

EDA

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Basic Info:

```
## [1] 370 10
```

```
## [1] 74 14
```

```
##      ID      team.id      Age      Gender
## Min.   :102.0   Min.    : 2.00   Min.   :23.00   Length:370
## 1st Qu.:343.2   1st Qu.: 35.00   1st Qu.:26.00   Class :character
## Median :552.5   Median : 63.00   Median :27.00   Mode  :character
## Mean   :530.3   Mean    : 60.79   Mean    :27.45
## 3rd Qu.:729.8   3rd Qu.: 87.75   3rd Qu.:28.00
## Max.   :874.0   Max.    :111.00   Max.    :37.00
##                                     NA's    :13
## Ethnicity      Cortisol      Testosterone      log.cortisol
## Length:370     Min.    :0.0300   Min.    : 15.28   Min.    : -3.5066
## Class :character 1st Qu.:0.1060   1st Qu.: 62.58   1st Qu.: -2.2443
## Mode  :character Median :0.1700   Median :101.24   Median : -1.7720
##                  Mean    :0.2195   Mean    :110.45   Mean    : -1.7627
##                  3rd Qu.:0.2700   3rd Qu.:148.05   3rd Qu.: -1.3093
##                  Max.    :2.1800   Max.    :541.23   Max.    : 0.7793
##                  NA's    :5       NA's    :5       NA's    :5
## log.testosterone Country
## Min.    :2.727   Length:370
## 1st Qu.:4.136   Class :character
## Median :4.617   Mode  :character
## Mean    :4.534
## 3rd Qu.:4.998
## Max.    :6.294
## NA's    :5
##      team.id      team.size final.performance time.of.day
## Min.    : 2.00   Min.    :3   Min.    : -3.0807   Min.    : 9.000
## 1st Qu.: 34.25   1st Qu.:5   1st Qu.: -0.4267   1st Qu.: 9.438
## Median : 62.50   Median :5   Median : 0.1817   Median :10.750
## Mean    : 60.08   Mean    :5   Mean    : 0.0000   Mean    :11.672
## 3rd Qu.: 86.75   3rd Qu.:5   3rd Qu.: 0.6012   3rd Qu.:14.250
## Max.    :111.00   Max.    :6   Max.    : 1.1099   Max.    :16.000
##
##      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
```

Individual dataset

- The individual dataset contains 370 observations, and 10 variables :
ID Participant ID number team.id ID number of the team this participant belonged to Age Age, in years
Gender Gender (Male or Female) Ethnicity Ethnicity of the participant Cortisol Participant's cortisol
levels, nMol/L Testosterone Participant's testosterone levels, pg/mL log.cortisol Natural logarithm of
the participant's cortisol level log.testosterone Natural logarithm of the participant's testosterone level
Country Country of citizenship of the participant
- 18 rows contain at least one missing value in one of the columns

Team dataset

- The team dataset contains 74 teams and 14 variables:
team.id Team ID number team.size Number of people on the team final.performance The team's final
performance score time.of.day The time of day the team's hormone sample was collected (hh.mm)
females Number of females in the group final.cash Total cash earned by the team final.contracts
Total number of contracts won by the team final.reorders Total number of reorders won by the team
final.rank Team's final rank at the end of the project, relative to other teams in their class section
interim.performance Same as above, but measured at Day 5 of the study (missing for some teams)
interim.cash
interim.contracts
interim.reorders
interim.rank
- 22 teams have no interim.rank, interim.reorders, interim.contracts, interim.cash, and interim.performance

```
#factorize certain variables and create diversity score for each group
indi_dat <- indi_dat %>%
  mutate_if(sapply(indi_dat, is.character), as.factor) %>%
  group_by(team.id) %>%
  mutate(diversity_score = n_distinct(Gender, Ethnicity, Country))
```

```

#intermediate step of calculating aggregated statistics by group
agg_indi_dat <- indi_dat %>%
  group_by(team.id) %>%
  summarise(mean_testo = mean(Testosterone), mean_log_testo = mean(log.testosterone), sd_testo = sd(Tes

## `summarise()` ungrouping output (override with `.groups` argument)

#combing the info from the individual dataset to the team dataset, average/sd cortisol and testosterone
combo_dat <- team_dat %>%
  inner_join(agg_indi_dat, by = "team.id") %>%
  mutate(proportion_female = females/team.size)

write_csv(combo_dat, "../data/combined_processed.csv")

