Lipids Exploration

Nick Strayer

April 4, 2016

First we read data in

```
data <- read.csv("/Users/Nick/Dropbox/vandy/regression/bios6312_final/data/ivfedata-2013_full.csv")
```

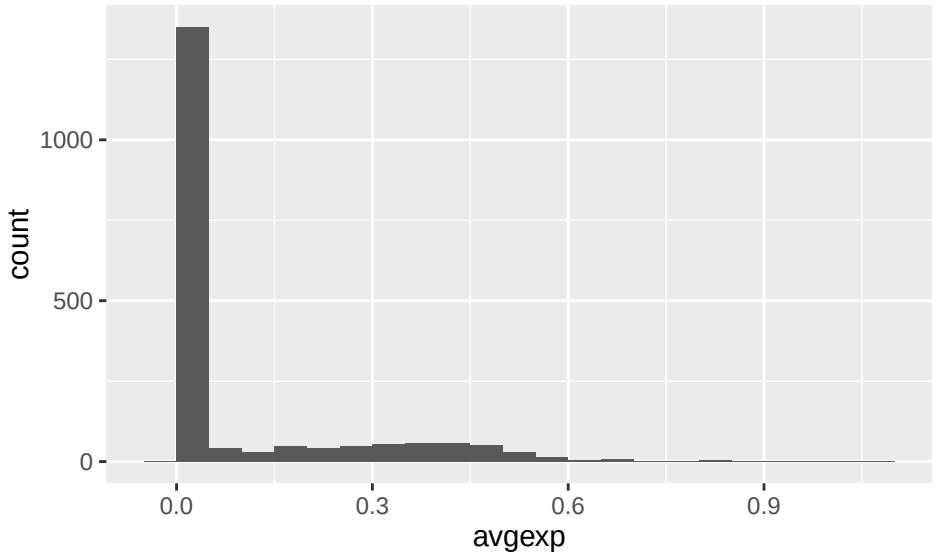
Now we recode the columns whos values are simply Ys and Ns to 1 and 0s respectively.

```
#y n columns
y_n_cols <- c("hosp.death","unit.death", "bsi.inf","eent.inf","gi.inf","lri.inf","pneu.inf","ssi.inf","s

#recode y and n values to 0=N, 1 = Y.
data[, y_n_cols] = ifelse(data[, y_n_cols] == "N", 0, 1)
```

We have a large portion of lipids users who have no exposure.

```
ggplot(data, aes(avgexp)) + geom_histogram(binwidth = 0.05)
```

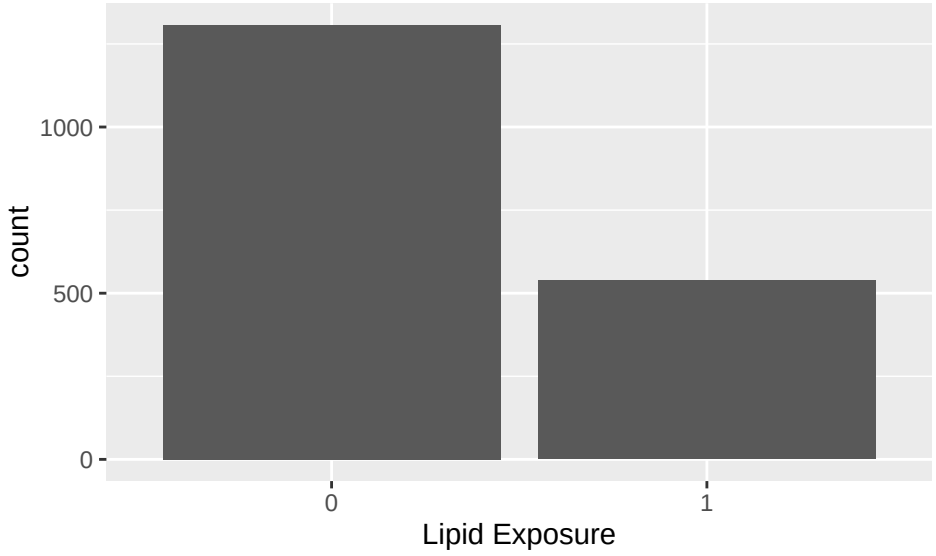


Because of this we will dichotomize on the exposure variable for logistic regression.

```
#make a binary column for if the patient recieved lipids during stay.
data$lipids = ifelse(data$avgexp >  0.0, 1, 0)
```

Now we check to see what the distribution of lipid use is.

```
ggplot(data, aes(x = factor(lipids))) + geom_bar(stat = "count") + labs(x = "Lipid Exposure")
```



