

w271 Lab 2: Cereal Shelf Placement

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- (h) Estimate odds ratios and calculate corresponding confidence intervals for each explanatory variable. Relate your interpretations back to the plots constructed for this exercise. 16

#Load libraries and insert a function to tidy up the code when they are printed out
`library(vcd)`

`## Loading required package: grid`

```
library(nnet)
library(car)
```

`## Loading required package: carData`

```
library(Hmisc)
```

`## Loading required package: lattice`

`## Loading required package: survival`

`## Loading required package: Formula`

`## Loading required package: ggplot2`

```
##
## Attaching package: 'Hmisc'

## The following objects are masked from 'package:base':
##
##      format.pval, units

library(skimr)
library(MASS)

rm(list = ls())
library(knitr)

##
## Attaching package: 'knitr'

## The following object is masked from 'package:skimr':
##
##      kable

opts_chunk$set(tidy.opts=list(width.cutoff=60),tidy=TRUE)

cereal <- read.csv("cereal_dillons.csv")
str(cereal)

## 'data.frame':    40 obs. of  7 variables:
## $ ID          : int  1 2 3 4 5 6 7 8 9 10 ...
## $ Shelf       : int  1 1 1 1 1 1 1 1 1 1 ...
## $ Cereal      : Factor w/ 38 levels "Basic 4","Capn Crunch",...: 17 34 19 13 16 9 2 3 30 8 ...
## $ size_g      : int  28 28 28 32 30 31 27 27 29 33 ...
## $ sugar_g     : int  10 2 2 2 13 11 12 9 11 2 ...
## $ fat_g       : num  0 0 0 2 1 0 1.5 2.5 0.5 0 ...
## $ sodium_mg   : int  170 270 300 280 210 180 200 200 220 330 ...

# Examine the data to check data validity before proceeding
# with the questions.
skim(cereal)

## Skim summary statistics
## n obs: 40
## n variables: 7
##
## -- Variable type:factor -----
## variable missing complete  n n_unique          top_counts
##   Cereal           0       40 40          38 Cap: 2, Foo: 2, Bas: 1, Cap: 1
## ordered
##   FALSE
##
## -- Variable type:integer -----
## variable missing complete  n  mean    sd p0    p25    p50    p75 p100
##      ID           0       40 40   20.5 11.69  1   10.75  20.5  30.25  40
```

```
##      Shelf      0      40 40      2.5  1.13  1      1.75      2.5      3.25      4
##      size_g      0      40 40     37.2 11.79 27     29.75     31      51      60
##    sodium_mg      0      40 40    195.5 81.67  0    157.5     200     262.5     330
##      sugar_g      0      40 40     10.4  5.67  0      6      11      14      20
##      hist
##
##
##
##
##
##
## -- Variable type:numeric -----
## variable missing complete  n mean  sd p0 p25 p50  p75 p100      hist
##      fat_g      0      40 40     1.2 1.1  0 0.5   1 1.62      5
```

There are 7 variables with 40 observations evenly distributed across 4 shelves. There's no missing data. There are 38 types of cereal, with sugar content ranging 0 to 20 gram, fat content ranging from 0 to 5 gram, sodium content from 0 to 330 gram, serving size ranging 27 to 60 gram.

(a) The explanatory variables need to be re-formatted before proceeding further. First, divide each explanatory variable by its serving size to account for the different serving sizes among the cereals. Second, re-scale each variable to be within 0 and 1.

