Testosterone, diversity, and group project performance project

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Assignment description

See: http://rosmarus.refsmmat.com/datasets/datasets/hormone-diversity/

Introduction and data summary

```
summary(ind_dat)
```

```
##        ID           team.id         Age           Gender
##  Min.   :102.0   2      :  6   Min.   :23.00   Female:133
##  1st Qu.:343.2   12     :  6   1st Qu.:26.00   Male  :237
##  Median :552.5   24     :  6   Median :27.00
##  Mean   :530.3   35     :  6   Mean   :27.45
##  3rd Qu.:729.8   44     :  6   3rd Qu.:28.00
##  Max.   :874.0   55     :  6   Max.   :37.00
##                  (Other):334   NA's   :13
##             Ethnicity      Cortisol       Testosterone
##  Asian           : 61   Min.   :0.0300   Min.   : 15.28
##  Black           : 17   1st Qu.:0.1060   1st Qu.: 62.58
##  Hispanic        : 40   Median :0.1700   Median :101.24
##  Other           :  9   Mean   :0.2195   Mean   :110.45
##  South Asian     : 35   3rd Qu.:0.2700   3rd Qu.:148.05
##  South East Asian:  5   Max.   :2.1800   Max.   :541.23
##  White           :203   NA's   :5        NA's   :5
##   log.cortisol     log.testosterone      Country
##  Min.   :-3.5066   Min.   :2.727    USA      :213
##  1st Qu.:-2.2443   1st Qu.:4.136    China    : 19
##  Median :-1.7720   Median :4.617    India    : 16
##  Mean   :-1.7627   Mean   :4.534    Korea    : 10
##  3rd Qu.:-1.3093   3rd Qu.:4.998    Argentina:  9
##  Max.   : 0.7793   Max.   :6.294    Canada   :  8
##  NA's   :5         NA's   :5        (Other)  : 95
```

```
summary(team_dat)
```

```
##     team.id     team.size final.performance  time.of.day
##  2      : 1   Min.   :3   Min.   :-3.0807   Min.   : 9.000
##  3      : 1   1st Qu.:5   1st Qu.:-0.4267   1st Qu.: 9.438
##  4      : 1   Median :5   Median : 0.1817   Median :10.750
##  5      : 1   Mean   :5   Mean   : 0.0000   Mean   :11.672
##  6      : 1   3rd Qu.:5   3rd Qu.: 0.6012   3rd Qu.:14.250
##  9      : 1   Max.   :6   Max.   : 1.1099   Max.   :16.000
##  (Other):68
##     females        final.cash      final.contracts final.reorders
##  Min.   :0.000   Min.   : 642783   Min.   :1.000   Min.   : 15.00
##  1st Qu.:2.000   1st Qu.:1362974   1st Qu.:2.000   1st Qu.: 81.25
```

```
##  Median :2.000   Median :1664432   Median :3.000   Median : 86.00
##  Mean   :1.784   Mean   :1600262   Mean   :2.662   Mean   : 84.54
##  3rd Qu.:2.000   3rd Qu.:1820144   3rd Qu.:3.000   3rd Qu.: 90.00
##  Max.   :2.000   Max.   :2050636   Max.   :3.000   Max.   :110.00
##
##    final.rank     interim.performance  interim.cash     interim.contracts
##  Min.   : 1.000   Min.   :-2.1978     Min.   : 396109   Min.   :1.000
##  1st Qu.: 4.000   1st Qu.:-0.2651     1st Qu.: 734886   1st Qu.:2.000
##  Median : 7.500   Median : 0.1456     Median : 806530   Median :3.000
##  Mean   : 7.257   Mean   : 0.0000     Mean   : 812429   Mean   :2.404
##  3rd Qu.:10.000   3rd Qu.: 0.6604     3rd Qu.: 925021   3rd Qu.:3.000
##  Max.   :14.000   Max.   : 1.0924     Max.   :1062138   Max.   :3.000
##                   NA's   :22          NA's   :22        NA's   :22
##  interim.reorders  interim.rank
##  Min.   : 20.00   Min.   : 1.00
##  1st Qu.: 75.75   1st Qu.: 4.00
##  Median : 85.00   Median : 8.00
##  Mean   : 81.40   Mean   : 8.00
##  3rd Qu.: 90.00   3rd Qu.:11.25
##  Max.   :108.00   Max.   :15.00
##  NA's   :22       NA's   :22
```

```r
# seems like interim.* columns contain a lot of missing data.
```