So we can see more people did not recieve them than recieved them.

```
kable(summary(data[, y_n_cols]))
```

hosp.death	unit.death	bsi.inf	eent.inf	gi.inf	lri.inf	pr
Min. :0.0000	Min. :0.00000	Min. :0.00000	Min. :0.000000	Min. :0.00000	Min. :0.000000	Min.
1st Qu.:0.0000	1st Qu.:0.00000	1st Qu.:0.00000	1st Qu.:0.000000	1st Qu.:0.00000	1st Qu.:0.000000	1st Q
Median :0.0000	Median :0.00000	Median :0.00000	Median :0.000000	Median :0.00000	Median :0.000000	Media
Mean :0.0878	Mean :0.05691	Mean :0.02927	Mean :0.000542	Mean :0.02114	Mean :0.007588	Mean
3rd Qu.:0.0000	3rd Qu.:0.00000	3rd Qu.:0.00000	3rd Qu.:0.000000	3rd Qu.:0.00000	3rd Qu.:0.000000	3rd Q
Max. :1.0000	Max. :1.00000	Max. :1.00000	Max. :1.000000	Max. :1.00000	Max. :1.000000	Max.

Descriptive Statistics of Patients.

First a quick function to generate a nice table output of `summary`.

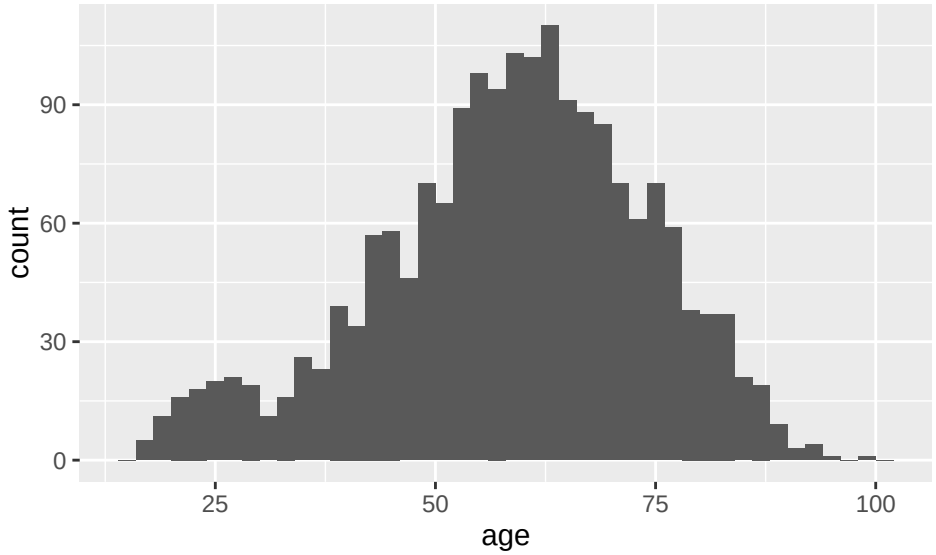
```
#this is tedious
summaryTable <- function(variable){ kable(as.data.frame(as.list(summary(variable)))) }
```

Ages

```
summaryTable(data$age)
```

Min.	X1st.Qu.	Median	Mean	X3rd.Qu.	Max.
17.02	49.4	59.66	58.47	69.08	98.64

```
ggplot(data, aes(age)) + geom_histogram(binwidth = 2) + labs(x = "age")
```

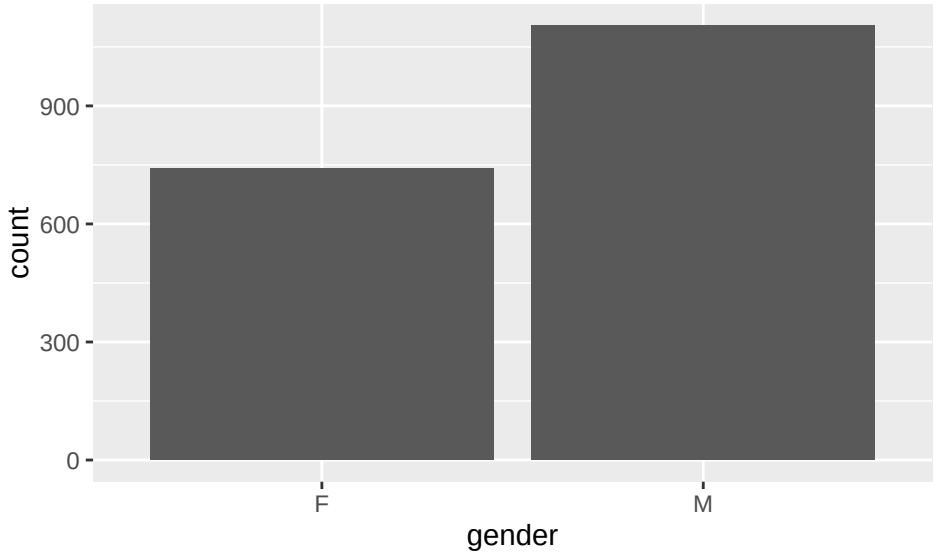


Gender

```
summaryTable(data$gender)
```

F	M
741	1104

```
ggplot(data, aes(x = factor(gender))) + geom_bar(stat = "count") + labs(x = "gender")
```



