the previous exercise.

Exercise 6.4. [Purpose: To connect HDIs to the real world, with iterative data collection.] Suppose an election is approaching, and you are interested in knowing whether the general population prefers candidate A or candidate B. A just-published poll in the newspaper states that of 100 randomly sampled people, 58 preferred candidate A and the remainder preferred candidate B.

(A) Suppose that before the newspaper poll, your prior belief was a uniform distribution. What is the 95% HDI on your beliefs after learning of the newspaper poll results? Use the function of Section 6.7.1 (BernGrid.R) to determine your answer.

```
pTheta = rep(1,1000)
pTheta = pTheta / sum( pTheta )
width = 1 / length(pTheta)
Theta = seq( from = width/2 , to = 1-width/2 , by = width )
post = BernGrid( Theta , pTheta , c(rep(1,58),rep(0,42)) )
```

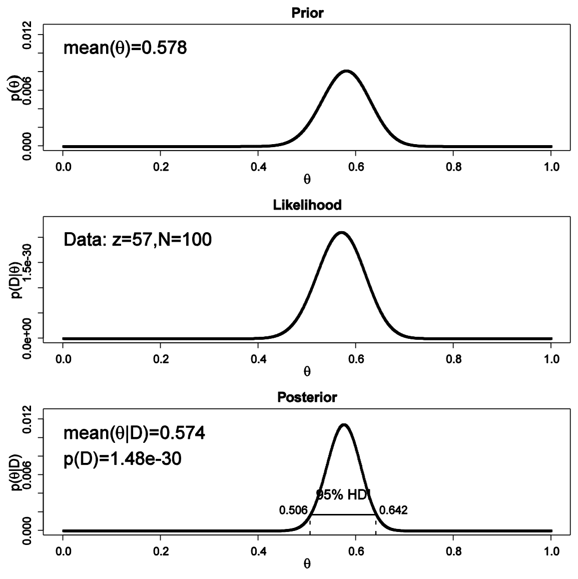


(B) Based in the newspaper poll, is it credible to believe that the population is equally divided in its preferences among candidates?

The 95% HDI includes 0.50, so an equally divided population is still credible.

(C) You want to conduct a follow-up poll to narrow down your estimate of the population's preference. In your follow-up poll, you randomly sample 100 people and find that 57 prefer candidate A and the remainder prefer candidate B. Assuming that peoples' opinions have not changed between polls, what is the 95% HDI on the posterior?

```
post = BernGrid( Theta , post , c(rep(1,57),rep(0,43)) )
```



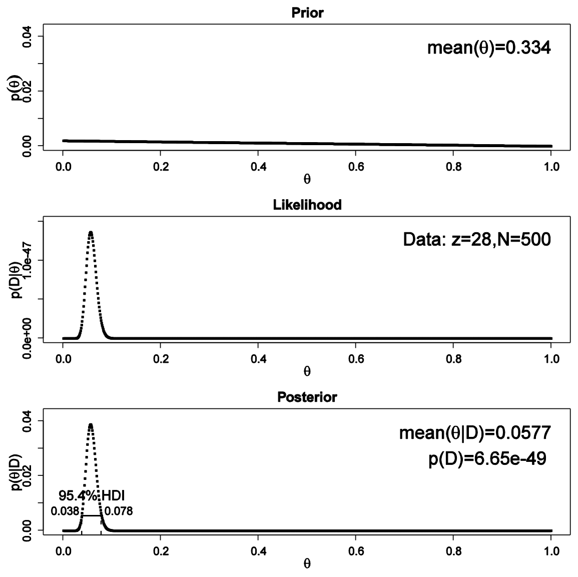
(D) Based on your follow-up poll, is it credible to believe that the population is equally divided in its preferences among candidates? (Hint: Compare your answer here to your answer for Exercise 5.2.)

The 95% HDI now excludes 0.5, and therefore we might decide to declare that an equally-divided population is not credible. Notice that the posterior found here by grid approximation closely matches the one found in Exercise 5.2 by analytical mathematics.

Exercise 6.5. [Purpose: To explore HDIs in the (almost) real world.] Suppose that the newly hired quality control manager at the Acme Widget factory is trying to convince the CEO that the proportion of defective widgets coming off the assembly line is less than 10%. No previous data are available regarding the defect rate at the factory. The manager randomly samples 500 widgets, and she finds that 28 of them are defective. What do you conclude about the defect rate? Justify your choice of prior. Include graphs to explain/support your conclusion.

There is no uniquely correct prior for this exercise. We can imagine that the CEO is very skeptical about quality, and believes that even very high defect rates are possible, although not as probable as low defect rates. Therefore the prior used here is linearly decreasing across the domain.

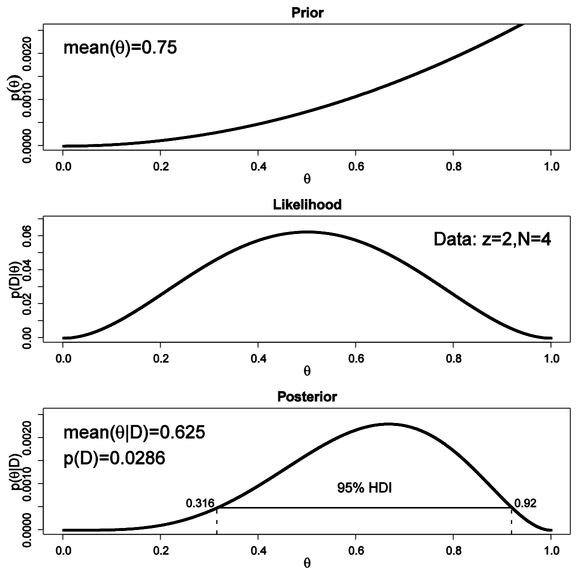
```
pTheta = 1000:1  # linearly decreasing prior
pTheta = pTheta / sum( pTheta )
width = 1 / length(pTheta)
Theta = seq( from = width/2 , to = 1-width/2 , by = width )
post = BernGrid( Theta , pTheta , c(rep(1,28),rep(0,500-28)) )
```



The 95% HDI falls entirely below 0.10, hence it is reasonable to decide that a defect rate of 10% is not credible (and that the actual defect rate is near 5.8%).

Exercise 6.6. [Purpose: To use grid approximation for prediction of subsequent data.] Suppose we believe that a coin is biased to come up heads, and we describe our prior belief as quadratically increasing: p(theta) is proportional to theta squared. Suppose we flip the coin four times and observe two heads and two tails. Based on the posterior distribution, what is the predicted probability that the next flip will yield a head? To answer this question, use the function of Section 6.7.1 (BernGrid.R). Define thetagrid as in the example in the comments at the beginning of the function. Then define relprob = thetagrid^2, and normalize it to specify the prior. The function returns a vector of discrete posterior masses, which you might call posterior. Apply Equation 6.4 by computing sum(thetagrid * posterior). (Bonus hint: The answer is also displayed in the output graphics.)

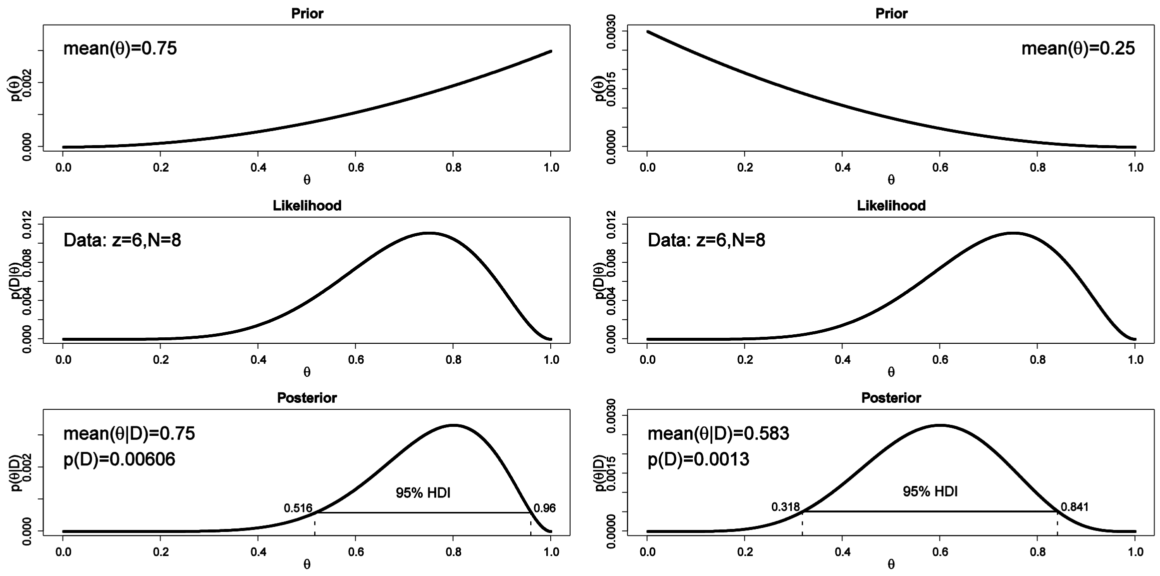
```
binwidth = 1/1000
thetagrid = seq( from=binwidth/2 , to=1-binwidth/2 , by=binwidth )
relprob = thetagrid^2
prior = relprob / sum(relprob)
posterior = BernGrid( thetagrid , prior , c(rep(1,2),rep(0,2)) )
predprob = sum( thetagrid * posterior )
show( predprob )
```



The predicted probability of heads for the next flip is the value of predprob, also shown in the graph of the posterior, which equals 0.625.

Exercise 6.7. [Purpose: To use grid approximation to compare models.] Suppose we have competing beliefs about the bias of a coin: One person believes the coin is head biased, and the second person believes the coin is tail biased. To make this specific, suppose the head-biased prior is p(theta|M1) proportional to theta^2 and the tail-biased prior is p(theta|M2) proportional to (1-theta)^2. Suppose that we are equally willing to entertain the two models, so p(M1) = p(M2) = 0.5. We flip the coin N = 8 times and observe z = 6 heads. What is the ratio of posterior beliefs? To answer this question, read the coding suggestion in Exercise 6.6 and look at p(D) in the graphical output.

```
binwidth = 1/1000
thetagrid = seq( from=binwidth/2 , to=1-binwidth/2 , by=binwidth )
relprob = thetagrid^2
prior = relprob / sum(relprob)
posterior = BernGrid( thetagrid , prior , c(rep(1,6),rep(0,2)) )

relprob = (1-thetagrid)^2
prior = relprob / sum(relprob)
posterior = BernGrid( thetagrid , prior , c(rep(1,6),rep(0,2)) )
```



The posteriors reveal that p(D|M1)=0.00606 and p(D|M2)=0.00130, and therefore the Bayes factor is 4.66 in favor of M1. Because the prior on the models was 50-50, the Bayes factor is also the posterior odds.

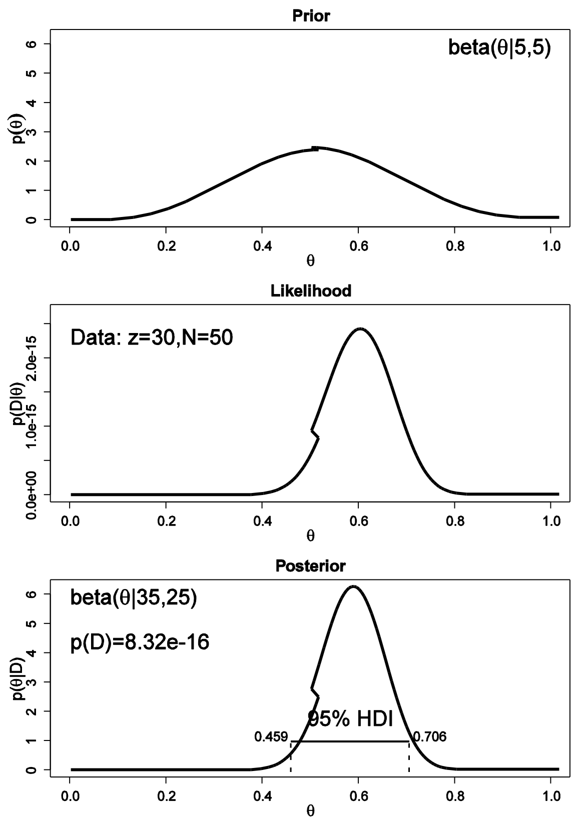
Exercise 6.8. [Purpose: To model comparison in the (almost) real world.] A pharmaceutical company claims that its new drug increases the probability that couples who take the drug will conceive a boy. The company has published no studies regarding this claim, so there is no public knowledge regarding the efficacy of the drug. Suppose you conduct a study in which 50 couples, sampled at random from the general population, take the drug during a period of time while trying to conceive a baby. Suppose that eventually all couples conceive; there are 30 boys and 20 girls (no multiple births).

(A) You want to estimate the probability of conceiving a boy for couples who take the drug. What is an appropriate prior belief distribution? It cannot be the general population probability, because that is a highly peaked distribution near 0.5 that refers to nondrugged couples. Instead, the prior needs to reflect our preexperiment uncertainty in the effect of the drug. Discuss your choice of prior with this in mind.

The most skeptical prior for drugged couples would be the nondrugged population prior. This prior would be sharply peaked around 0.5 and it would take a large amount of data to reallocate beliefs away from it. A less skeptical prior would be gently peaked at 0.5, with some modest prior belief in probabilities above and below 0.5. *Ultimately, the analysis needs to convince your audience, and therefore the prior needs to be agreeable to your audience.* Suppose we have some theoretical reason to believe that the drug may indeed alter the probability of conceiving a boy or girl, and the audience of the analysis would agree. Therefore we use, say, a beta(theta|5,5) prior. This is not the only correct answer; the point is to think carefully about where the prior comes from and what your audience would agree with.

(B) Using your prior from the previous part, show a graph of the posterior and decide whether it is credible that couples who take the drug have a 50% chance of conceiving a boy.

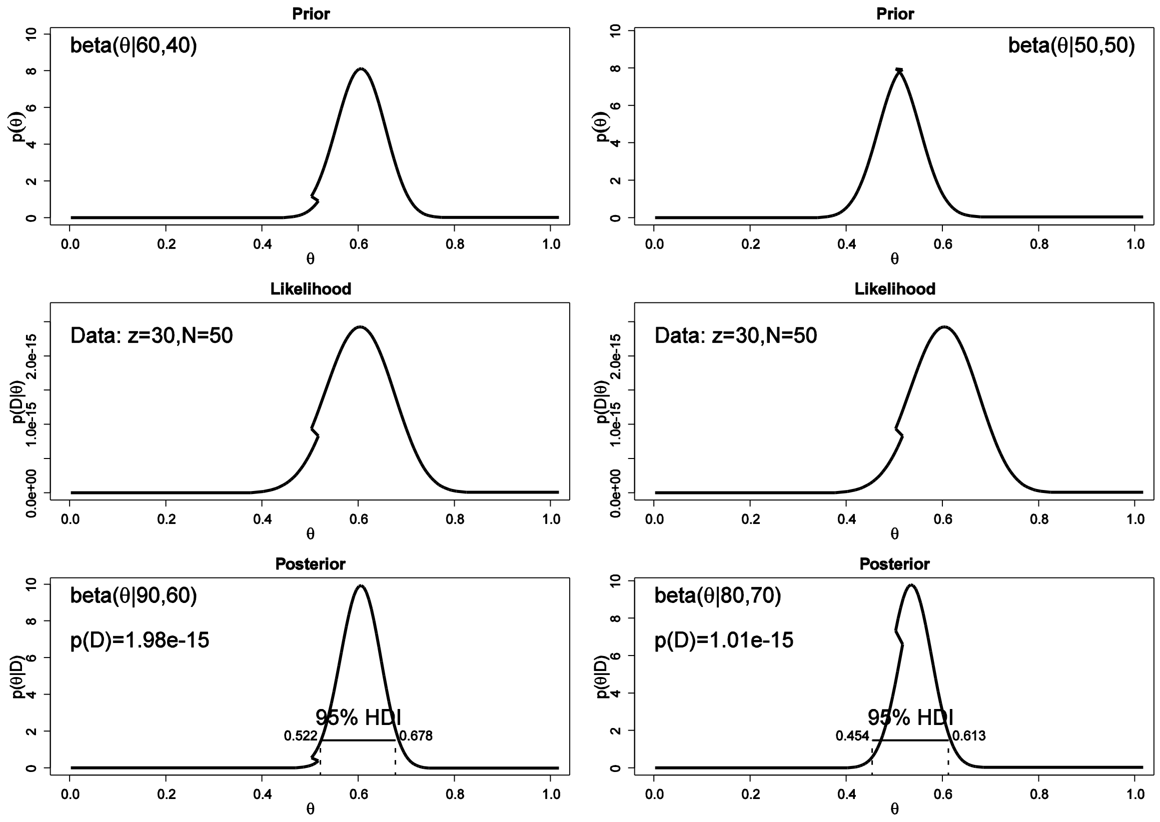
Because we're using beta priors, we can use BernBeta.R instead of BernGrid.R. The two programs should yield essentially identical results, of course.
post = BernBeta(c(5,5) , c(rep(1,30),rep(0,20)))
yields a posterior 95% HDI that includes 0.50, as shown below, so we decide not to believe the manufacturer's claim.



(The jagged parts of the graphs are caused by Word not rendering EPS correctly.)

(C) Suppose that the drug manufacturers make a strong claim that their drug sets the probability of conceiving a boy to nearly 60%, with high certainty. Suppose you represent that claim by a beta(theta|60,40) prior. Compare that claim against the skeptic who says there is no effect of the drug, and the probability of conceiving a boy is represented by a beta(theta|50,50) prior. What is the value of p(D) for each prior? What is the posterior belief in each claim? (Hint: Be careful when computing the posterior belief in each model, because you need to take into account the prior belief in each model. Is the prior belief in the manufacturer's claim as strong as the prior belief in the skeptical claim?)

```
post = BernBeta( c(60,40) , c(rep(1,30),rep(0,20)) )
post = BernBeta( c(50,50) , c(rep(1,30),rep(0,20)) )
```



The Bayes factor is 1.98e-15 / 1.01e-15 = 1.96 in favor of the 60-40 prior. This is not the posterior odds, however, because we have to factor in the prior odds of the model priors. Suppose, for example, that p(60-40 prior) is 0.33, and p(50-50 prior) is 0.67. Then the posterior odds are
p(60-40 prior | D) / p(50-50 prior | D)
= p(D | 60-40 prior) / p(D | 50-50 prior) * p(60-40 prior) / p(50-50 prior)
= 1.96 * 0.33/0.67
= 0.97
In other words, for the slightly skeptical prior odds, the posterior odds are essentially equal for the two models. Again, this is not the single "correct" answer, but illustrates the process.

Chapter 7.

Exercise 7.1. [Purpose: To see what happens in the Metropolis algorithm with different proposal distributions, and to get a sense how the proposal distribution must be "tuned" to the target distribution.] Use the home-grown Metropolis algorithm in the R script of Section 7.6.1 (BernMetropolisTemplate.R) for this exercise. See Figure 7.6 for examples of what your output might look like.

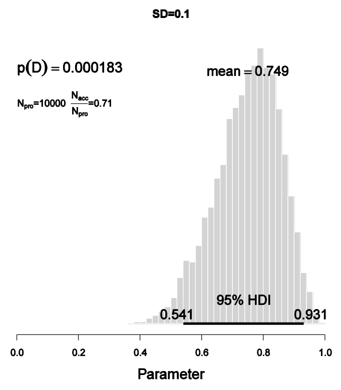
(A) The proposal distribution generates candidate jumps that are normally distributed with mean zero. Set the standard deviation of the proposal distribution to 0.1 (if it isn't already) and run the script. Save/print the graph and annotate it with SD = 0.1.
(B) Set the standard deviation of the proposal distribution to 0.001 and run the script. Save/print the graph and annotate it with SD = 0.001.
(C) Set the standard deviation of the proposal distribution to 100.0 and run the script. Save/print the graph and annotate it with SD = 100.0.

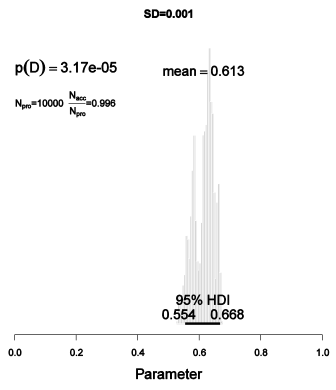
The line of code

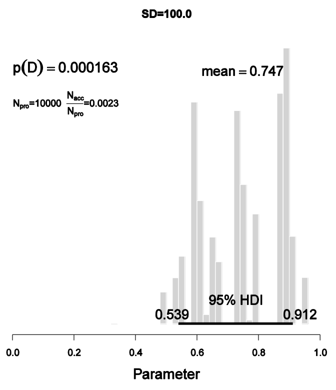
```
proposedJump = rnorm( 1 , mean = 0 , sd = 0.1 )
```

is the only line that needs changing to adjust the SD of the proposal. The graphs below had titles included by specifying the argument main in plotPost, e.g.,

```
plotPost( acceptedTraj , xlim=c(0,1) , breaks=30 , main="SD=0.1" )
```







(D) Which proposal distribution gave the most accurate representation of the posterior? Which proposal distribution had the fewest rejected proposals? Which proposal distribution had the most rejected proposals?

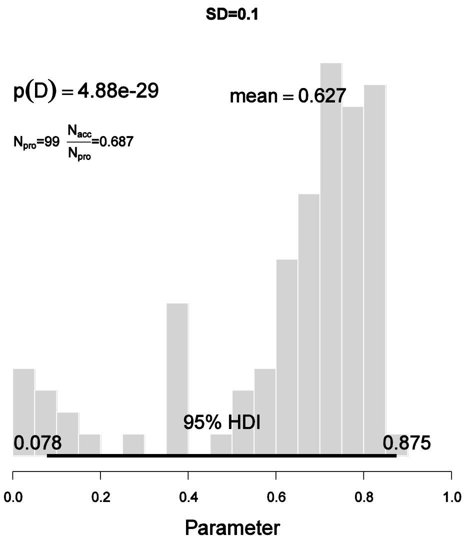
The proposal with SD=0.1 gave the most accurate representation of the posterior. The fewest rejected proposals came when SD=0.001 (because all proposals were so close to the current position and therefore the acceptance probability was usually close to 1.0) and the most rejected proposals came when SD=100.0 (because most proposals were far outside the range of acceptability and therefore rejected).

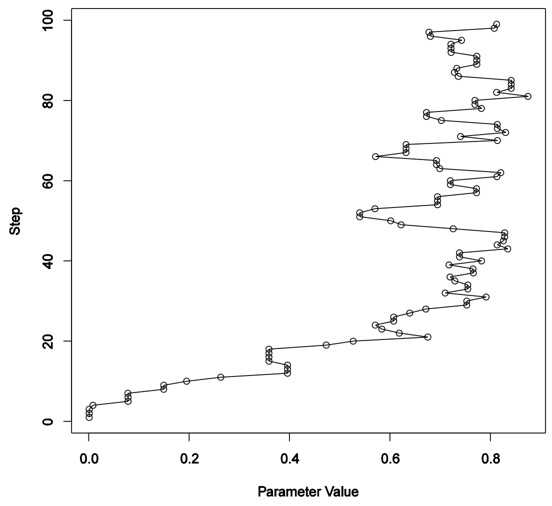
(E) If we didn't know from other techniques what the true posterior looked like, how would we know which proposal distribution generated the most accurate representation of the

posterior? (This does not have a quick answer; it's meant mostly as a question for pondering and motivating techniques introduced in later chapters.)

One signature of a representative sample chain is that it is not "clumpy" across steps. Both of the bad distributions above don't move around much from one step to the next. This lingering and clumping is called large "autocorrelation". We want to avoid sample chains that have large autocorrelation.

Exercise 7.2. [Purpose: To understand the influence of the starting point of the random walk, and why the walk doesn't necessarily go back to that region.] Edit the homegrown Metropolis algorithm of Section 7.6.1 (BernMetropolisTemplate.R) for this exercise. It is best to save it as a differently named script so you don't mess up the original version. Set trajlength = 100 and set burnin = ceiling(0.01 *trajlength). Finally, set trajectory[1] = 0.001. Now run the script and save the resulting histogram.





(A) How many jumps are proposed? How many steps are excluded as part of the burn-in portion? At what value of does the random walk start?

The resulting histogram is shown at the left. With trajlength=100, there are 100 steps proposed. With burnin = ceiling(0.01 *trajlength), there is only 1 burn-in step. The walk starts at 0.001 because trajectory[1]=0.001

(B) Why does the histogram have so many points below 0.5? That is, why does the chain stay below 0.5 as long as it does?

The initial value is 0.001, so the chain starts at the far left. It stays to the left side of 0.5 for quite a number of steps because the proposal distribution has a fairly small SD of 0.1, so proposed jumps are fairly small.

(C) Why does the histogram have so few points below 0.5? That is, why does the chain not go back below 0.5?

The chain eventually stays to the right of 0.5 because the posterior probability of values to the left of 0.5 is small.

These points might be made clearer by plotting the trajectory instead of histogram, as shown at

left, using the command
plot(acceptedTraj , 1:length(acceptedTraj) , type="o" , ylab="Step" , xlab="Parameter Value")

Exercise 7.3. [Purpose: To get some hands-on experience with applying the Metropolis algorithm, and to compare its results with the other methods we've learned about.] Suppose you have a coin that you believe is either fair, or biased to come up heads, or biased to come up tails. As an expression of your prior belief, you define your prior on theta (the probability of heads) to be proportional to $[\cos(4\pi\theta)+1]^2$. In other words, $p(\theta) = [\cos(4\pi\theta)+1]^2 / Z$, where Z is the appropriate normalizing constant. We flip the coin 12 times and we get 8 heads. See Figure 7.7 to see the prior, likelihood, and posterior.

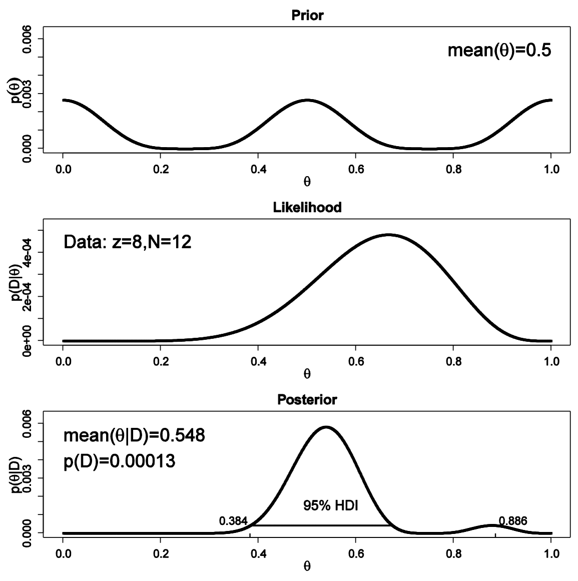
(A) Determine the formula for the posterior distribution exactly, using formal integration in Bayes' rule. Just kidding. Instead, do the following: Explain the initial setup if you wanted to try to determine the exact formula for the posterior. Show the explicit formulas involving the likelihood and prior in Bayes' rule. Do you think that the prior and likelihood are conjugate? That is, would the formula for the posterior have the "same form" as the formula for the prior?

$$p(\theta \mid D) = p(\theta \mid D) p(\theta) \Big/ \int d\theta \; p(\theta \mid D) p(\theta)$$
$$= \theta^8 (1-\theta)^4 (\cos(4\pi\theta)+1)^2 \Big/ \int d\theta \; \theta^8 (1-\theta)^4 (\cos(4\pi\theta)+1)^2$$

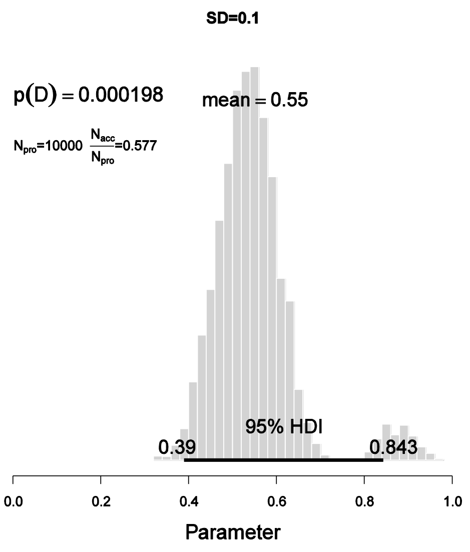
(Z does not appear in the formula above because it cancels out in the numerator and denominator.) It is doubtful that a formula for the posterior would have the same form as the prior. Also evident from the formula is that an analytical solution is not trivial if it is possible at all.

(B) Use a fine grid over and approximate the posterior. Use the R function of Section 6.7.1 (BernGrid.R), p. 109. (The R function also plots the prior distribution, so you can see that it really is trimodal.)

```
binwidth = 1/1000
thetagrid = seq( from=binwidth/2 , to=1-binwidth/2 , by=binwidth )
relprob = ( cos( 4*pi*thetagrid ) + 1 )^2
prior = relprob / sum(relprob)
datavec = c( rep(1,8) , rep(0,4) )
posterior = BernGrid( Theta=thetagrid , pTheta=prior , Data=datavec )
```



(C) Use a Metropolis algorithm to approximate the posterior. Use the R script of Section 7.6.1, (BernMetropolisTemplate.R) adapted appropriately for the prior function. You'll need to alter the definitions of the likelihood and prior functions in the R script; include that portion of the code with what you hand in (but don't include the rest of the code). Must you normalize the prior to generate a sample from the posterior? Is the value of p.D/ displayed in the graph correct?



There are only two program changes that need to be made. One is the specification of the data and the other is the specification of the prior:

```
myData = c( 1, 1, 1, 1, 1, 1, 1, 1, 0, 0, 0, 0 )

prior = function( theta ) {
  prior = ( cos( 4 * pi * theta ) + 1 )^2
  prior[ theta > 1 | theta < 0 ] = 0
  return( prior )
}
```

(Be sure that a long chain is generated, with sufficient burn-in!) This produces the following histogram:

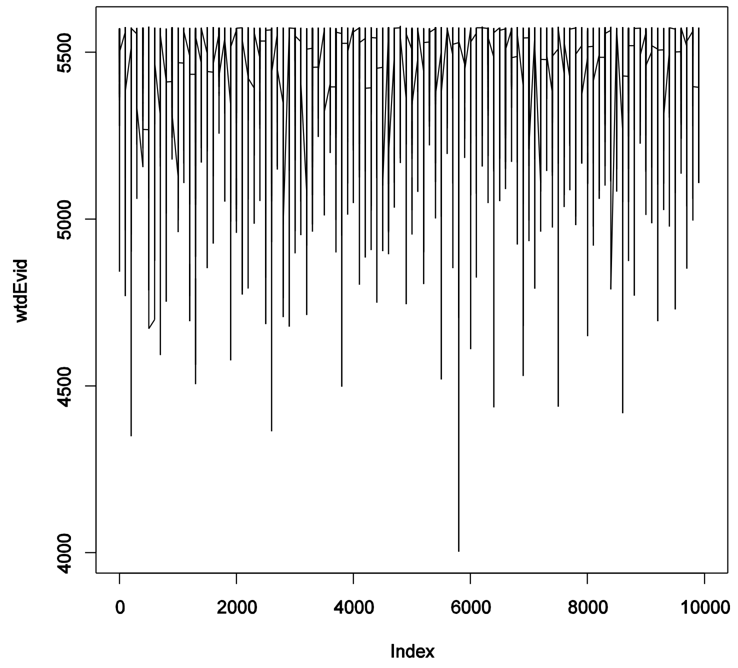
Notice that the histogram shows bimodality, just like the grid approximation. Also note that the HDI marked in the histogram is *not* appropriate, because the algorithm for approximating the HDI assumes a unimodal distribution.

(D) Could you apply BUGS to this situation? In particular, can you think of a way to specify the prior density in terms of distributions that BUGS knows about?

There is no simple way to specify this prior in BUGS.

Exercise 7.4. [Purpose: To approximate p.D/, explore other choices for h./ in Equation 7.8, and note that the one used in the R script of Section 7.6.1 (Bern- MetropolisTemplate.R) is a good one.] Edit the R script of Section 7.6.1 (BernMetropolisTemplate.R) for this exercise. It is best to save it as a differently named script so you don't mess up the original version. At the end of the script, add this line: windows() ; plot(wtdEvid,type="l").

(A) Select (i.e., highlight with the cursor) that line in the R editor and run it. Save the plot. Explain what the plot is plotting. That is, what is wtdEvid (on the y axis) and what is on the x axis?



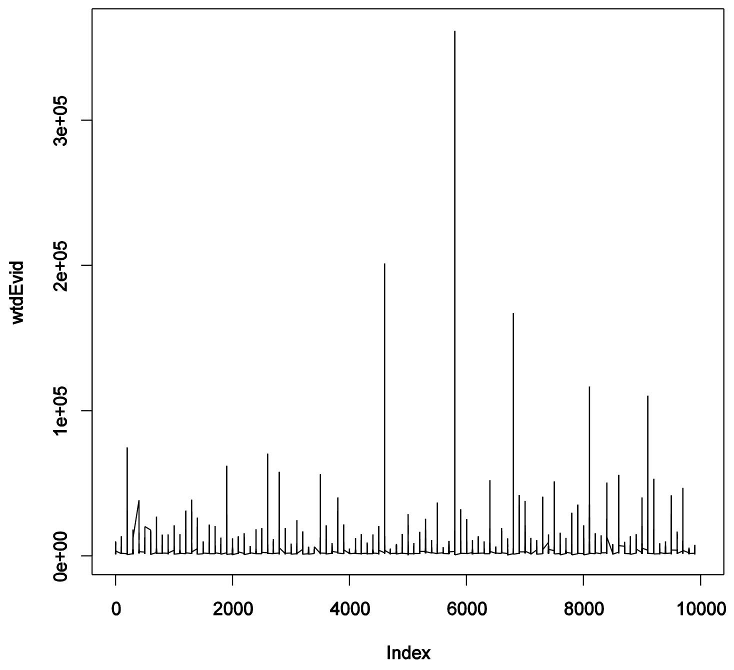
The plot shows the weighted evidence, denoted wtdEvid, at each step in the chain. The step in the chain is denoted "Index" on the x axis. The weighted evidence at step *i* is

$$\frac{1}{p(D)} = \frac{h(\theta_i)}{p(D \mid \theta_i)p(\theta_i)}$$

where $h(\theta)$ is a beta distribution with the same mean and standard deviation as the sampled posterior. Notice that the value of wtdEvid is usually between 4700 and 5700.

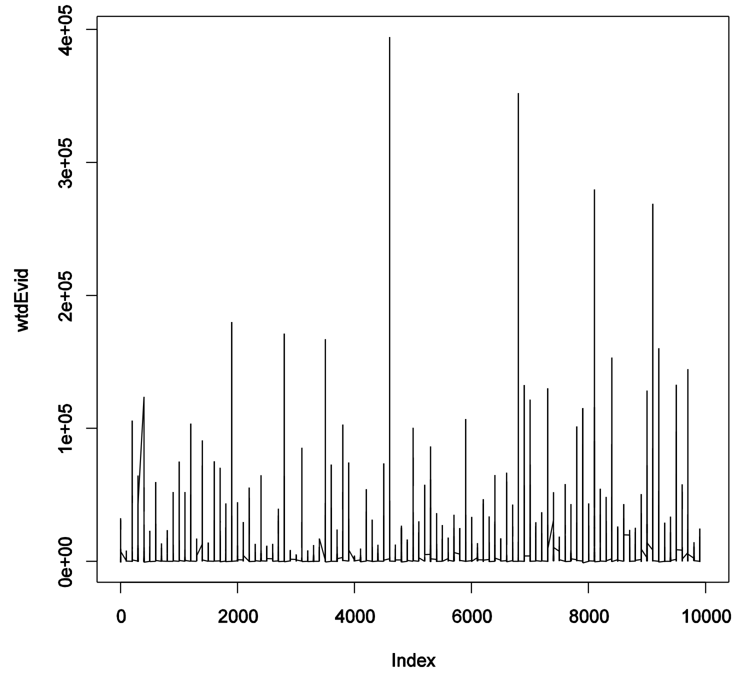
(B) Consider a different choice for the h(θ) in Equation 7.8. To do this, we'll leave it as a beta function, but change the choice of its a and b values. Find where a and b are specified in the R program (near the end, just before wtdEvid is defined), and type in a=1 and b=1 instead. Now select (i.e., highlight with the cursor) the portion of the program from the new

a and b definitions, through the computation of wtdEvid, and the new plot command. Run the selection, and save the resulting plot.



The plot above shows the result. Notice that there are spikes that shoot to extreme values, far beyond the usual magnitude of wtdEvid. Notice the scale on the y axis: 3e+05 is 300,000!

(C) Repeat, but this time with a=10 and b=10.



The plot above shows that wtdEvid shoots to extreme values, even more extreme than the previous part, up to 400,000.

(D) For which values of a and b are the values of wtdEvid most stable across the random walk? Which values of a and b would produce the most stable estimate of p(D)?

The most stable estimate of wtdEvid comes from using a,b values that produce h(θ) similar to the actual posterior.

Exercise 7.5. [Purpose: To explore the use of BUGS and consider model comparison.] Suppose there are three people with different beliefs about a coin. One person (M1) believes that the coin is biased toward tails; we'll model this person's beliefs as a uniform distribution over values between 0 and 0.4. The second person (M2) believes that the coin is approximately fair; we'll model this person's beliefs as a uniform distribution between 0.4 and 0.6. The third person (M3) believes that the coin is biased toward heads; we'll model this person's beliefs as a uniform distribution over values between 0.6 and 1.0. We won't favor any person a priori, and therefore we start by assuming that p(M1) = p(M2) = p(M3) = 1/3. We now flip the coin 14 times and observe 11 heads. Use BUGS to determine the evidences for the three models. Hints: For each person, compute p(D) by adapting the program BernBetaBugsFull.R of Section 7.4.1 in two steps. First, modify the model specification so that the prior is uniform over the limited range, instead of beta. Appendix I of the OpenBUGS User Manual (see Section 7.4) explains how to specify uniform distributions in BUGS. Second, include a new section at the end of the BUGS program that will compute p(D). Do this by copying the last section of the program BernMetropolisTemplate.R that computes p(D), pasting it onto the end of your BUGS program, and making additional necessary changes so that the output of BUGS can be

processed by the newly added code. In particular, before the newly added code, you'll have to include these lines:
acceptedTraj = thetaSample
meanTraj = mean(thetaSample)
sdTraj = sd(thetaSample)

The complete code is below. The major changes have been highlighted.

```
graphics.off()
rm(list=ls(all=TRUE))
library(BRugs)         # Kruschke, J. K. (2010). Doing Bayesian data analysis:
                       # A Tutorial with R and BUGS. Academic Press / Elsevier.
#------------------------------------------------------------------------------
# THE MODEL.

# Specify the model in BUGS language, but save it as a string in R:
modelString = "
# BUGS model specification begins ...
model {
    # Likelihood:
    for ( i in 1:nFlips ) {
        y[i] ~ dbern( theta )
    }
    # Prior distribution:
    theta ~ dunif( 0.6 , 1.0 )
}
# ... BUGS model specification ends.
" # close quote to end modelString

# Write the modelString to a file, using R commands:
writeLines(modelString,con="model.txt")
# Use BRugs to send the model.txt file to BUGS, which checks the model syntax:
modelCheck( "model.txt" )

#------------------------------------------------------------------------------
# THE DATA.

# Specify the data in R, using a list format compatible with BUGS:
dataList = list(
    nFlips = 14 ,
    y = c( 1,1,1,1,1,1,1,1,1,1,1,0,0,0 )
)

# Use BRugs commands to put the data into a file and ship the file to BUGS:
modelData( bugsData( dataList ) )

#------------------------------------------------------------------------------
# INTIALIZE THE CHAIN.

modelCompile()  # BRugs command tells BUGS to compile the model.
modelGenInits() # BRugs command tells BUGS to randomly initialize a chain.

#------------------------------------------------------------------------------
# RUN THE CHAINS.

# BRugs tells BUGS to keep a record of the sampled "theta" values:
samplesSet( "theta" )
# R command defines a new variable that specifies an arbitrary chain length:
chainLength = 10000
# BRugs tells BUGS to generate a MCMC chain:
```

```
modelUpdate( chainLength )

#------------------------------------------------------------------------------
# EXAMINE THE RESULTS.

thetaSample = samplesSample( "theta" ) # BRugs asks BUGS for the sample values.
thetaSummary = samplesStats( "theta" ) # BRugs asks BUGS for summary statistics.

# Make a graph using R commands:
windows(10,6)
layout( matrix( c(1,2) , nrow=1 ) )
plot( thetaSample[1:500] , 1:length(thetaSample[1:500]) , type="o" ,
      xlim=c(0,1) , xlab=bquote(theta) , ylab="Position in Chain" ,
      cex.lab=1.25 , main="BUGS Results" )
source("plotPost.R")
histInfo = plotPost( thetaSample , xlim=c(0,1) )

## Posterior prediction:
## For each step in the chain, use posterior theta to flip a coin:
#chainLength = length( thetaSample )
#yPred = rep( NULL , chainLength )  # define placeholder for flip results
#for ( stepIdx in 1:chainLength ) {
#  pHead = thetaSample[stepIdx]
#  yPred[stepIdx] = sample( x=c(0,1), prob=c(1-pHead,pHead), size=1 )
#}
## Jitter the 0,1 y values for plotting purposes:
#yPredJittered = yPred + runif( length(yPred) , -.05 , +.05 )
## Now plot the jittered values:
#windows(5,5.5)
#plot( thetaSample[1:500] , yPredJittered[1:500] , xlim=c(0,1) ,
#      main="posterior predictive sample" ,
#      xlab=expression(theta) , ylab="y (jittered)" )
#points( mean(thetaSample) , mean(yPred) , pch="+" , cex=2 )
#text( mean(thetaSample) , mean(yPred) ,
#      bquote( mean(y) == .(signif(mean(yPred),2)) ) ,
#      adj=c(1.2,.5) )
#text( mean(thetaSample) , mean(yPred) , srt=90 ,
#      bquote( mean(theta) == .(signif(mean(thetaSample),2)) ) ,
#      adj=c(1.2,.5) )
#abline( 0 , 1 , lty="dashed" , lwd=2 )

# Rename variables above so they are compatible with code pasted below
acceptedTraj = thetaSample
meanTraj = mean( thetaSample )
sdTraj = sd( thetaSample )
myData = dataList$y

# Code below is copied from BernMetropolisTemplate.R

likelihood = function( theta , data ) {
  z = sum( data == 1 )
  N = length( data )
  pDataGivenTheta = theta^z * (1-theta)^(N-z)
  pDataGivenTheta[ theta > 1 | theta < 0 ] = 0
  return( pDataGivenTheta )
}

prior = function( theta ) {
  prior = dunif( theta , min=0.6 , max=1.0 ) # uniform density
  prior[ theta > 1 | theta < 0 ] = 0
  return( prior )
}
```

```
# Compute evidence for model, p(D):

a =   meanTraj   * ( (meanTraj*(1-meanTraj)/sdTraj^2) - 1 )
b = (1-meanTraj) * ( (meanTraj*(1-meanTraj)/sdTraj^2) - 1 )

wtdEvid = dbeta( acceptedTraj , a , b ) / (
             likelihood( acceptedTraj , myData ) * prior( acceptedTraj ) )
pData = 1 / mean( wtdEvid )

# Display p(D) in the graph
if ( meanTraj > .5 ) { xpos = 0.0 ; xadj = 0.0
} else { xpos = 1.0 ; xadj = 1.0 }
densMax = max( histInfo$density )
text( xpos , 0.75*densMax , bquote( p(D)==.( signif(pData,3) ) ) ,
      adj=c(xadj,0) , cex=1.5 )

dev.copy2eps(file="Exercise7.5.eps")
```

The only changes from one model to the next involve the prior in *both* the BUGS model specification *and* the appended code for computing p(D):

M1:

```
    theta ~ dunif( 0.0 , 0.4 )
  prior = dunif( theta , min=0.0 , max=0.4 )
```

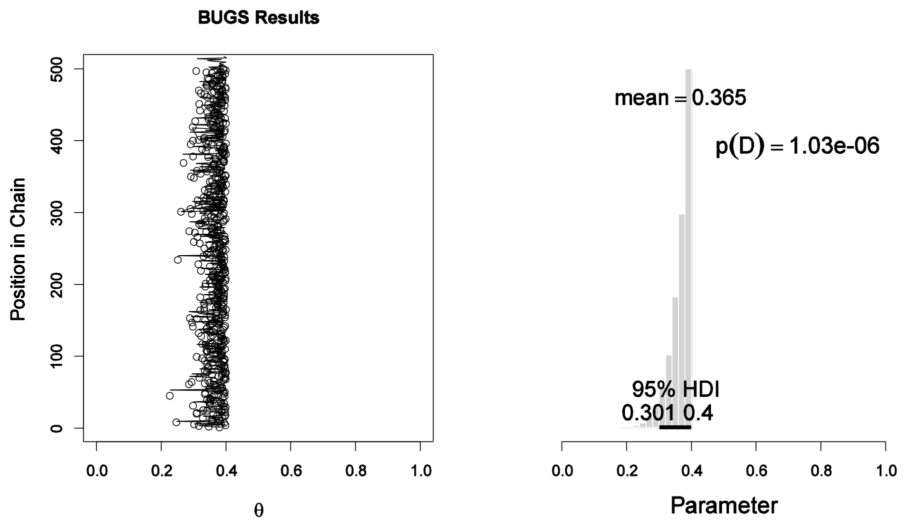
M2:

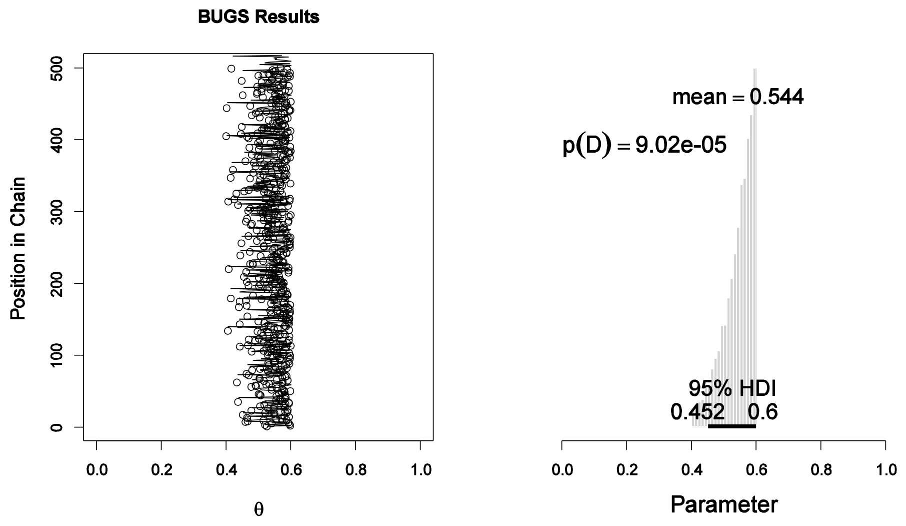
```
    theta ~ dunif( 0.4 , 0.6 )
  prior = dunif( theta , min=0.4 , max=0.6 )
```

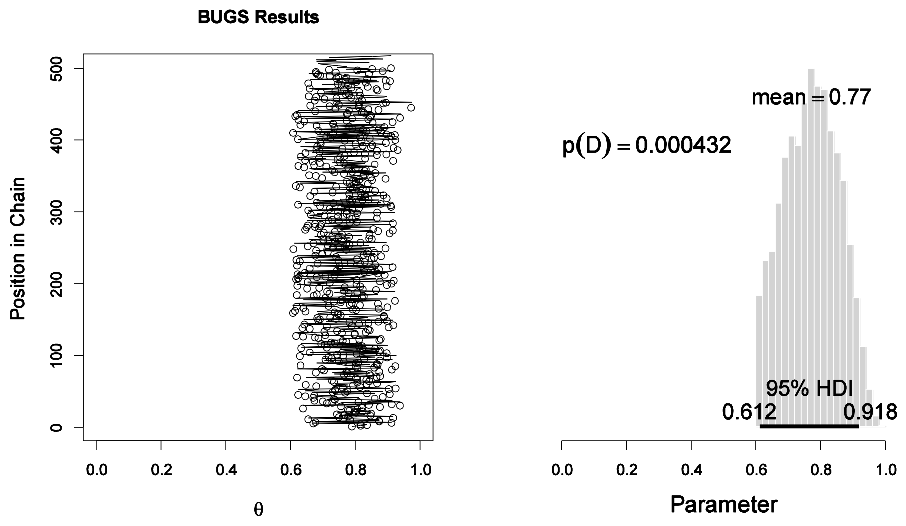
M3:

```
    theta ~ dunif( 0.6 , 1.0 )
  prior = dunif( theta , min=0.6 , max=1.0 )
```

The graphs on the next page are the result. We see that p(D|M1)=1.03e-06, p(D|M2)=9.02e-05, p(D|M3)=0.000432. Thus, M3 is strongly preferred over the other models.


BUGS Results
Position in Chain
θ
mean = 0.365
p(D) = 1.03e-06
95% HDI
0.301 0.4
Parameter


BUGS Results
Position in Chain
θ
mean = 0.544
p(D) = 9.02e-05
95% HDI
0.452 0.6
Parameter


BUGS Results
Position in Chain
θ
mean = 0.77
p(D) = 0.000432
95% HDI
0.612 0.918
Parameter

Chapter 8.

Exercise 8.1. [Purpose: To explore a real-world application about the difference of proportions.] Is there a “hot hand” in basketball? This question has been addressed in a frequently cited article by Gilovich, Vallone, & Tversky (1985).The idea of a hot hand is that the success of a shot depends on the success of a previous shot, as opposed to each shot being an independent flip of a coin (or toss of a ball). One way to address this idea is to consider pairs of free throws taken after fouls. If the player has a hot hand, then he should be more likely to make the second shot after a successful first shot than after a failed first shot. If the two shots are independent, however, then the probability of making the second shot after a successful first shot should equal the probability of making the second shot after failing the first shot. Thus, there is a hot hand if the probability of success after a success is better than the probability of success after failure.

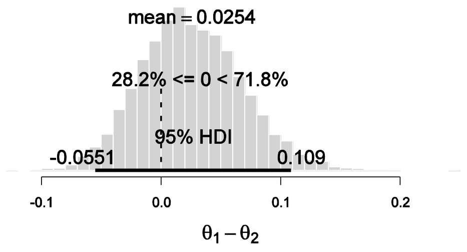
During 1980–1982, Larry Bird of the Boston Celtics had 338 pairs of free throws. He was successful on 285 first shots and failed on the remaining 53 first shots. After the 285 successful first shots, he was successful on 251 second shots (and failed on the other 34 second shots). After the 53 failed first shots, he was successful on 48 second shots (and failed on the other 5 second shots). Thus, we want to know if 251/285 (success after success) is different than 48/53 (success after failure).

Let θ_1 represent the proportion of success after a successful shot, and let θ_2 represent the proportion of success after a failed first shot. Suppose we have priors of beta(θ|30,10) on both, representing the belief that we think that professional players make about 75% of their free throws, regardless of when they are made.

(A) Modify the BRugs program of Section 8.8.3 (BernTwoBugs.R) to generate a histogram of credible differences between success-after-success and success-after-failure. Explain what modifications you made to the R code. (Hint: Your result should look like something like Figure 12.2, p. 299).

The model specification should include these priors:
```
theta1 ~ dbeta( 30 , 10 )
theta2 ~ dbeta( 30 , 10 )
```
The data specification should include the following inside its list:
```
N1 = 285,
y1 = c( rep(1,251) , rep(0,285-251) ),
N2 = 53,
y2 = c( rep(1,48) , rep(0,53-48) )
```

The resulting posterior distribution of differences looks like this:



(B) Based on your results from the previous part, does Larry Bird seem to have a hot hand? In other words, are almost all of the credible differences between success-after-success and success-after-failure well above zero, or is a difference of zero among the credible differences?

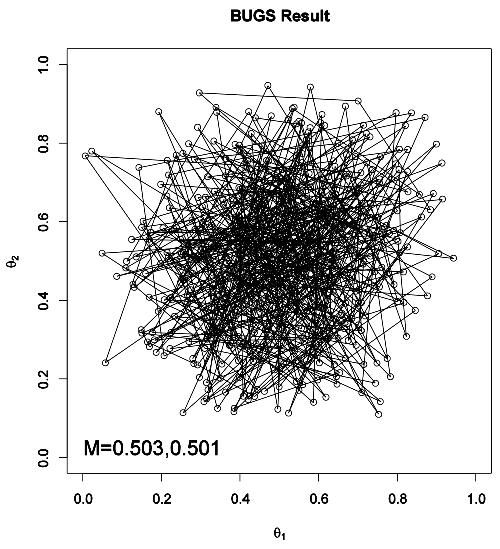
A difference of zero lies well within the 95% HDI, which means that a difference of zero is among the credible values, and there is not strong evidence for a hot hand.

Exercise 8.2. [Purpose: To examine the prior in BUGS by omitting references to data.] Reproduce and run the BUGS code that generated the chains in Figure 8.7. Show the sections of code that you modified from the program in Section 8.8.3 (BernTwoBugs.R), and show the resulting graphical output.

As shown on p. 175 of the textbook, the data list has the y1 and y2 values commented out, as follows:

```
N1 = 7 ,
# y1 = c( 1,1,1,1,1,0,0 ) ,
N2 = 7 #,
# y2 = c( 1,1,0,0,0,0,0 )
```

Notice that the N1 and N2 values remain specified, because those values are still used in the model specification. Notice also that the final comma is commented out, so that the list structure has the proper syntax. When the program is run, the resulting posterior sample looks much like Figure 8.7, as follows:

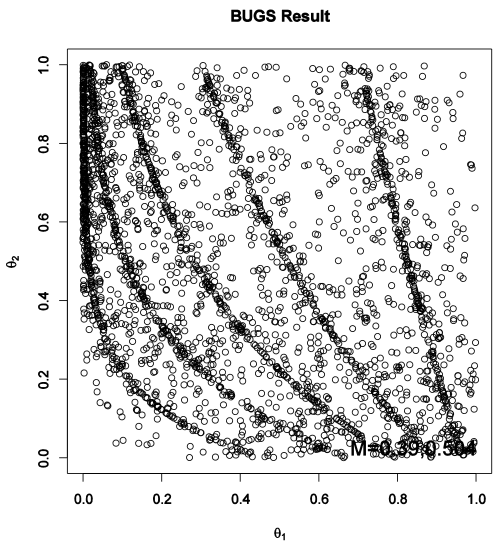


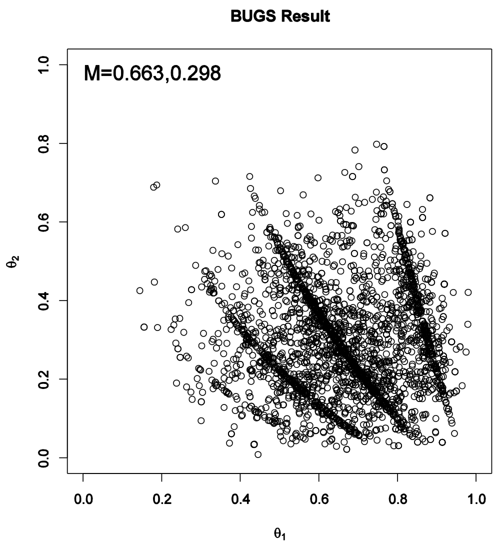
Exercise 8.3. [Purpose: To understand the limitations of prior specification in BUGS.] In BUGS, all priors must be specified in terms of probability distributions that BUGS knows about. These distributions include the beta, gamma, normal, uniform, and so on, as specified in the appendix of the BUGS User Manual. There are ways to program novel distributions into BUGS, but explaining how would take us too far afield at this point. Instead, we'll consider how unusual priors can be constructed from the built-in distributions. The left panel of Figure 8.9 shows the prior that results from this model specification (BernTwoFurrowsBugs.R):

```
model {
    # Likelihood. Each flip is Bernoulli.
    for ( i in 1 : N1 ) { y1[i] ~ dbern( theta1 ) }
    for ( i in 1 : N2 ) { y2[i] ~ dbern( theta2 ) }
    # Prior. Curved scallops!
    x ~ dunif(0,1)
    y ~ dunif(0,1)
    N <- 4
    xt <- sin( 2*3.141593*N * x ) / (2*3.141593*N) + x
    yt <- 3 * y + (1/3)
    xtt <- pow( xt , yt )
    theta1 <- xtt
    theta2 <- y
}
```

Adapt the program in Section 8.8.3 (BernTwoBugs.R) to use this prior, but with N set to 5 instead of 4. (Don't confuse N with N1 or N2.) Produce a graph of the prior and of the posterior, like those shown in Figure 8.9. This particular furrowed prior would never be used in actual research that I'm aware of; the point is that you can specify unusual priors if you need to.

