exercise_sheet_9_Immanuel_Albrecht

May 4, 2023

1 Exercise sheet 9 - Wine tasting

For this exercise, you will need to load the dataset (Wines2012) from the rethinking package that we discussed already in the class.

[2]:

```
library(rethinking)
data(Wines2012)
d <- Wines2012
```

```
Lade nötiges Paket: rstan

Lade nötiges Paket: StanHeaders


rstan version 2.26.16 (Stan version 2.26.1)


For execution on a local, multicore CPU with excess RAM we recommend calling
options(mc.cores = parallel::detectCores()).
To avoid recompilation of unchanged Stan programs, we recommend calling
rstan_options(auto_write = TRUE)
For within-chain threading using `reduce_sum()` or `map_rect()` Stan functions,
change `threads_per_chain` option:
rstan_options(threads_per_chain = 1)


Do not specify '-march=native' in 'LOCAL_CPPFLAGS' or a Makevars file

Lade nötiges Paket: cmdstanr

This is cmdstanr version 0.5.3

- CmdStanR documentation and vignettes: mc-stan.org/cmdstanr

- CmdStan path: D:/Users/Immanuel/Documents/.cmdstan/cmdstan-2.31.0

- CmdStan version: 2.31.0
```

```
A newer version of CmdStan is available. See ?install_cmdstan() to install it.
To disable this check set option or environment variable
CMDSTANR_NO_VER_CHECK=TRUE.

Lade nötiges Paket: parallel

rethinking (Version 2.31)


Attache Paket: 'rethinking'


Das folgende Objekt ist maskiert 'package:rstan':

    stan


Das folgende Objekt ist maskiert 'package:stats':

    rstudent
```

This dataset comes from the judgment of Princeton, which was a wine tasting event that took place in 2012 in Princeton (NJ, USA). The goal was to compare French wines to the ones produced by the New Jersey wine industry. This dataset contains the following variables that we will be using:

- score: rating assigned by each judge to each wine.
- wine: wine id
- judge: judge name
- flight: red or white wine
- wine.amer: american or french wine
- judge.amer: american or french (or belgian) judge

The goal is to model the score variable (standardise it to facilitate the exercises below) based on the predictors listed above. Mention clearly the priors you are using throughout the exercises.

1.1 Exercise 1

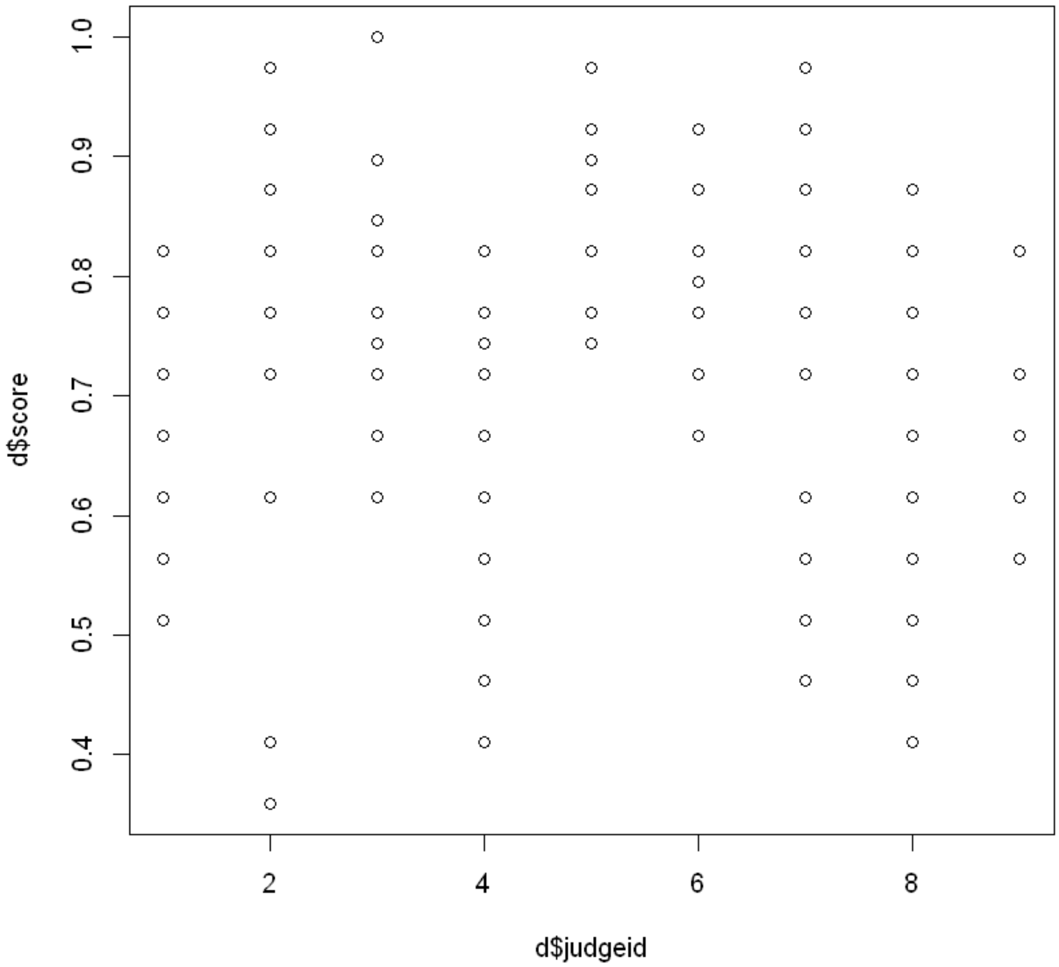
Focus on the interaction between the variables judge and wine. Use indices for these two variables, e.g. judgeid <- as.integer(d$judge). Start by using a simple linear model to measure the relationship between the score and the 9 judges and 20 wines. Use a figure to summarise the model output. Is there any visible pattern amongst the judges in the one hand and amongst the wines in the other hand? Are there wines that consistently got low/high ratings? Are there judges that are more severe than others?