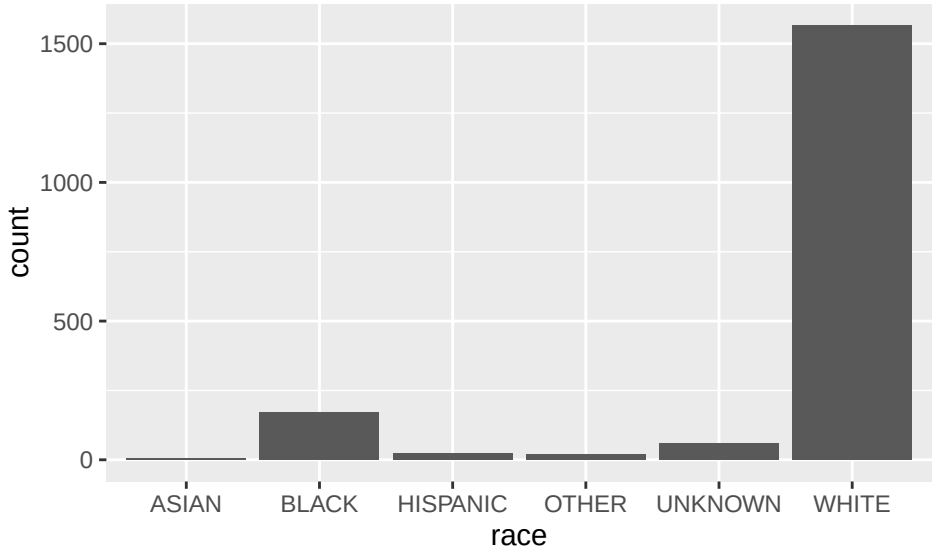
Race

```
#recode the ? race to unknown.
data[data$race == "?", "race"] = "UNKNOWN"

summaryTable(data$race)
```

X.	ASIAN	BLACK	HISPANIC	OTHER	UNKNOWN	WHITE
0	6	173	22	19	59	1566

```
ggplot(data, aes(x = factor(race))) + geom_bar(stat = "count") + labs(x = "race")
```

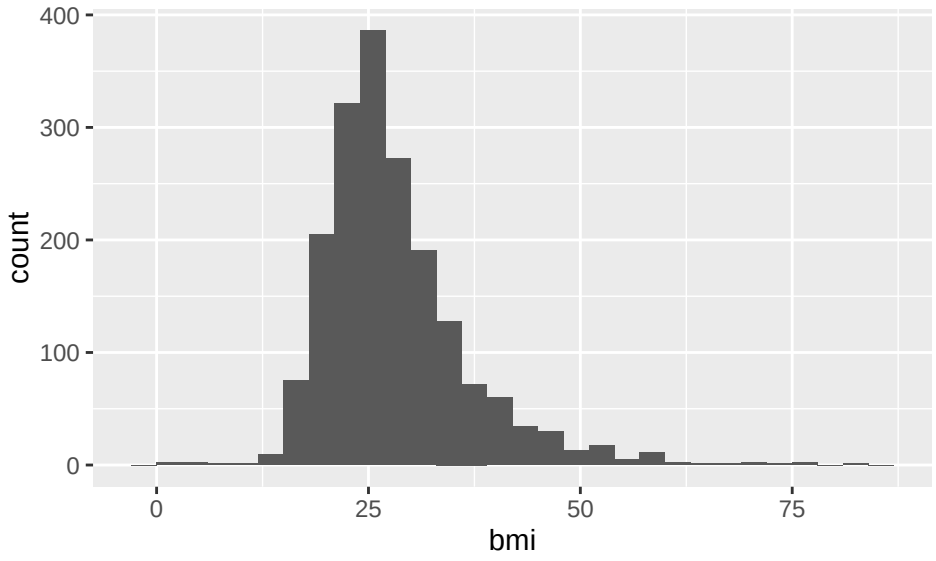


BMI

```
summaryTable(data$bmi)
```

Min.	X1st.Qu.	Median	Mean	X3rd.Qu.	Max.
0.15	22.61	26.26	28.09	31.43	83.12

```
ggplot(data, aes(bmi)) + geom_histogram(binwidth = 3)
```

