

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
```

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.

```
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])}))

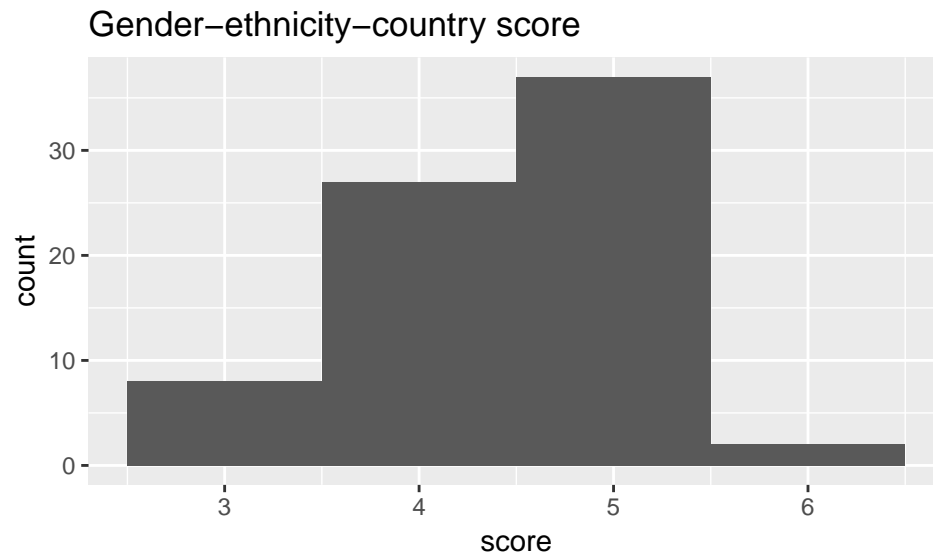
# calculate the average cortisol level for each group.
team_dat$avg.log.cortisol<- unlist(lapply(team_dat$team.id,
  function(x){mean(ind_dat$log.cortisol[ind_dat$team.id == x])}))
```

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?

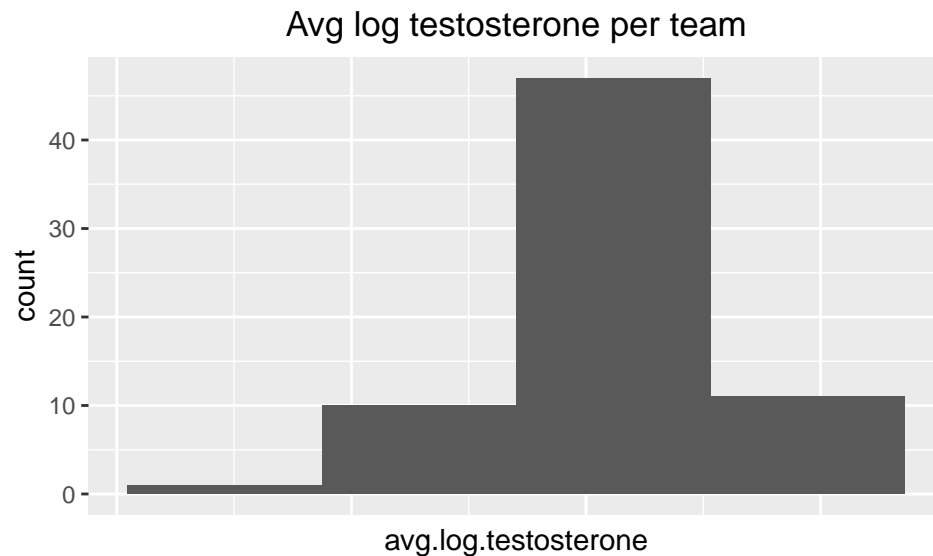
Composition of groups

```
# 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)) + theme_hw +
  geom_histogram(bins = 4) + labs(title="Avg log testosterone per team")
```

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

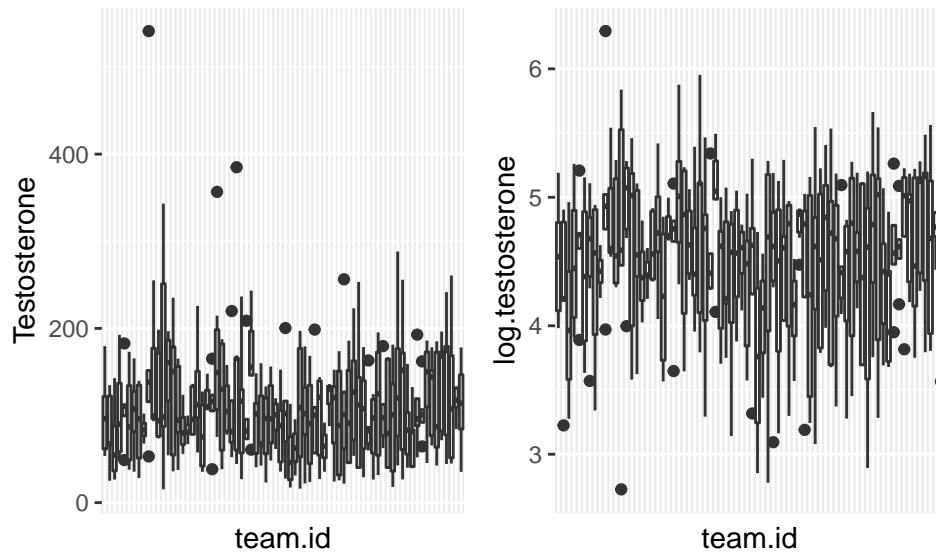