[3]:

```r
d$judgeid <- as.integer(d$judge)
# d$judgeid <- scale(d$judgeid)
```

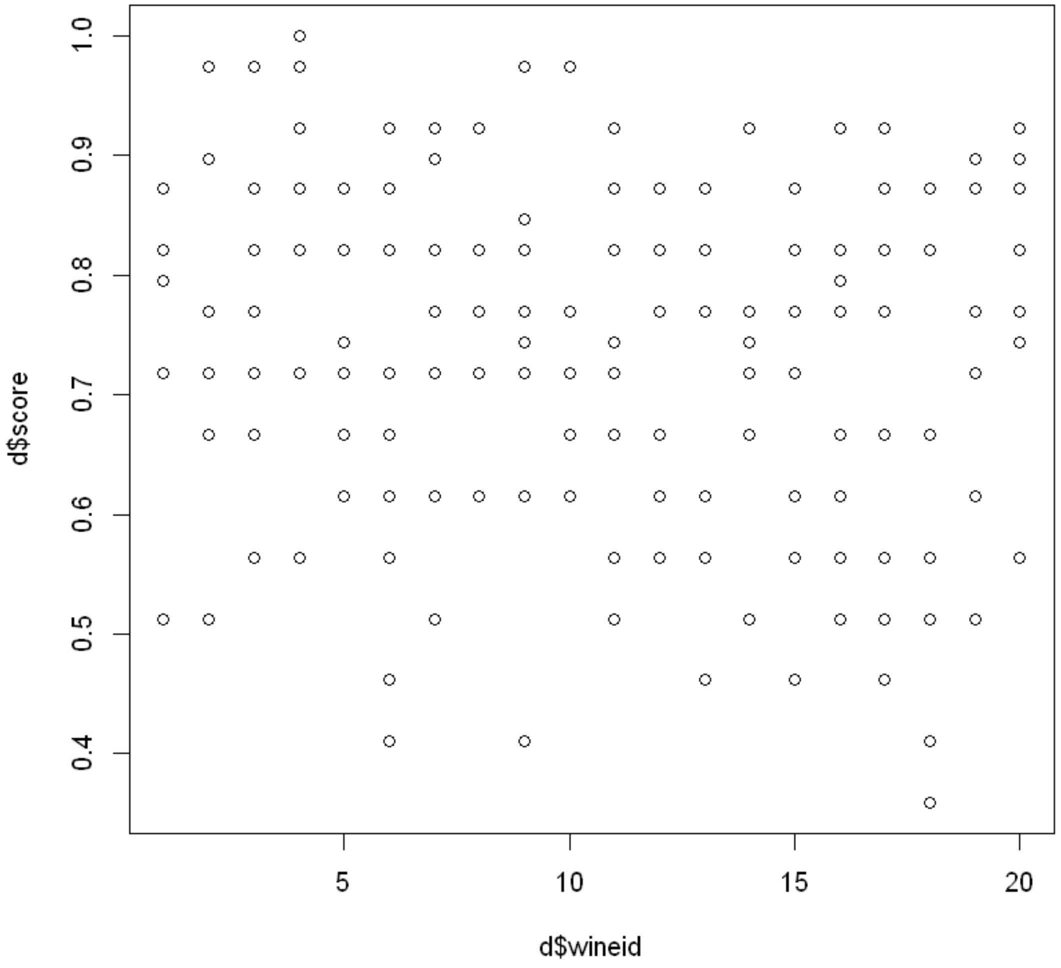
```
d$wineid <- as.integer(d$wine)
# d$wineid <- scale(d$wineid)
d.score.max <- max(d$score)
d$score <- d$score / d.score.max
d.score.mean <- mean(d$score)
d$flightid <- as.integer(d$flight) - 1
```

```
[4]: plot(d$judgeid, d$score)
     plot(d$wineid, d$score)
     d
```



A data.frame: 180 × 9

judge <fct>	flight <fct>	wine <fct>	score <dbl>	wine.amer <int>	judge.amer <int>	judgeid <int>	wine <int>
Jean-M Cardebat	white	A1	0.5128205	1	0	4	1
Jean-M Cardebat	white	B1	0.6666667	1	0	4	3
Jean-M Cardebat	white	C1	0.7179487	0	0	4	5
Jean-M Cardebat	white	D1	0.7692308	0	0	4	7
Jean-M Cardebat	white	E1	0.4102564	1	0	4	9
Jean-M Cardebat	white	F1	0.6666667	1	0	4	11
Jean-M Cardebat	white	G1	0.7692308	1	0	4	13
Jean-M Cardebat	white	H1	0.5641026	0	0	4	15
Jean-M Cardebat	white	I1	0.4615385	1	0	4	17
Jean-M Cardebat	white	J1	0.6153846	0	0	4	19
Tyler Colman	white	A1	0.8205128	1	1	9	1
Tyler Colman	white	B1	0.7179487	1	1	9	3
Tyler Colman	white	C1	0.7179487	0	1	9	5
Tyler Colman	white	D1	0.8205128	0	1	9	7
Tyler Colman	white	E1	0.6153846	1	1	9	9
Tyler Colman	white	F1	0.5641026	1	1	9	11
Tyler Colman	white	G1	0.5641026	1	1	9	13
Tyler Colman	white	H1	0.7179487	0	1	9	15
Tyler Colman	white	I1	0.5641026	1	1	9	17
Tyler Colman	white	J1	0.7179487	0	1	9	19
John Foy	white	A1	0.8205128	1	1	5	1
John Foy	white	B1	0.8717949	1	1	5	3
John Foy	white	C1	0.8205128	0	1	5	5
John Foy	white	D1	0.7692308	0	1	5	7
John Foy	white	E1	0.7435897	1	1	5	9
John Foy	white	F1	0.7435897	1	1	5	11
John Foy	white	G1	0.8205128	1	1	5	13
John Foy	white	H1	0.8717949	0	1	5	15
John Foy	white	I1	0.7692308	1	1	5	17
John Foy	white	J1	0.8974359	0	1	5	19
Daniele Meulder	red	A2	0.7179487	0	0	1	2
Daniele Meulder	red	B2	0.8205128	0	0	1	4
Daniele Meulder	red	C2	0.5641026	1	0	1	6
Daniele Meulder	red	D2	0.8205128	1	0	1	8
Daniele Meulder	red	E2	0.7179487	1	0	1	10
Daniele Meulder	red	F2	0.7692308	1	0	1	12
Daniele Meulder	red	G2	0.6666667	0	0	1	14
Daniele Meulder	red	H2	0.5641026	1	0	1	16
Daniele Meulder	red	I2	0.5128205	1	0	1	18
Daniele Meulder	red	J2	0.7692308	0	0	1	20
Jamal Rayyis	red	A2	0.7692308	0	0	3	2
Jamal Rayyis	red	B2	1.0000000	0	0	3	4
Jamal Rayyis	red	C2	0.7179487	1	0	3	6
Jamal Rayyis	red	D2	0.6153846	1	0	3	8
Jamal Rayyis	red	E2	0.6666667	1	0	3	10
Jamal Rayyis	red	F2	0.8205128	1	0	3	12
Jamal Rayyis	red	G2	0.7435897	0	0	3	14
Jamal Rayyis	red	H2	0.7692308	1	0	3	16
Jamal Rayyis	red	I2	0.8205128	1	0	3	18
Jamal Rayyis	red	J2	0.8205128	0	0	3	20