```

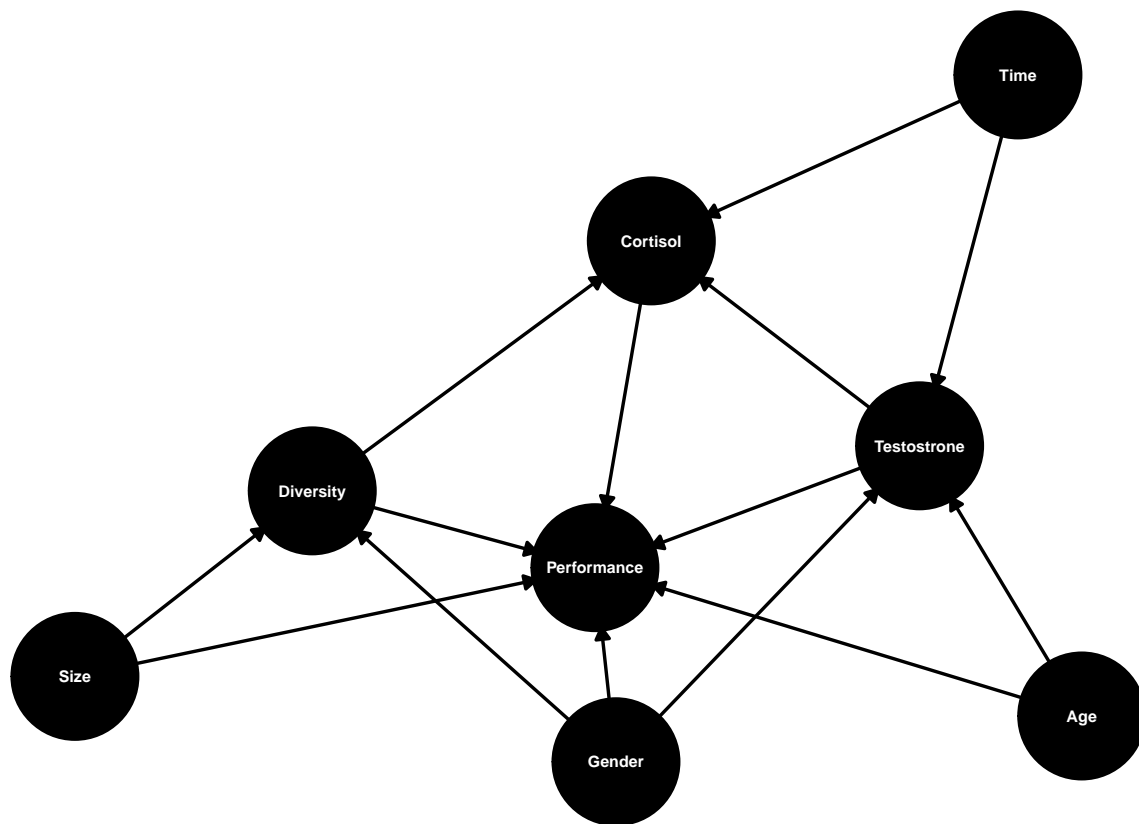
Causal DAG

```

tidy_ggdag <- dagify(
  Testosterone ~ Time + Gender + Age,
  Cortisol ~ Time + Testosterone + Diversity,
  Diversity ~ Size + Gender,
  Performance ~ Testosterone + Cortisol + Diversity + Size + Age + Gender,
  exposure = "Diversity",
  outcome = "Performance"
) %>%
  tidy_dagitty()

ggdag(tidy_ggdag, node_size = 22, text_size = 2.2) +
  theme_dag()

```



Understanding the variables

Typical amount of diversity present:

```
diversity_vars <- indi_dat %>% select(Gender, Ethnicity, Country)
```

