Exploring the ProPublica COMPAS data

Loading and filtering data

```
library(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
```

```
library(ggplot2)
library(grid)
library(gridExtra)
```

```
##
## Attaching package: 'gridExtra'
```

```
## The following object is masked from 'package:dplyr':
##
##     combine
```

```
raw_data <- read.csv("~/My Drive/tex-documents/working-papers/algo-fairness/algo-fairness-m/rutgers-pres
nrow(raw_data)
```

```
## [1] 7214
```

Filtering the data a bit:

```
df <- dplyr::select(raw_data, age, c_charge_degree, race, age_cat, score_text, sex, priors_count,
                    days_b_screening_arrest, decile_score, is_recid, two_year_recid, c_jail_in, c_jail_
        filter(days_b_screening_arrest <= 30) %>%
        filter(days_b_screening_arrest >= -30) %>%
        filter(is_recid != -1) %>%
        filter(c_charge_degree != "O") %>%
        filter(score_text != 'N/A')
nrow(df)
```

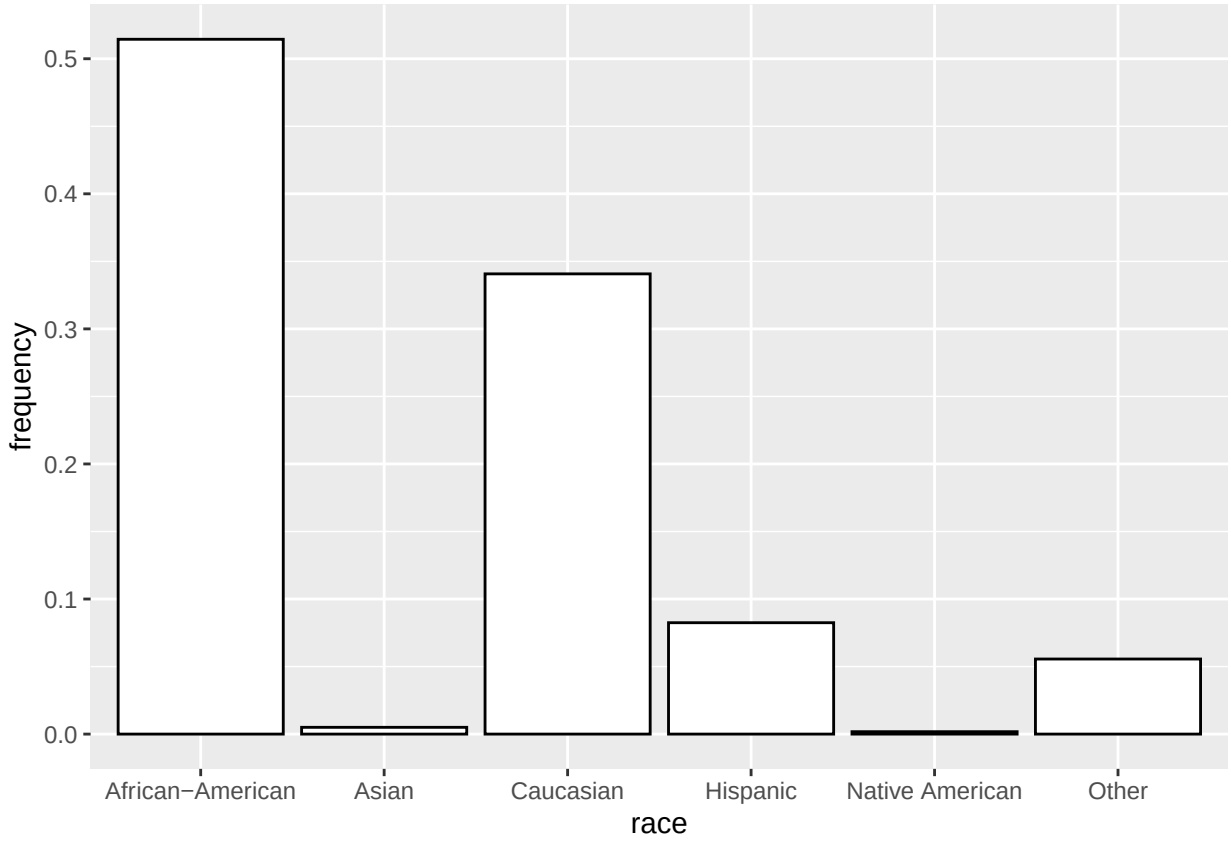
```
## [1] 6172
```

Race breakdown

The database is mostly constituted of blacks, whites and Hispanics. Asians and native-Americans are a small percentage.

```
race <- ggplot(df, aes(x=race)) +
          # geom_histogram(aes(y=..count../sum(..count..)), colour="black", fill="grey100")  +
```

```
          geom_bar(aes(y=..count../sum(..count..)), colour="black", fill="grey100") +
          xlab("race") +
          ylab("frequency")
race
```