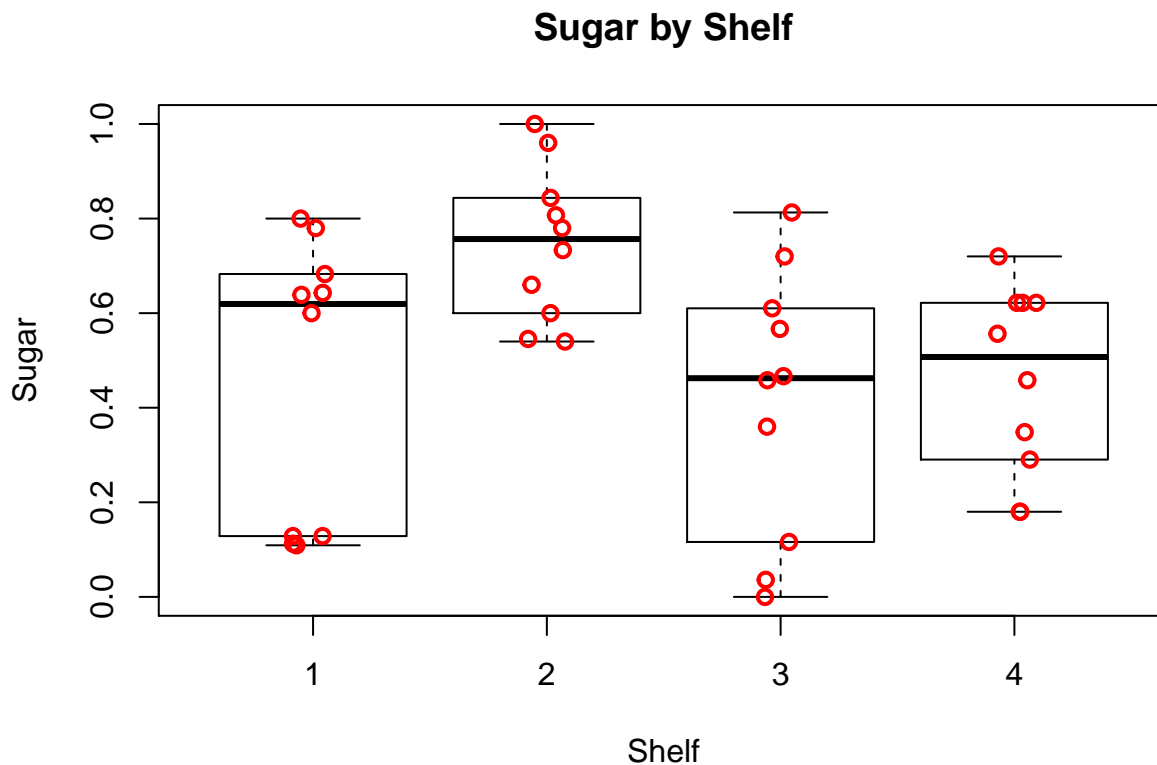
```
# the formula is from textbook
standardize <- function(x) {
  (x - min(x))/(max(x) - min(x))
}
cereal2 <- data.frame(Shelf = cereal$Shelf, Cereal = cereal$Cereal,
  sugar = standardize(cereal$sugar_g/cereal$size_g), fat = standardize(cereal$fat_g/cereal$size_g),
  sodium = standardize(cereal$sodium/cereal$size_g))

head(cereal2)
```

```
##      Shelf      Cereal      sugar      fat      sodium
## 1      1 Kellogg's Razzle Dazzle Rice Crispies 0.6428571 0.000 0.5666667
## 2      1      Post Toasties Corn Flakes 0.1285714 0.000 0.9000000
## 3      1      Kellogg's Corn Flakes 0.1285714 0.000 1.0000000
## 4      1      Food Club Toasted Oats 0.1125000 0.675 0.8166667
## 5      1      Frosted Cheerios 0.7800000 0.360 0.6533333
## 6      1      Food Club Frosted Flakes 0.6387097 0.000 0.5419355
```

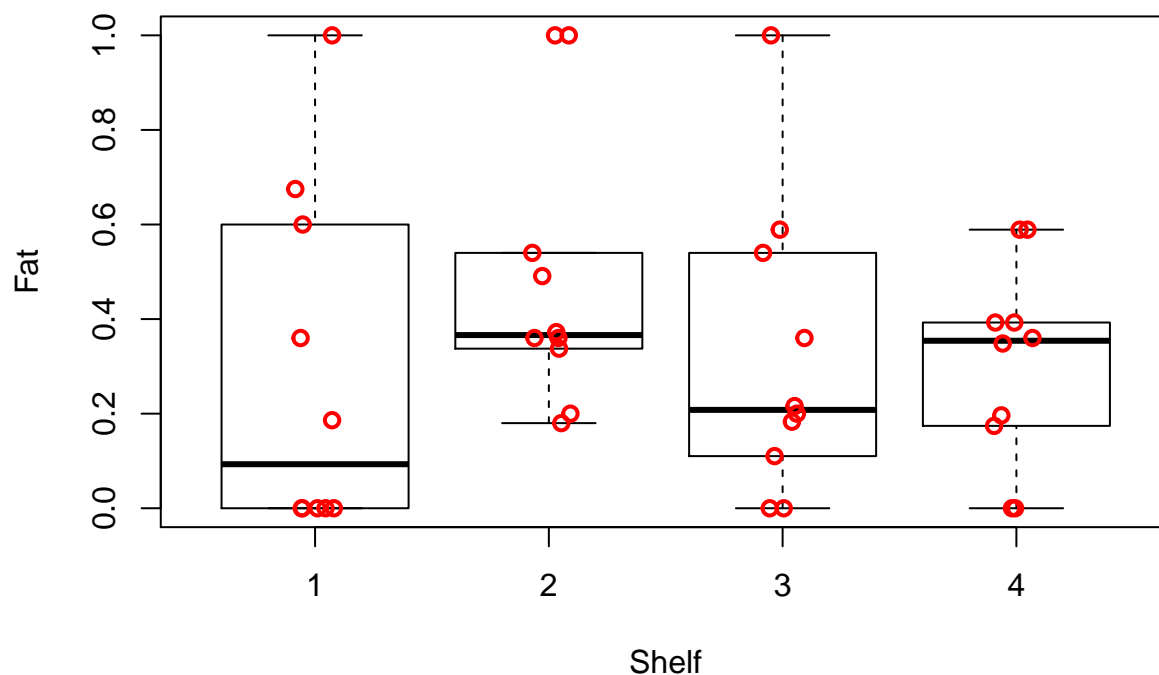
(b) Construct side-by-side box plots with dot plots overlaid for each of the explanatory variables. Also, construct a parallel coordinates plot for the explanatory variables and the shelf number. Discuss if possible content differences exist among the shelves.

```
# this code is from textbook
boxplot(formula = sugar ~ Shelf, data = cereal2, ylab = "Sugar",
        xlab = "Shelf", main = "Sugar by Shelf", pars = list(outpch = NA))
stripchart(x = cereal2$sugar ~ cereal2$Shelf, lwd = 2, col = "red",
          method = "jitter", vertical = TRUE, pch = 1, add = TRUE)
```