The result when `N<-5` is shown below (prior on left, posterior on right). Notice that there are five ridges in the prior, not four ridges as in Figure 8.9 of the textbook.

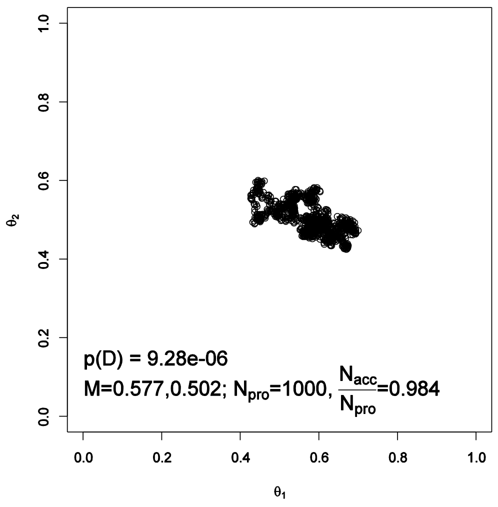




Exercise 8.4. [Purpose: To understand Metropolis sampling, and to see the importance of tuning the proposal distribution.] For this exercise, assume the prior and data used in Figure 8.1.

(A) In the R code of Section 8.8.2 (BernTwoMetropolis.R), set the standard deviations (both sd1 and sd2) of the proposal distribution to 0.005, and run the program. Does the resulting distribution of sampled values resemble Figures 8.1 or 8.3? What is wrong with the choice of standard deviations?

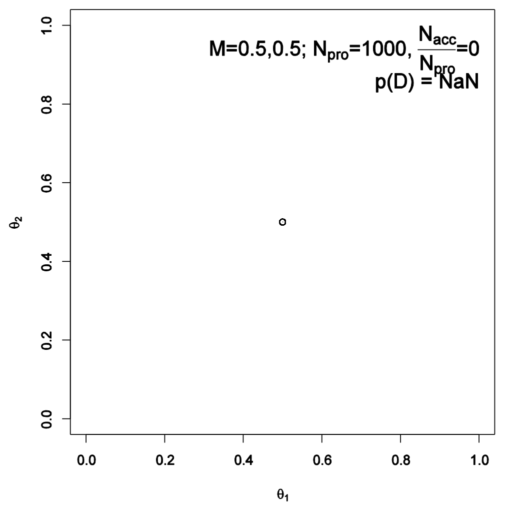
Changing line 57 of the program to
```
nDim = 2 ; sd1 = 0.005 ; sd2 = 0.005  # was 0.2
```
yields



which is a very clumpy, autocorrelated chain. The standard deviation for the proposal distribution is much too small, yielding successive steps too close to each other. Notice that the acceptance proportion is 98.4%, meaning that almost every proposal is accepted.

(B) In the R code of Section 8.8.2 (BernTwoMetropolis.R), set the standard deviations (both sd1 and sd2) of the proposal distribution to 5.0, and run the program. Does the resulting distribution of sampled values resemble Figures 8.1 or 8.3? What is wrong with the choice of standard deviations?

Changing line 57 of the program to
```
nDim = 2 ; sd1 = 5.0 ; sd2 = 5.0  # was 0.2
```
yields



Notice that the acceptance proportion is zero, meaning that no proposal is ever accepted, and the chain remains stuck at its starting point. This results from the proposals all being far beyond the reasonable range of the posterior.

Exercise 8.5. [Purpose: To remember how to do posterior prediction with BUGS.] For this exercise, assume the prior and data used in Figure 8.1. From the posterior, what is the probability that the next flip of the two coins will have $y_1^* = 1$ and $y_2^* = 0$? To answer this question, expand the code of Section 8.5 so that it includes posterior predictions. See the example in Section 7.4.2, (p. 143), and simply repeat the same structure for each theta and y value. Include your code with your answer.

Starting with the program BernTwoBugs.R, we add the following lines of code and the end of the program:

```
# Posterior prediction. For each step in the chain, use the posterior thetas
# to flip the coins.
chainLength = length( theta1Sample )
# Create matrix to hold results of simulated flips:
yPred = matrix( NA , nrow=2 , ncol=chainLength )
for ( stepIdx in 1:chainLength ) { # step through the chain
  # flip the first coin:
  pHead1 = theta1Sample[stepIdx]
  yPred[1,stepIdx] = sample( x=c(0,1), prob=c(1-pHead1,pHead1), size=1 )
  # flip the second coin:
  pHead2 = theta2Sample[stepIdx]
  yPred[2,stepIdx] = sample( x=c(0,1), prob=c(1-pHead2,pHead2), size=1 )
}
# Now determine the proportion of times that y1==1 and y2==0
pY1eq1andY2eq0 = sum( yPred[1,]==1 & yPred[2,]==0 ) / chainLength
```

The result is that pY1eq1andY2eq0 is 0.37. (The code above is merely suggestive. You may have more elegant code that accomplishes the same result.)

Chapter 9.

Exercise 9.1. [Purpose: To investigate research design—more coins versus more flips per coin.] In Section 9.2.5, p. 219, it was argued that if the goal of the research is to get a good estimate of the group average μ, then it is better to collect data from more coins than to collect more flips per coin. This exercise has you generate simulated data to bolster this conclusion.

(A) Use the R code of Section 9.5.1 (BernBetaMuKappaBugs.R) for this exercise. In the data section of that program, comment out the lines that specify N and z. Insert the following lines:

```
ncoins = 50 ; nflipspercoin = 5
muAct = .7 ; kappaAct = 20
thetaAct = rbeta( ncoins , muAct*kappaAct , (1-muAct)*kappaAct )
z = rbinom( n=ncoins , size=nflipspercoin , prob=thetaAct )
N = rep( nflipspercoin , ncoins )
```

Explain in words what that code does. This is important; if you don't understand this code, the rest of the exercise will not make much sense. (Hint: It's generating random data, for specific "actual" parameter values; explain in detail.)

thetaAct is a vector of length ncoins (i.e., 50). Each component of thetaAct is the actual bias of the corresponding coin. The theta values are sampled randomly from a beta distribution with mean muAct and certainty kappaAct.

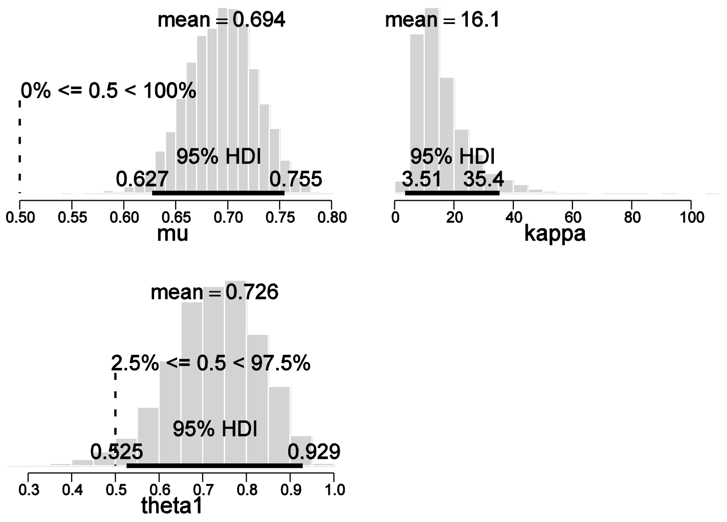
z is a vector of number of heads randomly generated when each coin is flipped nflipspercoin with actual probability thetaAct.

N is the vector of number of flips for each coin. For example, when the above code is run, it produces (randomly) the following:

```
thetaAct
 [1] 0.7853951 0.8073966 0.4982677 0.8523268 0.7040792 0.6331948 0.6236083
 [8] 0.8444975 0.8437521 0.6940055 0.6072397 0.4525766 0.7907075 0.8159670
[15] 0.6158728 0.6934655 0.7720326 0.7363004 0.6251704 0.7225201 0.7853685
[22] 0.6898285 0.7206907 0.7581194 0.6733569 0.7329841 0.7543905 0.6074791
[29] 0.7277989 0.8674680 0.5884220 0.6229580 0.6880705 0.6004323 0.6318800
[36] 0.7357017 0.8505620 0.5595014 0.8726786 0.7874657 0.5362301 0.8735407
[43] 0.8071881 0.6113401 0.5950920 0.8011553 0.8088236 0.7643088 0.4644073
[50] 0.7772480

z
 [1] 4 3 3 5 3 2 2 5 4 3 2 3 5 5 2 2 4 5 4 4 4 2 2 2 3 4 4 4 5 5 3 2 1 1 3 5 3 3
[39] 5 5 4 4 4 1 3 3 5 4 2 3

N
 [1] 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5
[39] 5 5 5 5 5 5 5 5 5 5 5 5
```

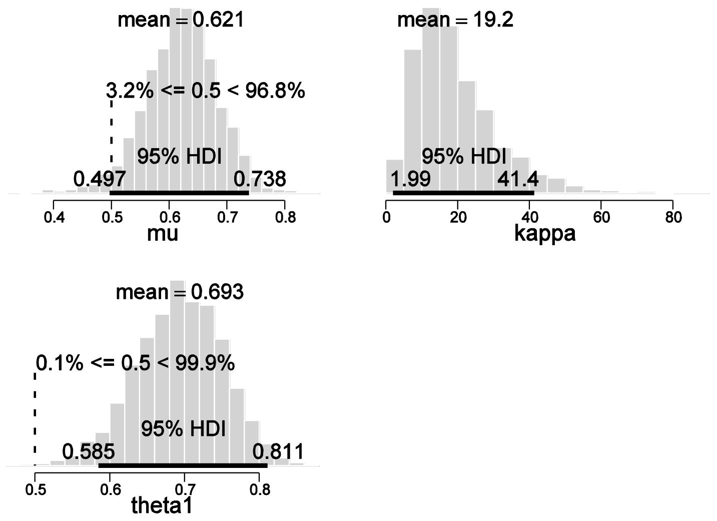
(B) At the bottom of the program, UNcomment the lines that plot the posteriors of muSample, kappaSample, and thetaSample[1,]. (Don't plot thetaSample[28,], because it doesn't exist.) You should also Uncomment the windows() and layout(. . .) command, so that the plots don't overwrite each other. Run the program a few times and include the graphs of one typical run in your write-up.

Notice that the HDI for mu is always well above .5, but the HDI for theta1 has its left edge near .5.



(C) Now change the data-generation code so that the number of coins is 5 (instead of 50) and the number of flips per coin is 50 (instead of 5). Run the program a few times and include the graphs of one typical run in your write-up.

Notice that the HDI for mu has its left edge near .5, but the HDI for theta1 is always well above .5.



(D) Is the posterior estimate of μ more certain for 5 coins or for 50 coins? Is the posterior estimate of θ1 more certain for 5 coins (50 flips per coin) or for 50 coins (5 flips per coin)? Is it better to use more coins or more flips per coin if the goal is to estimate μ?

As mentioned in the descriptions of the posterior distributions, the uncertainty on mu is smaller when there are more coins, but the posterior uncertainty of theta1 is smaller when there are more flips per coin. If the goal is to estimate mu, then there should be more coins.

Exercise 9.2. [Purpose: To examine the effect of different assumptions about across-group constraints. Specifically, different assumptions about κ_c in the analysis of data from the filtration-condensation experiment.] For this exercise, we will perform alternative analyses of the data from the filtration-condensation experiment described in Section 9.3.1. You will adapt the code listed in Section 9.5.2 (FilconBrugs.R), which implements the hierarchical model diagrammed in Figure 9.7, to implement the alternative hierarchical models diagrammed in Figure 9.17.

(A) The left side of Figure 9.17 shows a model in which the same κ value is used for all groups simultaneously. The idea here is that accuracies of individuals in each group depend on the group mean accuracy, and we are going to estimate the magnitude of that dependency of individuals on the group mean, but we assume that whatever the degree of dependency is, it is the same in every group. This assumption can be thought of as saying that the category structure (e.g., filtration or condensation) affects the mean accuracy of the group, but individual variation from the mean accuracy is caused only by other factors that are the same across groups, not by the category structure. To implement this assumption in the program, do the following: In the model specification, because κ does not depend on the group (i.e., the condition), move the line that specifies the distribution of κ outside the for loop that cycles through the conditions. Moreover, because there is only one κ, remove the index from κ (i.e., change kappa[condIdx] to kappa). Then, in the initialization of the chains, make sure that kappa is initialized to a single value instead of a vector of four values. To do this, set kappa to the mean of the four condition kappas. Now run the modified program. (Hint: For an example of results, see Figures 9.18 and 9.19, and compare the results with those in Figure 9.16.) In your answer: (1) Report the modified model-specification section of your code; (2) Show the graph of the estimated μ differences; (3) Answer this question: Why is the 95% HDI of the μ1 - μ2 differences farther away from zero than in the original analysis?

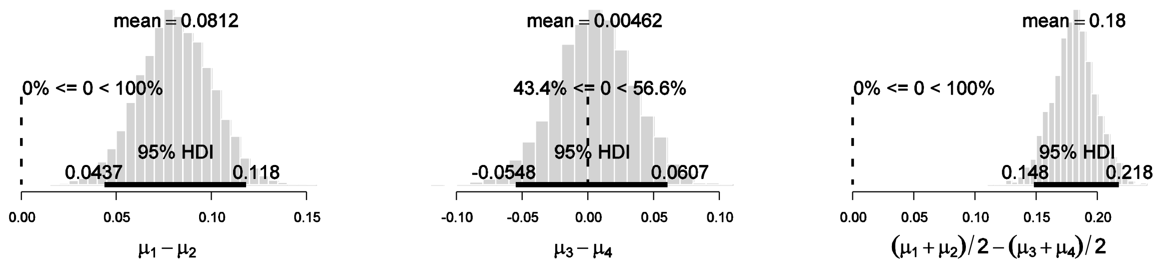
The modified model specification:

```
model {
   for ( subjIdx in 1:nSubj ) {
      # Likelihood:
      z[subjIdx] ~ dbin( theta[subjIdx] , N[subjIdx] )
      # Prior on theta: Notice nested indexing.
      theta[subjIdx] ~ dbeta( a[cond[subjIdx]] , b[cond[subjIdx]]
)I(0.001,0.999)
   }
   for ( condIdx in 1:nCond ) {
      a[condIdx] <- mu[condIdx] * kappa
      b[condIdx] <- (1-mu[condIdx]) * kappa
      # Hyperprior on mu and kappa:
      mu[condIdx] ~ dbeta( Amu , Bmu )
   }
   kappa ~ dgamma( Skappa , Rkappa )
   # Constants for hyperprior:
   Amu <- 1
   Bmu <- 1
   Skappa <- pow(meanGamma,2)/pow(sdGamma,2)
   Rkappa <- meanGamma/pow(sdGamma,2)
   meanGamma <- 10
   sdGamma <- 10
}
```

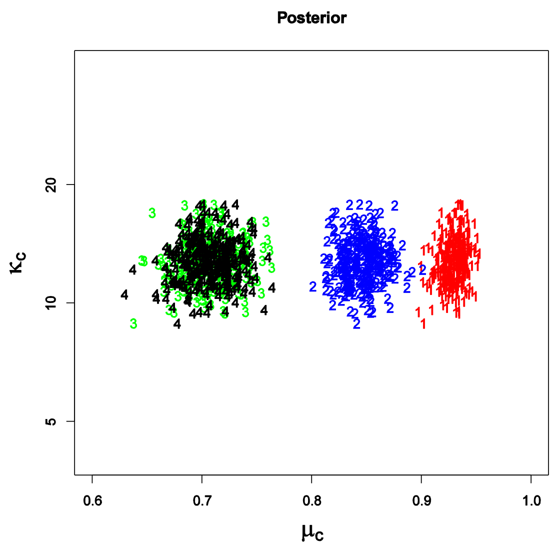
The modified initialization function:

```
  genInitList <- function() {
    sqzData = .01+.98*datalist$z/datalist$N
    mu = aggregate( sqzData , list(datalist$cond) , mean )[,"x"]
    sd = aggregate( sqzData , list(datalist$cond) , sd )[,"x"]
    kappa = mu*(1-mu)/sd^2 - 1
    return(
      list(
        theta = sqzData ,
        mu = mu ,
        kappa = mean( kappa )
      )
    )
  }
```

Graph of mu differences:



And here is a graph of the mu and kappa values, just for completeness:



In the scatterplot, the value of kappa is the same for all four groups at any step in the chain. The value of kappa changes from step to step.

Why are the mu differences farther away from zero than in the original analysis?

The difference, mu1-mu2, has a slightly higher mean than for the original analysis, and a narrower 95%HDI. Thus, constraining kappa to be the same in each group has made the mu1-mu2 difference apparently stronger. The reason is a bit subtle, but can be best explained by looking at the scatterplots in Figure 9.19 of the textbook. Notice that the scatter of kappa1 by mu1, and the scatter of kappa2 by mu2, shows positive correlation. In other words, if kappa1 is bigger, then the most credible mu1 is also a little bigger. Moreover, there is no constraint from one group to the other, so kappa1 is free to be large when kappa2 is randomly selected to be small. Thus, when considering only the difference mu1-mu2 and collapsing across kappa, the high variability of the two kappa's and the correlations of kappa's with mu's produces a bit of smearing of the mu difference. (So, you may ask, why are kappa1 and mu1 correlated? The answer is that the individual accuracies in group 1 are a bit skewed toward small values, so that if kappa increases, the data are better accommodated by a higher mu, where the bulk of the individuals are. Same for group 2.)

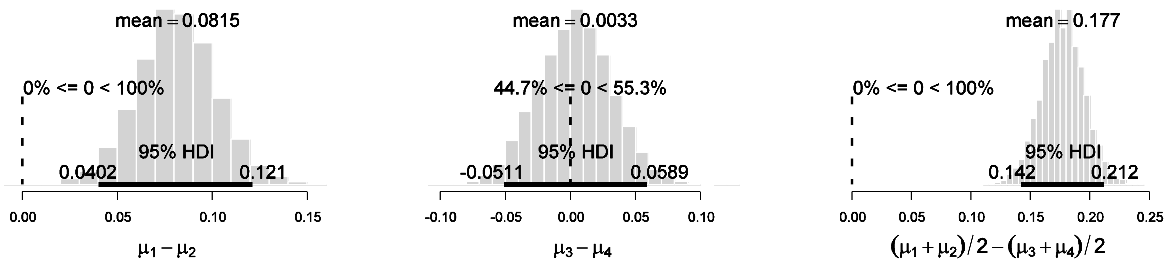
(B) The right side of Figure 9.17 shows a model in which the κ_c values for the different groups come an overarching distribution, the parameters of which are estimated by considering all the groups. The idea here is that accuracies of individuals in each group depend on the group mean accuracy, and we are going to estimate the magnitude of that dependency of individuals on group mean, but we assume that whatever the degree of dependency is, it will tend to be similar across groups, and we let the data inform our estimate of that similarity. To implement this assumption in the program, do the following: First, starting with the original program, in the model specification, change the lines that specify the mean and standard deviation of the gamma distribution, from constants to uniform distributions. Use ranges from 0.01 to 30. For example, change meanGamma <- 10 to meanGammadunif(0.01,30), and do the same for sdGamma. The resulting model specification could look like this (FilconCoKappaBrugs.R): […] Second, be sure that the

initialization of the chains give initial values to meanGamma and sdGamma; such as mean(kappa[]) and sd(kappa[]), respectively, where kappa[] are data-derived kappas for the four groups. Now run the modified program. (Hint: For an example of results, see Figures 9.18 and 9.19, and compare the results with those in Figure 9.16). In your answer: (1) Report the modified model-specification section of your code; (2) Show the graph of the estimated μ differences; (3) Answer this question: Why is the 95% HDI of the μ1 - μ2 differences farther away from zero than in the original analysis, but not as far away from zero as when assuming the same κ for all conditions?

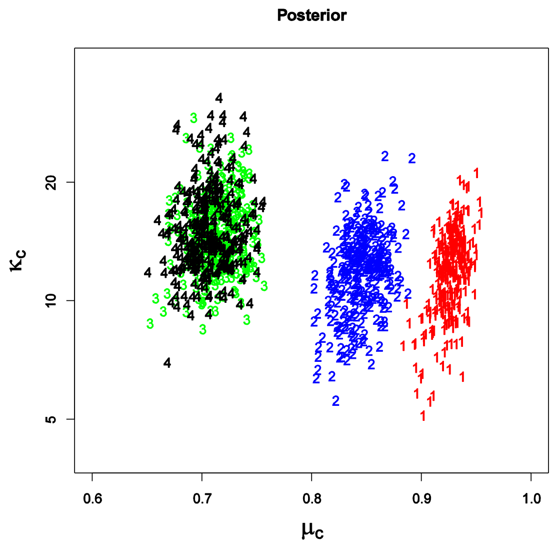
The modified model specification and the initialization:

```
model {
   for ( subjIdx in 1:nSubj ) {
      # Likelihood:
      z[subjIdx] ~ dbin( theta[subjIdx] , N[subjIdx] )
      # Prior on theta: Notice nested indexing.
      theta[subjIdx] ~ dbeta( a[cond[subjIdx]] , b[cond[subjIdx]]
)I(0.001,0.999)
   }
   for ( condIdx in 1:nCond ) {
      a[condIdx] <- mu[condIdx] * kappa[condIdx]
      b[condIdx] <- (1-mu[condIdx]) * kappa[condIdx]
      # Hyperprior on mu and kappa:
      mu[condIdx] ~ dbeta( Amu , Bmu )
      kappa[condIdx] ~ dgamma( Skappa , Rkappa )
   }
   # Constants for hyperprior:
   Amu <- 1
   Bmu <- 1
   Skappa <- pow(meanGamma,2)/pow(sdGamma,2)
   Rkappa <- meanGamma/pow(sdGamma,2)
   meanGamma ~ dunif( 0.01 , 30 )
   sdGamma ~ dunif( 0.01 , 30 )
}

  genInitList <- function() {
    sqzData = .01+.98*datalist$z/datalist$N
    mu = aggregate( sqzData , list(datalist$cond) , mean )[,"x"]
    sd = aggregate( sqzData , list(datalist$cond) , sd )[,"x"]
    kappa = mu*(1-mu)/sd^2 - 1
    return(
      list(
        theta = sqzData ,
        mu = mu ,
        kappa = kappa ,
        meanGamma = mean( kappa ),
        sdGamma = sd( kappa )
      )
    )
  }
```

Graph of mu differences:



And here is the scatterplot of kappa's and mu's:



Why are the mu differences farther away from zero than in the original analysis, but not as far away as in the equal-kappa model?

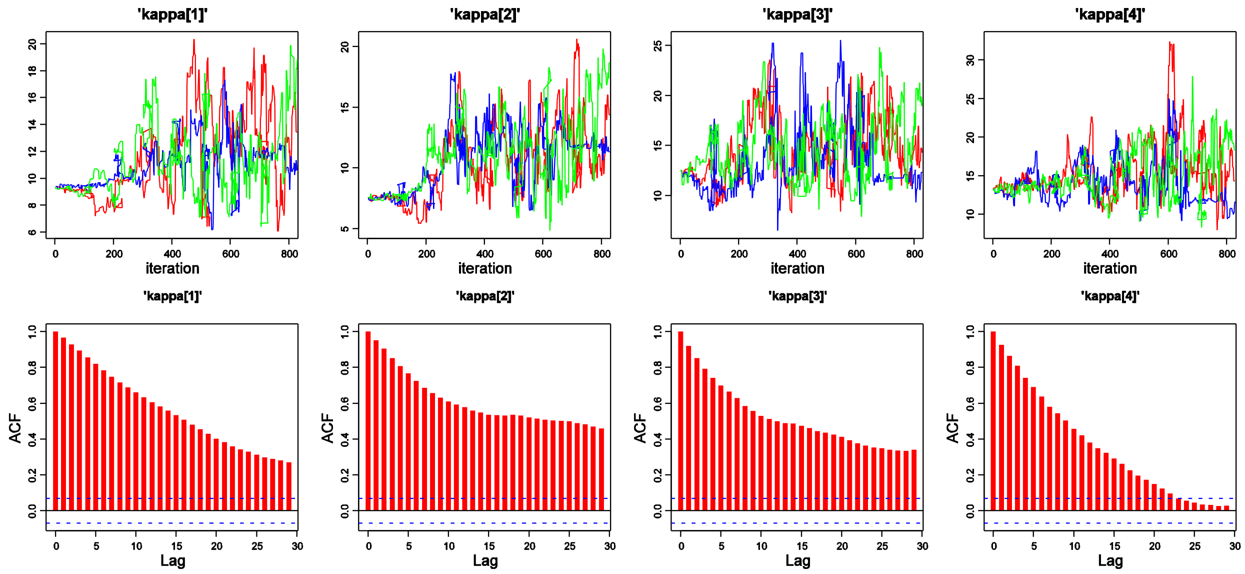
As explained in the previous part, the variability of the kappa's and the correlation of kappa with mu produces greater variability in the mu's, hence weaker differences between mu's. The scatter plots of mu and kappa (all shown in Figure 9.19 in the textbook) reveal that the variability of the kappa's is slightly less for this model than for the independent-kappa's model. This makes sense, because the current model has the four groups mutually inform each other's kappa values. Thus, because this model has intermediate constraint on the kappa values, and the kappa's are correlated with the mu's, this model also has intermediate sensitivity on the mu1-mu2 difference.

Exercise 9.3. [Purpose: To see, graphically, the importance of burning-in the chains, and the meaning of autocorrelation.] This exercise uses the BUGS program you created in the last part of the previous exercise (i.e., the model for the right side of Figure 9.17). You might find it useful to refer to Section 23.2, p. 623, when doing this exercise. Set the burn-in to zero and the thinning to zero. In other words, don't burn-in at all, and remove the the thin argument. Have the model go for 800 steps. What do the graphs of the chains look like, in particular for kappa? See, for example, Figure 9.20. Are the chains thoroughly overlapping? Include a relevant graph and discuss both burn-in and autocorrelation.

Change the modelUpdate section to this:

```
#burninSteps = 2000
#modelUpdate( burninSteps )
samplesSet( c("mu","kappa","theta","meanGamma","sdGamma") )
nPerChain = 800    # was ceiling(5000/nChain)
modelUpdate( nPerChain )   # was ,thin=10
```

The resulting chains for the kappa's look like this:



Notice that it takes a few hundred steps for the chains to diverge from their equal starting values, and to settle into their group-specific values. Notice also that the chains can get stuck and clumpy, as revealed also by the large autocorrelation function (ACF) values shown in the second row of graphs above. Thus, these chains show the need for burn-in (the period of time it takes for the chains to diverge and independently sample their posterior-appropriate values) and thinning (to reduce unrepresentative clumpiness in the posterior sample).

Chapter 10.

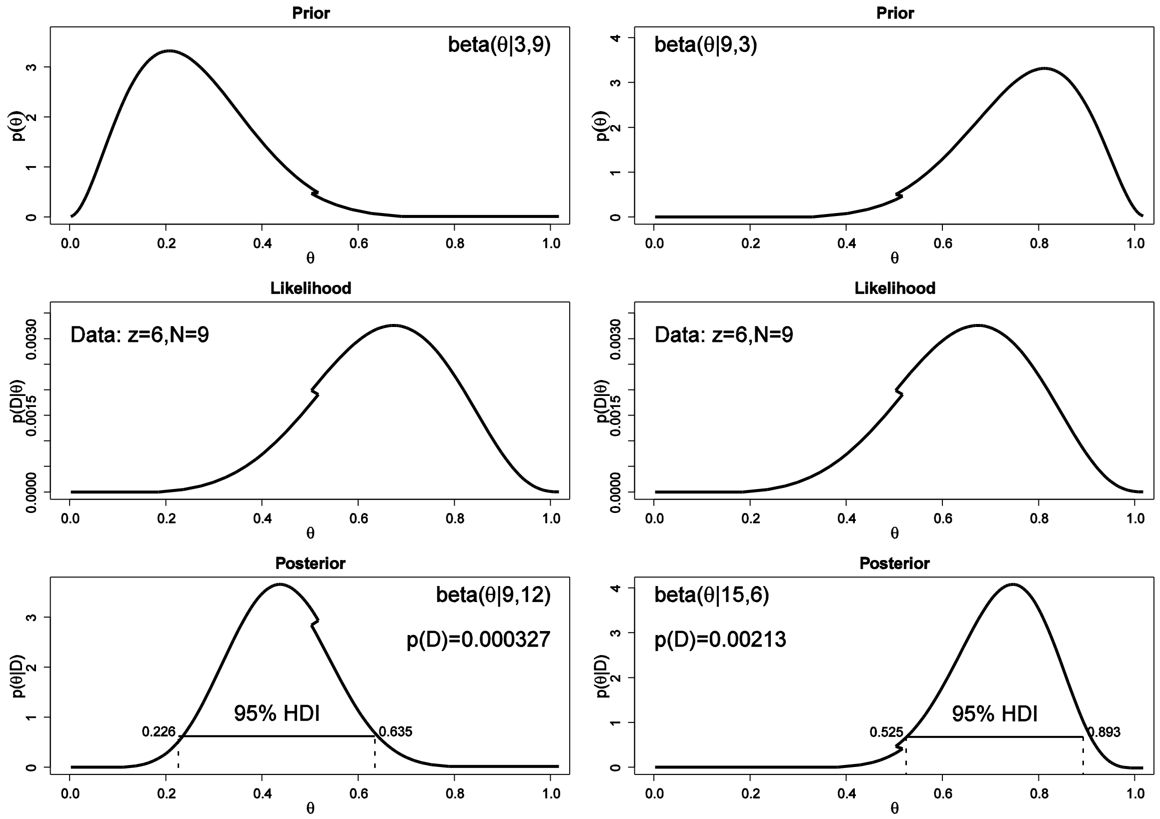
Exercise 10.1. [Purpose: To see how first-level model comparison is like hierarchical modeling with just two values of a hyperparameter.]

(A) Use the R code of Section 5.5.1 (BernBeta.R) (p. 91) to compare the model M1 : beta(θ|3,9) and the model M2 : beta(θ|9,3), when the observed data are z = 6 heads in N = 9 flips. What is the Bayes factor for the two models?

The R commands

```
postShape = BernBeta( priorShape=c(3,9) , dataVec=c(rep(1,6),rep(0,9-6)) )
postShape = BernBeta( priorShape=c(9,3) , dataVec=c(rep(1,6),rep(0,9-6)) )
```

yield these graphs:



(The original graphs are smooth but the EPS graphics are rendered incorrectly by Word.)
The Bayes factor is p(D|M2) / p(D|M1) = 0.00213/0.000327 = 6.51.

(B) Verify the values of p(D) by using Equation 5.10, p. 88.

Eqn 5.10 is p(z,N) = B(z+a,N−z+b) / B(a,b). Hence

p(6,9|M2) = B(6+9,9-6+3) / B(9,3) = 0.002128483
p(6,9|M1) = B(6+3,9-6+9) / B(3,9) = 0.000327459

(C) From the right panel of the fourth row of Figure 10.1 (p. 243), visually estimate p(μ=0.75|D) and p(μ=0.25|D), and compute their ratio. Does that ratio nearly match the Bayes factor that you computed in the first two parts? (It should.)

Visual inspection reveals that the value of p(μ=0.75|D) is about 26, and p(μ=0.75|D) is about 4. The ratio is 26/4 = 6.5, which is nearly the same as what was computed in parts A and B.

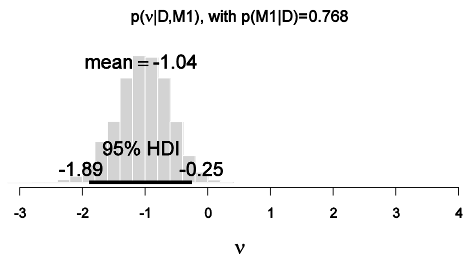
Exercise 10.2. [Purpose: To see that the prior can strongly affect the outcome of a model comparison.] In this exercise we consider a "toy" model comparison to illustrate how the priors on the parameters in two models can strongly affect the outcome of the comparison. The models: Consider two models for the bias of a coin. For both models, the probability of getting a "head" is a Bernoulli distribution of the bias θ, but each model has a different expression for determining the value of θ in terms of a different parameter:
M1 : θ = 1/(1 + exp(-ν)), where ν is any real value ("ν" is Greek "nu"), and
M2 : θ = exp(-η), where η is non-negative ("η" is Greek "eta").
(You can easily graph those two function in R if you want to see what they look like. Figure 14.6, p. 375, shows variations of model M1.) For model 1, we put a normal prior on ν, and for model 2, we put a gamma prior on η. The data: Suppose we flip the coin and find that we get 8 heads out of 30 flips.

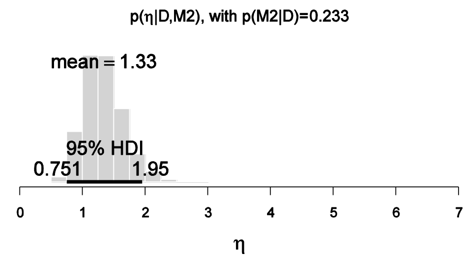
(A) Suppose the prior on ν is normal with mean 0 and precision 0.1, whereas the prior on η is gamma with shape 0.1 and rate 0.1. What are the resulting posterior probabilities of the models (if the prior on the models is 50/50)? […]

The following model specification

```
model {
   for ( i in 1:nFlip ) {
      # Likelihood:
      y[i] ~ dbern( theta )
   }
   # Prior
   theta <- ( (2-mdlIdx) * 1/(1+exp( -nu )) # theta from model index 1
            + (mdlIdx-1) * exp( -eta ) )    # theta from model index 2
   nu ~ dnorm(0,.1)      #  0,.1  vs  1,1
   eta ~ dgamma(.1,.1)   # .1,.1  vs  1,1
   # Hyperprior on model index:
   mdlIdx ~ dcat( modelProb[] )
   modelProb[1] <- .5
   modelProb[2] <- .5
}
```

yields





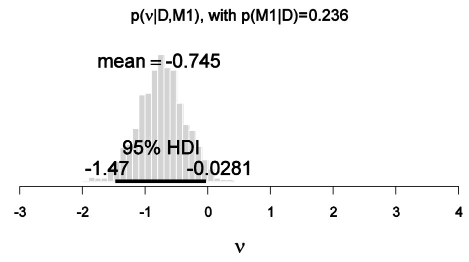
which is a preference for M1.

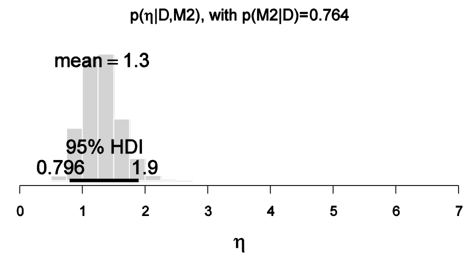
(B) Suppose the prior on ν is normal with mean 1 and precision 1, while the prior on η is gamma with shape 1 and rate 1. What are the resulting posterior probabilities of the models (if the prior on the models is 50/50)? Which model is preferred? (Hint: See Figure 10.7 for the posterior on the parameters and the model probabilities.

Changing the prior specification to

```
   nu ~ dnorm(1,1)       #  0,.1  vs  1,1
   eta ~ dgamma(1,1)    # .1,.1  vs  1,1
```

yields





which favors M2.

(C) Why does the choice of prior within each model (when the prior on p(M1) and p(M2) remains unchanged) have such a big influence on the posterior of the model believabilities? (Hint: Notice in Figure 10.7 that the posterior on the parameter values is in roughly the same place regardless of the prior—that is, the location of the posterior on the parameter values is dominated by the data. But notice that the prior probabilities at those posterior-favored values are rather different, and remember that p(D|M) = …

Inspection of the prior distributions in Figure 10.7 shows that for part A, the prior on ν (M1) is high around -1, which is the value that best accommodates the data, but for part B the prior on ν is very low around -1. On the other hand, for part A, the prior on η (M2) is very small around 1.3, which is the value that best accommodates the data, but for part B the prior on η is much larger around 1.3.

(D) Discuss how we might decide which choice of priors on ν and η would put the priors on an equal playing field. (Technically, in this case, the priors can be reparameterized to yield exact equivalence, but that's not the answer being sought for this exercise. In general, different models cannot be reparameterized into equivalence. Your discussion should address what to do in the general case, when models cannot be reparameterized to equivalence, but be motivated by considering the present toy example.) Here's one scheme to consider: Suppose we have some modest pilot data, or even some audience-agreeable plausible fictitious data, that in 7 flips there were 2 heads. To generate a prior for the subsequent new data, we start each model with an extremely vague proto-prior and update it with the modest pilot data. For example, suppose that the proto-prior on ν is normal with mean zero and precision of 0.0001 (i.e., standard deviation of 100), and the proto-prior on η has rate = 0.01 and shape = 0.01. Notice that both of the resulting priors (i.e., the extremely vague protopriors updated with the modest pilot data) are now reasonably "in the ballpark" of realistic data, and therefore the models are starting on a more equal playing field.

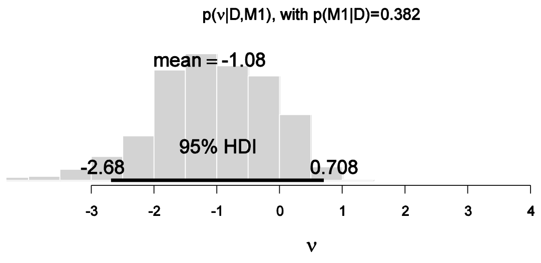
We specify the vague "proto-prior"

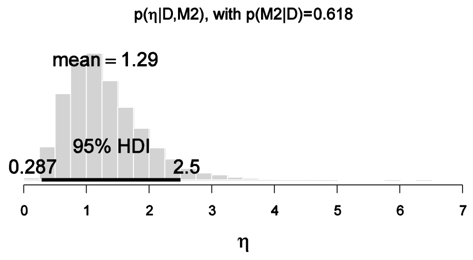
```
   nu ~ dnorm( 0 , 0.0001 )     #  0,.1  vs  1,1
   eta ~ dgamma( 0.01 , 0.01 )  # .1,.1  vs  1,1
```

and the hypothetical data

```
 N = 7 # 30
 z = 2 # 8
 datalist = list(
    y = c( rep(1,z) , rep(0,N-z) ) ,
    nFlip = N
 )
```

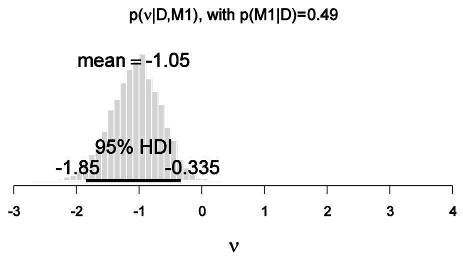
It turns out that the chains are badly outcorrelated, so we thin them to saving 1 step in 20.
The resulting posterior looks like this:

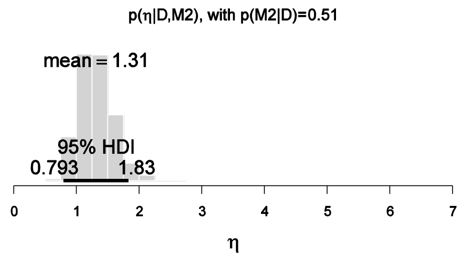




The p(M|D) values displayed in the graph are irrelevant because the protopriors are not of interest to us. The nu distribution for M1 looks roughly normal and has mean = -1.08 and a precision (1/var) = 1.14. The eta distribution for M2 looks roughly gamma and has mean = 1.29 and SD = 0.62, which corresponds to a gamma with shape = 4.33 and rate = 3.35 (see Figure 9.8, p. 209). These posteriors could then be used as the priors for subsequent real data. The priors are much more comparable for the two models because they were comparably informed by prior knowledge.

If those priors are used, i.e.,
```
   nu ~ dnorm(-1.08,1.14)     #  0,.1  vs  1,1
   eta ~ dgamma(4.33,3.35)    # .1,.1  vs  1,1
```
with the actual data, then the posterior is





Notice that p(M1|D) nearly equals p(M2|D)!

Exercise 10.3. [Purpose: To gain hands-on experience with the pseudopriors approach.] For this exercise, we'll consider a situation very similar to the filtration-condensation experiment that has been used repeatedly in recent pages, and was introduced in Section 9.3.1. The new experiment also involved people learning to categorize shapes. There were again four different groups, but this time the groups differed on the type of structural shift from an initial category structure to a new category structure (Kruschke, 1996). Theories of learning are concerned with this type of situation because different theories predict different types of transfer from one phase to the next. Our goal in this exercise is to determine whether the kappa values for the four groups are equivalent, just as we asked this question of the filtration-condensation data in Section 10.2.2, p. 246. Modify the program FilconModelCompPseudoPriorBrugs.R for this exercise. […]

(A) Run the program. Notice that the pseudopriors are not well matched to the posterior distribution. Change the pseudopriors so that they have the same mean and standard deviation as the posterior. Show this section of your modified code (i.e., the lines that set the shape and rate constants of the pseudopriors). (Hint: Use mean(kappa1sampleM1) and sd(kappa1sampleM1) to get the mean and standard deviation of the posterior. Then use the identities described in Figure 9.8 to determine the shape and rate parameters of a gamma distribution with that mean and standard deviation.)

Your results might differ a bit from the following, but should be near these values:

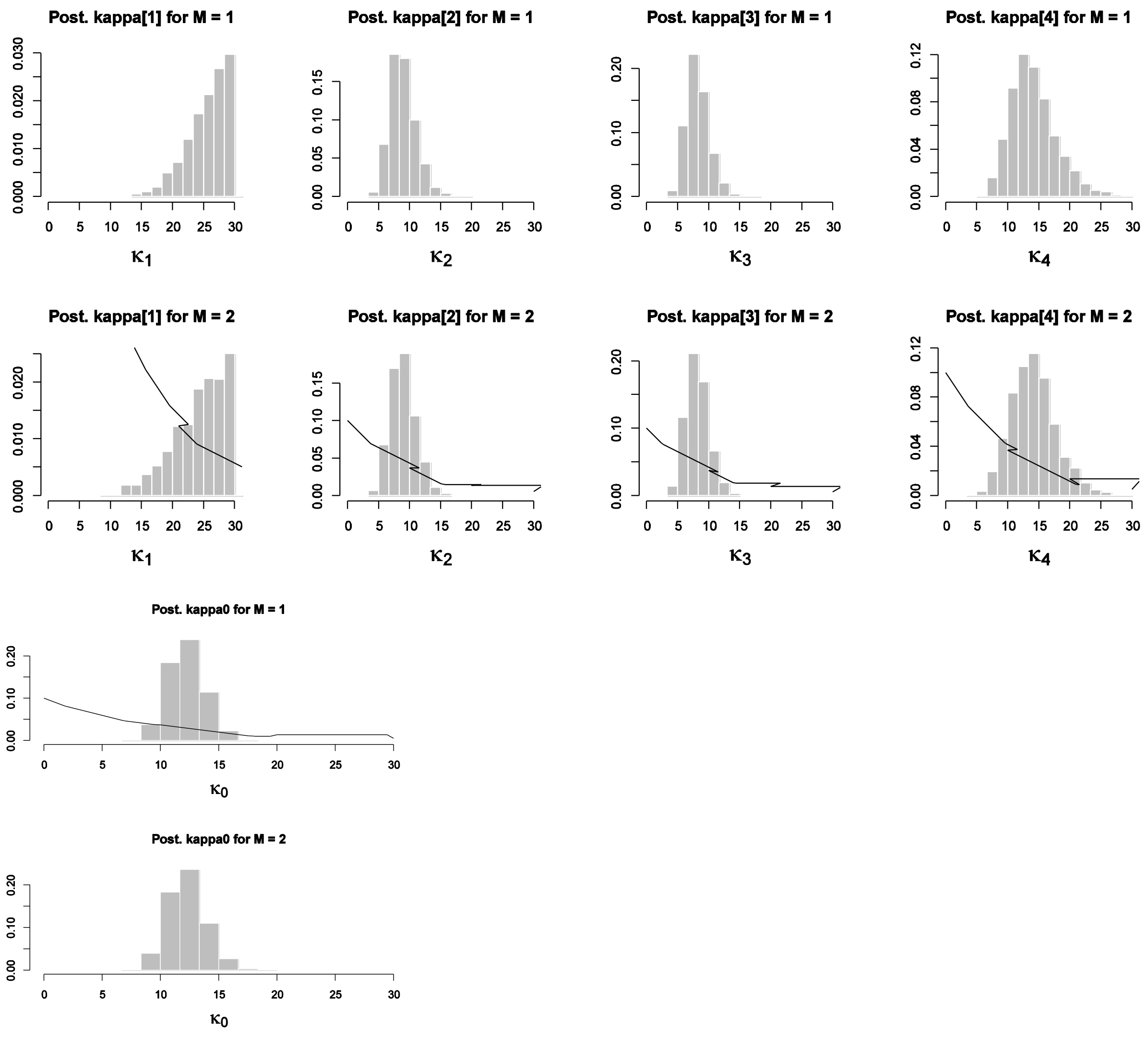
- Shape for kappa0 is `mean(kappa0sampleM2)^2 / sd(kappa0sampleM2)^2` which is approximately 62.8. Rate for kappa0 is `mean(kappa0sampleM2) / sd(kappa0sampleM2)^2` which is approximately 5.13.
- Shape for kappa1 is `mean(kappa1sampleM1)^2 / sd(kappa1sampleM1)^2` which is approximately 8.81. Rate for kappa1 is `mean(kappa1sampleM1) / sd(kappa1sampleM1)^2` which is approximately 0.213.
- Shape for kappa2 is `mean(kappa2sampleM1)^2 / sd(kappa2sampleM1)^2` which is approximately 19.3. Rate for kappa2 is `mean(kappa2sampleM1) / sd(kappa2sampleM1)^2` which is approximately 2.17.
- Shape for kappa3 is `mean(kappa3sampleM1)^2 / sd(kappa3sampleM1)^2` which is approximately 21.2. Rate for kappa3 is `mean(kappa3sampleM1) / sd(kappa3sampleM1)^2` which is approximately 2.59.
- Shape for kappa4 is `mean(kappa4sampleM1)^2 / sd(kappa4sampleM1)^2` which is approximately 14.9. Rate for kappa4 is `mean(kappa4sampleM1) / sd(kappa4sampleM1)^2` which is approximately 1.05.

These values get coded into the pseudo priors of the model as follows:

```
# Pseudo priors:
# shape, rate kappa0[ model ]
shk0[1] <- 62.8
rak0[1] <- 5.13
# shape kappa[ condition , model ]
shk[1,2] <- 8.81
shk[2,2] <- 19.3
shk[3,2] <- 21.2
shk[4,2] <- 14.9
```

```
# rate kappa[ condition , model ]
rak[1,2] <- 0.213
rak[2,2] <- 2.17
rak[3,2] <- 2.59
rak[4,2] <- 1.05
```

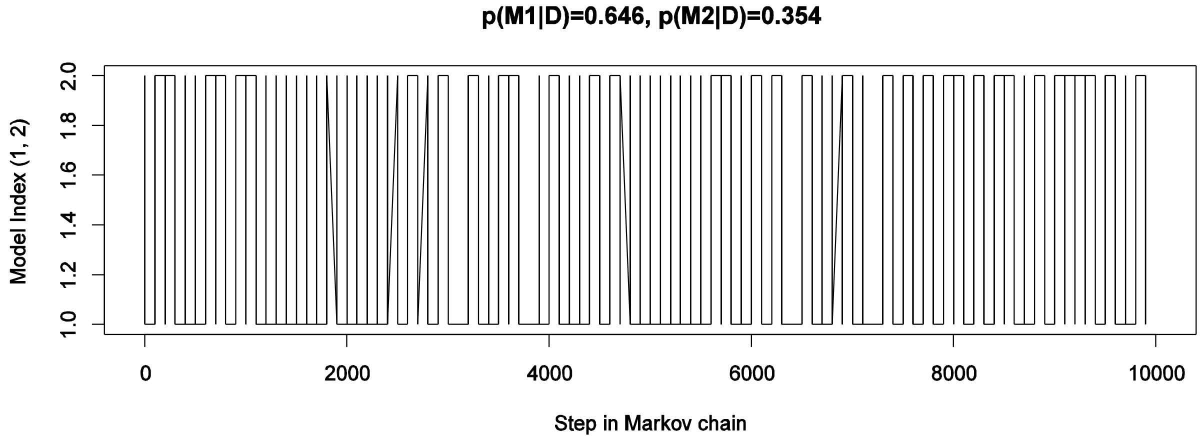
(B) Rerun the program with the better-tuned pseudopriors that you determined in the previous part. Show histograms of the kappa distributions like those in Figure 10.4. (Hint: Your histograms in the top and bottom rows should be similar, because the pseudoprior is supposed to mimic the actual posterior. You will find that the histogram for kappa1 falls largely above 30; that is, it exceeds the right limit of the x axis as it is presently set.)



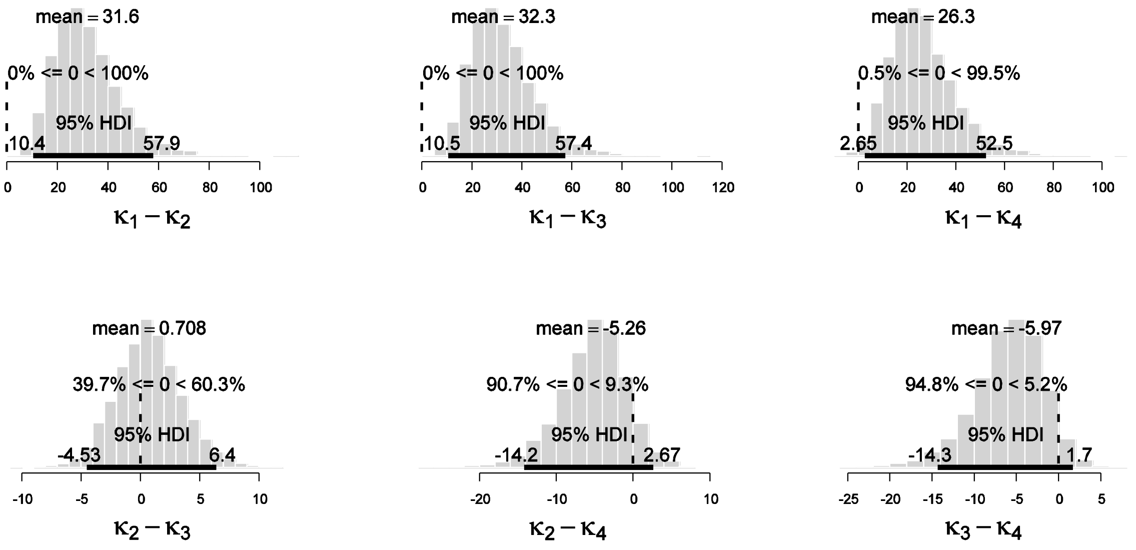
(The curves representing the vague prior are smooth in the original but rendered incorrectly by Word.) The distributions in the two rows look very similar, as intended by the setting of the pseudoprior.

(C) Are the kappa values of the four groups the same or different? Answer this question two ways, as follows. First, what is the value of the Bayes factor in favor of the different-kappa model? Be careful to take into account that the BUGS simulation used priors that were not 50-50. (Hint: It's about 600 to 1. Explain how to get that value.) Does the Bayes factor alone tell us anything about which groups are different? (The correct answer to that last question is no. Briefly explain why.) Second, considering only the different-kappa model, what are the distributions of the differences between kappas for model 1? Specifically, which kappas are different from which other kappas? Does the Bayes factor tell us anything that the kappa estimates do not? (The correct answer to that last question is no. Briefly explain why.) (Hint: Your histograms of kappa differences should look something like Figure 10.8).

First, according to the model-index posterior (see figure below – still a bit autocorrelated; thinning would help), the posterior odds are p(M1|D)/p(M2|D) = .646/.354 = 1.82. The Bayes factor is not the posterior, however. Recall that the prior was set at p(M1)=.003 and p(M2)=.997. Hence the Bayes factor is [p(M1|D)/p(M2|D)] [p(M2)/p(M1)] = 1.82 x .997/.003 = 608, i.e., M1 is favored by about 600 to 1. In other words, the model comparison strongly favors the different-kappa model.



Second, considering only the different-kappa model, the posterior reveals differences of kappa's as shown below:



We see that k1 is credibly different from all the other kappas, but the other kappas are not credibly different from each other. Thus, the estimates of the four kappas tell us that the kappas are different, which is the same conclusion as the model comparison, but the four-kappa model tells us more: We have explicit posterior estimates of all four kappas (and their conjoint distribution).

Chapter 11.

Exercise 11.1. [Purpose: To determine critical values for a two-tailed test, conduct the test, and notice the dependence of the conclusion on the intended stopping rule.] Suppose we flip a coin N = 17 times. Our goal is to determine what values for the number of heads would be extreme enough to reject the hypothesis that the coin is fair. We want the total probability of false alarm to be less than 5%. In other words, if the null hypothesis is really true, we will mistakenly reject it less than 5% of the time. Therefore, we desire critical values zlow and zhigh for the number of observed heads…

(A) What is the value of zlow? Explain how you got your answer. Hint: Try cumsum(dbinom(0:17 , 17 , .5)) < .025 and carefully explain what that does!

dbinom(0:17 , 17 , .5)
yields the binomial probability for z in 0:17 for N=17 and theta=.5, which is the vector

```
 7.629395e-06 1.296997e-04 1.037598e-03 5.187988e-03 1.815796e-02
 4.721069e-02 9.442139e-02 1.483765e-01 1.854706e-01 1.854706e-01
 1.483765e-01 9.442139e-02 4.721069e-02 1.815796e-02 5.187988e-03
 1.037598e-03 1.296997e-04 7.629395e-06
```

cumsum(dbinom(0:17 , 17 , .5))
yields the cumulative sum of the binomial density for z in 0:17 for N=17 and theta=.5, which is the vector

```
 7.629395e-06 1.373291e-04 1.174927e-03 6.362915e-03 2.452087e-02
 7.173157e-02 1.661530e-01 3.145294e-01 5.000000e-01 6.854706e-01
8.338470e-01 9.282684e-01 9.754791e-01 9.936371e-01 9.988251e-01
9.998627e-01 9.999924e-01 1.000000e+00
```

Notice that its last component is exactly 1.0, as it should be for the sum of a probability distribution.

cumsum(dbinom(0:17 , 17 , .5)) < .025
indicates whether each component of the cumulative sum vector is less than .025, which yields the vector

```
 TRUE  TRUE  TRUE  TRUE  TRUE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
 FALSE FALSE FALSE FALSE FALSE FALSE.
```

The 5th component is the largest component that is TRUE, which corresponds to z=4 (because z starts at 0). Hence zlow is 4, which means that when z is 4 or less, the null hypothesis is rejected.

(B) What is the value of zhigh? Explain how you got your answer. Hint: Try cumsum(dbinom(17:0 , 17 , .5)) < .025 and carefully explain what that does!

cumsum(dbinom(17:0 , 17 , .5)) < .025
is analogous to part A above, but orders the z values from 17 to 0 (instead of from 0 to 17). This way the cumulative sum starts at the high end of z and works down. The result is

```
 TRUE  TRUE  TRUE  TRUE  TRUE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
 FALSE FALSE FALSE FALSE FALSE FALSE.
```

The 5th component is the largest that is TRUE, which corresponds to z=13 (because z starts at 17). Hence zhigh is 13, which means that when z is 13 or higher, the null hypothesis is rejected.

(C) Suppose we flip the coin 17 times and get 4 heads. How many heads would we expect to get if the coin were fair? Can we reject the null hypothesis "at the 0.05 level" (which means, with two-tailed false alarm rate less than 0.05)?

If the coin were fair, we would expect to get .5 * 17 = 8.5 heads. The observed value of z=4 is *less* than the expected value, so we want to know if z is less than or equal to the critical zlow determined in part A. Because observed z=4 is indeed less than or equal to zlow=4, we reject the null hypothesis, with p<.05 two-tailed.

(D) New scenario: We have a six-sided die, and we want to know whether the probability that the six-dotted face comes up is fair. Thus, we are considering two possible outcomes: six dots or not six dots. If the die is fair, the probability of the six-dot face is 1/6. Suppose we roll the die N = 45 times, intending to stop at that number of rolls. What are the values of zlow and zhigh, using a two-tailed false alarm rate of 5%? Explain how you got your answer. Suppose we get 3 six-dot rolls. Can we reject the null hypothesis that the die is fair? (See the upper panel of Figure 11.7 for guidance.)

cumsum(dbinom(0:45 , 45 , 1/6)) < .025
yields TRUE up to its third component, which is z=2, hence zlow is 2.

cumsum(dbinom(45:0 , 45 , 1/6)) < .025
yields TRUE up to its 32nd component, which is z=14, hence zhigh is 14.

If the observed z=3, then we do not reject the null, because it is not as low as zlow=2.

