

MATH 208 Assignment2

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2019-10-07

Question 1

Load libraries and data:

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

Data exploration:

```
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
##
##
##
##
```

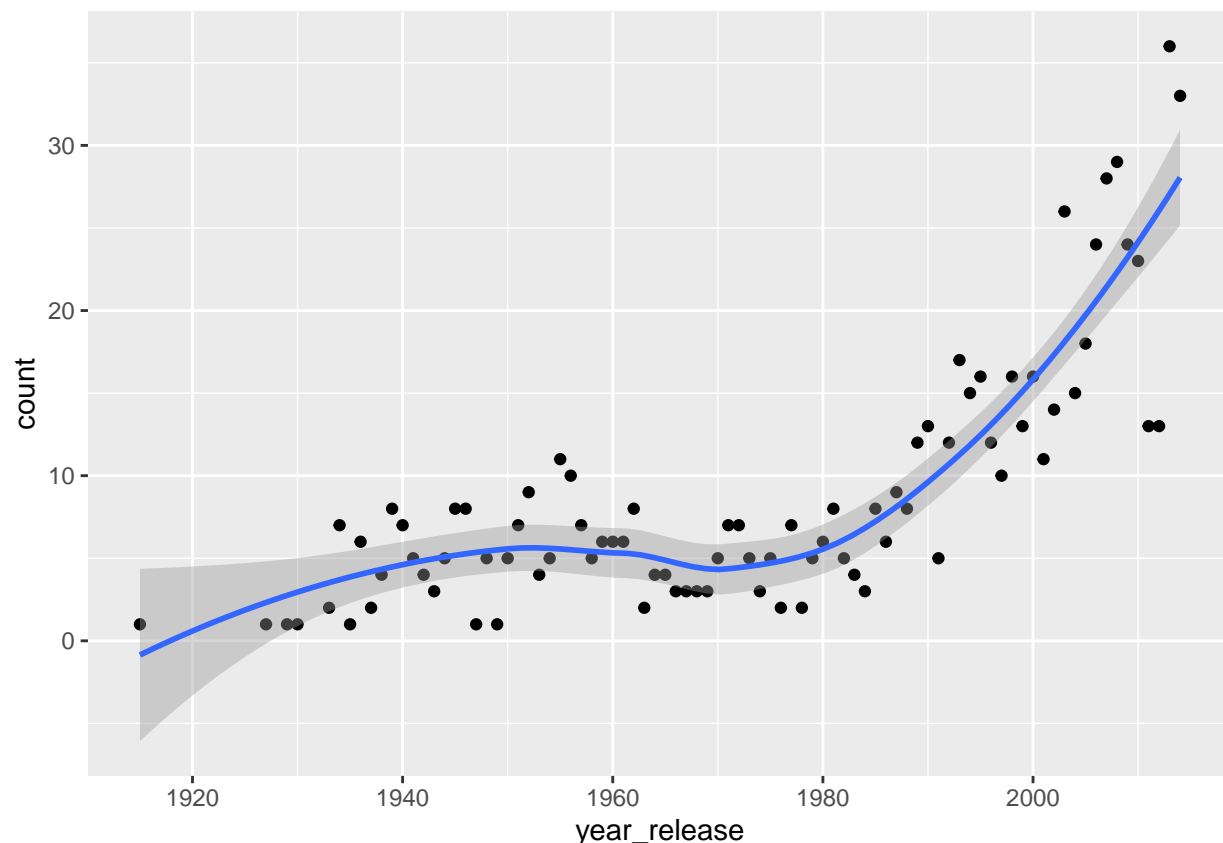
```
head(biopics)
```

```
## # 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)

```
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')
```

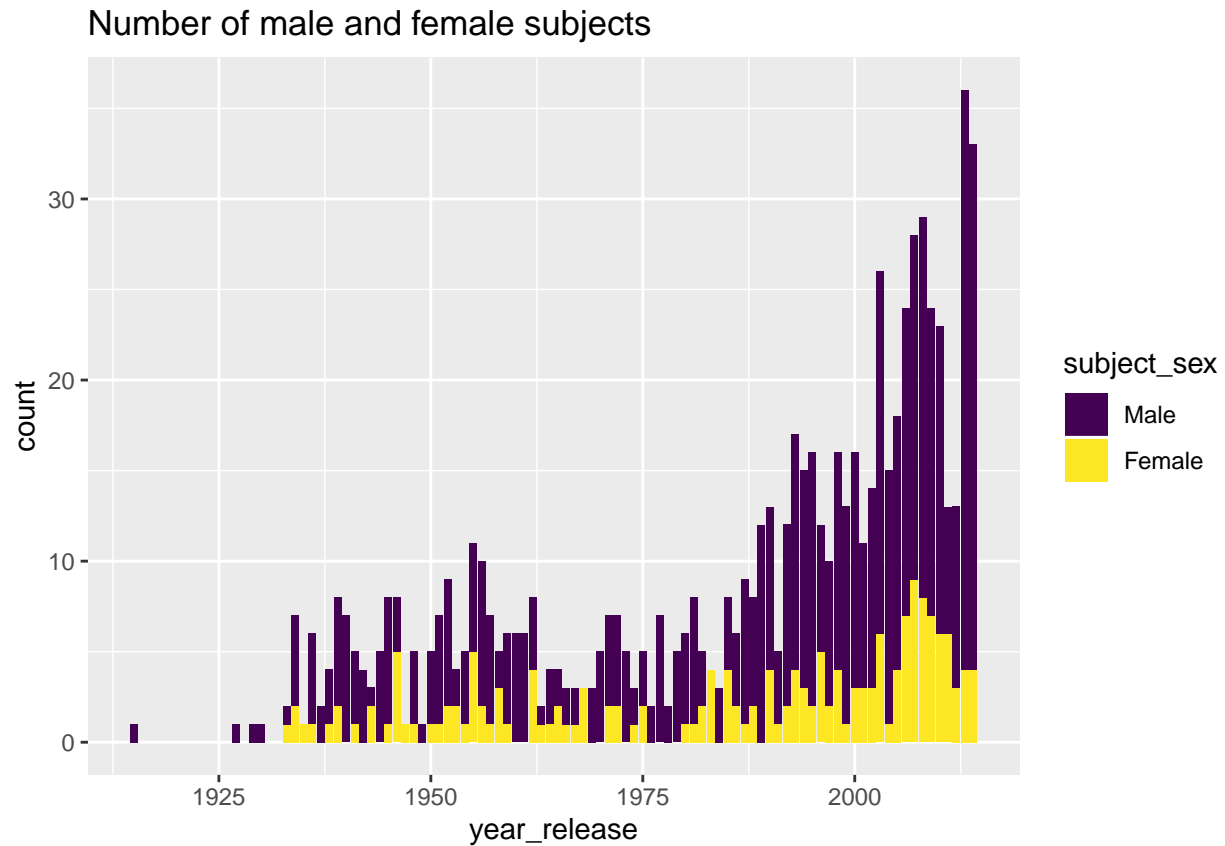
```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```