Questions

Q1

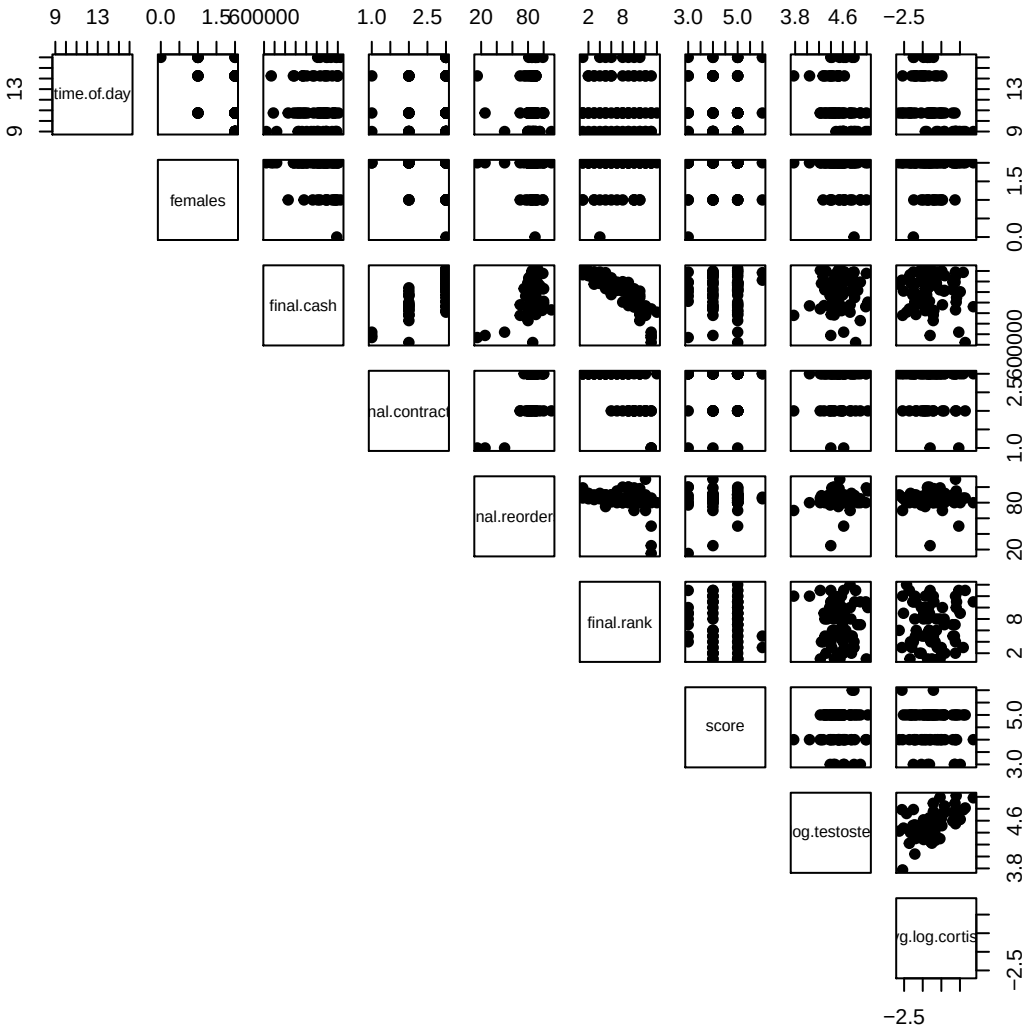
For each group, calculate the number of unique gender-ethnicity-country combinations (such as female-white-Russia or male-Indian-USA) among the group members, and store this with the other group information such as team size and performance. Also calculate the average testosterone level for each group.

```r
get_score <-function(group){
  score <- length(unique(ind_dat$combo[ind_dat$team.id == group,]))
  return(score)
}
#  calculate the number of unique gender-ethnicity-country combinations
ind_dat$combo <-paste(ind_dat$Gender, ind_dat$Ethnicity, ind_dat$Country)
team_dat$score<- unlist(lapply(team_dat$team.id,
               function(x){length(unique(ind_dat$combo[ind_dat$team.id == x]))}))

#  calculate the average testosterone level for each group.
team_dat$avg.log.testosterone<- unlist(lapply(team_dat$team.id,
               function(x){mean(ind_dat$log.testosterone[ind_dat$team.id == x])}))

#  calculate the average cortisol level for each group.
team_dat$avg.log.cortisol<- unlist(lapply(team_dat$team.id,
               function(x){mean(ind_dat$log.cortisol[ind_dat$team.id == x])}))
```

```r
# check relationships of all variables of interest
vars <- colnames(team_dat)[c(4:9, 15:17)]
#cor(team_dat)
pairs(team_dat[vars], pch = 19,  lower.panel=NULL)
```