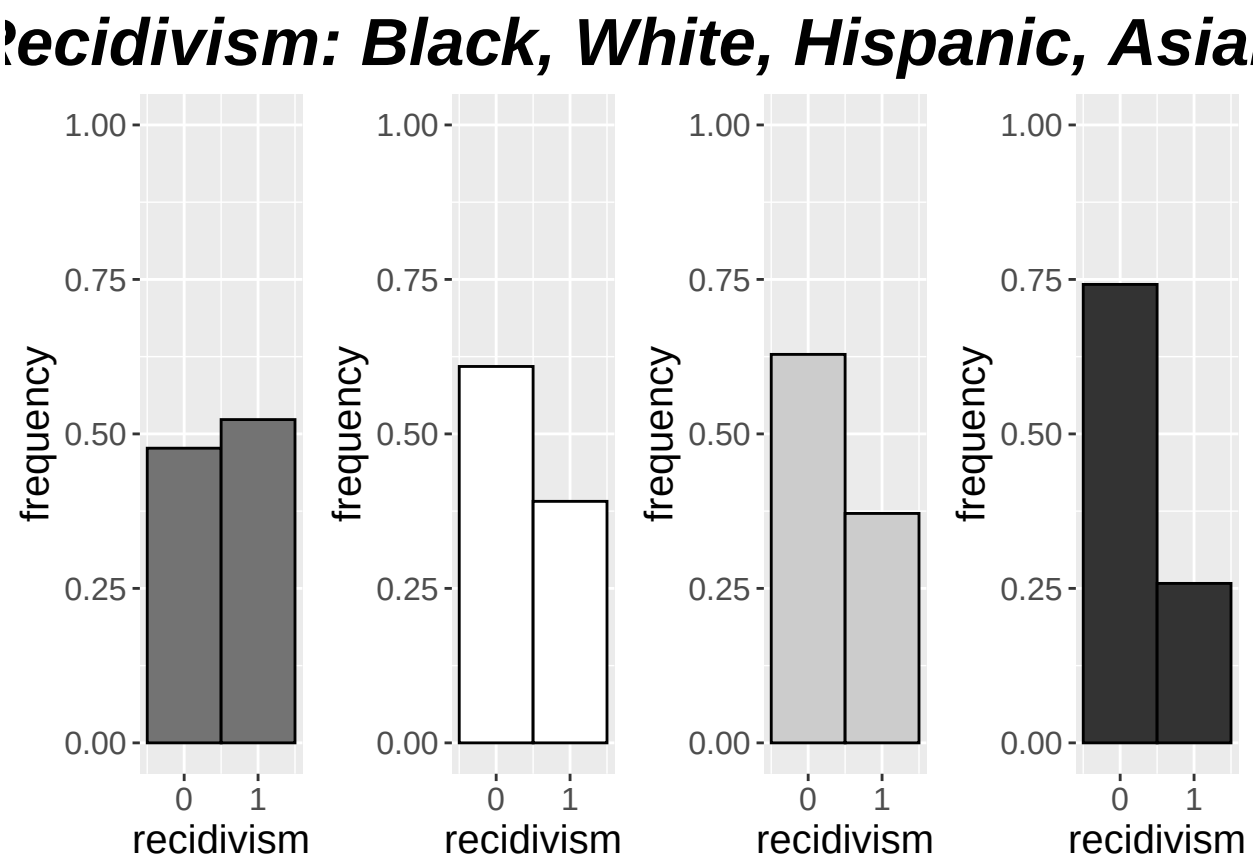


Recidivism

The recidivism rate is different across races. It is higher among blacks (almost 50%), while it is comparably lower among whites and Hispanics (about 40%) and even lower among Asians (about 35%). Recidivism is defined as a rearrest for a criminal offense that occurred within two years after the COMPAS risk assessment took place. Arrest is therefore used as as proxy for criminal activity.

```
pblack <- ggplot(data=filter(df, race =="African-American"), aes(x=two_year_recid)) +
          geom_histogram(aes(y=..count../sum(..count..)), binwidth = 1,  colour="black", fill="grey45")
          ylab("frequency") +
          ylim(0, 1) +
          scale_x_continuous(breaks = seq(0, 1, by = 1)) +
          theme(plot.title = element_text(hjust = 0.5)) +
          theme(text=element_text(size = 15))

pwhite <- ggplot(data=filter(df, race =="Caucasian"), aes(x=two_year_recid)) +
          geom_histogram(aes(y=..count../sum(..count..)), binwidth = 1,  colour="black", fill="grey100"
          ylab("frequency") +
          ylim(0, 1) +
          scale_x_continuous(breaks = seq(0, 1, by = 1)) +
          theme(plot.title = element_text(hjust = 0.5)) +
          theme(text=element_text(size = 15))
```