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>
```

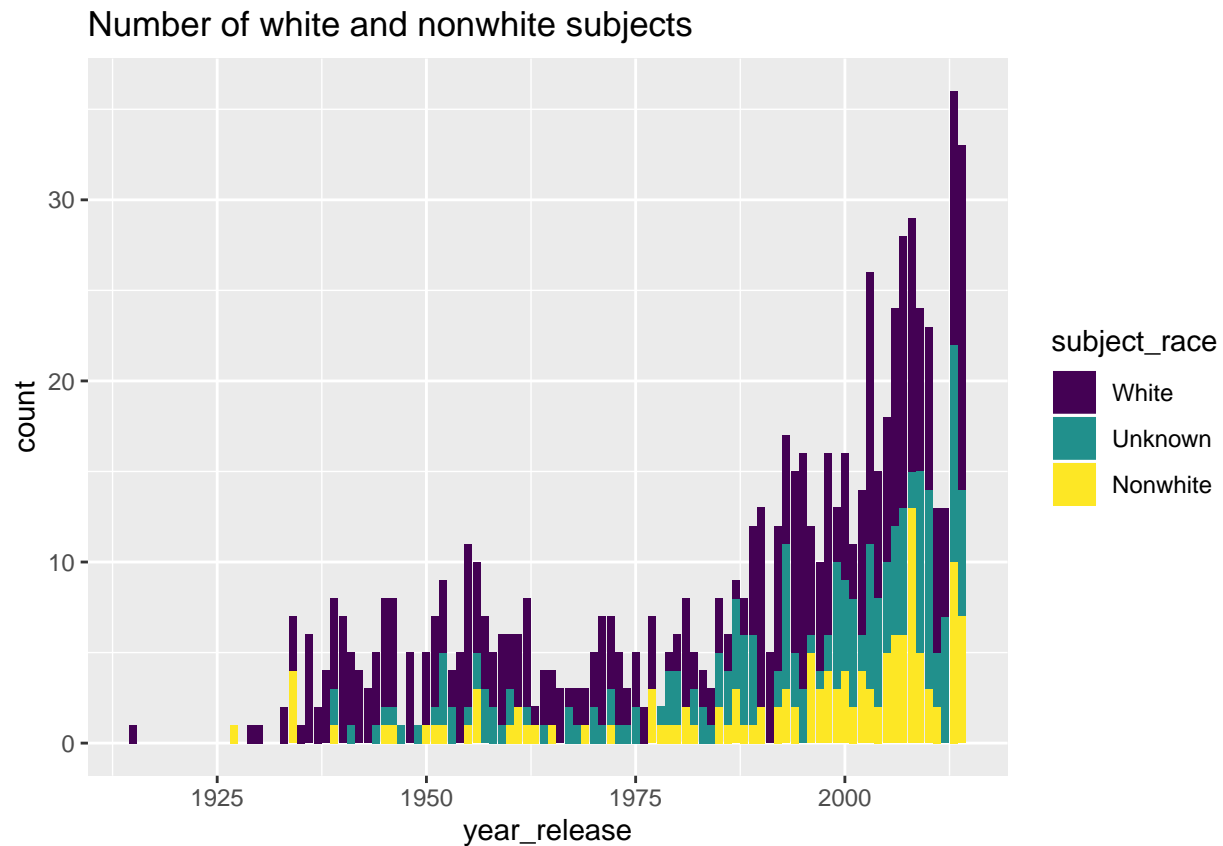
```
( c )
```

Recategorizing subject race into "White", "Nonwhite", and "Unknown":

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

```
head(biopics$subject_race)
```

```
## [1] "Unknown" "Nonwhite" "Unknown" "White" "Unknown" "Nonwhite"
c = biopics %>% 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)

```
c$years[(c$year_release >= 1915) & (c$year_release < 1934)] <- "1915~1934"
```

```
## Warning: Unknown or uninitialised column: 'years'.
```

```
c$years[(c$year_release >= 1934) & (c$year_release < 1954)] <- "1934~1954"
c$years[(c$year_release >= 1954) & (c$year_release < 1974)] <- "1954~1974"
c$years[(c$year_release >= 1974) & (c$year_release < 1994)] <- "1974~1994"
c$years[(c$year_release >= 1994) & (c$year_release <= 2014)] <- "1994~2014"
```

```
head(c$years)
```