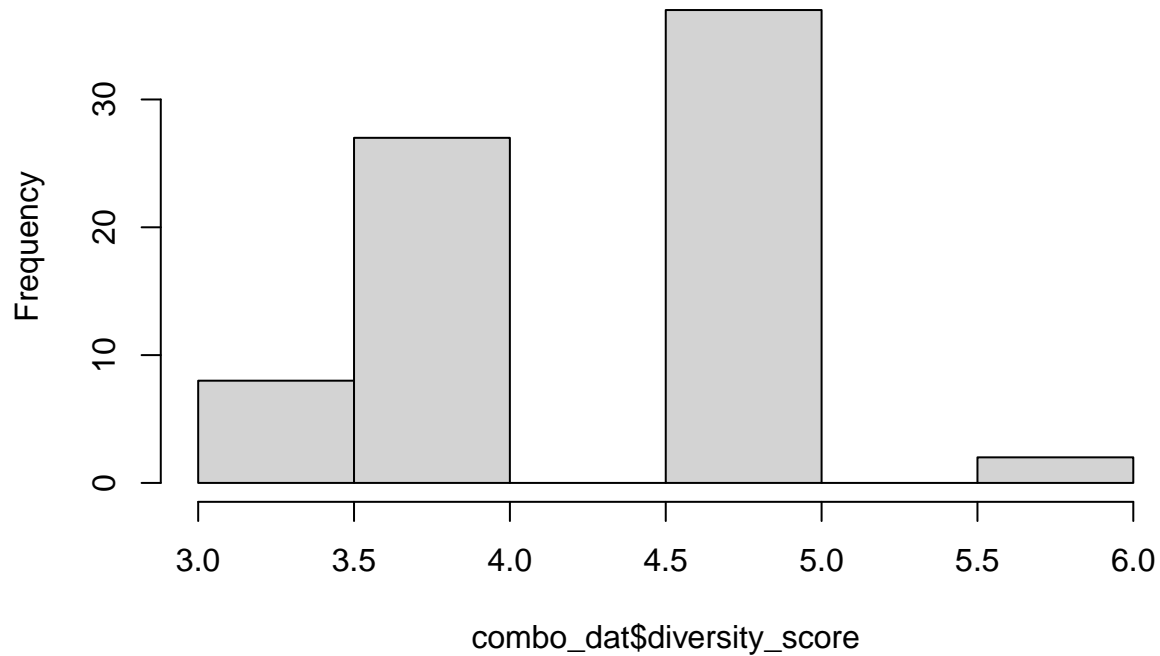
```
## Adding missing grouping variables: `team.id`
```

```
summary(diversity_vars[, -1])
```

```
##      Gender      Ethnicity      Country
## Female:133  Asian      : 61  USA      :213
## Male  :237  Black      : 17  China    : 19
##                               Hispanic : 40  India    : 16
##                               Other    : 9   Korea    : 10
##                               South Asian : 35  Argentina: 9
##                               South East Asian: 5  Canada   : 8
##                               White      :203  (Other)  : 95
```

```
hist(combo_dat$diversity_score)
```