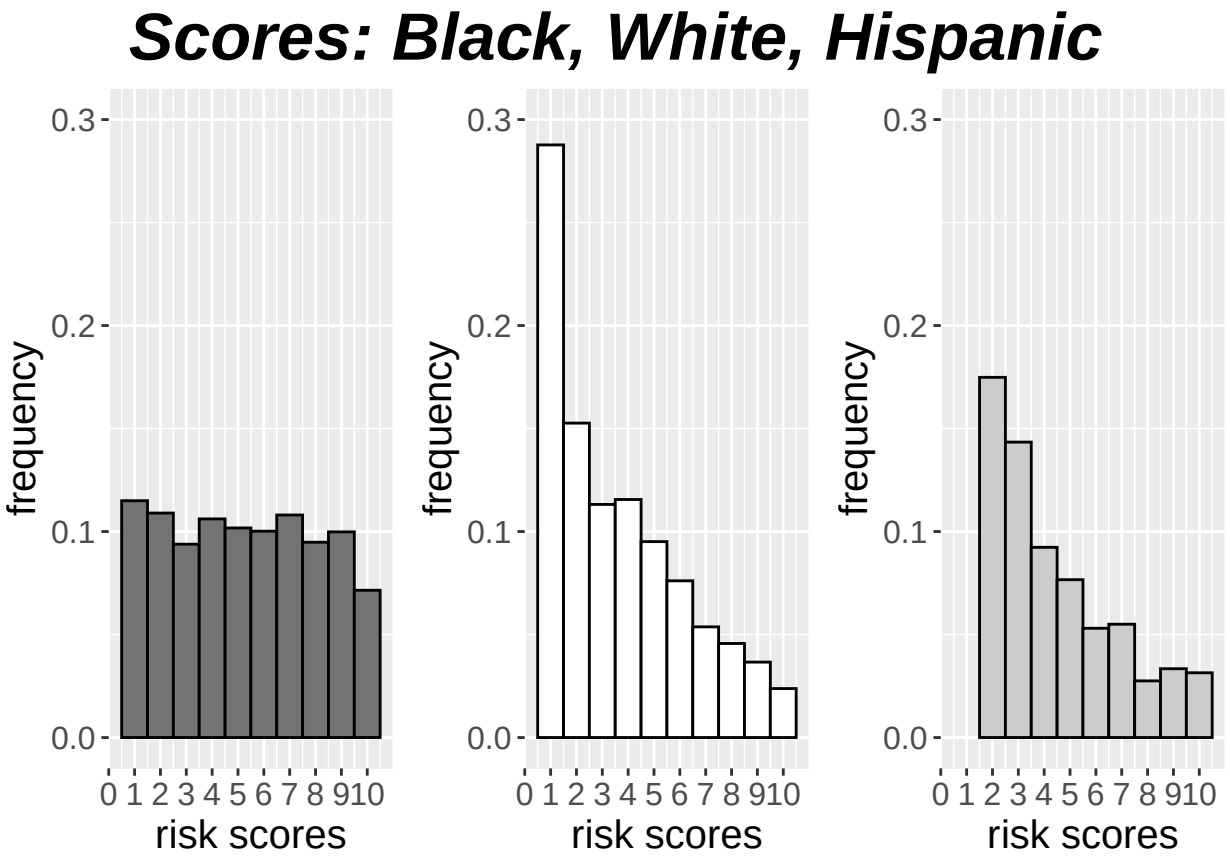
```
phispanic <- ggplot(data=filter(df, race =="Hispanic"), aes(x=two_year_recid)) +
          geom_histogram(aes(y=..count../sum(..count..)), binwidth = 1,  colour="black", fill="grey80")
          ylab("frequency") +
          ylim(0, 1) +
          scale_x_continuous(breaks = seq(0, 1, by = 1)) +
          theme(plot.title = element_text(hjust = 0.5)) +
          theme(text=element_text(size = 15))

pasian <- ggplot(data=filter(df, race =="Asian"), aes(x=two_year_recid)) +
          geom_histogram(aes(y=..count../sum(..count..)), binwidth = 1,  colour="black", fill="grey20")
          ylab("frequency") +
          ylim(0, 1) +
          scale_x_continuous(breaks = seq(0, 1, by = 1)) +
          theme(plot.title = element_text(hjust = 0.5)) +
          theme(text=element_text(size = 15))

grid.arrange(pblack, pwhite, phispanic, pasian, ncol = 4, top=textGrob("Recidivism: Black, White, Hispa
```