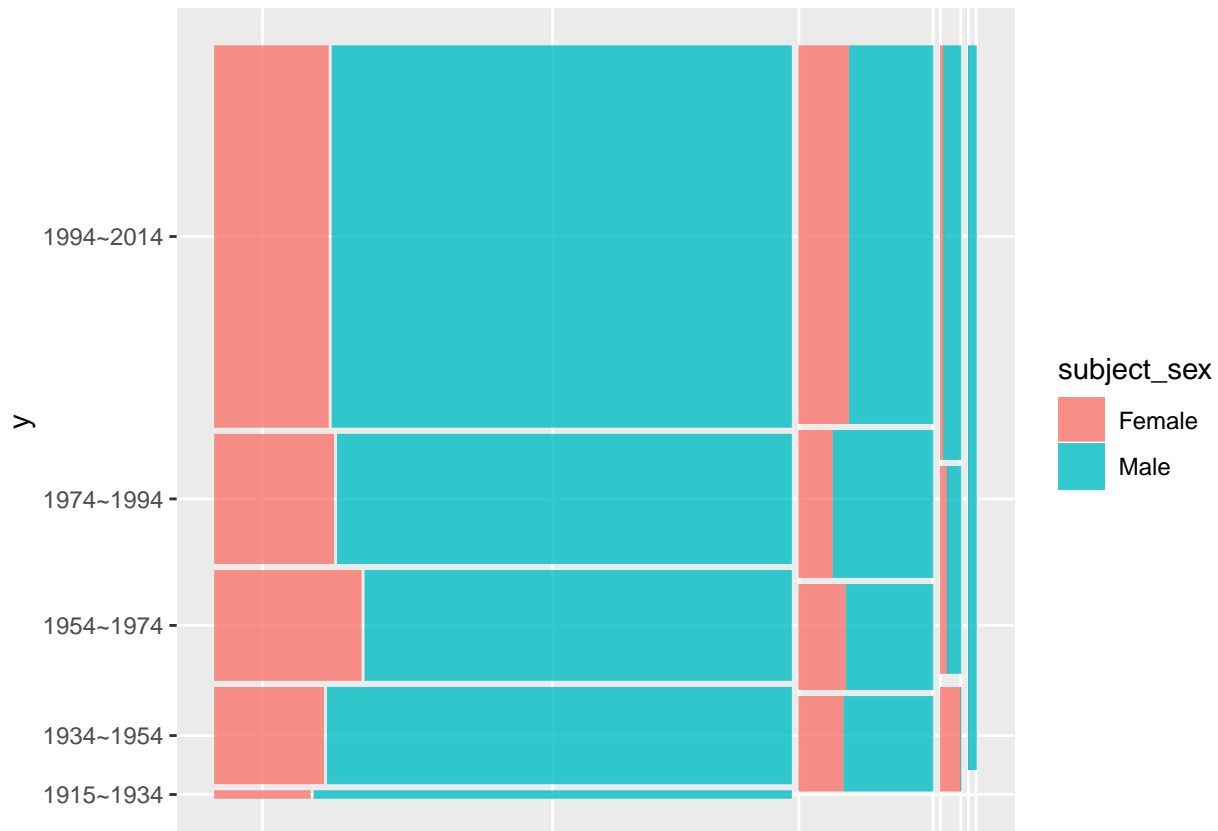
```
## [1] "1954~1974" "1994~2014" "1994~2014" "1994~2014" "1994~2014" "1994~2014"
```

```
ggplot(c) + geom_mosaic(aes(x=product(years, number_of_subjects),
  fill=subject_race)) +
  theme(axis.title.x =element_blank(),axis.text.x =element_blank(),
  axis.ticks.x=element_blank())
```



From the above plot, we can see that the “Nonwhite” group is the most underrepresented in biopics based on number of subjects since the blue areas are relatively smaller than the other two.

```
ggplot(c) + geom_mosaic(aes(x=product(years, number_of_subjects),
                             fill=subject_race)) +
theme(axis.title.x =element_blank(),axis.text.x =element_blank(),
axis.ticks.x=element_blank())
```



From the above plot, we can see that the “Female” group is the most underrepresented in biopics based on number of subjects since the the total red areas are relatively smaller than the blue areas.

(e)

```
d1 <- c %>% group_by(year_release,subject_race) %>%
  summarise(count=n()) %>% mutate(prop=count/sum(count))
d1
```

```
## # A tibble: 192 x 4
## # Groups:   year_release [86]
##   year_release subject_race count  prop
##   <int> <fct>         <int> <dbl>
## 1     1915 White             1 1
## 2     1927 Nonwhite          1 1
## 3     1929 White             1 1
## 4     1930 White             1 1
## 5     1933 White             2 1
## 6     1934 White             3 0.429
## 7     1934 Nonwhite          4 0.571
## 8     1935 White             1 1
## 9     1936 White             6 1
## 10    1937 White             2 1
## # ... with 182 more rows
```

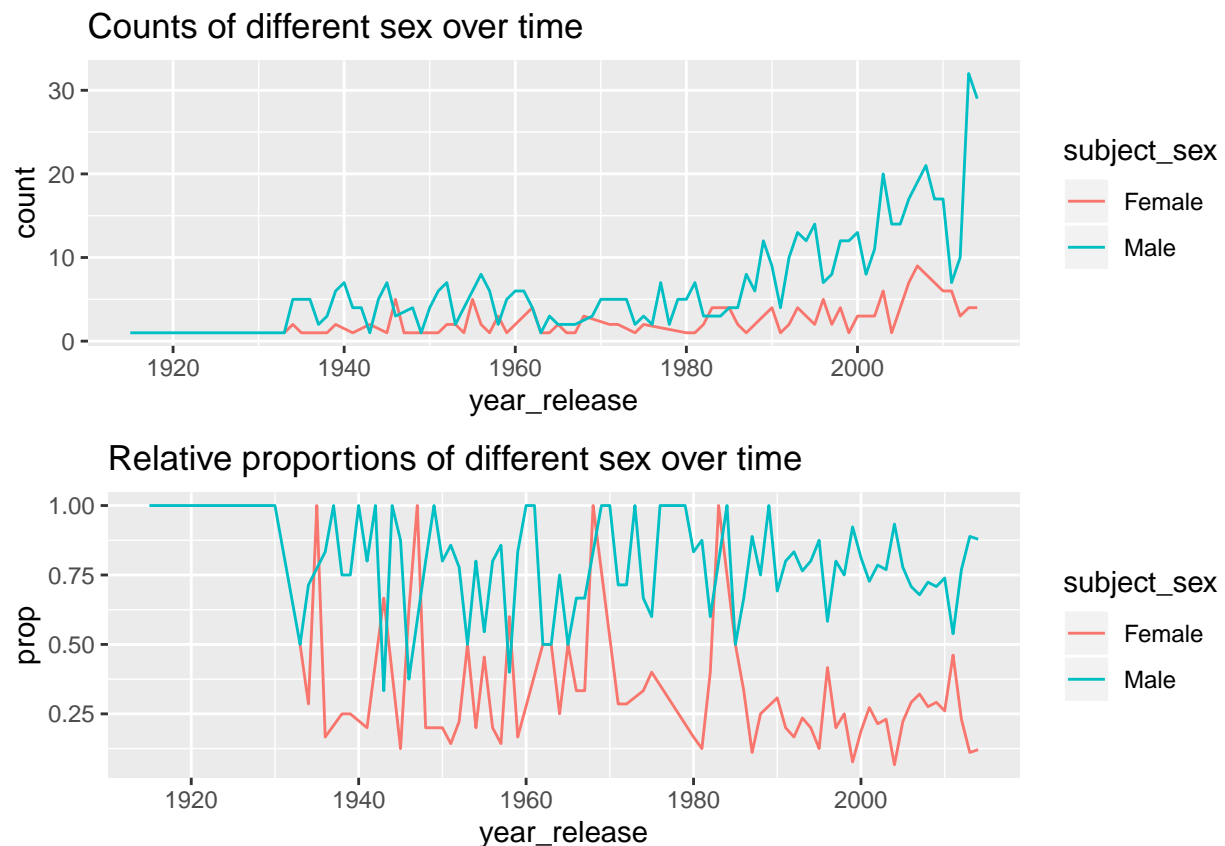
```
d2 <- c %>% group_by(year_release,subject_sex) %>%
  summarise(count=n()) %>% mutate(prop=count/sum(count))
d2
```

```
## # A tibble: 148 x 4
```

