

140SL MIDTERM

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2019/2/6

1.

```
# rm(list=ls())
pkg <- c("readr", "readxl", "dplyr", "stringr", "ggplot2", "tidyr")
pkgload <- lapply(pkg, require, character.only = TRUE)
```

```
## Loading required package: readr
## Loading required package: readxl
## Loading required package: dplyr
##
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##
##   filter, lag
## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union
## Loading required package: stringr
## Loading required package: ggplot2
## Loading required package: tidyr
```

1.

- Provide a demographic profile for both test components (AnionGap and SODIUM).

```
data1 <- read_excel("/Users/MichaelMiao/UCLA/uclatextbook/140sl/140\ review\ from\ Wilbur/demographicDa
```

```
## readxl works best with a newer version of the tibble package.
## You currently have tibble v1.4.2.
## Falling back to column name repair from tibble <= v1.4.2.
## Message displays once per session.
```

```
load("/Users/MichaelMiao/UCLA/uclatextbook/140sl/140\ review\ from\ Wilbur/LAB4PM.RData")
data2 <- LAB4PM
summary(data1)
```

```
##   STUDY_ID      Gender      Race
## Length:18721   Length:18721   Length:18721
## Class :character Class :character Class :character
## Mode  :character Mode  :character Mode  :character
## Ethnicity
## Length:18721
## Class :character
## Mode  :character
```

```
summary(data2)
```

```
##      STUDY_ID      AnionGap      Age      Year
## Length:14161      Min.   : 4.00      Min.   :30.00      Min.   :2016
## Class :character      1st Qu.:12.00      1st Qu.:32.00      1st Qu.:2016
## Mode  :character      Median :14.00      Median :34.00      Median :2016
##                                     Mean  :13.77      Mean  :34.45      Mean  :2016
##                                     3rd Qu.:15.00      3rd Qu.:37.00      3rd Qu.:2017
##                                     Max.   :35.00      Max.   :40.00      Max.   :2017
## Inpatient_Outpatient      SODIUM
## Length:14161      Min.   :123.0
## Class :character      1st Qu.:139.0
## Mode  :character      Median :140.0
##                                     Mean  :140.1
##                                     3rd Qu.:142.0
##                                     Max.   :151.0
```

```
names(data1)
```

```
## [1] "STUDY_ID" "Gender" "Race" "Ethnicity"
```

```
names(data2)
```

```
## [1] "STUDY_ID" "AnionGap" "Age"
## [4] "Year" "Inpatient_Outpatient" "SODIUM"
```

```
datajoin <- inner_join(data1,data2,by = "STUDY_ID")
```

```
#View(datajoin)
```

```
datajoind <- distinct(datajoin)
```

```
attach(datajoin)
```

```
summary(datajoin)
```

```
##      STUDY_ID      Gender      Race
## Length:14161      Length:14161      Length:14161
## Class :character      Class :character      Class :character
## Mode  :character      Mode  :character      Mode  :character
##
##
##
##      Ethnicity      AnionGap      Age      Year
## Length:14161      Min.   : 4.00      Min.   :30.00      Min.   :2016
## Class :character      1st Qu.:12.00      1st Qu.:32.00      1st Qu.:2016
## Mode  :character      Median :14.00      Median :34.00      Median :2016
##                                     Mean  :13.77      Mean  :34.45      Mean  :2016
##                                     3rd Qu.:15.00      3rd Qu.:37.00      3rd Qu.:2017
##                                     Max.   :35.00      Max.   :40.00      Max.   :2017
## Inpatient_Outpatient      SODIUM
## Length:14161      Min.   :123.0
## Class :character      1st Qu.:139.0
## Mode  :character      Median :140.0
##                                     Mean  :140.1
##                                     3rd Qu.:142.0
##                                     Max.   :151.0
```

```
tapply(datajoin$AnionGap,datajoin$Race,mean)
```

```
##      American Indian or Alaska Native
```

```
##          14.23913
##          Asian
##          13.83436
##          Black or African American
##          13.15815
##          Multiple Races
##          13.61905
##          NA
##          13.13636
## Native Hawaiian or Other Pacific Islander
##          14.45946
##          Other
##          13.80646
##          Patient Refused
##          14.21692
##          Unknown
##          13.92087
##          White or Caucasian
##          13.65992
```

```
tapply(datajoin$AnionGap,datajoin$Gender,mean)