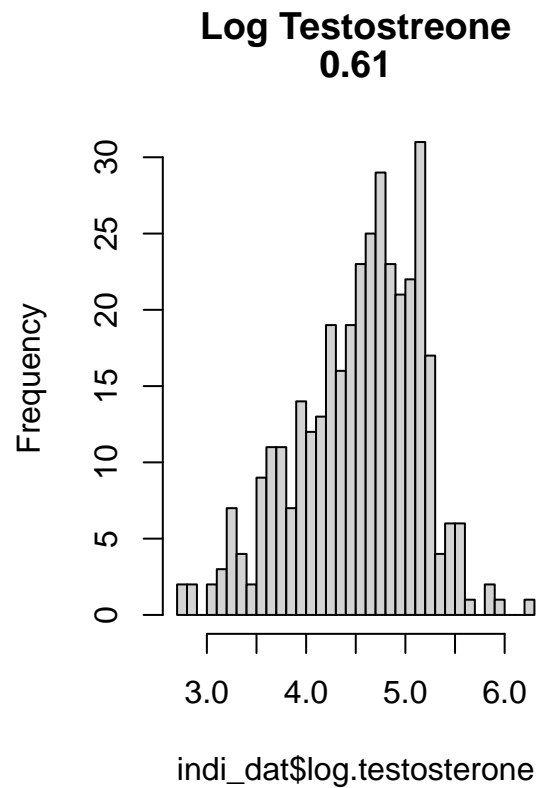
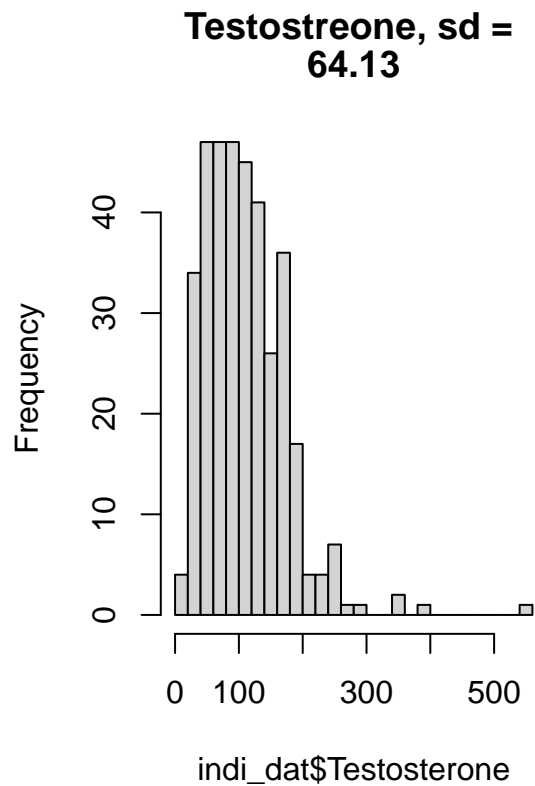
Histogram of combo_dat\$diversity_score



This dataset has a lot more men than women and mostly white Americans. There is a adequate amount of variability in the diversity scores.

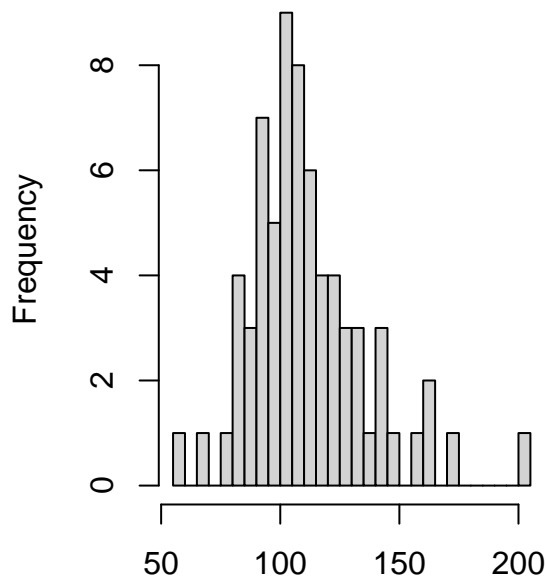
testostreone vs log testostreone

```
par(mfrow=c(1,2))
sd_testo = round(sd(indi_dat$Testosterone, na.rm = T),2)
sd_log_testo = round(sd(indi_dat$log.testosterone, na.rm = T),2)
hist(indi_dat$Testosterone, breaks = 30, main = c("Testostreone, sd = ",sd_testo))
hist(indi_dat$log.testosterone, breaks = 30, main = c("Log Testostreone", sd_log_testo))
```



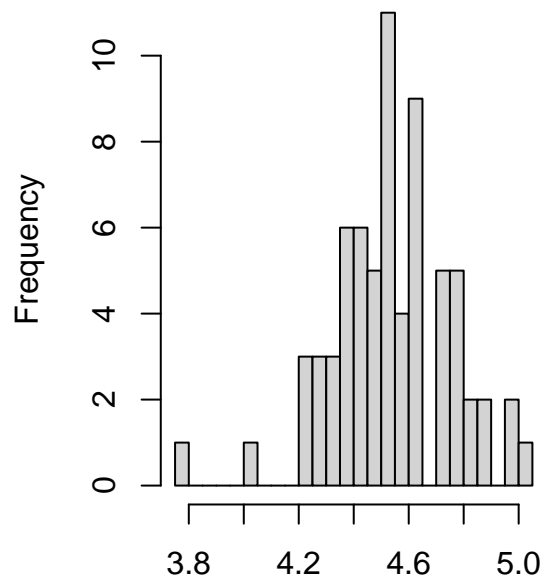
```
par(mfrow=c(1,2))
sd_testo = round(sd(agg_indi_dat$mean_testo, na.rm = T),2)
sd_log_testo = round(sd(agg_indi_dat$mean_log_testo, na.rm = T),2)
hist(agg_indi_dat$mean_testo, breaks = 30, main = c("Mean Group Testostreone, sd = ",sd_testo))
hist(agg_indi_dat$mean_log_testo, breaks = 30, main = c("Mean Group Log Testostreone", sd_log_testo))
```

