MATH 208 Assignment2

Yan Miao

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Question 1

Load libraries and data:

```r
library(fivethirtyeight)
library(ggplot2)
library(gridExtra)
library(ggmosaic)
library(tidyverse)
data(biopics)
```

Data exploration:

```r
summary(biopics)
```

```
    title               site              country          year_release 
 Length:761         Length:761         Length:761         Min.   :1915  
 Class :character   Class :character   Class :character   1st Qu.:1969  
 Mode  :character   Mode  :character   Mode  :character   Median :1995  
                                                          Mean   :1987  
                                                          3rd Qu.:2007  
                                                          Max.   :2014  
                                                                        
   box_office          director         number_of_subjects
 Min.   :     3150   Length:761         Min.   :1.000     
 1st Qu.:  1170000   Class :character   1st Qu.:1.000     
 Median :  6140000   Mode  :character   Median :1.000     
 Mean   : 22981174                      Mean   :1.268     
 3rd Qu.: 30500000                      3rd Qu.:1.000     
 Max.   :350000000                      Max.   :4.000     
 NA's   :324                                              
   subject          type_of_subject     race_known       
 Length:761         Length:761         Length:761        
 Class :character   Class :character   Class :character  
 Mode  :character   Mode  :character   Mode  :character  
                                                         
                                                         
                                                         
                                                         
 subject_race       person_of_color subject_sex        lead_actor_actress
 Length:761         Mode :logical   Length:761         Length:761        
 Class :character   FALSE:661       Class :character   Class :character  
 Mode  :character   TRUE :100       Mode  :character   Mode  :character  
```

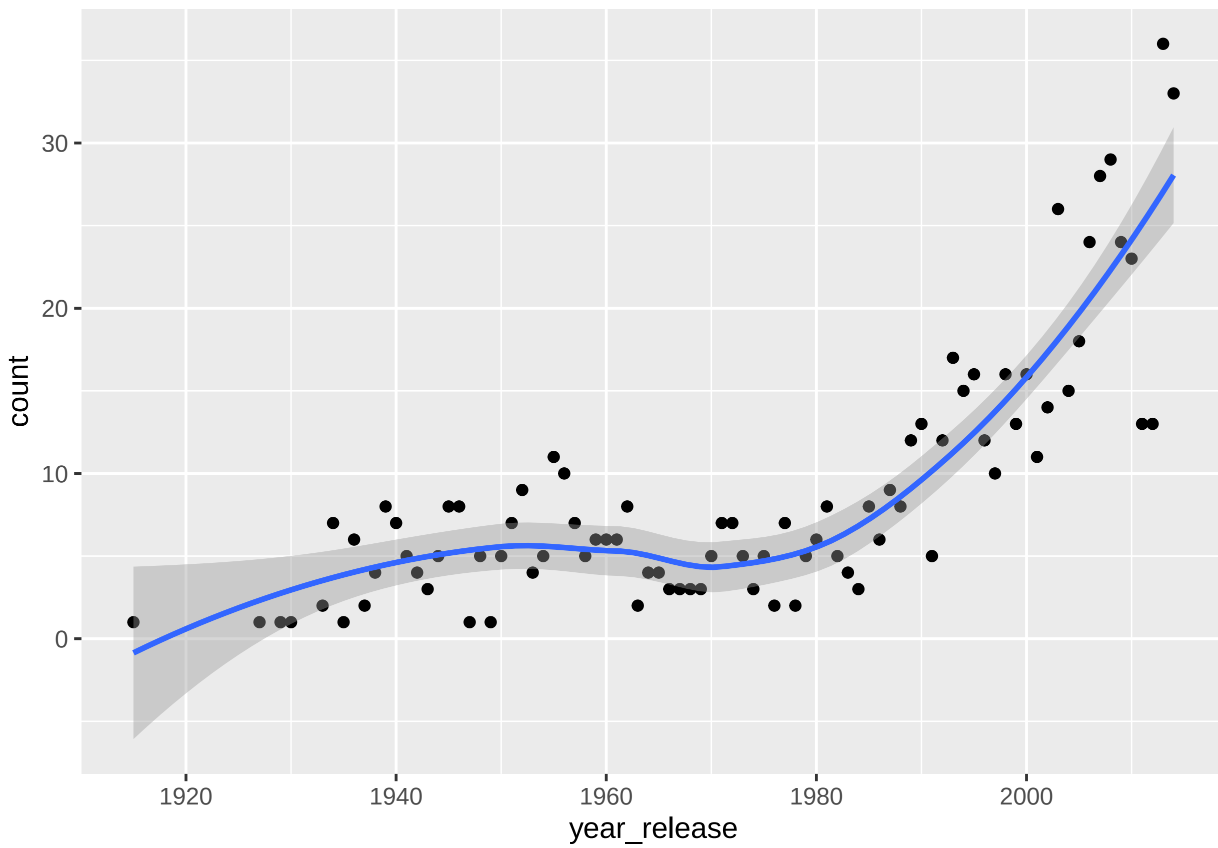
```r
head(biopics)
```

```
# A tibble: 6 x 14
  title site  country year_release box_office director number_of_subje~
  <chr> <chr> <chr>          <int>      <dbl> <chr>               <int>
1 10 R~ tt00~ UK              1971         NA Richard~                1
2 12 Y~ tt20~ US/UK           2013   56700000 Steve M~                1
3 127 ~ tt15~ US/UK           2010   18300000 Danny B~                1
4 1987  tt28~ Canada          2014         NA Ricardo~                1
5 20 D~ tt01~ US              1998     537000 Myles B~                1
6 21    tt04~ US              2008   81200000 Robert ~                1
# ... with 7 more variables: subject <chr>, type_of_subject <chr>,
#   race_known <chr>, subject_race <chr>, person_of_color <lgl>,
#   subject_sex <chr>, lead_actor_actress <chr>
```

(a)

```r
a <- biopics %>% group_by(year_release) %>% summarise(count = n())
a <- as.data.frame(a)
ggplot(a, aes(x = year_release, y = count)) +
  geom_point() + geom_smooth(method = 'auto')
```