Risk scores distribution by race

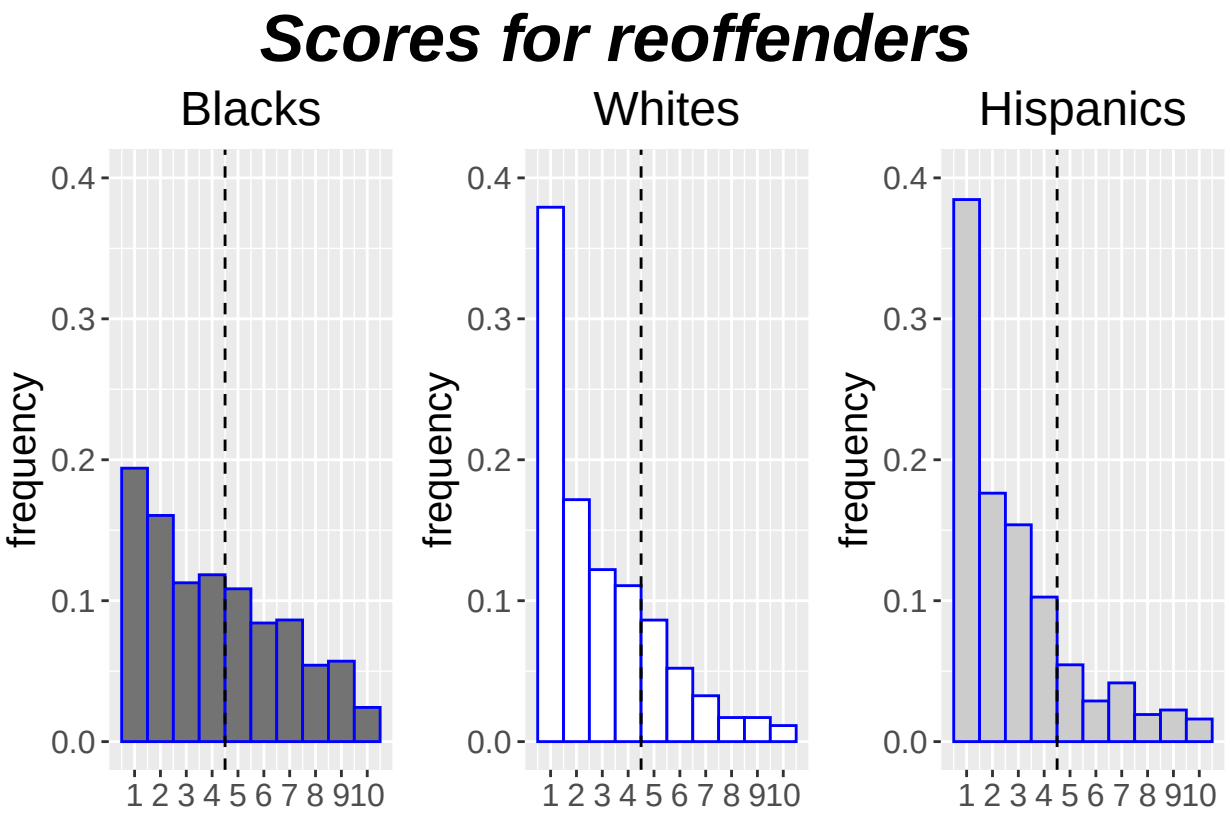
COMPAS assigns each individual a score between 1 (very low risk of recidivism) and 10 (high risk of recidivism). We can plot the distribution of these scores by race. The scores of blacks are evenly distributed across all values from 1 to 10. The scores of Hispanics tend to be more concentrated towards lower values. This trend is even more apparent for whites.

```
pblack_s <- ggplot(data=filter(df, race =="African-American"), aes(x=decile_score)) +
          geom_histogram(aes(y=..count../sum(..count..)), binwidth = 1,  colour="black", fill="grey45")
          ylab("frequency") +
          ylim(0, 0.3) +
          scale_x_continuous(breaks = seq(0, 10, by = 1)) +
          theme(plot.title = element_text(hjust = 0.5)) +
          theme(text=element_text(size = 15))

pwhite_s <- ggplot(data=filter(df, race =="Caucasian"), aes(x=decile_score)) +
          geom_histogram(aes(y=..count../sum(..count..)), binwidth = 1,  colour="black", fill="grey100"
          ylab("frequency") +
          ylim(0, 0.3) +
          scale_x_continuous(breaks = seq(0, 10, by = 1)) +
          theme(plot.title = element_text(hjust = 0.5)) +
          theme(text=element_text(size = 15))

phispanic_s <- ggplot(data=filter(df, race =="Hispanic"), aes(x=decile_score)) +
          geom_histogram(aes(y=..count../sum(..count..)), binwidth = 1,  colour="black", fill="grey80")
          ylab("frequency") +
          ylim(0, 0.3) +
          scale_x_continuous(breaks = seq(0, 10, by = 1)) +
          theme(plot.title = element_text(hjust = 0.5)) +
          theme(text=element_text(size = 15))

grid.arrange(pblack_s, pwhite_s, phispanic_s, ncol = 3, top=textGrob("Scores: Black, White, Hispanic",
```