**Mean Group Testosterone, sd =
24.93**



agg_indi_dat\$mean_testo

**Mean Group Log Testosterone
0.22**



agg_indi_dat\$mean_log_testo

The above plots shows the histogram of the testosterone level compared to the log of the testosterone level, for overall as well as group mean. The log transformation helps with lessen the impact of outliers on our analysis. We don't want to let the group that contain the individual with really high testosterone level impact our analysis disproportionately since mean is very sensitive to outliers. The standard deviation is drastically reduced in the log transformed variable in both cases and the histogram approximate a normal distribution.

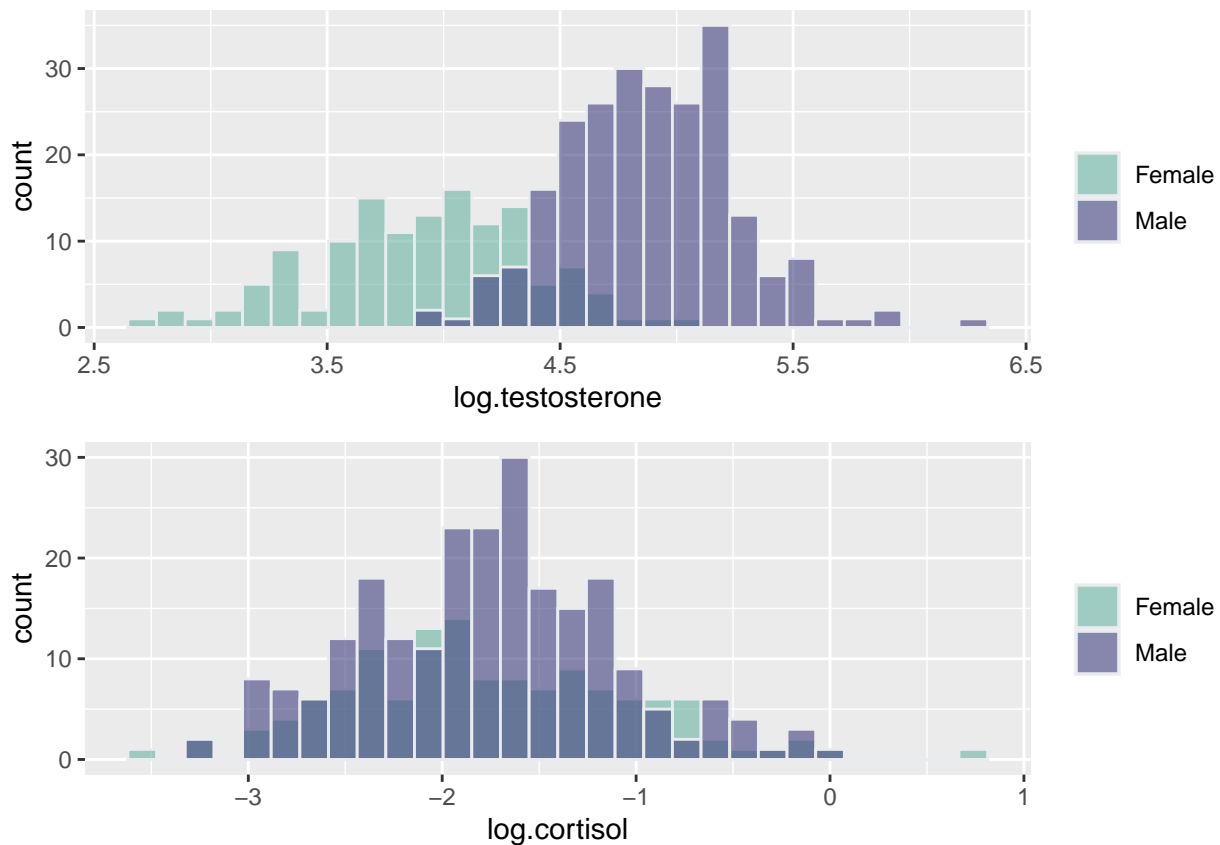
testosterone, cortisol by gender

```
testo <- indi_dat %>%