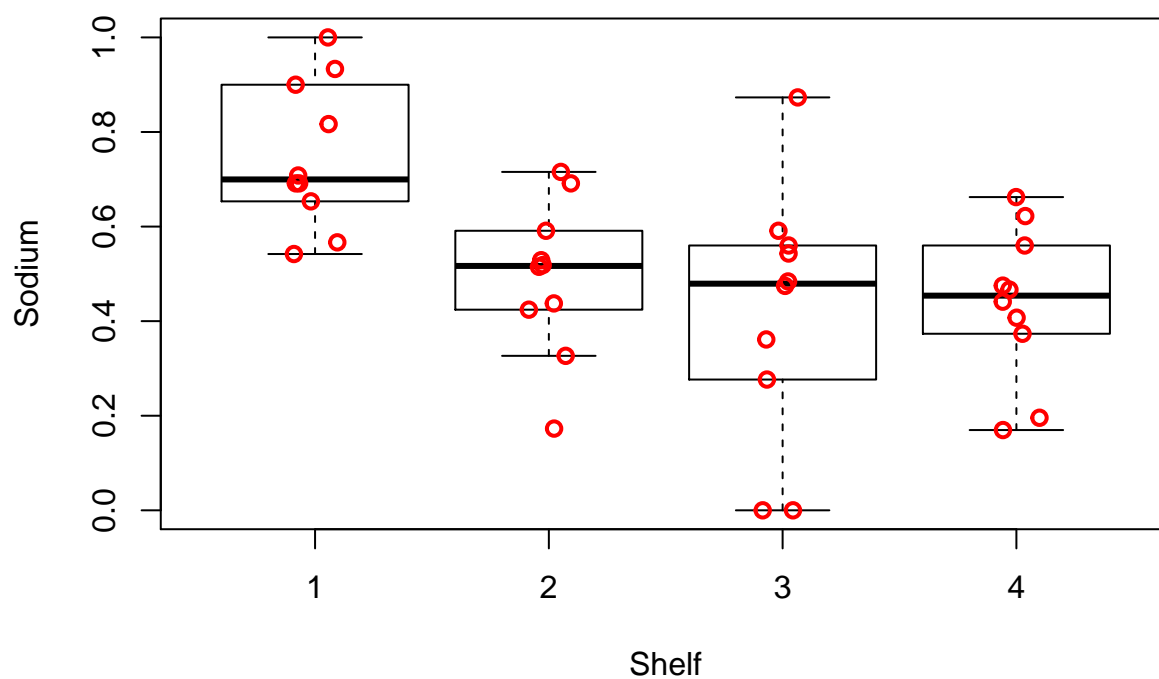
```
boxplot(formula = fat ~ Shelf, data = cereal2, ylab = "Fat",
        xlab = "Shelf", main = "Fat by Shelf", pars = list(outpch = NA))
stripchart(x = cereal2$fat ~ cereal2$Shelf, lwd = 2, col = "red",
          method = "jitter", vertical = TRUE, pch = 1, add = TRUE)
```

Fat by Shelf



```
boxplot(formula = sodium ~ Shelf, data = cereal2, ylab = "Sodium",
        xlab = "Shelf", main = "Sodium by Shelf", pars = list(outpch = NA))
stripchart(x = cereal2$sodium ~ cereal2$Shelf, lwd = 2, col = "red",
          method = "jitter", vertical = TRUE, pch = 1, add = TRUE)
```

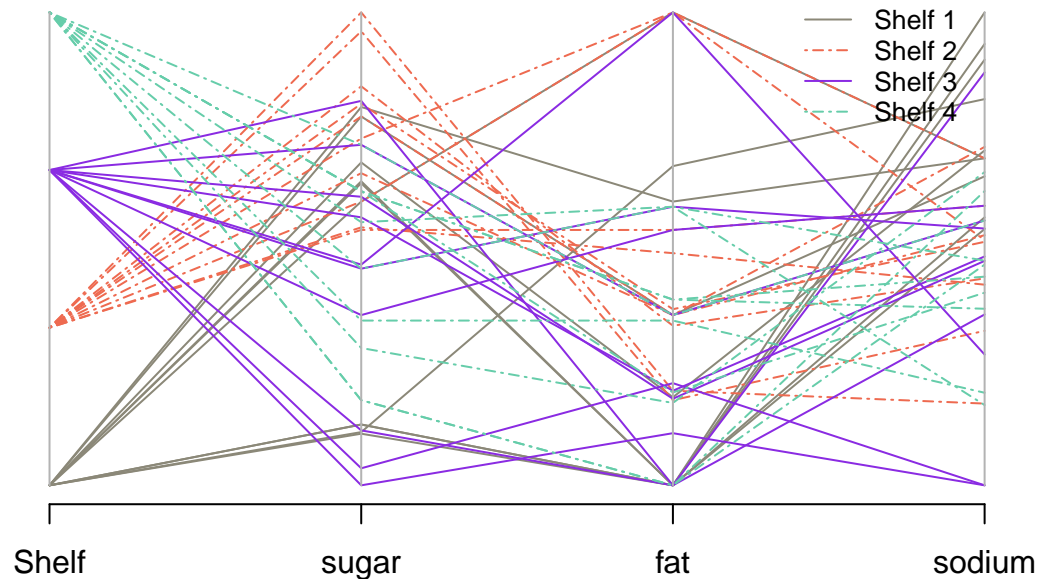
Sodium by Shelf



```
cereal3 <- data.frame(cereal2[1], cereal2[, 3:5])

# Colors by condition:
cereal.colors <- ifelse(test = cereal2$Shelf == 1, yes = "cornsilk4",
  no = ifelse(test = cereal2$Shelf == 2, yes = "coral2", no = ifelse(test = cereal2$Shelf ==
    3, yes = "blueviolet", no = "aquamarine3")))
# Line type by condition:
cereal.lty <- ifelse(test = cereal2$Shelf == 1, yes = "solid",
  no = ifelse(test = cereal2$Shelf == 2, yes = "twodash", no = ifelse(test = cereal2$Shelf ==
    3, yes = "solid", no = "twodash")))

parcoord(x = cereal3, col = cereal.colors, lty = cereal.lty) # Plot
legend(x = 3.35, y = 1.05, legend = c("Shelf 1", "Shelf 2", "Shelf 3",
  "Shelf 4"), lty = c("solid", "twodash", "solid", "twodash"),
  col = c("cornsilk4", "coral2", "blueviolet", "aquamarine3"),
  cex = 0.8, bty = "n")
```