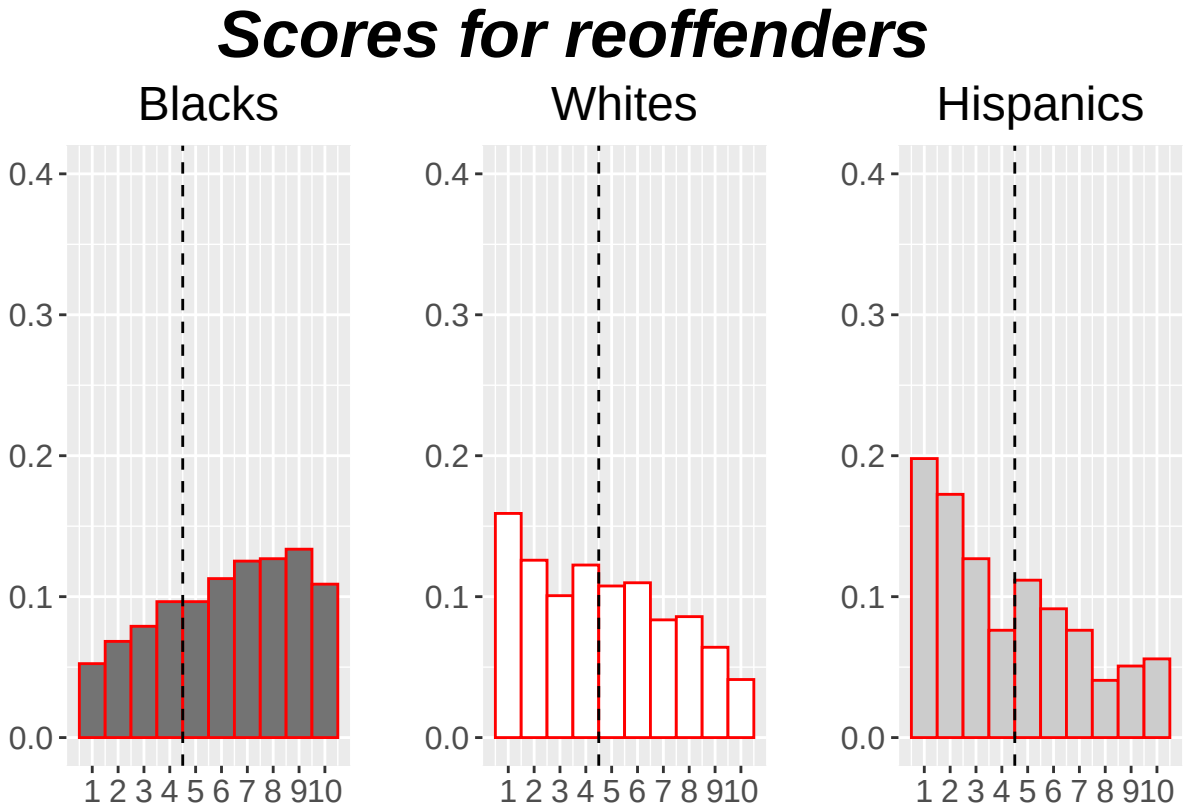
Risk scores distribution by race (non re-offenders only)

Let's focus on those individuals in the database for whom no criminal activity (i.e. arrest) was recorded within a period of two years. Call them non re-offenders. The distribution of the scores for these individuals should be different, mostly concentrated toward lower values. If they did not re-offend, COMPAS should have been able to predict that and assign them lower scores. This is the case for the three racial groups – a sign that COMPAS is, to some extent, tracking future criminal behavior (i.e. arrest). However, the scores are more clearly concentrated towards lower values for whites and Hispanics, and much less clearly for blacks.



Risk scores distribution by race (re-offenders only)

Let's focus on those individuals in the database for whom criminal activity (i.e. arrest) was recorded within a period of two years. Call them re-offenders. The distribution of the scores for these individuals should be concentrated toward higher values. If they did re-offend, COMPAS should have been able to predict that and assign them higher scores. This is the case for blacks, but not for whites and Hispanics – a sign that COMPAS is, to some extent, tracking future criminal behavior (i.e. arrest) for blacks, but much less so for whites and Hispanics.



Racial Disparities in false positives

The false positives rates is higher for blacks compared to whites and Hispanics. COMPAS does not return a yes/decision, but simply a risk score between 1 and 10. Let's first stipulate that anyone with a score of at least 5 is classified as a re-offenders by COMPAS. So, a false positive occurs when someone who is not a reoffenders is classified as such by COMPAS. The false positive rate is defined as following fraction:

$$\frac{\text{\# classified as reoffenders and reoffenders}}{\text{\# reoffenders}}$$

```
black_I <- subset(df, race =="African-American" & is_recid==0)
black_I_Cg <- subset(df, race =="African-American" & is_recid==0 & decile_score>4)

fp_black <- nrow(black_I_Cg)/nrow(black_I)

print(paste0("Compas false positive rate for blacks: ", fp_black))
```

```
## [1] "Compas false positive rate for blacks: 0.414407988587732"
```

```
white_I <- subset(df, race =="Caucasian" & is_recid==0)
white_I_Cg <- subset(df, race =="Caucasian" & is_recid==0 & decile_score>4)

fp_white <- nrow(white_I_Cg)/nrow(white_I)

print(paste0("Compas false positive rate for Whites: ", fp_white))
```

```
## [1] "Compas false positive rate for Whites: 0.216436126932465"
```