(E) Suppose we roll the die until we get 3 six-dot outcomes. It takes 45 rolls. (Notice this is the same result as the previous part.) How many six-dot outcomes would we expect to get if the coin were fair? Can we reject the null hypothesis that the die is fair, at the 0.05 level? (See the lower panel of Figure 11.7 for guidance.)

A plot much like the lower-right of Figure 11.7 can be created by the following two lines of code:
nbin = function(N , z , theta) { z * dbinom(z,N,theta) / N }
plot(3:52 , nbin(3:52 , 3 , 1/6) , type="h")

We can use the nbin function, defined above, to find the critical values:
cumsum(nbin(3:52 , 3 , 1/6)) < .025
is TRUE only to its second component, which corresponds to Nlow=4.

sum(nbin(3:41 , 3 , 1/6))
is 0.9761868, which means that N=42 is the smallest N in the high rejection tail, i.e., Nhigh=42.

The observed N=45 exceeds Nhigh, therefore we reject the null hypothesis. Notice that this contradicts the conclusion from the previous part.

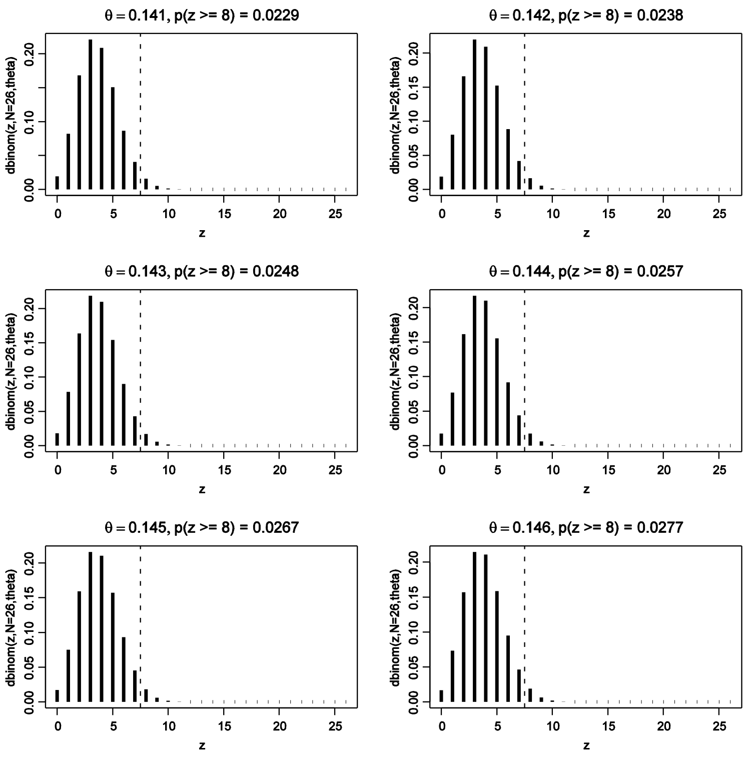
Exercise 11.2. [Purpose: To determine NHST confidence intervals and notice that they depend on the experimenter's intention.] Suppose we flip a coin N = 26 times and observe z = 8 heads. Assume that the intention was to stop when N = 26.

(A) Show that when θ=0.144, the probability of z ≥8 is just over 2.5%, but for smaller values of θ, the probability of z ≥ 8 is less than 2.5%. Hint: Try
for(theta in seq(.140 , .150 , .001))
{ show(c(theta , sum(dbinom(8:26 ,26 , theta)))) }
and explain carefully what that does.

The code increments theta in steps of .001 and shows the sum of the binomial distribution from 8 to 26. A more elaborate version of the code produces graphs along with the sum:

```
windows(7,7)
layout( matrix( 1:6 , ncol=2 , byrow=T ) )
par( mar=c(4,4,2.5,1) , mgp=c(2,0.7,0) )
for( theta in seq( .141 , .146 , 0.001 ) )  {
      plot( 0:26 , dbinom( 0:26 , 26 , theta ) , type="h" , lwd=3 ,
                   xlab="z" , ylab="dbinom(z,N=26,theta)" ,
                   main=bquote( list(
                   theta==.(theta) ,
                   "p(z >= 8) = "*.(round(sum(dbinom(8:26,26,theta)),4))
                   )) )
      abline( v=7.5 , lty="dashed" )
}
```

which yields this graph:

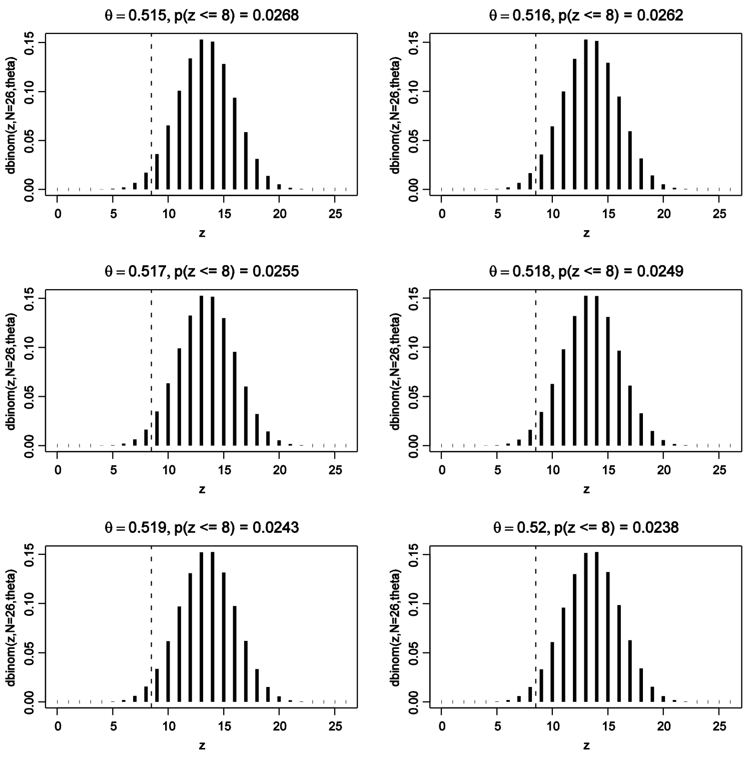


You can see in the middle row that as theta increases from .143 to .144, p(z>=8) increases from .0248 to .0257. In other words, a result of z=8 does reject theta=.143, but does not reject theta=.144.

(B) Show that when theta = 0.517, the probability of z <= 8 is just over 2.5%, but when theta exceeds 0.517, then p(z<=8) drops below 2.5%.

Analogously to the answer of the previous part, we can graph the binomial as theta increments:

```
windows(7,7)
layout( matrix( 1:6 , ncol=2 , byrow=T ) )
par( mar=c(4,4,2.5,1) , mgp=c(2,0.7,0) )
for( theta in seq( .515 , .520 , 0.001 ) )  {
       plot( 0:26 , dbinom( 0:26 , 26 , theta ) , type="h" , lwd=3 ,
                     xlab="z" , ylab="dbinom(z,N=26,theta)" ,
                     main=bquote( list(
                     theta==.(theta) ,
                     "p(z <= 8) = "*.(round(sum(dbinom(0:8,26,theta)),4))
                     )) )
       abline( v=8.5 , lty="dashed" )
}
```



It can be seen in the middle row that as theta goes from .517 to .518, the left-tail probability goes from .0255 to .0249. Hence z=8 rejects theta=.518, but z=8 does not reject theta=.517.

(C) What is the 95% confidence interval for theta? (Just summarize the results of the previous two parts.)

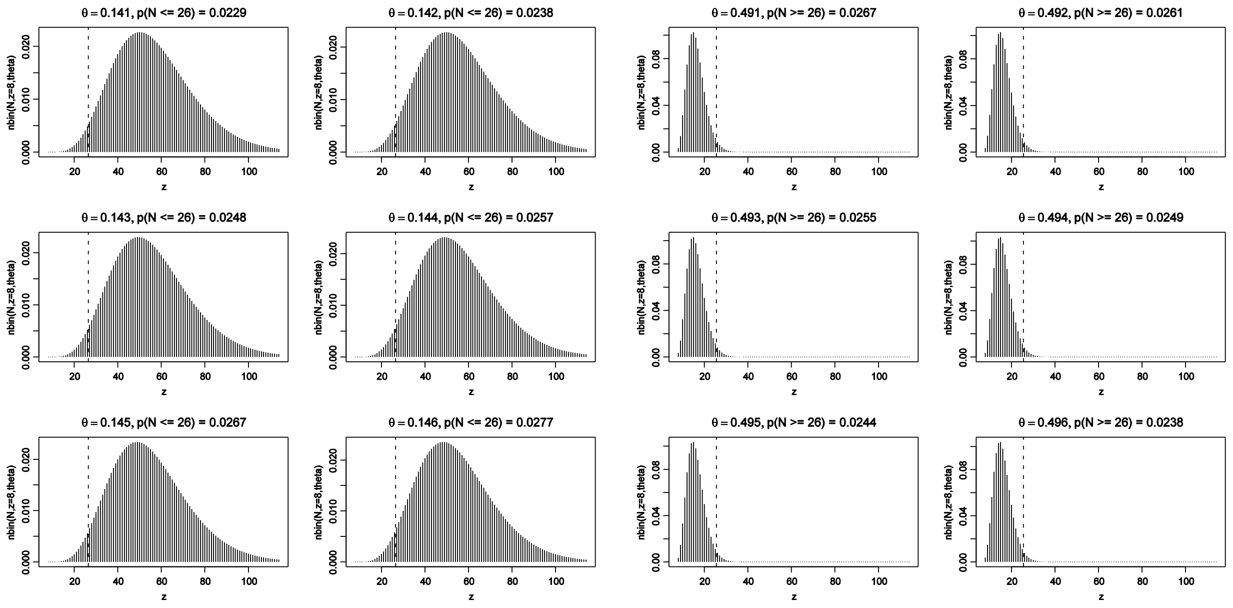
The range of theta's that is *not* rejected by z=8 (with N=26) extends from theta=.144 to theta=.517.

(D) Suppose that the intention was to stop when z = 8 heads. Explain how to determine the NHST confidence interval, and include R code as appropriate. (Compare to Figure 11.5.)

This code, analogous to the previous parts, produces the graphs that follow:

```
windows(7,7)
layout( matrix( 1:6 , ncol=2 , byrow=T ) )
par( mar=c(4,4,2.5,1) , mgp=c(2,0.7,0) )
for( theta in seq( .141 , .146 , 0.001 ) )  {
       plot( 8:114 , nbin( 8:114 , 8 , theta ) , type="h" , lwd=1 ,
                     xlab="z" , ylab="nbin(N,z=8,theta)" ,
                     main=bquote( list(
                     theta==.(theta) ,
                     "p(N <= 26) = "*.(round(sum(nbin(8:26,8,theta)),4))
                     )) )
       abline( v=26.5 , lty="dashed" )
}

windows(7,7)
layout( matrix( 1:6 , ncol=2 , byrow=T ) )
par( mar=c(4,4,2.5,1) , mgp=c(2,0.7,0) )
```

```
for( theta in seq( .491 , .496 , 0.001 ) )  {
      plot( 8:114 , nbin( 8:114 , 8 , theta ) , type="h" , lwd=1 ,
                   xlab="z" , ylab="nbin(N,z=8,theta)" ,
                   main=bquote( list(
                   theta==.(theta) ,
                   "p(N >= 26) = "*.(round(1-sum(nbin(8:25,8,theta)),4))
                   )) )
      abline( v=25.5 , lty="dashed" )
}
```



The left panels show that theta=.144 is not rejected, but theta=.143 is rejected.
The right panels show that theta=.493 is not rejected, but theta=.494 is rejected.
Hence the confidence interval, of values not rejected by N=26 (for fixed z=8), goes from theta=.144 to theta=.493. Notice that this is different than the confidence interval for z=8 with fixed N=26, computed in the previous part.

Exercise 11.3. [Purpose: To determine the p value if a coin is flipped for a fixed period of time instead of for a fixed number of flips.] (For another example of NHST for fixed-duration samples, see Kruschke, 2010a.) An experimenter is investigating whether there are more conservatives or liberals in her subject pool. She recruits 46 subjects and finds that 30 of them are liberal. We are interested in testing the null hypothesis that the population is split 50-50; (i.e., theta = 0.5).

(A) If we assume that the experimenter intended to stop when N = 46, what is the probability of getting 30 or more liberals in a sample according to the null hypothesis? Do we reject the null hypothesis? Hint: sum(dbinom(30:46 , 46 , .5)) < 0.025

The Hint code indicates whether the probability of getting 30 or more flips out of N=46 is less than .025. The result is FALSE, because sum(dbinom(30:46,46,.5)) = .0270. Therefore we do not reject the null hypothesis. (We ask about 30 or more because 30 is larger than the expected value of 23.)

(B) We ask the experimenter why she chose N = 46. She replies that she didn't; in fact, she chose to run the experiment for 1 week, and she just happened to get 46 subjects. (This is typical in real-world research. There is nothing wrong with this procedure because we are assuming that every person polled is independent of every other person polled and uninfluenced by the poller's intentions.) With these intentions regarding duration, we cannot assume that N is fixed at 46, and therefore the space of possible experiment outcomes is much larger. … Is the probability of getting the observed proportion less than 2.5%? Do we reject the null hypothesis? How does this compare with the conclusion from the previous part of the exercise?

The code stated in the exercise, namely

```
z_obs = 30 ; N_obs = 46
nulltheta = .5
tail_prob = 0  # Zero initial value for accumulation over possible N.
for ( N in 1 : (3*N_obs) ) {  # Start at 1 to avoid /0. 3*N_obs is arbitrary.
  # Create vector of z values such that z/N >= z_obs/N_obs
  zvec = (0:N)[ (0:N)/N >= z_obs/N_obs ]
  tail_prob = tail_prob + (
              dpois( N , N_obs ) * sum( dbinom( zvec , N , nulltheta ) ) )
}
show( tail_prob )
```

yields p=.0209, which is <.025. In other words, contrary to the conclusion of the previous part, this analysis says we do reject the null hypothesis when the intention is to run the experiment for 1 week.

(C) Repeat the previous two parts, for z = 26 and N = 39.

When N=39 is fixed, we get p = sum(dbinom(26:39 , 39 , .5)) = 0.02662, hence we do not reject the null hypothesis.

When the duration is fixed with a mean rate of 26/39, then the code above produces p=.0229, hence we do reject the null hypothesis, contrary to when N is fixed.

Exercise 11.4. [Purpose: To determine the false alarm rate for a two-tiered data collection process (compare to Berger & Berry, 1988).] …
(A) For N = 30, what are zlow and zhigh, assuming a two-tailed false alarm rate of .05 or less? (See Exercise 11.1.) (Hint: The answer is 9 and 21; your job is to explain how to get that answer.)

Using the techniques of Exercise 11.1, we simply see which indices of the vector 0:30 or 30:0 have cumulative sums less than .025:

```
max( (0:30)[ cumsum( dbinom( 0:30 , 30 , .5 ) ) < .025 ] ) = 9
min( (30:0)[ cumsum( dbinom( 30:0 , 30 , .5 ) ) < .025 ] ) = 21
```

(B) For N = 45, what are zlow and zhigh, assuming a two-tailed false alarm rate of .05 or less? (See Exercise 11.1.) (Hint: The answer is 15 and 30; your job is to explain how to get that answer.)

As in the previous part:

```
max( (0:45)[ cumsum( dbinom( 0:45 , 45 , .5 ) ) < .025 ] ) = 15
min( (45:0)[ cumsum( dbinom( 45:0 , 45 , .5 ) ) < .025 ] ) = 30
```

For the next parts of the exercise, consider Table 11.1. Each cell of Table 11.1 corresponds to a certain outcome from the first 30 flips and a certain outcome from the second 15 flips. A cell is marked by a dagger, †, if it has a result for the first 30 flips that would reject the null hypothesis. A cell is marked by a double dagger, ‡, if it has a result for the total of 45 flips that would reject the null hypothesis. For example, the cell with 10 heads from the first 30 flips and 1 head from the second 15 flips is marked with a ‡ because the total number of heads for that cell, 10 + 1 = 11, is less than 15 (which is zlow for N = 45). That cell has no single dagger, †, because getting 10 heads in the first 30 flips is not extreme enough to reject the null.

(C) Denote the number of heads in the first 30 flips as z1, and the number of heads in the second 15 flips as z2. Explain why it it true that the z1, z2 cell of the table has conjoint probability equal to dbinom(z1,30,.5) * dbinom(z2,15,.5).

The first 30 flips (event 1) and the next 15 flips (event 2) are independent of each other. Hence the conjoint probability of the outcomes of the two events is simply the product of the individual event probabilities.

(D) What is the sum of the probabilities of all the cells that contain a † (whether or not it contains a ‡)? Explain how you got your answer! (Hint: The answer is not greater than 0.05. See also the Hint at the end of the exercise).

The Hint provides this R code:

```
N1 = 30       # Number of flips for first test. Try 17.
N2 = 15       # Number of _additional_ flips for second test. Try 27 or 50.

theta = .5    # Hypothesized bias of coin.
FAmax = .05   # False Alarm maximum for a single test.
NT = N1 + N2  # Total number of flips.

# Determine critical values for N1:
# EXPLAIN what each function does and why, including
# dbinom, cumsum, which, max, and (0:N)[...]
loCritN1 = (0:N1)[ max( which( cumsum( dbinom(0:N1,N1,theta) ) <= FAmax/2 ) ) ]
hiCritN1 = (N1:0)[ max( which( cumsum( dbinom(N1:0,N1,theta) ) <= FAmax/2 ) ) ]
# Compute actual false alarm rate for those critical values.
# EXPLAIN what this does and why.
FA1 = sum( ( 0:N1 <= loCritN1 | 0:N1 >= hiCritN1 ) * dbinom(0:N1,N1,theta) )
cat( "N1:",N1 , ", lo:",loCritN1 , ", hi:",hiCritN1 , ", FA:",FA1 , "\n" )

# Determine critical values for NT:
# EXPLAIN what each function does and why, including
# dbinom, cumsum, which, max, and (0:N)[...]
loCritNT = (0:NT)[ max( which( cumsum( dbinom(0:NT,NT,theta) ) <= FAmax/2 ) ) ]
hiCritNT = (NT:0)[ max( which( cumsum( dbinom(NT:0,NT,theta) ) <= FAmax/2 ) ) ]
# Compute actual false alarm rate for those critical values.
# EXPLAIN what this does and why.
FAT = sum( ( 0:NT <= loCritNT | 0:NT >= hiCritNT ) * dbinom(0:NT,NT,theta) )
cat( "NT:",NT , ", lo:",loCritNT , ", hi:",hiCritNT , ", FA:",FAT , "\n" )
```

```
# Determine actual false alarm rate for the two-tier test:
# EXPLAIN each of the matrices below --- what is in each one?
Z1mat = matrix( 0:N1 , nrow=N2+1 , ncol=N1+1 , byrow=TRUE )
ZTmat = outer( 0:N2 , 0:N1 , "+" )
pZTmat = outer( dbinom( 0:N2 , N2 , theta ) , dbinom( 0:N1 , N1 , theta ) )
# EXPLAIN the matrices in computation below.
FA1or2 = sum( ( ( ZTmat <= loCritNT | ZTmat >= hiCritNT ) # double dagger matrix
              | ( Z1mat <= loCritN1 | Z1mat >= hiCritN1 ) # single dagger matrix
              ) * pZTmat )
cat( "Two tier FA:" , FA1or2 , "\n" )
```

The first sections of the code simply find the critical values, as was done in parts A and B of this exercise. Those sections also compute the actual false alarm rate when using those critical values, by summing the tail probabilities of the binomial distributions.

For 30 flips, the rejection-tail probability is .0428.

(E) What is the sum of the probabilities of all the cells that contain a ‡ (whether or not it contains a †)? Explain how you got your answer! (Hint: The answer is not greater than 0.05. See also the Hint at the end of the exercise.)

From the middle section of the code, we find that the rejection-tail probability for the 15 flips is .0357.

(F) What is the sum of the probabilities of all the cells that contain either a † or a ‡? Note: This is the false alarm rate for the two-stage design, because these are all the ways you would decide to reject the null even when it's true. Explain how you got your answer! (Hint: The answer is greater than 0.05. See also the Hint at the end of the exercise.)

The last section of code is the important part for the two-tier procedure. The matrix Z1mat represents the outcome of the first 30 flips. Its size is 16x31 and has all 0's in its first column, all 1's in its second column, and so on, with all 30's in its 31st column. The ZTmat matrix represents the sum total of the all 45 flips. Its size is also 16x31. It has a 0 in the top left cell, 1's in cells [1,2] and [2,1], 2's in the next diagonal, and so on, until cell [16,31] contains the value 45.

The matrix pZTmat contains the probability of each outcome, namely, the product of the binomial probability of the first 30 flips and the binomial probability of the next 15 flips. The matrix is constructed by using R's outer() function.

The single-dagger matrix is computed as
`Z1mat <= loCritN1 | Z1mat >= hiCritN1`
which yields TRUE only where Z1mat has entries below loCritN1 or above hiCritN1.
The double-dagger matrix is similarly computed as
`ZTmat <= loCritNT | ZTmat >= hiCritNT`
By taking the logical OR of those two matrices, the result is TRUE anywhere there is a single or double dagger. That matrix is component-multiplied by pZTmat to isolate only the probabilities of the single or double-dagger cells. The matix is then summed.

The resulting sum is p=.061. Thus, the two-tier procedure has a false alarm rate greater than .05.

(G) Suppose that the researcher intends to run an experiment using this two-stage stopping criterion. She collects the first 30 flips and finds 8 heads. She therefore rejects the null hypothesis and reports that p < 0.05. Is that correct? Explain. (Hint: The answer is no, it's not correct, because the design of the experiment included a larger potential sampling space.)

Even though the researcher stopped after the first 30 flips, the design of experiment considered the larger sample space involving the second 15 flips. Thus, because the researcher intended to continue if the first 30 did not yield a significant result, the researcher must report the probability of false alarm from the intended design. Thus, the researcher should report that p<.061.

(H) Whenever we run an experiment and get a result that trends away from the null expectation, but isn't quite significant, it's natural to consider collecting more data. We saw in the previous part that even intending to collect more data, but not actually doing it, inflates the false alarm rate. Doesn't the fact that we always consider collecting more data mean that we always have a much higher false alarm risk than we pretend we do? Doesn't the actual false alarm rate of an experiment depend on the maximal number of data points we'd be willing to collect over the course of our lifetimes?

Yes! And that is another reason why NHST is so strange --- the p value depends on our (un-)willingness to collect more data.

This is another manifestation of the same problem that arose in the context of multiple comparisons (section 11.4.1). When we contemplate including another condition in a study, which will be compared with existing conditions, we enlarge the space of possible comparisons and therefore inflate the false alarm rate. We don't actually need to have collected the data in the addition condition, we merely need to intend to compare with that condition once we collect the data. That situation is analogous to the present scenario; it's just that here we merely intend to collect more data in the same condition instead of in a different condition.

Chapter 12.

Exercise 12.1. [Purpose: To investigate model comparison for different partitions of group means.] The program in Section 12.4.1(OneOddGroupModelComp.R) does a model comparison in which M1 has different means for every group and M2 has the same mean for all groups. In this exercise, we consider a different model comparison, with a different partition of the conditions.

(A) Consider a comparison for which M1 has one mean for condition 1 and a second mean for conditions 2 through 4, and M2 has the same mean for all groups. A quick-and-dirty way to program this is by changing the model specification to (OneOddGroupModelCompEx12.1.R)

```
for ( j in 1:2 ) {
   mu[j] ~ dbeta( a[j,mdlIdx] , b[j,mdlIdx] )
}
mu[3] <- mu[2]
mu[4] <- mu[2]
```

Explain in English what the modified code does.

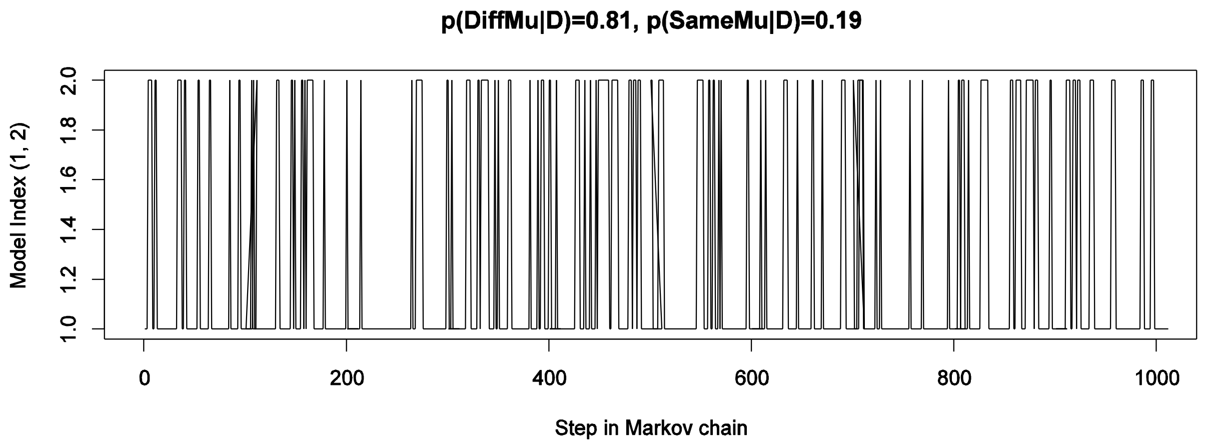
Answer: The code puts beta priors on mu[1] and mu[2], but sets mu[3] and mu[4] equal to mu[2].

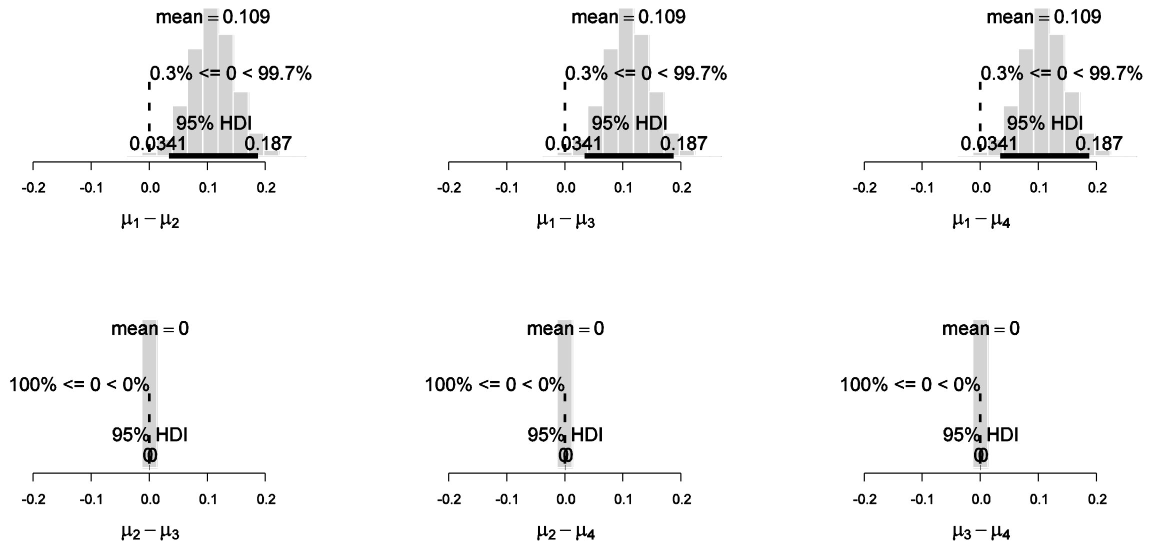
Unfortunately, the modified model structure is not amenable to automatic initialization in BUGS. We can "manually" initialize it this way (OneOddGroupModelCompEx12.1.R):

```
genInitList <- function() {
  sqzData = .01+.98*datalist$nCorrOfSubj/datalist$nTrlOfSubj
  mu = aggregate( sqzData , list(datalist$CondOfSubj) , "mean" )[,"x"]
  sd = aggregate( sqzData , list(datalist$CondOfSubj) , "sd" )[,"x"]
  kappa = mu*(1-mu)/sd^2 - 1
  return(
    list(
      theta = sqzData ,
      mu = c( mu[1] , mean( mu[2:4] ) , NA , NA ) ,
      mu0 = mean(mu) ,
      kappa = kappa ,
      mdlIdx = 1
    )
  )
}
for ( chainIdx in 1 : nchain ) {
  modelInits( bugsInits( genInitList ) )
}
```

The initialization uses the same technique introduced in Section 9.5.2 (FilconBrugs.R), with only one novel nuance: The last two components of mu are specified as NA because those components are not stochastic, but are instead fixed (in the model specification) to equal mu[2]. …

Run the modified program, and show the resulting graphs analogous to those in Figure 12.5. Why are the upper histograms all the same, and why are the lower histograms (e.g., mu2 - mu3) so strange looking?





The upper histograms are all the same because mu2 = mu3 = mu4, hence mu1-mu2 = mu1-mu3 = mu1-mu4.

The lower histograms are strange looking because the differences are all zero. That is, because mu2=mu3=mu4, mu2-mu3=0 and mu2-mu4=0 and mu3-mu4=0. Hence the histograms must be spikes over zero.

(B) What should we conclude from the model comparison of the previous part? (Be careful to express your conclusion as a statement about relative believabilities.) Should we conclude that the means of conditions 2 through 4 are actually equal?

The prior on the two model indices was 50/50, and the posterior of the index (shown in the chain above) shows 81% vs 19% in favor of the different-mu model. This means that of these two models, the different-mu model is more than four times more believable than the same-mu model. But this does not imply that the different-mu model is correct, it merely implies that it is better than the same-mu model. In particular, the different-mu model asserts that mu2=mu3=mu4, but this might not be an accurate description of the groups.

Exercise 12.2. [Purpose: To estimate a difference, including a ROPE (and the hot hand example with a better prior).]

(A) Consider again the hot hand example from Exercise 8.1, p. 188. In this part of the exercise we establish a better prior: We know from general basketball statistics that professional players tend to make about 75% of their free throws, with some players almost as low as 50% and some players almost as high as 95%. A beta(theta|16,6) distribution nicely captures this prior knowledge. But what we do not know from prior statistics is the difference between success after success and success after failure in pairs of free throws. To be as vague as possible about the difference, we'll put a uniform distribution on the difference. Notice that when the overall success rate is, say, 90%, the difference could be anything from +20% (i.e., 100% versus 80%) to -20% (i.e., 80% versus 100%), but when the overall success rate is, say, 70%, then the difference could be anything from +60% to -60%. The specification of the prior needs to accommodate this range that depends on the overall success. Here is one way to specify this in the BUGS model:

```
theta1 <- mu + deflect
theta2 <- mu - deflect
mu ~ dbeta( 16 , 6 )
delta ~ dbeta( 1 , 1 )
deflect <- (delta-.5)*2 * min(mu,1-mu)
```

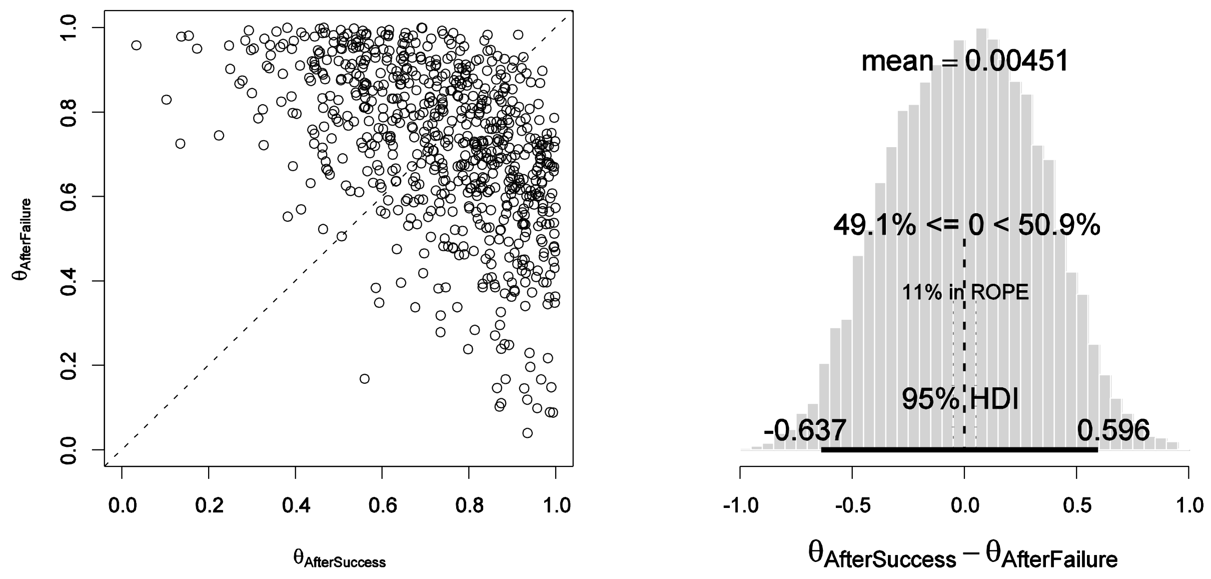
The variable mu is the overall success rate. The variable deflect is the deflection away from mu created by a previous success or a previous failure. The value of deflect is just a linearly transformed value of the random variable delta, which has a uniform prior. Incorporate this code into the model and run without the data, so you can see the prior. Show your complete model specification and a graph of the MCMC sample, which should look much like the upper row of Figure 12.6.

Here is the complete program used to generate Figure 12.6:

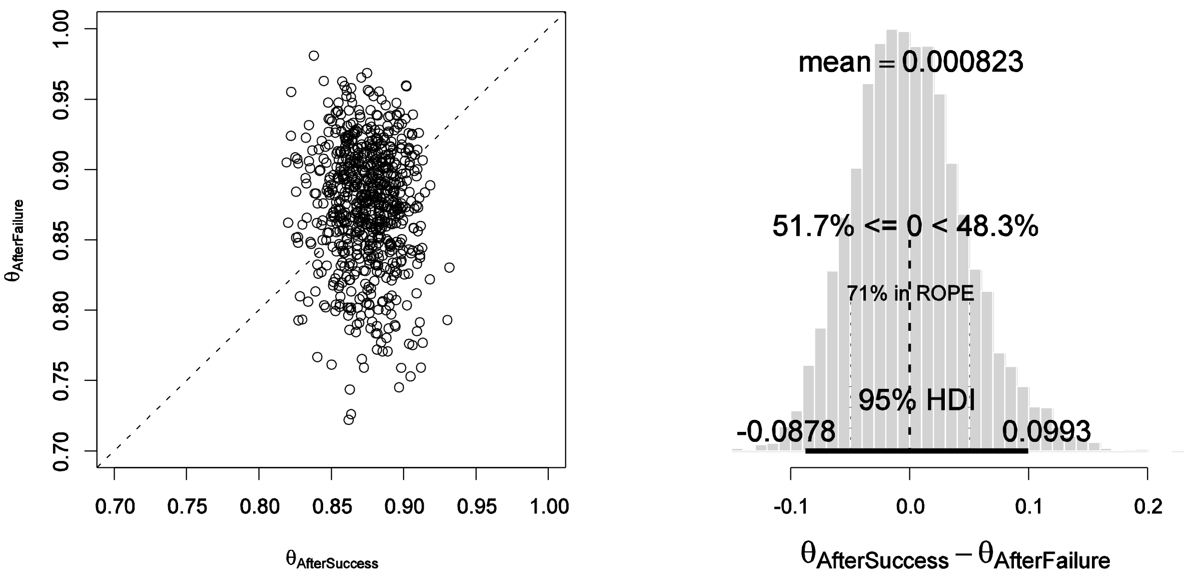
```
graphics.off()
library(BRugs)
priorOnly = T           # Kruschke, J. K. (2010). Doing Bayesian data analysis:
                        # A Tutorial with R and BUGS. Academic Press / Elsevier.
#------------------------------------------------------------------------------
# THE MODEL.

modelstring = "
# BUGS model specification begins here...
model {
    # Likelihood. Each flip is Bernoulli.
    for ( i in 1 : N1 ) { y1[i] ~ dbern( theta1 ) }
    for ( i in 1 : N2 ) { y2[i] ~ dbern( theta2 ) }
    # Prior.
    theta1 <- mu + deflect
    theta2 <- mu - deflect
    mu ~ dbeta( 16 , 6 ) # mean about 75%, range about 50% to 95%
    delta ~ dbeta(1,1)   # prior on hot-hand difference is uniform
    deflect <- (delta-.5)*2 * min(mu,1-mu)
}
```

```
# ... end BUGS model specification
" # close quote for modelstring
# Write model to a file:
.temp = file("model.txt","w") ; writeLines(modelstring,con=.temp) ; close(.temp)
# Load model file into BRugs and check its syntax:
modelCheck( "model.txt" )

#------------------------------------------------------------------------------
# THE DATA.

# Specify the data in a form that is compatible with BRugs model, as a list:
z1 = 251 ; N1 = 285 ; z2 = 48 ; N2 = 53 # data are specified here
if ( priorOnly ) {
  datalist = list(
    N1 = N1 ,
    #y1 = c( rep(1,z1) , rep(0,N1-z1) ) ,
    N2 = N2 #,
    #y2 = c( rep(1,z2) , rep(0,N2-z2) )
  )
} else {
  datalist = list(
    N1 = N1 ,
    y1 = c( rep(1,z1) , rep(0,N1-z1) ) ,
    N2 = N2 ,
    y2 = c( rep(1,z2) , rep(0,N2-z2) )
  )
}
# Get the data into BRugs:
modelData( bugsData( datalist ) )

#------------------------------------------------------------------------------
# INTIALIZE THE CHAIN.

modelCompile()
modelGenInits()

#------------------------------------------------------------------------------
# RUN THE CHAINS.

samplesSet( c( "theta1" , "theta2" ) ) # Keep a record of sampled "theta" values
chainlength = 10000                     # Arbitrary length of chain to generate.
modelUpdate( chainlength )             # Actually generate the chain.

#------------------------------------------------------------------------------
# EXAMINE THE RESULTS.

if ( priorOnly ) {
   fnrt = "Exercise12.2.prior"
} else {
   fnrt = "Exercise12.2.post"
}

theta1Sample = samplesSample( "theta1" ) # Put sampled values in a vector.
theta2Sample = samplesSample( "theta2" ) # Put sampled values in a vector.

# Plot a histogram of the posterior differences of theta values.
source("plotPost.R")
windows(10,5.5)
layout( matrix( 1:2 , ncol=2 ) )
thetaDiff = theta1Sample - theta2Sample
thindex = round(seq(1,length(theta1Sample),len=700))
if ( priorOnly ) {
   xlimits = c(0,1) ; ylimits = c(0,1)
} else {
   xlimits = c(.7,1) ; ylimits = c(.7,1)
}

plot( theta1Sample[thindex] , theta2Sample[thindex] ,
      ylab=expression(theta[AfterFailure]) , xlim=xlimits ,
      xlab=expression(theta[AfterSuccess]) , ylim=ylimits )
abline(0,1,lty="dashed")
plotPost( thetaDiff , xlab=expression(theta[AfterSuccess]-theta[AfterFailure]) ,
          breaks=30 , compVal=0.0 , main="" , ROPE=c(-.05,.05) )

rope = c(-0.05,0.05)
probPracEqZero = ( sum( thetaDiff > rope[1] & thetaDiff < rope[2] )
                   / length( thetaDiff ) )
cat( paste( "ROPE:" , rope[1] , "," , rope[2] , "\n" ,
            "Proportion in ROPE:" , signif(probPracEqZero,3) , "\n" ,
            "Ratio in ROPE to out of ROPE:" ,
            signif(probPracEqZero/(1-probPracEqZero),3) , "\n" ) )

dev.copy2eps(file=paste(fnrt,".eps",sep=""))
```

The resulting graphs look like this (just like Figure 12.6). First, the prior:



And the posterior:



(B) Suppose we establish a ROPE on the difference of success after success and success after failure. We will arbitrarily set it at +/-5%. Run the program with the data included, and display the posterior. The plotPost.R function allows specification of a ROPE, with output as shown in Figure 12.6. Include your output graph, and say in English what the ROPE indicates.

The plots with the ROPE are included above (see the specification in the code above, too). The ROPE indicates that in the posterior *71% of the credible differences are practically equivalent to zero*, where "practically equivalent" means within 5 percentage points.

Exercise 12.3. [Purpose: To apply the approaches to a real-world example.] The thematic apperception test (TAT) is a method for assessing personality and other aspects of interpersonal attitudes. The subject is shown pictures of people in ambiguous scenes, and the subject is asked to make up a story about what the pictured people are doing. In a study reported by Werner, Stabenau, & Pollin (1970, Table 4),2 pictures showing parent-child interactions were shown to women who had children. The stories invented by the mothers were scored for whether or not they expressed "personally involved, child-centered, flexible interactions." Twenty mothers of normal children and 20 mothers of schizophrenic children were each shown 10 pictures. The number of stories, out of 10, that expressed a flexible interaction, were as follows:
Mothers of normal children: 8, 4, 6, 3, 1, 4, 4, 6, 4, 2, 2, 1, 1, 4, 3, 3, 2, 6, 3, 4.
Mothers of schizophrenic children: 2, 1, 1, 3, 2, 7, 2, 1, 3, 1, 0, 2, 4, 2, 3, 3, 0, 1, 2, 2.
For purposes of this exercise, we will assume that the prior is informed from previous research, which indicates that the typical number of stories that express flexible interactions for this picture set is around 3 or 4, and can be well described by a

beta(3.5,6.5) distribution. This is the distribution of flexible-narrative tendencies across mothers.

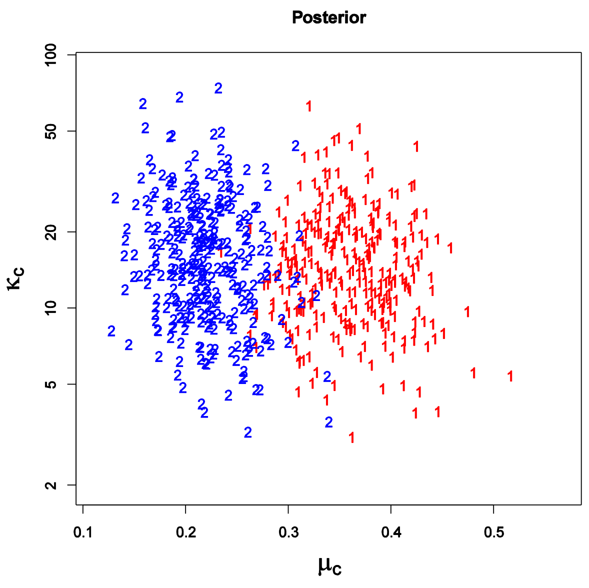
(A) Estimate the difference between TAT scores of the two groups of mothers. Be sure to use the prior knowledge. Is zero among the credible differences? If you assume that the difference has a ROPE from -0.1 to +0.1, is the ROPE excluded from the 95% HDI? (Hints: Set up a hierarchical model in BUGS, using the filtration-condensation example as a guide. The prior applies to the distribution of individual theta[i] values, and the data are distributed as a binomial with bias theta[i].)

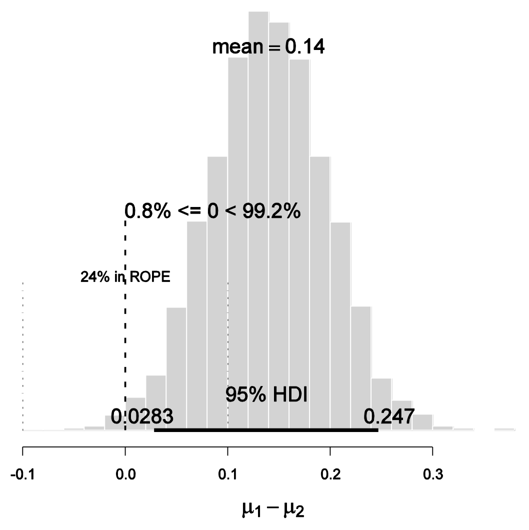
The prior knowledge stated in the exercise needs to be extended in some reasonable way so that it can be expressed in the model structure. The stated prior knowledge (i.e., about 3.5 flexible interactions out of 10) suggests that the shape parameters of the hyperdistribution that generates mu[j] should have a mean of .35 = 3.5/(3.5+6.5), but with only modest certainty, say kappa=2. Hence, perhaps
  mu[j] ~ dbeta(.35*2 , .65*2)
But BUGS won't parse the multiplication inside a density function, so we say
  mu[j] ~ dbeta(.7 , 1.3)
Analogously, shapeGamma and rateGamma should yield a beta distribution with mean of 10=3.5+6.5, but not with much certainty, say SD=10. Hence, perhaps
  kappa[j] ~ dgamma(10^2/10^2 , 10/10^2) # BUGS won't parse this --- put in (1,.1)

The resulting program looks like this:

```
graphics.off()
rm(list=ls(all=TRUE))
fileNameRoot=”Exercise12.3.A" # for constructing output filenames
#install.packages("BRugs")
library(BRugs)

#------------------------------------------------------------------------------
# THE MODEL.

modelstring = "
# BUGS model specification begins here...
model {
   for ( subjIdx in 1:nSubj ) {
      # Likelihood:
      z[subjIdx] ~ dbin( theta[subjIdx] , N[subjIdx] )
      # Prior on theta: Notice nested indexing.
      theta[subjIdx] ~ dbeta( a[cond[subjIdx]] , b[cond[subjIdx]] )
   }
   for ( condIdx in 1:nCond ) {
      a[condIdx] <- mu[condIdx] * kappa[condIdx]
      b[condIdx] <- (1-mu[condIdx]) * kappa[condIdx]
      # Hyperprior on mu and kappa:
      mu[condIdx] ~ dbeta( Amu , Bmu )
      kappa[condIdx] ~ dgamma( Skappa , Rkappa )
   }
   # Constants for hyperprior:
   Amu <- 0.35 * 2
   Bmu <- 0.65 * 2
   Skappa <- pow(meanGamma,2)/pow(sdGamma,2)
   Rkappa <- meanGamma/pow(sdGamma,2)
   meanGamma <- 10
   sdGamma <- 10
}
# ... end BUGS model specification
" # close quote for modelstring
# Write model to a file:
writeLines(modelstring,con="model.txt")
# Load model file into BRugs and check its syntax:
modelCheck( "model.txt" )

#------------------------------------------------------------------------------
# THE DATA.

nCorrOfSubj = c( 8, 4, 6, 3, 1, 4, 4, 6, 4, 2, 2, 1, 1, 4, 3 ,3 ,2 ,6, 3, 4,
                 2, 1, 1, 3, 2, 7, 2, 1, 3, 1, 0, 2, 4, 2, 3, 3, 0, 1, 2, 2 )
CondOfSubj = c( rep(1,20) , rep(2,20) )
nTrlOfSubj = rep(10,40)
nSubj = length(CondOfSubj)
nCond = length(unique(CondOfSubj))

# Specify the data in a form that is compatible with BRugs model, as a list:
datalist = list(
 nCond = nCond ,
 nSubj = nSubj ,
 cond = CondOfSubj ,
 N = nTrlOfSubj ,
 z = nCorrOfSubj
)

# Get the data into BRugs:
# Function bugsData stores the data file (default filename is data.txt).
# Function modelData loads data file into BRugs (default filename is data.txt).
modelData( bugsData( datalist ) )

#------------------------------------------------------------------------------
# INTIALIZE THE CHAINS.

modelCompile( numChains=3 )
modelGenInits()

#------------------------------------------------------------------------------
# RUN THE CHAINS.

burninSteps = 1000
modelUpdate( burninSteps )
samplesSet( c("mu","kappa","theta") )
nPerChain = 1000
modelUpdate( nPerChain , thin=5 )

#------------------------------------------------------------------------------
# EXAMINE THE RESULTS.

source("plotPost.R")
source("plotChains.R")

# Check for convergence, mixing and autocorrelation:
plotChains( "mu" , saveplots=T , fileNameRoot )
plotChains( "kappa" , saveplots=F )
plotChains( "theta[1]" , saveplots=F )

# Extract parameter values and save them.
mu = NULL
kappa = NULL
for ( condIdx in 1:nCond ) {
   mu = rbind( mu , samplesSample( paste("mu[",condIdx,"]",sep="") ) )
   kappa = rbind( kappa , samplesSample( paste("kappa[",condIdx,"]",sep="") ) )
}
save( mu , kappa , file=paste(fileNameRoot,"MuKappa.Rdata",sep="") )
chainLength = NCOL(mu)

# Histograms of mu differences:
windows()
plotPost( mu[1,]-mu[2,] , xlab=expression(mu[1]-mu[2]) , main="" ,
          breaks=20 , compVal=0 , ROPE=c(-.1,.1) )
dev.copy2eps(file=paste(fileNameRoot,"MuDiffs.eps",sep=""))

# Scatterplot of mu,kappa in each condition:
windows()
muLim = c(min(mu),max(mu))
kappaLim = c(min(kappa),max(kappa))
mainLab="Posterior"
thindex = round( seq( 1 , chainLength , len=300 ) )
plot( mu[1,thindex] , kappa[1,thindex] , main=mainLab ,
      xlab=expression(mu[c]) , ylab=expression(kappa[c]) , cex.lab=1.75 ,
      xlim=muLim , ylim=kappaLim , log="y" , col="red" , pch="1" )
points( mu[2,thindex] , kappa[2,thindex] , col="blue" , pch="2" )
dev.copy2eps(file=paste(fileNameRoot,"Scatter.eps",sep=""))
```

The results look like this:





The posterior on the difference of mu's indicates that the 95% HDI excludes zero, but the 95% HDI does not fall outside the ROPE. Indeed, 24% of the posterior falls inside the ROPE. Thus, depending on how wide a ROPE we use, we may or may not declare that zero difference is credible.

(B) Using model compareson, determine the posterior probability of a model that uses one hyperparameter to describe both groups, relative to a model that uses a different hyperparameter for each group. For this application, the prior on the hyperparameters should not be informed, but instead should be extremely vague and broad, because the model comparison is supposed to be "automatic." What is the posterior probability of the different-hyperparameter model? If it is the preferred model, can we use it to estimate the

difference between groups? (Answer: Not necessarily, because it does not use the prior knowledge.)

Running the program (below) once with vague pseudopriors yields a sample for resetting to more plausible pseudopriors. For example, the first run with vague pseudopriors yields the mean and SD of mu0 in model 2:
m = mean(mu0sampleM2) = 0.2875809
s = sd(mu0sampleM2) = 0.02942183
Converting those to shape parameters for the beta distribution, using Eqn. 5.6 p. 83, yields
a = m*(m*(1-m)/s^2 - 1) = 67.77622
b = (1-m)*(m*(1-m)/s^2 - 1) = 167.9008
These values are used in the pseudoprior on the second run.