```
p1 <- ggplot(ind_dat, aes(x= team.id, y=Testosterone)) +
  geom_boxplot() + theme_hw

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

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

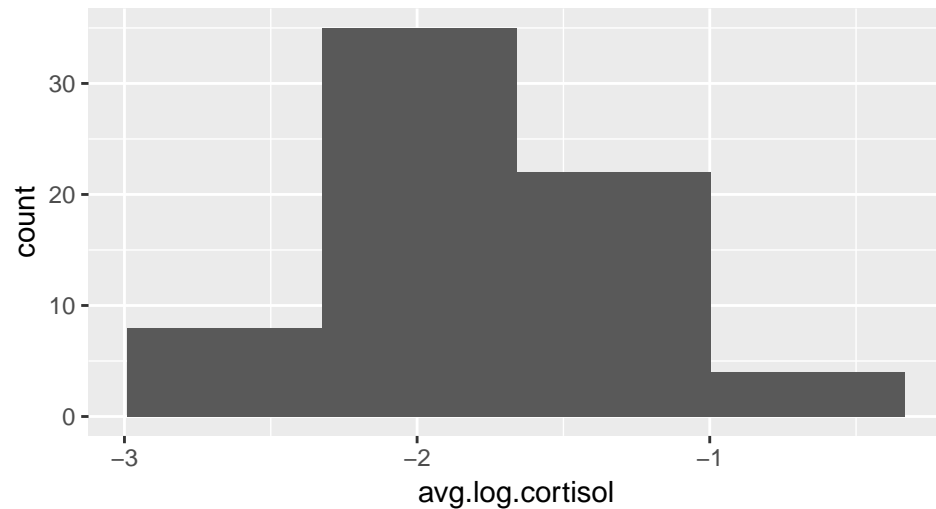
```
## Warning: Removed 5 rows containing non-finite values (stat_boxplot).
## Warning: Removed 5 rows containing non-finite values (stat_boxplot).
```



```
# 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).
```

Avg log cortisol per team



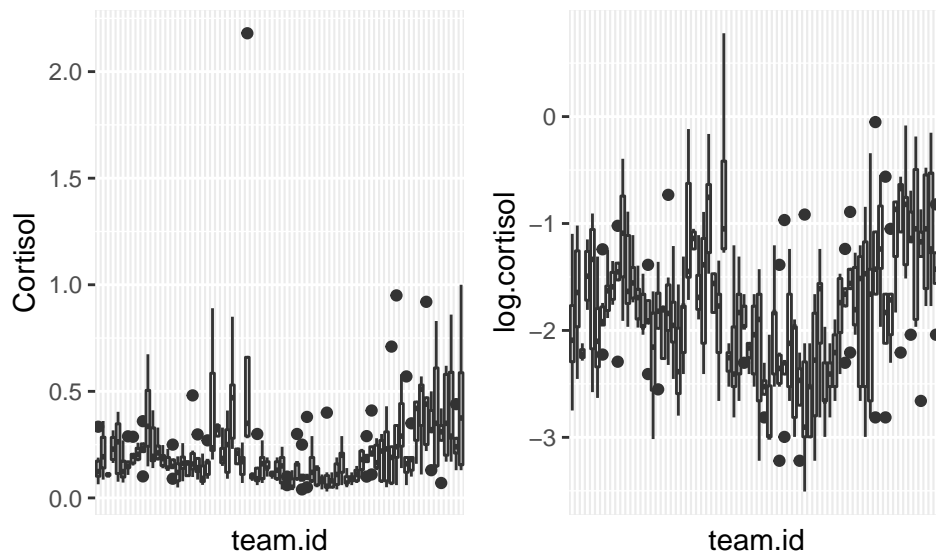
```
p1 <- ggplot(ind_dat, aes(x= team.id, y=Cortisol)) +
  geom_boxplot() + theme_hw

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).
```

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



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