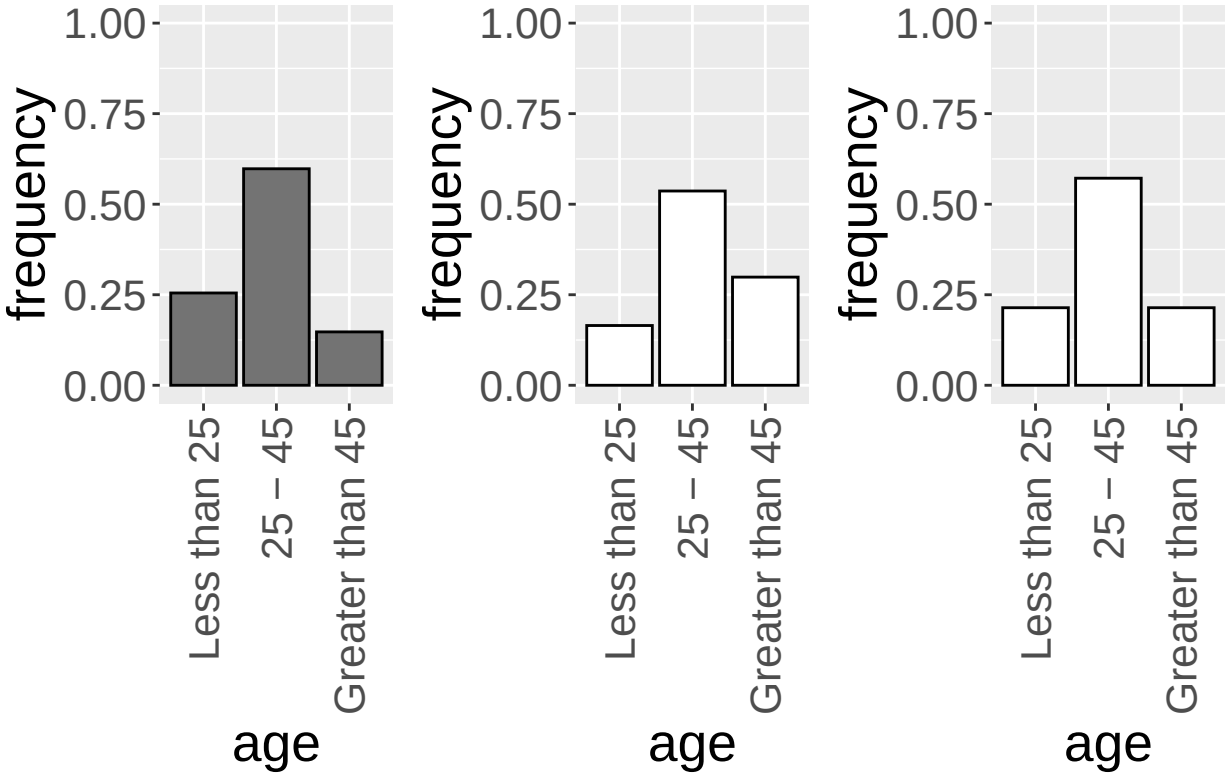
```
hispanic_I <- subset(df, race =="Hispanic" & is_recid==0)
hispanic_I_Cg <- subset(df, race =="Hispanic" & is_recid==0 & decile_score>4)
```

```r
fp_hispanic <- nrow(hispanic_I_Cg)/nrow(hispanic_I)

print(paste0("Compas false positive rate for Hispanics: ", fp_hispanic))
```

```
## [1] "Compas false positive rate for Hispanics: 0.182692307692308"
```

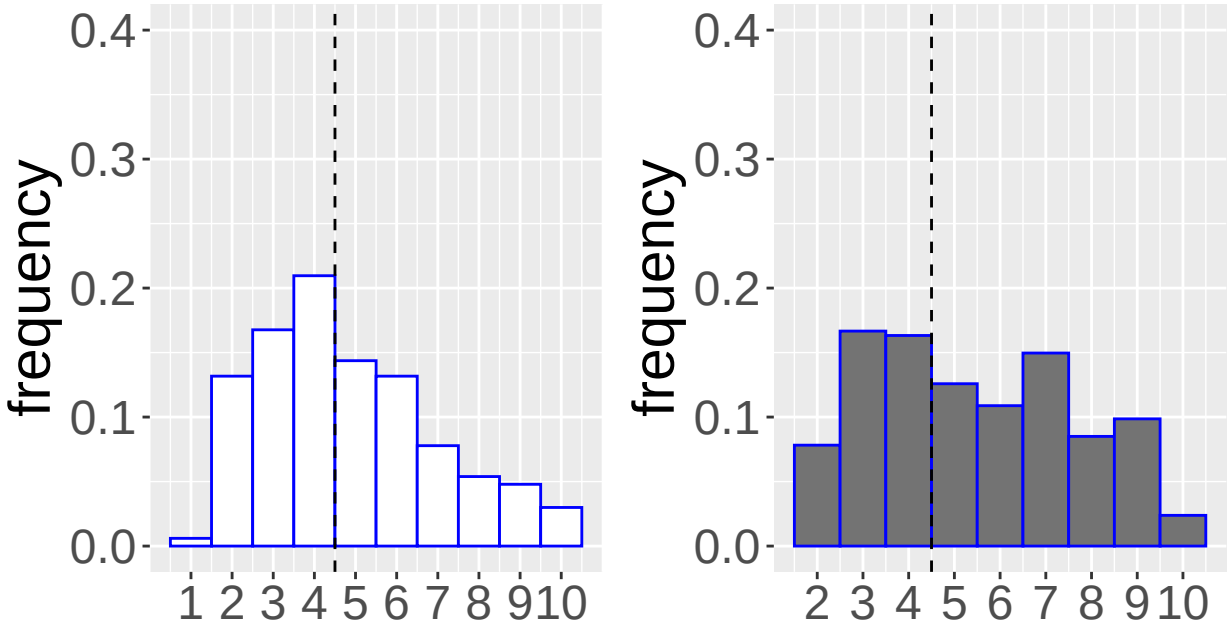
```r
black_age <- ggplot(data=filter(df, race =="African-American"), aes(x=age_cat)) +
          # geom_histogram(aes(y=..count../sum(..count..)), colour="black", fill="grey45")  +
          geom_bar(aes(y=..count../sum(..count..)), colour="black", fill="grey45") +
          xlab("age") +
          ylab("frequency") +
          ylim(0, 1) +
          theme(plot.title = element_text(hjust = 0.5)) +
          theme(text=element_text(size = 20)) +
          theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1)) +
          scale_x_discrete(limits = c("Less than 25", "25 - 45", "Greater than 45"))

white_age <- ggplot(data=filter(df, race =="Caucasian"), aes(x=age_cat)) +
          # geom_histogram(aes(y=..count../sum(..count..)), colour="black", fill="grey100")  +
          geom_bar(aes(y=..count../sum(..count..)), colour="black", fill="grey100") +
          xlab("age") +
          ylab("frequency") +
          ylim(0, 1) +
          theme(plot.title = element_text(hjust = 0.5)) +
          theme(text=element_text(size = 20)) +
          theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1)) +
          scale_x_discrete(limits = c("Less than 25", "25 - 45", "Greater than 45"))

hispanic_age <- ggplot(data=filter(df, race =="Hispanic"), aes(x=age_cat)) +
          # geom_histogram(aes(y=..count../sum(..count..)), colour="black", fill="grey80")  +
          geom_bar(aes(y=..count../sum(..count..)), colour="black", fill="grey100") +
          xlab("age") +
          ylab("frequency") +
          ylim(0, 1) +
          theme(plot.title = element_text(hjust = 0.5)) +
          theme(text=element_text(size = 20)) +
          theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1)) +
          scale_x_discrete(limits = c("Less than 25", "25 - 45", "Greater than 45"))

grid.arrange(black_age, white_age, hispanic_age, ncol = 3, top=textGrob("Age: Black, White, Hispanic",
```