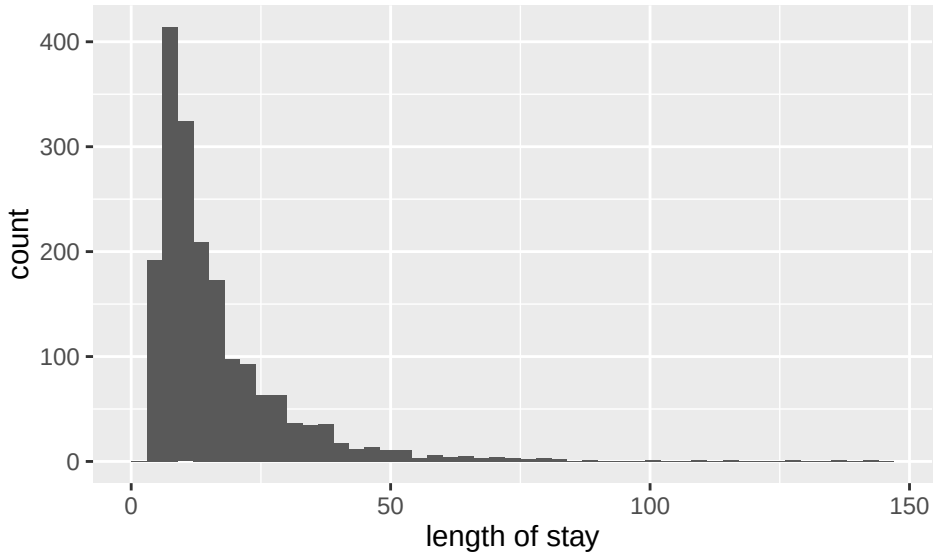


Hospital Length of Stay

```
summaryTable(data$hosp.los)
```

Min.	X1st.Qu.	Median	Mean	X3rd.Qu.	Max.
3.003	8.005	11.87	16.41	20.24	141.4

```
ggplot(data, aes(hosp.los)) + geom_histogram(binwidth = 3) + labs(x = "length of stay")
```

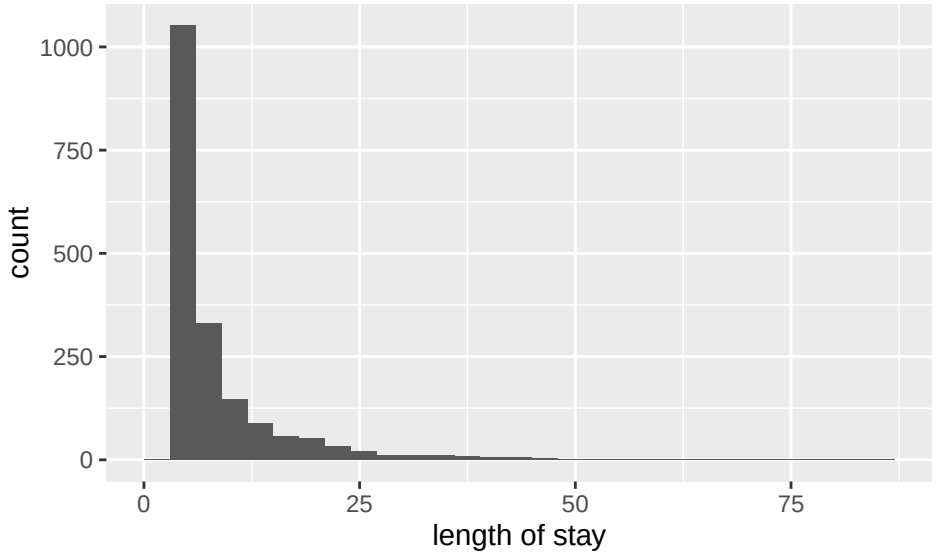


Unit Length of Stay

```
summaryTable(data$unit.los)
```

Min.	X1st.Qu.	Median	Mean	X3rd.Qu.	Max.
3.001	3.898	5.265	8.287	9.024	82.51

```
ggplot(data, aes(unit.los)) + geom_histogram(binwidth = 3) + labs(x = "length of stay")
```

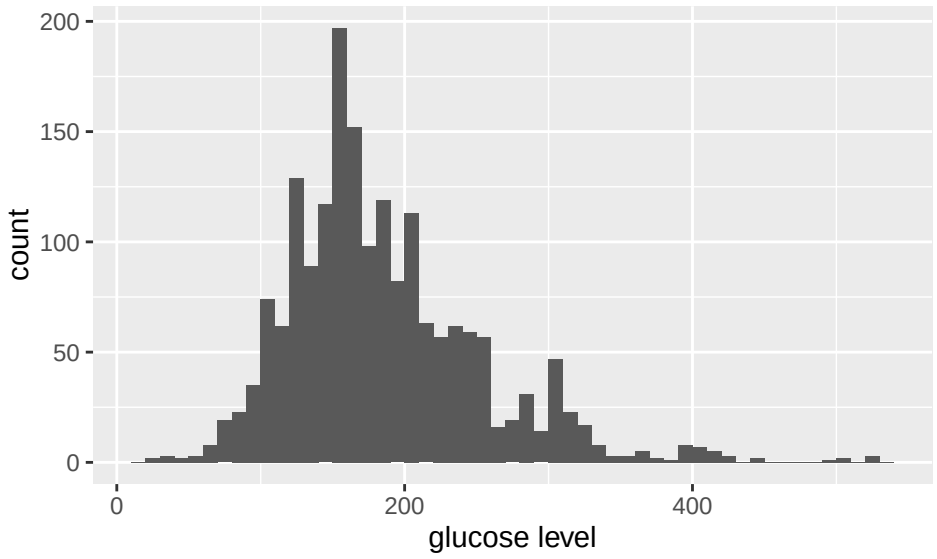


Glucose

```
summaryTable(data$glucose)
```

Min.	X1st.Qu.	Median	Mean	X3rd.Qu.	Max.
29	140	170	184.1	218	523

```
ggplot(data, aes(glucose)) + geom_histogram(binwidth = 10) + labs(x = "glucose level")
```