  ggplot( aes(x=log.testosterone, fill=Gender)) +
  geom_histogram( color="#e9ecef", alpha=0.6, position = 'identity') +
  scale_fill_manual(values=c("#69b3a2", "#404080")) +
  labs(fill="")

cortisol <- indi_dat %>%
  ggplot( aes(x=log.cortisol, fill=Gender)) +
  geom_histogram( color="#e9ecef", alpha=0.6, position = 'identity') +
  scale_fill_manual(values=c("#69b3a2", "#404080")) +
  labs(fill="")

grid.arrange(testo, cortisol)
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

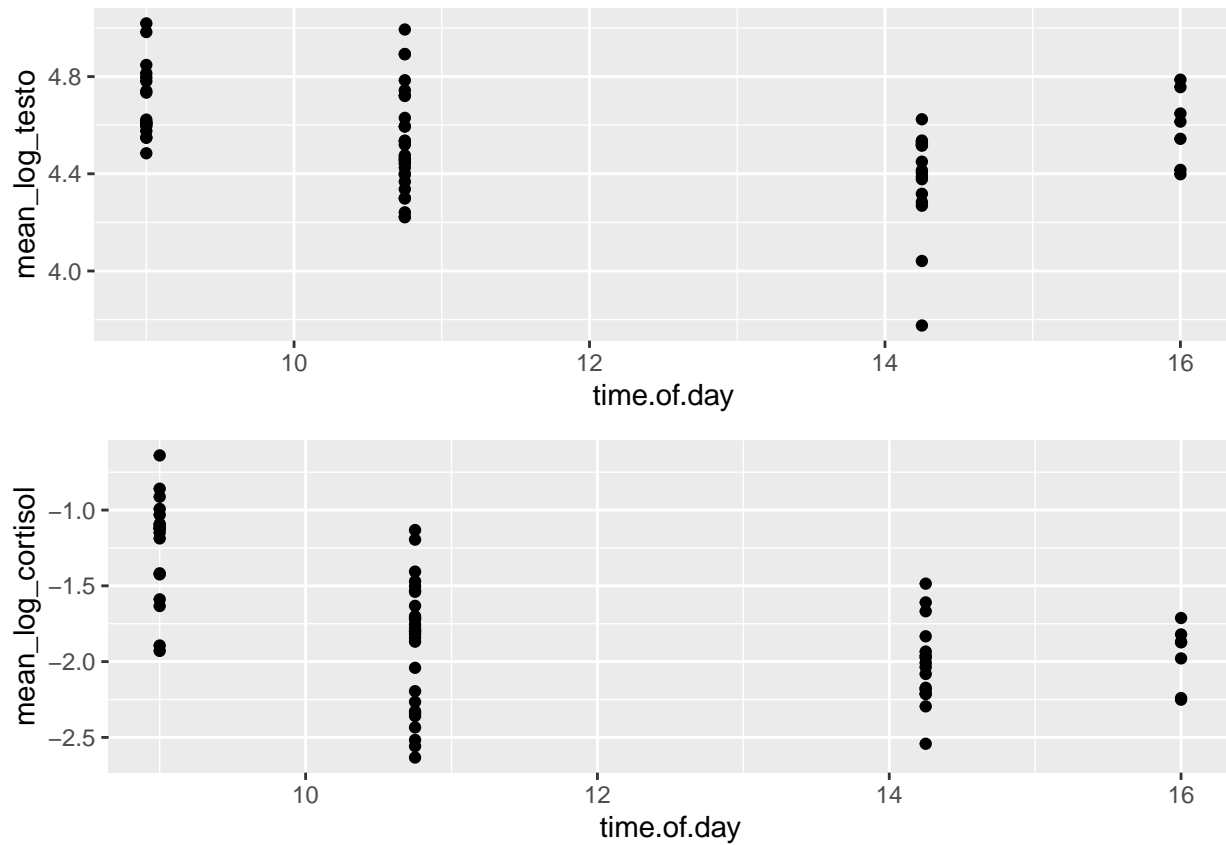


It makes sense that gender is correlated to the level of testosterone so special attention, since women tend to have lower testosterone level than men. Gender seem to have no impact on cortisol level. ### testosterone, cortisol by time of the day