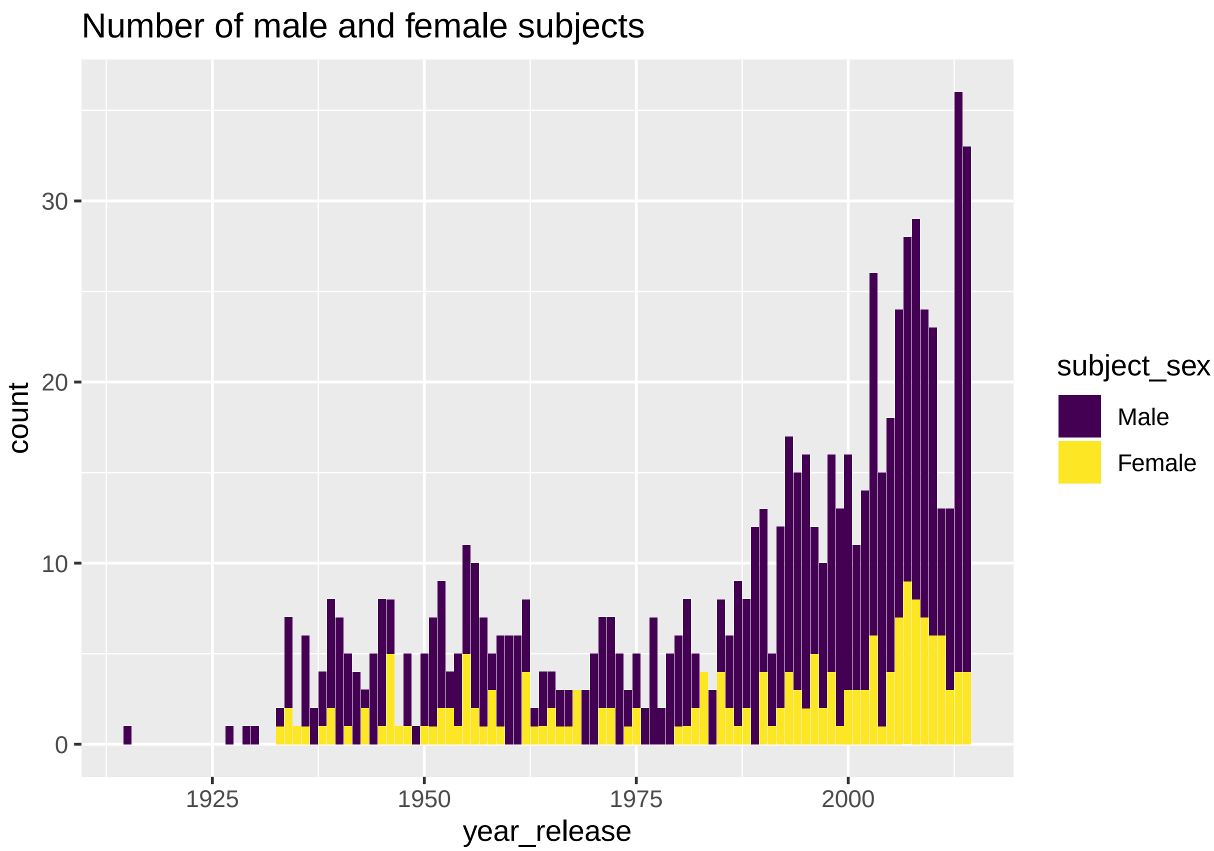
```
`geom_smooth()` using method = 'loess' and formula 'y ~ x'
```



Clearly, from the above plot, the total number of biopics released per year has increased over time.

(b)

```
b = biopics %>% mutate(subject_sex = fct_infreq(subject_sex))
ggplot(b,aes(x=year_release,fill=subject_sex)) +
geom_bar() + scale_fill_viridis_d() + labs(title="Number of male and female subjects")
```




```
head(b)
```

```
# A tibble: 6 x 14
  title site  country year_release box_office director number_of_subje~
  <chr> <chr> <chr>          <int>      <dbl> <chr>               <int>
1 10 R~ tt00~ UK              1971         NA Richard~                1
2 12 Y~ tt20~ US/UK           2013   56700000 Steve M~                1
3 127 ~ tt15~ US/UK           2010   18300000 Danny B~                1
4 1987  tt28~ Canada          2014         NA Ricardo~                1
5 20 D~ tt01~ US              1998     537000 Myles B~                1
6 21    tt04~ US              2008   81200000 Robert ~                1
# ... with 7 more variables: subject <chr>, type_of_subject <chr>,
#   race_known <chr>, subject_race <chr>, person_of_color <lgl>,
#   subject_sex <fct>, lead_actor_actress <chr>
```

(c)

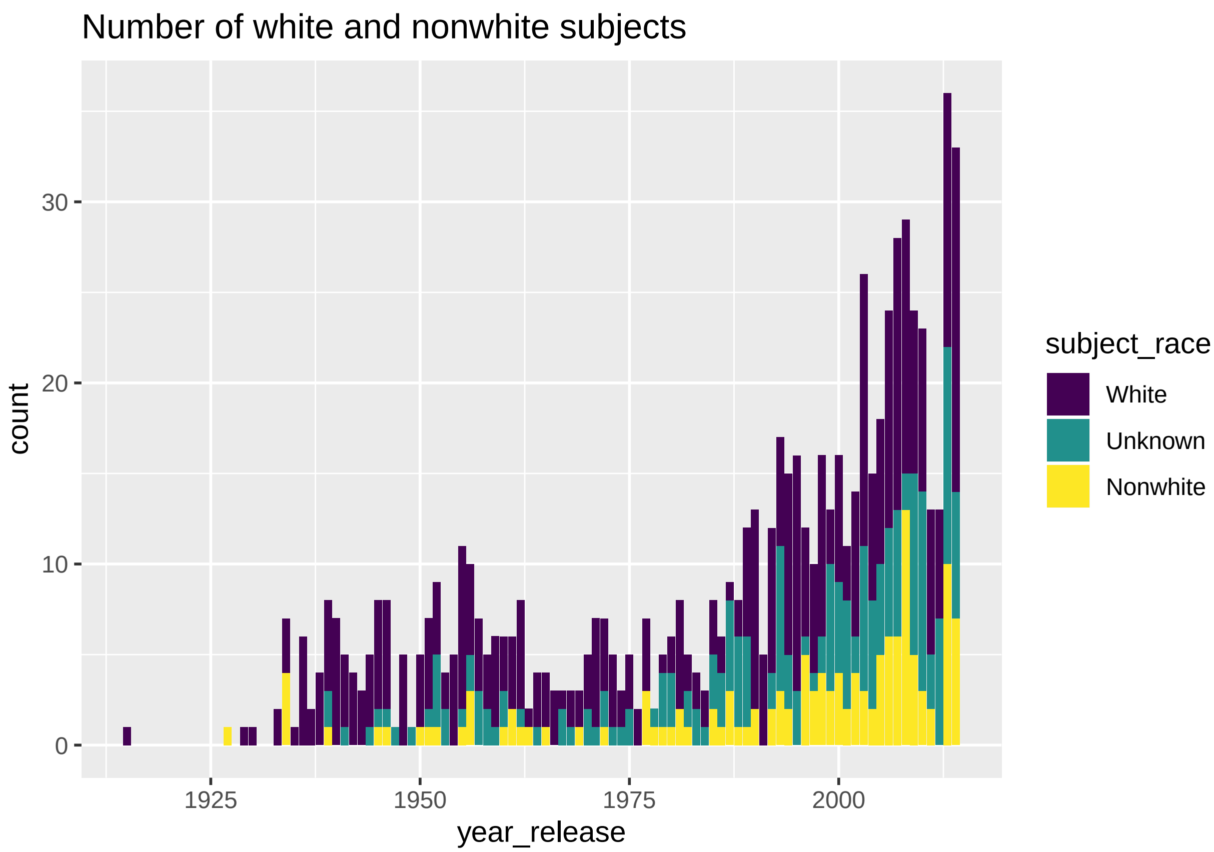
Recategorizing subject race into “White”, “Nonwhite”, and “Unknown”:

```
b$subject_race[is.na(b$subject_race)] <- "Unknown"
b$subject_race[b$subject_race != "White" &
                        b$subject_race != "Unknown"] <- "Nonwhite"
```

```
head(b$subject_race)
```

```
[1] "Unknown"  "Nonwhite" "Unknown"  "White"    "Unknown"  "Nonwhite"
```

```r
c = b %>% mutate(subject_race = fct_infreq(subject_race))
ggplot(c,aes(x=year_release,fill=subject_race)) +
geom_bar() + scale_fill_viridis_d() + labs(title="Number of white and nonwhite subjects")
```