Analogously, for mu1 in model 1:
> m = mean(mu1sampleM1)
> s = sd(mu1sampleM1)
> m*(m*(1-m)/s^2 - 1) yields 42.13674
> (1-m)*(m*(1-m)/s^2 - 1) yields 75.26989
And so forth. For the kappa values, use the gamma-conversion equations from Figure 9.8, p. 209. For example,
> m = mean(kappa0sampleM2)
> s = sd(kappa0sampleM2)
> m^2/s^2 ; m/s^2 yields 5.495545, 0.3886324
Then be careful to put those constants in the correct place in the model specification! The complete program is shown below:

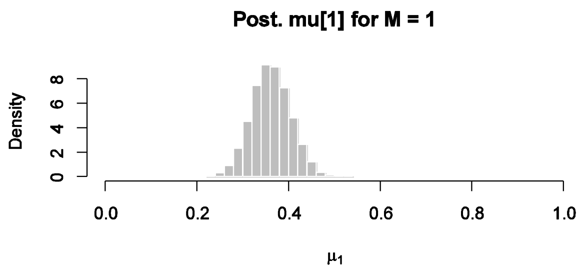
```
graphics.off()
rm(list=ls(all=TRUE))
#install.packages("BRugs")
library(BRugs)

filenamebase = "Exercise12.3.B"

#------------------------------------------------------------------------------
# THE MODEL.

modelstring = "
# BUGS model specification begins here...
model {
   for ( i in 1:nSubj ) {
      # Likelihood:
      nCorrOfSubj[i] ~ dbin( theta[i] , nTrlOfSubj[i] )
      # Prior on theta: Notice nested indexing.
      theta[i] ~ dbeta( aBeta[ CondOfSubj[i] ] , bBeta[ CondOfSubj[i] ] )
   }
   # Hyperprior on mu and kappa:
   mu0 ~ dbeta( aMu0[mdlIdx] , bMu0[mdlIdx] )
   kappa0 ~ dgamma( shk0[mdlIdx] , rak0[mdlIdx] )
   for ( j in 1:nCond ) {
      mu[j] ~ dbeta( aMu[j,mdlIdx] , bMu[j,mdlIdx] )
      kappa[j] ~ dgamma( shk[j,mdlIdx] , rak[j,mdlIdx] )
   }
   for ( j in 1:nCond ) {
      aBeta[j] <- (       ( (mu[j]*(2-mdlIdx))+(mu0*(mdlIdx-1)) )
                  * ((kappa[j]*(2-mdlIdx))+(kappa0*(mdlIdx-1))) )
      bBeta[j] <- ( ( 1 - ( (mu[j]*(2-mdlIdx))+(mu0*(mdlIdx-1)) ) )
                  * ((kappa[j]*(2-mdlIdx))+(kappa0*(mdlIdx-1))) )
   }
   # Constants for hyperprior true models:
   aP <- 1
   bP <- 1
   shP <- 1.0
   raP <- 0.1

   # Prior for true model:
   aMu0[2] <- aP
   bMu0[2] <- bP
   shk0[2] <- shP
   rak0[2] <- raP
   aMu[1,1] <- aP
   aMu[2,1] <- aP
   bMu[1,1] <- bP
   bMu[2,1] <- bP
   shk[1,1] <- shP
   shk[2,1] <- shP
   rak[1,1] <- raP
   rak[2,1] <- raP

   # Pseudo-prior for place-holding model:
   aMu0[1] <- 67.8
   bMu0[1] <- 167.9
   shk0[1] <- 5.49
   rak0[1] <- 0.389
   aMu[1,2] <- 42.1
   aMu[2,2] <- 27.4
   bMu[1,2] <- 75.3
   bMu[2,2] <- 97.3
   shk[1,2] <- 3.04
   shk[2,2] <- 2.75
   rak[1,2] <- 0.197
   rak[2,2] <- 0.154

   # Hyperprior on model index:
   mdlIdx ~ dcat( modelProb[] )
   modelProb[1] <- .5
   modelProb[2] <- .5
}
# ... end BUGS model specification
" # close quote for modelstring
# Write model to a file:
.temp = file("model.txt","w") ; writeLines(modelstring,con=.temp) ; close(.temp)
# Load model file into BRugs and check its syntax:
modelCheck( "model.txt" )

#------------------------------------------------------------------------------
# THE DATA.

# For each subject, specify the condition she was in,
# the number of trials she experienced, and the number correct.

nCorrOfSubj = c( 8, 4, 6, 3, 1, 4, 4, 6, 4, 2, 2, 1, 1, 4, 3 ,3 ,2 ,6, 3, 4,
                 2, 1, 1, 3, 2, 7, 2, 1, 3, 1, 0, 2, 4, 2, 3, 3, 0, 1, 2, 2 )
CondOfSubj = c( rep(1,20) , rep(2,20) )
nTrlOfSubj = rep(10,40)
nSubj = length(CondOfSubj)
nCond = length(unique(CondOfSubj))
```

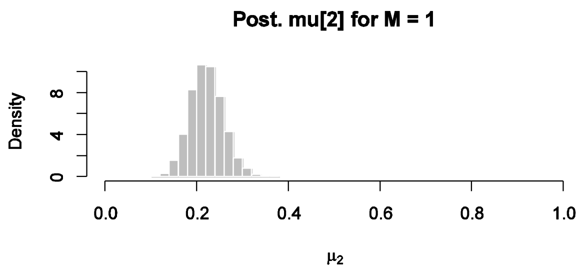
```
# Specify the data in a form that is compatible with BRugs model, as a list:
datalist = list(
 nCond = nCond ,
 nSubj = nSubj ,
 CondOfSubj = CondOfSubj ,
 nTrlOfSubj = nTrlOfSubj ,
 nCorrOfSubj = nCorrOfSubj
)

# Get the data into BRugs:
# Function bugsData stores the data file (default filename is data.txt).
# Function modelData loads data file into BRugs (default filename is data.txt).
modelData( bugsData( datalist ) )

#------------------------------------------------------------------------------
# INTIALIZE THE CHAINS.

nchain = 1
modelCompile( numChains=nchain )
modelGenInits()

#------------------------------------------------------------------------------
# RUN THE CHAINS.

burninSteps = 1000
modelUpdate( burninSteps )
samplesSet( c("mu","mu0","kappa","kappa0","theta","mdlIdx") )
nPerChain = ceiling(10000/nchain)
modelUpdate( nPerChain , thin=5 ) # takes nPerChain * thin steps

#------------------------------------------------------------------------------
# EXAMINE THE RESULTS.

source("plotChains.R")
source("plotPost.R")

modelIdxSample = samplesSample( "mdlIdx" )
pM1 = sum( modelIdxSample == 1 ) / length( modelIdxSample )
pM2 = 1 - pM1
string1 =paste("p(M1:DiffMu|D)=",round(pM1,3),sep="")
string2 =paste("p(M2:SameMu|D)=",round(pM2,3),sep="")
windows(10,4)
nStepsToPlot = length(modelIdxSample)
plot( 1:nStepsToPlot , modelIdxSample[1:nStepsToPlot] , type="l" ,
      xlab="Step in Markov chain" , ylab="Model Index (1, 2)" ,
      main=paste(string1,", ",string2,sep="") )
dev.copy2eps(file=paste(filenamebase,"_mdlIdx",".eps",sep=""))


mu0sampleM1 = samplesSample( "mu0" )[ modelIdxSample == 1 ]
mu0sampleM2 = samplesSample( "mu0" )[ modelIdxSample == 2 ]
windows()
layout( matrix(1:2,nrow=2) )
hist( mu0sampleM1 , main="Post. mu0 for M1 (Diff)" ,
      xlab=expression(mu[0]) , xlim=c(0,1) ,
      freq=F , col="grey" , border="white" )
#lines( seq(0,30,.1) , dgamma( seq(0,30,.1) , 1 , .1 ) )
hist( mu0sampleM2 , main="Post. mu0 for M2 (Same)"  ,
      xlab=expression(mu[0]) , xlim=c(0,1) ,
      freq=F , col="grey" , border="white" )
dev.copy2eps(file=paste(filenamebase,"_mu0",".eps",sep=""))

kappa0sampleM1 = samplesSample( "kappa0" )[ modelIdxSample == 1 ]
```

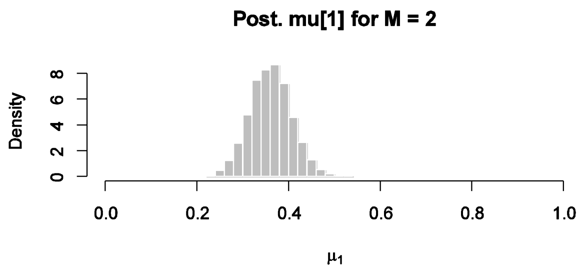
```
kappa0sampleM2 = samplesSample( "kappa0" )[ modelIdxSample == 2 ]
windows()
layout( matrix(1:2,nrow=2) )
hist( kappa0sampleM1 , main="Post. kappa0 for M1 (Diff)" ,
      xlab=expression(kappa[0]) , xlim=c(0,30) ,
      freq=F , col="grey" , border="white" )
#lines( seq(0,30,.1) , dgamma( seq(0,30,.1) , 1 , .1 ) )
hist( kappa0sampleM2 , main="Post. kappa0 for M2 (Same)"  ,
      xlab=expression(kappa[0]) , xlim=c(0,30) ,
      freq=F , col="grey" , border="white" )
dev.copy2eps(file=paste(filenamebase,"_kappa0",".eps",sep=""))

mu1sampleM1 = samplesSample( "mu[1]" )[ modelIdxSample == 1 ]
mu2sampleM1 = samplesSample( "mu[2]" )[ modelIdxSample == 1 ]
mu1sampleM2 = samplesSample( "mu[1]" )[ modelIdxSample == 2 ]
mu2sampleM2 = samplesSample( "mu[2]" )[ modelIdxSample == 2 ]
windows(10,5)
layout( matrix(1:4,nrow=2,byrow=T) )
hist( mu1sampleM1 , main="Post. mu[1] for M = 1" ,
      xlab=expression(mu[1]) , xlim=c(0,1) ,
      freq=F , col="grey" , border="white" )
hist( mu2sampleM1 , main="Post. mu[2] for M = 1" ,
      xlab=expression(mu[2]) , xlim=c(0,1) ,
      freq=F , col="grey" , border="white" )
hist( mu1sampleM2 , main="Post. mu[1] for M = 2" ,
      xlab=expression(mu[1]) , xlim=c(0,1) ,
      freq=F , col="grey" , border="white" )
#lines( seq(0,30,.1) , dgamma( seq(0,30,.1) , 1 , .1 ) )
hist( mu2sampleM2 , main="Post. mu[2] for M = 2" ,
      xlab=expression(mu[2]) , xlim=c(0,1) ,
      freq=F , col="grey" , border="white" )
#lines( seq(0,30,.1) , dgamma( seq(0,30,.1) , 1 , .1 ) )
dev.copy2eps(file=paste(filenamebase,"_mucond",".eps",sep=""))

kappa1sampleM1 = samplesSample( "kappa[1]" )[ modelIdxSample == 1 ]
kappa2sampleM1 = samplesSample( "kappa[2]" )[ modelIdxSample == 1 ]
kappa1sampleM2 = samplesSample( "kappa[1]" )[ modelIdxSample == 2 ]
kappa2sampleM2 = samplesSample( "kappa[2]" )[ modelIdxSample == 2 ]
windows(10,5)
layout( matrix(1:4,nrow=2,byrow=T) )
hist( kappa1sampleM1 , main="Post. kappa[1] for M = 1" ,
      xlab=expression(kappa[1]) , xlim=c(0,30) , freq=F ,
      col="grey" , border="white" )
hist( kappa2sampleM1 , main="Post. kappa[2] for M = 1" ,
      xlab=expression(kappa[2]) , xlim=c(0,30) , freq=F ,
      col="grey" , border="white" )
hist( kappa1sampleM2 , main="Post. kappa[1] for M = 2" ,
      xlab=expression(kappa[1]) , xlim=c(0,30) , freq=F ,
      col="grey" , border="white" )
#lines( seq(0,30,.1) , dgamma( seq(0,30,.1) , 1 , .1 ) )
hist( kappa2sampleM2 , main="Post. kappa[2] for M = 2" ,
      xlab=expression(kappa[2]) , xlim=c(0,30) , freq=F ,
      col="grey" , border="white" )
#lines( seq(0,30,.1) , dgamma( seq(0,30,.1) , 1 , .1 ) )
dev.copy2eps(file=paste(filenamebase,"_kcond",".eps",sep=""))

muSample = rbind( mu1sampleM1 , mu2sampleM1 )
windows()
plotPost( muSample[1,]-muSample[2,] , xlab=bquote(mu[.(1)]-mu[.(2)]) ,
                  breaks=20 , main="M1" )
dev.copy2eps(file=paste(filenamebase,"_mudiff",".eps",sep=""))

kSample = rbind( kappa1sampleM1 , kappa2sampleM1 )
```

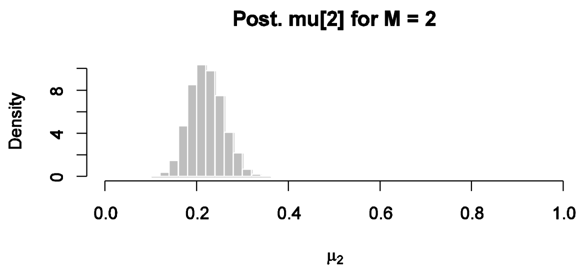
```
windows()
plotPost( kSample[1,]-kSample[2,] , xlab=bquote(kappa[.(1)]-kappa[.(2)]) ,
                  breaks=20 , xlim=c(-25,25) , main="M1" )
dev.copy2eps(file=paste(filenamebase,"_kdiff",".eps",sep=""))
```

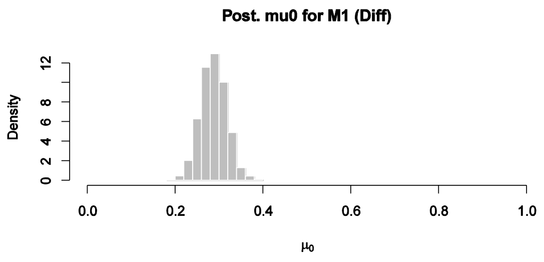
The results are shown below. First, notice that the pseudopriors do indeed well match the actual posteriors:

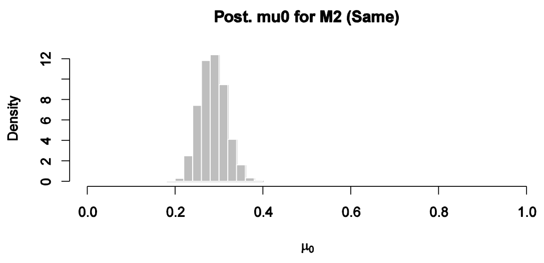




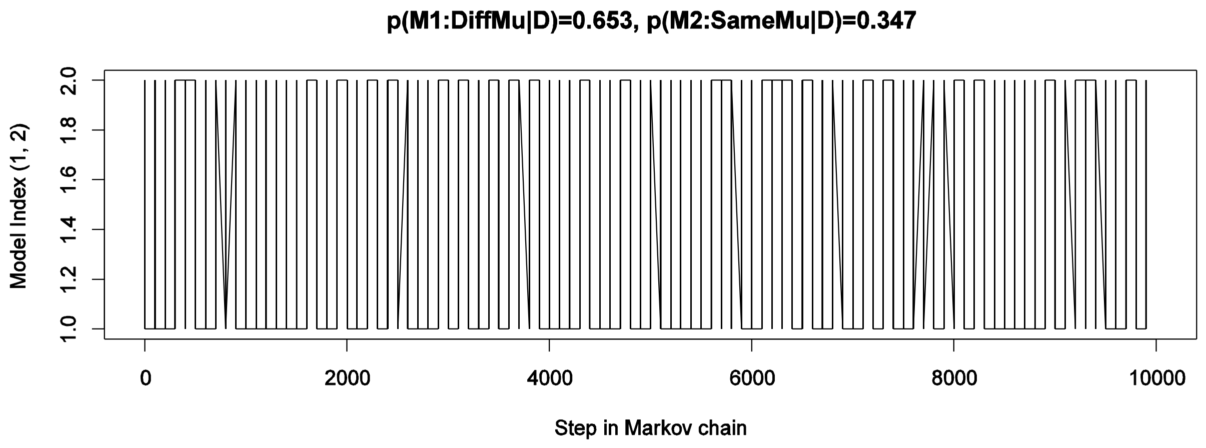






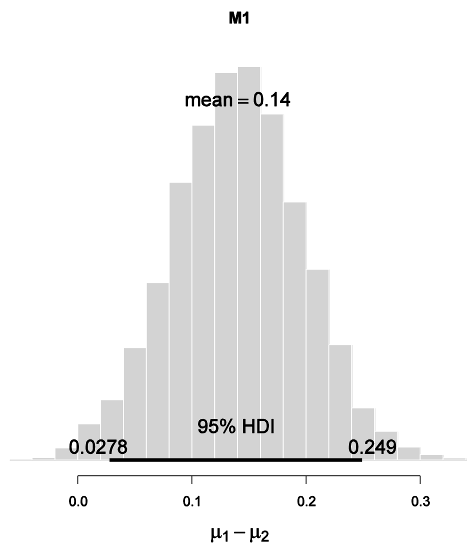


Next, notice that the Different-Means model is only a little preferred to the Same-Means model:



The prior on the model index was set to 50/50, so the probability displayed in the title of the chain is the posterior probability of the models.

Even though the different-means model is not strongly preferred, if we use it as the "winning" model we can examine the difference of the means, which looks like this:



It is very similar to the posterior found in the previous part A of this exercise, but it is a little different. Other than random sampling in the MCMC chain, the difference between the posteriors is caused by different priors. Here, the prior was vague. In part A, the prior was informed. The part A posterior is therefore more appropriate (assuming that our audience agrees to the informed prior).

Chapter 13.

Exercise 13.2. [Purpose: To understand power for flipping a single coin in Tables 13.1 and 13.2.] For this exercise, consider flipping a single coin and inferring its bias.

(A) Table 13.2 indicates that when the data-generating distribution is vague, with kappa = 10 and theta = 0.80, then 85 flips are needed for an 80% chance of getting the 95% HDI width to be less than 0.2. What is the minimal N needed if the data-generating distribution is certain, with kappa = 2000? Show the command you used, and report the exact power for the smallest N that has power greater than 0.8.

```
minNforHDIpower( genPriorMean=.80 , genPriorN=2000 , HDImaxwid=.2 )
…
 For sample size = 67, power = 0.823923
```

(B) Regarding the previous part, why might a researcher pursue a goal of precision if the data-generating hypothesis is already precise? (Hint: The audience prior may be different than the data-generating hypothesis. Discuss briefly, perhaps with an example.)

The audience may have a more diffuse prior than the researcher. (The minNforHDIpower function defaults to an audience prior that is uniform, i.e., beta(1,1).) So the researcher wants to know how big a sample size is needed to convince an audience, even though the researcher has a fairly precise data-generating hypothesis.

(C) Table 13.1 indicates that when the data-generating distribution is highly certain, with kappa = 2000 and theta = 0.80, then 18 flips are needed for an 80% chance of getting the 95% HDI to exclude theta = 0.5. What is the minimal N needed if the data-generating distribution is vague, with kappa = 2? Show the command you used, and report the exact power for the smallest N that has power greater than 0.8.

```
 minNforHDIpower( genPriorMean=.8 , genPriorN=2 , nullVal=.5 )
…
 For sample size = 21, power = 0.803802
```

(D) For the previous part, the goal was for the HDI to exclude the null value (i.e., 0.5). Notice that the goal can be satisfied if the HDI is above the null value or if the HDI is below the null value. (1) When the data generating prior is a beta distribution with theta = 0.8 and kappa = 2, as in the previous part, what proportion of the data-generating biases are greater than the null value? (2) If the goal is for the HDI to fall entirely above the null value, what sample size is needed to achieve a power of 0.8? (Hint: Use minNforHDIpower.R with the argument ROPEHc(0,.5).) Watch the sample size increase and increase and increase, with the power creeping toward an asymptote. Why does the power never exceed the proportion you computed for (1)?

Please note an error in the statement of the exercise! The desired power should be 0.9, not 0.8.

(1) The proportion of data-generating biases greater than the null value of .8 is given by the amount of the data-generating beta distribution, beta(.8*2 , (1-.8)*2), above theta=.5. In R, the cumulative beta distribution is the function pbeta(theta,a,b). It returns the probability between zero and theta. We want the probability above theta. Hence we want
1 - pbeta(.5 , 0.8*2 , (1-0.8)*2) which is 0.8681836.

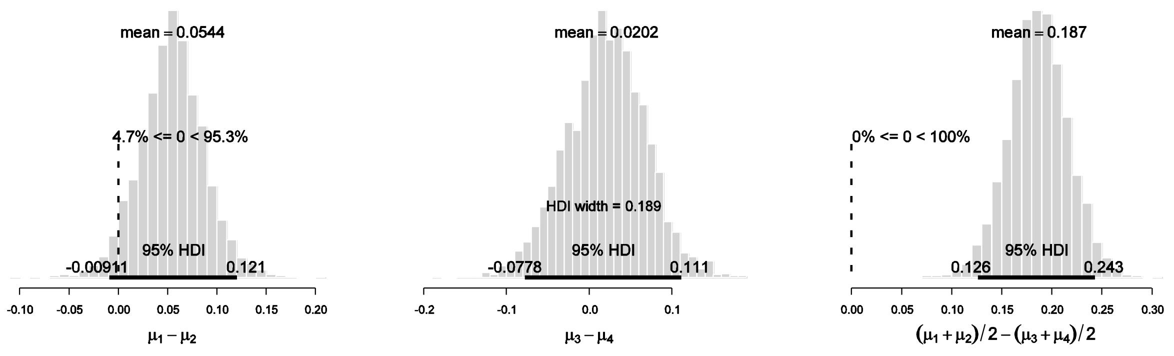
(2) *We use a desired power of 0.9* in minNforHDIpower(), as follows:

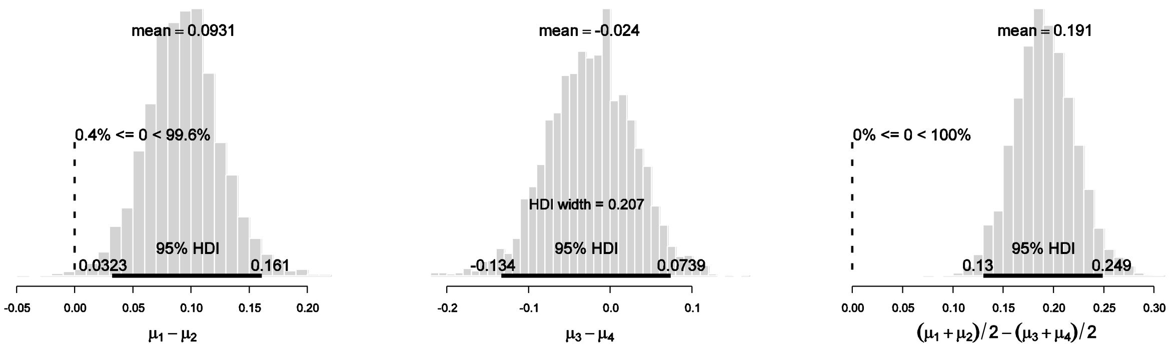
```
minNforHDIpower( genPriorMean=.8 , genPriorN=2 , nullVal=.5 , ROPE=c(0,.5) ,
desiredPower=0.9 )
…
For sample size = 500, power = 0.8450405
…
```

The power never exceeds 0.868, computed in (1), because even an infinite sample size can only reveal the data-generating theta value. Because the data-generating theta values are above .5 only 86.8% of the time, the power can never exceed that.

Exercise 13.3. [Purpose: To determine power for groups of coins, when the goal is precision.] Consider the filtration-condensation experiment summarized in Section 13.3. Suppose we want the 95% HDI on the difference, mu3 - mu4, to have a width less than 0.20. What sample size (N per group) is needed to achieve this goal at least 80% of the time? Determine the answer by running the program in Section 13.6.2 (FilconBrugsPower.R) with various values for nPerGroup. (Hint: N is about 17; your job is to find the minimal N and discuss how you did it.)

Notice that the third goal checked in the program FilconBrugsPower.R is the goal sought here. See lines 141-143 of the program (p. 344 of the textbook). The number of simulated subjects per condition is specified on line 170. It is set at nSubjPerCond=15, but you can change it to other values to explore power as a function of number of subjects. Beware, this takes time, because a stable estimate of power takes a couple hundred simulated experiments, which must be conducted for every sample size. When N=17, the proportion of times that the third goal is achieved hovers around .8, which is the desired power. When N is less than 17, the estimated power tends to be less than .8. Although not asked for by the exercise, here are a couple posterior distributions from simulated data when N=17:





You can see that in the first one, the 95%HDI of mu3-mu4 is less than .2, but in the second one, the 95%HDI of mu3-mu4 is larger than .2.

Exercise 13.4. [Purpose: This is a capstone exercise that uses real data to review many techniques of the previous chapters, including generating priors in BUGS, checking credibility of null values, estimating retrospective power, and conducting a posterior predictive check.] This exercise examines a learning experiment that investigated how easy it is for people to learn new category structures after having previously learned an initial structure (Kruschke, 1996). Some new structures had relevant stimulus dimensions that were also previously relevant in the initial structure, while other new structures had relevant stimulus dimensions that were previously irrelevant in the initial structure. […]

(A) [Purpose: To create a BUGS model that has an estimated hyperprior on μ_c and on κ_c.] […] Discuss why we would want to estimate higher-level distributions across the μ_c and κ_c. You may want to mention commonalities across conditions, such as all the learners being the same species, and all learners experiencing the same sort of stimuli on the same computer display. It is also important to discuss shrinkage of estimates. Finally, discuss why the particular higher-level distribution might not be appropriate.

It is reasonable to model all the condition means (and certainties) as coming from a common hyperdistribution because all the conditions used the same task (predictive learning with feedback) with the same stimuli (schematic box cars) and the same type of learners (college students). Without a specific theory of the different conditions, therefore, the conditions should be roughly the same, or at least share enough that they can be mutually informative. The hyperdistribution therefore provides some shrinkage on the estimates of the condition means and certainties, attenuating outlying conditions especially if they have a small sample size.

It would be unreasonable to put a hyperprior on the condition means and certainties if we have prior belief that the conditions are radically different or have subclusters or are otherwise not mutually informative. For example, if we have prior knowledge that some of the conditions produce very low performance while others produce very high performance, we might not want to put all the conditions under one hyperdistribution because that would be contrary to our prior knowledge.

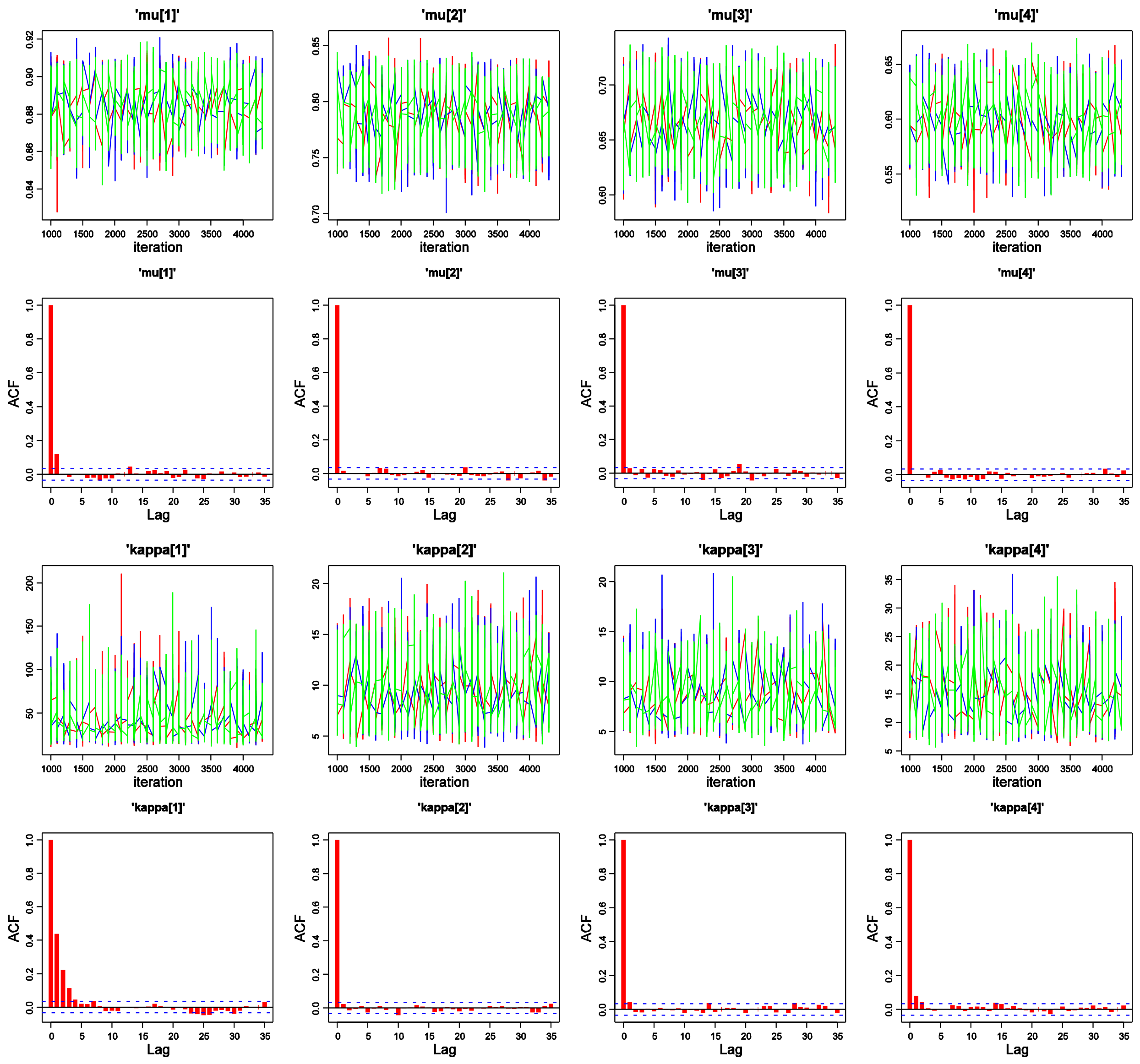
(B) [Purpose: To check for convergence, mixing, and autocorrelation.] With the data included, run the BUGS model and check for convergence, mixing, and autocorrelation. The model can be initialized automatically, using modelGenInits(), but unfortunately it takes forever for the chains to converge because some are initialized too far away from the mode of the posterior. Instead, manually initialize the chains at reasonable values, as indicated by the data. The same method as was used in Section 9.5.2 (FilconBrugs.R) is used and extended here (Kruschke1996CSbugs.R): […] Run the model and determine reasonable burn-in and thinning. Show the autocorrelation and chain plots for μ_c and κ_c. You may find it useful to refer to Section 23.2, p. 623.

For completeness, here are excerpts of the code that was used to generate the plots:

```
model {
   for ( i in 1:nSubj ) {
      nCorrOfSubj[i] ~ dbin( theta[i] , nTrlOfSubj[i] )
      theta[i] ~ dbeta( a[ CondOfSubj[i] ] , b[ CondOfSubj[i] ] )I(0.0001,0.9999)
   }
   for ( cond in 1:nCond ) {
      a[cond] <- mu[cond] * kappa[cond]
      b[cond] <- (1-mu[cond]) * kappa[cond]
      mu[cond] ~ dbeta( aMu , bMu )
      kappa[cond] ~ dgamma( sGamma , rGamma )
   }
   aMu <- max( .01 , mMu * kMu )
   bMu <- max( .01 , (1-mMu) * kMu )
   mMu ~ dunif(0,1)
   kMu ~ dgamma(1,.1)
   sGamma <- max( .005 , pow(muGamma,2)/pow(sigmaGamma,2) )
   rGamma <- max( .005 , muGamma/pow(sigmaGamma,2) )
   muGamma ~ dgamma(1,.1)
   sigmaGamma ~ dgamma(1,.1)
}

…

genInitList <- function() {
    sqzData = .01+.98*datalist$nCorrOfSubj/datalist$nTrlOfSubj
    mu = aggregate( sqzData , list(datalist$CondOfSubj) , "mean" )[,"x"]
    sd = aggregate( sqzData , list(datalist$CondOfSubj) , "sd" )[,"x"]
    kappa = mu*(1-mu)/sd^2 - 1
    mMu = mean( mu )
    kMu = mMu * (1-mMu) / sd(mu)^2
    muGamma = mean( kappa )
    sigmaGamma = sd( kappa )
    return( list( theta = sqzData ,
                  mu = mu ,
                  kappa = kappa ,
                  mMu = mMu ,
                  kMu = kMu ,
                  muGamma = muGamma ,
                  sigmaGamma = sigmaGamma ) )
}

…

burninSteps = 1000 # Because initialization is good, doesn't need much burnin
modelUpdate( burninSteps )
samplesSet( c("mu","kappa","theta","mMu","kMu","muGamma","sigmaGamma") )
thinStep = 20
```

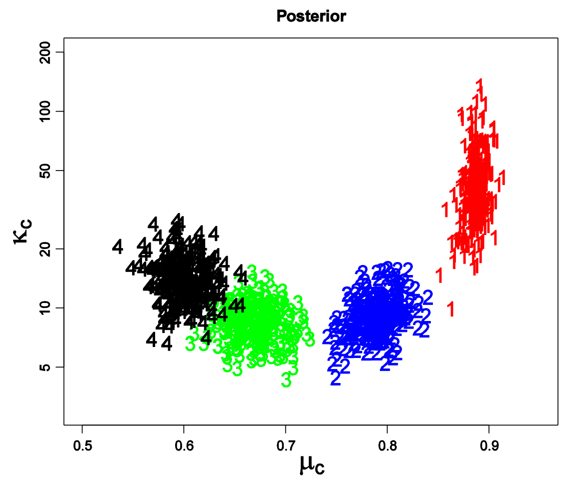
```
stepsPerChain = ceiling(10000/nchain)
modelUpdate( stepsPerChain , thin=thinStep )

…

sumInfo = plotChains( "mu" , saveplots=T , filenameroot=fileNameRoot )
sumInfo = plotChains( "kappa" , saveplots=T , filenameroot=fileNameRoot )
```

Below are the autocorrelation and chain plots for the condition means and certainties. The plots indicate that the chains are well burned-in, converged, and not autocorrelated.

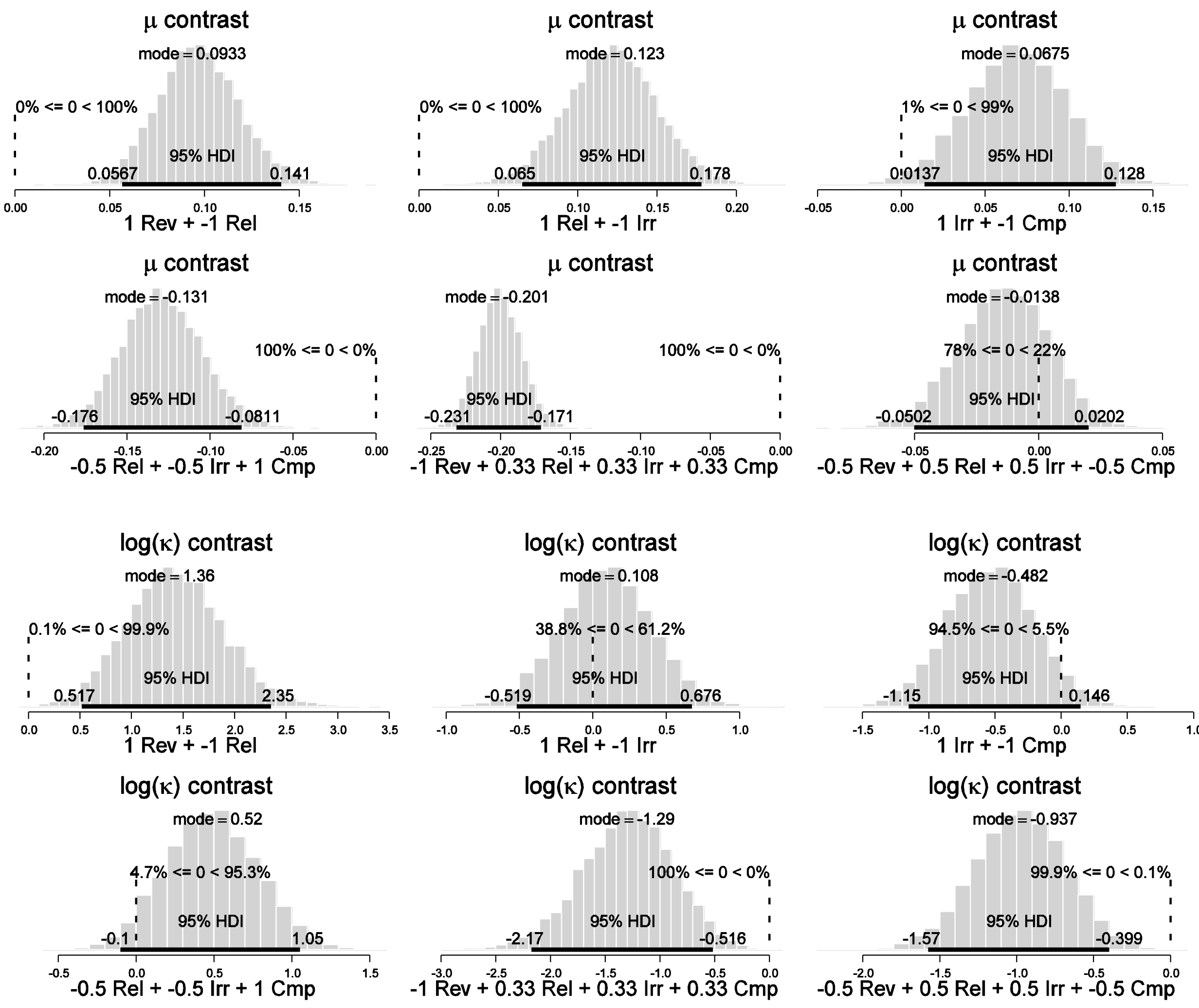


(C) [Purpose: To examine and interpret the posterior distribution of differences.] Which groups are different from each other, on which parameters? (Hint: See Figure 13.4.)

Here is a scatter plot of the condition mu's and kappa's:



Note that the scatter does not reveal which points at at the same step in the chain; i.e., the plot does not indicate which point marked "1" is at the same step in the chain as a point marked "2" or "3" or "4". The marginals of that distribution are used in the plots below.



The graphs of the kappa differences use log(kappa) merely to make the distributions more readable. The conclusions are the same in this case when using the original scale. *It should be noted, however, that HDIs can change when the scale is non-linearly transformed, because dense regions might be stretched into not-dense regions and not-dense regions might be compressed into dense regions. Thus, when the edge of an HDI is near the null value or ROPE, use the most meaningful scale for the parameter, which is presumably the scale on which its prior was defined.*

The posterior histograms indicate that the four group's mu's are very credibly different from each other, with $\mu_{REV} > \mu_{REL} > \mu_{IRR} > \mu_{CMP}$. For the kappa's, only the kappa of the Reversal conditions is credibly higher than the others, which are roughly the same (i.e., their differences are small compared to the uncertainty in their estimates).

(D) [Purpose: To check the robustness of the posterior when the prior is changed in reasonable ways.] Do the posterior differences change much if the prior changes? (1) Specifically, try this alternative vague prior: Wherever the top-level prior specifies dgamma(1,.1), change it to dgamma(0.1,.1). (2) Also, try this prior that forces all κ_c to be close to 15:

```
  muGamma ~ dgamma(22500,1500)
  sigmaGamma ~ dgamma(25,250)
```

Show your results. Which prior is more reasonable, and why?

(1) Results for

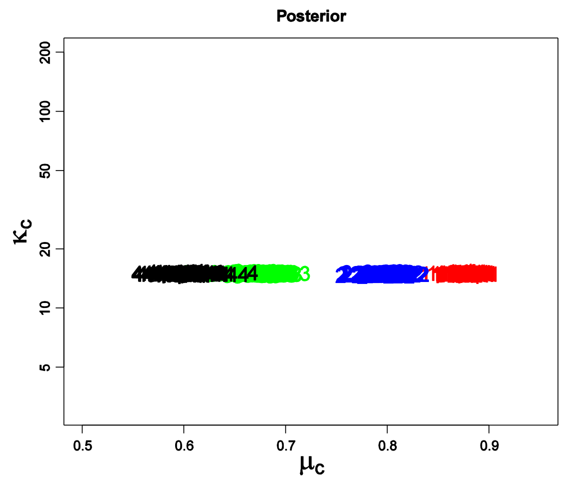
```
   muGamma ~ dgamma(.1,.1)
   sigmaGamma ~ dgamma(.1,.1)
```

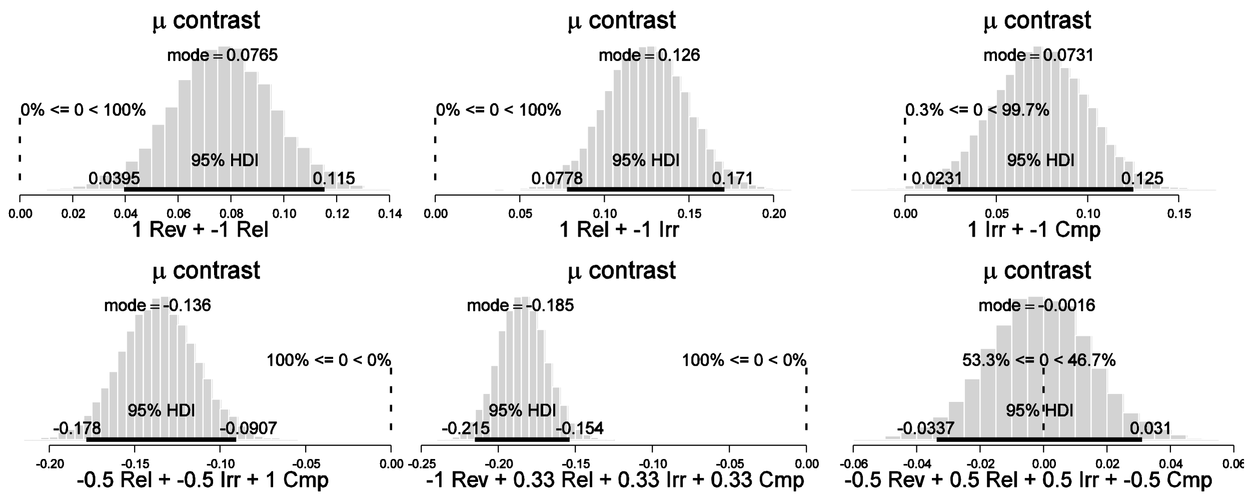
are remarkably similar to the results shown in previous parts. In other words, this change of prior from one vague prior to another has no notable effect on the posterior.

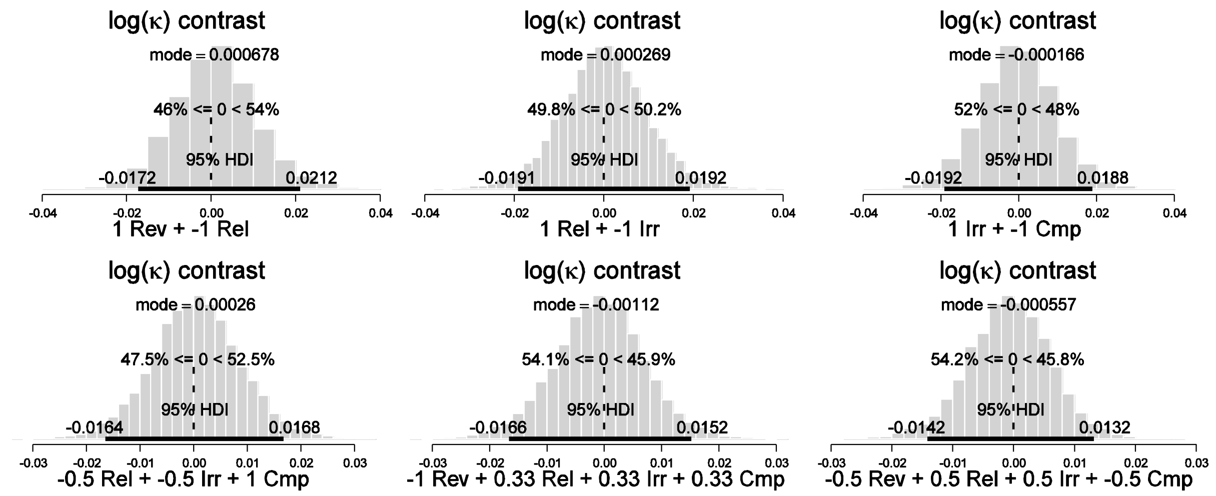
(2) Results for

```
   muGamma ~ dgamma(22500,1500)
   sigmaGamma ~ dgamma(25,250)
```

are quite different, of course, because of the strong prior constraint on kappa. The chains are converged and well mixed, but noticeably autocorrelated. Because the chains are fairly long, however, and there is more than one chain, the autocorrelation will be tolerated for purposes of this exercise. Here are plots of the posterior:



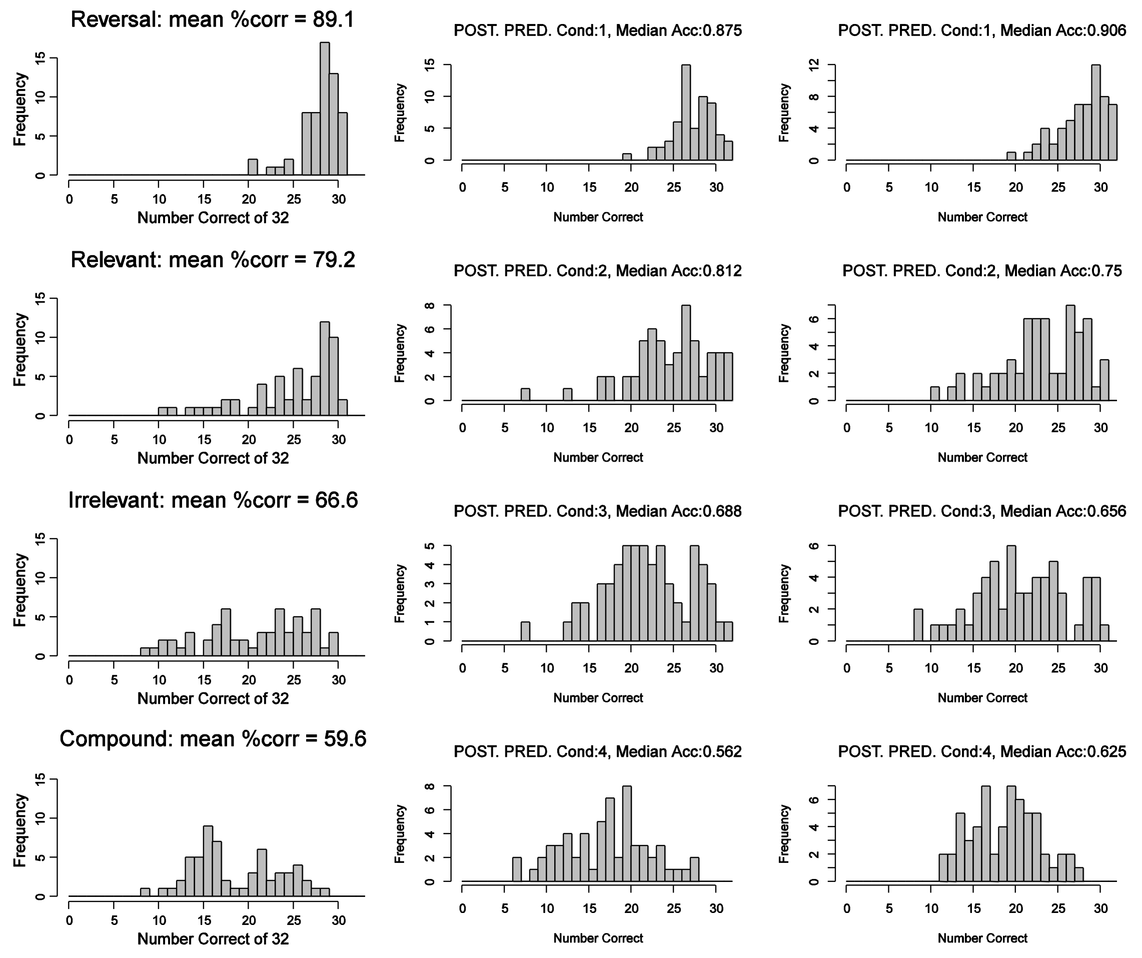




Notice that all kappa values are nearly 15, as demanded by the prior. Hence the kappa differences, in the lower histograms, are very small. The differences in the mu values, across conditions, are qualitatively the same as with the vague prior, but slightly different quantitatively.

(E) [Purpose: To conduct a posterior predictive check.] For this part, use the plausible dgamma(1,.1) prior, not the less-plausible other priors explored in the previous part. Conduct a posterior predictive check by generating simulated data from the sampled posterior parameter values. This can be done in R as follows (Kruschke1996CSbugs.R): […] This code puts each randomly generated sample of data into a row of the matrix nCorrOfSubjPredMat. Figure 13.5 shows histograms of simulated data. The preceding code relied on previously extracting the parameter chains from BUGS, as follows (Kruschke1996CSbugs.R): […]

```
# Extract chains from BUGS for subsequent examination
mu = NULL
kappa = NULL
for ( condIdx in 1:nCond ) {
    nodeName = paste( "mu[" , condIdx , "]" , sep="" )
    mu = rbind( mu , samplesSample( nodeName ) )
    nodeName = paste( "kappa[" , condIdx , "]" , sep="" )
    kappa = rbind( kappa , samplesSample( nodeName ) )
}
save( mu , kappa , file=paste(fileNameRoot,"MuKappa.Rdata",sep="") )
chainLength = NCOL(mu)

# Posterior predictive check.
# This code allows specification of different number of subjects, trials.
nSimExps = min(500,chainLength) # number of simulated experiments
nSubjPerCond = sum( CondOfSubj == 1 ) # number of subjects per condition
nTrlPerSubj = nTrlOfSubj[1] # number of trials per subject
nCorrOfSubjPredMat = matrix( 0 , nrow=nSimExps , ncol=nSubjPerCond*nCond )
CondOfSubjPredMat =  matrix( 0 , nrow=nSimExps , ncol=nSubjPerCond*nCond )
nTrlOfSubjPredMat =  matrix( 0 , nrow=nSimExps , ncol=nSubjPerCond*nCond )
for ( stepIdx in 1:nSimExps ) {
    for ( condIdx in 1:nCond ) {
        m = mu[condIdx,stepIdx]
        k = kappa[condIdx,stepIdx]
        a = m*k
        b = (1-m)*k
        for ( subjIdx in 1:nSubjPerCond ) {
            colIdx = (condIdx-1)*nSubjPerCond + subjIdx
            theta = rbeta( 1 , a , b )
            nCorrOfSubjPredMat[stepIdx,colIdx] = rbinom( 1 ,
                                   size=nTrlPerSubj , prob=theta )
            CondOfSubjPredMat[stepIdx,colIdx] = condIdx
            nTrlOfSubjPredMat[stepIdx,colIdx] = nTrlPerSubj
        }
    }
}
save( nCorrOfSubjPredMat , nTrlOfSubjPredMat , CondOfSubjPredMat ,
      file=paste(fileNameRoot,"PredData.Rdata",sep="") )
# Make plots
nToPlot = 5 # number of simulated data sets to plot
stepIdx = round(seq(1,nSimExps,len=nToPlot)) # which steps in chain to plot
for ( plotIdx in 1:nToPlot ) {
    # Display predicted data summary:
    windows(4,10)
    layout( matrix( 1:4 , nrow=4 , byrow=T ) )
    for ( condIdx in 1:4 ) {
        dataToPlot = nCorrOfSubjPredMat[ stepIdx[plotIdx] ,
              CondOfSubjPredMat[stepIdx[plotIdx],]==condIdx ]
        maxTrl = max(nTrlOfSubjPredMat[stepIdx[plotIdx],])
        hist( dataToPlot , xlim=c(0,maxTrl) , breaks=0:maxTrl ,
              xlab="Number Correct" , col="grey" ,
              main=bquote("POST. PRED. Cond:"*.(condIdx)*
              ", Median Acc:"*.( round( median(dataToPlot)/maxTrl , 3 ) ) ) )
    }
    dev.copy2eps(file=paste(fileNameRoot,"Pred",plotIdx,".eps",sep=""))
}
```



The actual data are shown in the left column above, and two posterior-predicted data sets are shown in the middle and right columns. The conclusion to be drawn is that the simulated data "look" fairly similar to the actual data, and therefore the model seems to be a fairly good description of the data.

The only possible point of discrepancy is that the data for the Compound shift (lower left graph) look like they might possibly be bimodal. Such bimodality does occur from time to time in simulated data sets, however, so it is not clear that the apparent bimodality in the data is caused by chance or by two different kinds of learners.

The verisimilitude of the simulated data (i.e., resemblance with the actual data) is important for the next parts of the exercise, which consider power analysis based on simulated data. If the simulated data did not mimic the actual data, then the power analysis would not be very meaningful.

(F) [Purpose: To do a retrospective power analysis.] Using the method of Figure 13.3, which is exemplified by the code explained in Section 13.6.2 (FilconBrugsPower.R), conduct a retrospective power analysis, and estimate the power of four goals: $\mu_{REV} - \mu_{REL} > 0$, $\mu_{REL} - \mu_{IRR} > 0$, $\mu_{IRR} - \mu_{CMP} > 0$, $\kappa_{REV} - \kappa_{REL} > 0$ (condition 1 is Reversal, condition 2 is Relevant, condition 3 is Irrelevant, and condition 4 is Compound). To do this, … Run at least 100 simulated data sets, and report your tally for how many times the goals were achieved. …

For 200 simulated data sets, the estimated probability of achieving the four goals is 0.985, 0.935, 0.630, and 0.390. For the mu goals, the Reversal versus Relevant comparison may have been uselessly overpowered, while the Irrelevant versus Compound comparison was underpowered. Thus, if the primary purpose was evaluating the mu values of the groups, the experiment may have been more efficiently conducted with fewer subjects in the Reversal condition but more subjects in the Compound condition. If the primary purpose was evaluating the kappa values of groups (which it was not), then the experiment was very underpowered.

Some of the code for the analysis is reproduced here:

```
GoalAchievedForSample = function( dataList , plotResults=F ,
                                  fileNameRoot="DeleteMe" ) {
library(BRugs)
#------------------------------------------------------------------------------
# THE MODEL.

modelstring = "
# BUGS model specification begins ...
model {
   for ( i in 1:nSubj ) {
      nCorrOfSubj[i] ~ dbin( theta[i] , nTrlOfSubj[i] )
      theta[i] ~ dbeta( a[ CondOfSubj[i] ] , b[ CondOfSubj[i] ] )
   }
   for ( cond in 1:nCond ) {
      a[cond] <- max( .01 , mu[cond] * kappa[cond] )
      b[cond] <- max( .01 , (1-mu[cond]) * kappa[cond] )
      mu[cond] ~ dbeta( aMu , bMu )
      kappa[cond] ~ dgamma( sGamma , rGamma )
   }
   aMu <- max( .01 , mMu * kMu )
   bMu <- max( .01 , (1-mMu) * kMu )
   mMu ~ dunif(0,1)
   kMu ~ dgamma(1,.1)
   sGamma <- max( .005 , pow(muGamma,2)/pow(sigmaGamma,2) )
   rGamma <- max( .005 , muGamma/pow(sigmaGamma,2) )
   muGamma ~ dgamma(1,.1)
   sigmaGamma ~ dgamma(1,.1)
}
# ... end of BUGS model specification
" # close quote for modelstring
writeLines(modelstring,con="model.txt") # write model to a file.
modelCheck( "model.txt" ) # Load model file into BRugs and check its syntax.

#------------------------------------------------------------------------------
# THE DATA.

modelData( bugsData( dataList ) )
```

```
#------------------------------------------------------------------------------
# INTIALIZE THE CHAINS.

nchain = 1 # instead of 3, to prevent BUGS crashes?
modelCompile( numChains=nchain )
genInitList <- function() {
    theta = .01 + .98 * dataList$nCorrOfSubj / dataList$nTrlOfSubj
    mu = rep( 0 , dataList$nCond )
    kappa = rep( 0 , dataList$nCond )
    for ( condIdx in 1:dataList$nCond ) {
       mu[condIdx] = mean( theta[ dataList$CondOfSubj == condIdx ] )
       kappa[condIdx] = ( mu[condIdx] * (1-mu[condIdx])
                          / sd( theta[ dataList$CondOfSubj == condIdx ] )^2 )
    }
    mMu = mean( mu )
    kMu = mMu * (1-mMu) / sd(mu)^2
    muGamma = mean( kappa )
    sigmaGamma = sd( kappa )
    return( list(
         theta = theta ,
         mu = mu ,
         kappa = kappa ,
         mMu = mMu ,
         kMu = kMu ,
         muGamma = muGamma ,
         sigmaGamma = sigmaGamma
    ))
}
for ( chainIdx in 1 : nchain ) {
    modelInits( bugsInits( genInitList ) )
}

#------------------------------------------------------------------------------
# RUN THE CHAINS.

burninSteps = 1000 # Because initialization is good, doesn't need much burnin
modelUpdate( burninSteps )
samplesSet( c("mu","kappa","theta","mMu","kMu","muGamma","sigmaGamma") )
stepsPerChain = ceiling(5000/nchain)
thinStep = 20
modelUpdate( stepsPerChain , thin=thinStep )

#------------------------------------------------------------------------------
# EXAMINE THE RESULTS.

source("plotPost.R")

# Extract chains from BUGS for subsequent examination
mu = NULL
kappa = NULL
for ( condIdx in 1:nCond ) {
    nodeName = paste( "mu[" , condIdx , "]" , sep="" )
    mu = rbind( mu , samplesSample( nodeName ) )
    nodeName = paste( "kappa[" , condIdx , "]" , sep="" )
    kappa = rbind( kappa , samplesSample( nodeName ) )
}
chainLength = NCOL(mu)

if ( plotResults ) {
# show graphs of posterior …
} # end if plotResults
```

```
# Specify goals and check whether they are achieved:
source("HDIofMCMC.R")
# Goal is Reversal Mu minus Relevant Mu 95% HDI exceeds zero:
goal1Ach = ( HDIofMCMC( mu[1,] - mu[2,] )[1] > 0.0 )
# Goal is Relevant Mu minus Irrelevant Mu 95% HDI exceeds zero:
goal2Ach = ( HDIofMCMC( mu[2,] - mu[3,] )[1] > 0.0 )
goal3Ach = ( HDIofMCMC( mu[3,] - mu[4,] )[1] > 0.0 )
goal4Ach = ( HDIofMCMC( kappa[1,] - kappa[2,] )[1] > 0.0 )
goalAchieved = c( goal1Ach , goal2Ach , goal3Ach , goal4Ach )

return( goalAchieved )
} # end of function GoalAchievedForSample

#==============================================================================
# Now call the function defined above, using simulated data.

analysisType = c("Retro","Repli")[1] # specify [1] or [2]
fileNameRoot = paste("Kruschke1996CSbugsPower",analysisType,sep="")

# Load original data, for use in replication probability analysis:
load("Kruschke1996CSdatsum.Rdata") # loads CondOfSubj, nCorrOfSubj, nTrlOfSubj
# Rename the original data so they don't get overwritten:
CondOfSubjOrig = CondOfSubj
nCorrOfSubjOrig = nCorrOfSubj
nTrlOfSubjOrig = nTrlOfSubj
nSubjOrig = length(CondOfSubjOrig)
nCondOrig = length(unique(CondOfSubjOrig))

# Load previously computed posterior mu[cond,step], kappa[cond,step] values.
load( file="Kruschke1996CSbugsPostMuKappa.Rdata" )
chainLength = NCOL(mu)
nCond = NROW(mu) # should be 4, of course

# SPECIFY NUMBER OF SUBJECTS PER GROUP FOR SIMULATED DATA:
nSubjPerCond = 60
fileNameRoot = paste(fileNameRoot,"N",nSubjPerCond,sep="")

# Specify number of simulated experiments:
nSimExperiments = min(200,chainLength)
nSubj = nSubjPerCond * nCond # Number of subjects total.
nTrlPerSubj = 32 # Number of trials per subject; fixed by design at 32.
nGoal=4 # Determined in function above.

# If previous record of power estimation exists, load it and continue the runs.
filelist = dir( pattern=paste(fileNameRoot,"Result.Rdata",sep="") )
if ( length( filelist ) > 0 ) {
   load(paste(fileNameRoot,"Result.Rdata",sep="")) # loads expIdx and nSuccess
   prevExpIdx = expIdx
   chainIdxVec = round(seq(1,chainLength,len=(prevExpIdx+nSimExperiments))) # Use
these chains.
} else {
  prevExpIdx = 0
  nSuccess = rep(0,nGoal) # Initialize success counter.
  chainIdxVec = round(seq(1,chainLength,len=nSimExperiments)) # Use these chains.
}

# Simulated experiment loop begins here:
for ( expIdx in (1+prevExpIdx):(nSimExperiments+prevExpIdx) ) {

    # Generate random data from posterior parameters
    chainIdx=chainIdxVec[expIdx]
    CondOfSubj = sort( rep( 1:nCond , nSubjPerCond ) )
    nTrlOfSubj = rep( nTrlPerSubj , nSubj )
    nCorrOfSubj = rep( 0 , nSubj )
    for ( condIdx in 1:nCond ) {
        m = mu[condIdx,chainIdx]
        k = kappa[condIdx,chainIdx]
        a = m*k
        b = (1-m)*k
        # Generate random theta and z values for simulated subjects:
        thetaVec = rbeta( nSubjPerCond , a , b )
        zVec = rbinom( n=nSubjPerCond , size=nTrlPerSubj , prob=thetaVec )
        nCorrOfSubj[ CondOfSubj==condIdx ] = zVec
    }
    # Put data into list for BUGS program
    if ( analysisType == "Retro" ) { # retrospective power
       dataList = list(
             nCond = nCond ,
             nSubj = nSubj ,
             CondOfSubj = CondOfSubj ,
             nTrlOfSubj = nTrlOfSubj ,
             nCorrOfSubj = nCorrOfSubj
             )
    }
    if ( analysisType == "Repli" ) { # replication probability
       dataList = list(
             nCond = nCond ,
             nSubj = nSubj + nSubjOrig ,
             CondOfSubj = c( CondOfSubj , CondOfSubjOrig ) ,
             nTrlOfSubj = c( nTrlOfSubj , nTrlOfSubjOrig ) ,
             nCorrOfSubj = c( nCorrOfSubj , nCorrOfSubjOrig )
             )
    }

    # For monitoring, make plots for first 5 simulated experiments:
    if ( expIdx <= 5 ) { plotRes = T } else { plotRes = F }

    # Call BUGS program and tally number of successes:
    nSuccess = nSuccess + GoalAchievedForSample( dataList ,
                                                 plotRes , fileNameRoot )
    estPower = nSuccess / expIdx
    cat( "\n*** nSubjPerCond:",nSubjPerCond, ", nSimExp:",expIdx,
      " , nSuccess:",nSuccess, ", estPower:",round(estPower,2), "\n\n" )
    flush.console()
    save( nSuccess , expIdx , estPower ,
          file=paste(fileNameRoot,"Result.Rdata",sep="") )

} # end of simulated experiment loop.
```

(G) [Purpose: To do a replication power analysis.] Suppose you repeat the experiment, using the posterior of the first experiment as the prior for the second experiment. Estimate the probability of achieving the four goals of the previous part. … This task is easy to do if you successfully accomplished the previous part. In each step of the chain, instead of using only the simulated data, concatenate the simulated data to the actual data. …

Code for this part is included in the listing of the previous part; notice near the end of listing the section beginning with

```
    if ( analysisType == "Repli" ) { # replication probability
```

Results from 200 simulated experiments show that the probabilities of achieving the fours goals are 1.000, 0.995, 0.850, and 0.960. In other words, if the posterior from the first experiment is used as the prior for a replication, there is very high probability of achieving any of the four goals in the replication.