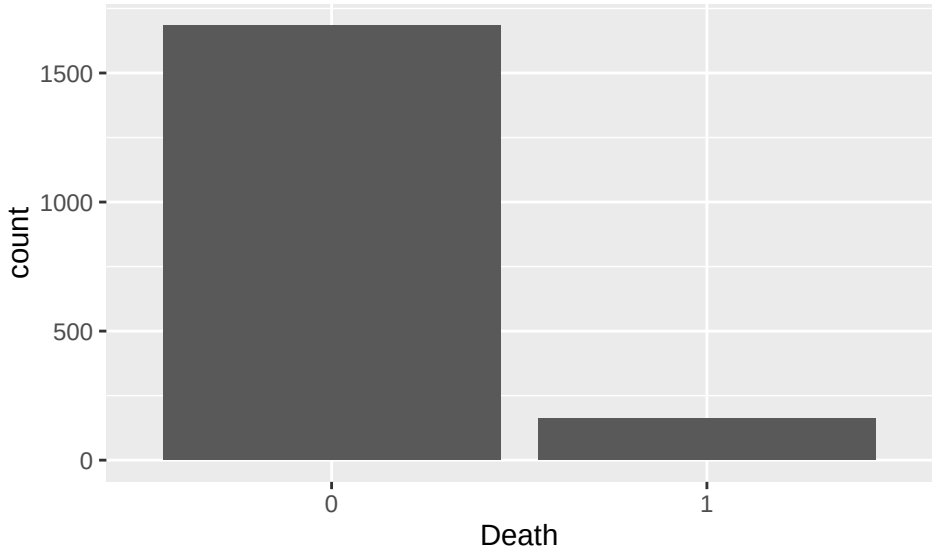


Hospital Deaths

```
summaryTable(data$hosp.death)
```

Min.	X1st.Qu.	Median	Mean	X3rd.Qu.	Max.
0	0	0	0.0878	0	1

```
ggplot(data, aes(x = factor(hosp.death))) + geom_bar(stat = "count") + labs(x = "Death")
```



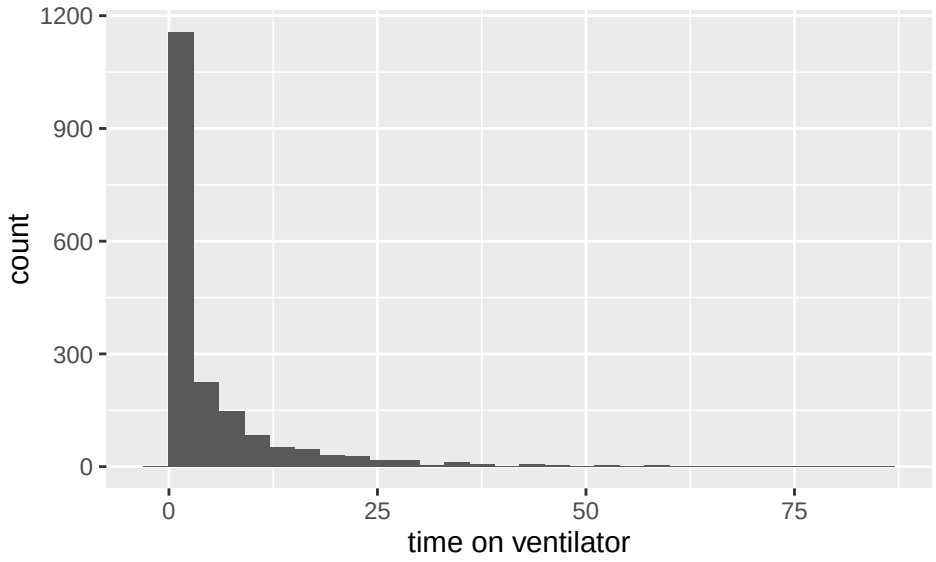
A much greater amount of people didn't die.