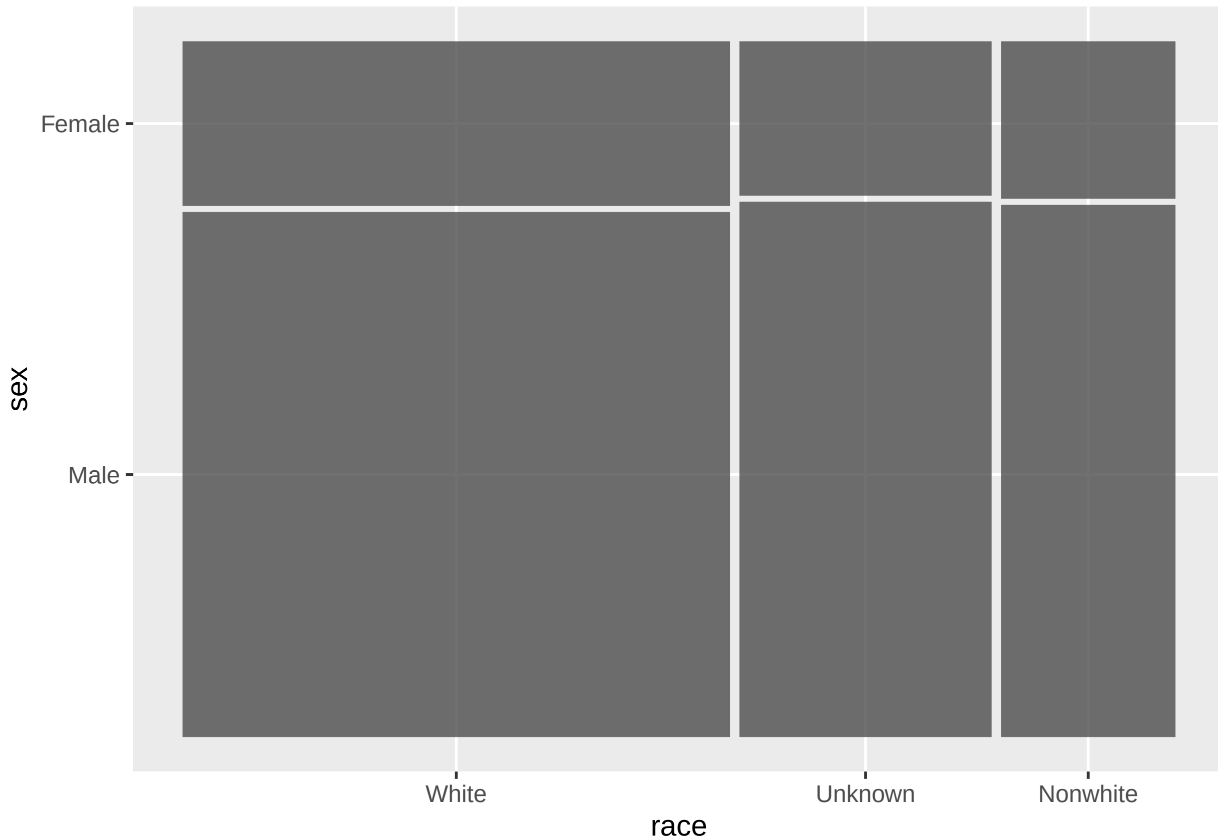


(d)

```r
head(c)
```

```
# A tibble: 6 x 14
  title site  country year_release box_office director number_of_subje~
  <chr> <chr> <chr>          <int>      <dbl> <chr>               <int>
1 10 R~ tt00~ UK              1971         NA Richard~                1
2 12 Y~ tt20~ US/UK           2013   56700000 Steve M~                1
3 127 ~ tt15~ US/UK           2010   18300000 Danny B~                1
4 1987  tt28~ Canada          2014         NA Ricardo~                1
5 20 D~ tt01~ US              1998     537000 Myles B~                1
6 21    tt04~ US              2008   81200000 Robert ~                1
# ... with 7 more variables: subject <chr>, type_of_subject <chr>,
#   race_known <chr>, subject_race <fct>, person_of_color <lgl>,
#   subject_sex <fct>, lead_actor_actress <chr>
```

```r
ggplot(c) + geom_mosaic(aes(x=product(subject_sex, subject_race))) + labs(x = "race", y = "sex")
```



From the above plot, we can see that the "Nonwhite Female" group is the most underrepresented in biopics based on number of subjects since it has the smallest area in the plot.

(e)

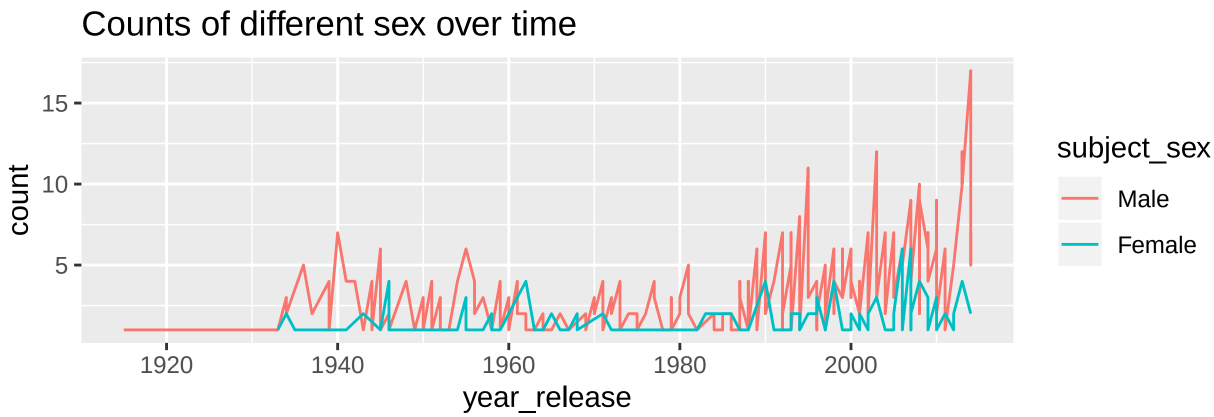
```
d <- c %>% group_by(year_release,subject_race,subject_sex) %>%
  summarise(count=n()) %>% mutate(prop=count/sum(count))
d
```