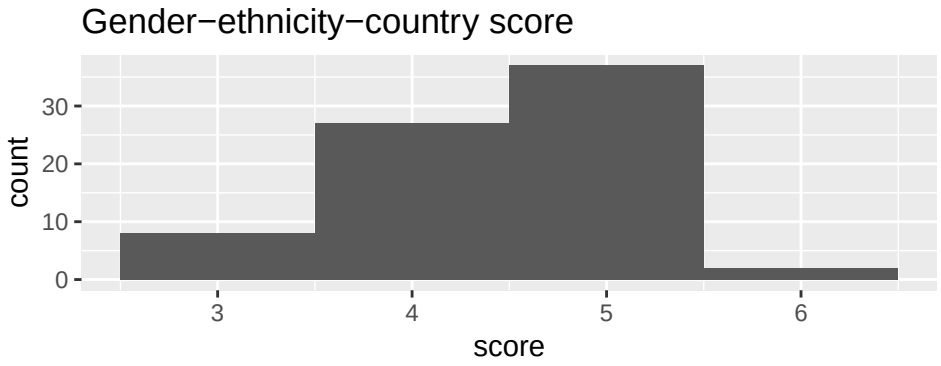


Q2

Do exploratory data analysis to explore the composition of groups, the typical amount of diversity, and the typical amounts of testosterone. Note particularly that the data includes the logs of the cortisol and testosterone levels as well as the raw levels; does your EDA suggest you should use the logs or the raw values?

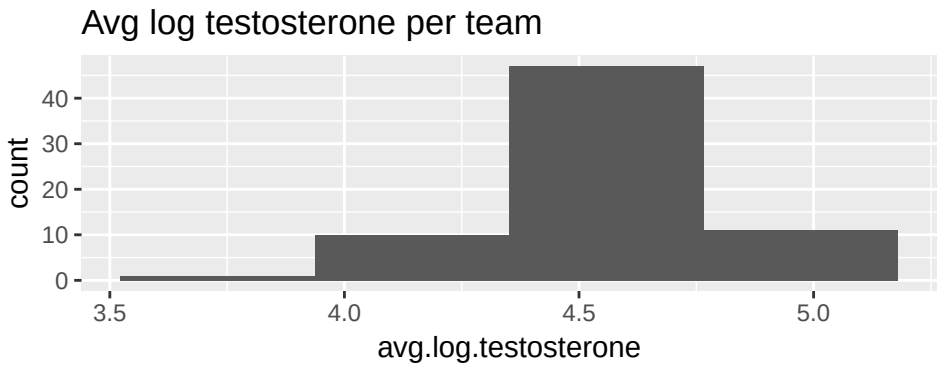
Composition of groups

```
# visualise the distribution of diversity
ggplot(team_dat, aes(x = score)) +
  geom_histogram(bins = 4)+ labs(title="Gender-ethnicity-country score")
```




```
# visualise the distribution of testosterone
ggplot(team_dat, aes(x = avg.log.testosterone)) +
  geom_histogram(bins = 4)+ labs(title="Avg log testosterone per team")
```

```
## Warning: Removed 5 rows containing non-finite values (stat_bin).
```



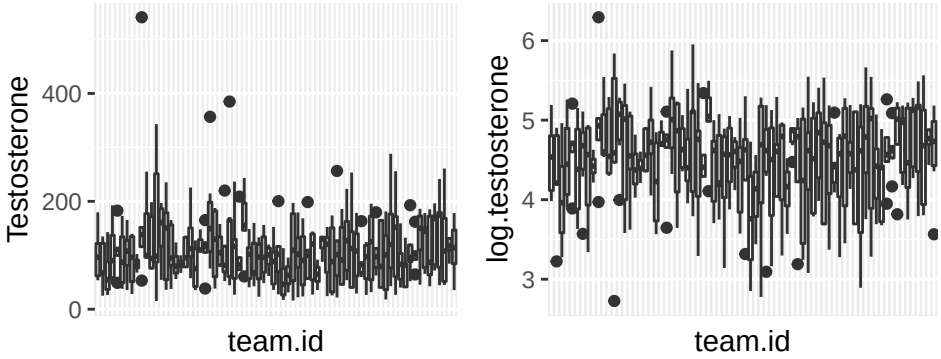

```
p1 <-ggplot(ind_dat, aes(x= team.id, y=Testosterone))+
  geom_boxplot()+theme_hw

p2 <-ggplot(ind_dat, aes(x= team.id, y=log.testosterone))+
  geom_boxplot()+theme_hw

grid.arrange(p1, p2, ncol = 2)
```

```
## Warning: Removed 5 rows containing non-finite values (stat_boxplot).
```