Time on Ventilator

```
summaryTable(data$ventdays.unit)
```

Min.	X1st.Qu.	Median	Mean	X3rd.Qu.	Max.
0	0	1.328	4.878	6	82.51

```
ggplot(data, aes(ventdays.unit)) + geom_histogram(binwidth = 3) + labs(x = "time on ventilator")
```

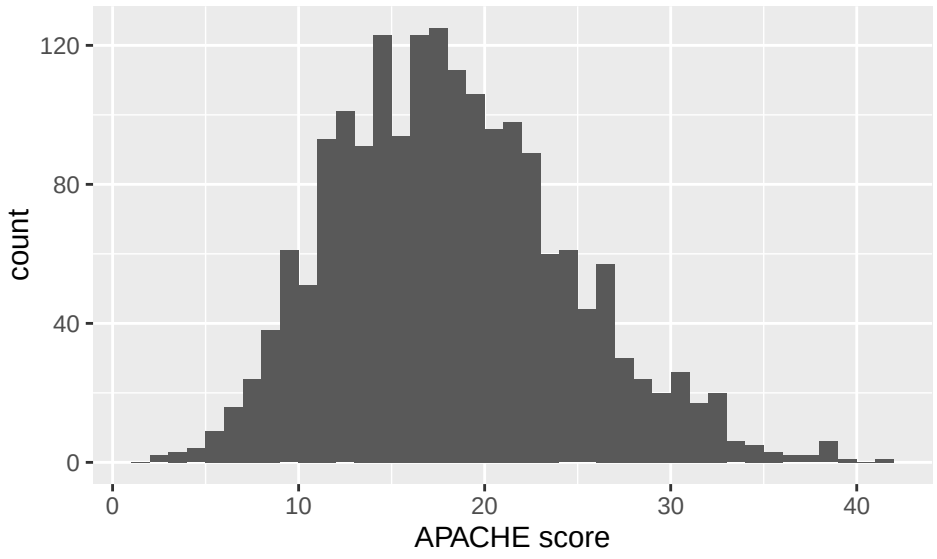


Apache Score.

```
summaryTable(data$apache2)
```

Min.	X1st.Qu.	Median	Mean	X3rd.Qu.	Max.
2	13	17	17.72	22	41

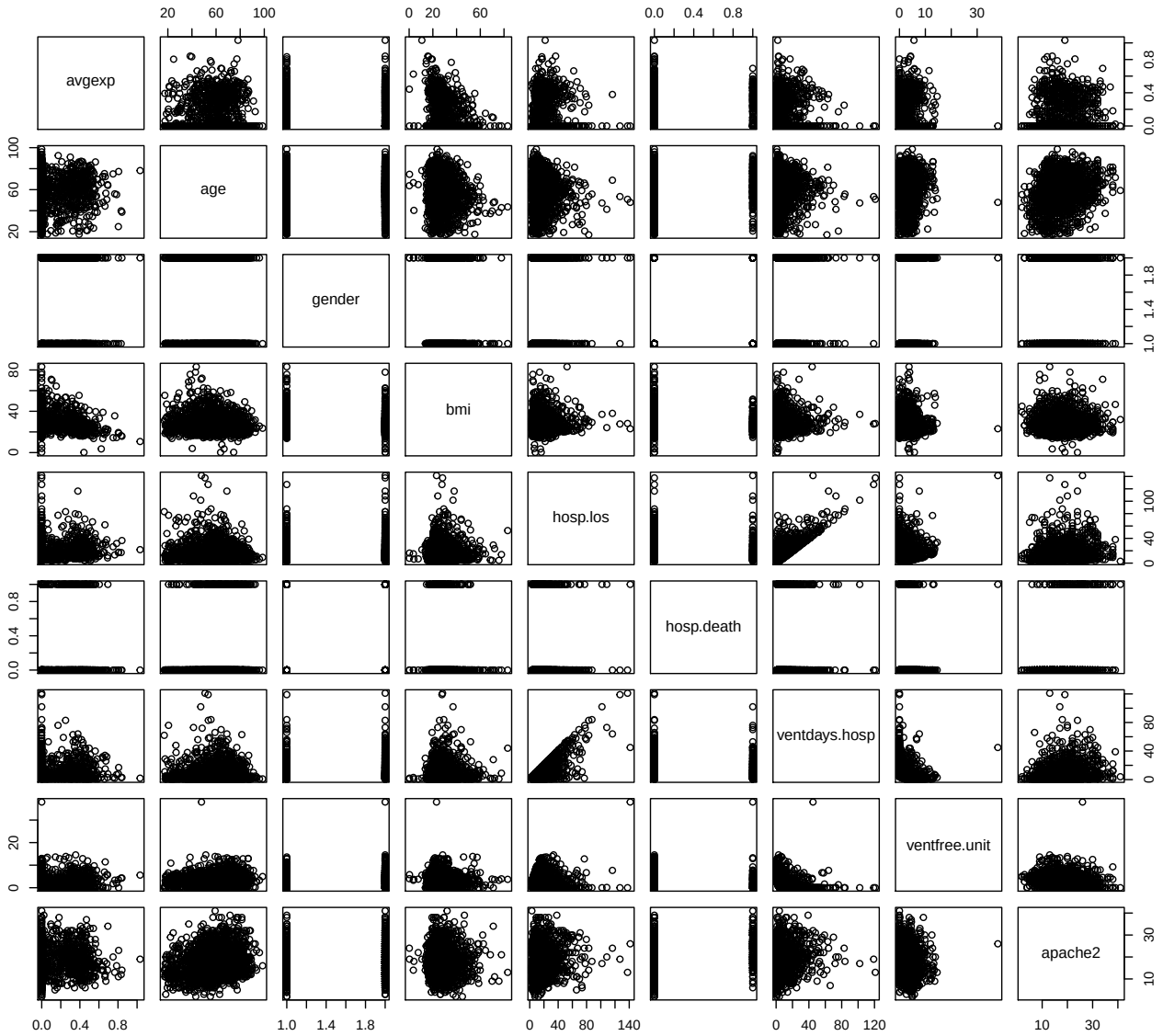
```
ggplot(data, aes(apache2)) + geom_histogram(binwidth = 1) + labs(x = "APACHE score")
```