High sugar content seems to be most prevalent among Shelf 2. The other shelves have a pretty wide spread of sugar content, with means roughly in the same places. Of note is Shelf 1's bimodal distribution of sugar, with one cluster of cereals with nearly no sugar and the other cluster having above average sugar content. Without that low sugar cluster, the rest of the shelf would have a mean sugar content much closer to Shelf 2.

Fat content seems to be pretty evenly distributed across shelves. In cereal this most likely corresponds to contents like nuts and oilseeds. There is a heavy occurrence of fat content at both extremes (1 and 0). Shelf 1 has so many 0 fat score cereals that its mean is lower than the others. Perhaps also notable is that shelf 2 is the only shelf with no cereals with a 0 score for fat, and that shelf 4 is the only shelf with no cereals with a 1 score, but visually, that information does not add much in light of the rest of the fat content plots.

Sodium content is notably highest on Shelf 1, but otherwise the other shelves have a more or less similar mean, with Shelf 3 showing the most breadth of sodium levels within that shelf.

(c) The response has values of 1, 2, 3, and 4. Under what setting would it be desirable to take into account ordinality. Do you think this occurs here?

Answer: If we believed that there was a natural ordering to the shelves, or that they could be arranged in an order such that shelf 1 < shelf 2 < shelf 3, etc. - then we would be desirable to take into account ordinality (especially if we believed that the “distance” between each level were equal). However, we do not believe that is the case with this data, as it is not clear whether being on a low shelf is objectively better than on a high shelf, or vice versa. There are attractors/detractors from each shelf height and for different customers - for example, children are at the height of lower shelves than adults are - but that ordering is not universal and therefore not desirable to take into account in our modeling. If other data could be brought in that demonstrated the desirability or marketability of each shelf had some order (which probably does exist), that could also be used as a factor for ordinality.

(d) Estimate a multinomial regression model with linear forms of the sugar, fat, and sodium variables. Perform LRTs to examine the importance of each explanatory variable.

```
levels(as.factor(cereal2$Shelf))

## [1] "1" "2" "3" "4"

mod1 <- multinom(as.factor(Shelf) ~ sugar + fat + sodium, data = cereal2)

## # weights:  20 (12 variable)
## initial  value 55.451774
## iter   10 value 37.329384
## iter   20 value 33.775257
## iter   30 value 33.608495
## iter   40 value 33.596631
## iter   50 value 33.595909
## iter   60 value 33.595564
## iter   70 value 33.595277
## iter   80 value 33.595147
## final   value 33.595139
## converged

summary(mod1)

## Call:
## multinom(formula = as.factor(Shelf) ~ sugar + fat + sodium, data = cereal2)
##
## Coefficients:
##   (Intercept)      sugar      fat      sodium
## 2    6.900708    2.693071    4.0647092 -17.49373
## 3   21.680680 -12.216442  -0.5571273 -24.97850
## 4   21.288343 -11.393710  -0.8701180 -24.67385
##
```

```
## Std. Errors:
## (Intercept)    sugar      fat    sodium
## 2    6.487408 5.051689 2.307250 7.097098
## 3    7.450885 4.887954 2.414963 8.080261
## 4    7.435125 4.871338 2.405710 8.062295
##
## Residual Deviance: 67.19028
## AIC: 91.19028
```

```
Anova(mod1)
```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: as.factor(Shelf)
##      LR Chisq Df Pr(>Chisq)
## sugar   22.7648 3  4.521e-05 ***
## fat      5.2836 3    0.1522
## sodium  26.6197 3  7.073e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- We cannot use mcprofile package for likelihood ratio, as nnet package author does not believe that one at a time intervals should be calculated. We use value of c equal to 1 standard deviation instead. *

```
sd.cereal <- apply(X = cereal2[, -c(2)], MARGIN = 2, FUN = sd)
c.value <- c(sd.cereal)[2:4]
round(c.value, 2)
```

```
## sugar    fat sodium
## 0.27    0.30  0.23
```

```
# coefficients(mod1)
beta.hat2 <- coefficients(mod1)[1, 2:4]
beta.hat3 <- coefficients(mod1)[2, 2:4]
beta.hat4 <- coefficients(mod1)[3, 2:4]
# OR for j = 2 (Shelf 2 vs Shelf 1)
print("OR for j = 2")
```

```
## [1] "OR for j = 2"
```

```
round(exp(c.value * beta.hat2), 2)
```

```
## sugar    fat sodium
## 2.06    3.37  0.02
```

```
round(1/exp(c.value * beta.hat2), 2)
```

```
## sugar    fat sodium
## 0.48    0.30 55.74
```



```
# OR for j = 3 (Shelf 3 vs Shelf 1)
print("OR for j = 3")
```

```
## [1] "OR for j = 3"
```

```
round(exp(c.value * beta.hat3), 2)
```

```
## sugar    fat sodium
##  0.04    0.85   0.00
```

```
round(1/exp(c.value * beta.hat3), 2)
```

```
## sugar    fat sodium
## 26.81    1.18 311.36
```

```
# OR for j = 4 (Shelf 4 vs Shelf 1)
print("OR for j = 3")
```

```
## [1] "OR for j = 3"
```

```
round(exp(c.value * beta.hat4), 2)
```

```
## sugar    fat sodium
##  0.05    0.77   0.00
```

```
round(1/exp(c.value * beta.hat4), 2)
```

```
## sugar    fat sodium
## 21.48    1.30 290.31
```