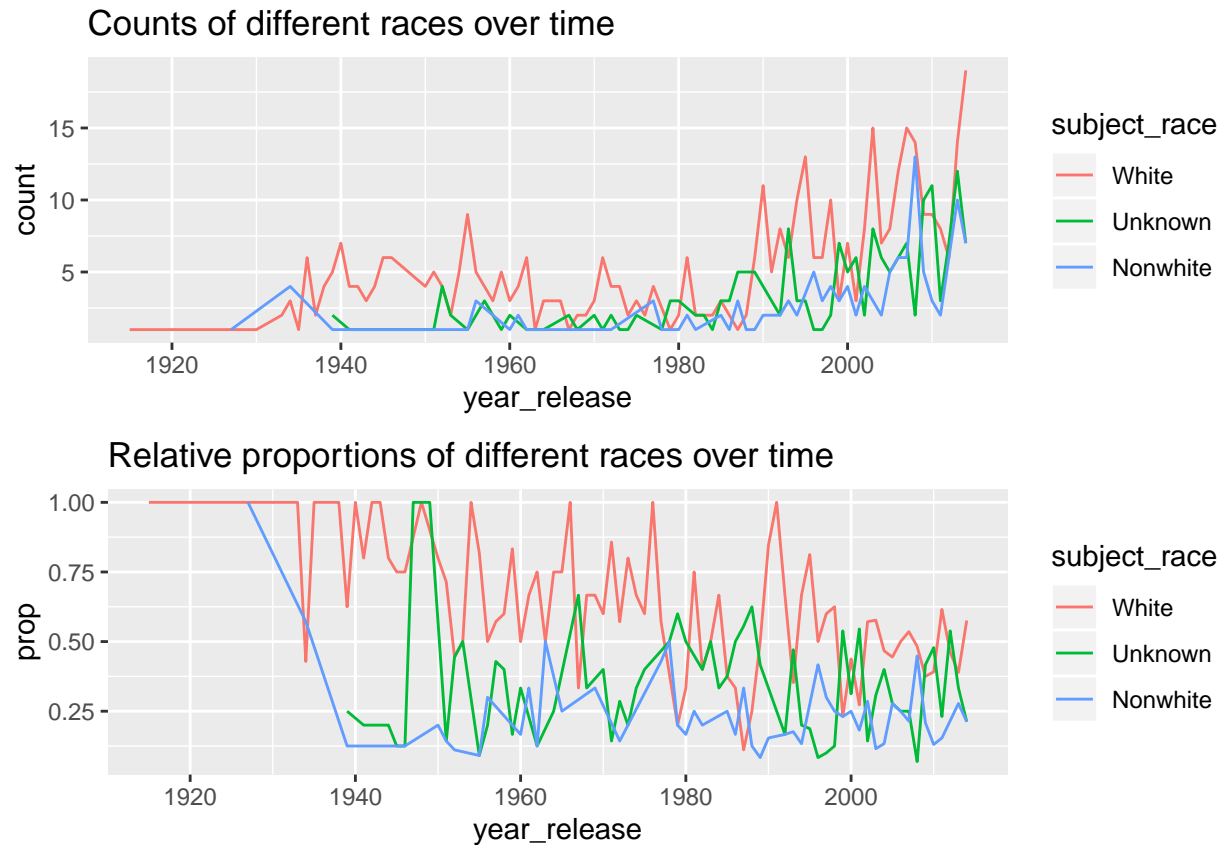
```
## # Groups:   year_release [86]
##   year_release subject_sex count  prop
##   <int> <chr>      <int> <dbl>
## 1     1915 Male         1  1
## 2     1927 Male         1  1
## 3     1929 Male         1  1
## 4     1930 Male         1  1
## 5     1933 Female        1  0.5
## 6     1933 Male         1  0.5
## 7     1934 Female        2  0.286
## 8     1934 Male         5  0.714
## 9     1935 Female        1  1
## 10    1936 Female        1  0.167
## # ... with 138 more rows
```

(f)

```
p1 = ggplot(d2, aes(year_release, y=count)) + geom_line(aes(colour=subject_sex)) +
  labs(title = "Counts of different sex over time")
p2 = ggplot(d2, 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(d1, aes(year_release, y=count)) + geom_line(aes(colour=subject_race)) +
  labs(title = "Counts of different races over time")
p4 = ggplot(d1, 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 a smaller and smaller 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

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

Data exploration

```
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
```

```
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)

```
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))
```