Looking at relationships between variables.

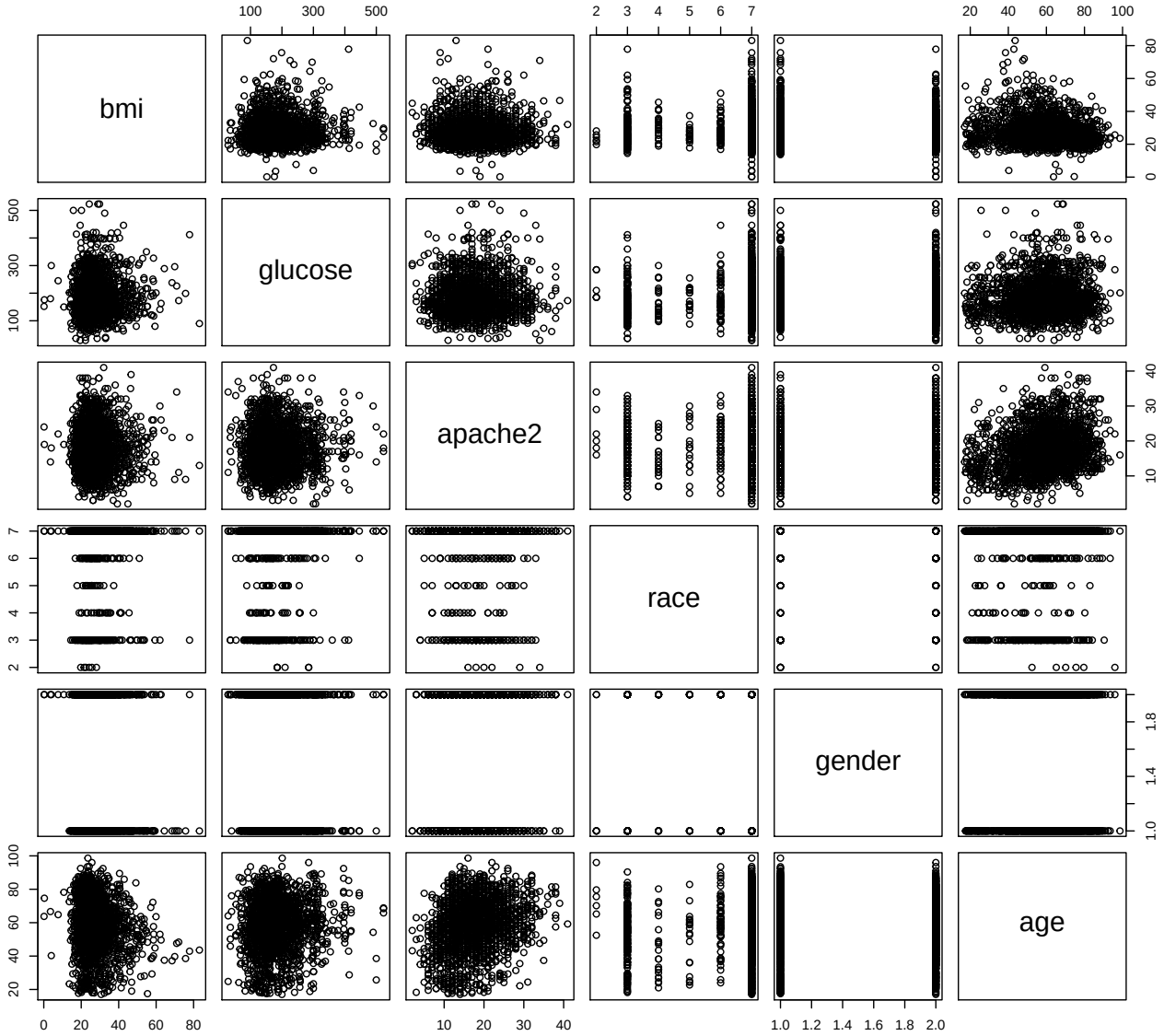
```
demoCols  <- c("avgexp",    "age",  "gender",   "bmi",  "hosp.los", "hosp.death",   "ventdays.hosp",

plot(data[,demoCols])
```