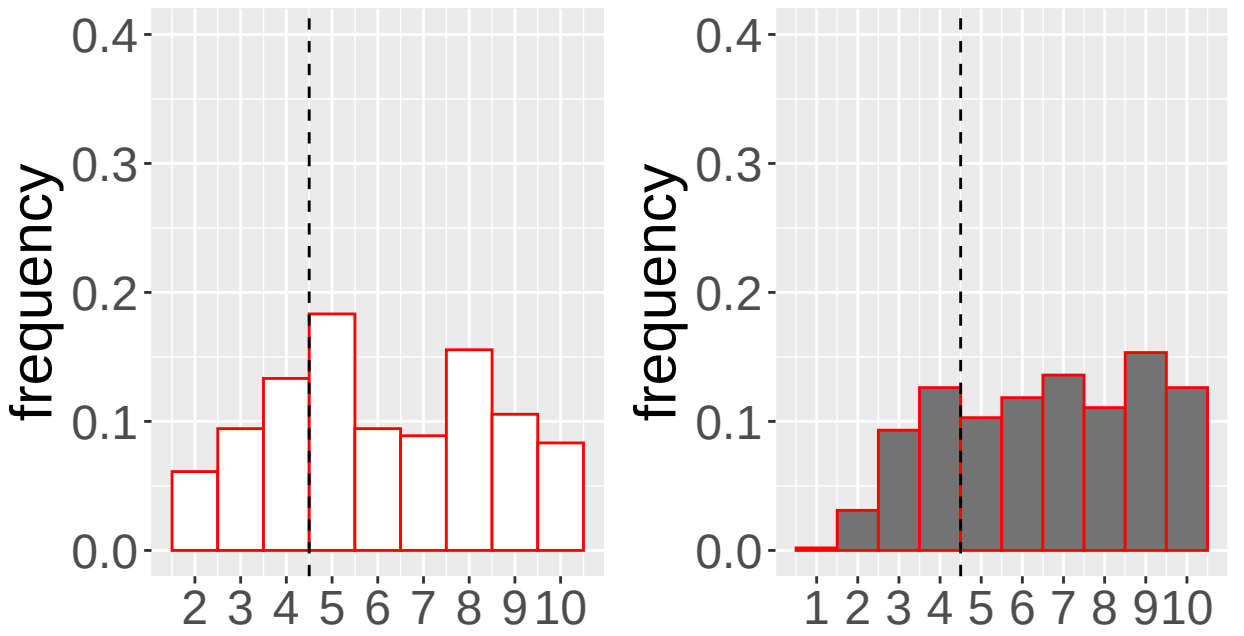
Age: Black, White, Hispanic



on−reoffenders: Scores by Race and Ag

White and < 25 Black and < 25





Disparities

```
black <- subset(df, race =="African-American")
b <- nrow(black)/nrow(df)

print(paste0("Black: ", b))
```

```
## [1] "Black: 0.514419961114712"
```

```
white <- subset(df, race =="Caucasian")
w <- nrow(white)/nrow(df)

print(paste0("White: ", w))
```

```
## [1] "White: 0.340732339598185"
```

```
hispanic <- subset(df, race =="Hispanic")
h <- nrow(hispanic)/nrow(df)

print(paste0("Hispanic: ", h))
```

```
## [1] "Hispanic: 0.0824692158133506"
```