```

```
##   Female      Male  Unknown
## 13.67799 13.87348 16.00000
```

```
tapply(datajoin$AnionGap,datajoin$Ethnicity,mean)
```

```
##          Cuban          Hispanic or Latino
##          16.00000          13.59548
## Hispanic/Spanish origin Other Mexican, Mexican American, Chicano/a
##          14.01170          13.00000
##          Not Hispanic or Latino          Patient Refused
##          13.69819          14.19592
##          Puerto Rican          Unknown
##          12.50000          13.93228
```

```
tapply(datajoin$SODIUM,datajoin$Race,mean)
```

```
##          American Indian or Alaska Native
##          139.3261
##          Asian
##          140.1168
##          Black or African American
##          140.0032
##          Multiple Races
##          139.7738
##          NA
##          139.9545
## Native Hawaiian or Other Pacific Islander
##          139.7297
##          Other
##          140.1326
##          Patient Refused
##          140.2988
##          Unknown
##          140.2171
```

```
##           White or Caucasian
##           140.1332
```

```
tapply(datajoin$SODIUM,datajoin$Gender,mean)
```

```
##   Female      Male   Unknown
## 139.7425 140.6421 143.0000
```

```
tapply(datajoin$SODIUM,datajoin$Ethnicity,mean)
```

```
##           Cuban           Hispanic or Latino
##           141.2500           139.9774
##   Hispanic/Spanish origin Other Mexican, Mexican American, Chicano/a
##           140.2047           139.7419
##           Not Hispanic or Latino           Patient Refused
##           140.1228           140.3020
##           Puerto Rican           Unknown
##           140.7500           140.2659
```

```
prop.table(table(datajoin$Gender))
```

```
##
##   Female      Male      Unknown
## 5.528564e-01 4.470729e-01 7.061648e-05
```

```
prop.table(table(datajoin$Race))
```

```
##
##   American Indian or Alaska Native
##           0.003248358
##           Asian
##           0.102746981
##   Black or African American
##           0.044205918
##           Multiple Races
##           0.005931784
##           NA
##           0.003107125
##   Native Hawaiian or Other Pacific Islander
##           0.002612810
##           Other
##           0.170397571
##           Patient Refused
##           0.078454911
##           Unknown
##           0.149918791
##           White or Caucasian
##           0.439375750
```

```
table(Gender)
```

```
## Gender
##   Female      Male   Unknown
##    7829    6331         1
```

```
table(Race)
```

```
## Race
##   American Indian or Alaska Native
```

```
##          46
##          Asian
##          1455
##          Black or African American
##          626
##          Multiple Races
##          84
##          NA
##          44
## Native Hawaiian or Other Pacific Islander
##          37
##          Other
##          2413
##          Patient Refused
##          1111
##          Unknown
##          2123
##          White or Caucasian
##          6222
```

```
table(Ethnicity)
```

```
## Ethnicity
##          Cuban          Hispanic or Latino
##          4          1372
##          Hispanic/Spanish origin Other Mexican, Mexican American, Chicano/a
##          171          124
##          Not Hispanic or Latino          Patient Refused
##          9042          1225
##          Puerto Rican          Unknown
##          8          2215
```

```
datajoinnew <- datajoin %>% mutate(.,Noinfo = replace(Race, Race=="Patient Refused","Unknown"))
table(datajoinnew$Noinfo)
```

```
##
##          American Indian or Alaska Native
##          46
##          Asian
##          1455
##          Black or African American
##          626
##          Multiple Races
##          84
##          NA
##          44
## Native Hawaiian or Other Pacific Islander
##          37
##          Other
##          2413
##          Unknown
##          3234
##          White or Caucasian
##          6222
```

```

datajoinnew <- datajoinnew %>% select_at(.,vars(-c(Race)))
datajoinnew <- rename(datajoinnew, Race = Noinfo)
dim(datajoinnew)

## [1] 14161      9

datajoinnew <- datajoinnew %>% mutate(., NO = replace(Ethnicity, Ethnicity == "Patient Refused", "Unknown"))
datajoinnew <- datajoinnew %>% select_at(.,vars(-c(Ethnicity)))
dim(datajoinnew)

## [1] 14161      9

datajoinnew <- rename(datajoinnew, Ethnicity = NO)