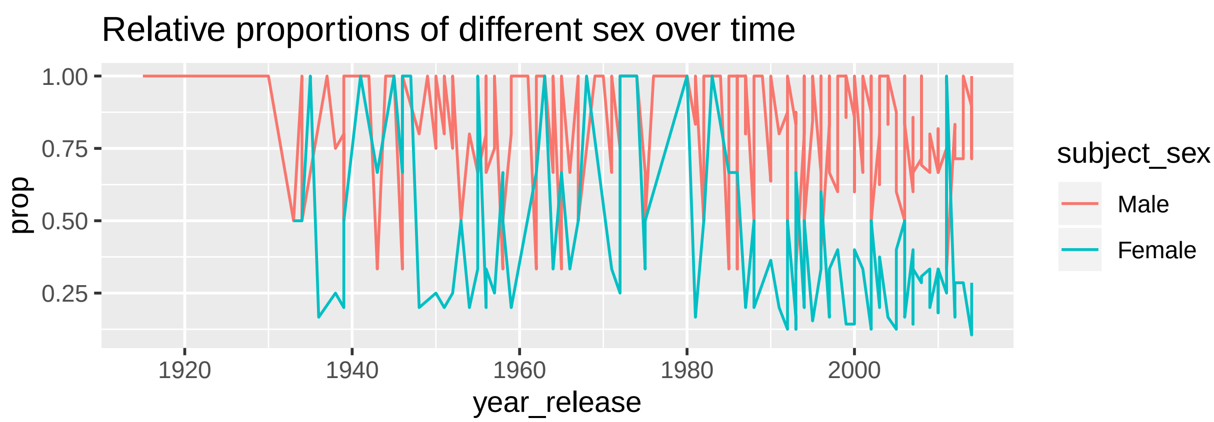
```
# A tibble: 281 x 5
# Groups:   year_release, subject_race [192]
   year_release subject_race subject_sex count  prop
          <int> <fct>        <fct>       <int> <dbl>
 1         1915 White        Male            1   1
 2         1927 Nonwhite     Male            1   1
 3         1929 White        Male            1   1
 4         1930 White        Male            1   1
 5         1933 White        Male            1   0.5
 6         1933 White        Female          1   0.5
 7         1934 White        Male            3   1
 8         1934 Nonwhite     Male            2   0.5
 9         1934 Nonwhite     Female          2   0.5
10         1935 White        Female          1   1
# ... with 271 more rows
```

(f)

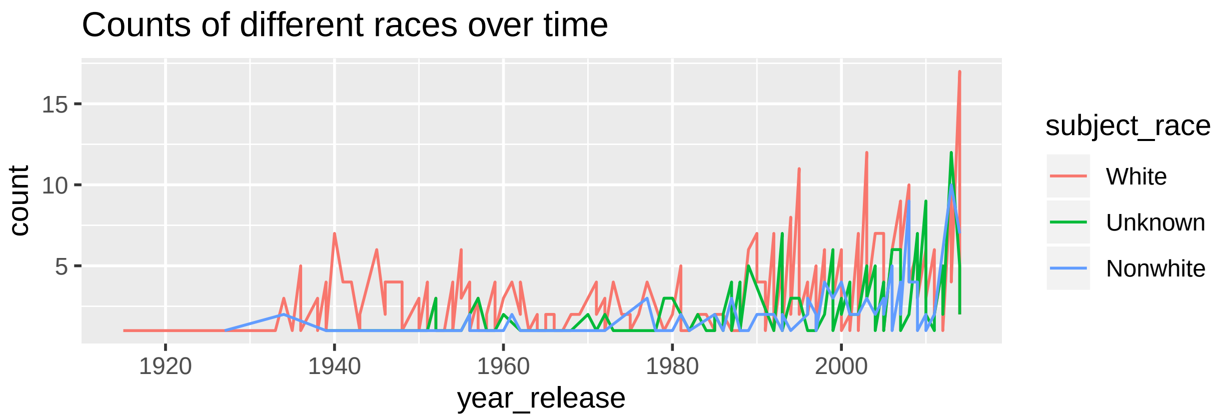
```
p1 = ggplot(d, aes(year_release, y=count)) + geom_line(aes(colour=subject_sex)) +
  labs(title = "Counts of different sex over time")
```

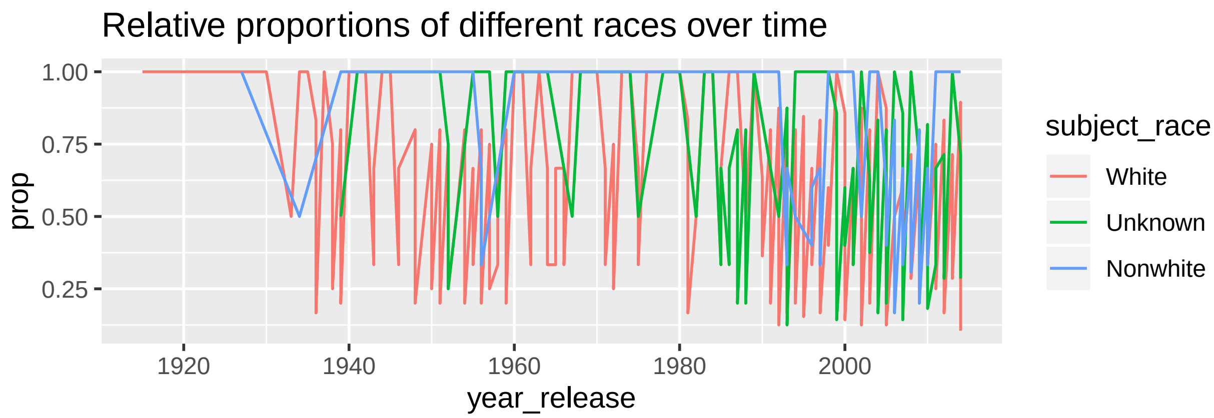
```
p2 = ggplot(d, aes(year_release, y=prop)) + geom_line(aes(colour=subject_sex)) +
  labs(title = "Relative proportions of different sex over time")
grid.arrange(p1,p2)
```






```
p3 = ggplot(d, aes(year_release, y=count)) + geom_line(aes(colour=subject_race)) +
  labs(title = "Counts of different races over time")
p4 = ggplot(d, aes(year_release, y=prop)) + geom_line(aes(colour=subject_race)) +
  labs(title = "Relative proportions of different races over time")
grid.arrange(p3,p4)
```





Based on the above plots, we conclude that although the imbalance of different races is improving over the time, it is still a huge problem when it comes to different sex. The line plot showing the counts of different sex and races over time indicates that the number of different races increases in a more and more consistent pace while the number of the male subjects has a more significant growth than that of the female subjects as time passes by. Moreover, from the line plot showing the relative proportions of subjects over time, the lines of different races tend to fluctuate within more and more similar range while the line representing the relative proportions of male subjects stays at the top of the plot almost all the time. The above reasons all lead to the conclusion stated previously.