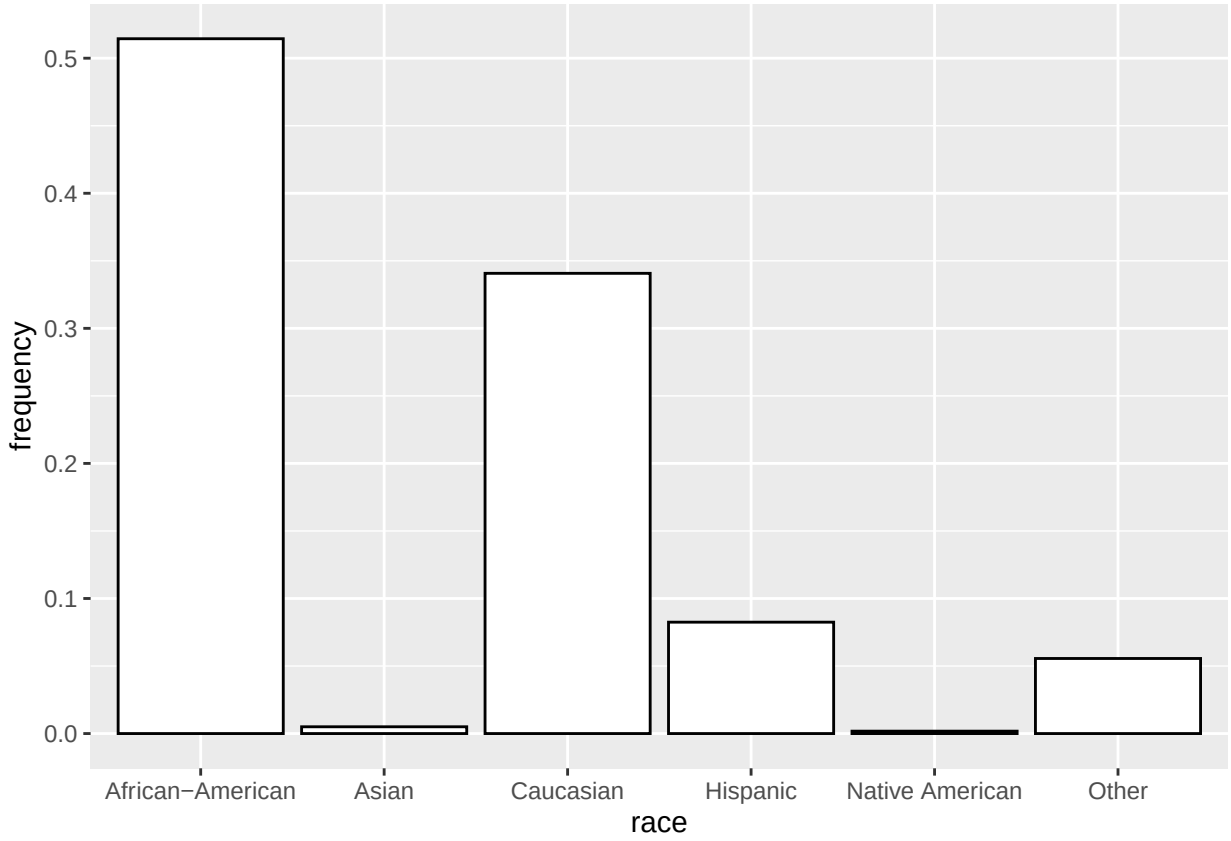
```
other <- subset(df, race =="Other")
o <- nrow(other)/nrow(df)

print(paste0("Other: ", o))
```

```
## [1] "Other: 0.0555735580038885"
```

```
asian <- subset(df, race =="Asian")
a <- nrow(asian)/nrow(df)

print(paste0("Asian: ", a))
```

```
## [1] "Asian: 0.00502268308489955"
```

```
race <- ggplot(df, aes(x=race)) +
          # geom_histogram(aes(y=..count../sum(..count..)), colour="black", fill="grey100")  +
          geom_bar(aes(y=..count../sum(..count..)), colour="black", fill="grey100") +
          xlab("race") +
          ylab("frequency")
race
```




```
black_old_I <- subset(df, race =="African-American" & is_recid==0 & age_cat=="Greater than 45")
black_old_I_Cg <- subset(df, race =="African-American" & is_recid==0 & decile_score>4 & age_cat=="Great

nrow(black_old_I)
```

```
## [1] 261
```

```
nrow(black_old_I_Cg)
```

```
## [1] 65
```

```
fp_old_black <- nrow(black_old_I_Cg)/nrow(black_old_I)

print(paste0("COMPAS false positive rate for blacks (> 45): ", fp_old_black))
```

```
## [1] "COMPAS false positive rate for blacks (> 45): 0.24904214559387"
```

```r
white_old_I <- subset(df, race =="Caucasian" & is_recid==0 & age_cat=="Greater than 45")
white_old_I_Cg <- subset(df, race =="Caucasian" & is_recid==0 & decile_score>4 & age_cat=="Greater than

nrow(white_old_I)
```

```
## [1] 442
```

```r
nrow(white_old_I_Cg)
```

```
## [1] 34
```

```r
fp_old_white <- nrow(black_old_I_Cg)/nrow(white_old_I)

print(paste0("COMPAS false positive rate for whites (> 45): ", fp_old_white))
```

```
## [1] "COMPAS false positive rate for whites (> 45): 0.147058823529412"
```