```
testo <- combo_dat %>%
  ggplot(aes(x=time.of.day, y=mean_log_testo)) +
  geom_point()

cortisol <- combo_dat %>%
  ggplot(aes(x=time.of.day, y=mean_log_cortisol)) +
  geom_point()

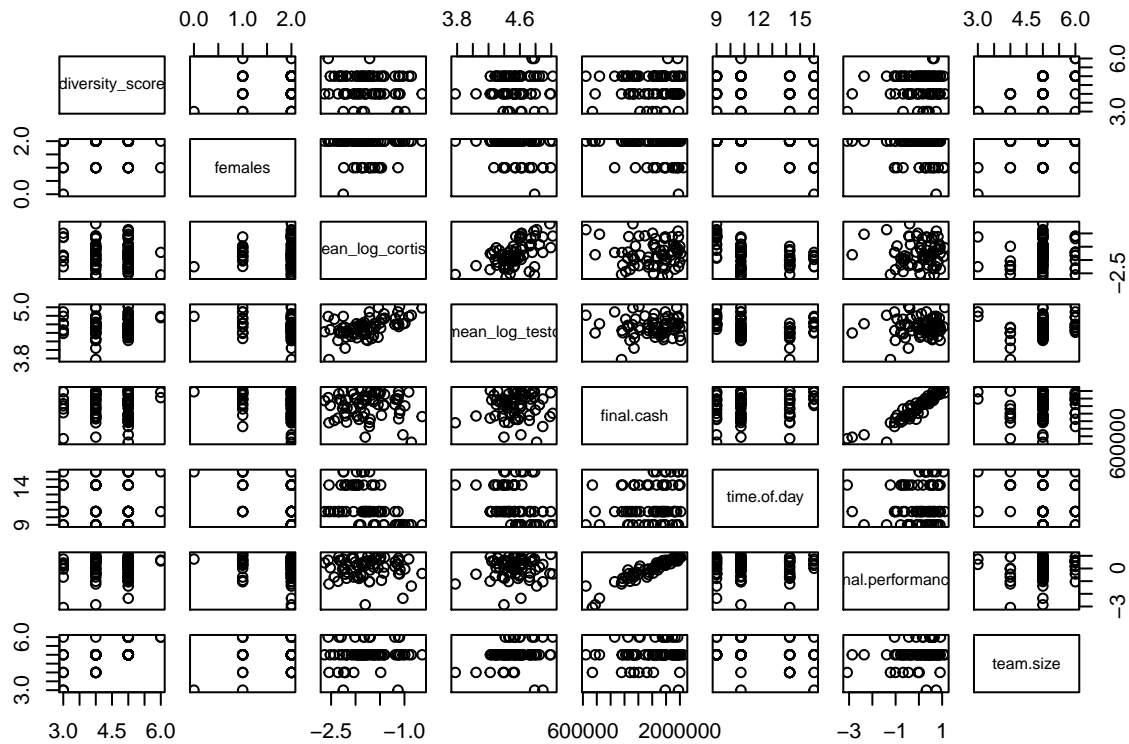
grid.arrange(testo, cortisol)
```

Time of the day could also be a confounder since the testosterone and cortisol level could change base on what time of the day you measure it.

relationships between a subset of variables

```
combo_dat_subset <- combo_dat %>% select(diversity_score,females, mean_log_cortisol, mean_log_testo, f
pairs(combo_dat_subset) # not including team id
```



- Worth noting that there are exactly 2 females in all the groups, if we want to control for gender it would make more sense to use percentage.
- Cortisol seems to be correlated with Testosterone levels, since Cortisol is related to stress maybe it will help test/explain why there could be an interaction effect between diversity and testosterone (through causing stress on the team).