Question 2

```r
library(heplots)
data(Diabetes)
```

Data exploration

```r
summary(Diabetes)
```

```
     relwt          glufast         glutest          instest     
 Min.   :0.7100   Min.   : 70   Min.   : 269.0   Min.   : 10.0  
 1st Qu.:0.8800   1st Qu.: 90   1st Qu.: 352.0   1st Qu.:118.0  
 Median :0.9800   Median : 97   Median : 413.0   Median :156.0  
 Mean   :0.9773   Mean   :122   Mean   : 543.6   Mean   :186.1  
 3rd Qu.:1.0800   3rd Qu.:112   3rd Qu.: 558.0   3rd Qu.:221.0  
 Max.   :1.2000   Max.   :353   Max.   :1568.0   Max.   :748.0  
      sspg                     group   
 Min.   : 29.0   Normal           :76  
```

```
 1st Qu.:100.0   Chemical_Diabetic:36
 Median :159.0   Overt_Diabetic   :33
 Mean   :184.2
 3rd Qu.:257.0
 Max.   :480.0
```

```r
head(Diabetes)
```

```
  relwt glufast glutest instest sspg  group
1  0.81      80     356     124   55 Normal
2  0.95      97     289     117   76 Normal
3  0.94     105     319     143  105 Normal
4  1.04      90     356     199  108 Normal
5  1.00      90     323     240  143 Normal
6  0.76      86     381     157  165 Normal
```

(a)

```r
Diabetes %>% group_by(group) %>% summarise_all(list(Avg=mean,Med=median)) %>%
  pivot_longer(cols=c("relwt_Avg", "relwt_Med", "glufast_Avg", "glufast_Med",
                      "glutest_Avg", "glutest_Med", "instest_Avg",
                      "instest_Med", "sspg_Avg", "sspg_Med"),names_to = "Measure") %>%
  pivot_wider(id_cols=Measure,names_from=group) %>% arrange(desc(Measure))
```

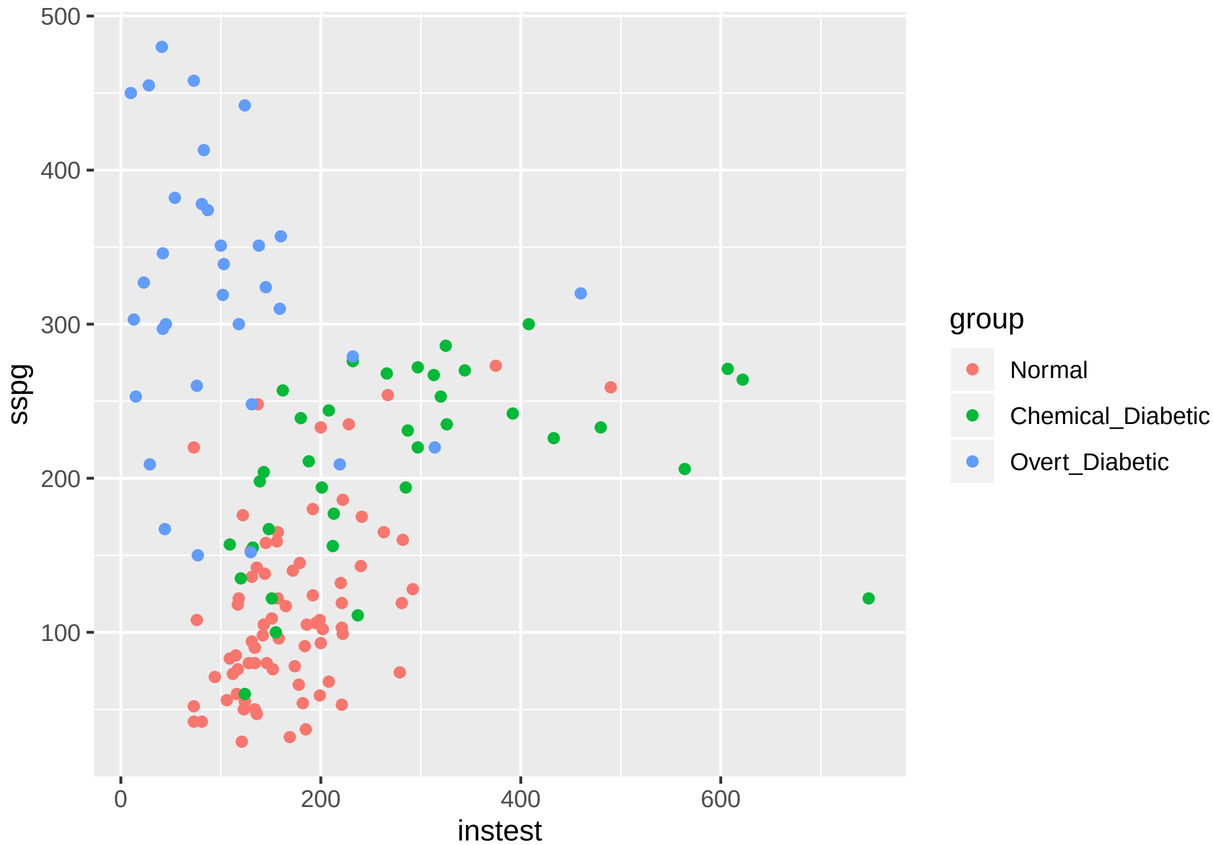
```
# A tibble: 10 x 4
   Measure      Normal Chemical_Diabetic Overt_Diabetic
   <chr>         <dbl>             <dbl>          <dbl>
 1 sspg_Med    105               223            320
 2 sspg_Avg    114               209.           319.
 3 relwt_Med     0.95              1.06           0.98
 4 relwt_Avg     0.937             1.06           0.984
 5 instest_Med 157               252.            83
 6 instest_Avg 173.              288            106
 7 glutest_Med 353               476.           972
 8 glutest_Avg 350.              494.          1044.
 9 glufast_Med  90                99.5          203
10 glufast_Avg  91.2              99.3          218.
```

From the table above, variable “sspg”, “instest”, and “glutest” seem to differentiate amongst the different types of diabetes very well.

(b)