Chapter 14.

Exercise 14.1. [Purpose: For real-world examples of research, to identify which statistical model is relevant.] For each of the following examples, identify the predicted variable and its scale type, identify the predictor variable(s) and its scale type, and identify the cell of Table 14.1 to which the example belongs.

(A) Guber (1999) examined average performance by public high school students on the Scholastic Aptitude Test (SAT) as a function of how much money was spent per pupil by the state and what percentage of eligible students actually took the exam.

Predicted Variable: SAT Score: Metric
Predictor Variable(s): How much money was spent by the state per pupil (metric), and the percentage of students who took the test (metric).
Cell: y(Metric) & Two or More Metric x factors.

(B) Hahn, Chater, & Richardson (2003) were interested in perceived similarity of simple geometric patterns. Human observers rated pairs of patterns for how similar the patterns appeared, by circling one of the digits 1 to 7 printed on the page, where 1 meant "very dissimilar" and 7 meant "very similar." The authors presented a theory of perceived similarity, in which patterns are perceived to be dissimilar to the extent that it takes more geometric transformations to produce one pattern from the other. The theory specified the exact number of transformations needed to get from one pattern to the other.

Predicted Variable: Geometric/Shape similarity: Ordinal
Predictor Variable(s): The number of transformations needed to get from one shape to the other: Metric
Cell: y(Ordinal) & Single Metric x factor.

(C) R.L. Berger et al. (1988) were interested in the longevity of rats, measured in days, as a function of the rats' diet. One group of rats fed freely, another group of rats had a very low calorie diet.

Predicted Variable: Longevity of rats in days: Metric
Predictor Variable(s): Diet (free feeding vs. low calorie dies): Nominal
Cell: y(Metric) & Single Nominal x factor.

(D) McIntyre (1994) was interested in predicting the tar content of a cigarette (measured in milligrams) from the weight of the cigarette.

Predicted Variable: Tar Content of Cigarette (milligrams): Metric
Predictor Variable(s): Weight of the cigarette: Metric
Cell: y(Metric) & Single Metric x factor.

(E) You are interested in predicting the gender of a person, based on the person's height and weight.

Predicted Variable: Gender: Dichotomous
Predictor Variable(s): Height and Weight: Metric
Cell: y(Dichotomous) & Two or More Metric x factors.

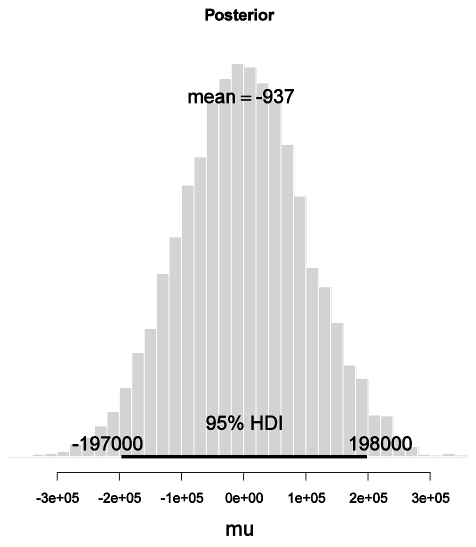
(F) You are interested in predicting whether a respondent will agree or disagree with the statement "The United States needs a federal health care plan with a public option," on the basis of the respondent's political party affiliation.

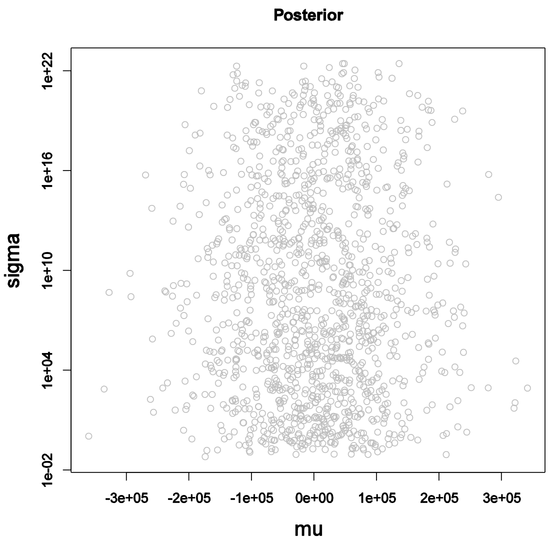
Predicted Variable: Will respondents Agree Or Disagree with the statement: Dichotomous
Predictor Variable(s): Political Party Affiliation: Nominal
Cell: y(Dichotomous) & Single nominal x factor.

Chapter 15.

Exercise 15.1. [Purpose: To view the prior from BUGS.] For the program in Section 15.4.1 (YmetricXsingleBrugs.R), generate graphs of prior distribution, analogous to Figure 15.3. To do this, comment out the data in the data specification, as explained in Section 8.5.1, p. 174. But also beware of the following: Automatically initialize the chains from the prior, and, when plotting the results, comment out the plotChains commands because the MCMC sigma values are too extreme for some of the BUGS graphics routines.

Notice the huge values of the scales below. In particular, notice that the prior on mu was specified as mu ~ dnorm(0 , 1.0E-10), which means that the SD on mu should be 1/sqrt(1.0E-10) = 1e+05 = 100000. For a normal distribution with SD=100000, the 95%HDI should go from about -196000 to +196000, which is very nearly what the posterior sample shows.



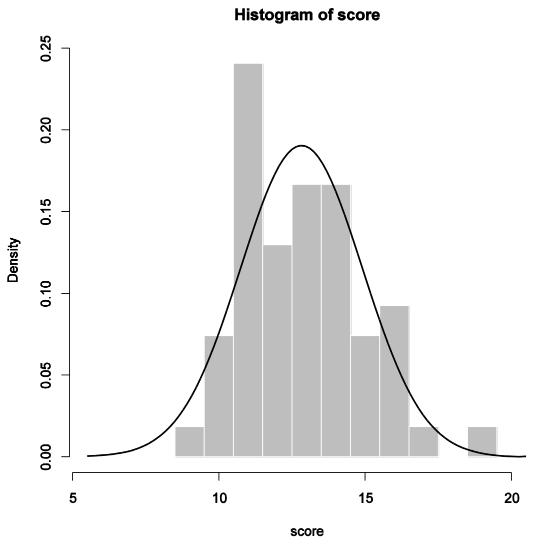


Exercise 15.2. [Purpose: To explore a realistic example of estimating a single mean, with consideration of priors.] University students who agreed to participate in a problem-solving experiment were also tested for their vocabulary level, using the Wechsler Adult Intelligence Scale Revised (WAIS-R), which is normed to have a general-population mean of 10 and standard deviation of 3. Here are the data from the university students (data from Hand et al., 1994, set #392, p. 322):
14 11 13 13 13 15 11 16 10 13 14 11 13 12 10 14 10 14 16 14 14 11 11 11
13 12 13 11 11 15 14 16 12 17 9 16 11 19 14 12 12 10 11 12 13 13 14 11
11 15 12 16 15 11

(A) Are the data roughly normal, that is, essentially unimodal and symmetrically distributed? (No formal analysis is required here; only an "eyeball" assessment is expected.) Therefore, can a normal likelihood function be applied?

The code below generated the accompanying graph:

```
score = c( 14, 11, 13, 13, 13, 15, 11, 16, 10, 13, 14, 11, 13, 12, 10, 14, 10, 14, 16,
14, 14, 11, 11, 11, 13, 12, 13, 11, 11, 15, 14, 16, 12, 17, 9, 16, 11, 19, 14, 12, 12,
10, 11, 12, 13, 13, 14, 11, 11, 15, 12, 16, 15, 11 )
m = mean( score )
s = sd( score )
hist( score , breaks=seq(5.5,20.5,1) , prob=T , col="grey" , border="white" )
xVals = seq(5.5,20.5,len=101)
lines( xVals , dnorm( xVals, m , s ) , lwd=2 )
dev.copy2eps(file="Exercise15.2.A.eps")
```



The graph plots a histrogram of the data, with a superimposed normal curve that has the same mean and SD as the data. Visual inspection show a bit of a spike in the data at 11, and perhaps an outlier on the high end, but the data are not wildly non-normal. Therefore a normal distribution may be used as a default model of the data unless other (e.g., theoretical) considerations suggest otherwise.

(B) Discuss the rationale for a prior distribution. Justify the constants you choose for the hyperprior. (Hint: The results of the analysis will be presented to a skeptical audience, who may doubt any claims about how prior knowledge of the general population informs an analysis of university students. Therefore, your prior should be very vague and widely dispersed around the general population values.)

Because this is a subgroup (i.e., university students) and not the general population, the prior knowledge about the general population is only indirectly applicable to the group. Therefore we might suppose that mu is somewhere around 10, but because we are uncertain, we might give the prior on mu a large uncertainty, such as 10 (this makes negative values possible in the prior, which is not really appropriate for this application, but negative values will be rendered unlikely by the data). Thus, the prior on mu might be mu ~ dnorm(10 , 1/10^2).

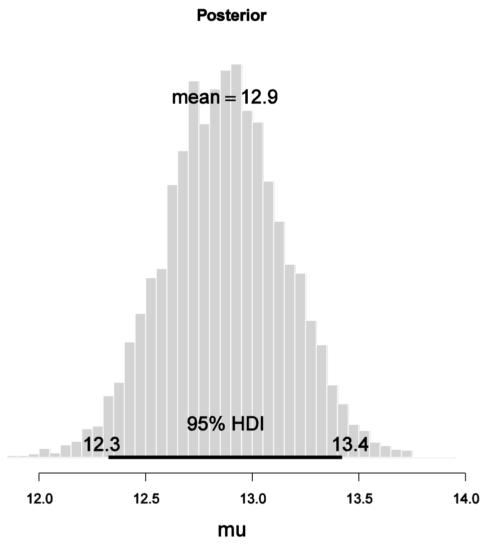
For the prior on the precision, tau, the general population has tau=1/3^2 (because SD=3), but our special group might have a larger or smaller precision. To be encompassing, we might suppose that the prior on tau is a gamma distribution with mean 3 and standard deviation 3, hence tau ~ dgamma(3^2/3^2 , 3/3^2).

These are not the only "correct" answers, but your justification should be similar.

(C) Is the mean vocabulary score of the university students credibly different from the general population mean of 10? Report the 95% HDI on mu for the various priors you considered in the previous part.

```
model {
    # Likelihood:
    for( i in 1 : N ) {
        y[i] ~ dnorm( mu , tau ) # tau is precision, not SD
    }
    # Prior:
    tau ~ dgamma( 1 , 0.333 )
    mu ~ dnorm( 10 , 0.01 )
}
```

yields



The 95% HDI is far above 10.0, which the general population mean.

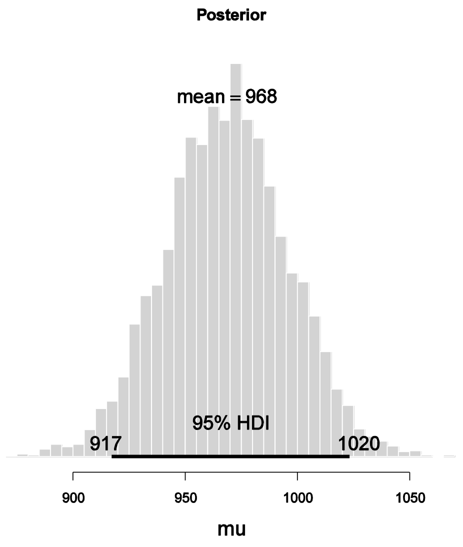
Exercise 15.3. [Purpose: To observe a realistic example of estimating a mean, with consideration of whether a normal likelihood distribution is appropriate.] Suppose we know that the mean life time of rats that eat ad lib is 700 days. This value is, in fact, about right for lab rats; see Figure 15.10, which shows data from R.L. Berger et al. (1988), as reported in Hand et al. (1994, data set #242), and which are available in the file RatLives.Rdata. This is an Rdata file, which stores values in compressed format, not text format. To get the data into R, type load("RatLives.Rdata"). It will look like nothing happens when you type that command, but the variables are now loaded into R; you can see the variables that R knows about by typing ls(). You will see listed the two vectors

adlibDiet and restrictedDiet. When rats are placed on a restricted diet, their longevity can be affected. Figure 15.10 shows the results.

(A) Using the raw data from the restricted-diet longevities, estimate mu and its 95% HDI. Be sure to report the prior you used. (Hint: The HDI extends from about 917 to 1020 days.)

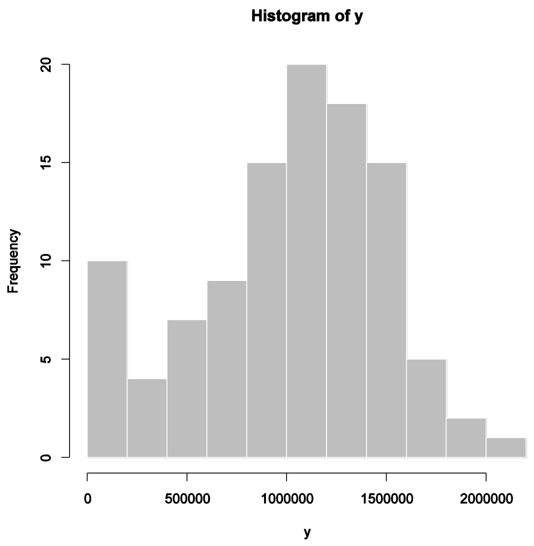
Using the data from the ad-lib diet as a source of prior information (assuming that previous experiments have revealed similar data --- it's the restricted diet that's not known yet), we set on prior on mu centered at the ad lib mean of 700, but leave it very broad, with an SD of 700 (or something of your own choice motivated the same way), and we set the prior on tau centered at the ad lib precision of 5.6E-05, but leave it very broad, with an SD also of 5.6E-05. This yields:

```
model {
    # Likelihood:
    for( i in 1 : N ) {
        y[i] ~ dnorm( mu , tau ) # tau is precision, not SD
    }
    # Prior for Exercise 15.3
    tau ~ dgamma( 1 , 18000 ) # m = s = 5.6E-05
    mu ~ dnorm( 700 , 2.0E-06 ) # precision = 1/700^2
}
…
load("RatLives.Rdata")
y = restrictedDiet
```



(B) Is it appropriate to apply a normal likelihood function to these data? Transform the data by squaring the longevities. Estimate mu and its 95% HDI (now in days squared). Be careful to use an appropriate prior! (Hint: The HDI extends from about 967^2 to 1053^2 days.)

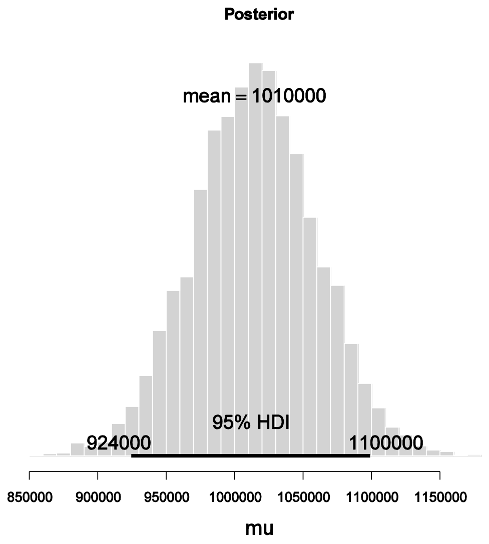
The squared data look like this:



The transformed data are far less skewed to the left than that original data. They are better described by a normal than the original data.

We use the transformed ad lib data to inform the priors. The transformed ad lib data have a mean of about 486000 and a precision of about 4.3E-11.

```
tau ~ dgamma( 1 , 2.3E+10 ) # m = s = 4.3E-11
mu ~ dnorm( 486000 , 4.2E-12 ) # precision = 1/486000^2
…
load("RatLives.Rdata")
y = restrictedDiet^2
```



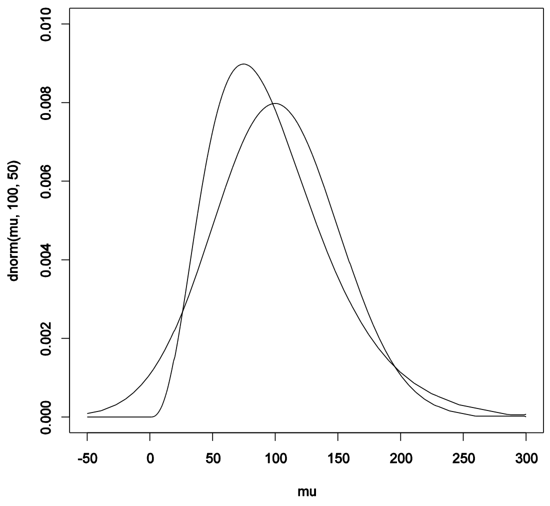
The 95%HDI limits in days, computed as sqrt(HDIofMCMC(muSample)), are 961.5 to 1048.3.

(C) Why is the first estimate lower than the second estimate? Which estimate is more appropriate and why?

The first estimate, using original-scale data, is lower because of the extreme leftward skew in the original data. The normal model is pulled down by the left-skew in the data. Because the original data are not very well modeled by a normal, the estimate from the transformed data is more trustworthy.

Exercise 15.4. [Purpose: To think about specifying an informed prior, and non-normal, non-gamma priors.] In the program of Section 15.4.1 (YmetricXsingleBrugs.R), the prior on the group mean uses an extremely small precision. This diffuse prior is silly, because we know that individual IQ scores from the general population should be near 100 with a standard deviation of about 15. Special populations might have IQ scores consistently above or below 100 but almost certainly within, say, 100 points above or below 100. Consider the following expressions of the prior belief on mu:
(1) mu ~ dnorm(100 , sd=50) # that's sd=50, so tau=pow (50,-2)
(2) mu ~ dgamma(4 , 0.04)
(3) mu ~ dunif(0 , 200)
(4) mu ~ dgamma(3 , 0.03)

(A) Plot the densities of (1) and (2) on the same graph, superimposed. (Hint:
mu = seq(-50 , 300 , length=501)
plot(mu , dnorm(mu , 100 , 50) , type="l" , ylim=c(0,0.01))
lines(mu , dgamma(mu , 4 , 0.04))
What do the densities of (1) and (2) have in common? (Hint: Compute the mean and sd of the gamma distribution.) Should either of (1) or (2) be preferred over the other? (Hint: Consider negative IQ scores, which should not be allowed.)

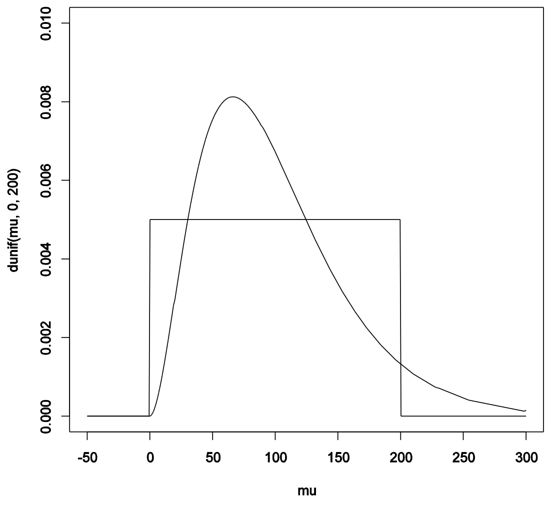


The mean of the gamma distribution is s/r = 4/0.04 = 100, and the sd of the gamma distribution is sqrt(s)/r = 2/0.04 = 50 (see Fig. 9.8, p. 209). In other words, the gamma and normal have the same mean and SD.

Despite that similarity, the gamma is to be preferred as a prior for IQ scores because IQ scores can not be negative. The graph shows that the normal distribution givess negative scores some credibility.

(B) Plot the densities of (3) and (4) on the same graph, superimposed. What do the densities of (3) and (4) have in common? Should one of (3) or (4) be preferred over the other? (Hint: Consider IQ scores greater than 200, which should be allowed.)

```
plot( mu , dunif( mu , 0 , 200 ) , type="l" , ylim=c(0,0.01))
lines( mu , dgamma( mu , 3 , 0.03 ) )
```



The mean of the gamma is 3/0.03 = 100, and the sd of the gamma is sqrt(3)/0.03 = 57.7.
The mean of the uniform is 100 (obviously), and its sd can be easily approximated by a large random sample, sd(runif(1000000,0,200)), which yields 57.7. In other words, the two distributions have very nearly the same mean and SD.

Despite the similarity, the gamma distribution is a better prior for IQ because the uniform makes IQ scores above 200 impossible, which should be allowed.

In the program of Section 15.4.1 (YmetricXsingleBrugs.R), the prior on the group precision is a general diffuse distribution. This diffuse prior is silly, because we know that individual IQ scores have a standard deviation around 15 (i.e., a precision of 1/15^2 = 0.00444...) in the general population. The SD might be a bit smaller within special populations.

(C) Suppose we believe that the smallest SD we would find in a specialized population is 5. What is the corresponding precision? (Notice that it is larger than 1/15^2.)

The corresponding precision is 1/5^2 = 0.04. That’s the smallest SD, hence the largest precision.

(D) We want to create a gamma distribution for precision that has a mean corresponding to 1/15^2, such that most of the gamma distribution is less than the precision corresponding to an IQ precision of 1/5^2, because, as mentioned in the previous part, we

don’t think that precisions much greater than 1/5^2 are tenable. Therefore, to be sure that our prior encompasses that maximum but still allows for considerable uncertainty, we will set the standard deviation of the gamma distribution to half of the difference between the precisions determined in the previous two parts. What is the value of half of the difference between the precisions determined in the previous two parts? (Hint: The answer is 0.01777… . Explain.)

The largest precision is 0.04, and the mean precision is 0.00444. Half the difference is
0.5 * (1/5^2 - 1/15^2) which yields 0.01777…

(E) What are the values of the shape and rate parameters for a gamma distribution that has mean of 0.00444 and standard deviation of 0.01777?

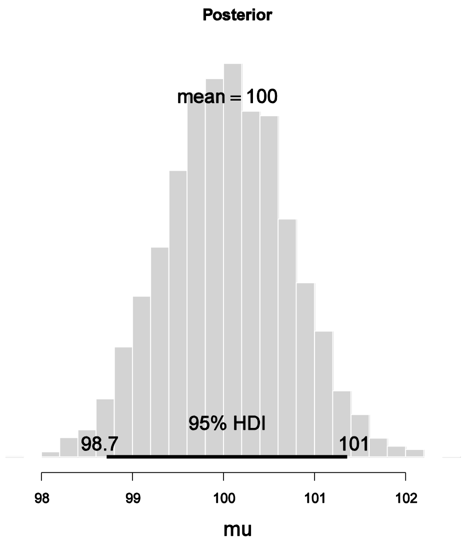
s = m^2/sd^2 = 0.625
r = m/sd^2 = 14.0625

(F) Rerun the program of Section 15.4.1 (YmetricXsingleBrugs.R) using a prior for tau from the previous part, and a prior for mu that is the most appropriate from (1)–(4) above. Include the posterior histogram of mu with your answer. Does the conclusion differ noticeably from the diffuse priors?

The most appropriate prior on mu is either of the gamma distributions; I’ll use gamma(3,.03) because it is more vague.

```
tau ~ dgamma( 0.625 , 14.0625 )
mu ~ dgamma( 3 , 0.03 )
```

yields



The posterior is essentially the same as diffuse priors. In this case there are so many data points that the prior is overwhelmed.

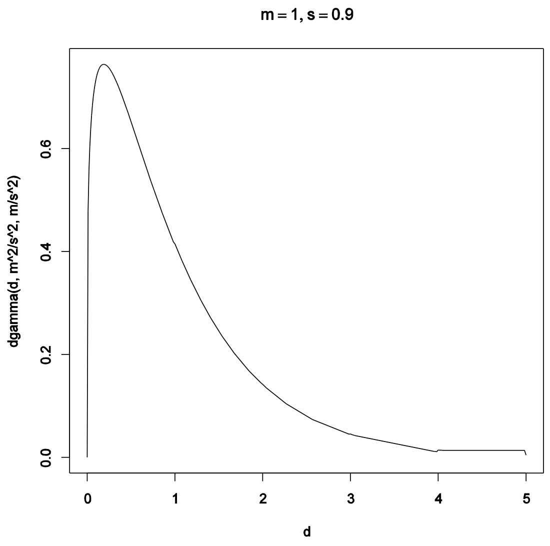
Exercise 15.5. [Purpose: With repeated measures, to see how the group estimate and individual estimates reflect different sources of variation in the data.] Consider the data, y, with different assignments to subjects, s, as follows:
y values: 1 2 3 21 22 23 41 42 43
s, large between subj. var.: 1 1 1 2 2 2 3 3 3
s, small between subj. var.: 1 2 3 1 2 3 1 2 3
The first row shows nine data values. The second row indicates a situation in which the first three data points come from subject 1, the second three data points come from subject 2, and so on. The third row indicates a different situation, in which the first, fourth, and seventh data points come from subject 1, and so forth. The assignment of data to subjects in the second row produces large between-subject variance, whereas the assignment of data to subjects in the third row produces small between-subject variance. Notice that for both situations, however, the overall mean is the same because the data are the same. We are interested in which situation gives a more precise estimate of the group-level mean. Modify the program of Section 15.4.2 (SystemsBrugs.R) for use with these data. (No need to be too fancy. For example, in the datalist, just type in y = c(1, 2, 3, 21, 22, 23, 41, 42, 43) and subj = c(1,1,1, 2,2,2, 3,3,3).) Be sure to make the prior appropriate for these data. Run the program twice, once for each assignment of data to subjects (using the same prior for both runs). (Hint: Your results should look something like those in Figure 15.11). Notice that the mean of the posterior of muG is essentially the same for both runs, but the HDI widths are quite different. Explain why.

The prior on muG should be appropriate for data in the range 0-50, without being very certain. Hence we could set muG ~ dnorm(25 , 0.0001).

The prior on tauG should be appropriate for groups that have between-group SDs in the range of 1 to 20 (because the two sets of data do). So we could set a prior on SD with a mean of 10 and a very uncertain. So, we could use a gamma distribution on precision with a mean of 0.01 (i.e., SD=10) and a sd the same: tauG ~ dgamma(.01^2/.01^2 , .01/.01^2).

The within-group SDs also range from 1 to 20 across data sets, so the prior on tau[j] should have a mean m around 1/10^2. The hyperprior on m can therefore be set analogous to the prior on tauG, namely m ~ dgamma(.01^2/.01^2 , .01/.01^2).

Finally, the within-group variances are identical across groups for these fictitious data sets (which would never happen in the real world), and therefore care must be taken when setting the prior on d, so that the posterior does not collapse into degeneracy with d=0. We'll put a prior on d such that the sd of the gamma distribution is slightly less than the mean, thereby prohibiting d=0. For example, d ~ dgamma(1 , 1.23), as shown in this graph:



It is worth emphasizing that this choice of prior is not uniquely correct. Other priors could also be justified. Indeed, other priors will yield different posteriors because the data are so few! The graphs in Figure 15.11 of the textbook were generated from different priors.

The full model specification is

```
model {
    for( i in 1 : Ndata ) {
        y[i] ~ dnorm( mu[ subj[i] ] , tau[ subj[i] ] )
    }
    for ( j in 1 : Nsubj ) {
        mu[j] ~ dnorm( muG , tauG )
        tau[j] ~ dgamma( sG , rG )
    }
    muG ~ dnorm( 25 , 0.0001 )
    tauG ~ dgamma( 1 , 100 )
    sG <- pow(m,2) / pow(d,2)
    rG <- m / pow(d,2)
    m ~ dgamma( 1 , 100 )
    d ~ dgamma( 1 , 1.23 )
}
```

The data can be specified thus:

```
datalist = list(
   y    = c( 1,2,3, 21,22,23, 41,42,43 ) ,
   subj = c( 1,1,1,  2, 2, 2,  3, 3, 3 ) ,
   #subj = c( 1,2,3,  1, 2, 3,  1, 2, 3 ) ,
   Ndata = 9 ,
   Nsubj = 3
)
```

Unfortunately, BUGS does not always like automatically initializing the chains when the priors are vague. Therefore we can manually start the chains at values consistent with the data:

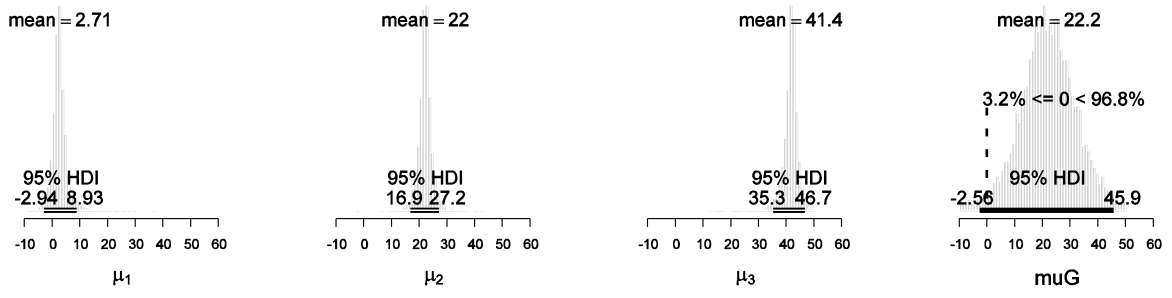
```
y = datalist$y
s = datalist$s
```

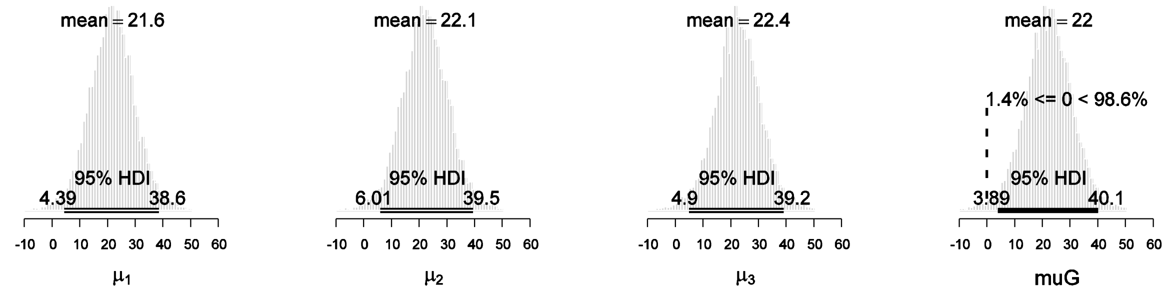
```
# Overall mean:
muGinit = mean( y )
# Group means:
muVec = aggregate( y ~ as.factor(s), data=cbind(y,s), mean )[,2]
# Precision across group means:
tauGinit = 1 / sd( muVec )^2
# Groups SDs:
sdVec = aggregate( y ~ as.factor(s), data=cbind(y,s), sd )[,2]
dInit = max( 0.01 , sd( sdVec ) )
# manually initialize chains near the data:
genInitList <- function() {
        list( muG = muGinit ,
              tauG = tauGinit ,
         m = mean(1/sdVec^2) ,
         d = dInit ,
         mu = muVec ,
         tau = 1/sdVec^2 )
}
for ( chainIdx in 1 : nchain ) {
        modelInits( bugsInits( genInitList ) )
}
```

The posterior mu values can be plotted thus

```
windows(10,3)
layout( matrix( 1:4 , nrow=1 , byrow=T ) )
for ( sIdx in 1:3 ) {
    histInfo = plotPost( muSample[sIdx,] , xlab=bquote(mu[.(sIdx)]) ,
                         xlim=c(-10,60) , breaks=c(-5000,seq(-10,50,len=61),5000) )
}
histInfo = plotPost( muGsample , xlab=bquote(muG) , xlim=c(-10,60) ,
                        breaks=c(-5000,seq(-10,50,len=61),5000) , compVal=0 )
```

which yields, for the two data sets, the following graphs:





These graphs differ from Figure 15.11 of the textbook because different priors were used. But the qualitative nature is the same: When the data are re-assigned to subjects/groups such that there is larger between group variance, then the estimate of muG is larger.

Chapter 16.

Exercise 16.1. [Purpose: To see the influence of individual slope differences on the estimate of the group-average slope.] The data shown in Figure 16.10 indicate that all subjects had similar rates of decline in retention, and therefore the estimate of the group average is fairly certain. In this exercise, we change the data so that the individual slopes differ more dramatically and examine the effect on the estimate of the group average.

(A) Alter the data as follows: In the program listed in Section 16.5.3 (SimpleLinearRegressionRepeatedBrugs.R), just before the data are renamed from dataMat to x and y (at about line 65), subtract .030x from subject 1, subtract .015x from subject 2, do nothing to subject 3, and add .015x to subject 4. Here is an example of code for subject 1:

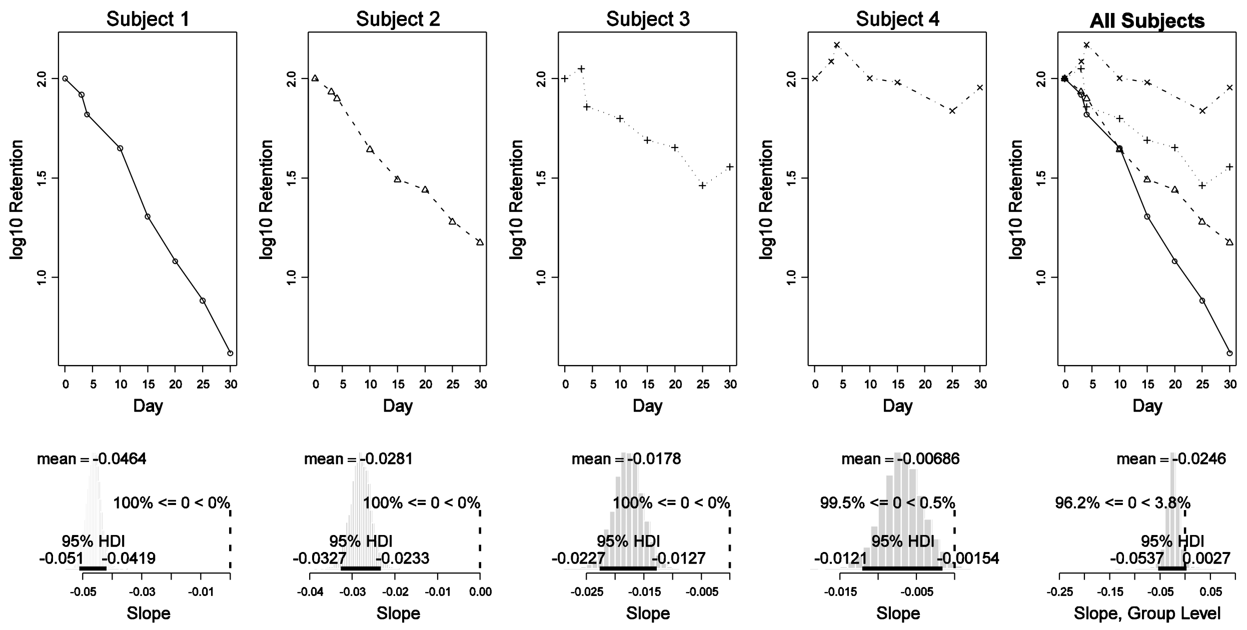
```
  subjRowVec H ( dataMat[,subjColName] HH 1 )
  dataMat[ subjRowVec , yColName ] H ( dataMat [ subjRowVec , yColName ]
     - .030 * dataMat[ subjRowVec , xColName ] )
```

Repeat and modify for the remaining subjects. Run the program and include the plot of the data. (See Figure 16.12.) The data curves for the four subjects should have four very different slopes.

Here is the complete data-modification code, executed *after* the conversion to log10:

```
subjRowVec = ( dataMat[,"subjID"] == 1 )
dataMat[ subjRowVec , "retention" ] = ( dataMat[ subjRowVec , "retention" ]
          - .030 * dataMat[ subjRowVec , "time" ] )
subjRowVec = ( dataMat[,"subjID"] == 2 )
dataMat[ subjRowVec , "retention" ] = ( dataMat[ subjRowVec , "retention" ]
          - .015 * dataMat[ subjRowVec , "time" ] )
subjRowVec = ( dataMat[,"subjID"] == 4 )
dataMat[ subjRowVec , "retention" ] = ( dataMat[ subjRowVec , "retention" ]
          + .015 * dataMat[ subjRowVec , "time" ] )
```

And here is the resulting graph:



(B) Relative to the original data, has the posterior mean of the group slopes gotten farther away from zero or closer to zero? Include the histogram of the posterior in your write-up. Are all the individual slopes believably different from zero (according to the 95% HDI)? Is the group slope believably different from zero (according to the 95% HDI)? Why is the group-level slope, which is now farther away from zero on average, less believably different from zero than in the original data?

The posterior mean of the group slopes (lower right of graph above) has gotten farther away from zero, i.e., more negative. And all the individual slopes are credibly below zero, as shown by the posterior histograms in columns 1-4 above. But the 95%HDI of the group-level slope includes zero, i.e., the group-level slope is very uncertain and might even include zero. This seems like a contradiction: All the individual slopes are less than zero, but the group slope might include zero. It's not a contradiction, though. The reason is that the individual slopes differ from each other very much. Hence there is lots of uncertainty in the group average slope. This uncertainty means that the 95%HDI at the group level is wide.

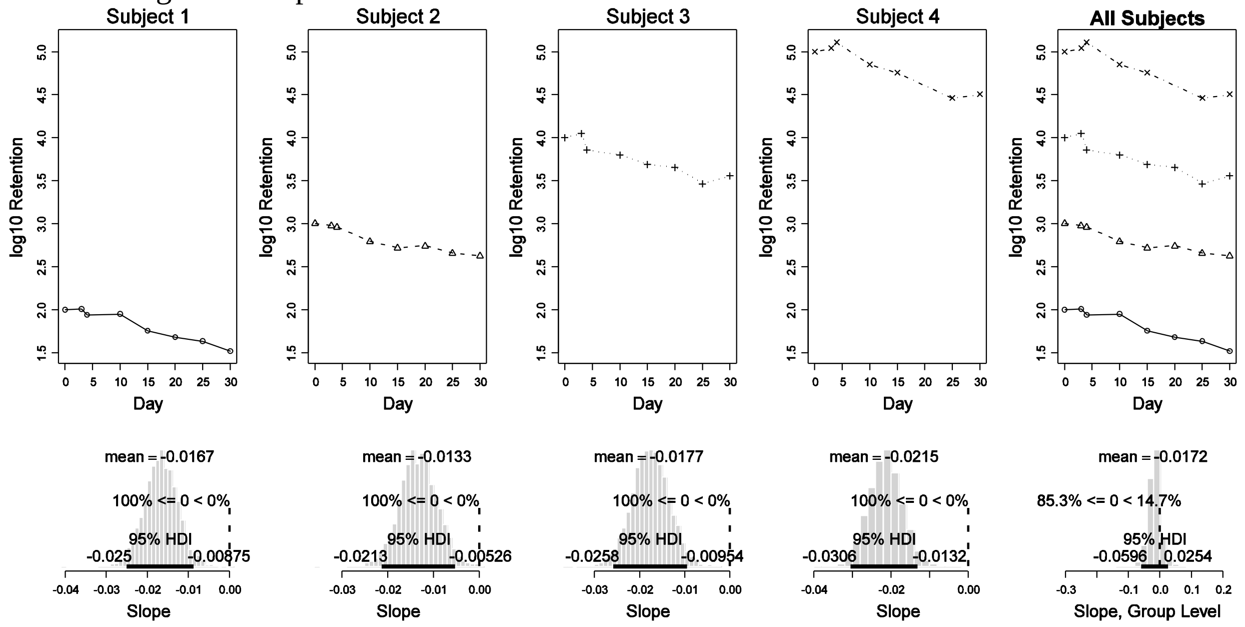
Exercise 16.2. [Purpose: To see the influence of differences in individual intercepts on the estimate of group-average slope.] The data shown in Figure 16.10 all start at 2.0 because that is log10(100), and the data were measured as percentage of original value. Suppose that the data were kept in their raw magnitudes instead of converted to percentage of first magnitude. This would merely change the intercepts of the individual data curves, without changing their slopes …. In this exercise we find out whether this change would have any effect on the estimate of the group slope.

(A) Alter the data as follows: In the program listed in Section 16.5.3 (SimpleLinearRegressionRepeatedBrugs.R), right before the data are converted to log10 on line 42, insert this code: … Run the program and include the plot of the data. (See Figure 16.13.) The data curves for the four subjects should have four very different intercepts.

Before the conversion to log10, include this transformation:

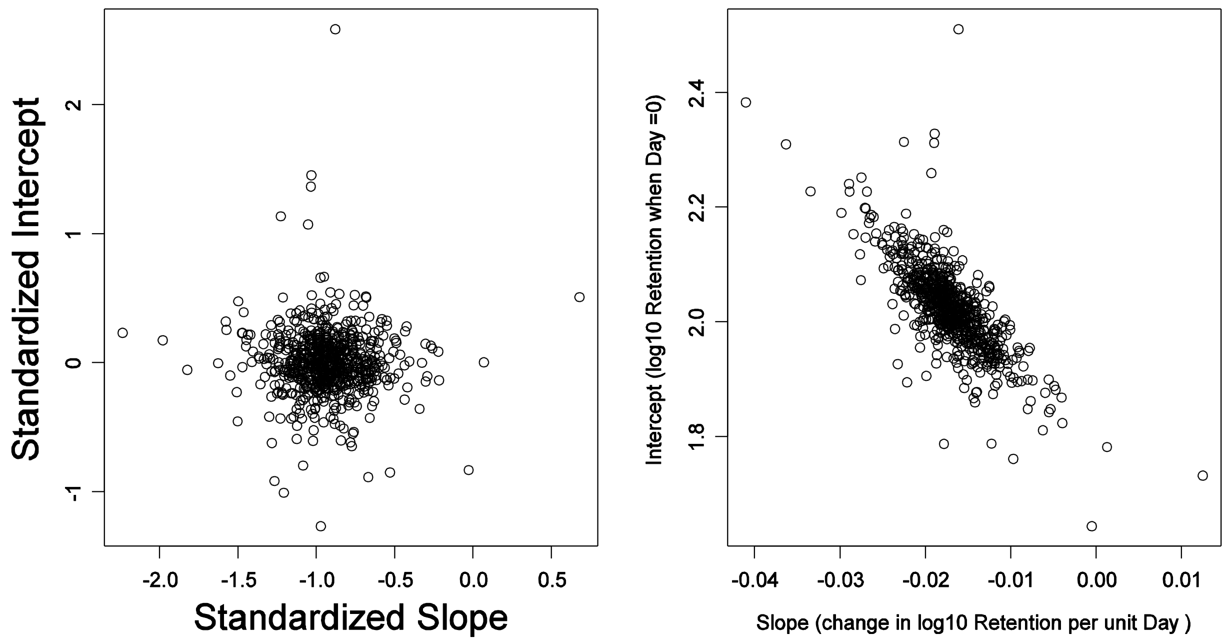
```
for ( subjIdx in 1:4 ) {
    rowIdx = ( dataMat[,"subjID"] == subjIdx )
    dataMat[rowIdx,"retention"] = dataMat[rowIdx,"retention"] * 10^(subjIdx-1)
}
```

The resulting data and posterior look like this:

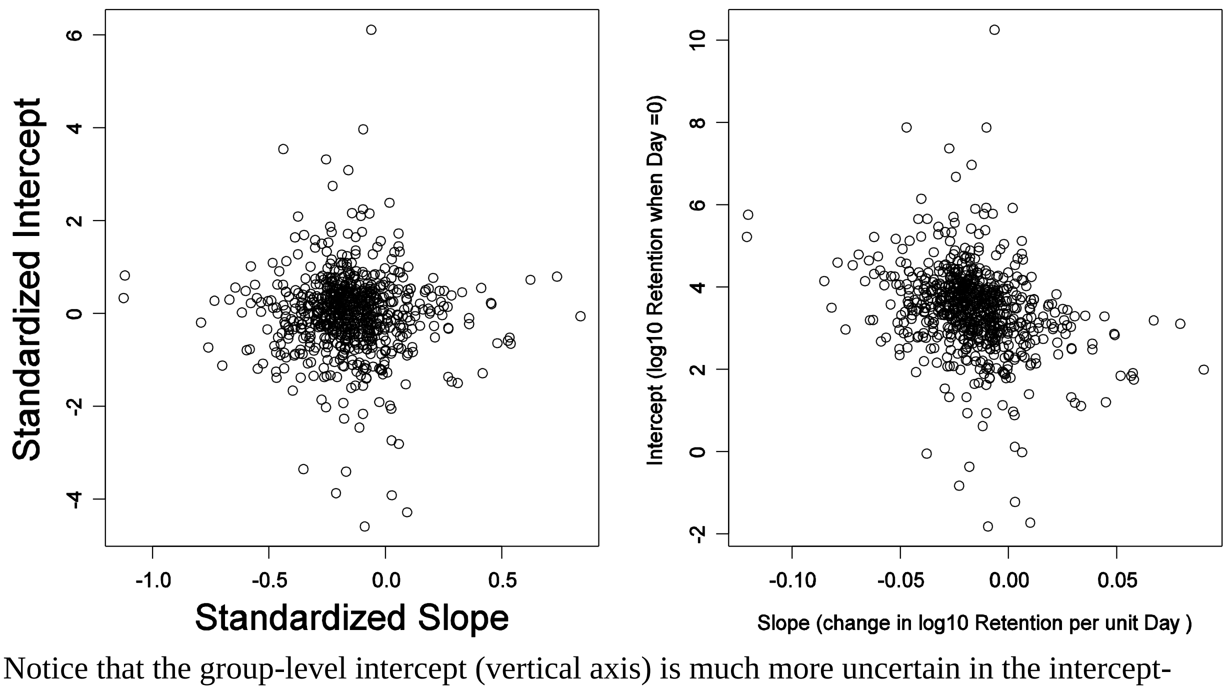


(B) Relative to the original data, are the estimates of the individual slopes different? Relative to the original data, is the posterior mean of the estimated group slope different? Include the histogram of the posterior of the group slope. Is the group slope believably different from zero (according to the 95% HDI)? Why is the group-level slope less believably different from zero, compared to the original data? (Hint: The individual intercepts affect the certainty of the group-average intercept. The group-average intercept trades off with the group-average slope; consider scatter plots of mu0G and mu1G.)

For the individual slope estimates, the means of the posteriors are about the same as in the original data, which makes sense because the individual slopes in the data are unchanged. But the uncertainties of the estimates have increased. For example, Subject 4 in the original data had a slope estimate with 95%HDI from -0.0256 to -0.0164, but in the intercept-altered data the HDI goes from -0.0306 to -0.0132. For the group-level slope, the mean of the posterior is the same for the original and intercept-altered data, which makes sense because there has been no change in the individual slopes. But, the uncertainty on the group-level slope has increased; in particular, the 95%HDI now includes zero! The reason is provided by the hint in the statement of the exercise. Because the individual intercepts are now very different, the estimate of the group-level intercept is now very uncertain. The uncertainty in the group-level intercept implies that the group-level slope also has more flexibility, because different group-level intercepts can trade-off with more extreme group-level slopes. Hence the group-level slope is more uncertain. Plots of the group-level slope and intercept are shown below. First, for the original data:



Next, for the intercept-altered data:



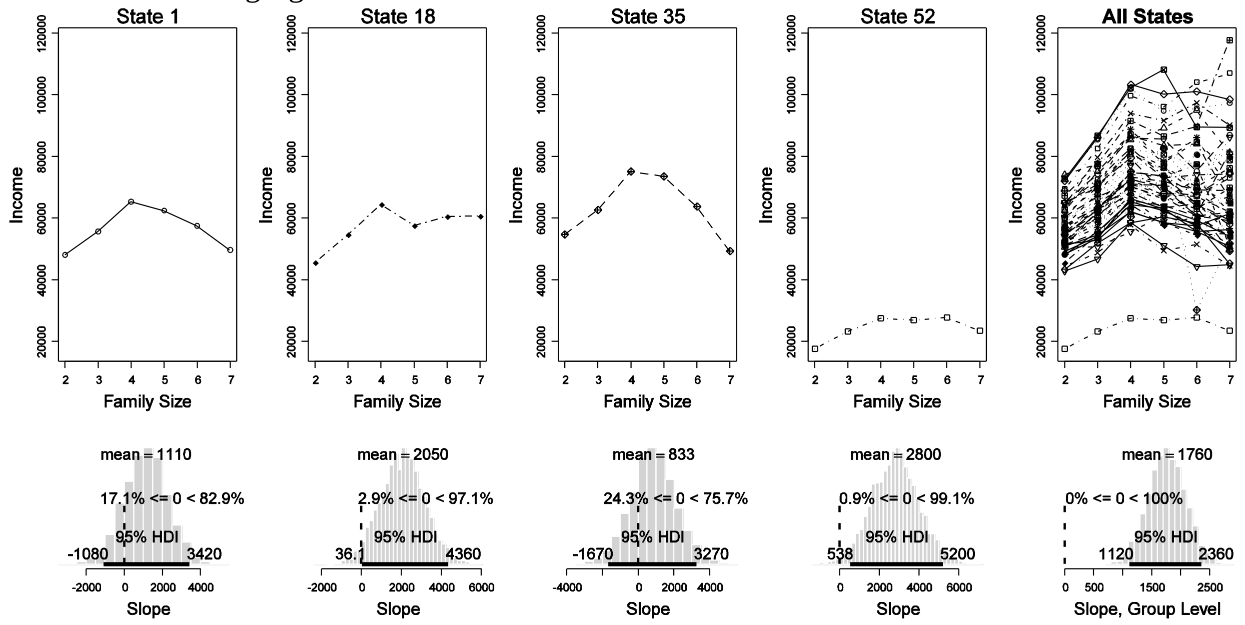
Notice that the group-level intercept (vertical axis) is much more uncertain in the intercept-altered data.

Exercise 16.3. [Purpose: To observe real data for repeated measures of individual regression, with an outlying individual and nonlinear trend.] Suppose we are interested in whether families with more members have higher incomes. The U.S. Census Bureau has published data that indicate the median family income as a function of number of persons

in the family, for all 50 states and the District of Columbia and Puerto Rico. The data are plotted in Figure 16.14.

(A) Run the program of Section 16.5.3 (SimpleLinearRegressionRepeatedBrugs.R) with the income data. Examine the data section of the program, and you will find that the necessary lines of code are already available. The program should generate a figure much like Figure 16.14, p. 451.

Here is the resulting figure:



For lack of space, the figure does not plot all 52 individual "States" (50 States plus D.C. and Puerto Rico).

(B) There is suggestion of outliers in these data. One curve (for Puerto Rico) falls barely above 20,000, which is far lower than all the others. This suggests an outlier for the distribution of intercepts. Some single data points fall far from the individual linear trends. For example, the six-person family in the District of Columbia has an income of only about 30,000, whereas the five-person family has an income of more than 80,000. This suggests an outlier for points around linear trends. Finally, some individual slopes might seem quite steep compared to others. For example, the income in Hawaii rises about $50,000 from twoperson to seven-person families. This increase might or might not be an outlier relative to other states. Which distributions in the hierarchical model of Figure 16.11 should be changed to t distributions to address these outliers? Change the model specification to accommodate these t distributions. Use the example in Section 16.5.2 (SimpleRobustLinearRegressionBrugs. R) as a guide. Report your model specification in your write-up. Show the posterior estimate of the intercept of Puerto Rico for small-df t bias and for large-df t bias. Show the posterior estimate of the slope of Hawaii for small-df t bias and for large-df t bias.

The low curve suggests that the subject intercepts, b0[s], have an outlier and could use a t distributed prior. The outlying single data point suggests that the single data points, y[r], could use a t distributed likelihood. And the outlying slope suggests that subject slopes, b1[s], could use a t distributed prior. Therefore, the parameters that were originally given normal priors, as

```
  y[r] ~ dnorm( mu[r] , tau[ subj[r] ])
  b0[s] ~ dnorm( mu0G , tau0G )
  b1[s] ~ dnorm( mu1G , tau1G )
```

should be changed to

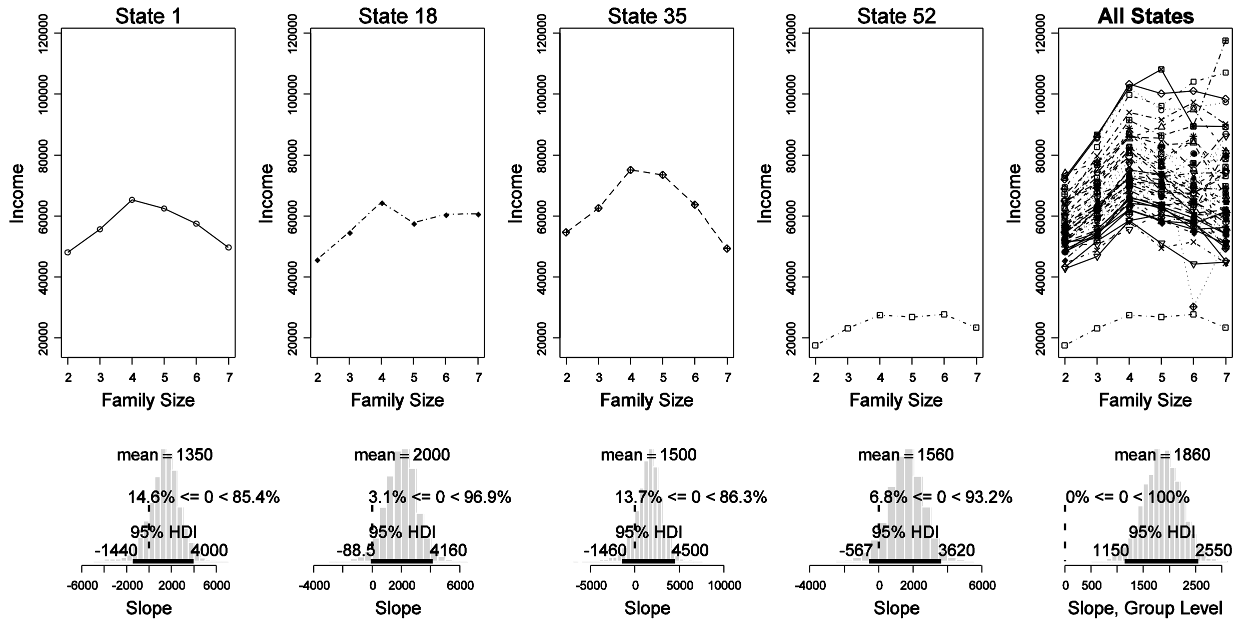
```
  y[r] ~ dt( mu[r] , tau[subj[r]] , tdf )
  b0[s] ~ dt( mu0G , tau0G , tdf )
  b1[s] ~ dt( mu1G , tau1G , tdf )
```

with

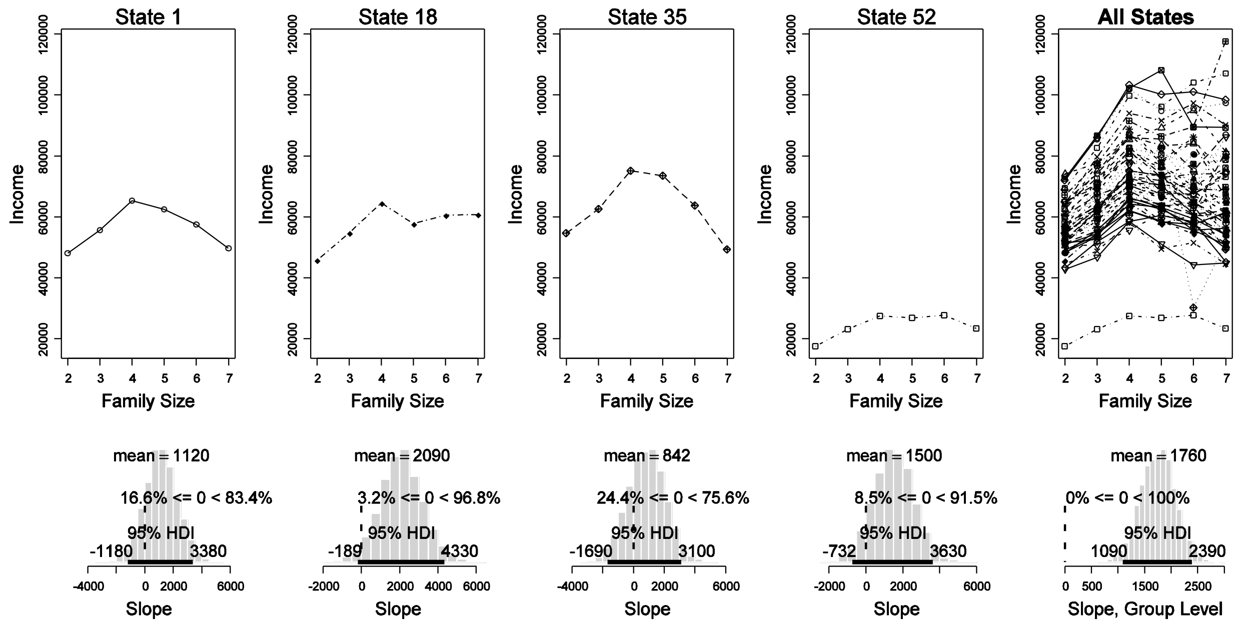
```
  tdf <- 2 # for low, or 100 for high
```

The specific tdf values could be different, or even specified with a hyperdistribution that favors small or large values.