```

- There are about 55% females and 44% males enroll in this test. There are many unknowns and I would like to make the patient refused as unknown for both race and ethnicity. The two component seems to have no specific pattern but they distribute well.

2

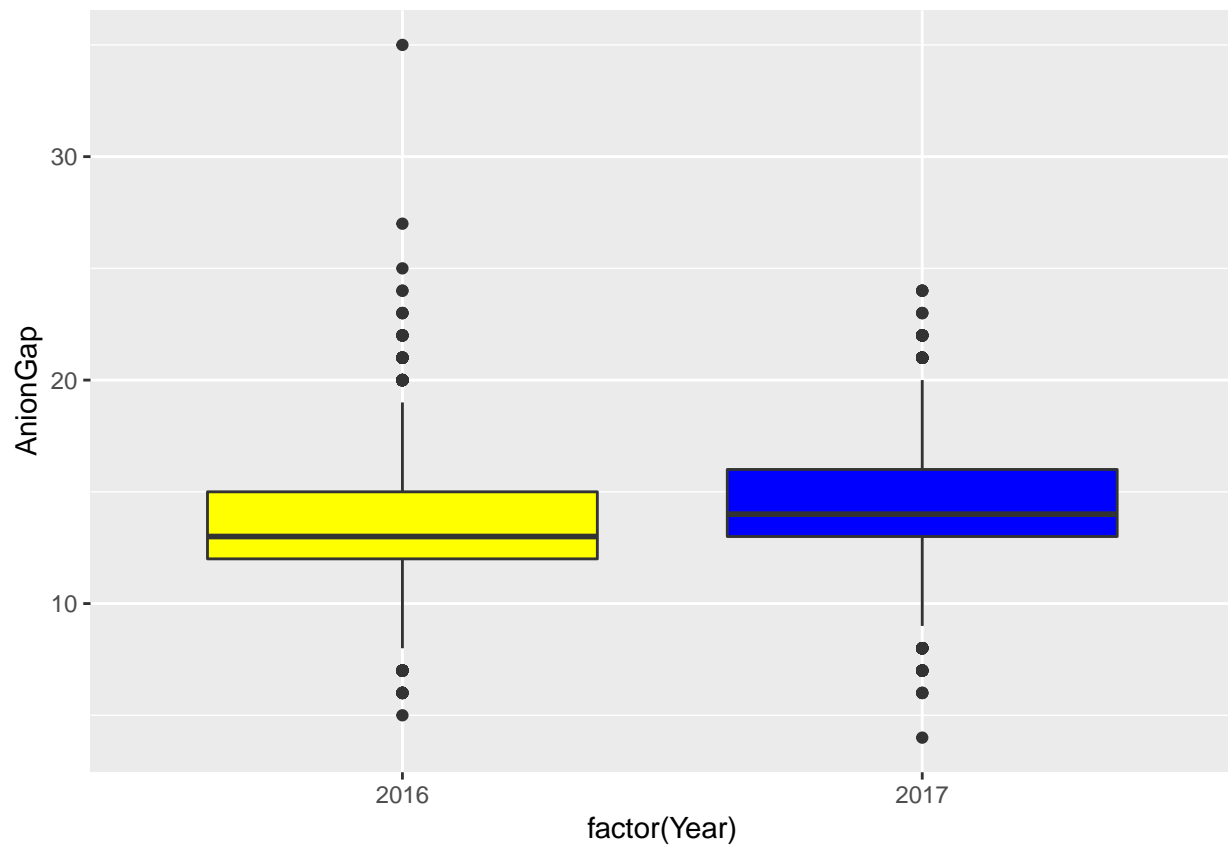
```

str(datajoinnew)

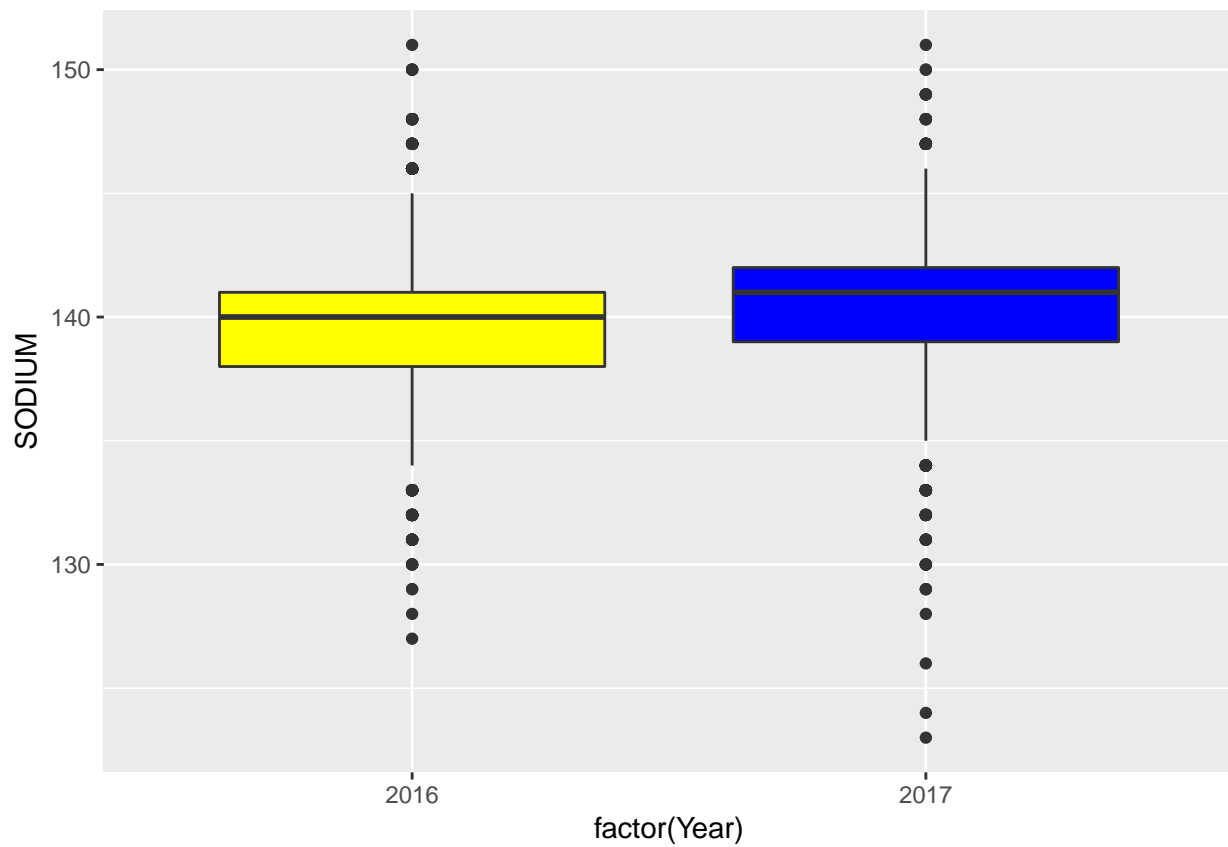
## Classes 'tbl_df', 'tbl' and 'data.frame': 14161 obs. of 9 variables:
## $ STUDY_ID : chr "000EA425FFF3622052E55966D027AEC7" "0013E732CFD6284BBBDC47C8B3D6132A" ...
## $ Gender : chr "Female" "Female" "Female" "Female" ...
## $ AnionGap : num 13 15 13 15 14 15 16 14 12 11 ...
## $ Age : int 33 35 38 39 33 33 32 31 35 32 ...
## $ Year : int 2016 2016 2016 2016 2016 2016 2017 2016 2017 2017 2016 ...
## $ Inpatient_Outpatient: chr "IP" "OP" "OP" "OP" ...
## $ SODIUM : num 141 140 141 143 141 142 141 144 139 136 ...
## $ Race : chr "Other" "Other" "White or Caucasian" "White or Caucasian" ...
## $ Ethnicity : chr "Not Hispanic or Latino" "Unknown" "Not Hispanic or Latino" "Not Hispanic or Latino" ...

par(mfrow=c(1,2))
ggplot(data = datajoinnew,aes(factor(Year),AnionGap))+geom_boxplot(fill = c("yellow","blue"))