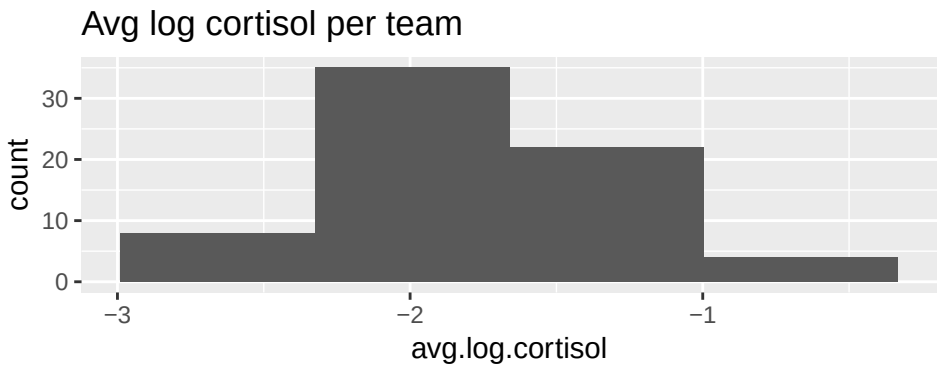
```
## Warning: Removed 5 rows containing non-finite values (stat_boxplot).
```




```
# visualise the distribution of cortisol
ggplot(team_dat, aes(x = avg.log.cortisol)) +
```

```
  geom_histogram(bins = 4)+ labs(title="Avg log cortisol per team")
```

```
## Warning: Removed 5 rows containing non-finite values (stat_bin).
```




```
p1 <-ggplot(ind_dat, aes(x= team.id, y=Cortisol))+
  geom_boxplot()+theme_hw

p2 <-ggplot(ind_dat, aes(x= team.id, y=log.cortisol))+
  geom_boxplot()+theme_hw

grid.arrange(p1, p2, ncol = 2)
```

```
## Warning: Removed 5 rows containing non-finite values (stat_boxplot).

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```
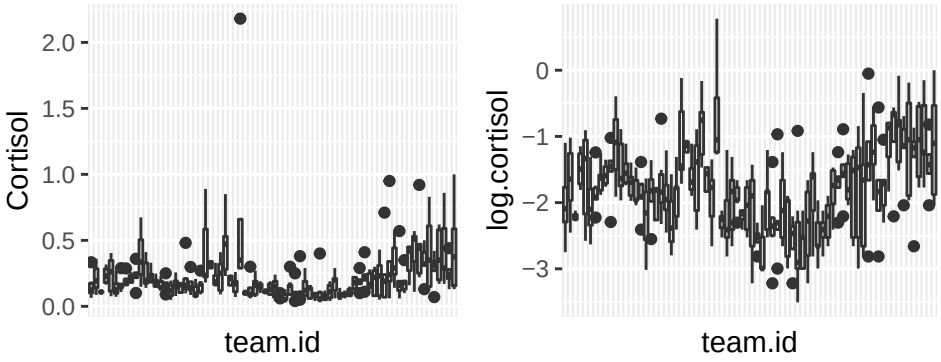
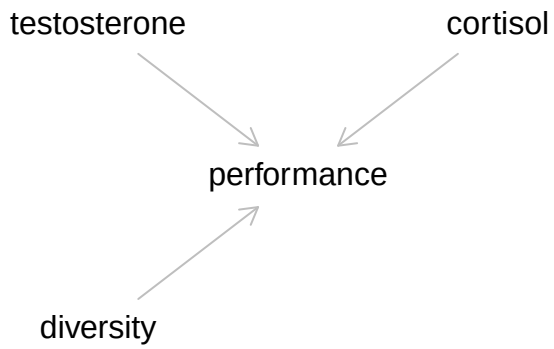



Sketch out causal diagrams

The findings suggest that diversity is beneficial for performance, but only if group-level testosterone is low; diversity has a negative effect on performance if group-level testosterone is high.

```
library(dagitty)

g <- dagitty('dag {
    testosterone  [pos="0,0"]
    diversity [pos="0,1"]
    performance [pos="1,0.5"]
    cortisol [pos="2,0"]

    testosterone -> performance <- diversity
    cortisol-> performance
```

```
}')
plot(g)
```




```
impliedConditionalIndependencies( g )
```

```
## cortisol _||_ diversity
## cortisol _||_ testosterone
## diversity _||_ testosterone
```

Q3

Q4

Q5