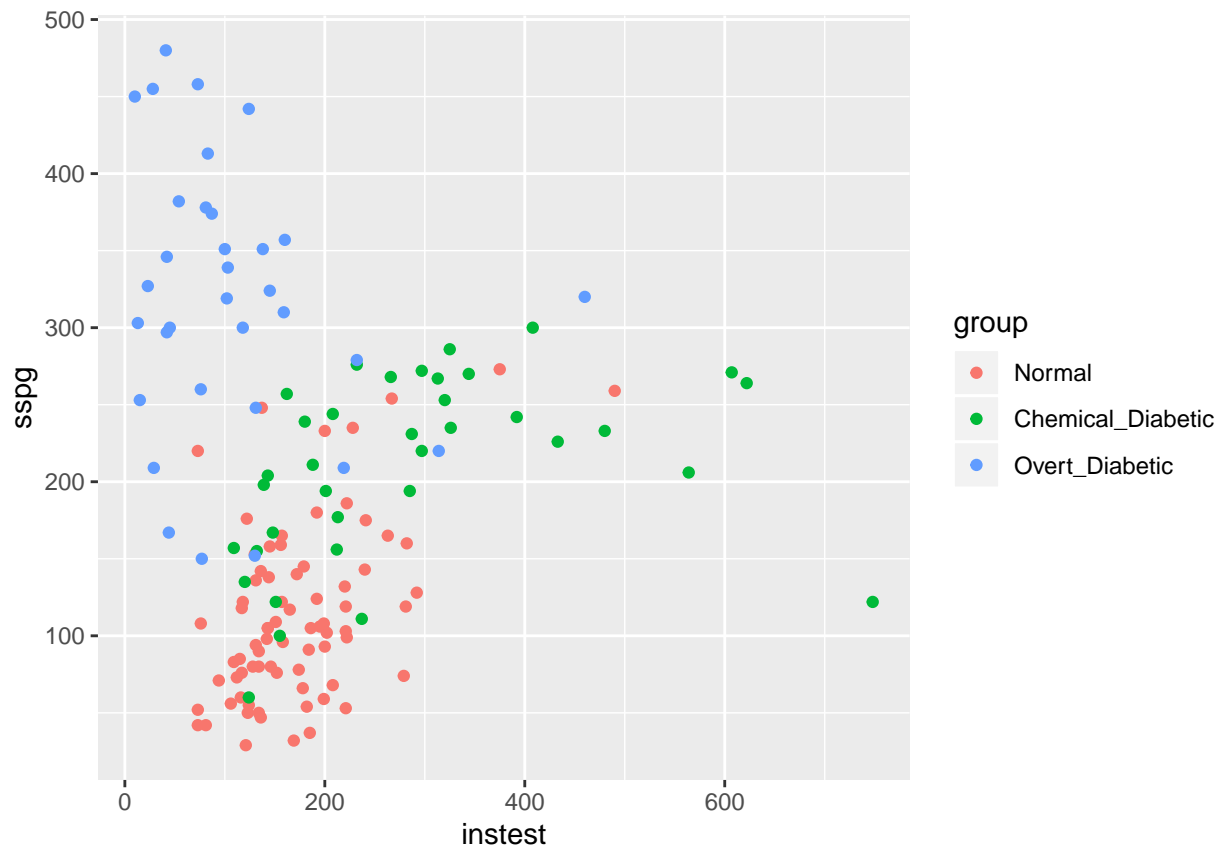
```
## # A tibble: 10 x 4
## Measure Normal Chemical_Diabetic Overt_Diabetic
## <chr> <dbl> <dbl> <dbl>
## 1 sspg_Med 105 223 320
## 2 sspg_Avg 114 209. 319.
## 3 relwt_Med 0.95 1.06 0.98
## 4 relwt_Avg 0.937 1.06 0.984
## 5 instest_Med 157 252. 83
## 6 instest_Avg 173. 