Same thing but with the variables we chose as controls in our regressions.

```
controls = c("bmi", "glucose", "apache2", "race", "gender", "age")
plot(data[, controls])
```

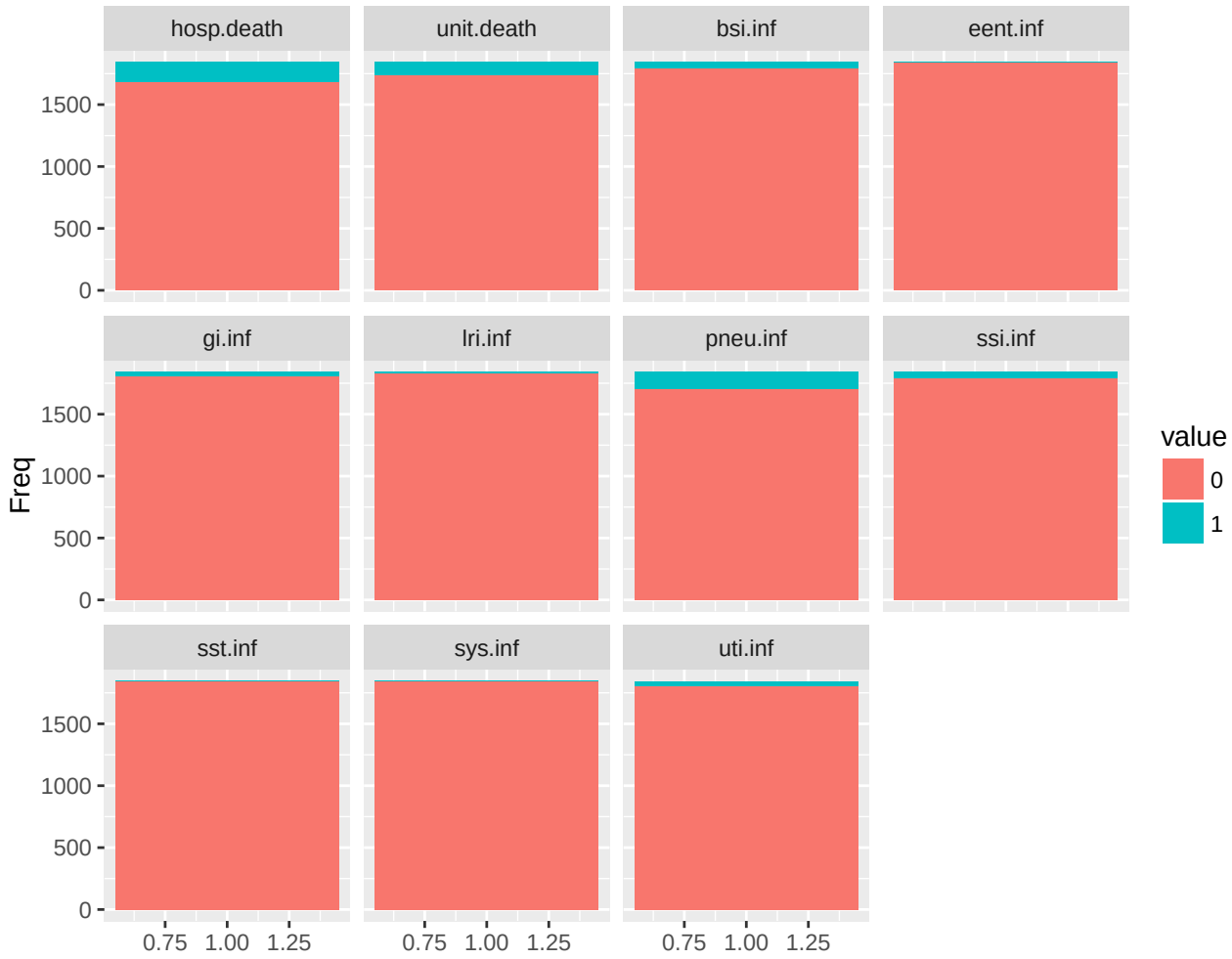


Outcomes plot:

```
library(reshape)
tp <- melt(data[, y_n_cols])
```

```
## Using  as id variables
```

```
ggplot(data.frame(table(tp)), aes(x = 1, y = Freq, fill = value)) +
  geom_bar(stat="identity", position=position_stack()) +
  facet_wrap( ~ variable) + labs(x = "")
```




```
summary(lm(data$apache2 ~ data$age))
```

```
##
## Call:
## lm(formula = data$apache2 ~ data$age)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -15.4003  -4.4598  -0.6392   3.8900  23.2065
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 11.823725   0.557604   21.20   <2e-16 ***
## data$age     0.100806   0.009223   10.93   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 6.09 on 1843 degrees of freedom
## Multiple R-squared:  0.06088,    Adjusted R-squared:  0.06037
## F-statistic: 119.5 on 1 and 1843 DF,  p-value: < 2.2e-16
```