When tdf=2, the result looks like this:



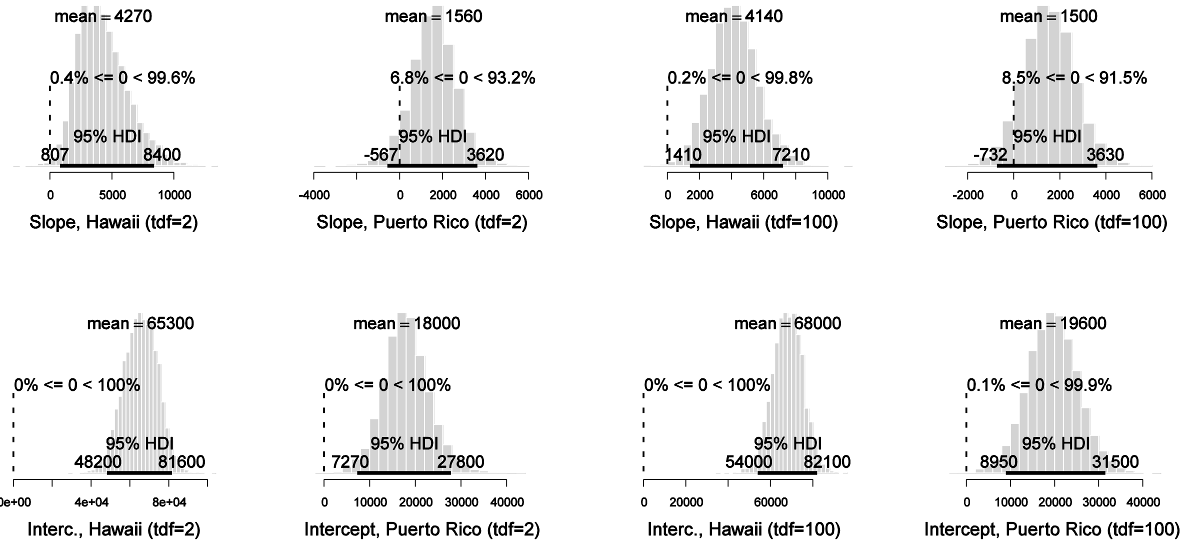
For tdf=100, the results look like this:



To answer the specific questions about Hawaii and Puerto Rico, we need to determine the index value of those states. Then we can plot the relevant parameter values. One way to do that appears below (this code is appended to the end of the program):

```
windows()
layout( matrix( 1:4 , nrow=2 ) )
# Hawaii:
HawaiiIdx = which( unique(dataMat[,"State"]) == "Hawaii" )
histInfo = plotPost( b1samp[HawaiiIdx,] , xlab=paste("Slope, Hawaii (tdf=",tdf,")",sep="") ,
               compVal=0.0 , breaks=30 )
histInfo = plotPost( b0samp[HawaiiIdx,] , xlab=paste("Interc., Hawaii (tdf=",tdf,")",sep="") ,
               compVal=0.0 , breaks=30 )
# Puerto Rico:
PRIdx = which( unique(dataMat[,"State"]) == "Puerto Rico" )
histInfo = plotPost( b1samp[PRIdx,] , xlab=paste("Slope, Puerto Rico (tdf=",tdf,")",sep="") ,
               compVal=0 , breaks=30 )
histInfo = plotPost( b0samp[PRIdx,] , xlab=paste("Intercept, Puerto Rico (tdf=",tdf,")",sep="") ,
               compVal=0 , breaks=30 )
```

The resulting histograms look like the following:



The results for tdf=2 are on the left, and the results for tdf=100 are on the right. Notice that the mean credible slope for Hawaii is steeper (farther from the group mean slope) when tdf=2, and the mean credible intercept for Puerto Rico is smaller (farther from the group mean intercept) when tdf=2. In other words, there appears to be less shrinkage of outliers when tdf=2 than when tdf=100.

(C) The data also suggest a nonlinear trend in the data. Incomes appear to rise for two-, three-, and four-person families, but they then level off and decline as family size gets larger. Include in the original (non-t) model another term that can capture "quadratic curvature" in the income level … . The prior on b2 is analogous to the prior on b1. Is the group-average estimate of curvature credibly nonzero?

Here's the model statement. The new parts are in bold font.

```
model {
    for( r in 1 : Ndata ) {
        y[r] ~ dnorm( mu[r] , tau[ subj[r] ] )
        mu[r] <- b0[subj[r]] + b1[subj[r]] * x[r] + b2[subj[r]] * pow(x[r],2)
    }
    for ( s in 1 : Nsubj ) {
        b0[s] ~ dnorm( mu0G , tau0G )
        b1[s] ~ dnorm( mu1G , tau1G )
        b2[s] ~ dnorm( mu2G , tau2G )
        tau[s] ~ dgamma( sG , rG )
    }
    mu0G ~ dnorm(0,.01)
    tau0G ~ dgamma(.1,.1)
    mu1G ~ dnorm(0,.01)
    tau1G ~ dgamma(.1,.1)
    mu2G ~ dnorm(0,.01)
    tau2G ~ dgamma(.1,.1)
    sG <- pow(m,2)/pow(d,2)
    rG <- m/pow(d,2)
    m ~ dgamma(1,.1)
    d ~ dgamma(1,.1)
}
```

The model must also be initialized with the new variables. Although there is a simple way to get R's lm() function to do regression on quadratic terms, that's not the purpose of this exercise, and so we'll do lazy initialization and let burn-in do the work of finding the posterior.

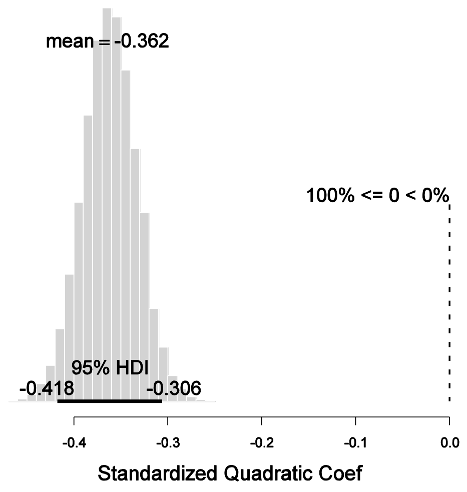
```
genInitList <- function() {
    b0 = b1 = tau = rep(0,length=Nsubj)
    for ( sIdx in 1:Nsubj ) {
       yVec = datalist$y[datalist$subj==sIdx]
       xVec = datalist$x[datalist$subj==sIdx]
       lmInfo = lm( yVec ~ xVec )
       b0[sIdx] = lmInfo$coef[1]
       b1[sIdx] = lmInfo$coef[2]
       tau[sIdx] = length(yVec) / sum(lmInfo$res^2)
    }
    mu0G = mean(b0)
    tau0G = 1/sd(b0)^2
    mu1G = mean(b1)
    tau1G = 1/sd(b1)^2
    m = mean(tau)
    d = sd(tau)
    list( b0=b0 , b1=b1 ,
          b2=0*b1 , # lazy
          tau=tau ,
          mu0G=mu0G , tau0G=tau0G ,
          mu1G=mu1G , tau1G=tau1G ,
          mu2G=0 , tau2G=.5*tau1G , # lazy
          m=m , d=d )
}
for ( chainIdx in 1 : nchain ) {
    modelInits( bugsInits( genInitList ) )
}
```

The new variables must also be monitored and extracted:

```
samplesSet( c( "b0","b1","b2","tau" , "mu0G","tau0G", "mu1G","tau1G", "mu2G","tau2G",
"m","d" ) )
…
zmu2Gsamp = samplesSample( "mu2G" )
```

The resulting posterior on mu2G looks like this:

```
histInfo = plotPost( zmu2Gsamp , xlab="Standardized Quadratic Coef" ,
compVal=0 , breaks=30 )
```



Thus, there does indeed appear to be a credible quadratic trend, on average, across the 52 states.

Chapter 17.

Exercise 17.1. [Purpose: To view the prior on the regression coefficients, when there is a hyperprior.] The hyperprior on regression coefficients in Figure 17.6 may be difficult to intuit. Therefore, generate graphs of the prior distribution on the regression coefficients for the program in Section 17.5.2 (MultiLinRegressHyperBrugs.R), when tdf is set at different values. To accomplish this, do the following: … Run the program and display the prior for tdfBgain=1 and for tdfBgain=100. Point out and discuss any differences in the priors for those different hyperprior constants.

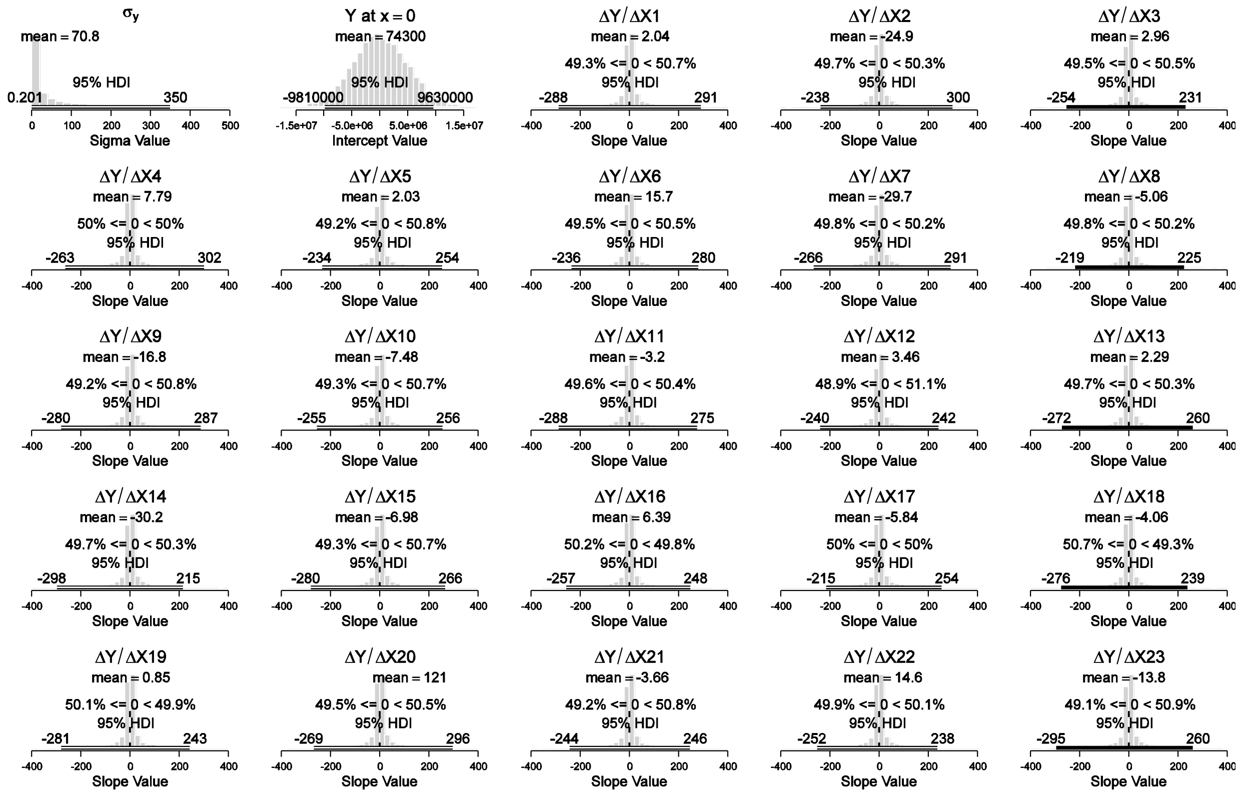
Please note that the suggested change for the plotting limits is appropriate for the randomly generated data.

The changes to the code are listed here:

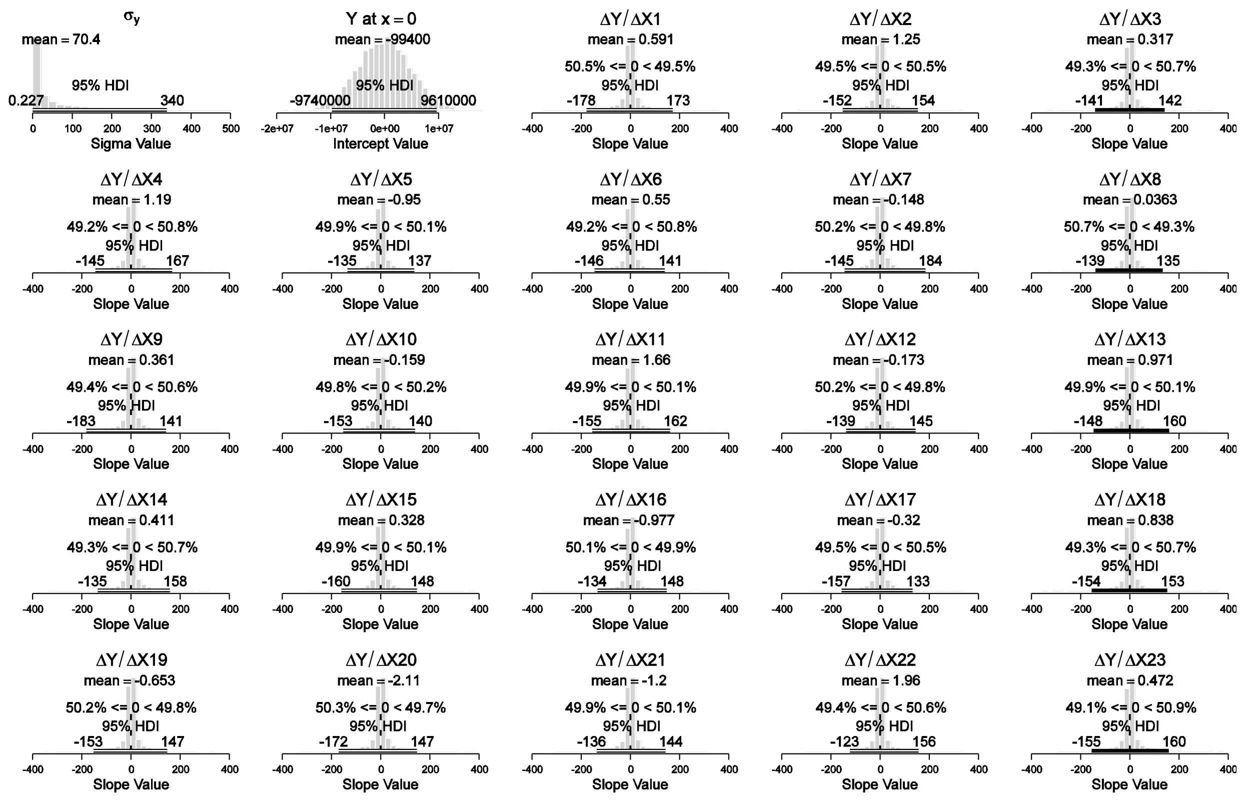
```
model {
    for( i in 1 : nData ) {
        y[i] ~ dnorm( mu[i] , tau )
        mu[i] <- b0 + inprod( b[] , x[i,] )
    }
    tau ~ dgamma(.01,.01)I(0.0001,10000)
    b0 ~ dnorm(0,1.0E-12)
    for ( j in 1:nPredictors ) {
        b[j] ~ dt( muB , tauB , tdfB )
    }
    muB ~ dnorm( 0 , .100 )
    tauB ~ dgamma(.01,.01)I(0.0001,10000)
    udfB ~ dunif(0,1)
    tdfB <- 1 + tdfBgain * ( -log( 1 - udfB ) )
}

…

tdfBgain = 100 # or 1

…

datalist = list(
           x = zx ,
#           y = as.vector( zy ) ,
           nPredictors = nPredictors ,
           nData = nData ,
           tdfBgain = tdfBgain
)

…


#genInitList <- function(nPred=nPredictors) {
#    lmInfo = lm( y ~ x ) # R function returns least-squares (normal MLE) fit.
#    bInit = lmInfo$coef[-1] * apply(x,2,sd) / sd(y)
#    tauInit = (length(y)*sd(y)^2)/sum(lmInfo$res^2)
#    list(
#        b0 = 0 ,
#        b = bInit ,
#        tau = tauInit ,
#        muB =  mean( bInit ) ,
#        tauB = 1 / sd( bInit )^2 ,
#        udfB = 0.95 # tdfB = 4
#    )
#}
#for ( chainIdx in 1 : nChain ) {
#    modelInits( bugsInits( genInitList ) )
#}

modelGenInits()

…

checkConvergence = F
if ( checkConvergence ) {
  b0Sum  = plotChains( "b0"  , saveplots=F , filenameroot=fname )
  bSum   = plotChains( "b"   , saveplots=F , filenameroot=fname )
  tauSum = plotChains( "tau" , saveplots=F , filenameroot=fname )
  muBSum = plotChains( "muB" , saveplots=F , filenameroot=fname )
  tauBSum = plotChains( "tauB" , saveplots=F , filenameroot=fname )
  tdfBSum = plotChains( "tdfB" , saveplots=F , filenameroot=fname )
}

…

# Display the posterior:
nPlotPerRow = 5
nPlotRow = ceiling((2+nPredictors)/nPlotPerRow)
nPlotCol = ceiling((2+nPredictors)/nPlotRow)
windows(3.5*nPlotCol,2.25*nPlotRow)
layout( matrix(1:(nPlotRow*nPlotCol),nrow=nPlotRow,ncol=nPlotCol,byrow=T) )
par( mar=c(4,3,2.5,0) , mgp=c(2,0.7,0) )
histInfo = plotPost( sigmaSamp , xlab="Sigma Value" , compVal=NULL ,
                     breaks=30 , main=bquote(sigma[y]) ,
                     cex.main=1.67 , cex.lab=1.33 )
histInfo = plotPost( b0Samp , xlab="Intercept Value" , compVal=NULL ,
                     breaks=30 , main=bquote(.(predictedName) *" at "* x==0) ,
                     cex.main=1.67 , cex.lab=1.33 )
for ( sIdx in 1:nPredictors ) {
histInfo = plotPost( bSamp[,sIdx] , xlab="Slope Value" , compVal=0.0 ,
                     breaks=c(-1000000,seq(-400,400,21),1000000) , xlim=c(-400,400) ,
                     main=bquote( Delta * .(predictedName) /
                                  Delta * .(predictorNames[sIdx]) ) ,
                     cex.main=1.67 , cex.lab=1.33 )
}
```

Please note that the suggested change for the plotting limits is appropriate for the randomly generated data.

The posterior for tdfBgain=1 looks like this:



The posterior for tdfBgain=100 looks like the following. *Notice that the 95%HDI on the slopes extends from roughly -150 to +150, which is much less than when tdfBgain=1 (above).* The means of the intercept and slope are all very close to zero relative to the widths of the distributions. The means are thrown off from zero because there are some extreme outliers in these prior distributions.



Notice that for either prior, the priors distributions are *extremely* broad compared to the posteriors displayed in Figure 17.7 (pp. 465-466) of the textbook. Thus, these priors are very vague indeed.

Exercise 17.2. [Purpose: To conduct a power analysis for multiple regression.] Consider the SAT data shown in Figure 17.3, p. 457, and the posterior for a linear regression model (with no interaction) shown in Figure 17.5, p. 461. The marginal posterior distribution for the slope on spending per pupil has a 95% HDI that excludes zero, and has a width of very nearly 17. Consider two different goals for the research. One goal is to show that the 95% HDI on spending per pupil excludes a ROPE of [-1,+1], and the second goal is to show that the width of the 95% HDI is less than 10. … Answer these questions:

What is the retrospective power for each of the two goals? (Hint: It's about 0.67 and 0.00, when the x points are randomly sampled with replacement from the 50 actual points.)

The hint gives the answer. You need to show how to get the answer. Here's the code:

```
GoalAchievedForSample = function( xOrig , yOrig , plotResults=F ,
                                  fileNameRoot="DeleteMe" ) {
fname=fileNameRoot

library(BRugs)

#------------------------------------------------------------------------------
# THE MODEL.
```

```
modelstring = "
# BUGS model specification begins here...
model {
    for( i in 1 : nData ) {
        y[i] ~ dnorm( mu[i] , tau )
        mu[i] <- b0 + inprod( b[] , x[i,] )
    }
    tau ~ dgamma(.01,.01)
    b0 ~ dnorm(0,1.0E-12)
    for ( j in 1:nPredictors ) {
        b[j] ~ dnorm(0,1.0E-12)
    }
}
# ... end BUGS model specification
" # close quote for modelstring
writeLines(modelstring,con="model.txt")
modelCheck( "model.txt" )

#------------------------------------------------------------------------------
# THE DATA.
# Takes raw data as input so that program can convert back to original scale,
# and goals can be expressed on original scale.

nPredictors = NCOL(xOrig)
nData = NROW(xOrig)

# Re-center data at mean, to reduce autocorrelation in MCMC sampling.
# Standardize (divide by SD) to make prior specification easier.
standardizeCols = function( dataMat ) {
    zDataMat = dataMat
    for ( colIdx in 1:NCOL( dataMat ) ) {
        mCol = mean( dataMat[,colIdx] )
        sdCol = sd( dataMat[,colIdx] )
        zDataMat[,colIdx] = ( dataMat[,colIdx] - mCol ) / sdCol
    }
    return( zDataMat )
}
zx = standardizeCols( xOrig )
zy = standardizeCols( yOrig )

# Get the data into BUGS:
datalist = list(
           x = zx ,
           y = as.vector( zy ) , # BUGS does not treat 1-column mat as vector
           nPredictors = nPredictors ,
           nData = nData
)
modelData( bugsData( datalist ) )

#------------------------------------------------------------------------------
# INTIALIZE THE CHAINS.

nChain = 3
modelCompile( numChains = nChain )

genInitList <- function(nPred=nPredictors) {
    lmInfo = lm( datalist$y ~ datalist$x ) # R function returns MLE
    bInit = lmInfo$coef[-1]
    tauInit = length(datalist$y) / sum(lmInfo$res^2)
    list(
        b0 = 0 ,
        b = bInit ,
        tau = tauInit
    )
}
for ( chainIdx in 1 : nChain ) {
    modelInits( bugsInits( genInitList ) )
}

#------------------------------------------------------------------------------
# RUN THE CHAINS

# burn in
BurnInSteps = 100
modelUpdate( BurnInSteps )
# actual samples
samplesSet( c( "b0" , "b" , "tau" ) )
stepsPerChain = ceiling(50000/nChain)
thinStep = 2
modelUpdate( stepsPerChain , thin=thinStep )

#------------------------------------------------------------------------------
# EXAMINE THE RESULTS

source("plotPost.R")

# Extract chain values:
zb0Samp = matrix( samplesSample( "b0" ) )
zbSamp = NULL
for ( j in 1:nPredictors ) {
   zbSamp = cbind( zbSamp , samplesSample( paste("b[",j,"]",sep="") ) )
}
zTauSamp = matrix( samplesSample( "tau" ) )
zSigmaSamp = 1 / sqrt( zTauSamp ) # Convert precision to SD
chainLength = length(zTauSamp)

# Convert to original scale:
bSamp = zbSamp * matrix( sd(yOrig)/apply(xOrig,2,sd) , byrow=TRUE ,
                     ncol=nPredictors , nrow=NROW(zbSamp) )
b0Samp = ( zb0Samp * sd(yOrig)
          + mean(yOrig)
          - rowSums( zbSamp
          * matrix( sd(yOrig)/apply(xOrig,2,sd) , byrow=TRUE ,
                    ncol=nPredictors , nrow=NROW(zbSamp) )
          * matrix( apply(xOrig,2,mean) , byrow=TRUE ,
                    ncol=nPredictors , nrow=NROW(zbSamp) ) ) )
sigmaSamp = zSigmaSamp * sd(yOrig)

# Display the posterior:
if ( plotResults ) {
nPlotPerRow = 5
nPlotRow = ceiling((2+nPredictors)/nPlotPerRow)
nPlotCol = ceiling((2+nPredictors)/nPlotRow)
windows(3.5*nPlotCol,2.25*nPlotRow)
layout( matrix(1:(nPlotRow*nPlotCol),nrow=nPlotRow,ncol=nPlotCol,byrow=T) )
par( mar=c(4,3,2.5,0) , mgp=c(2,0.7,0) )
histInfo = plotPost( sigmaSamp , xlab="Sigma Value" , compVal=NULL ,
                     breaks=30 , main=bquote(sigma[y]) ,
                     cex.main=1.67 , cex.lab=1.33 )
histInfo = plotPost( b0Samp , xlab="Intercept Value" , compVal=NULL ,
                     breaks=30 , main=bquote(.(predictedName) *" at "* x==0) ,
                     cex.main=1.67 , cex.lab=1.33 )
for ( sIdx in 1:nPredictors ) {
  histInfo = plotPost( bSamp[,sIdx] , xlab="Slope Value" , compVal=0.0 ,
                       breaks=30 , cex.main=1.67 , cex.lab=1.33 ,
                       main=bquote( Delta * .(predictedName) /
                                    Delta * .(predictorNames[sIdx]) ) )
}
}

#-------------------------------------------------------------------------------

source("HDIofMCMC.R")

# Goal 1 is HDI of b1 excludes ROPE .
# Goal 2 is HDI of b1 has desired precision .
HDIlims = HDIofMCMC( bSamp[,1] )
ROPE = c(-1,1)
goalAch1 = ( HDIlims[1] > ROPE[2] | HDIlims[2] < ROPE[1]  )
#goalAch1 = ( HDIlims[1] > ROPE[2] )  # If you want HDI to fall ABOVE the ROPE
goalAch2 = ( HDIlims[2] - HDIlims[1] < 10 ) # 10
goalAchieved = c( goalAch1 , goalAch2 )

return( goalAchieved )
} # end of function GoalAchievedForSample

#===============================================================================
# Now call the function defined above, using simulated data.

analysisType = c("Retro","Repli")[1] # specify [1] or [2]
fileNameRoot = paste("Exercise17.2",analysisType,sep="")

# Load original data, for use in replication probability analysis:
dataMat = read.table( file="Guber1999data.txt" ,
                      col.names = c( "State","Spend","StuTchRat","Salary",
                                     "PrcntTake","SATV","SATM","SATT") )
predictedName = "SATT"
predictorNames = c( "Spend" , "PrcntTake" )
nData = NROW( dataMat )
yActual = as.matrix( dataMat[,predictedName] )
xActual = as.matrix( dataMat[,predictorNames] )

# Load previously computed posterior chains for parameters
# b0Samp , bSamp , sigmaSamp
load( file="MultipleLinearRegressionBrugsGuber1999.Rdata" )
chainLength = length(b0Samp)

# SPECIFY NUMBER OF (ADDITIONAL) DATA POINTS:
nPts = 50

# Specify number of simulated experiments:
nSimExperiments = min(200,chainLength)
nGoal=2 # Determined in function above.

# If previous record of power estimation exists, load it and continue the runs.
filelist = dir( pattern=paste( fileNameRoot, "N",nPts, "Result.Rdata",
                               sep="") )
if ( length( filelist ) > 0 ) { # if the file already exists...
   # load  previous expIdx, nSuccess
   load(paste(fileNameRoot,"N",nPts,"Result.Rdata",sep=""))
   prevExpIdx = expIdx
   # Use just some of the MCMC steps, distributed among the whole chain:
   chainIdxVec = round(seq(1,chainLength,len=(prevExpIdx+nSimExperiments)))
} else { # ... otherwise, start a new record
  prevExpIdx = 0
  nSuccess = rep(0,nGoal) # Initialize success counter.
  chainIdxVec = round(seq(1,chainLength,len=nSimExperiments))
}
```

```
# Simulated experiment loop begins here:
for ( expIdx in (1+prevExpIdx):(nSimExperiments+prevExpIdx) ) {

    # Generate random data from posterior parameters
    chainIdx=chainIdxVec[expIdx]
    b0 = b0Samp[chainIdx]
    b1 = bSamp[chainIdx,1]
    b2 = bSamp[chainIdx,2]
    sigma = sigmaSamp[chainIdx]
    cat( "b0=",b0, ", b1=",b1, ", b2=",b2, ", sigma=",sigma, "\n")
    flush.console()
    ySim = cbind( rep(0,nPts) )
    xSim = matrix( 0 , nrow=nPts , ncol=NCOL(xActual) )
    for ( ptIdx in 1:nPts ) {
        xIdx = sample( NROW(xActual) , size=1 ) # selects randomly from xActual
        x1 = xActual[xIdx,1]
        x2 = xActual[xIdx,2]
        ySim[ptIdx] = b0 + b1*x1 + b2*x2 + rnorm(1,0,sd=sigma)
        xSim[ptIdx,] = c(x1,x2)
    }
    if ( analysisType == "Repli" ) { # if replication probability
       xSim = rbind( xActual , xSim )
       ySim = rbind( yActual , ySim )
    }

    # Make plots for first 10 simulated experiments:
    if ( expIdx <= 10 ) { plotRes = T } else { plotRes = F }

    # Call BUGS program and tally number of successes:
    nSuccess = ( nSuccess
                 + GoalAchievedForSample( xSim , ySim , plotRes, fileNameRoot ))
    estPower = nSuccess / expIdx
    cat( "\n*** nPts:",nPts, ", nSimExp:",expIdx,
      " , nSuccess:",nSuccess, ", estPower:",round(estPower,2), "\n\n" )
    flush.console()
    save( nSuccess , expIdx , estPower ,
          file=paste(fileNameRoot,"N",nPts,"Result.Rdata",sep="") )

} # end of simulated experiment loop.
```

What is the power for each of the two goals when N = 130? (Hint: It’s about 0.85 and 0.30.)

The hint provides the answer. But your answer should include the number of simulated experiments you ran and the number of times each goal was achieved.

What’s the minimal N needed to achieve a power of 0.80 for the second goal?

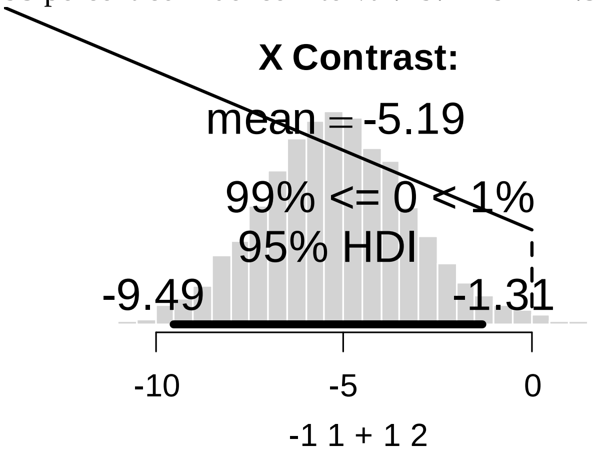
It’s about 180. Again, your answer should include the number of simulated experiments you ran and the number of times each goal was achieved.

Chapter 18.

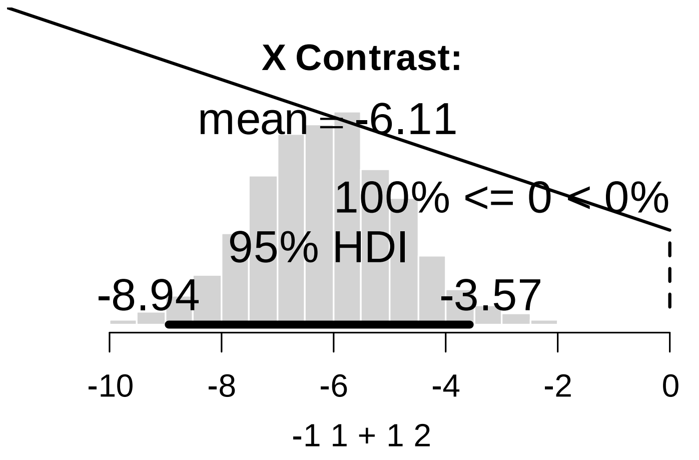
Exercise 18.1. [Purpose: To notice that Bayesian ANOVA with two groups tends to agree with an NHST t test.] The BRugs program of Section 18.4.1 (ANOVAonewayBRugs.R) allows you to specify random data. It executes a Bayesian ANOVA, and at the end of the program it also conducts an NHST ANOVA and t tests (using R's aov and t.test functions). Run the program ten times with different random data by commenting out the set.seed command. Specify ysdtrue = 4.0, atrue = c(2,-2) (which implies two groups because there are two deflections) and npercell = 8. For each run, record, by hand,
(1) how much of the posterior difference between means falls on one side of zero (see the posterior histogram with the main title "X Contrast" and x axis labeled "-1 1 + 1 2"),
(2) whether the 95% HDI excludes zero, and
(3) the confidence interval and p value of the NHST t test.
Do the t test and the BANOVA usually agree in their decisions about whether the group means are different?

Here are results from 10 runs. The t-test is shown first, followed by the Bayesian posterior. Your results may differ, because the data are randomly generated.

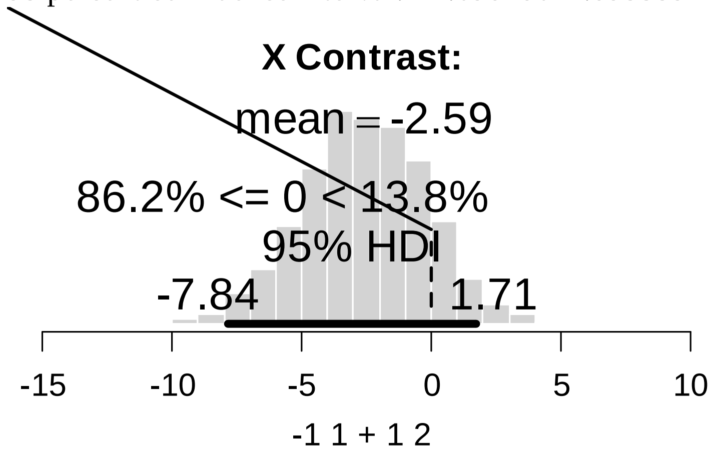
1. M2-M1 = -5.410669
t = -3.0047, df = 14, p-value = 0.009464
95 percent confidence interval: -9.272914 -1.548425



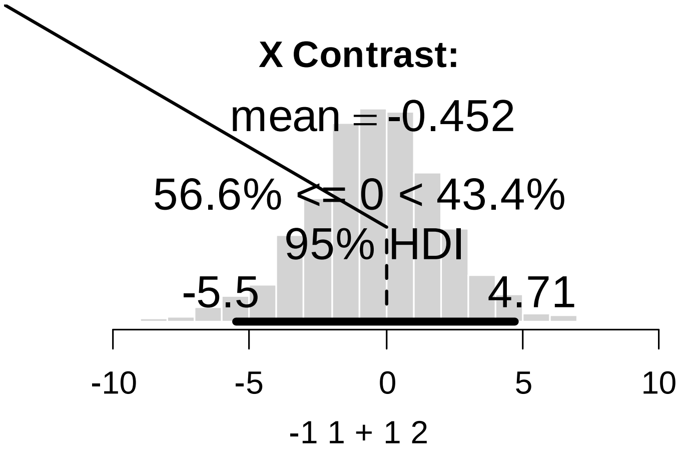
2. M2-M1 = -6.222964
t = -5.1686, df = 14, p-value = 0.0001426
95 percent confidence interval: -8.805289 -3.640639



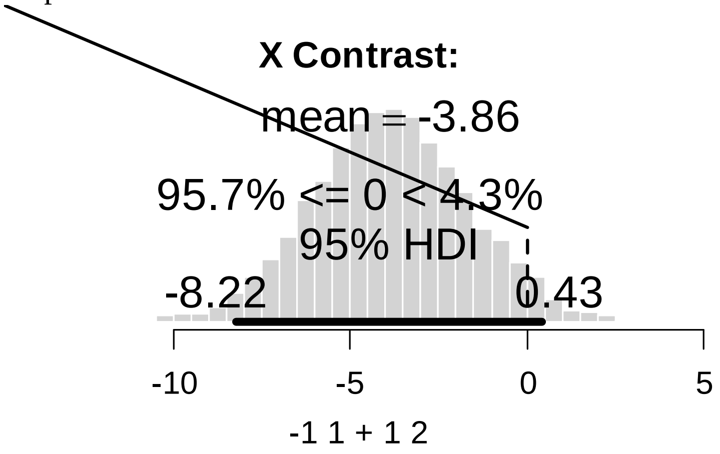
3. M2-M1 = -2.902464
t = -1.298, df = 14, p-value = 0.2153
95 percent confidence interval: -7.698286 1.893359



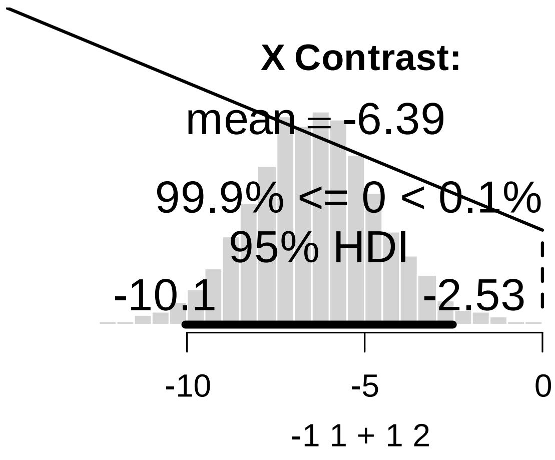
4. M2-M1 = -0.5305656
t = -0.222, df = 14, p-value = 0.8275
95 percent confidence interval: -5.657225 4.596094



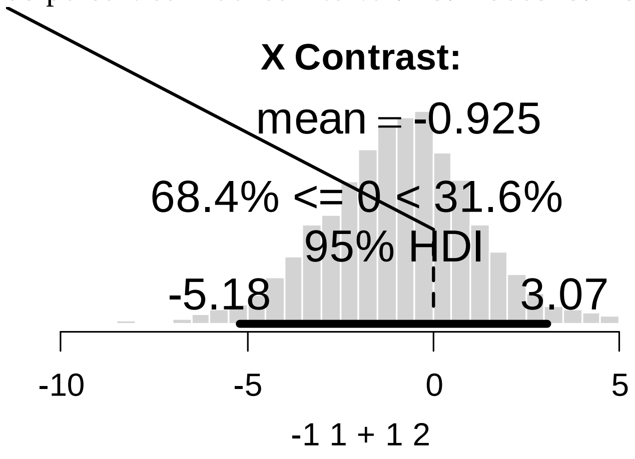
5. M2-M1 = -4.198784
t = -2.115, df = 14, p-value = 0.05284
95 percent confidence interval: -8.45665094 0.05908298



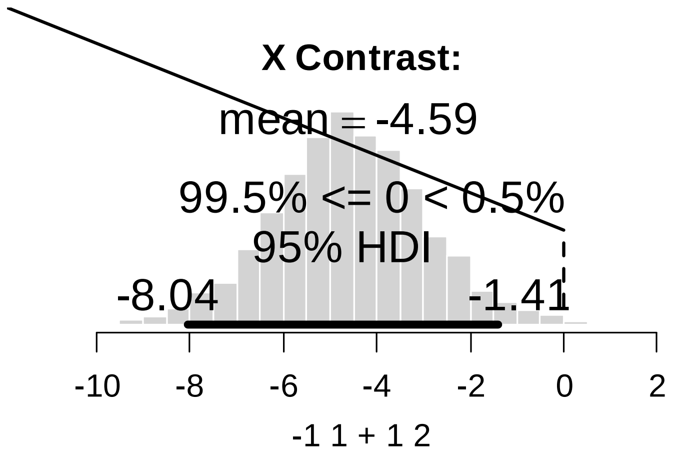
6. M2-M1 = -6.570604
t = -4.0425, df = 14, p-value = 0.001211
95 percent confidence interval: -10.056668 -3.084539



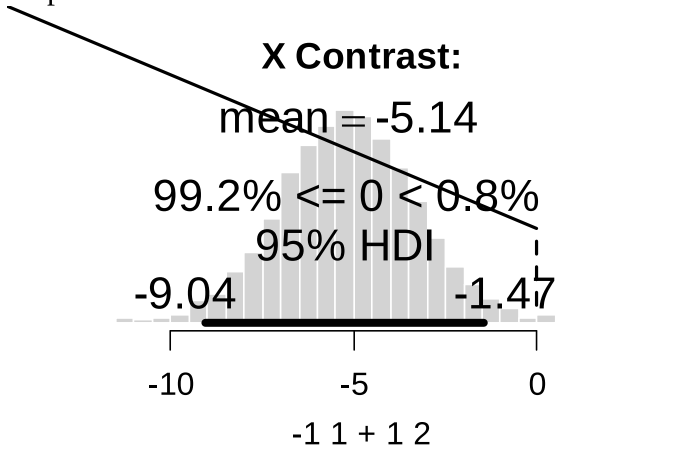
7. M2-M1 = -1.071621
t = -0.5287, df = 14, p-value = 0.6053
95 percent confidence interval: -5.418663 3.275421



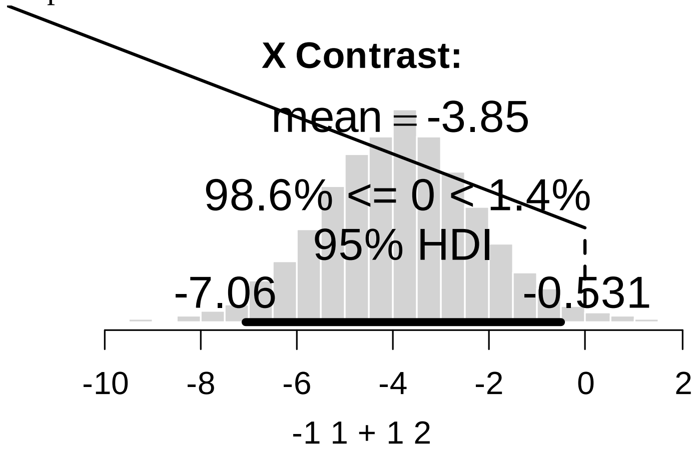
8. M2-M1 = -4.763127
t = -3.3178, df = 14, p-value = 0.005079
95 percent confidence interval: -7.842266 -1.683988



9. M2-M1 = -5.308085
t = -3.2347, df = 14, p-value = 0.005993
95 percent confidence interval: -8.827658 -1.788511



10. M2-M1 = -4.022563
t = -2.7984, df = 14, p-value = 0.01422
95 percent confidence interval: -7.105540 -0.939587



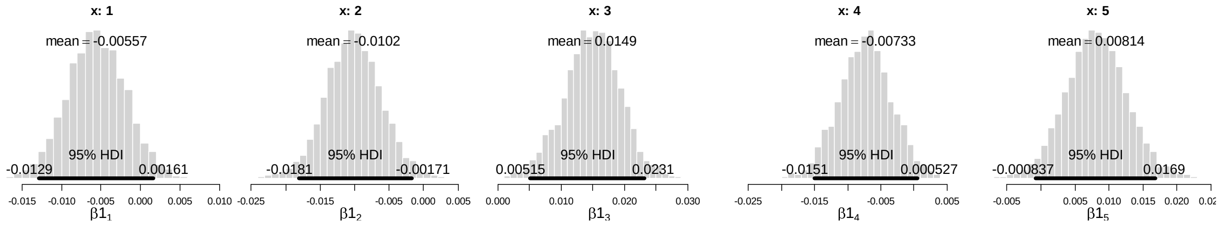
In all ten cases, the conclusion regarding the null value is the same for the t-test and the Bayesian HDI. Typically, the 95%HDI is a bit more conservative, i.e., wider, than the 95% confidence interval. The Bayesian conclusion comes without ever computing a *p* value.

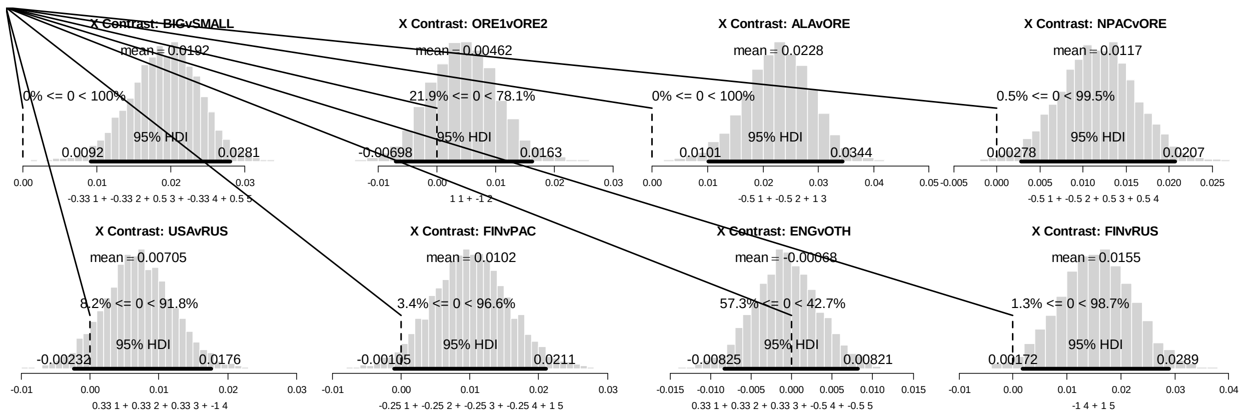
Exercise 18.2. [Purpose: To understand the influence of the prior in Bayesian ANOVA.] In the model section of the BRugs program of Section 18.4.1 (ANOVAonewayBRugs.R), and correspondingly in the diagram of Figure 18.1, there are several constants that determine the prior. These constants include the mean value of the baseline (M0 in the diagram), the precision on the baseline (T0 in the diagram), the precision of the folded-t distribution (Tt in the diagram), and the upper value of the uniform distribution on y (Hy in the diagram). Because the data are standardized, M0 should be set at zero, and T0 can be modest (not terribly small). Hy also can be set to a modest value because the data are standardized. But what about the precision of the folded-t distribution, Tt? This constant modulates the degree of shrinkage: A large value of Tt indicates prior knowledge that the groups do not differ much, and it imposes a high degree of shrinkage that must be overcome by the data. Run the program on the mussel data using a small value of Tt , such as 1.0E-6, and a large value of Tt , such as 1000. Are the results very different? Discuss which prior value might be appropriate.

Using a small precision on Tt:

```
model {
  for ( i in 1:Ntotal ) {
    y[i] ~ dnorm( mu[i] , tau )
    mu[i] <- a0 + a[x[i]]
  }
  #
  tau <- pow( sigma , -2 )
  sigma ~ dunif(0,10) # y values are assumed to be standardized
  #
  a0 ~ dnorm(0,0.001) # y values are assumed to be standardized
  #
  for ( j in 1:NxLvl ) { a[j] ~ dnorm( 0.0 , atau ) }
  atau <- 1 / pow( aSD , 2 )
  aSD <- abs( aSDunabs ) + .1
  aSDunabs ~ dt( 0 , 1.0E-6 , 2 )
}
```

yields

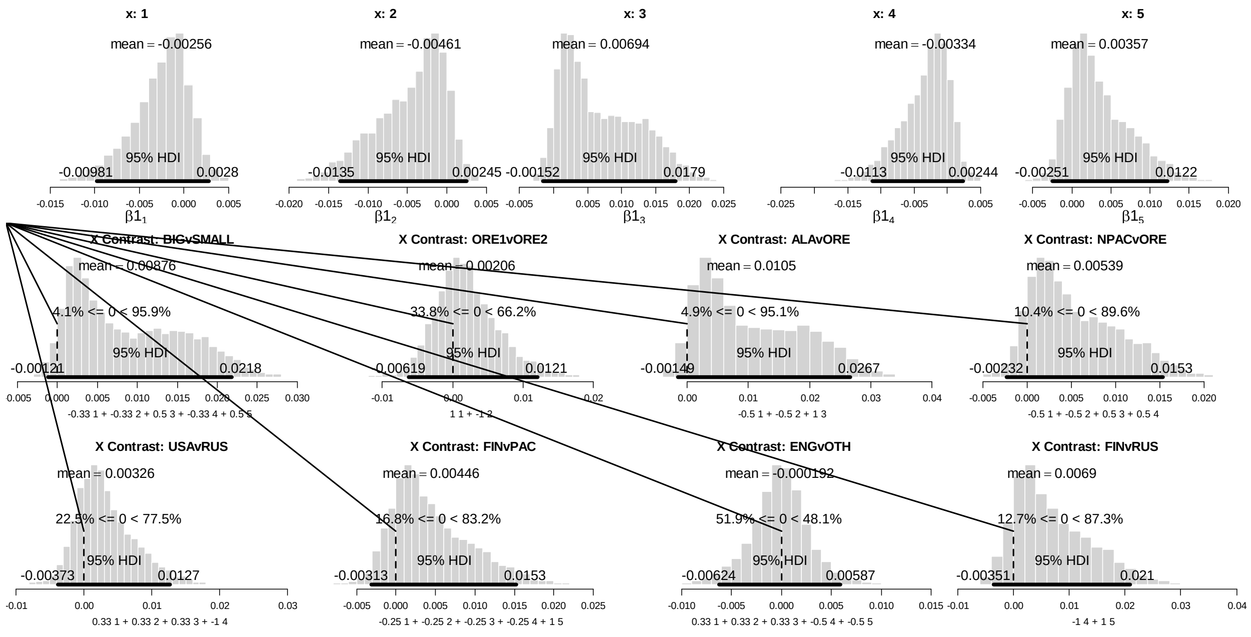




Using a large precision on Tt:

```
  aSDunabs ~ dt( 0 , 1000 , 2 )
```

yields



The results are dramatically different. In particular, the extremely large precision in the prior essentially insists that there is no variation between groups, and therefore the credible group deflections are all near zero, and therefore the differences between groups are all near zero.

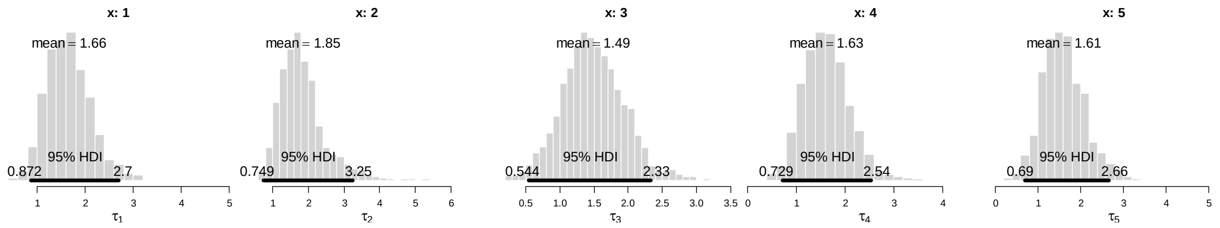
The low-precision prior is much more appropriate here, unless for some reason we really do have an extremely strong prior belief that there can be no differences between groups. In that case, it would take an enormous sample size to overcome the prior.

Exercise 18.3. [Purpose: To understand Bayesian ANOVA without assuming equal variances.] Modify the program in Section 18.4.1 (ANOVAonewayBRugs.R) so that it allows a different variance for each group, with the different variances coming from a hyperdistribution that has its precision informed by the data. In other words, instead of assuming the same tauy for all the levels of x, we allow each group to have its own variance. Denote the precision of the jth group as tauj, analogous to the deflection betaj. Just as the group deflections are assumed to come from a higher-level distribution, we will assume that the group SDs come from a higher-level distribution. Because SDs must be non-negative, use a gamma density for the higher-level distribution. The gamma distribution has two parameters for which you need to establish a prior. See the right side of Figure 16.11 for guidance. Corresponding code is offered in a hint, below. Run the program on the mussel muscle data. Are the conclusions about the group means any different than when assuming equal variances across groups?

Hint regarding the conclusion: The posteriors on the group means are only a little different in this case, because the group variances are roughly the same. But because the group variances are less constrained when they are all allowed to be different, they are less certain. Therefore, the group means are a little less certain, and thus the differences of means are a little less certain.

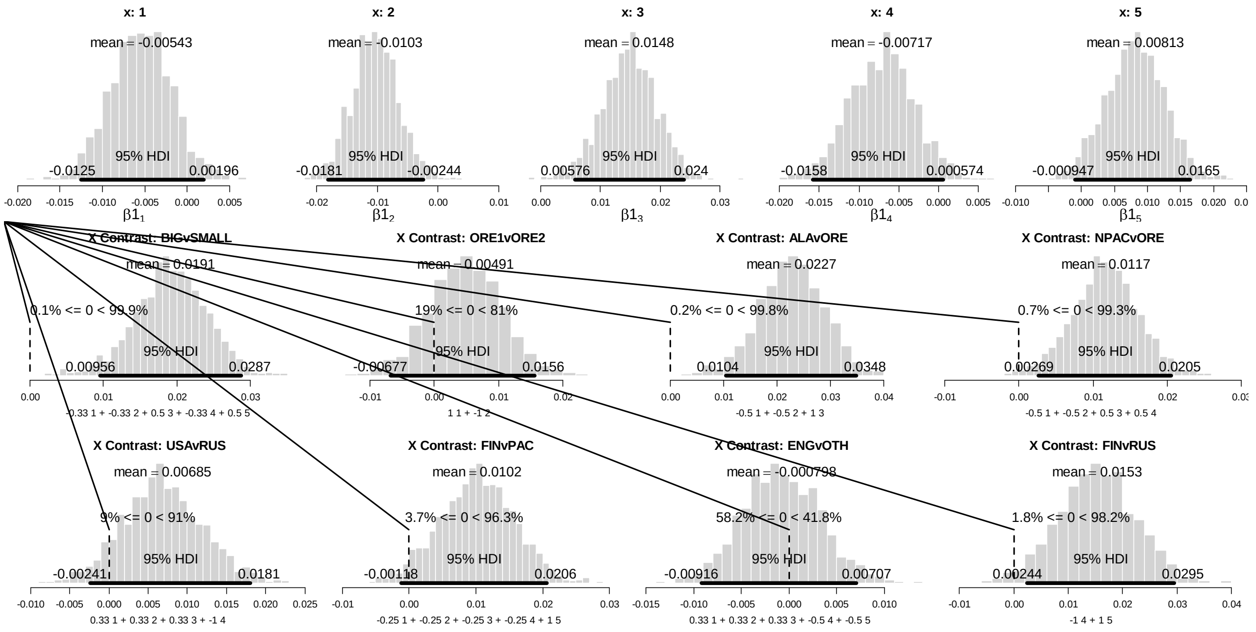
```
model {
  for ( i in 1:Ntotal ) {
    y[i] ~ dnorm( mu[i] , tau[x[i]] )
    mu[i] <- a0 + a[x[i]]
  }
  a0 ~ dnorm(0,0.001)
  for ( j in 1:NxLvl ) {
     a[j] ~ dnorm( 0.0 , atau )
     tau[j] ~ dgamma( sG , rG )
  }
  sG <- pow(m,2)/pow(d,2)
  rG <- m/pow(d,2)
  m ~ dgamma(1,1)
  d ~ dgamma(1,1)
  atau <- 1 / pow( aSD , 2 )
  aSD <- abs( aSDunabs ) + .1
  aSDunabs ~ dt( 0 , 0.001 , 2 )
}

…

  theData = data.frame( y=datalist$y , x=factor(x,labels=xnames) )
  a0 = mean( theData$y )
  a = aggregate( theData$y , list( theData$x ) , mean )[,2] - a0
  tau = 1/(aggregate( theData$y , list( theData$x ) , sd )[,2])^2
  genInitList <- function() {
    return(
        list(
            a0 = a0 ,
            a = a ,
            tau = tau ,
            m = mean( tau ) ,
            d = sd( tau ) ,
            aSDunabs = sd(a)
        )
    )
  }
  for ( chainIdx in 1 : nchain ) {
    modelInits( bugsInits( genInitList ) )
  }
```

Here are the posterior tau values:



They are fairly homogeneous because the groups happen to have similar SDs for these data.