288 106
## 7 glutest_Med 353 476. 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)

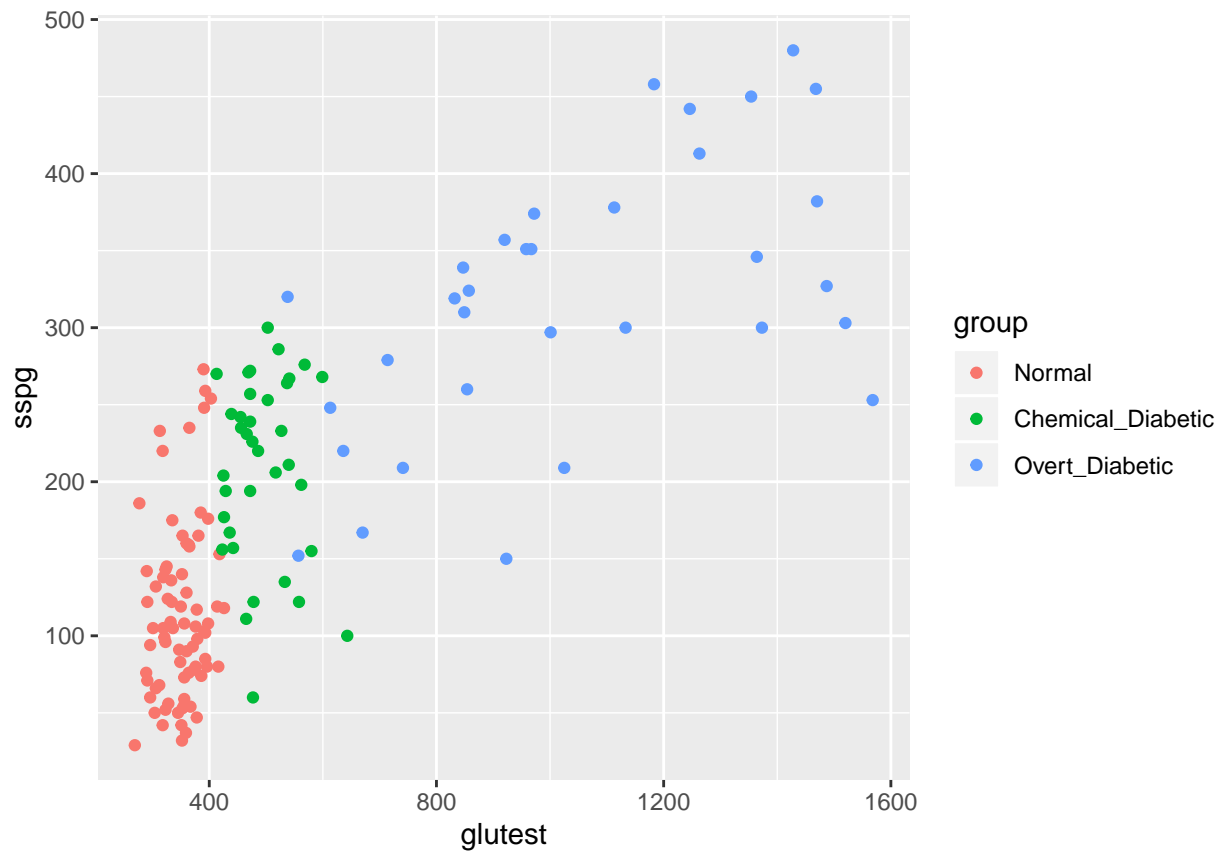
“sspg” versus “insulin test”:

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



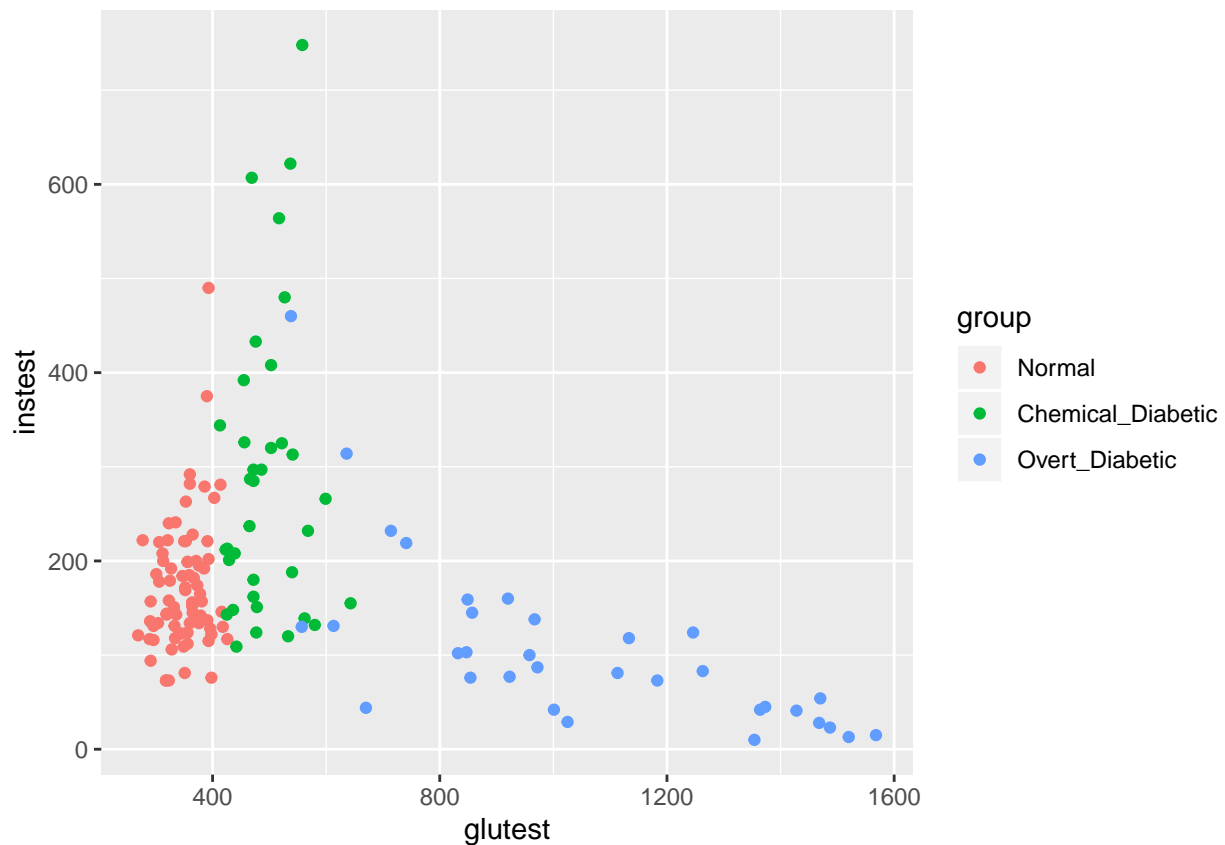
“sspg” versus “glucose test”:

```
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()
```



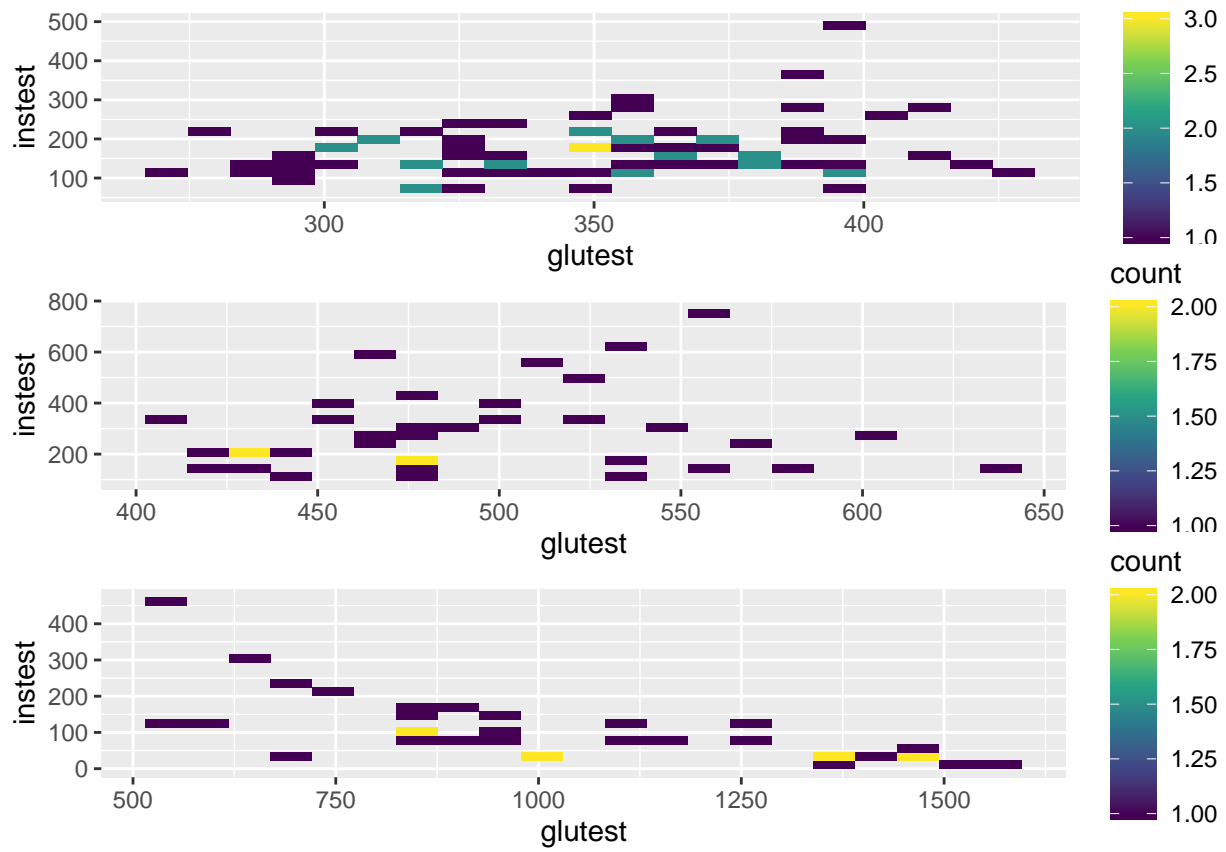
The pair "insulin test" and "glucose test" seems to allow for the strongest distinction amongst the three groups.

(c)

Histograms:

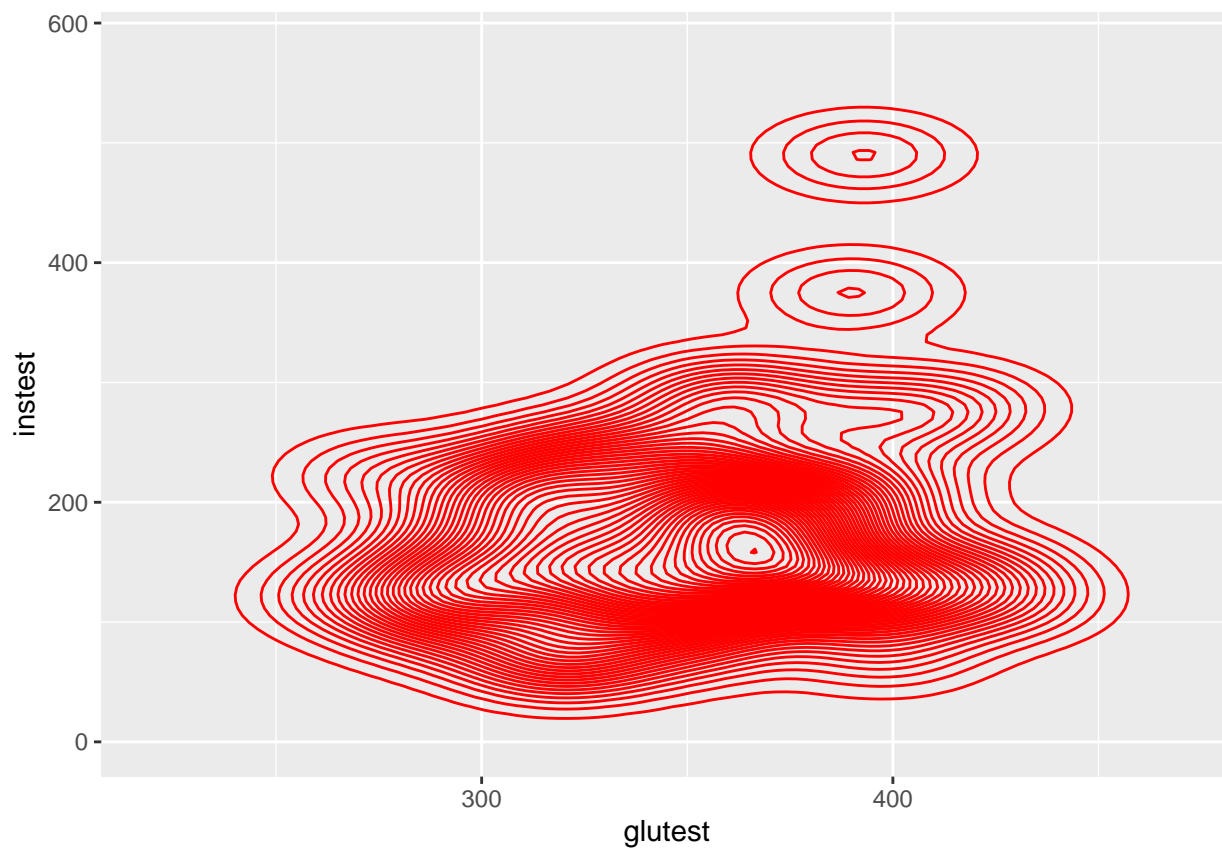
```
normal <- Diabetes %>% filter(group == "Normal")
chemical <- Diabetes %>% filter(group == "Chemical_Diabetic")
overt <- Diabetes %>% filter(group == "Overt_Diabetic")