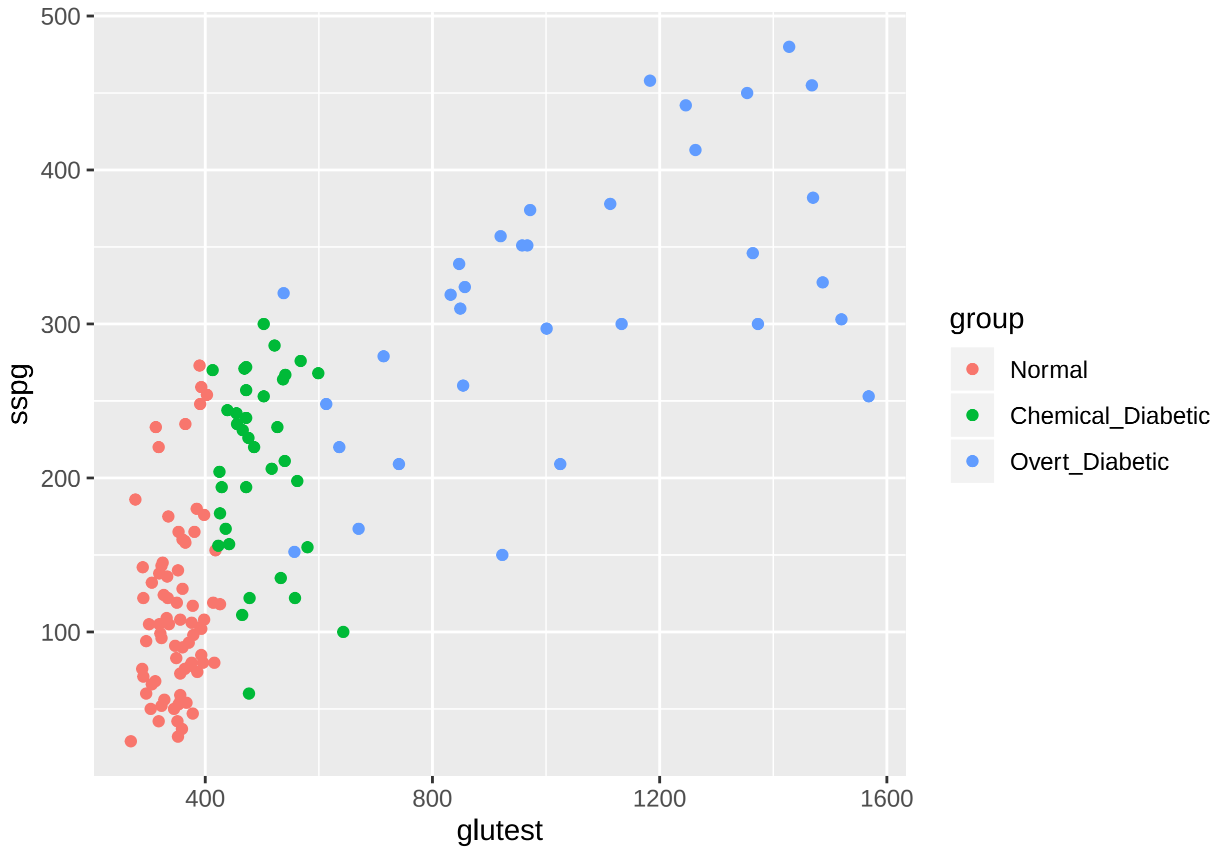
“sspg” versus “insulin test”:

```r
ggplot(Diabetes, aes(x = instest, y = sspg, colour = group)) + geom_point()
```



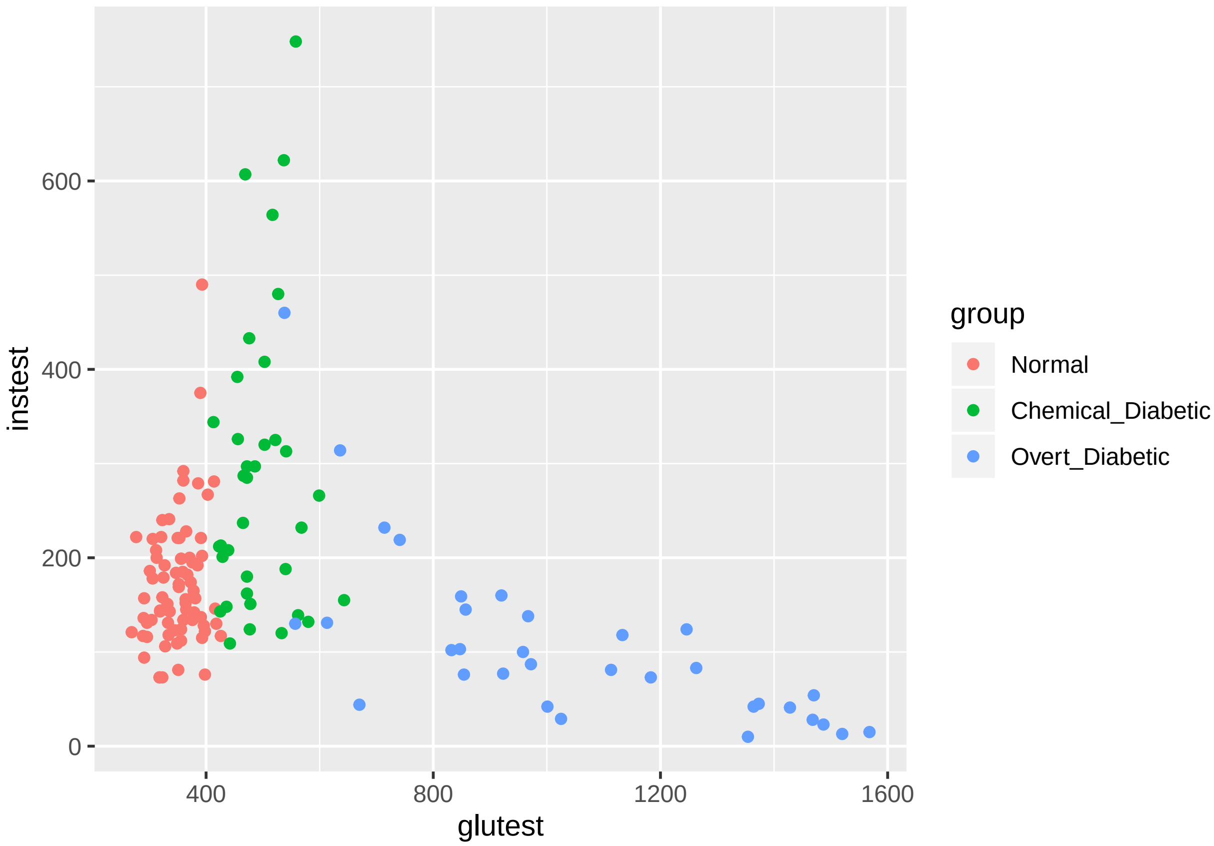
"sspg" versus "glucose test":

```
ggplot(Diabetes, aes(x = glutest, y = sspg, colour = group)) + geom_point()
```



"insulin test" versus "glucose test":

```
ggplot(Diabetes, aes(x = glutest, y = instest, colour = group)) + geom_point()
```