[5]:

```
model <- map(
        alist(
                score <- dnorm(mu, sigma),
                mu <- a + bj * judgeid + bw * wineid + bjw * judgeid * wineid,
                a ~ dnorm(mean(d$score), 10),
                bj ~ dnorm(0, 10),
                bw ~ dnorm(0, 10),
                bjw ~ dnorm(0, 10),
                sigma ~ dunif(0, 20)
        ),
        data = d
)
```

```
post <- extract.samples(model)
mu.link <- function(judgeid, wineid) post$a + post$bj * judgeid + post$bw *␣
 ↪wineid + post$bjw * judgeid * wineid
mu.link.judgeid <- function(judgeid) mu.link(judgeid, wineid = mean(d$wineid))
mu.link.wineid <- function(wineid) mu.link(judgeid = mean(d$judgeid), wineid)
```

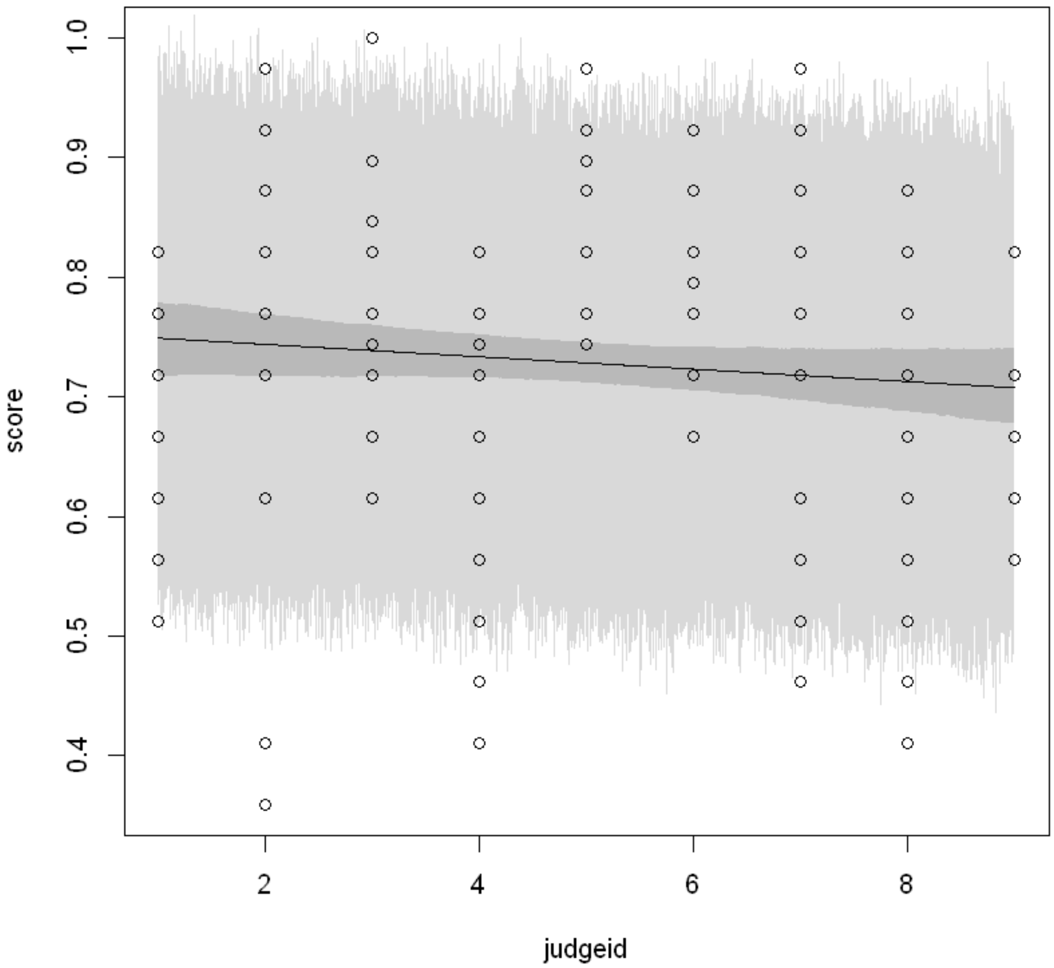
[6]:

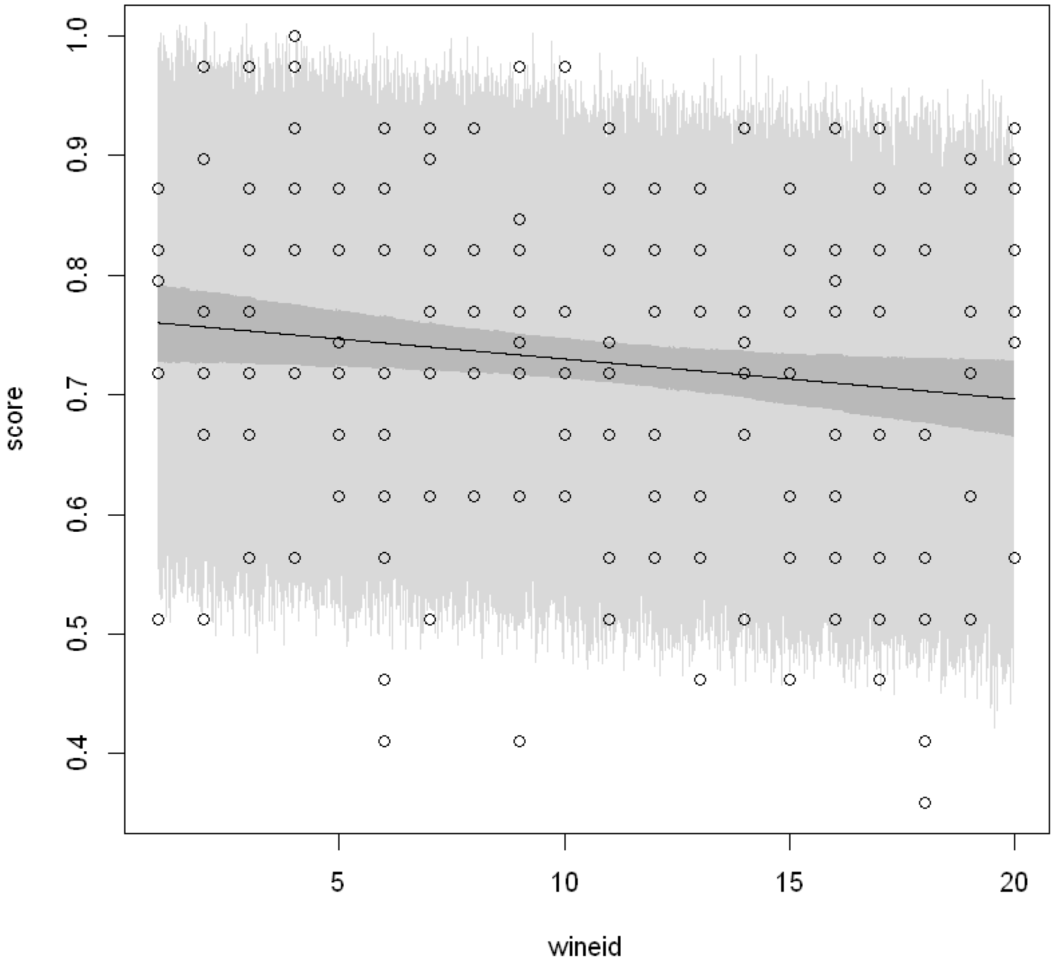
```
judgeid.seq <- seq(from = min(d$judgeid), to = max(d$judgeid), by = 0.01)
wineid.seq <- seq(from = min(d$wineid), to = max(d$wineid), by = 0.01)
```

[7]:

```
# This function plots a given model with shades
plot_with_shade_judgeid <- function(output, mu.link) {
# For each weight value we calculate a 91 percent credible interval
mu <- sapply(judgeid.seq, mu.link)
mu.mean <- apply(mu, 2, mean)
mu.HPDI <- apply(mu, 2, HPDI, prob = 0.91)

plot(score ~ judgeid, d)
lines(judgeid.seq, mu.mean)
shade(mu.HPDI, judgeid.seq)

# We calculate the 91 percent credible interval of the height variables by␣
 ↪taking into account the uncertainty of the slope and the standard deviation
sim.score <- sim(output, data = list(judgeid = judgeid.seq, wineid =␣
 ↪mean(d$wineid)))
score.HPDI <- apply(sim.score, 2, HPDI, prob = 0.91)
shade(score.HPDI, judgeid.seq)
}

plot_with_shade_wineid <- function(output, mu.link) {
# For each weight value we calculate a 91 percent credible interval
mu <- sapply(wineid.seq, mu.link)
mu.mean <- apply(mu, 2, mean)
mu.HPDI <- apply(mu, 2, HPDI, prob = 0.91)

plot(score ~ wineid, d)
lines(wineid.seq, mu.mean)
shade(mu.HPDI, wineid.seq)

# We calculate the 91 percent credible interval of the height variables by␣
 ↪taking into account the uncertainty of the slope and the standard deviation
sim.score <- sim(output, data = list(wineid = wineid.seq, judgeid =␣
 ↪mean(d$judgeid)))
score.HPDI <- apply(sim.score, 2, HPDI, prob = 0.91)
shade(score.HPDI, wineid.seq)
}

plot_with_shade_judgeid(model, mu.link.judgeid)
```

```
plot_with_shade_wineid(model, mu.link.wineid)
```