(e) Show that there are no significant interactions among the explanatory variables (including an interaction among all three variables).

```
## Not actually sure if this is what the question means?
```

```
modA <- multinom(as.factor(Shelf) ~ sugar + fat + sodium + sugar:fat,
  data = cereal2)
```

```
## # weights:  24 (15 variable)
## initial  value 55.451774
## iter   10 value 37.518284
## iter   20 value 33.008954
## iter   30 value 31.923790
## iter   40 value 31.590382
## iter   50 value 31.417819
## iter   60 value 31.212591
## iter   70 value 31.158365
## iter   80 value 31.068476
## iter   90 value 31.042861
## iter  100 value 30.998934
```

```
## final value 30.998934
## stopped after 100 iterations
```

```
Anova(modA)
```

```
## Analysis of Deviance Table (Type II tests)
```

```
##
```

```
## Response: as.factor(Shelf)
```

```
##          LR Chisq Df Pr(>Chisq)
```

```
## sugar      22.7648  3  4.521e-05 ***
```

```
## fat         5.2836  3    0.1522
```

```
## sodium     30.8407  3  9.183e-07 ***
```

```
## sugar:fat   5.1924  3    0.1582
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
modB <- multinom(as.factor(Shelf) ~ sugar + fat + sodium + sugar:sodium,
  data = cereal2)
```

```
## # weights:  24 (15 variable)
```

```
## initial value 55.451774
```

```
## iter  10 value 36.577939
```

```
## iter  20 value 33.026993
```

```
## iter  30 value 32.740384
```

```
## iter  40 value 32.604061
```

```
## iter  50 value 32.452790
```

```
## iter  60 value 32.427677
```

```
## iter  70 value 32.423013
```

```
## iter  80 value 32.420834
```

```
## iter  90 value 32.420382
```

```
## iter 100 value 32.420219
```

```
## final value 32.420219
```

```
## stopped after 100 iterations
```

```
Anova(modB)
```

```
## Analysis of Deviance Table (Type II tests)
```

```
##
```

```
## Response: as.factor(Shelf)
```

```
##          LR Chisq Df Pr(>Chisq)
```

```
## sugar      22.7648  3  4.521e-05 ***
```

```
## fat         6.1167  3    0.1061
```

```
## sodium     26.6197  3  7.073e-06 ***
```

```
## sugar:sodium  2.3498  3    0.5030
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
modC <- multinom(as.factor(Shelf) ~ sugar + fat + sodium + fat:sodium,
  data = cereal2)
```

```
## # weights:  24 (15 variable)
```

```
## initial value 55.451774
## iter 10 value 36.936754
## iter 20 value 32.546388
## iter 30 value 32.211409
## iter 40 value 32.085217
## iter 50 value 31.709427
## iter 60 value 31.095835
## iter 70 value 30.872944
## iter 80 value 30.734369
## iter 90 value 30.653914
## iter 100 value 30.639405
## final value 30.639405
## stopped after 100 iterations
```

```
Anova(modC)
```

```
## Analysis of Deviance Table (Type II tests)
```

```
##
```

```
## Response: as.factor(Shelf)
```

```
##          LR Chisq Df Pr(>Chisq)
```

```
## sugar      19.2525  3 0.0002424 ***
```

```
## fat         5.2836  3 0.1521727
```

```
## sodium     26.6197  3 7.073e-06 ***
```

```
## fat:sodium  5.9115  3 0.1159978
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
modD <- multinom(as.factor(Shelf) ~ sugar + fat + sodium + fat:sodium:sugar,
  data = cereal2)
```

```
## # weights: 24 (15 variable)
```

```
## initial value 55.451774
```

```
## iter 10 value 37.410894
```

```
## iter 20 value 33.855213
```

```
## iter 30 value 33.056977
```

```
## iter 40 value 32.715781
```

```
## iter 50 value 32.677949
```

```
## iter 60 value 32.592524
```

```
## iter 70 value 32.578128
```

```
## iter 80 value 32.550159
```

```
## iter 90 value 32.541053
```

```
## iter 100 value 32.535394
```

```
## final value 32.535394
```

```
## stopped after 100 iterations
```

```
Anova(modD)
```

```
## Analysis of Deviance Table (Type II tests)
```

```
##
```

```
## Response: as.factor(Shelf)
```

```
##              LR Chisq Df Pr(>Chisq)
## sugar          22.7648  3  4.521e-05 ***
## fat            5.2836  3    0.1522
## sodium        26.6197  3  7.073e-06 ***
## sugar:fat:sodium 2.1195  3    0.5480
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

modE <- multinom(as.factor(Shelf) ~ sugar + fat + sodium + sugar:fat +
  sugar:sodium + fat:sodium + fat:sodium:sugar, data = cereal2)

## # weights:  36 (24 variable)
## initial  value 55.451774
## iter   10 value 36.170336
## iter   20 value 31.166546
## iter   30 value 29.963705
## iter   40 value 28.414027
## iter   50 value 27.891712
## iter   60 value 27.763967
## iter   70 value 27.622579
## iter   80 value 27.438263
## iter   90 value 27.015534
## iter  100 value 26.772481
## final   value 26.772481
## stopped after 100 iterations

Anova(modE)

## Analysis of Deviance Table (Type II tests)
##
## Response: as.factor(Shelf)
##              LR Chisq Df Pr(>Chisq)
## sugar          19.2525  3  0.0002424 ***
## fat            6.1167  3  0.1060686
## sodium        30.8407  3  9.183e-07 ***
## sugar:fat       3.2309  3  0.3573733
## sugar:sodium    3.0185  3  0.3887844
## fat:sodium      3.1586  3  0.3678151
## sugar:fat:sodium 2.5884  3  0.4595299
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

(f) Kellogg's Apple Jacks (<http://www.applejacks.com>) is a cereal marketed toward children. For a serving size of 28 grams, its sugar content is 12 grams, fat content is 0.5 grams, and sodium content is 130 milligrams. Estimate the shelf probabilities for Apple Jacks.

Alice's solution:

```

# recall rescale function from textbook stand01 <-
# function(x) { (x - min(x))/(max(x) - min(x)) } cereal has
# the pre-scaled variable numbers. Don't use cereal2
stand02 <- function(x, variable) {
  (x - min(variable))/(max(variable) - min(variable))
}
sugar1 <- stand02(x = 12/28, variable = cereal$sugar)
fat1 <- stand02(x = 0.5/28, variable = cereal$fat)
sodium1 <- stand02(x = 1.3/28, variable = cereal$sodium)
newdata <- data.frame(sugar = sugar1, fat = fat1, sodium = sodium1)
lin.pred.hat <- predict(object = mod1, newdata = newdata, type = "probs",
  se = TRUE)
round(lin.pred.hat, 7)

```

```

##          1          2          3          4
## 0.0000000 0.0000003 0.5928551 0.4071446

```

Jessica's solution:

```

stand.new <- function(meas, serv_size, comparison) {
  (meas/serv_size - min(comparison))/(max(comparison) - min(comparison))
}

newdata <- data.frame(sugar = stand.new(12, 28, cereal$sugar_g/cereal$size_g),
  fat = stand.new(0.5, 28, cereal$fat_g/cereal$size_g), sodium = stand.new(130,
  28, cereal$sodium_mg/cereal$size_g))

round(predict(object = mod1, newdata = newdata, type = "probs",
  se.fit = TRUE), 7)

```

```

##          1          2          3          4
## 0.0532685 0.4719426 0.2004274 0.2743615

```

(g) Construct a plot similar to Figure 3.3 where the estimated probability for a shelf is on the y-axis and the sugar content is on the x-axis. Use the mean overall fat and sodium content as the corresponding variable values in the model. Interpret the plot with respect to sugar content.

Alice's solution:

```

newfat <- c(rep(mean(cereal2$fat), 11))
newsodium <- c(rep(mean(cereal2$sodium), 11))
newsugar <- c(seq(0, 1, 0.1))
simulated.data <- data.frame(sugar = newsugar, fat = newfat,
  sodium = newsodium)
pi.hat.sim <- predict(mod1, newdata = simulated.data, type = "probs")
plot.new()
x <- seq(0, 1, 0.1)