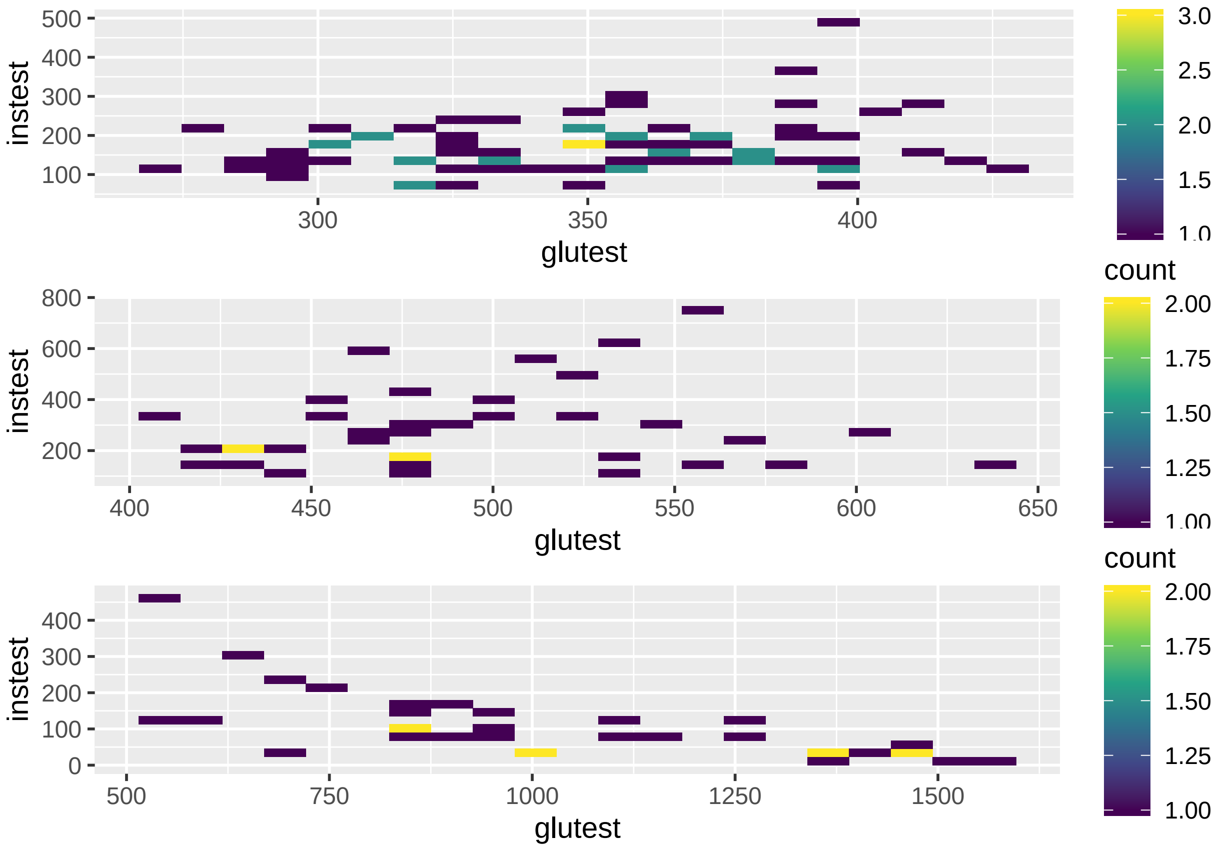
The pair "“insulin test” & “glucose test” seems to allow for the strongest distinction amongst the three groups.

(c)

Histograms:

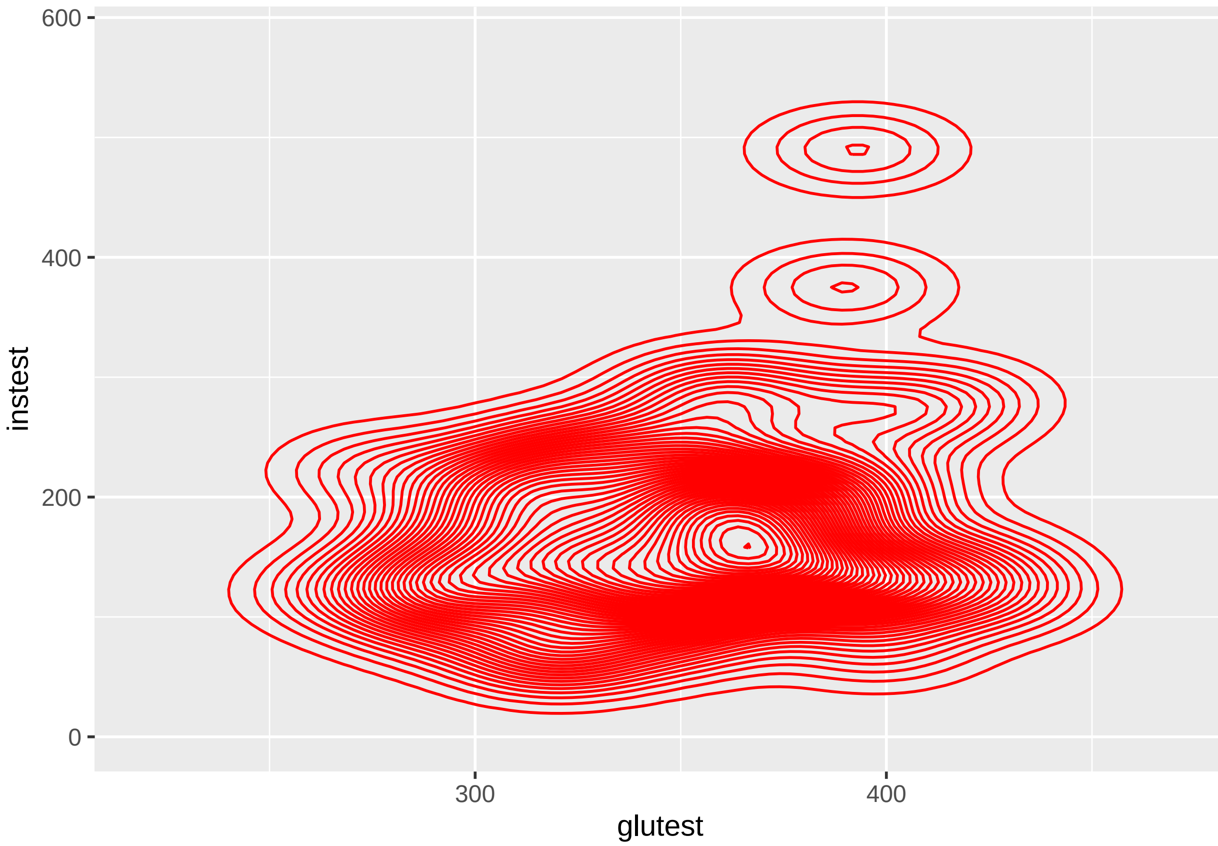
```
normal <- Diabetes %>% filter(group == "Normal")
chemical <- Diabetes %>% filter(group == "Chemical_Diabetic")
overt <- Diabetes %>% filter(group == "Overt_Diabetic")
```

```
p = ggplot(normal,aes(x=glutest,y=instest)) + geom_bin2d(bins=20) +
  scale_fill_continuous(type = "viridis") + labs(x="glutest",y="instest")
q = ggplot(chemical,aes(x=glutest,y=instest)) + geom_bin2d(bins=20) +
  scale_fill_continuous(type = "viridis") + labs(x="glutest",y="instest")
n = ggplot(overt,aes(x=glutest,y=instest)) + geom_bin2d(bins=20) +
  scale_fill_continuous(type = "viridis") + labs(x="glutest",y="instest")
grid.arrange(p,q,n)
```