```



```
ggplot(data = datajoinnew,aes(factor(Year),SODIUM))+geom_boxplot(fill = c("yellow","blue"))
```



```
attach(datajoinnew)
```

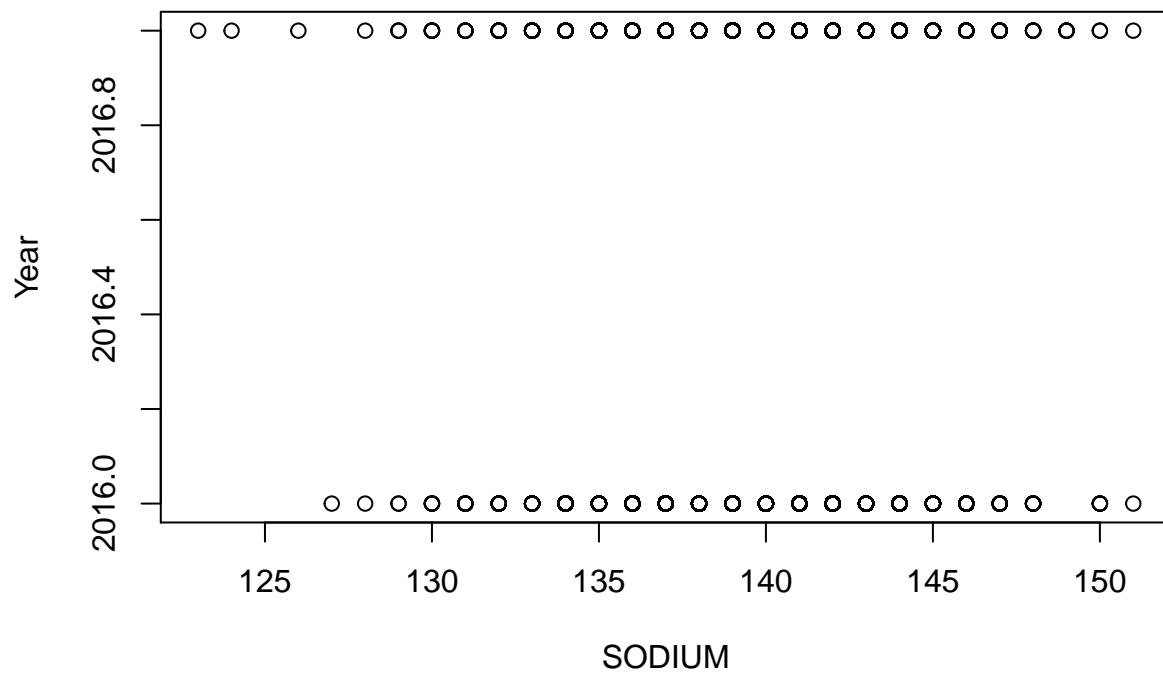
```
## The following objects are masked from datajoin:
```

```
##
```

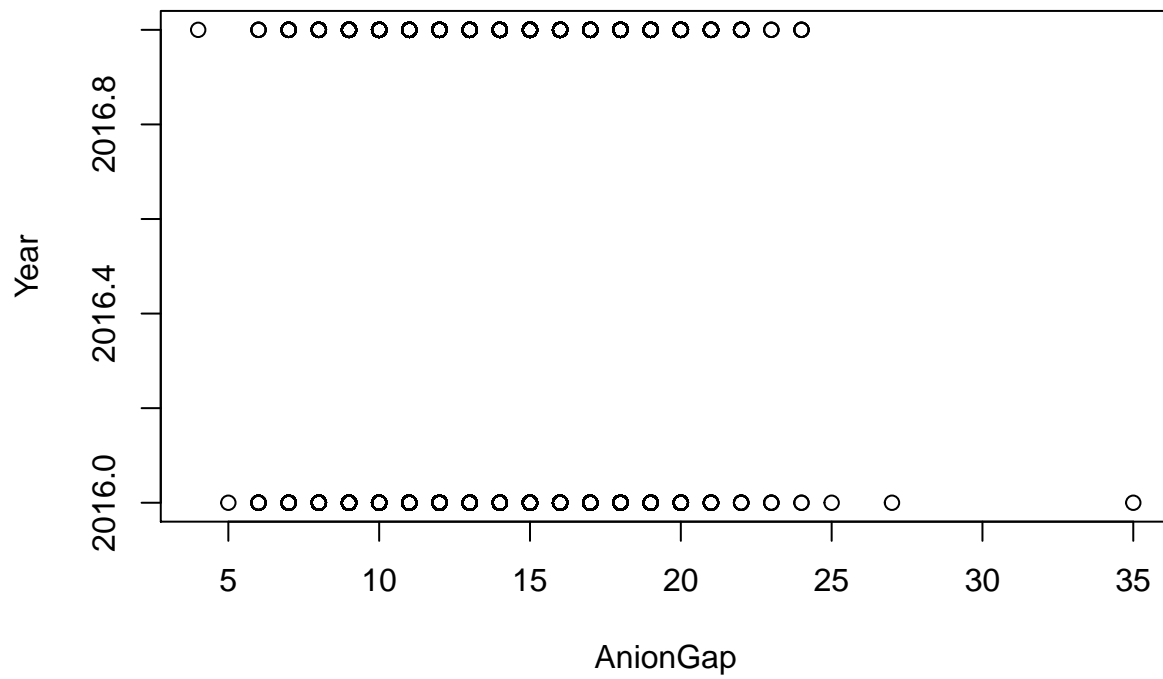
```
##   Age, AnionGap, Ethnicity, Gender, Inpatient_Outpatient, Race,
```

```
##   SODIUM, STUDY_ID, Year
```