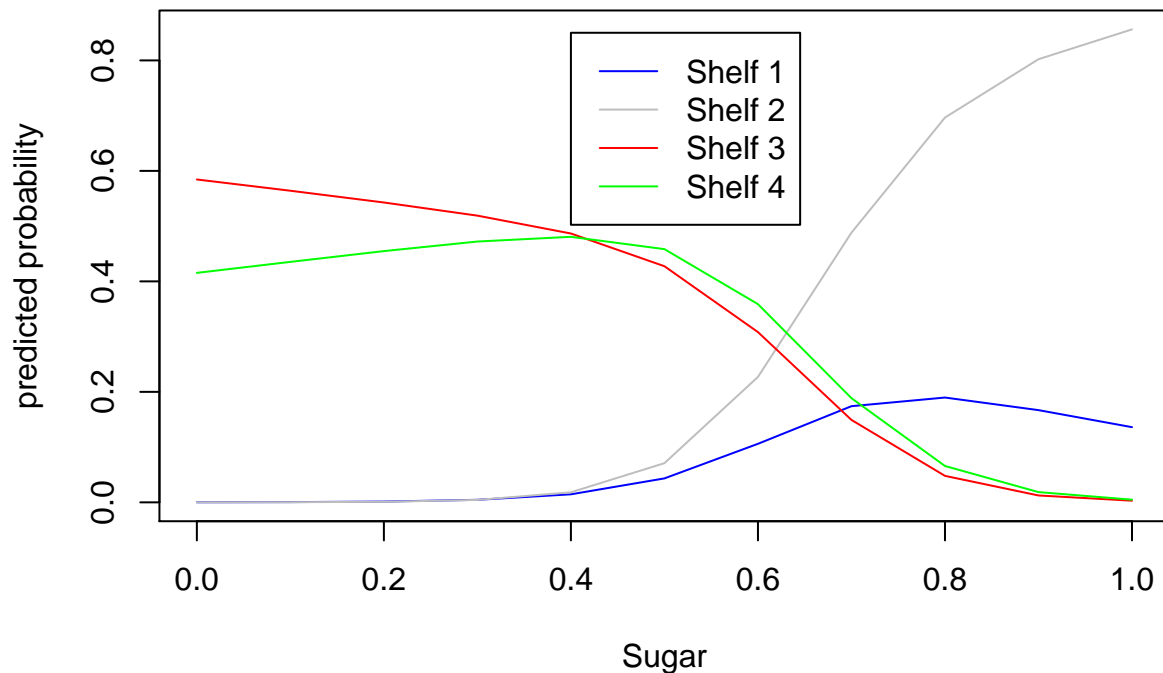
```

```

plot(x, pi.hat.sim[, 1], type = "l", col = "blue", ylim = range(min(pi.hat.sim),
  max(pi.hat.sim)), xlab = "Sugar", ylab = "predicted probability")
lines(x, pi.hat.sim[, 2], col = "gray")
lines(x, pi.hat.sim[, 3], col = "red")
lines(x, pi.hat.sim[, 4], col = "green")

legend(x = 0.4, y = 0.85, legend = c("Shelf 1", "Shelf 2", "Shelf 3",
  "Shelf 4"), col = c("blue", "gray", "red", "green"), lty = "solid")

```



Jessica's solution:

```

## Open question: in figure 3.3, they have each line stop at
## the min/max for each type of kernel (equivalent to each
## shelf in our example). Is this what we want, or do we want
## it to go from 0 to 1 for each shelf? (code for both below,
## 0-1 is commented out.)

```

```

beta.hat <- coefficients(mod1)
beta.hat

```

```

## (Intercept)      sugar      fat      sodium
## 2      6.900708    2.693071  4.0647092 -17.49373
## 3     21.680680   -12.216442 -0.5571273 -24.97850
## 4     21.288343   -11.393710 -0.8701180 -24.67385

```

```

mean_fat <- mean(cereal2$fat)
mean_sodium <- mean(cereal2$sodium)

```

```

# Create plotting area first to make sure get the whole
# region with respect to x-axis
curve(expr = 1/(1 + exp(beta.hat[1, 1] + beta.hat[1, 2] * x) +
  exp(beta.hat[2, 1] + beta.hat[2, 2] * x)), ylab = expression(hat(pi)),
  xlab = "sugar", xlim = c(min(cereal2$sugar), max(cereal2$sugar)),
  ylim = c(0, 1), col = "black", lty = "solid", lwd = 2, n = 1000,
  type = "n", panel.first = grid(col = "gray", lty = "dotted"))

## Plot each pi_j Shelf1
curve(expr = 1/(1 + exp(beta.hat[1, 1] + beta.hat[1, 2] * x +
  beta.hat[1, 3] * mean_fat + beta.hat[1, 4] * mean_sodium) +
  exp(beta.hat[2, 1] + beta.hat[2, 2] * x + beta.hat[2, 3] *
    mean_fat + beta.hat[2, 4] * mean_sodium) + exp(beta.hat[3,
  1] + beta.hat[3, 2] * x + beta.hat[3, 3] * mean_fat + beta.hat[3,
  4] * mean_sodium))), col = "black", lty = "solid", lwd = 2,
  n = 1000, add = TRUE, xlim = c(min(cereal2$sugar[cereal2$Shelf ==
    1]), max(cereal2$sugar[cereal2$Shelf == 1])))
# xlim = c(0,1))

# Shelf2
curve(expr = exp(beta.hat[1, 1] + beta.hat[1, 2] * x + beta.hat[1,
  3] * mean_fat + beta.hat[1, 4] * mean_sodium)/(1 + exp(beta.hat[1,
  1] + beta.hat[1, 2] * x + beta.hat[1, 3] * mean_fat + beta.hat[1,
  4] * mean_sodium) + exp(beta.hat[2, 1] + beta.hat[2, 2] *
  x + beta.hat[2, 3] * mean_fat + beta.hat[2, 4] * mean_sodium) +
  exp(beta.hat[3, 1] + beta.hat[3, 2] * x + beta.hat[3, 3] *
    mean_fat + beta.hat[3, 4] * mean_sodium))), col = "green",
  lty = "longdash", lwd = 2, n = 1000, add = TRUE, xlim = c(min(cereal2$sugar[cereal2$Shelf ==
    2]), max(cereal2$sugar[cereal2$Shelf == 2])))
# xlim = c(0,1))