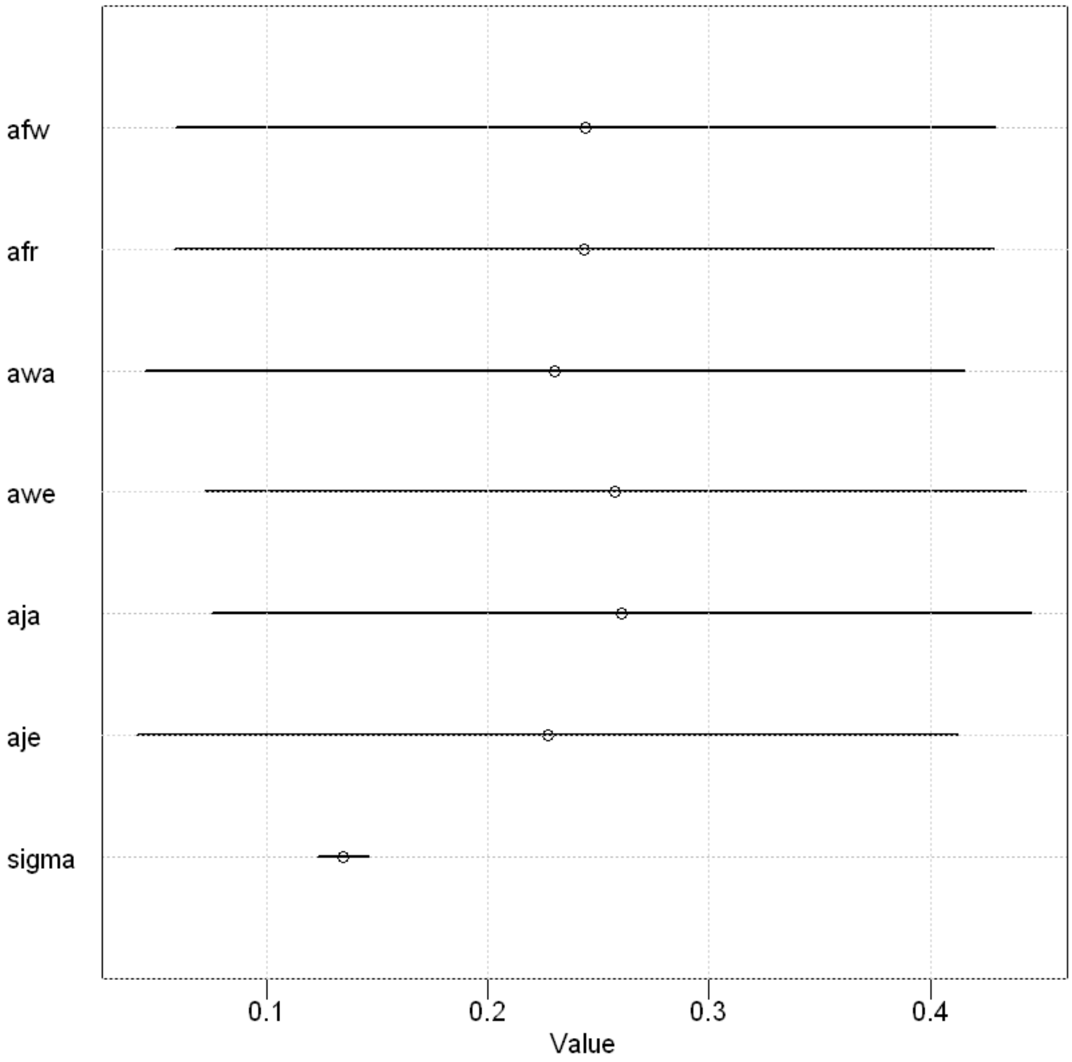


This was a dud. The linear model obviously doesnt tell us anything. We see that some wines have a little better scores than others, and some judges give on average better scores than others. For the useless model we used quite harmless priors that nearly dont restrict the parameters.

1.2 Exercise 2

Focus now on the flight, wine.amer and judge.amer variables. Build a linear model (without interactions for the time being) to model the score form these three predictors. Is there an identifiable bias between judge and wine regions? Is one flight favoured over the other? Compute posterior differences to aid in your analysis of the results.

[8]:
```
model1 <- map(
        alist(
                score ~ dnorm(mu, sigma),
                mu <- afw * flightid + afr * (1 - flightid) + awa * wine.amer + awe * (1 - wine.amer) + aja * judge.amer + aje * (1 - judge.amer),
                afw ~ dnorm(d.score.mean, 0.2),
                afr ~ dnorm(d.score.mean, 0.2),
                awa ~ dnorm(d.score.mean, 0.2),
                awe ~ dnorm(d.score.mean, 0.2),
                aja ~ dnorm(d.score.mean, 0.2),
                aje ~ dnorm(d.score.mean, 0.2),
                sigma ~ dunif(0, 2)
        ),
        data = d
)

plot(summary(model1))
grid()
```

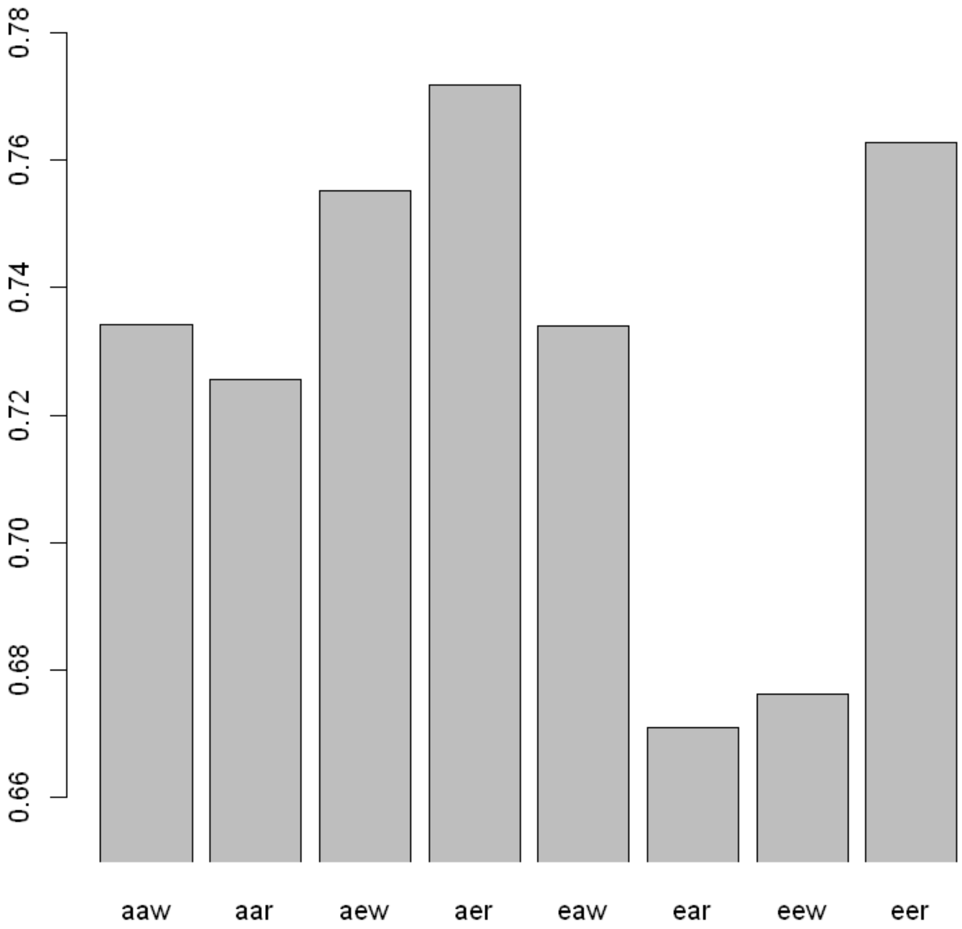


Okay, the exercise is worded so weirdly, that ill just answer the second part, if there is identifiable bias of judge, wine region and if one flight is favoured over another. We create a dataset for all possible combinations of judges, wines and flights

[19]:

```
d$aaw <- d$judge.amer * d$wine.amer * d$flightid
d$aar <- d$judge.amer * d$wine.amer * (1 - d$flightid)
d$aew <- d$judge.amer * (1 - d$wine.amer) * d$flightid
d$aer <- d$judge.amer * (1 - d$wine.amer) * (1 - d$flightid)
d$eaw <- (1 - d$judge.amer) * d$wine.amer * d$flightid
d$ear <- (1 - d$judge.amer) * d$wine.amer * (1 - d$flightid)
d$eew <- (1 - d$judge.amer) * (1 - d$wine.amer) * d$flightid
d$eer <- (1 - d$judge.amer) * (1 - d$wine.amer) * (1 - d$flightid)
```

```r
means <- c(mean(d$score[d$aaw == 1]), mean(d$score[d$aar == 1]), mean(d$score[d$aew == 1]), mean(d$score[d$aer == 1]), mean(d$score[d$eaw == 1]), mean(d$score[d$ear == 1]), mean(d$score[d$eew == 1]), mean(d$score[d$eer == 1]))
names <- c("aaw", "aar", "aew", "aer", "eaw", "ear", "eew", "eer")

barplot(means, names.arg = names, ylim = c(0.65, 0.78), xpd = FALSE)
```