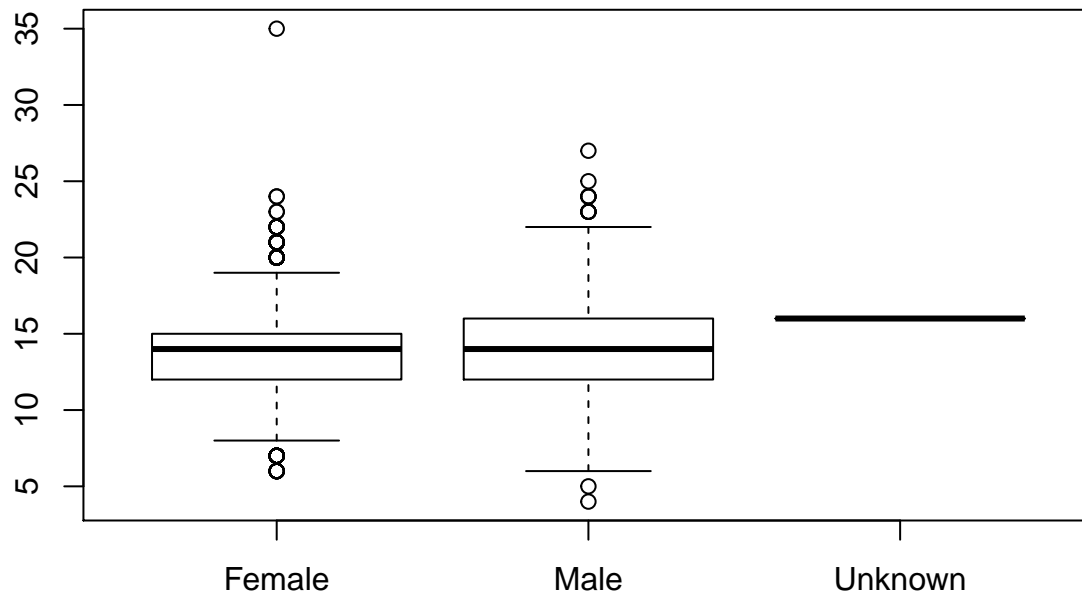
```
plot(SODIUM,Year)
```

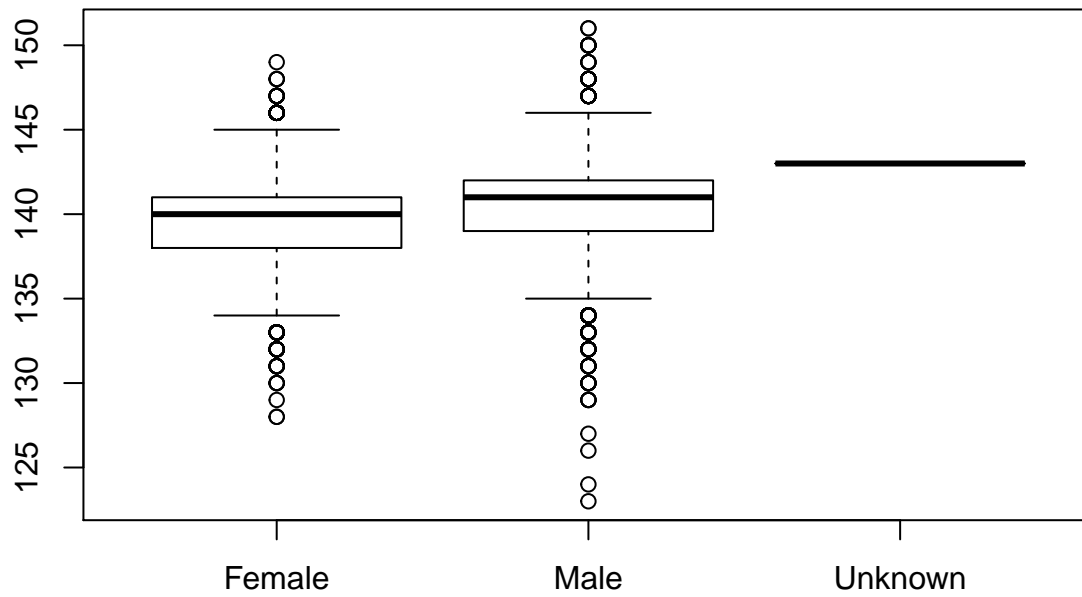
```
plot(AnionGap,Year)
```



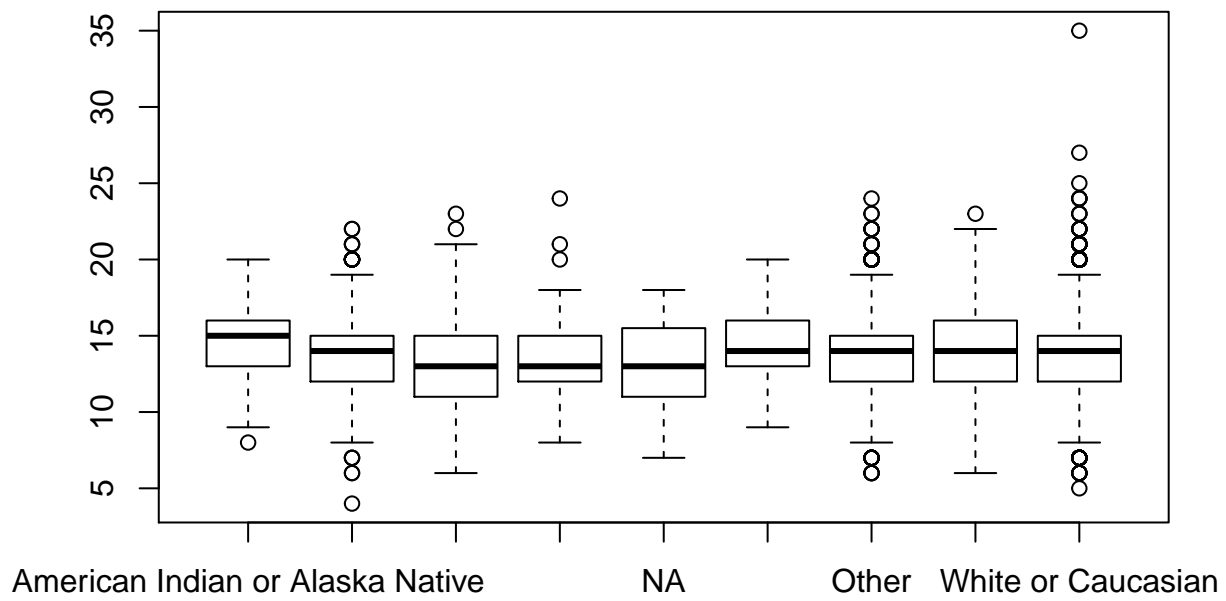
```
plot(as.factor(Gender),AnionGap)
```