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)
```

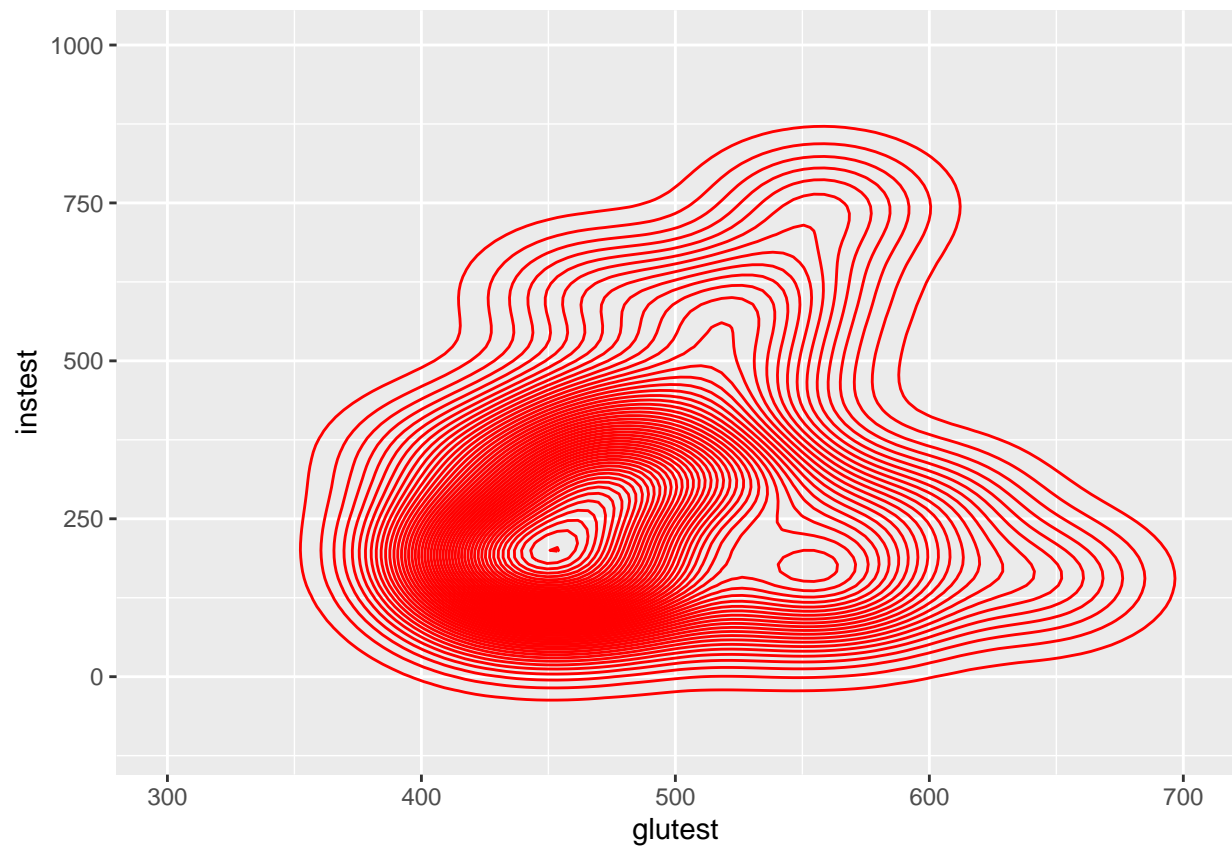


Contour plots:

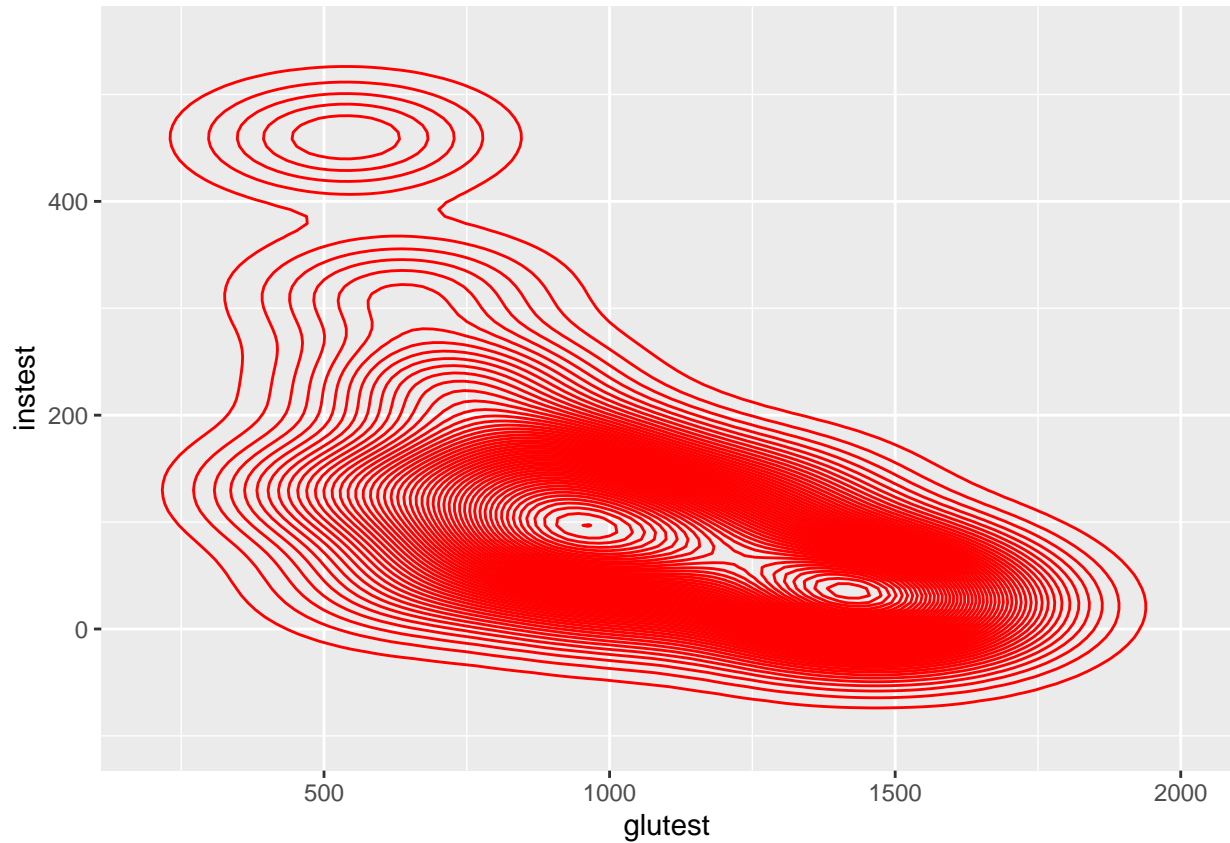
```
ggplot(normal,aes(x=glutest,y=instest)) + geom_density_2d(col="red",bins=50) +
  labs(x="glutest",y="instest") +
  ylim(c(0,580)) + xlim(c(220,470))
```



```
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” \times “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.