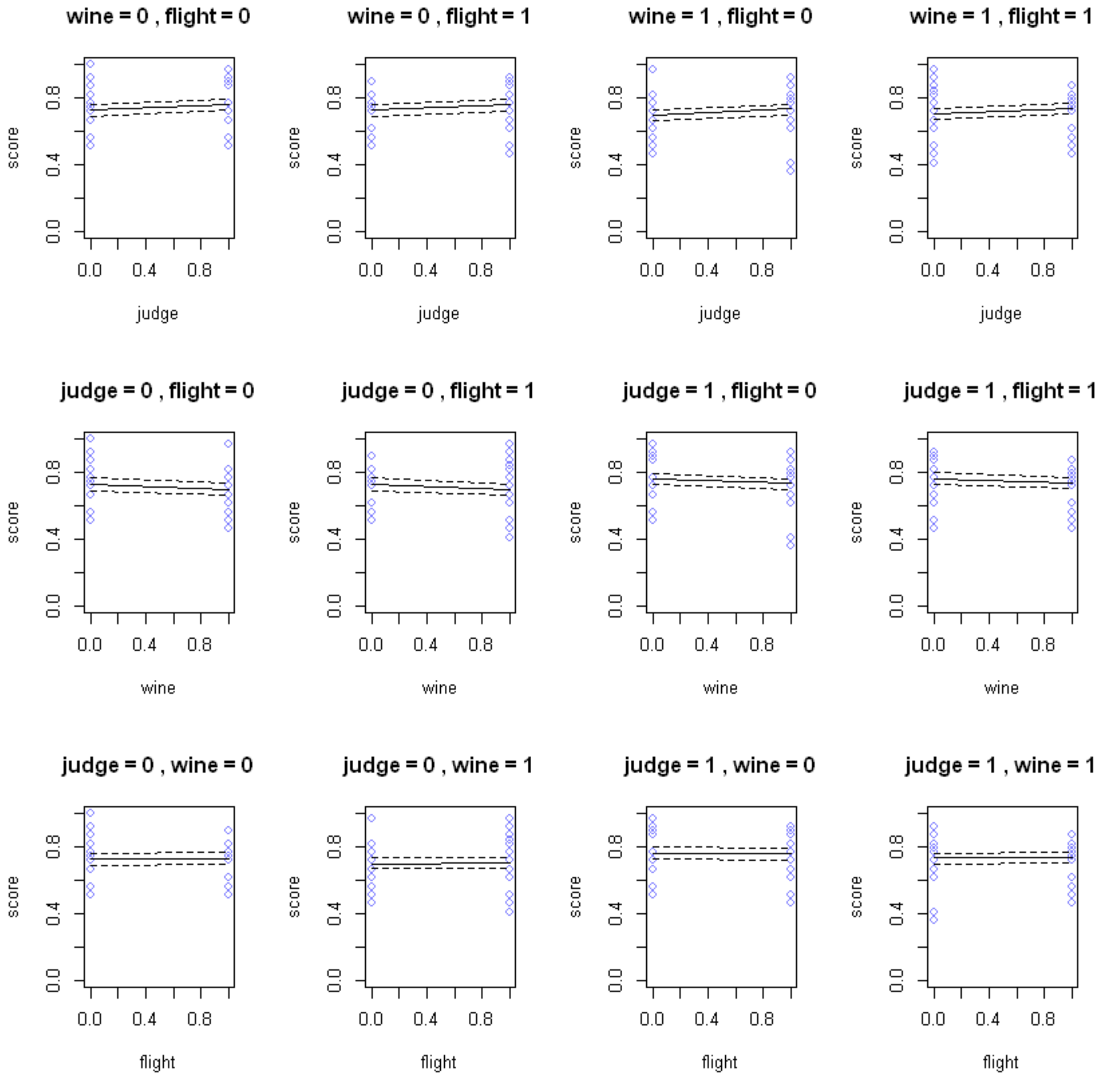


We see that american judges like european wine more than american one. European red has better scores than european white and american white has better scores than american red. Red american wine has the lowerst scores over all and red european has the best scores. Europeans like white american more than white european, and it is inverted for american judges.

Here we see the same results as above.

[62]:

```
# make a plot window with three panels in a single row
par(mfrow=c(3,4)) # 3 row, 4 columns
# loop over values of water.c and plot predictions
my_seq <- c(0, 1)
for (w in my_seq) {
        for (f in my_seq) {
                dt <- d[d$wine.amer == w & d$flightid == f, ]
                plot(score ~ judge.amer, data=dt, col=rangi2,
                main=paste("wine =", w, ", flight =", f), xlim=c(0, 1),␣
 ↪ylim=c(0, 1),
                xlab="judge")
                mu <- link(model1 , data=list(judge.amer = my_seq, wine.amer =␣
 ↪w, flightid = f))
                mu.mean <- apply(mu, 2, mean)
                mu.HPDI <- apply(mu, 2, HPDI, prob=0.91)
                lines(my_seq, mu.mean )
                lines(my_seq, mu.HPDI[1,], lty=2)
                lines(my_seq, mu.HPDI[2,], lty=2)
        }
}
for (j in my_seq) {
        for (f in my_seq) {
                dt <- d[d$judge.amer == j & d$flightid == f, ]
                plot(score ~ wine.amer, data=dt, col=rangi2,
                main=paste("judge =", j, ", flight =", f), xlim=c(0, 1),␣
 ↪ylim=c(0, 1),
                xlab="wine")
                mu <- link(model1 , data=list(wine.amer = my_seq, judge.amer =␣
 ↪j, flightid = f))
                mu.mean <- apply(mu, 2, mean)
                mu.HPDI <- apply(mu, 2, HPDI, prob=0.91)
                lines(my_seq, mu.mean )
                lines(my_seq, mu.HPDI[1,], lty=2)
                lines(my_seq, mu.HPDI[2,], lty=2)
        }
}
for (j in my_seq) {
        for (w in my_seq) {
                dt <- d[d$judge.amer == j & d$wine.amer == w, ]
                plot(score ~ flightid, data=dt, col=rangi2,
                main=paste("judge =", j, ", wine =", w), xlim=c(0, 1), ylim=c(0,␣
 ↪1),
                xlab="flight")
                mu <- link(model1 , data=list(flightid = my_seq, wine.amer = w,␣
 ↪judge.amer = j))
                mu.mean <- apply(mu, 2, mean)
                mu.HPDI <- apply(mu, 2, HPDI, prob=0.91)
                lines(my_seq, mu.mean )
                lines(my_seq, mu.HPDI[1,], lty=2)
                lines(my_seq, mu.HPDI[2,], lty=2)
        }
}
```