# Shelf3
curve(expr = exp(beta.hat[2, 1] + beta.hat[2, 2] * x + beta.hat[2,
  3] * mean_fat + beta.hat[2, 4] * mean_sodium)/(1 + exp(beta.hat[1,
  1] + beta.hat[1, 2] * x + beta.hat[1, 3] * mean_fat + beta.hat[1,
  4] * mean_sodium) + exp(beta.hat[2, 1] + beta.hat[2, 2] *
  x + beta.hat[2, 3] * mean_fat + beta.hat[2, 4] * mean_sodium) +
  exp(beta.hat[3, 1] + beta.hat[3, 2] * x + beta.hat[3, 3] *
    mean_fat + beta.hat[3, 4] * mean_sodium))), col = "red",
  lty = "dotdash", lwd = 2, n = 1000, add = TRUE, xlim = c(min(cereal2$sugar[cereal2$Shelf ==
    3]), max(cereal2$sugar[cereal2$Shelf == 3])))
# xlim = c(0,1))

# Shelf4
curve(expr = exp(beta.hat[3, 1] + beta.hat[3, 2] * x + beta.hat[3,
  3] * mean_fat + beta.hat[3, 4] * mean_sodium)/(1 + exp(beta.hat[1,
  1] + beta.hat[1, 2] * x + beta.hat[1, 3] * mean_fat + beta.hat[1,
  4] * mean_sodium) + exp(beta.hat[2, 1] + beta.hat[2, 2] *
  x + beta.hat[2, 3] * mean_fat + beta.hat[2, 4] * mean_sodium) +
  exp(beta.hat[3, 1] + beta.hat[3, 2] * x + beta.hat[3, 3] *
    mean_fat + beta.hat[3, 4] * mean_sodium))), col = "blue",
  lty = "solid", lwd = 2, n = 1000, add = TRUE, xlim = c(min(cereal2$sugar[cereal2$Shelf ==
    4]), max(cereal2$sugar[cereal2$Shelf == 4])))
# xlim = c(0,1))

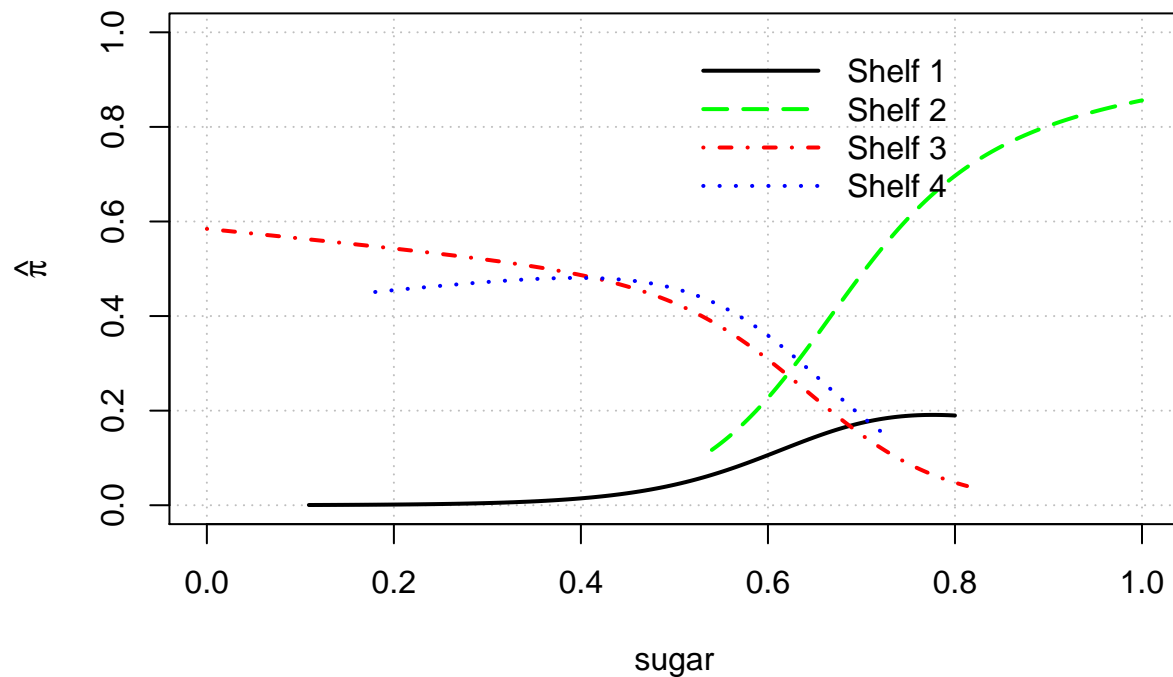
```

```

4] * mean_sodium) + exp(beta.hat[2, 1] + beta.hat[2, 2] *
x + beta.hat[2, 3] * mean_fat + beta.hat[2, 4] * mean_sodium) +
exp(beta.hat[3, 1] + beta.hat[3, 2] * x + beta.hat[3, 3] *
mean_fat + beta.hat[3, 4] * mean_sodium)), col = "blue",
lty = "dotted", lwd = 2, n = 1000, add = TRUE, xlim = c(min(cereal2$sugar[cereal2$Shelf ==
4]), max(cereal2$sugar[cereal2$Shelf == 4])))
# xlim = c(0,1))

legend(x = 0.5, y = 1, legend = c("Shelf 1", "Shelf 2", "Shelf 3",
"Shelf 4"), lty = c("solid", "longdash", "dotdash", "dotted"),
col = c("black", "green", "red", "blue"), bty = "n", lwd = c(2,
2, 2), seg.len = 4)

```



(h) Estimate odds ratios and calculate corresponding confidence intervals for each explanatory variable. Relate your interpretations back to the plots constructed for this exercise.