Here are the posterior group deflections and contrasts:



They do not differ much from the homogeneous-variance results (Figure 18.2, p. 498 of the textbook) because there is not much heterogeneity of variance. The group deflections are, however, slightly less deviant from zero, and their HDIs are slightly wider. This is caused by the larger freedom (uncertainty) in the group precisions allowing larger uncertainty in the group deflections.

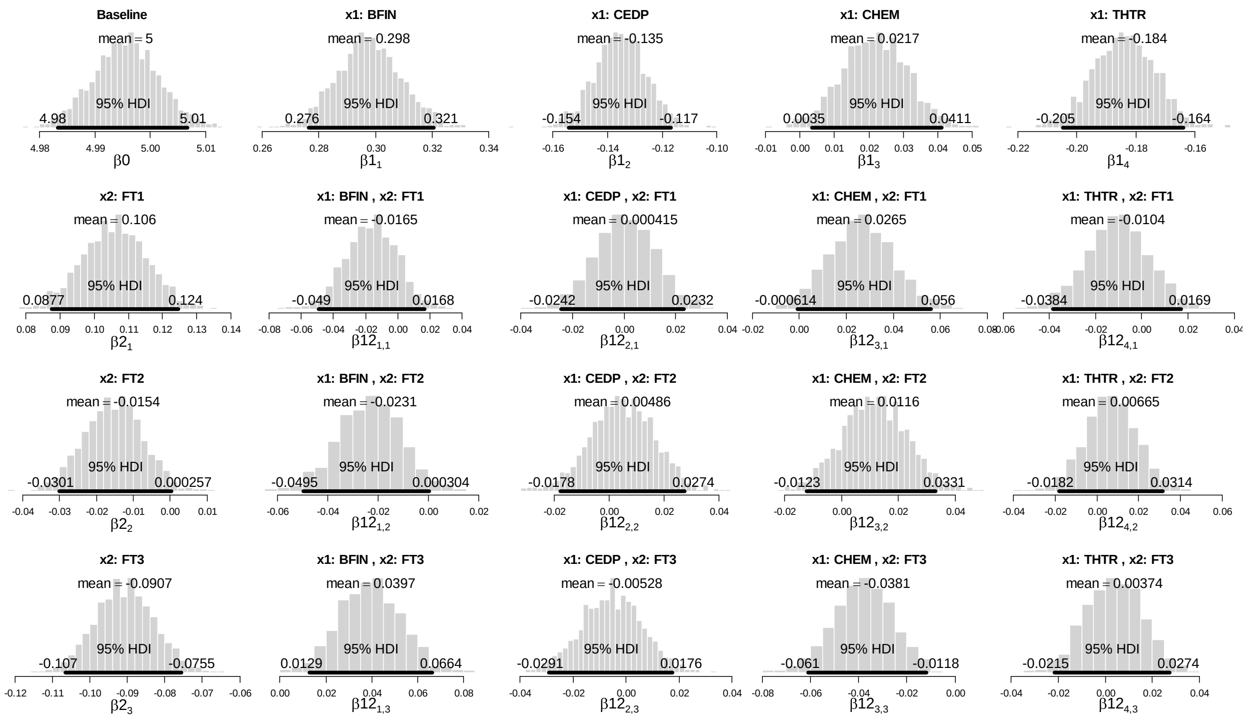
Chapter 19.

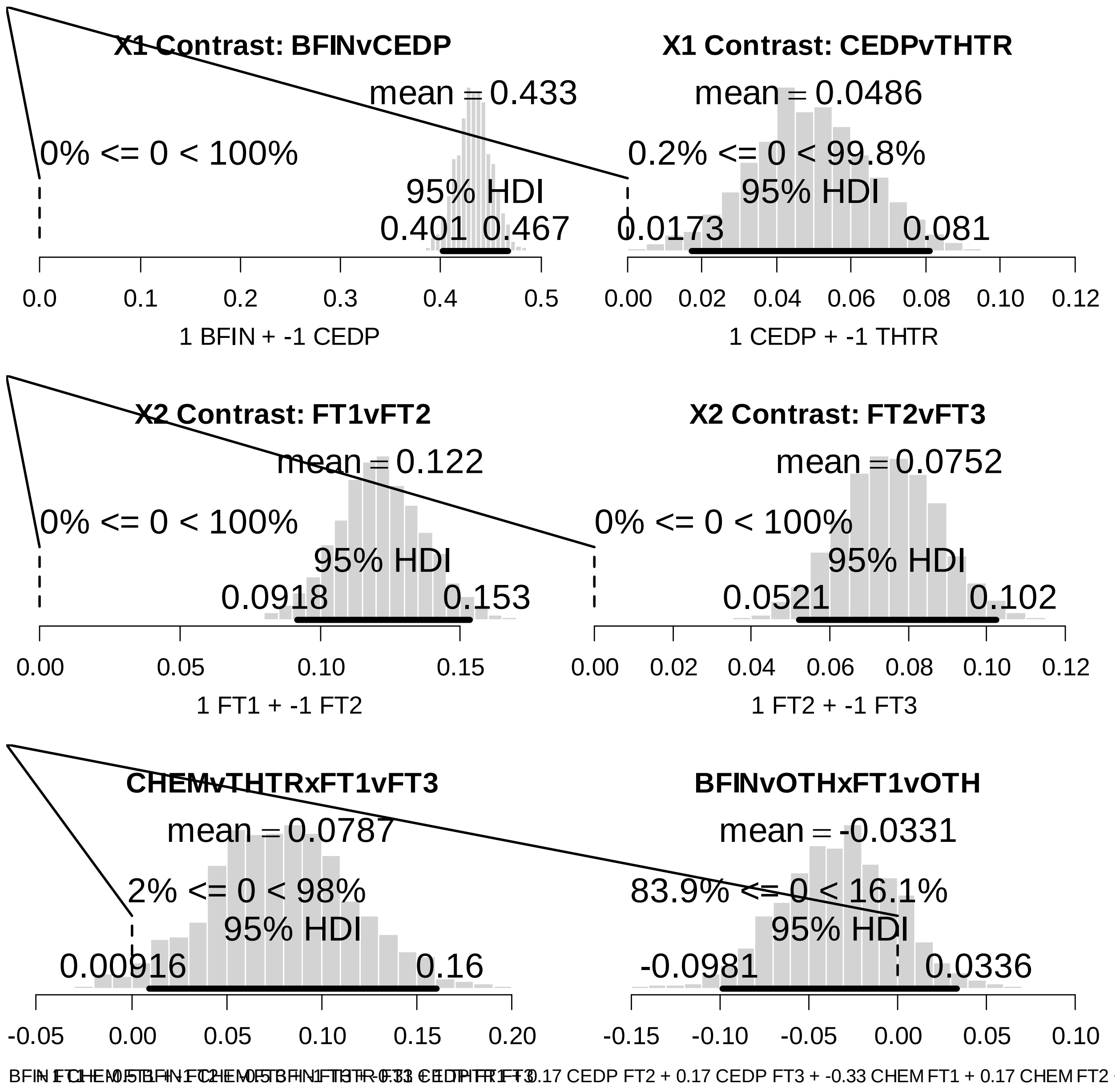
Exercise 19.1. [Purpose: To inspect an interaction for transformed data.] Consider the data plotted in Figure 19.3, p. 521.

(A) Is the interaction a crossover interaction or not? Briefly explain your answer.

The interaction is not a crossover interaction. The reason is that the ordering of levels on one factor is always the same at any level of the other factor. Specifically, the ordering of departments (x1) is THTR, CEDP, CHEM, BFIN at every level of seniority (x2). And, the ordering of seniority is FT3, FT2, FT1 in every department.

(B) Suppose we are interested in salaries thought of in terms of percentage (i.e., ratio) differences rather than additive differences. Therefore we take the logarithm, base 10, of the individual salaries (the R code has this option built into to the data section, where the salary data are loaded). Run the analysis on the transformed data, producing the results and contrasts analogous to those in Figures 19.4 and 19.5. Do any of the conclusions change?



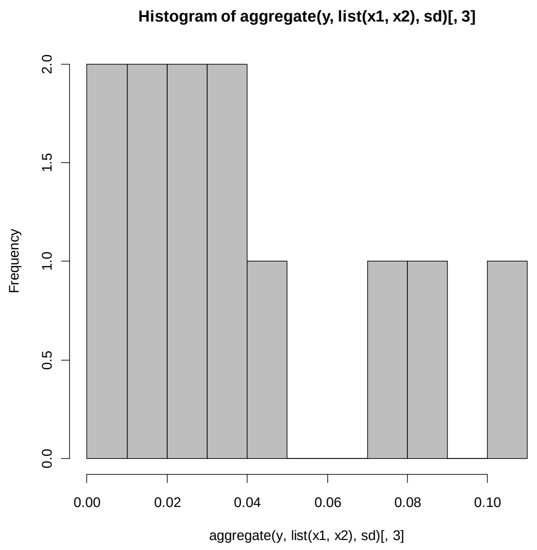


In terms of contrasts excluding zero, only one conclusion changes: For the logarithmic data, the contrast of CEDP vs THTR now excludes zero, whereas it did not for the original data (see top right of Figure 19.5, p. 524 of textbook).

(C) Examine the within-cell variances in the original and in the transformed data. (Hint: Try using the aggregate function on the data. As a guide, see how the function is used to initialize a1a2. Instead of applying the mean to the aggregated data, apply the standard deviation. The result is the within-cell standard deviations. Are they all roughly the same?) Do the original or the transformed data better respect the assumption of homogeneous variances?

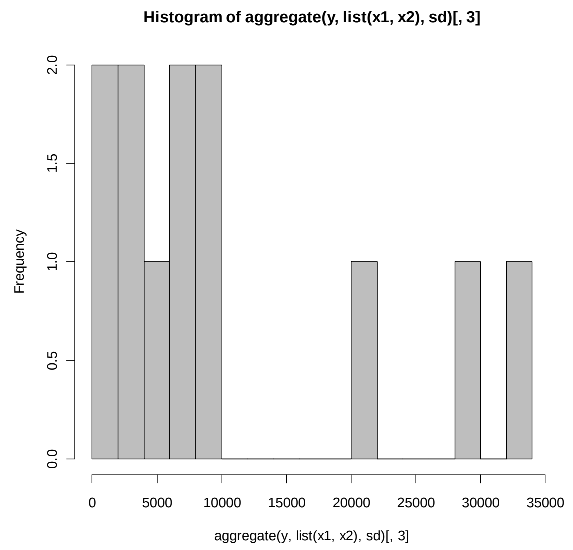
For the logarithmically transformed data,

```
aggregate( y, list(x1,x2), sd )
   Group.1 Group.2           x
1        1       1 0.005205083
2        2       1 0.037983957
3        3       1 0.101059931
4        4       1 0.033128985
5        1       2 0.072478142
6        2       2 0.048125947
7        3       2 0.085013176
8        4       2 0.027603123
9        1       3 0.018893844
10       2       3 0.007116409
11       3       3 0.020676694
12       4       3 0.014695818

hist( aggregate( y, list(x1,x2), sd )[,3] , breaks=12 , col="grey" )
```



Original data:

```
aggregate( y, list(x1,x2), sd )
   Group.1 Group.2          x
1        1       1  2828.4271
2        2       1  8191.0448
3        3       1 33969.2412
4        4       1  6020.9431
5        1       2 28794.5307
6        2       2  8062.0340
7        3       2 20566.9204
8        4       2  4183.0417
9        1       3  7736.9963
10       2       3   953.7838
11       3       3  3570.9237
12       4       3  1838.3906

hist( aggregate( y, list(x1,x2), sd )[,3] , breaks=12 , col="grey" )
```

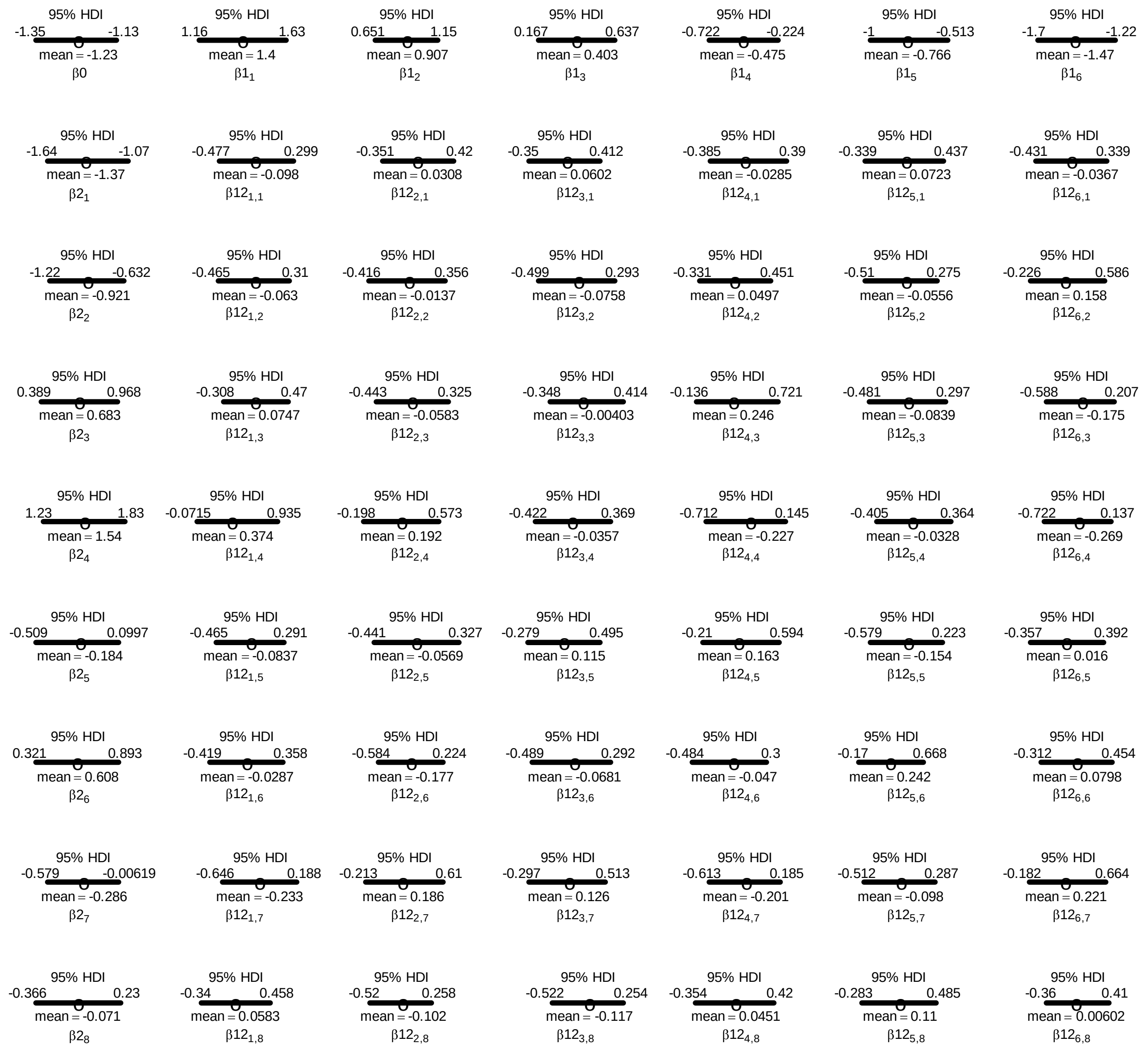


For both the original and logarithmically transformed data, the cell SDs show some outliers. But the degree of skew in the distribution of cell SDs seems to be a bit less for the logarithmically transformed data. By using this criterion alone, it seems that the transformed data better respect the assumption of homogeneous variances in the 12 cells.

We would also want to look at the distributions of data within cells to see if they are consistent with the assumption of normally distributed data. Because salaries tend to be skewed to the right, with a few people making very high salaries, the logarithmic transformation is likely to help the normality assumption too.

Exercise 19.2. [Purpose: To investigate a case of two-factor Bayesian ANOVA.] In the data specification of the program in Section 19.3.1 (ANOVAtwowayBRugs), you can load data from Qian & Shen (2007), regarding how quickly seaweed regenerates when in the presence of different types of grazers. Data were collected from eight different tidal areas of the Oregon coast; this predictor (x2) is referred to as the Block. In each of the eight Blocks, there were six different combinations of seaweed grazers established by the researchers. This predictor (x1) had six levels: control, with no grazers allowed; only small fish allowed; small and large fish allowed; only limpets allowed; limpets and small fish allowed; and all three grazers allowed. The predicted variable was the percentage of the plot covered by regenerated seaweed, logarithmically transformed.

(A) Load the data and run the program. You will find that there are too many levels of the two predictors to fit all the posterior histograms into a single multipanel display. Therefore, modify the plotPost.R program so that it produces only the mean and HDI limits, marked by a horizontal bar with a circle at the mean (without a histogram) and perhaps without a main title. Name your program something other than plotPost.R, and use it in the plotting section at the end of the program instead of plotPost.R. Show your results. (A secondary goal of this part of the exercise is to give you experience modifying graphics in R to suit your own purposes.) Hints: …



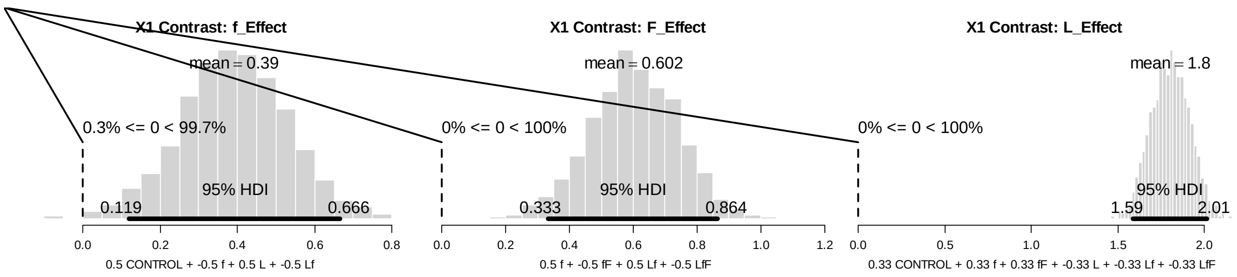
The above plot was generated with the following code. First, in the main program, the plotting commands were altered as indicated by the bold highlighted text:

```
source("plotPost19.2.R")
windows((datalist$Nx1Lvl+1)*2.75,(datalist$Nx2Lvl+1)*2.0)
layoutMat = matrix( 0 , nrow=(datalist$Nx2Lvl+1) , ncol=(datalist$Nx1Lvl+1) )
layoutMat[1,1] = 1
layoutMat[1,2:(datalist$Nx1Lvl+1)] = 1:datalist$Nx1Lvl + 1
layoutMat[2:(datalist$Nx2Lvl+1),1] = 1:datalist$Nx2Lvl + (datalist$Nx1Lvl + 1)
layoutMat[2:(datalist$Nx2Lvl+1),2:(datalist$Nx1Lvl+1)] = matrix(
    1:(datalist$Nx1Lvl*datalist$Nx2Lvl) + (datalist$Nx2Lvl+datalist$Nx1Lvl+1) ,
    ncol=datalist$Nx1Lvl , byrow=T )
layout( layoutMat )
par( mar=c(4,0.5,2.5,0.5) , mgp=c(1,0.7,0) )
histinfo = plotPost19.2( b0Sample , xlab=expression(beta * 0) , main="Baseline" ,
                     breaks=30  )
for ( x1idx in 1:datalist$Nx1Lvl ) {
  histinfo = plotPost19.2( b1Sample[x1idx,] , xlab=bquote(beta*1[.(x1idx)]) ,
                       main=paste("x1:",x1names[x1idx]) , breaks=30 )
}
for ( x2idx in 1:datalist$Nx2Lvl ) {
  histinfo = plotPost19.2( b2Sample[x2idx,] , xlab=bquote(beta*2[.(x2idx)]) ,
                       main=paste("x2:",x2names[x2idx]) , breaks=30 )
}
for ( x2idx in 1:datalist$Nx2Lvl ) {
  for ( x1idx in 1:datalist$Nx1Lvl ) {
    histinfo = plotPost19.2( b1b2Sample[x1idx,x2idx,] , breaks=30 ,
              xlab=bquote(beta*12[.(x1idx)*","*.(x2idx)]) ,
              main=paste("x1:",x1names[x1idx],", x2:",x2names[x2idx])  )
  }
}
```

The plotPost19.2.R function was adapted from plotPost.R as indicated by the bold highlighted text:

```
plotPost19.2 = function( paramSampleVec , credMass=0.95 , compVal=NULL ,
           HDItextPlace=0.7 , ROPE=NULL , yaxt=NULL , ylab=NULL ,
           xlab=NULL , cex.lab=NULL , cex=NULL , xlim=NULL , main=NULL ,
           showMode=F , ... ) {
    # Override defaults of hist function, if not specified by user:
    # (additional arguments "..." are passed to the hist function)
    if ( is.null(xlab) ) xlab="Parameter"
    if ( is.null(cex.lab) ) cex.lab=1.0
    if ( is.null(cex) ) cex=1.0
    if ( is.null(xlim) ) xlim=range( c( compVal , paramSampleVec ) )
    if ( is.null(main) ) main=""
    if ( is.null(yaxt) ) yaxt="n"
    if ( is.null(ylab) ) ylab=""
    # Plot histogram.
    par(xpd=NA)
    histinfo = hist( paramSampleVec , xlab=xlab , yaxt=yaxt , ylab=ylab ,
                     freq=F , col="lightgrey" , border="white" ,
                     xlim=xlim , main=main , cex=cex , cex.lab=cex.lab ,
                     plot=F ,
                     ... )
    plot( 0 , type="n" , bty="n" , xlim=xlim , xaxt="n" , yaxt="n" ,
                xlab=xlab , ylab=ylab ) # creates empty plot
    # Display mean or mode:
    if ( showMode==F ) {
        meanParam = mean( paramSampleVec )
        text( meanParam , 0*max(histinfo$density) ,
              bquote(mean==.(signif(meanParam,3))) , adj=c(.5,1.5) , cex=cex )
        points( meanParam , 0 , pch="o" , cex=1.5 )
    } else {
        dres = density( paramSampleVec )
        modeParam = dres$x[which.max(dres$y)]
        text( modeParam , 0*max(histinfo$density) ,
              bquote(mode==.(signif(modeParam,3))) , adj=c(.5,1.5) , cex=cex )
        points( modeParam , 0 , pch="o" , cex=1.5 )
    }
…# remainder is unchanged
}
```

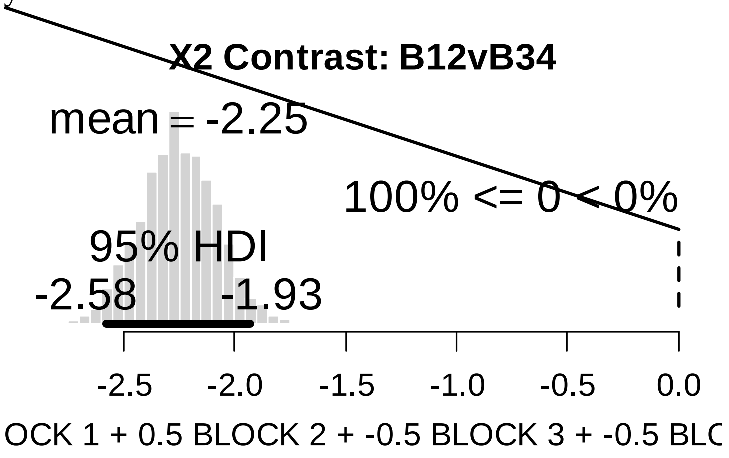
(B) The program already includes contrasts that consider whether there is an effect of small fish, an effect of large fish, and an effect of limpets. What conclusions do you reach from the posteriors of these contrasts?



The posterior histograms indicate clearly that all three effects are credibly greater than zero.

(C) Construct a contrast of the average of Blocks 3 and 4 versus the average of Blocks 1 and 2. Show your specification, the graph of the posterior on the contrast, and state your conclusion.

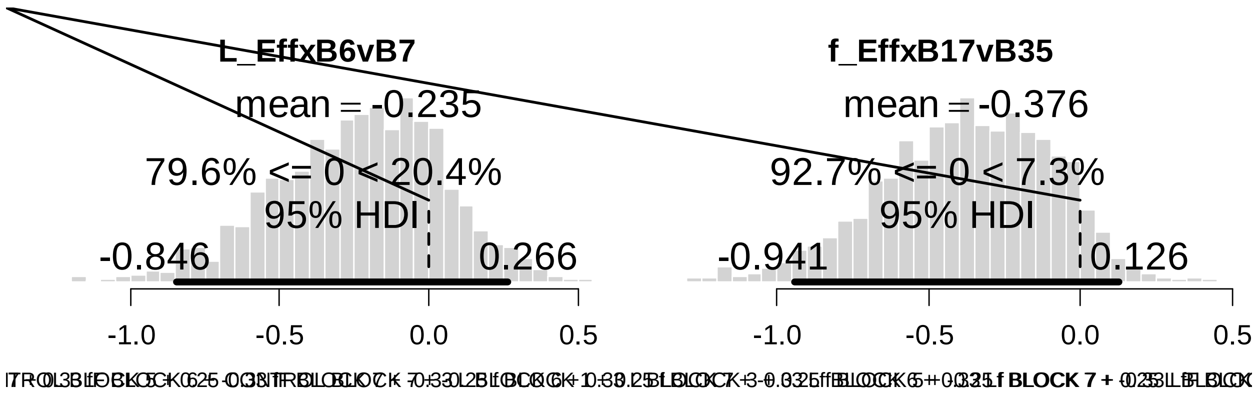
```
x2contrastList = list( B12vB34 = c( 1/2 , 1/2 , -1/2 , -1/2 ,0,0,0,0) )
```
yields



which indicates that there is a highly credible difference between the average of blocks 1 & 2 and the average of blocks 3 & 4.

(D) Is the effect of limpets different in Block 6 than in Block 7? To answer this question, construct an interaction contrast using an outer product (Hint: refer to the already-coded L effect for the contrast that specifies the effect of limpets). Is the effect of small fish different in Blocks 1 and 7 than in Blocks 3 and 5? For both questions, show the contrast vectors that you constructed and show the posterior of the contrast, and state your conclusion.

```
x1x2contrastList = list(
  L_EffxB6vB7 = outer( c(1/3,1/3,1/3,-1/3,-1/3,-1/3) , c(0,0,0,0,0,1,-1,0) ) ,
  f_EffxB17vB35 = outer( c(1/2,-1/2,0,1/2,-1/2,0) , c(1/2,0,-1/2,0,-1/2,0,1/2,0) ) )
```
yields the posterior histograms below

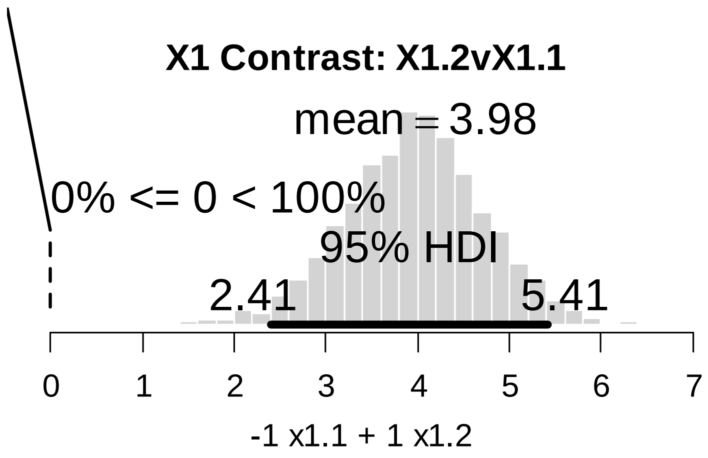


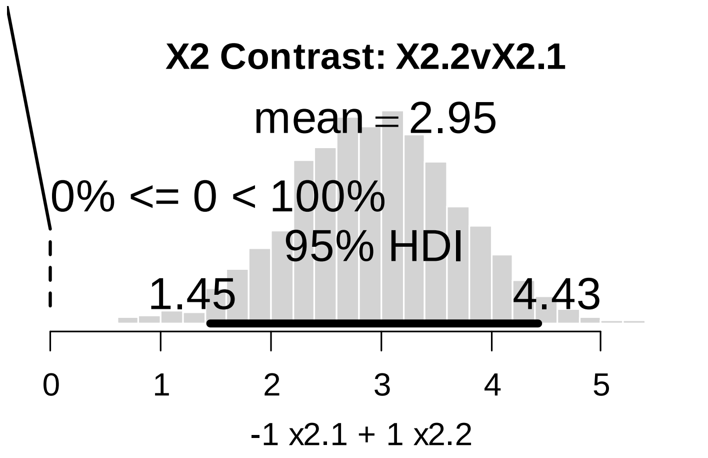
hence both interaction contrasts include zero among their credible values.

Exercise 19.3. [Purpose: To notice that within-subject designs can be more sensitive (hence more powerful) than between-subject designs.] Consider these data: …

(A) Ignoring the last column, which indicates the subject who generated the data, conduct a Bayesian ANOVA using x1 and x2 as predictors of y. Show the code you used to load the data, and show the resulting posterior histograms of . Also show the posterior of the contrast (i.e., the marginal difference between levels 1 and 2 of factor 1, also called the main effect of factor 1) and the posterior of the contrast (i.e., the marginal difference between levels 1 and 2 of factor 2, also called the main effect of factor 2).

```
  y = c( 101,102,103,105,104, 104,105,107,106,108, 105,107,106,108,109,
109,108,110,111,112 )
  x1 = c( 1,1,1,1,1, 1,1,1,1,1, 2,2,2,2,2, 2,2,2,2,2 )
  x2 = c( 1,1,1,1,1, 2,2,2,2,2, 1,1,1,1,1, 2,2,2,2,2 )
  # S = c( 1,2,3,4,5, 1,2,3,4,5, 1,2,3,4,5, 1,2,3,4,5 )
  x1names = c("x1.1","x1.2")
  x2names = c("x2.1","x2.2")
  # Snames = c("S1","S2","S3","S4","S5")
  Ntotal = length(y)
  Nx1Lvl = length(unique(x1))
  Nx2Lvl = length(unique(x2))
  # NSLvl = length(unique(S))
  x1contrastList = list( X1.2vX1.1 = c( -1 , 1 ) )
  x2contrastList = list( X2.2vX2.1 = c( -1 , 1 ) )
  x1x2contrastList = NULL # list( matrix( 1:(Nx1Lvl*Nx2Lvl) , nrow=Nx1Lvl ) )
```

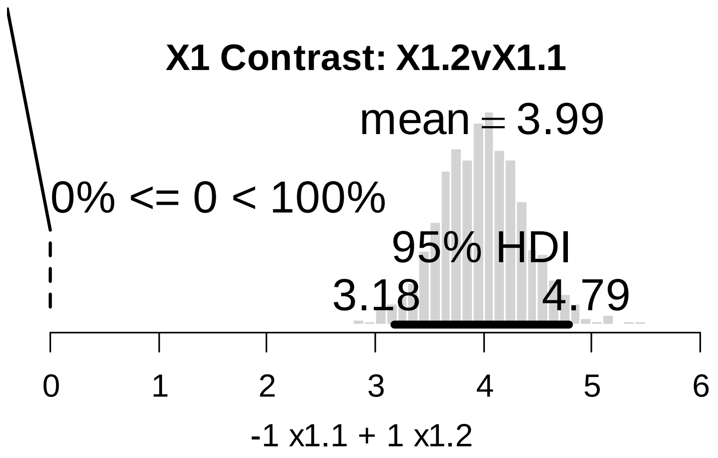


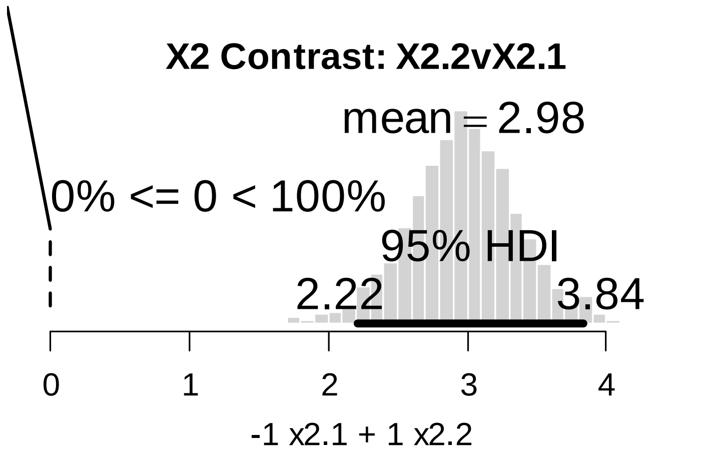


(B) Now include the subject as a predictor by expanding the model to include a deflection from baseline due to subject. (Do not include any subject interaction terms.) Again show the posteriors of the beta's requested in the previous part. Are the certainties on the estimates and contrasts different than in the previous part? In what way, and why? (Hint regarding the answer: Figure 19.7 shows posterior histograms for the main effect of factor 2, when the data are considered to be between subject or within subject. Notice that the means are essentially the same in both histograms, but the uncertainties are very different! Programming hints: …)

Here are sections of the modified code:

```
model {
  for ( i in 1:Ntotal ) {
    y[i] ~ dnorm( mu[i] , tau )
    mu[i] <- a0 + a1[x1[i]] + a2[x2[i]] + a1a2[x1[i],x2[i]] + aS[S[i]]
  }
  #
  tau <- pow( sigma , -2 )
  sigma ~ dunif(0,10) # y values are assumed to be standardized
  #
  a0 ~ dnorm(0,0.001) # y values are assumed to be standardized
  #
  for ( j1 in 1:Nx1Lvl ) { a1[j1] ~ dnorm( 0.0 , a1tau ) }
  a1tau <- 1 / pow( a1SD , 2 )
  a1SD <- abs( a1SDunabs ) + .1
  a1SDunabs ~ dt( 0 , 0.001 , 2 )
  #
  for ( j2 in 1:Nx2Lvl ) { a2[j2] ~ dnorm( 0.0 , a2tau ) }
  a2tau <- 1 / pow( a2SD , 2 )
  a2SD <- abs( a2SDunabs ) + .1
  a2SDunabs ~ dt( 0 , 0.001 , 2 )
  #
  for ( j1 in 1:Nx1Lvl ) { for ( j2 in 1:Nx2Lvl ) {
    a1a2[j1,j2] ~ dnorm( 0.0 , a1a2tau )
  } }
  a1a2tau <- 1 / pow( a1a2SD , 2 )
  a1a2SD <- abs( a1a2SDunabs ) + .1
  a1a2SDunabs ~ dt( 0 , 0.001 , 2 )
  #
  for ( jS in 1:NSLvl ) { aS[jS] ~ dnorm( 0.0 , aStau ) }
  aStau <- 1 / pow( aSSD , 2 )
  aSSD <- abs( aSSDunabs ) + .1
  aSSDunabs ~ dt( 0 , 0.001 , 2 )
}

…

  #  initialization based on data
  theData = data.frame( y=datalist$y , x1=factor(x1,labels=x1names) ,
                        x2=factor(x2,labels=x2names) , S=factor(S,labels=Snames) )
  a0 = mean( theData$y )
  a1 = aggregate( theData$y , list( theData$x1 ) , mean )[,2] - a0
  a2 = aggregate( theData$y , list( theData$x2 ) , mean )[,2] - a0
  aS = aggregate( theData$y , list( theData$S ) , mean )[,2] - a0
  linpred = as.vector( outer( a1 , a2 , "+" ) + a0 )
  a1a2 = aggregate( theData$y, list(theData$x1,theData$x2), mean)[,3] - linpred
  genInitList <- function() {
    return(
        list(
            a0 = a0 ,
            a1 = a1 ,
            a2 = a2 ,
            aS = aS ,
            a1a2 = matrix( a1a2 , nrow=Nx1Lvl , ncol=Nx2Lvl ) ,
            sigma = sd(theData$y)/2 , # lazy
            a1SDunabs = sd(a1) ,
            a2SDunabs = sd(a2) ,
            a1a2SDunabs = sd(a1a2) ,
            aSSDunabs = sd(aS)
        )
    )
  }
  for ( chainIdx in 1 : nchain ) {
    modelInits( bugsInits( genInitList ) )
  }

…

# Convert the a values to zero-centered b values.
# m12Sample is predicted cell means at every step in MCMC chain:
m12Sample = array( 0, dim=c( datalist$Nx1Lvl , datalist$Nx2Lvl ,
                             datalist$NSLvl , chainLength ) )
for ( stepIdx in 1:chainLength ) {
  for ( a1idx in 1:Nx1Lvl ) {
    for ( a2idx in 1:Nx2Lvl ) {
      for ( aSidx in 1:NSLvl ) {
        m12Sample[ a1idx , a2idx , aSidx , stepIdx ] = (
           a0Sample[stepIdx]
           + a1Sample[a1idx,stepIdx]
           + a2Sample[a2idx,stepIdx]
           + a1a2Sample[a1idx,a2idx,stepIdx]
           + aSSample[aSidx,stepIdx] )
      }
    }
  }
}

# b0Sample is mean of the cell means at every step in chain:
b0Sample = apply( m12Sample , 4 , mean )
# b1Sample is deflections of factor 1 marginal means from b0Sample:
b1Sample = ( apply( m12Sample , c(1,4) , mean )
           - matrix(rep( b0Sample ,Nx1Lvl),nrow=Nx1Lvl,byrow=T) )
# b2Sample is deflections of factor 2 marginal means from b0Sample:
b2Sample = ( apply( m12Sample , c(2,4) , mean )
           - matrix(rep( b0Sample ,Nx2Lvl),nrow=Nx2Lvl,byrow=T) )
# bSSample is deflections of factor S marginal means from b0Sample:
bSSample = ( apply( m12Sample , c(3,4) , mean )
           - matrix(rep( b0Sample ,NSLvl),nrow=NSLvl,byrow=T) )
# linpredSample is linear combination of the marginal effects:
linpredSample = 0*m12Sample
for ( stepIdx in 1:chainLength ) {
  for ( a1idx in 1:Nx1Lvl ) {
    for ( a2idx in 1:Nx2Lvl ) {
      for ( aSidx in 1:NSLvl ) {
        linpredSample[a1idx,a2idx,aSidx,stepIdx ] = (
           b0Sample[stepIdx]
           + b1Sample[a1idx,stepIdx]
           + b2Sample[a2idx,stepIdx]
           + bSSample[aSidx,stepIdx] )
      }
    }
  }
}
# b1b2Sample is the interaction deflection, i.e., the difference
# between the cell means and the linear combination:
b1b2Sample = apply( m12Sample - linpredSample , c(1,2,4) , mean )

# Convert from standardized b values to original scale b values:
b0Sample = b0Sample * ySDorig + yMorig
b1Sample = b1Sample * ySDorig
b2Sample = b2Sample * ySDorig
bSSample = bSSample * ySDorig
b1b2Sample = b1b2Sample * ySDorig
```





For both main effects, the means are the same whether or not the subject variable is included, but the HDI widths are dramatically different. By including the subject factor, the certainty of the main effects has greatly increased.

Why? Because subject 1 tends to have low scores, subject 5 tends to have high scores, and so on. When the subject identity is excluded, then the variation between subjects can only be attributed to within-cell noise. But when the subject identity is included, then the variation between subjects can be attributed to the subject factor, and the residual noise is much less.

Exercise 19.4. [Purpose: To conduct a power analysis for Bayesian ANOVA, for within-subject versus between-subject designs.] Conduct power analyses for the between-subject and within-subject versions of the previous exercise. Specifically, suppose the goal is for the 95% HDI of the contrast on factor 2 to have a width of 2.0 or less. Conduct a retrospective power analysis for this goal, for the within-subject version and the between-subject version. Caution: This exercise demands a lot of programming and could be time consuming, but the results drive home the point that within-subject designs can be more powerful than between-subject designs.

Answer to be included in a future edition of this solutions manual. Stay tuned.

Chapter 20.

Exercise 20.1. [Purpose: To observe correlated predictors in logistic regression.] For this exercise, we'll use some fictitious data regarding whether or not a patient suffered a heart attack within a year after a check-up that included measurements of systolic and diastolic blood pressures, cholesterol, weight, height, and age. The data are completely fabricated and fictional, for illustrative purposes only. The data are generated by the program BloodDataGenerator.R

(A) For this part, we will generate two data sets. In one set, the six predictors have correlations of zero with each other. In the second set, the first two predictors have a strong positive correlation, but still zero correlation with all the other predictors. For both sets, the true regression coefficient on the first predictor is zero, but the true regression coefficient on the second predictor is positive. Use the program BloodDataGenerator.R to generate these two data sets by selecting the relevant correlation matrix at the top of the program. For each data set, conduct a Bayesian analysis using the program in Section 20.5.1 (MultipleLogisticRegressionBrugs.R). Be sure to specify that the only predictors are the first two, namely, systolic and diastolic pressure. Include the posterior contour plots, which should look similar to those in Figure 20.7. Be sure also to include the histograms of the marginal posterior distributions. In which case are the HDIs narrower?

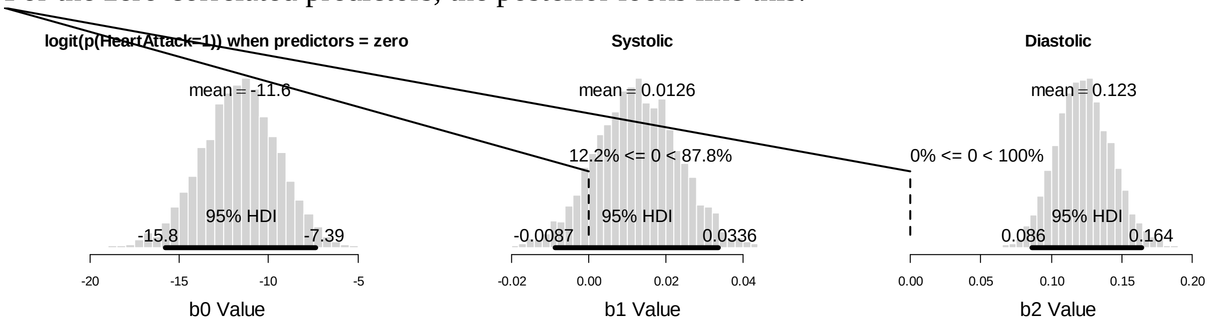
In the data generating program, for the first data set we specify the TRUE and FALSE conditions as follows:

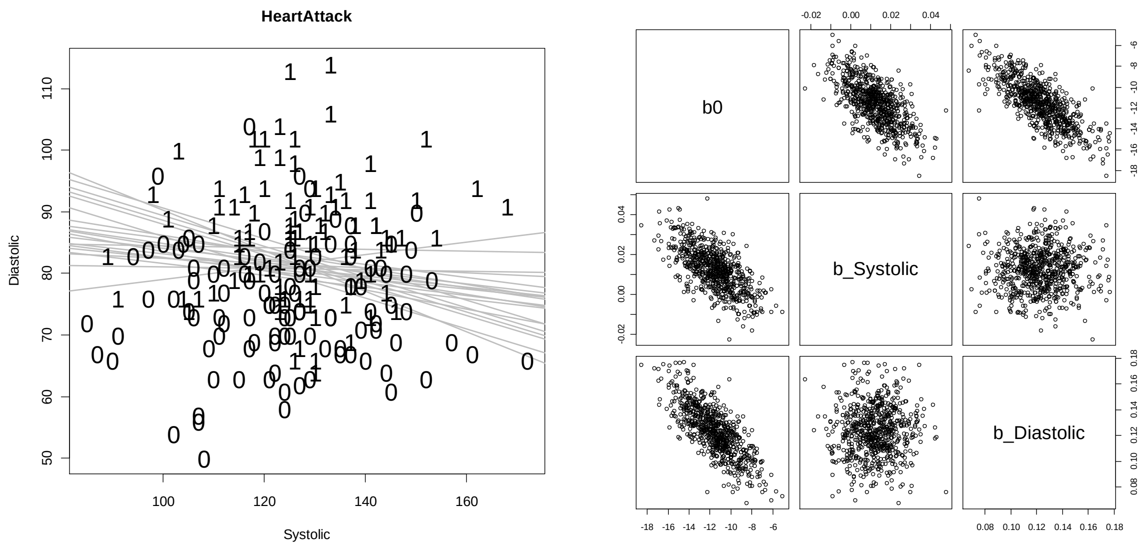
```
if ( T ) { # zero correlations everywhere
rMat = matrix( c(   1 ,  0 ,  0 ,  0 ,  0 ,  0 ,
                    0 ,  1 ,  0 ,  0 ,  0 ,  0 ,
                    0 ,  0 ,  1 ,  0 ,  0 ,  0 ,
                    0 ,  0 ,  0 ,  1 ,  0 ,  0 ,
                    0 ,  0 ,  0 ,  0 ,  1 ,  0 ,
                    0 ,  0 ,  0 ,  0 ,  0 ,  1  ) , ncol=nX ) }
if ( F ) { # first two predictors strongly correlated
rMat = matrix( c(   1 , .95,  0 ,  0 ,  0 ,  0 ,
                   .95,  1 ,  0 ,  0 ,  0 ,  0 ,
                    0 ,  0 ,  1 ,  0 ,  0 ,  0 ,
                    0 ,  0 ,  0 ,  1 ,  0 ,  0 ,
                    0 ,  0 ,  0 ,  0 ,  1 ,  0 ,
                    0 ,  0 ,  0 ,  0 ,  0 ,  1  ) , ncol=nX ) }
```

In the logistic regression program, we set the data specification to use only the first two predictors, as follows:

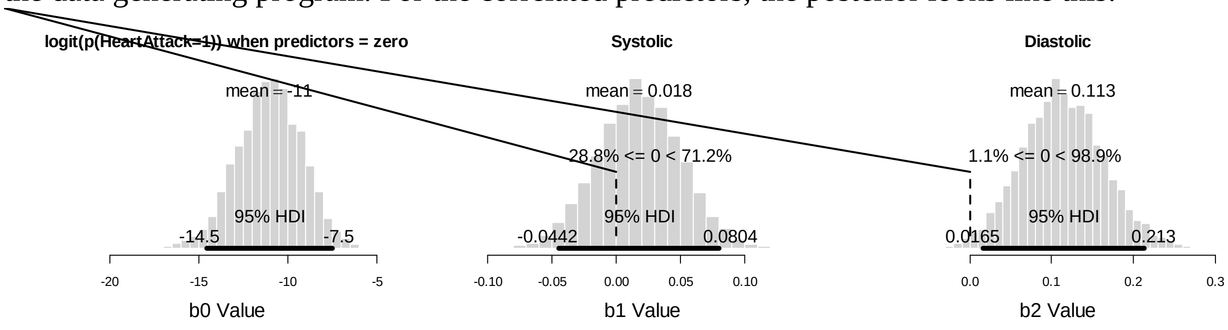
```
dataSource = c( "HtWt" , "Cars" , "HeartAttack" )[3]
…
if ( dataSource == "HeartAttack" ) {
  fname = paste( fname , dataSource , sep="" )
  dataMat = read.table(file="BloodDataGeneratorOutput.txt",header=T,sep=" ")
  predictedName = "HeartAttack"
#  predictorNames = c( "Systolic", "Diastolic", "Weight", "Cholesterol",
#                      "Height", "Age" )
  predictorNames = c( "Systolic", "Diastolic" )
  nData = NROW( dataMat )
  y = as.matrix( dataMat[,predictedName] )
  x = as.matrix( dataMat[,predictorNames] )
  nPredictors = NCOL( x )
}
```

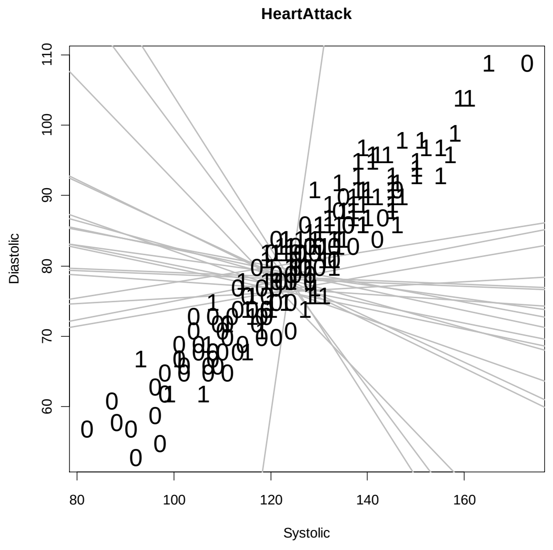
For the zero-correlated predictors, the posterior looks like this:

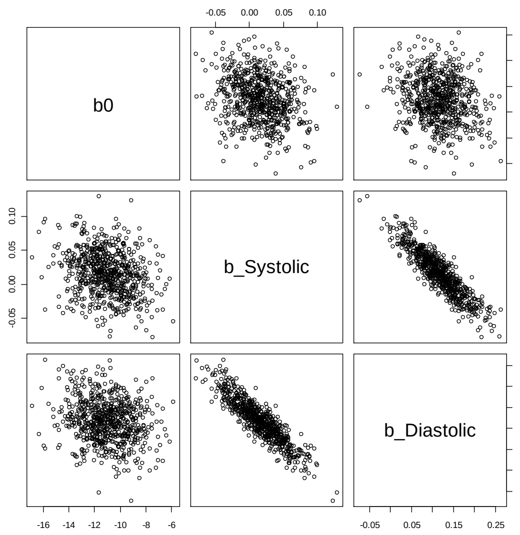




We re-run using correlated predictors by simply exchanging the TRUE and FALSE settings in the data generating program. For the correlated predictors, the posterior looks like this:







You can see that for the correlated predictors, there is a dramatic increase in the uncertainty of the estimated regression coefficients. The 95%HDIs are much wider on the b1 and b2 values for the correlated predictors than for the uncorrelated predictors. This increased uncertainty is clearly visible in the plot of the data with the logistic level contours, because the level contours are fairly tightly bundled for the uncorrelated predictors, but splayed at widely different angles for the correlated predictors.

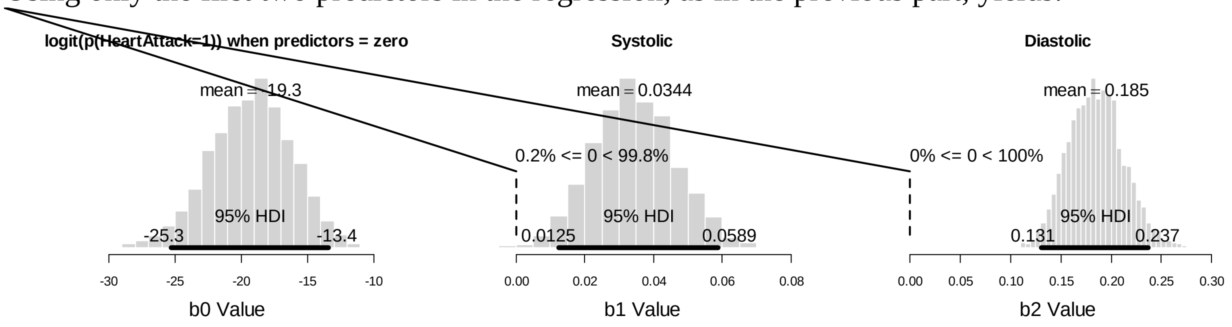
Also notice that the regression coefficients, b1 and b2, are strongly anticorrelated when the predictors are correlated. This anticorrlation indicates that uncertainty in the two regression coefficients trades off: If the slope on one predictor is large, the slope on the other must be small, if the logistic "surface" is to accommodate the data.

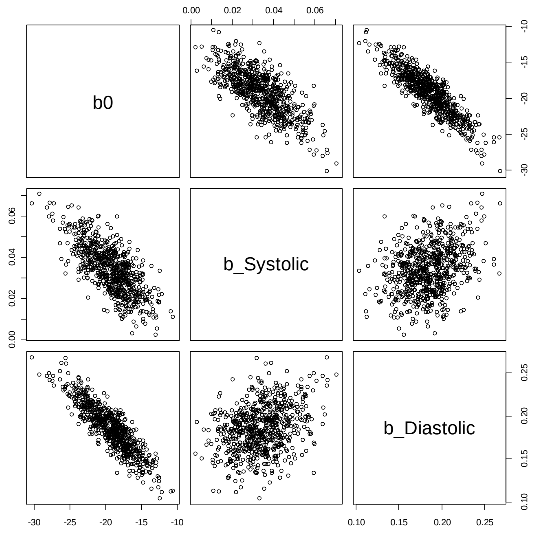
(B) For this part, we generate a different fictitious data set, in which the first two predictors (systolic and diastolic) have zero correlation with each other, but they are correlated with another predictor (weight). The first predictor (systolic) has a true regression coefficient of zero, but the second (diastolic) and third (weight) predictors have positive regression coefficients. Run the Bayesian logistic regression analysis using only the first two predictors. What is the estimate of the regression coefficient on the first predictor? Include the histograms of the marginals of the posterior. Now rerun the Bayesian logistic regression analysis including all six predictors. What is the estimate of the regression coefficient on the first predictor? Include the histograms of the marginals of the posterior (for which you might need to manually stretch the graph window or change the character sizes in the plot). Why are the estimates of the regression coefficient for the first predictor different in the two analyses?

We use this correlation matrix in the data generating program:

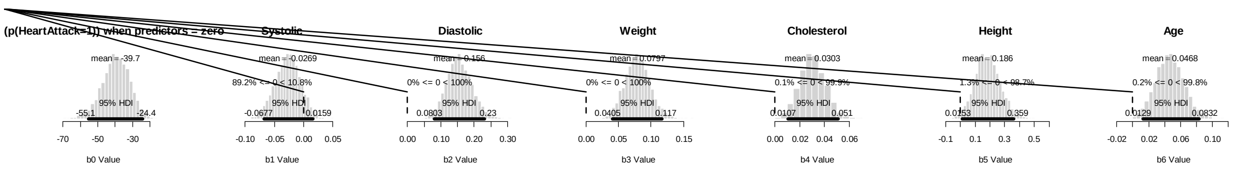
```
if ( T ) { # first two uncorrelated, but other predictors correlated
rMat = matrix( c(  1   ,  0   , .6 , .2 , .1 , .1 ,
                   0   ,  1   , .6 , .2 , .1 , .1 ,
                  .6   , .6   ,  1 , .4 , .2 , .2 ,
                  .2  , .2  , .4 ,  1 ,  0 , .3 ,
                  .1  , .1  , .2 ,  0 ,  1 ,  0 ,
                  .1  , .1  , .2 , .3 ,  0 ,  1 ) , ncol=nX ) }
```

Using only the first two predictors in the regression, as in the previous part, yields:

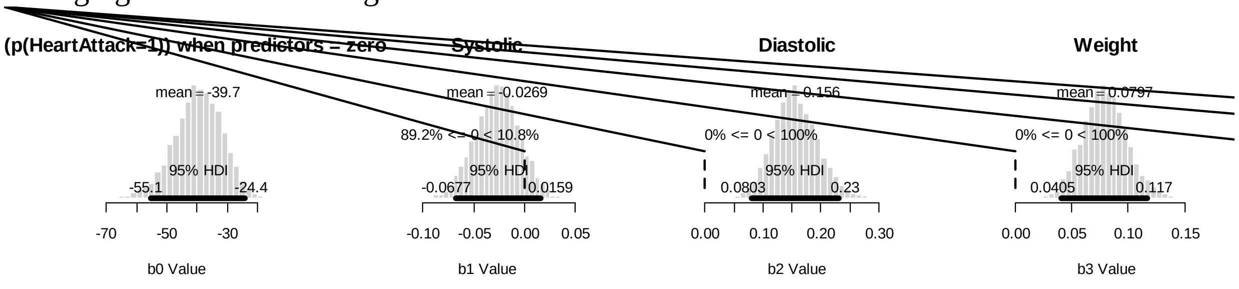




When using all six predictors, by uncommenting the predictorNames in the data specification (see code in previous part), the result is:



Enlarging the first few histograms:



We see that the estimated regression coefficient on b1 (Systolic) has changed dramatically. When including only the first two predictors, the estimate of b1 was positive and excluded zero. When all the predictors are included, the estimate of b1 is slightly negative and credible values include zero, which is the true generating value. The reason for the false estimation in the first case is that the first two predictors are correlated. Because the second predictor has an influence on the predicted value, and the first predictor is correlated with the second predictor, the data are consistent with the first predictor having an influence on the predicted value too. It is only by including other predictors that the true zero influence of the first predictor can be discerned.