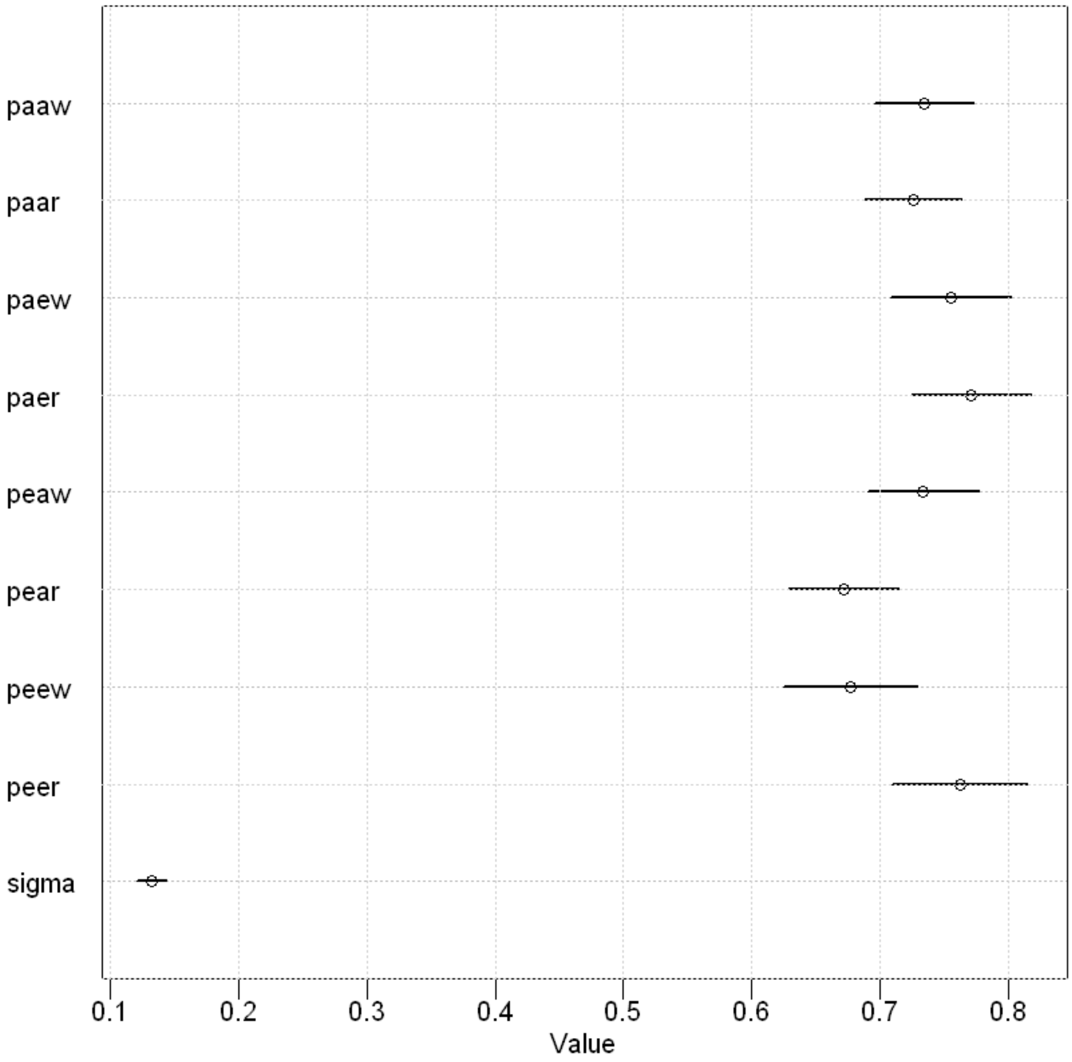


1.3 Exercise 3

Build a model that includes the three different interactions between the three variables of Exercise 2. Explain your choice of priors compared to Exercise 2 and detail how the interaction model affect the parameters. As in the class, use the link command to compute the predicted scores versus flight, wine region and judge nationality. In the interaction model, is there a preference (or not!) between judge's nationality and wine region? Discuss all other possible outcomes.