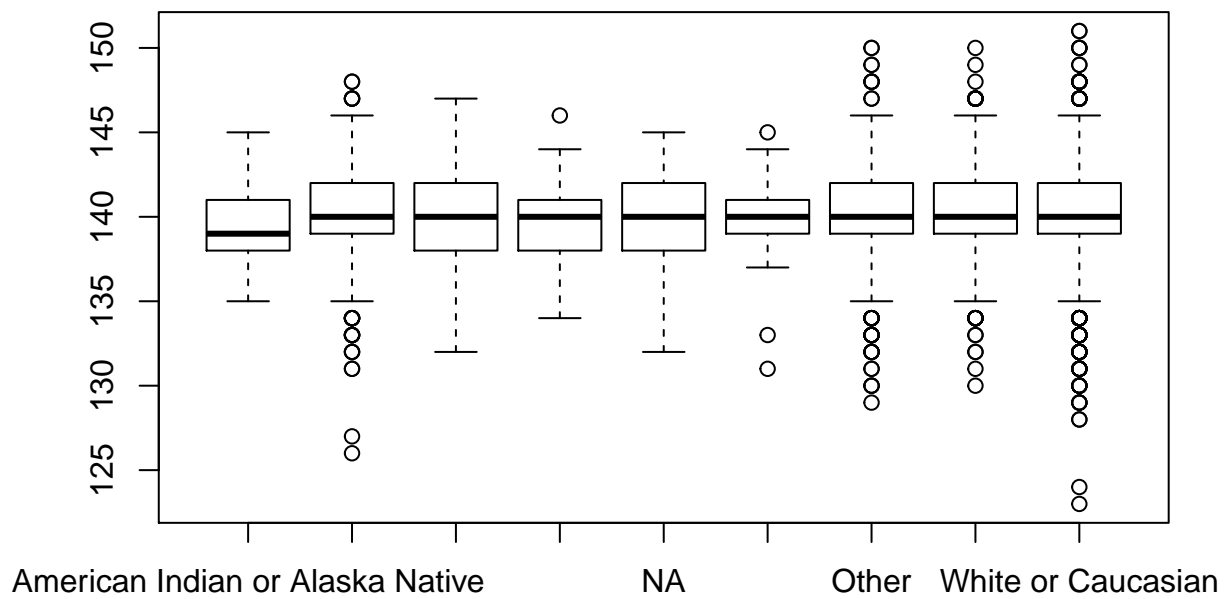
```
plot(as.factor(Gender),SODIUM)
```



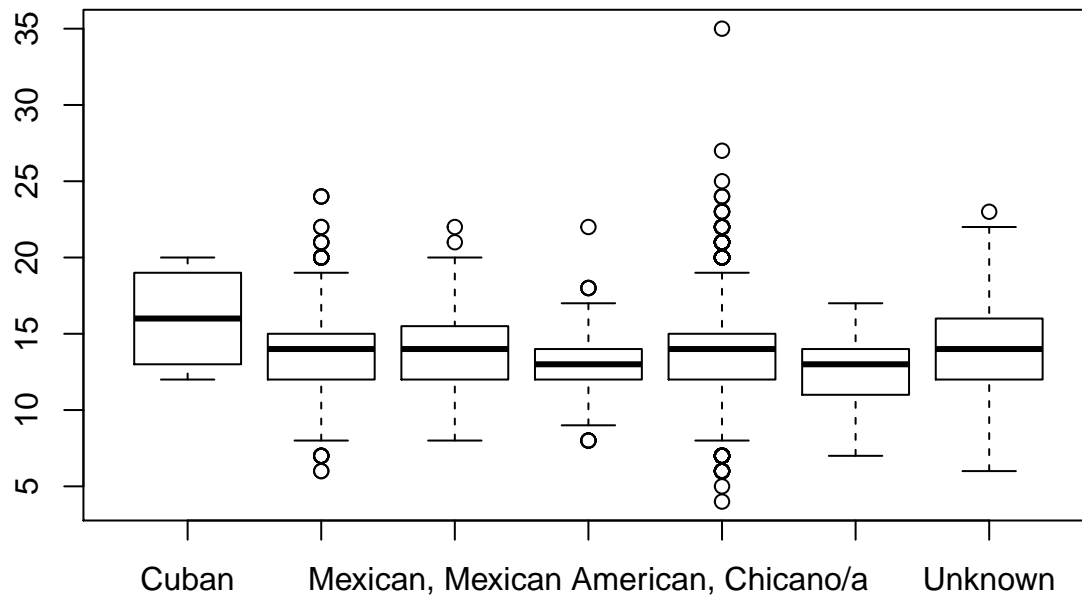
```
plot(as.factor(Race),AnionGap)
```



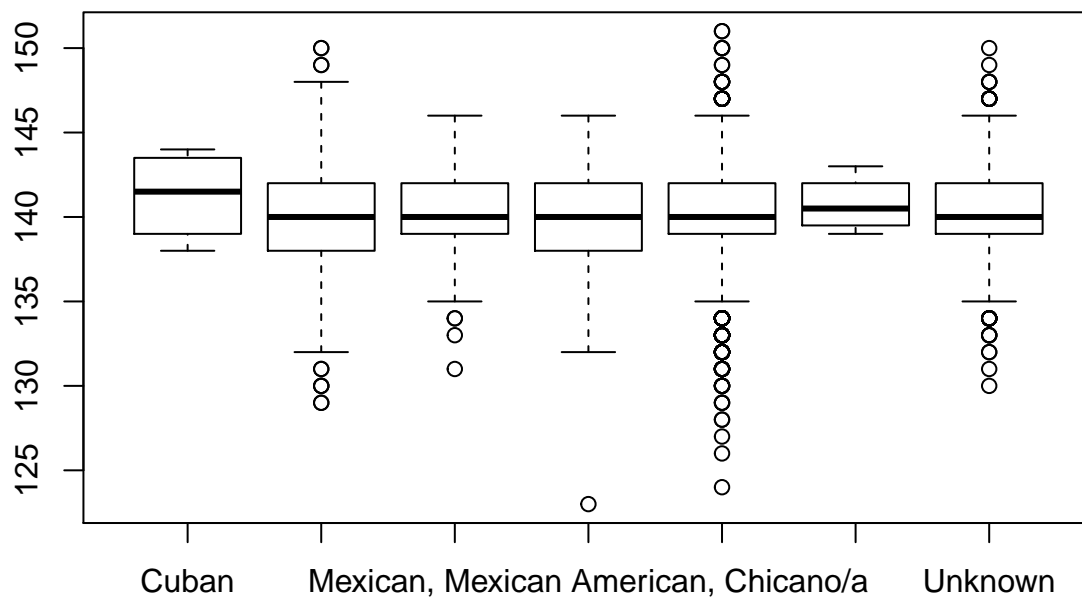
```
plot(as.factor(Race),SODIUM)
```



```
plot(as.factor(Ethnicity),AnionGap)
```



```
plot(as.factor(Ethnicity),SODIUM)
```