Exercise 20.2. [Purpose: To observe the consequences of a small proportion of 1's in logistic regression.] For this exercise, we again use fictitious data generated by the program BloodDataGenerator.R. Set all the inter-predictor correlations to zero by selecting the appropriate correlation matrix at the top of the program. Change the proportionOnes constant to 0.02. This causes the proportion of 1's in the data to be very small. In other words, the threshold for the sigmoidal function is set very high, so that the weighted sum of the predictors must be very large before p(y=1) gets very large. This sort of situation, in which there are few 1's, is not unusual in real data. In heart attack data, for example, there will be few people who have a heart attack in the year following a routine check-up. Run a Bayesian logistic regression on the data, using only the first two predictors. What are the estimates of the regression coefficients? Include the histograms of the marginals of the posterior, and include the posterior contour plot, which should look similar to the right panel of Figure 20.7. Compare the widths of the HDIs to the results of the first part of the previous exercise.

In the data generating program, set all correlation matrices to FALSE *except*

```
if ( T ) { # zero correlations everywhere
rMat = matrix( c(   1 ,  0 ,  0 ,  0 ,  0 ,  0 ,
                    0 ,  1 ,  0 ,  0 ,  0 ,  0 ,
                    0 ,  0 ,  1 ,  0 ,  0 ,  0 ,
                    0 ,  0 ,  0 ,  1 ,  0 ,  0 ,
                    0 ,  0 ,  0 ,  0 ,  1 ,  0 ,
                    0 ,  0 ,  0 ,  0 ,  0 ,  1  ) , ncol=nX ) }
```

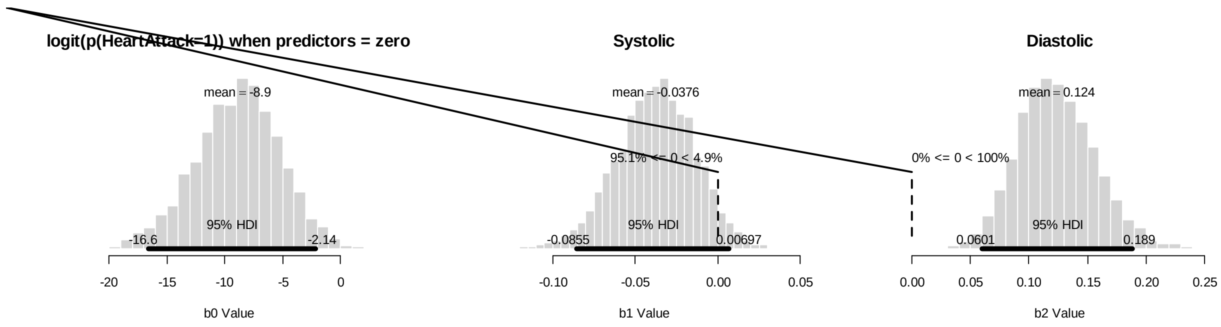
and set

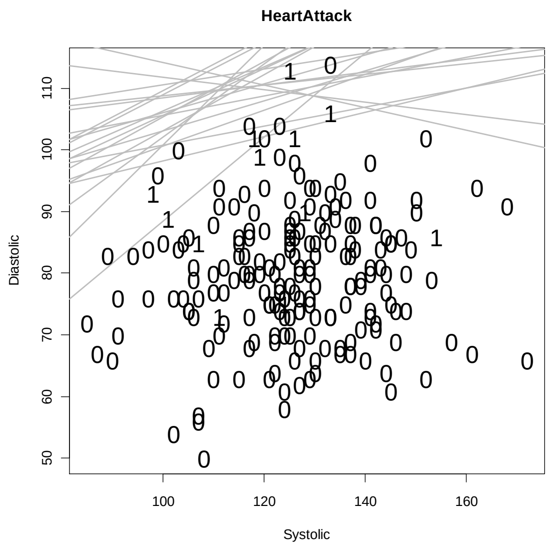
```
proportionOnes = 0.02  # e.g., about .05 for actual .10
```

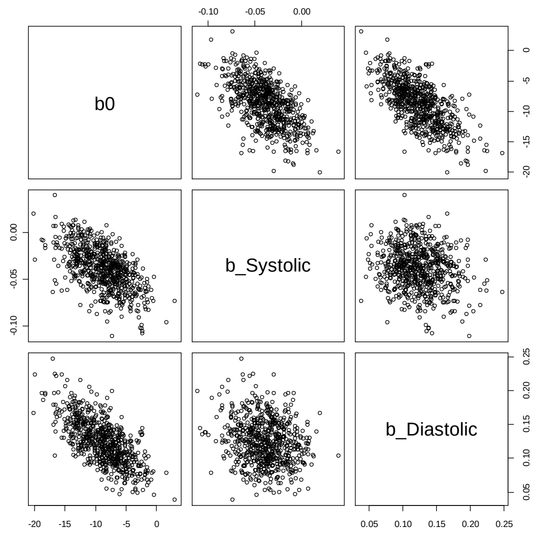
In the logistic regression program, set

```
dataSource = c( "HtWt" , "Cars" , "HeartAttack" )[3]
…
if ( dataSource == "HeartAttack" ) {
  fname = paste( fname , dataSource , sep="" )
  dataMat = read.table(file="BloodDataGeneratorOutput.txt",header=T,sep=" ")
  predictedName = "HeartAttack"
#  predictorNames = c( "Systolic", "Diastolic", "Weight", "Cholesterol",
#                      "Height", "Age" )
  predictorNames = c( "Systolic", "Diastolic" )
…
```

The result is:







Compared with the result of Exercise 20.1.A, the estimates here are less certain, even though the generating coefficients are the same. Most dramatically, the 95%HDI on the intercept extends from -16.6 to -2.14 here, but was much narrower, from -15.8 to -7.39, when the proportion of ones was 50%.

Exercise 20.3. [Purpose: To observe logistic ANOVA without assuming homogeneity of variance.] Extend the program of Section 20.5.2 (LogisticOnewayAnovaBrugs.R) so that it allows different certainty (kappa) parameters for each condition, with a hyperdistribution across conditions, just as in the model on the right side of Figure 9.17, p. 226. Apply the model to the filtration-condensation data, and compare the results with the results of Exercise 9.2, p. 236. If you already did Exercise 18.3, you can simply modify your program from that exercise. Programming hint: The model specification might look like this: (LogisticOnewayAnovaHeteroVarBrugs.R) …

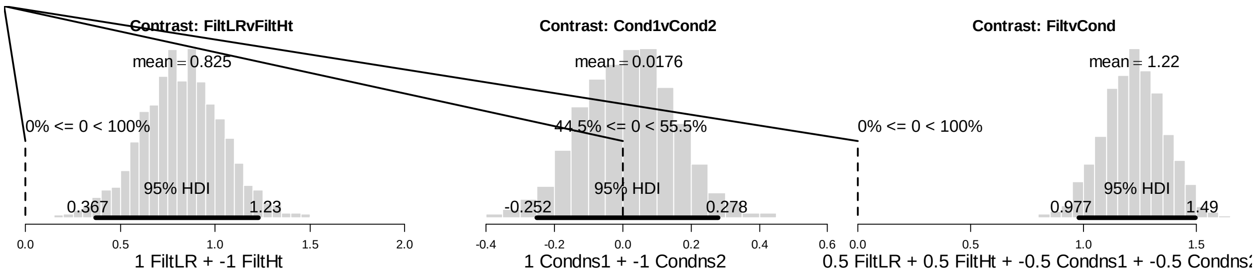
Model specification and chain initialization could look like this:

```
model {
  for ( i in 1:Ntotal ) {
    z[i] ~ dbin( theta[i] , n[i] )
    theta[i] ~ dbeta( aBeta[x[i]] , bBeta[x[i]] )I(0.001,0.999)
  }
  for ( j in 1:NxLvl ) {
    aBeta[j] <- mu[j] * k[j]
    bBeta[j] <- (1-mu[j]) * k[j]
    mu[j] <- 1 / ( 1 + exp( -( a0 + a[j] ) ) )
    a[j] ~ dnorm( 0.0 , atau )
    k[j] ~ dgamma( skappa , rkappa )
  }
  a0 ~ dnorm( 0 , 0.001 )
  atau <- 1 / pow( aSD , 2 )
  aSD <- abs( aSDunabs ) + .1
  aSDunabs ~ dt( 0 , 0.001 , 2 )
  skappa <- pow(mg,2)/pow(sg,2)
  rkappa <- mg/pow(sg,2)
  mg ~ dunif(0,50)
  sg ~ dunif(0,30)
}
```

…

```
  theData = data.frame( pr=.01+.98*datalist$z/datalist$n ,
                        x=factor(x,labels=xnames) )
  a0 = mean( logit(theData$pr) )
  a = aggregate( logit(theData$pr) , list( theData$x ) , mean )[,2] - a0
  mGrp = aggregate( theData$pr , list( theData$x ) , mean )[,2]
  sdGrp = aggregate( theData$pr , list( theData$x ) , sd )[,2]
  kGrp = mGrp*(1-mGrp)/sdGrp^2 - 1
  k = mean(kGrp)
  genInitList <- function() {
    return(
        list(
            a0 = a0 ,
            a = a ,
            aSDunabs = sd(a) ,
            theta = theData$pr ,
            k = kGrp ,
            mg = 10 ,
            sg = 10
        )
    )
  }
  for ( chainIdx in 1 : nchain ) {
    modelInits( bugsInits( genInitList ) )
  }
```

The resulting contrasts look like this:



In comparison with Figure 20.6, p. 560 of the textbook, we see that the basic qualitative conclusions are the same, in terms of excluding or not excluding zero difference. The magnitudes of the contrasts are slightly smaller here, however, because the added uncertainty of separate group precisions bleeds over into uncertainty in the group deflection values. As discussed on p. 560 of the textbook, although the "direct" model of chapter 9 and the logistic-ANOVA model of chapter 20 yield similar results, the logistic-ANOVA model is more easily generalized to two or more predictor variables.

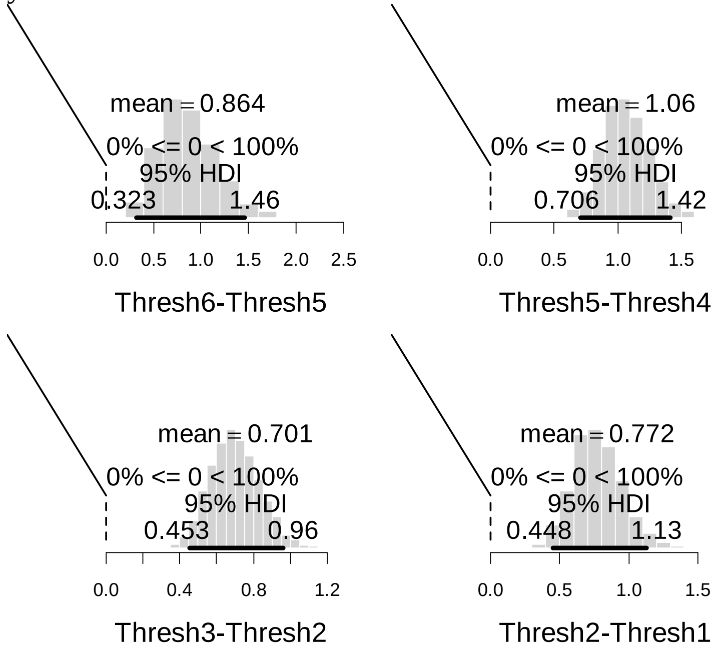
Chapter 21.

Exercise 21.1. [Purpose: To investigate posterior differences of thresholds.] Run the program in Section 21.5 (OrdinalProbitRegressionBrugs.R) on the Movies data (Moore, 2006). At the end of the program, notice that the posterior thresholds are stored in a matrix named threshSamp, one column per threshold.

(A) Make histograms of the differences between every pair of adjacent thresholds (i.e., threshSamp[,n]-threshSamp[,n-1], for n in 2:nYlevels). (Hint: Use plotPost with compVal=0.) Are any differences between adjacent thresholds close to zero?

```
windows(3.5,3)
t=6 ; histInfo=plotPost(threshSamp[,t]-threshSamp[,t-1],compVal=0,
 xlab=bquote("Thresh"*.(t)*"-Thresh"*.(t-1)))
t=5 ; histInfo=plotPost(threshSamp[,t]-threshSamp[,t-1],compVal=0,
 xlab=bquote("Thresh"*.(t)*"-Thresh"*.(t-1)))
t=4 ; histInfo=plotPost(threshSamp[,t]-threshSamp[,t-1],compVal=0,
 xlab=bquote("Thresh"*.(t)*"-Thresh"*.(t-1)))
t=3 ; histInfo=plotPost(threshSamp[,t]-threshSamp[,t-1],compVal=0,
 xlab=bquote("Thresh"*.(t)*"-Thresh"*.(t-1)))
t=2 ; histInfo=plotPost(threshSamp[,t]-threshSamp[,t-1],compVal=0,
 xlab=bquote("Thresh"*.(t)*"-Thresh"*.(t-1)))
```

yields

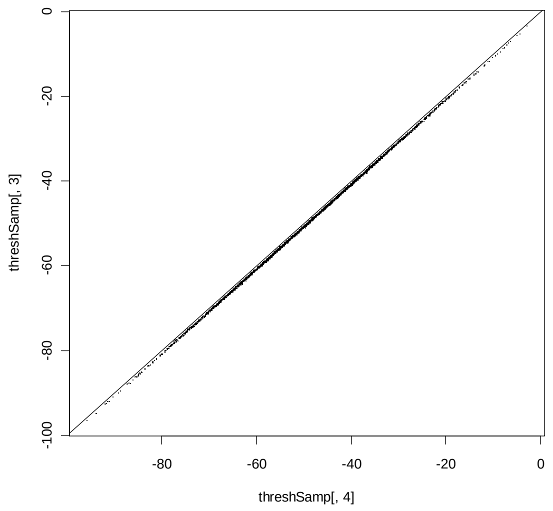


Clearly none of the adjacent threshold samples have overlapping values (i.e., no differences are less than zero).

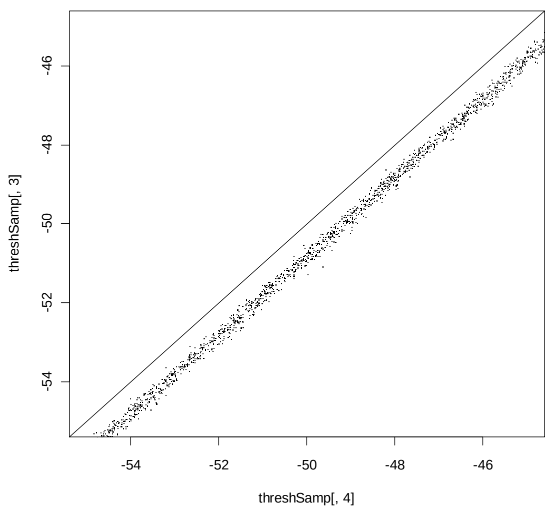
(B) Make a scatter plot of theta4 against theta3. (Hint: plot(threshSamp[,4], threshSamp[,3]).) Superimpose a line that marks theta4 = theta3. (Hint: abline(0,1).) What

is the relation of this scatter plot to the histogram you made in the previous part? In particular, what is the relation of the line in the scatter plot to the histogram?

```
plot( threshSamp[,4] , threshSamp[,3] , pch="." )
abline(0,1)
```
yields



Zooming in lets us see better:
```
plot( threshSamp[,4] , threshSamp[,3] , pch="." , xlim=c(-55,-45) , ylim=c(-55,-45) )
abline(0,1)
```



Notice that all the point lie below the diagonal line. The histogram in the previous part, which plots thresh4-thresh3, is just this scatterplot collapsed along the diagonal. The diagonal line here corresponds to the dashed line at compVal=0 in the histogram.

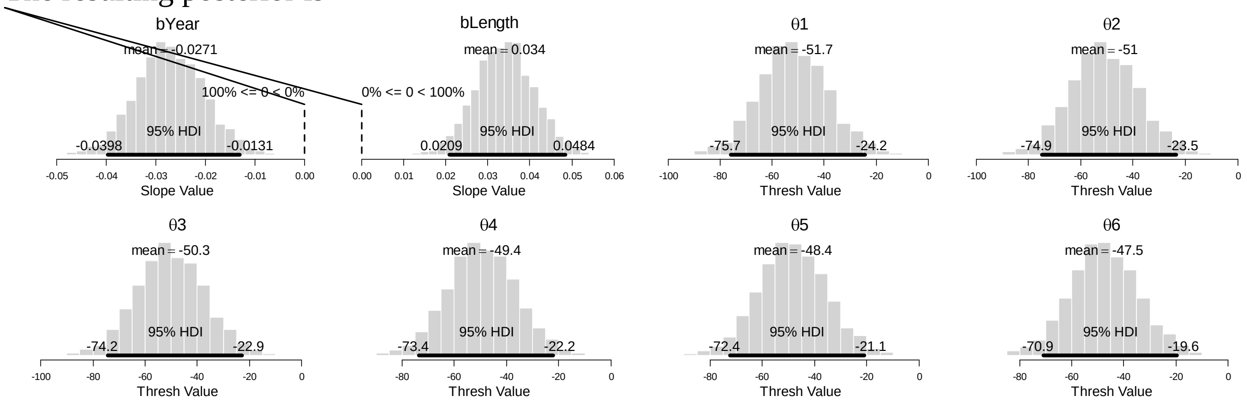
Exercise 21.2. [Purpose: To examine robustness when the prior is changed.] In the program in Section 21.5 (OrdinalProbitRegressionBrugs.R), the priors on the regression coefficients and thresholds are mildly informed. Consider the precision of the normal prior for the

regression coefficients. Because the predictors are standardized, their range is approximately -2 to +2. If we have a prior assumption that the steepest possible relationship between x and y maps the lowest value of x to the lowest value of y and the highest value of x to the highest value of y, then the steepest regression line would rise nYlevels as x goes from -2 to +2. Hence the steepest plausible slope is nYlevels/4, and the program makes that value the standard deviation of the prior on each regression coefficient. Consider now the prior on the thresholds. Because the thresholds are separated in the prior by 1 unit, and the thresholds should not violate consecutive ordering, it is reasonable to set their standard deviations no larger than 1.

(A) Set the prior on the regression coefficients so that the precision is very small, say, 1.0E-6. Run the program on the Movies data. Is the posterior much different?

In the model specification, change the prior as follows:
```
    bPrec <- 1.0E-06  # was  pow( nYlevels/4 , -2 )
```

The resulting posterior is

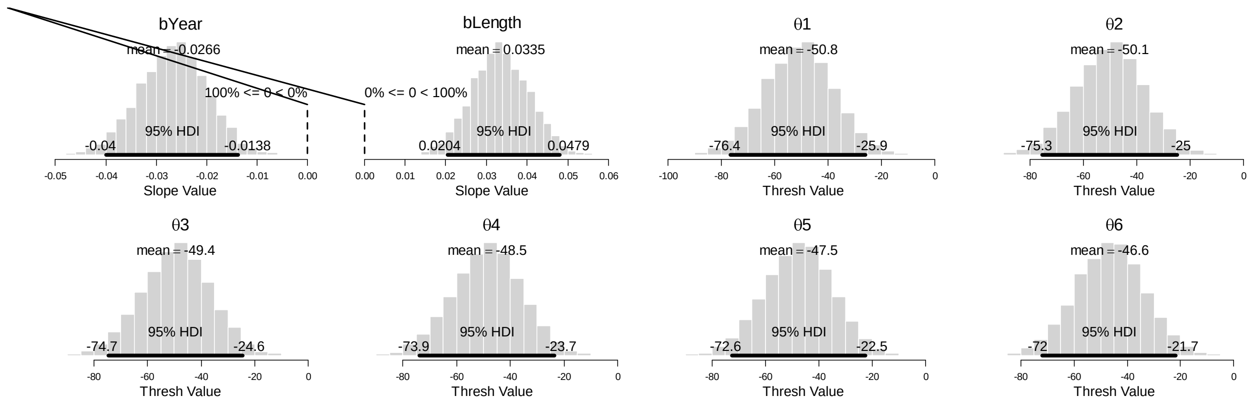


which is only very slightly different than the original posterior (see Figure 21.4, p. 585 of the textbook).

(B) Set the prior on the thresholds so that the precision is very small, say, 1.0E-6. (Set the prior on the regression coefficients back to the original setting.) Run the program on the Movies data. Is the posterior much different?

In the model specification, set the bPrec back to what it was, but change the following:
```
    threshPriorPrec <- 1.0E-6 # was 1
```

The resulting posterior is



which is only very slightly different than the original posterior (see Figure 21.4, p. 585 of the textbook). Thus, the posterior is very robust against changes in ways to specify a vague prior, and the mildly informed prior had no noticeable effect on the posterior relative to the extremely broad priors.

Exercise 21.3. [Purpose: To observe predicted values for novel predictor values.] Run the program in Section 21.5 (OrdinalProbitRegressionBrugs.R) on the movies data (Moore, 2006). Consider a movie that was not included in the rated movies. Suppose it was made in 1991, and had a length of 94 minutes. What is the probability of each rating for the movie? In other words, what is the probability that it would be rated 7, what is the probability that it would be rated 6, and so on. Answer the same question for a movie that had a length of 94 minutes but was made in 1931. (Hint: Use Equation 21.3, averaging the result across all the steps in the MCMC chain. Extra special bonus hint: Code for doing this is already included at the end of the program; your job is to understand what it's doing.)

The code at the end of the program below. The comments explain the code.
```
# Posterior prediction.
xProbe = c( 1991 , 94 ) # Note order of values: x1 is year and x2 is duration.
```
Added comment: xProbe, above, is the novel movie we want to make a prediction for.
```
# Set up a matrix for storing the values of p(y|xProbe) at each step in chain.
py = matrix( 0 , nrow=chainLength , ncol=nYlevels )
```
Added comment: py, above, has one row per MCMC step, and 7 columns for 7 possible rating values. Each column is the probability of the corresponding rating, for the parameter values at the step in the MCMC chain.
```
# Step through chain and compute p(y|xProbe) and each step:
for ( chainIdx in 1:chainLength ) {
    yValue = 1
    py[chainIdx,yValue] = (
        pnorm( threshSamp[chainIdx,yValue]
               - sum( bSamp[chainIdx,] * xProbe ) ) )
    for ( yValue in 2:(nYlevels-1) ) {
        py[chainIdx,yValue] = (
            pnorm( threshSamp[chainIdx,yValue]
                   - sum( bSamp[chainIdx,] * xProbe ) )
             - pnorm( threshSamp[chainIdx,yValue-1]
                      - sum( bSamp[chainIdx,] * xProbe ) ) )
    }
    yValue = nYlevels
    py[chainIdx,yValue] = ( 1 -
        pnorm( threshSamp[chainIdx,yValue-1]
               - sum( bSamp[chainIdx,] * xProbe ) ) )
}
# Now average across the chain:
pyAve = colMeans( py )
```

Added comment: pyAve, above is the average predicted probability of each rating, collapsed across all steps in the chain. In other words, that's the answer we're looking for!

```
round( pyAve , 3 )
```

yields

```
[1] 0.166 0.247 0.266 0.219 0.091 0.010 0.001
```

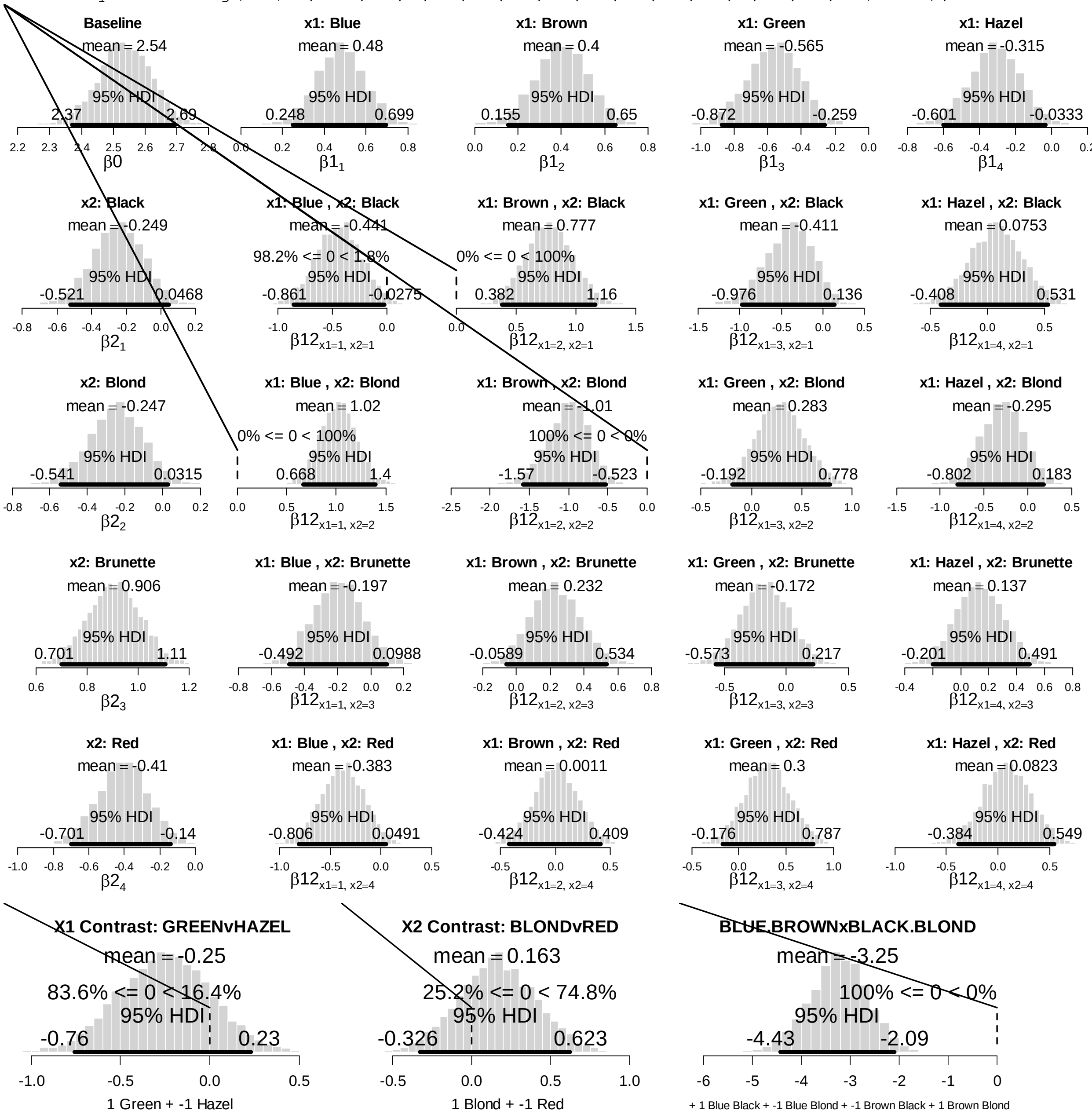
In other words, there is a 16.6% probability of rating "1", a 24.7% probability of rating "2", a 26.6% probability of rating "3", and so forth.

Chapter 22.

Exercise 22.1. [Purpose: To observe the influence of sample size on the precision of the estimate.] Consider the data regarding hair color and eye color in Table 22.1, which is available for use in the code of Section 22.4 (PoissonExponentialBrugs.R).

(A) Divide the original data frequencies by 2 and take the ceiling() of the result. Thus, the modified data are ceiling(c(68,...,16) / 2). This modification (nearly) preserves the relative proportions in each cell but halves the sample size. Run the program with these modified data, show the histograms, and compute the width of the 95% HDIs for the contrasts.

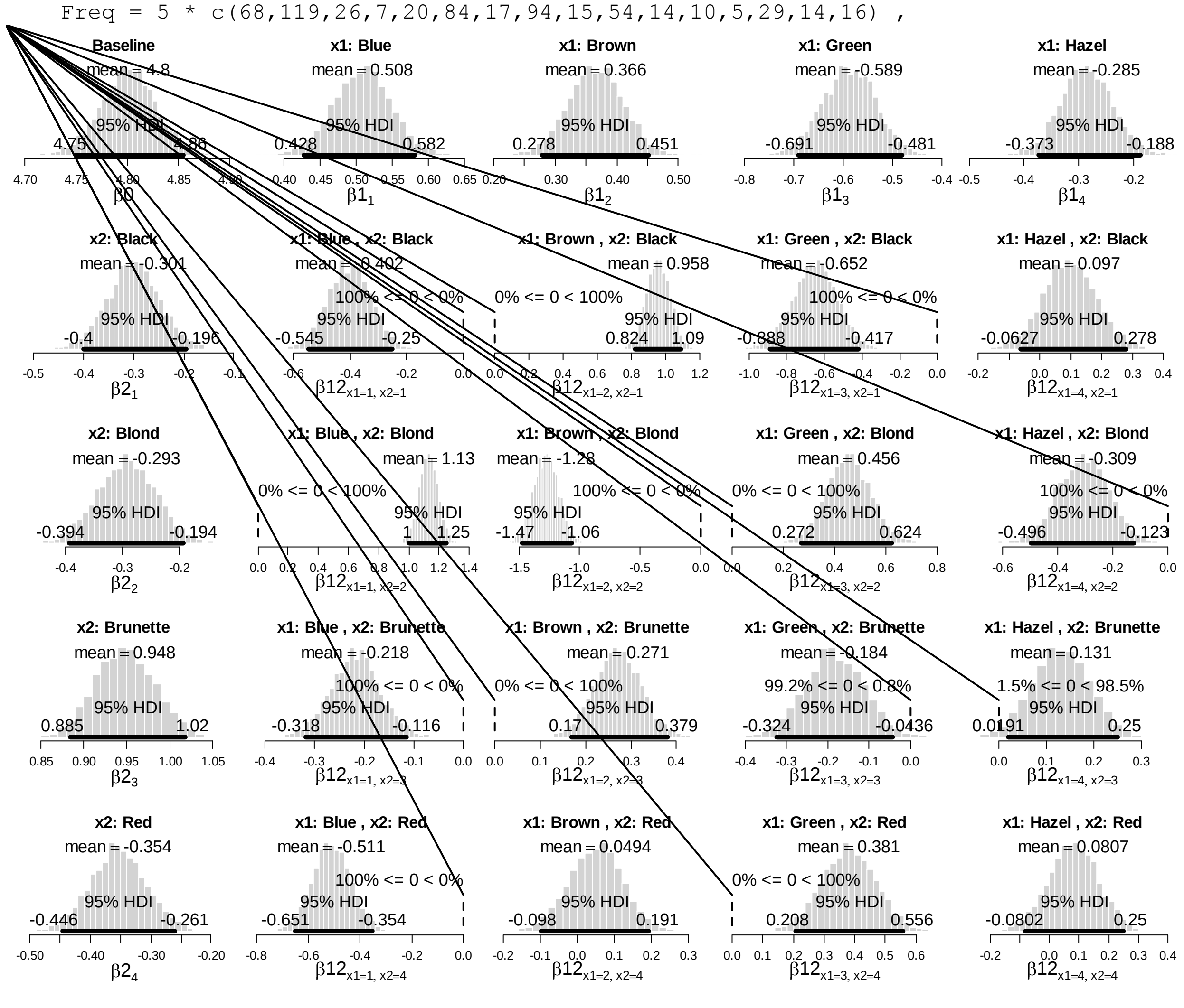
```
    Freq = ceiling( c(68,119,26,7,20,84,17,94,15,54,14,10,5,29,14,16) /2 ),
```

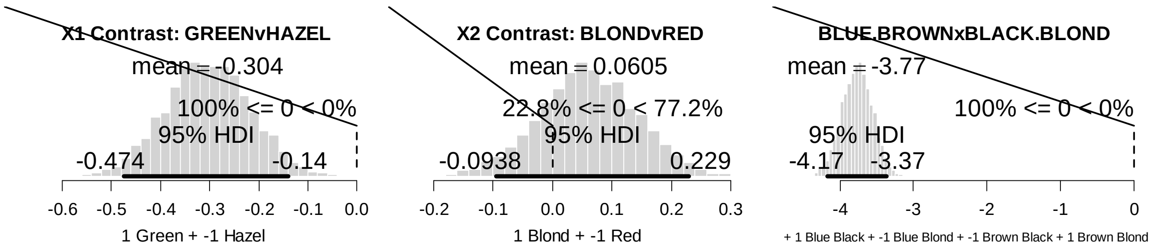


The HDIs are much wider for the halved frequencies than for the original data set (which are shown in Figure 22.3, p. 604 of the textbook). For example, the 95%HDI on the x2:Red deflection goes from -0.701 to -0.14 (a width of 0.561) for these halved frequencies, but from -0.575 to -0.174 (a width of 0.401) in the original frequencies.

(B) Multiply the original data vector by 5 so that all the cell frequencies are five times larger than the original. This modification preserves the relative proportions in each cell but quintuples the sample size. Run the program again. Show the histograms. Compute the width of the 95% HDIs for the contrasts. How do the precisions of the contrasts differ for the reduced and the enlarged data?

```
    Freq = 5 * c(68,119,26,7,20,84,17,94,15,54,14,10,5,29,14,16) ,
```



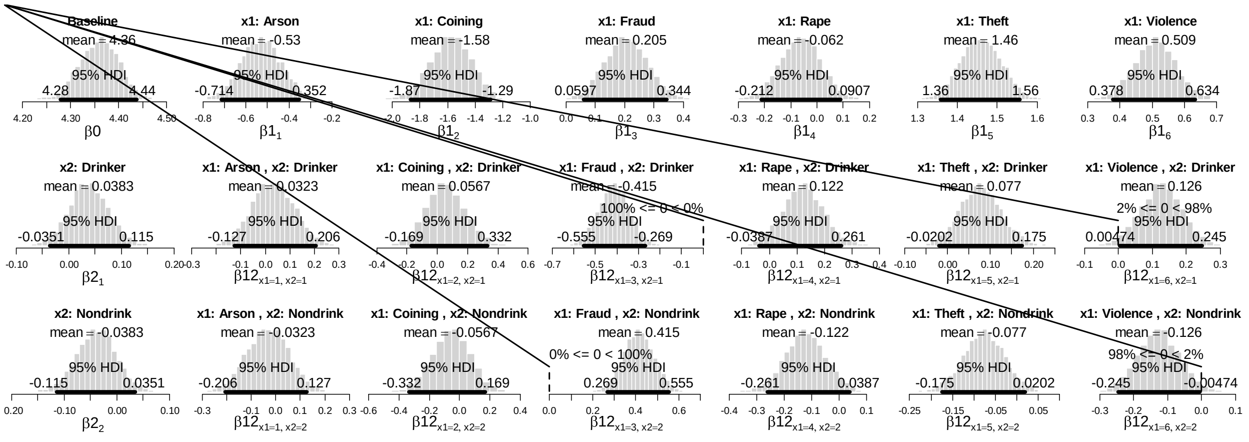


The HDIs are much narrower for the quintipled frequencies than for the original data set (which are shown in Figure 22.3, p. 604 of the textbook). For example, the 95%HDI on the x2:Red deflection goes from -0.446 to -0.261 (a width of 0.185) for these halved frequencies, but from -0.575 to -0.174 (a width of 0.401) in the original frequencies.

The contrasts have also had their HDIs greatly reduced. For example, in the halved data, the GREENvHAZEL contrast has an HDI that includes zero, but for the quintupled data, this contrast excludes zero. Thus, even though the relative proportions in the cells are the same as the original data, the increased sample size improves the certainty of the estimates and reduces the widths of the HDIs.

Exercise 22.2. [Purpose: To explore main effects and interactions in a contingency table.] The data section of the program in Section 22.4 (PoissonExponentialBrugs.R) includes data regarding the type of crime committed by convicted criminals and whether or not the criminal is a regular drinker of alcoholic beverages (Snee, 1974).

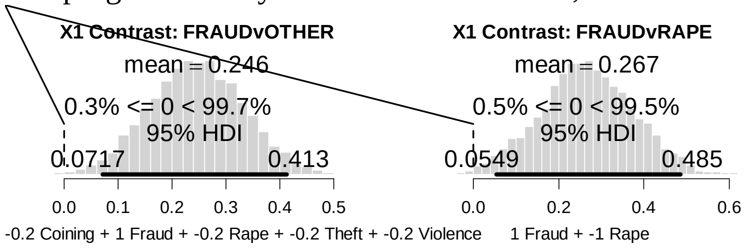
(A) Run the program with these data selected. Is there a credible nonindependence of the attributes? Describe the interaction in terms of the actual levels of the attributes (i.e., type of crime and drinker or nondrinker).



Yes, several of the interaction deflections exclude zero. (That is not a necessary condition for nonindependence, but it is sufficient.) For example, among criminals who committed fraud, there are fewer drinkers, i.e., more nondrinkers, than would be expected if the attributes were independent. In the opposite direction, among criminals who committed a violent crime (other than rape), there were more drinkers than would be expected if the attributes were independent.

(B) Is there a ("simple") main effect of fraud versus rape? That is, marginalizing across drinking, is there a credible difference in the proportion of criminals who committed fraud or committed rape? Show the results of an appropriate contrast.

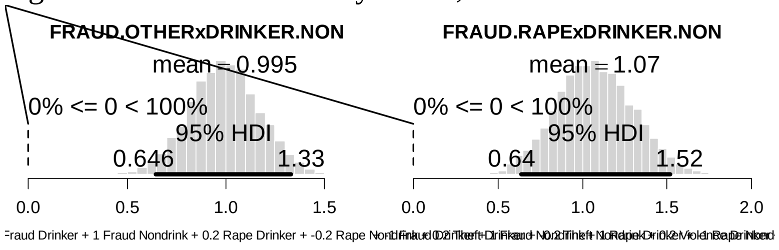
The program already has this contrast coded, and the result looks like this:



Thus, because the 95%HDI excludes zero, we say that it is highly credible that more criminals committed fraud than rape. (In fact, the contrast on the left shows that there was more fraud than the average of all the other categories of crimes.)

(C) Is the difference from the previous part the same among drinkers and nondrinkers? In other words, is the effect of criminal type the same at all levels of drinking? Show the results of an appropriate interaction contrast.

Again the contrast is already coded, and the result looks like this:



The right histogram shows the interaction contrast of fraud vs rape against drinker vs nondrinker. The distribution entirely excludes zero, and therefore we conclude that the interaction contrast is very credibly nonzero. There are two ways to state the interaction: Within these criminals, the ratio of rapists to fraud-committers is higher for drinkers than for nondrinker, or, the ratio of drinkers to nondrinkers is higher for rapists than for fraud-committers.

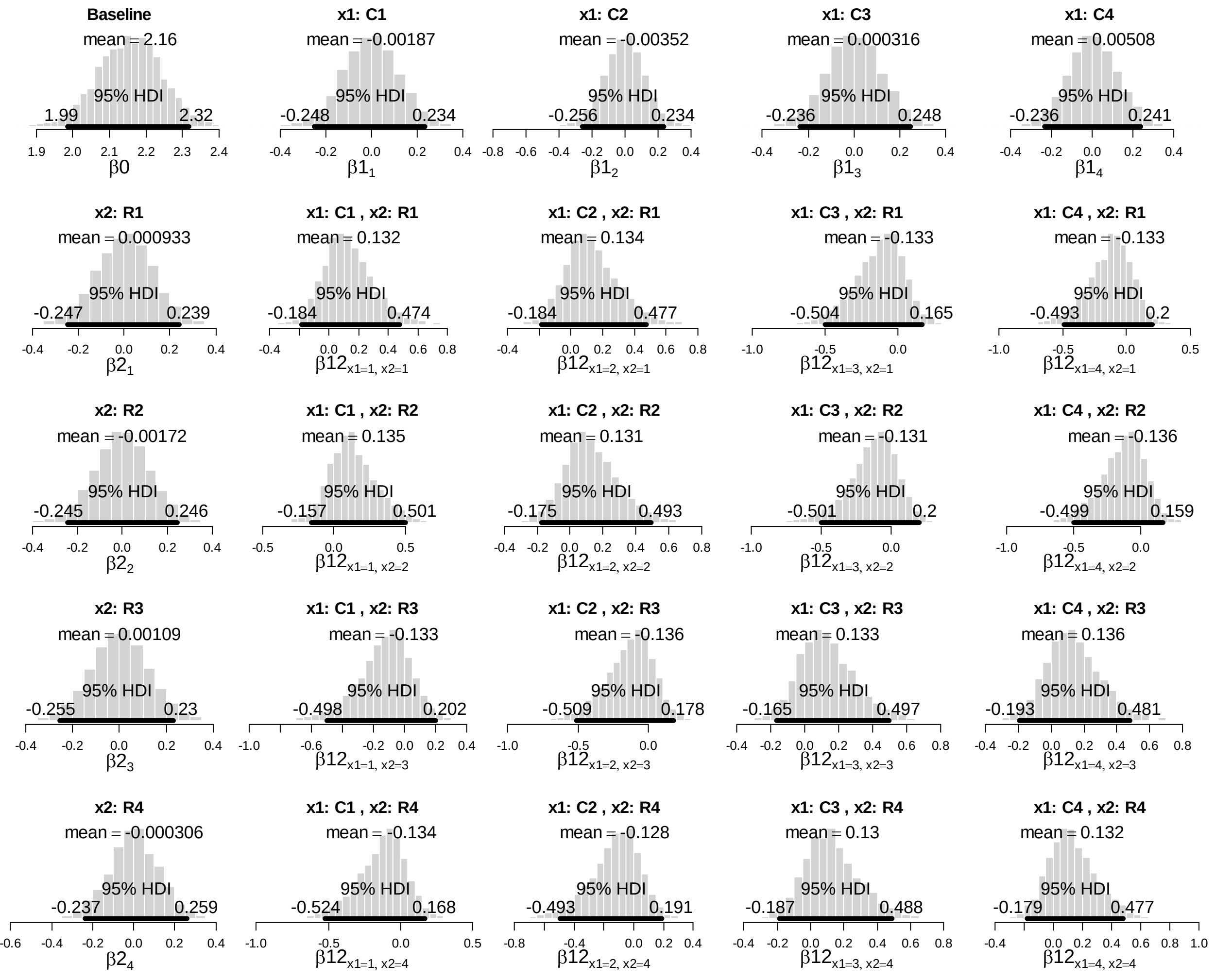
Exercise 22.3. [Purpose: To compare Bayesian analysis with chi-square test of independence.] This exercise assumes that you have some familiarity with traditional chi-square tests of independence. In the code of Section 22.4 (PoissonExponentialBrugs.R), the data section includes some simple fictitious data, which we can manipulate and then compare with results of Bayesian and chi-square analyses.

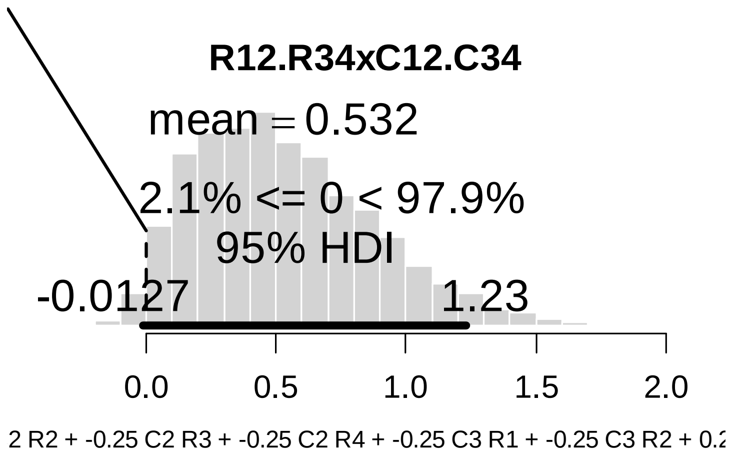
(A) Set the dataMultiplier to 6, and run the program. Include the histograms of the beta parameters and of the interaction contrast. Does the 95% HDI of the contrast include zero? The end of the program runs a chi-square test. What is the p value from the test? (Hint: See Figure 22.6.)

With the dataMultiplier set to 6, the data look like this (as shown in the R console window at the end of the run):

```
     [,1] [,2] [,3] [,4]
[1,]   12   12    6    6
[2,]   12   12    6    6
[3,]    6    6   12   12
[4,]    6    6   12   12
```
Notice that the marginals are uniform, i.e., all marginals have frequencies of 36. Only the interaction is not uniform. The question is whether the interaction is big enough that we can be very certain it is not zero.

The Bayesian posterior looks like this:





The marginal posteriors of the individual interaction deflections all include zero. The posterior of the interaction contrast includes zero in its 95%HDI (barely).

The chi-squared test at the end yields this result:

```
        Pearson's Chi-squared test
data:  obsFreq
X-squared = 16, df = 9, p-value = 0.06688
```

The p value is greater than .05, which means that the null hypothesis of independence is not rejected.

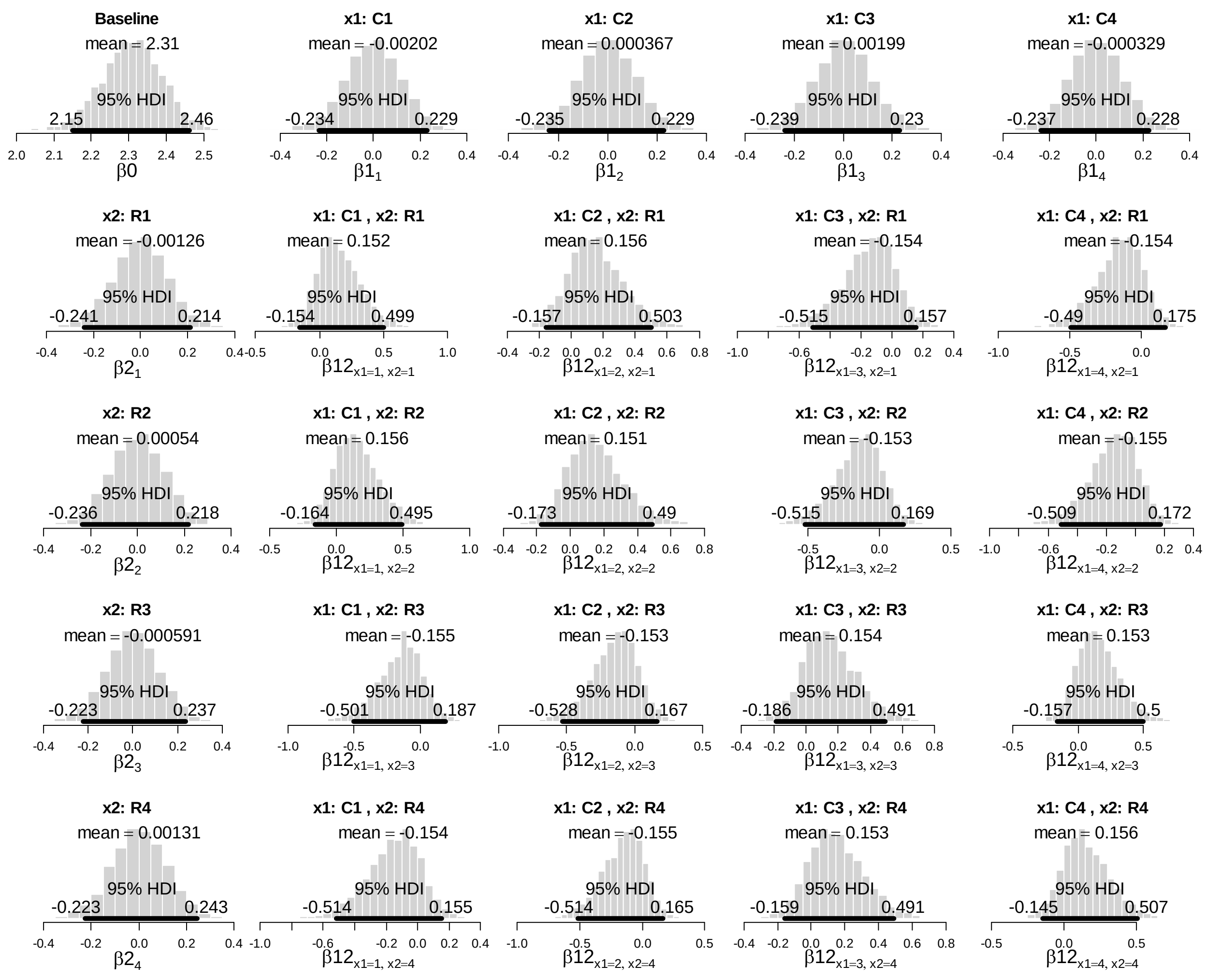
(B) Set the dataMultiplier to 7, and run the program. Include the histograms of the beta parameters and of the interaction contrast. Does the 95% HDI of the contrast include zero? The end of the program runs a chi-square test. What is the p value from the test? (Hint: See Figure 22.6.)

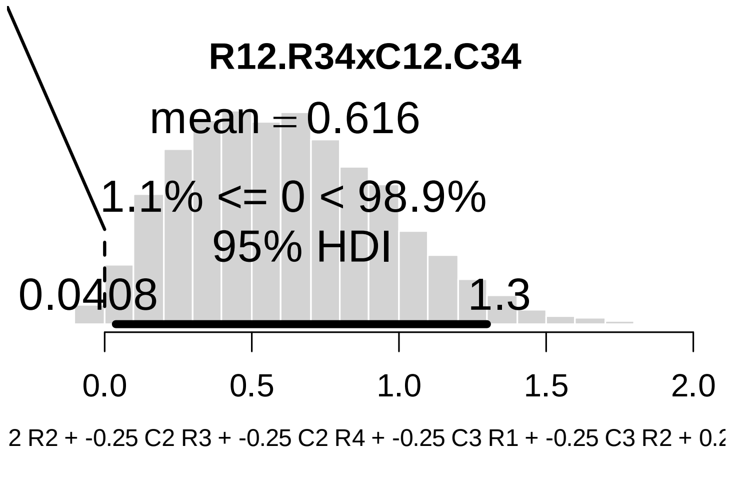
The data now look like this:

```
     [,1] [,2] [,3] [,4]
[1,]   14   14    7    7
[2,]   14   14    7    7
[3,]    7    7   14   14
[4,]    7    7   14   14
```

Like the previous part, the marginals are uniform.

The posterior now looks like this:





The individual cell interaction deflections all include zero, but the interaction contrast has a 95%HDI that excludes zero. In other words, by pooling across individual cells and computing an appropriate interaction contrast, we can see that there is variation across individual cells that is credibly different than pure independence or additivity.

The Pearson chi-squared test has these results:

```
        Pearson's Chi-squared test
data:  obsFreq
X-squared = 18.6667, df = 9, p-value = 0.02818
```

With p<.05, the user of NHST would reject the null hypothesis of independent attributes.

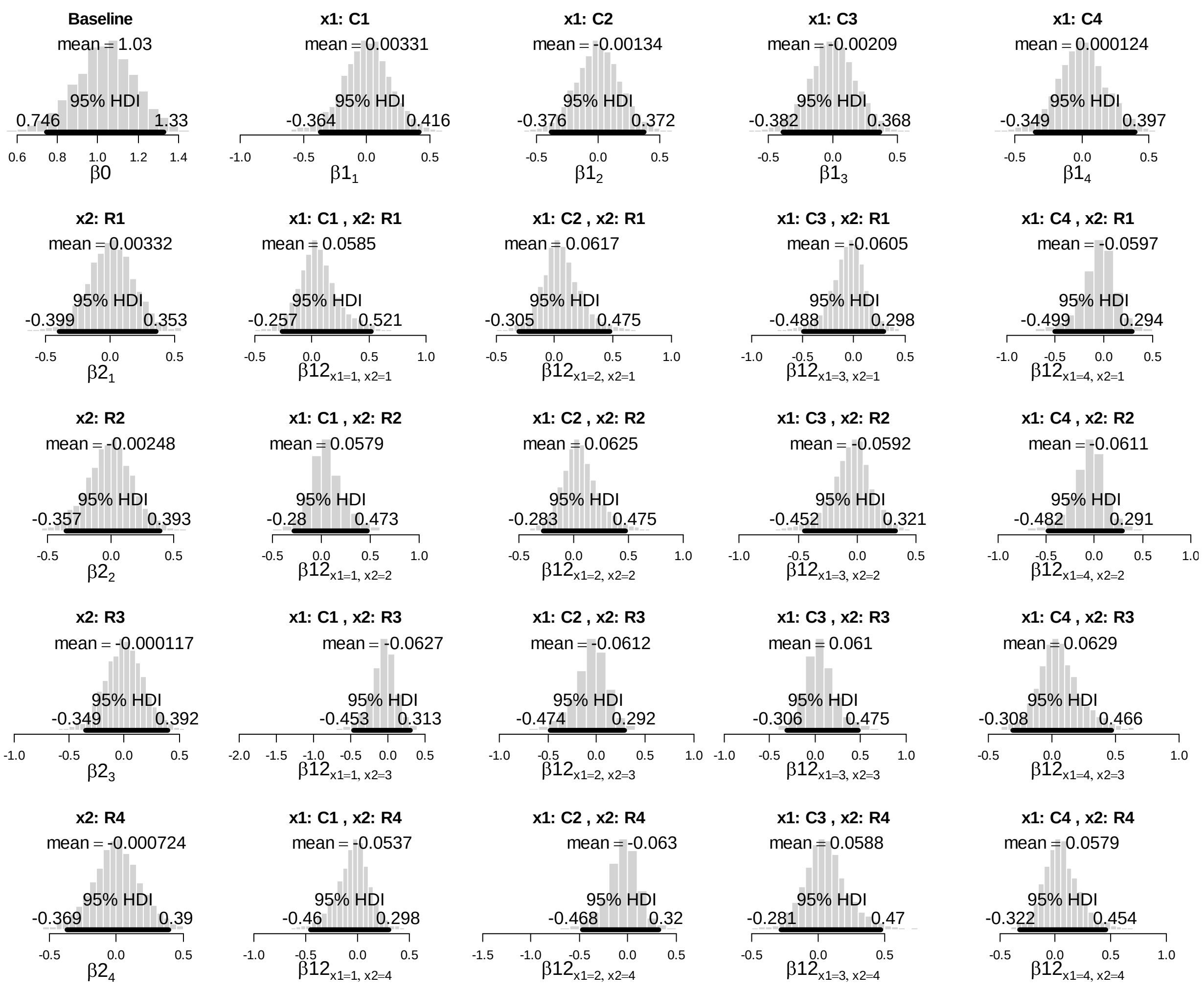
Across parts A and B, we see that the Bayesian and NHST analyses agree in their conclusions about whether or not nonindependence can be concluded from the data. The Bayesian analysis provides far more information, however, by showing individual cell posteriors and explicitly where the nonindependence arises. The Bayesian analysis also never computes a p value.

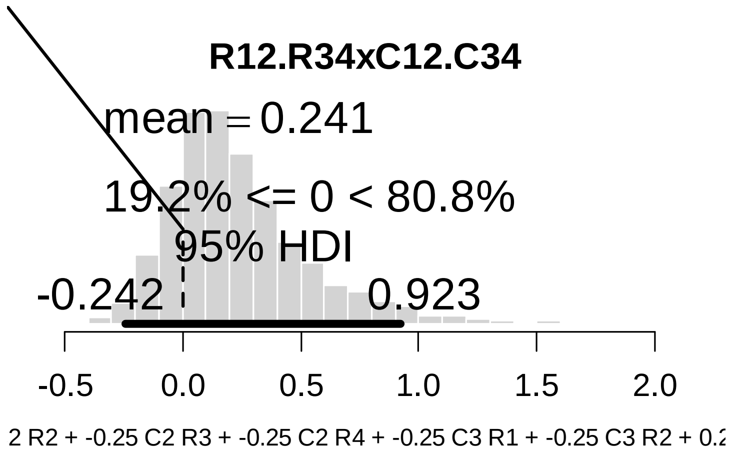
(C) Typical chi-square tests rely on approximating the sampling distribution of discrete Pearson chi-square values … with the continuous chi-square distribution (which derives from the sum of standardized normal samples). When the expected frequencies are too small, then the approximation is not good and the estimated p value may be wrong. A usual heuristic for declaring the chi-square test to be suspect is when (at least 10% of the) expected frequencies are less than 5. This is why computer packages issue warnings when expected values are too small. Bayesian analysis has no such problems. Set the dataMultiplier to 2, and run the program. Does the Bayesian analysis complain or do anything wrong? (No.) The end of the program runs a chi-square test. Is there a warning message? (Yes; report what it is.)

The data now are as follows:

```
     [,1] [,2] [,3] [,4]
[1,]    4    4    2    2
[2,]    4    4    2    2
[3,]    2    2    4    4
[4,]    2    2    4    4
```

The Bayesian posterior:





The point of showing the Bayesian posterior is that the Bayesian analysis proceeds as before, with no problems. The posterior shows that there is high uncertainty in the parameter estimates (because there data frequencies are so small).

The Pearson chi-squared test, however, gives this output with a warning message:

```
> chisqtest = chisq.test( obsFreq )
Warning message:
In chisq.test(obsFreq) : Chi-squared approximation may be incorrect
        Pearson's Chi-squared test
data:  obsFreq
X-squared = 5.3333, df = 9, p-value = 0.8043
```

The warning message is saying that the p value may be incorrect because it relies on approximating the discrete Pearson chi-square with the continuous chi-square, and the approximation is poor for small frequencies. The Bayesian analysis has no such problem with small frequencies.