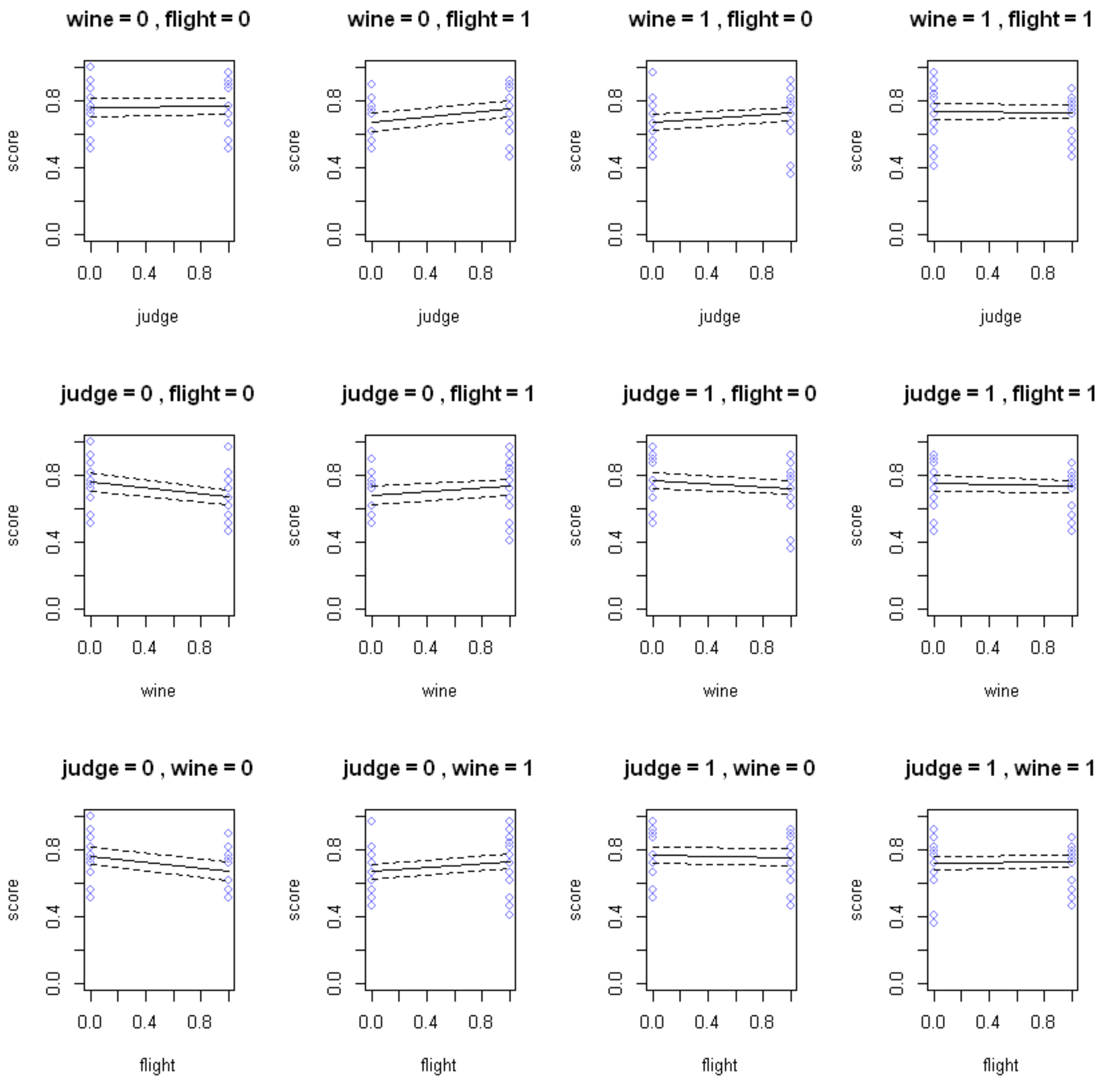
[46]:

```
model2 <- map(
        alist(
                score ~ dnorm(mu, sigma),
                mu <- paaw * judge.amer * wine.amer * flightid +
                paar * judge.amer * wine.amer * (1 - flightid) +
                paew * judge.amer * (1 - wine.amer) * flightid +
                paer * judge.amer * (1 - wine.amer) * (1 - flightid) +
                peaw * (1 - judge.amer) * wine.amer * flightid +
                pear * (1 - judge.amer) * wine.amer * (1 - flightid) +
                peew * (1 - judge.amer) * (1 - wine.amer) * flightid +
                peer * (1 - judge.amer) * (1 - wine.amer) * (1 - flightid),
                paaw ~ dnorm(d.score.mean, 0.3),
                paar ~ dnorm(d.score.mean, 0.3),
                paew ~ dnorm(d.score.mean, 0.3),
                paer ~ dnorm(d.score.mean, 0.3),
                peaw ~ dnorm(d.score.mean, 0.3),
                pear ~ dnorm(d.score.mean, 0.3),
                peew ~ dnorm(d.score.mean, 0.3),
                peer ~ dnorm(d.score.mean, 0.3),
                sigma ~ dunif(0, 2)
        ),
        data = d
)

plot(summary(model2))
grid()
```



```
[61]: # make a plot window with three panels in a single row
      par(mfrow=c(3,4)) # 3 row, 4 columns
      # loop over values of water.c and plot predictions
      my_seq <- c(0, 1)
      for (w in my_seq) {
              for (f in my_seq) {
                      dt <- d[d$wine.amer == w & d$flightid == f, ]
                      plot(score ~ judge.amer, data=dt, col=rangi2,
                      main=paste("wine =", w, ", flight =", f), xlim=c(0, 1),␣
       ↪ylim=c(0, 1),
                      xlab="judge")
                      mu <- link(model2 , data=list(judge.amer = my_seq, wine.amer =␣
       ↪w, flightid = f))
```

```
                mu.mean <- apply(mu, 2, mean)
                mu.HPDI <- apply(mu, 2, HPDI, prob=0.91)
                lines(my_seq, mu.mean )
                lines(my_seq, mu.HPDI[1,], lty=2)
                lines(my_seq, mu.HPDI[2,], lty=2)
        }
}
for (j in my_seq) {
        for (f in my_seq) {
                dt <- d[d$judge.amer == j & d$flightid == f, ]
                plot(score ~ wine.amer, data=dt, col=rangi2,
                main=paste("judge =", j, ", flight =", f), xlim=c(0, 1), ylim=c(0, 1),
                xlab="wine")
                mu <- link(model2 , data=list(wine.amer = my_seq, judge.amer = j, flightid = f))
                mu.mean <- apply(mu, 2, mean)
                mu.HPDI <- apply(mu, 2, HPDI, prob=0.91)
                lines(my_seq, mu.mean )
                lines(my_seq, mu.HPDI[1,], lty=2)
                lines(my_seq, mu.HPDI[2,], lty=2)
        }
}
for (j in my_seq) {
        for (w in my_seq) {
                dt <- d[d$judge.amer == j & d$wine.amer == w, ]
                plot(score ~ flightid, data=dt, col=rangi2,
                main=paste("judge =", j, ", wine =", w), xlim=c(0, 1), ylim=c(0, 1),
                xlab="flight")
                mu <- link(model2 , data=list(flightid = my_seq, wine.amer = w, judge.amer = j))
                mu.mean <- apply(mu, 2, mean)
                mu.HPDI <- apply(mu, 2, HPDI, prob=0.91)
                lines(my_seq, mu.mean )
                lines(my_seq, mu.HPDI[1,], lty=2)
                lines(my_seq, mu.HPDI[2,], lty=2)
        }
}
```



As discovered above, we see that the american judges prefer european white wine and europeans prefer american white wine. For red wine both nationalities prefer the european red wine.

As for the priors, I always used the same priors for all models.