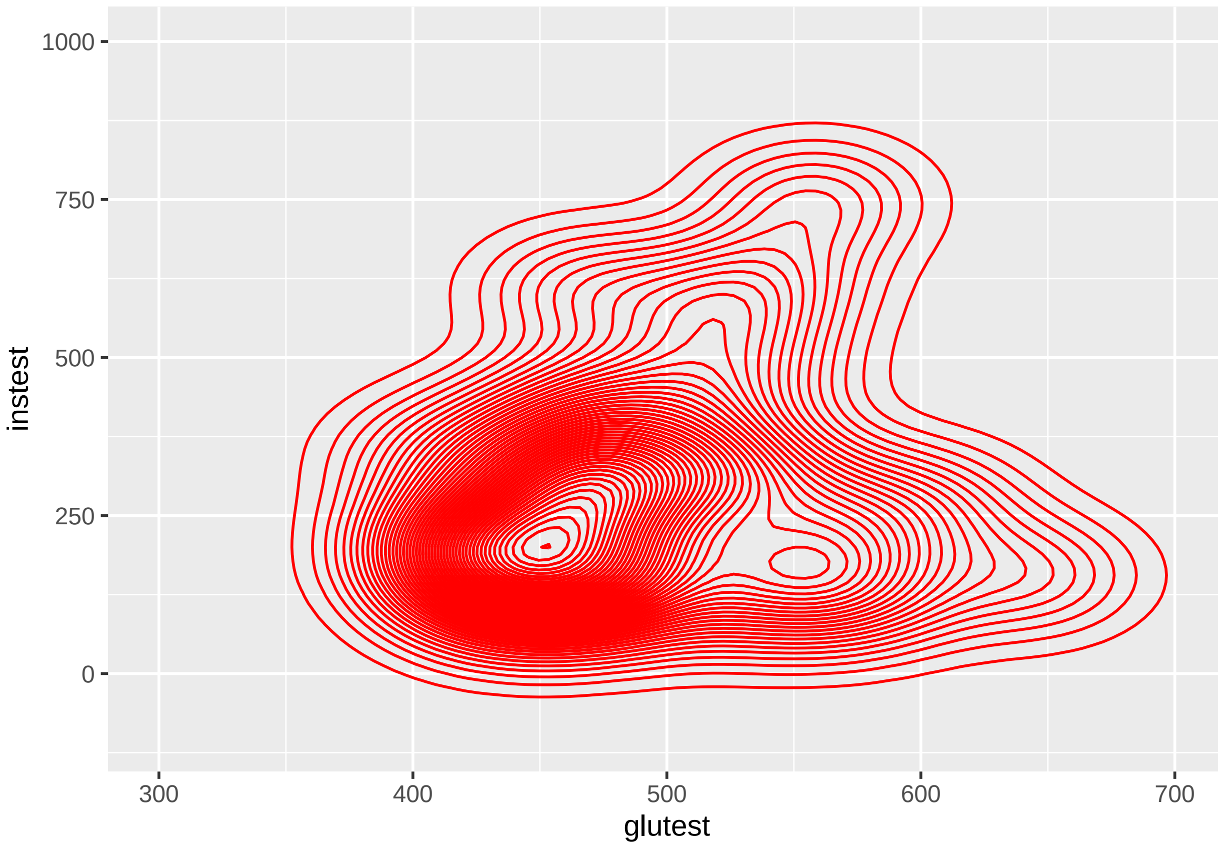


Contour plots:

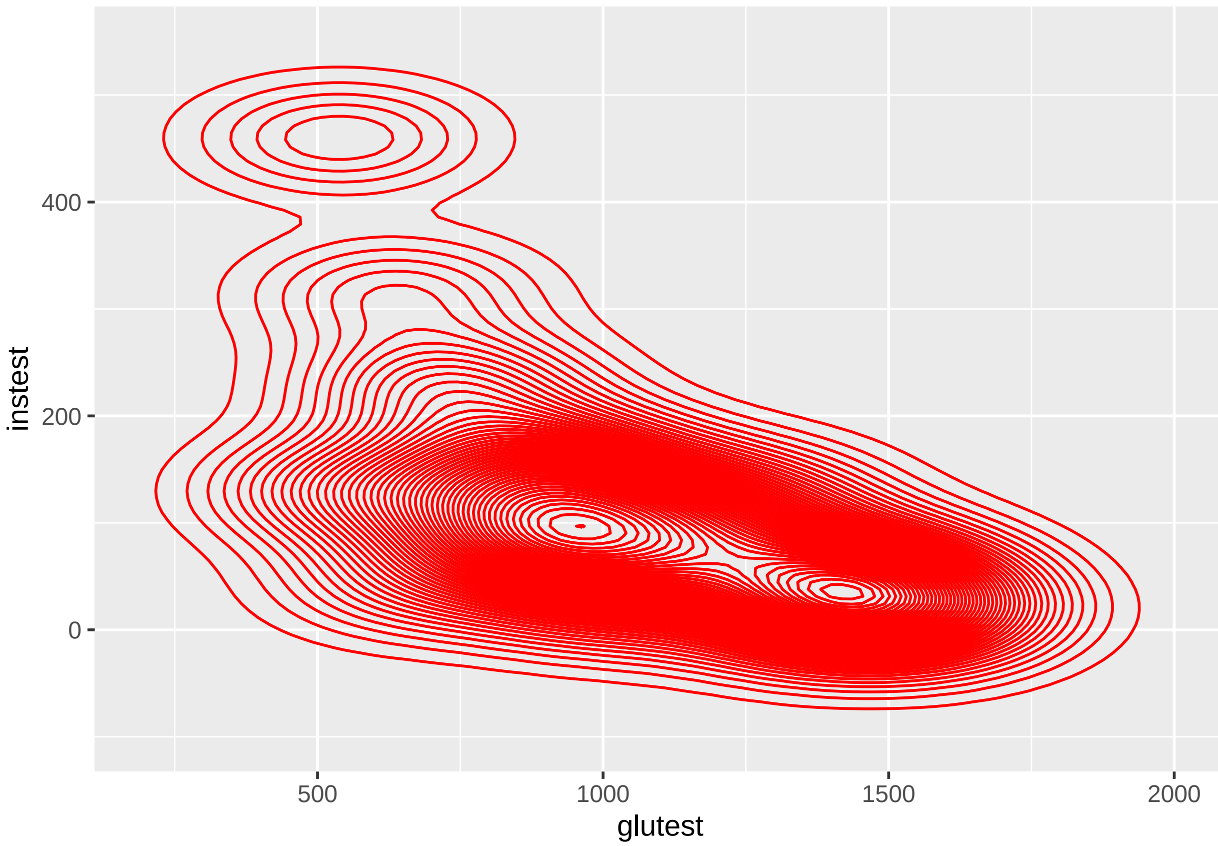
```
ggplot(normal,aes(x=glutest,y=instest)) + geom_density_2d(col="red",bins=50) +
  labs(x="glutest",y="instest") +
  ylim(c(0,580)) + xlim(c(220,470))
```




```
ggplot(chemical,aes(x=glutest,y=instest)) + geom_density_2d(col="red",bins=50) +
  labs(x="glutest",y="instest") +
  ylim(c(-100,1000)) + xlim(c(300,700))
```




```
ggplot(overt,aes(x=glutest,y=instest)) + geom_density_2d(col="red",bins=50) +
  labs(x="glutest",y="instest") +
  ylim(c(-100,550)) + xlim(c(200,2000))
```



These plots do provide useful summaries of the differences in distributions in the three groups. From the previous visualization, we picked out the subspace "instest"×"glutest" which "allows for the strongest distinction amongst the three groups". That is to say, these marginal distributions best describe the corresponding original distributions. Also, the histograms and contour plots gives information about the mode, mean, variance and other properties of the distributions. So the differences in distributions in the three groups are clearly visualized.