3

```
attach(datajoinnew)
```

```
## The following objects are masked from datajoinnew (pos = 3):
```

```
##
```

```
##   Age, AnionGap, Ethnicity, Gender, Inpatient_Outpatient, Race,
```

```
##   SODIUM, STUDY_ID, Year
```

```
## The following objects are masked from datajoin:
```

```
##
```

```
##   Age, AnionGap, Ethnicity, Gender, Inpatient_Outpatient, Race,
```

```
##      SODIUM, STUDY_ID, Year
modell1 <- glm(data = datajoinnew, SODIUM~ factor(Ethnicity)+ factor(Race) + factor(Gender))
summary(modell1)

##
## Call:
## glm(formula = SODIUM ~ factor(Ethnicity) + factor(Race) + factor(Gender),
##      data = datajoinnew)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -17.2885   -1.6203    0.2097    1.3797   10.3797
##
## Coefficients:
##                                     Estimate Std. Error
## (Intercept)                      140.12018    1.23701
## factor(Ethnicity)Hispanic or Latino    -1.19461    1.18805
## factor(Ethnicity)Hispanic/Spanish origin Other   -0.99804    1.20011
## factor(Ethnicity)Mexican, Mexican American, Chicano/a -1.39230    1.20539
## factor(Ethnicity)Not Hispanic or Latino    -1.06050    1.18649
## factor(Ethnicity)Puerto Rican            -0.49213    1.45296
## factor(Ethnicity)Unknown                 -0.88782    1.18953
## factor(Race)Asian                       0.73789    0.35554
## factor(Race)Black or African American      0.54781    0.36271
## factor(Race)Multiple Races                0.41494    0.43520
## factor(Race)NA                          0.25916    0.50791
## factor(Race)Native Hawaiian or Other Pacific Islander 0.27560    0.52417
## factor(Race)Other                       0.73058    0.35342
## factor(Race)Unknown                     0.59755    0.36162
## factor(Race)White or Caucasian           0.66737    0.35121
## factor(Gender)Male                      0.89330    0.04027
## factor(Gender)Unknown                   3.34386    2.37335
##
##                                     t value Pr(>|t|)
## (Intercept)                      113.273   <2e-16 ***
## factor(Ethnicity)Hispanic or Latino    -1.006    0.3147
## factor(Ethnicity)Hispanic/Spanish origin Other   -0.832    0.4056
## factor(Ethnicity)Mexican, Mexican American, Chicano/a -1.155    0.2481
## factor(Ethnicity)Not Hispanic or Latino    -0.894    0.3714
## factor(Ethnicity)Puerto Rican            -0.339    0.7348
## factor(Ethnicity)Unknown                 -0.746    0.4555
## factor(Race)Asian                       2.075    0.0380 *
## factor(Race)Black or African American      1.510    0.1310
## factor(Race)Multiple Races                0.953    0.3404
## factor(Race)NA                          0.510    0.6099
## factor(Race)Native Hawaiian or Other Pacific Islander 0.526    0.5990
## factor(Race)Other                       2.067    0.0387 *
## factor(Race)Unknown                     1.652    0.0985 .
## factor(Race)White or Caucasian           1.900    0.0574 .
## factor(Gender)Male                      22.185   <2e-16 ***
## factor(Gender)Unknown                   1.409    0.1589
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 5.627735)
```

```
##
## Null deviance: 82581 on 14160 degrees of freedom
## Residual deviance: 79599 on 14144 degrees of freedom
## AIC: 64672
##
## Number of Fisher Scoring iterations: 2
model2 <- glm(data = datajoinnew, AnionGap~ factor(Ethnicity)+ factor(Race) + factor(Gender))
summary(model2)

##
## Call:
## glm(formula = AnionGap ~ factor(Ethnicity) + factor(Race) + factor(Gender),
## data = datajoinnew)
##
## Deviance Residuals:
## Min 1Q Median 3Q Max
## -9.9460 -1.7726 0.0458 1.4140 21.4140
##
## Coefficients:
## Estimate Std. Error
## (Intercept) 16.48070 1.32351
## factor(Ethnicity)Hispanic or Latino -2.46108 1.27112
## factor(Ethnicity)Hispanic/Spanish origin Other -2.05224 1.28403
## factor(Ethnicity)Mexican, Mexican American, Chicano/a -3.06385 1.28968
## factor(Ethnicity)Not Hispanic or Latino -2.26967 1.26945
## factor(Ethnicity)Puerto Rican -3.50846 1.55455
## factor(Ethnicity)Unknown -2.07179 1.27271
## factor(Race)Asian -0.45157 0.38040
## factor(Race)Black or African American -1.13579 0.38807
## factor(Race)Multiple Races -0.60796 0.46563
## factor(Race)NA -1.36555 0.54342
## factor(Race)Native Hawaiian or Other Pacific Islander 0.17267 0.56082
## factor(Race)Other -0.42089 0.37814
## factor(Race)Unknown -0.45472 0.38690
## factor(Race)White or Caucasian -0.62499 0.37577
## factor(Gender)Male 0.18653 0.04308
## factor(Gender)Unknown 2.40128 2.53931
## t value Pr(>|t|)
## (Intercept) 12.452 < 2e-16 ***
## factor(Ethnicity)Hispanic or Latino -1.936 0.05287 .
## factor(Ethnicity)Hispanic/Spanish origin Other -1.598 0.11000
## factor(Ethnicity)Mexican, Mexican American, Chicano/a -2.376 0.01753 *
## factor(Ethnicity)Not Hispanic or Latino -1.788 0.07381 .
## factor(Ethnicity)Puerto Rican -2.257 0.02403 *
## factor(Ethnicity)Unknown -1.628 0.10358
## factor(Race)Asian -1.187 0.23521
## factor(Race)Black or African American -2.927 0.00343 **
## factor(Race)Multiple Races -1.306 0.19168
## factor(Race)NA -2.513 0.01199 *
## factor(Race)Native Hawaiian or Other Pacific Islander 0.308 0.75818
## factor(Race)Other -1.113 0.26570
## factor(Race)Unknown -1.175 0.23991
## factor(Race)White or Caucasian -1.663 0.09629 .
## factor(Gender)Male 4.330 1.5e-05 ***
```

```
## factor(Gender)Unknown                0.946  0.34435
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 6.442289)
##
##      Null deviance: 92020  on 14160  degrees of freedom
## Residual deviance: 91120  on 14144  degrees of freedom
## AIC: 66586
##
## Number of Fisher Scoring iterations: 2
model3 <- glm(data = datajoinnew, SODIUM ~ AnionGap)
summary(model3)
```

```
##
## Call:
## glm(formula = SODIUM ~ AnionGap, data = datajoinnew)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -16.9951  -1.4079   0.0049   1.5921  10.3964
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 137.45071    0.10905 1260.44  <2e-16 ***
## AnionGap      0.19572    0.00779   25.13  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 5.583425)
##
##      Null deviance: 82581  on 14160  degrees of freedom
## Residual deviance: 79056  on 14159  degrees of freedom
## AIC: 64545
##
## Number of Fisher Scoring iterations: 2
```

I think there is very tiny association of Sodium between gender(male) and race(asian) ; and some tiny association of Anigap between gender(male) and race(black). The association is very small overall. There is association between the Sodium and Aniongap. Also, the value goes up for the Sodium and Aniongap with year goes up.