LongitudinalDataAnalysis

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0. Introduction

The dataset contains information on patients who received renal graft(kidney transplant) The patients have been followed for at most 10 years.

Background: People with end-stage kidney disease who receive a kidney transplant generally live longer than people with ESRD who are on dialysis.

However, kidney transplant recipients must remain on immunosuppressants (medications to suppress the immune system) for the rest of their life to prevent their body from rejecting the new kidney. The long-term immunosuppression puts them at risk for infections and cancer.

The Haermatocrit level (HC level) usually differs with gender, Also the health condition of a person.

1. Task for week one

1.1 Import data

```
#install.packages("readxl")
library(readxl)
trenal <- read_excel("Trenal.XLS")
summary(trenal)
```

```
##       HC0             HC06            HC1             HC2             HC3
##  Min.   :14.00   Min.   :22.00   Min.   :20.00   Min.   :17.0   Min.   :20.00
##  1st Qu.:28.00   1st Qu.:35.00   1st Qu.:36.00   1st Qu.:36.0   1st Qu.:36.00
##  Median :32.00   Median :38.55   Median :39.00   Median :40.0   Median :39.00
##  Mean   :31.86   Mean   :38.83   Mean   :39.71   Mean   :39.7   Mean   :39.17
##  3rd Qu.:36.00   3rd Qu.:42.00   3rd Qu.:43.00   3rd Qu.:43.0   3rd Qu.:43.00
##  Max.   :60.00   Max.   :61.70   Max.   :63.00   Max.   :65.0   Max.   :60.00
##  NA's   :12                      NA's   :12      NA's   :1044   NA's   :2460
##       HC4             HC5             HC6             HC7
##  Min.   :23.00   Min.   :17.00   Min.   :20.00   Min.   :17.00
##  1st Qu.:35.00   1st Qu.:35.00   1st Qu.:36.00   1st Qu.:35.00
##  Median :39.00   Median :39.00   Median :39.00   Median :39.00
##  Mean   :39.16   Mean   :39.02   Mean   :39.11   Mean   :38.85
##  3rd Qu.:43.00   3rd Qu.:43.00   3rd Qu.:43.00   3rd Qu.:42.00
##  Max.   :55.00   Max.   :56.00   Max.   :55.00   Max.   :60.00
##  NA's   :3768    NA's   :5016    NA's   :6096    NA's   :7140
##       HC8             HC9             HC10            id
##  Min.   :23.00   Min.   :17.00   Min.   :24.10   Min.   :   1.0
##  1st Qu.:35.00   1st Qu.:35.00   1st Qu.:35.00   1st Qu.: 290.8
##  Median :38.05   Median :38.50   Median :38.00   Median : 580.5
```

```
##  Mean   :38.35   Mean   :38.57   Mean   :38.49   Mean   : 580.5
##  3rd Qu.:42.00   3rd Qu.:42.00   3rd Qu.:42.00   3rd Qu.: 870.2
##  Max.   :55.00   Max.   :55.00   Max.   :54.00   Max.   :1160.0
##  NA's   :8064    NA's   :8988    NA's   :9744
##       age             male            cardio           reject           const
##  Min.   :15.00   Min.   :0.0000   Min.   :0.0000   Min.   :0.0000   Min.   :1
##  1st Qu.:36.00   1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.:1
##  Median :48.00   Median :1.0000   Median :0.0000   Median :0.0000   Median :1
##  Mean   :46.43   Mean   :0.5741   Mean   :0.1784   Mean   :0.3164   Mean   :1
##  3rd Qu.:57.00   3rd Qu.:1.0000   3rd Qu.:0.0000   3rd Qu.:1.0000   3rd Qu.:1
##  Max.   :76.00   Max.   :1.0000   Max.   :1.0000   Max.   :1.0000   Max.   :1
##  NA's   :12
##        j            respons           time
##  Min.   : 1.00   Min.   :14.00   Min.   : 0.000
##  1st Qu.: 3.75   1st Qu.:34.00   1st Qu.: 1.750
##  Median : 6.50   Median :38.00   Median : 4.500
##  Mean   : 6.50   Mean   :38.24   Mean   : 4.625
##  3rd Qu.: 9.25   3rd Qu.:42.00   3rd Qu.: 7.250
##  Max.   :12.00   Max.   :65.00   Max.   :10.000
##                  NA's   :4362
```

remove a noninformative column const

```
trenal= trenal[,-18]
summary(trenal)
```

```
##       HC0             HC06            HC1             HC2             HC3
##  Min.   :14.00   Min.   :22.00   Min.   :20.00   Min.   :17.0   Min.   :20.00
##  1st Qu.:28.00   1st Qu.:35.00   1st Qu.:36.00   1st Qu.:36.0   1st Qu.:36.00
##  Median :32.00   Median :38.55   Median :39.00   Median :40.0   Median :39.00
##  Mean   :31.86   Mean   :38.83   Mean   :39.71   Mean   :39.7   Mean   :39.17
##  3rd Qu.:36.00   3rd Qu.:42.00   3rd Qu.:43.00   3rd Qu.:43.0   3rd Qu.:43.00
##  Max.   :60.00   Max.   :61.70   Max.   :63.00   Max.   :65.0   Max.   :60.00
##  NA's   :12                      NA's   :12      NA's   :1044   NA's   :2460
##       HC4             HC5             HC6             HC7
##  Min.   :23.00   Min.   :17.00   Min.   :20.00   Min.   :17.00
##  1st Qu.:35.00   1st Qu.:35.00   1st Qu.:36.00   1st Qu.:35.00
##  Median :39.00   Median :39.00   Median :39.00   Median :39.00
##  Mean   :39.16   Mean   :39.02   Mean   :39.11   Mean   :38.85
##  3rd Qu.:43.00   3rd Qu.:43.00   3rd Qu.:43.00   3rd Qu.:42.00
##  Max.   :55.00   Max.   :56.00   Max.   :55.00   Max.   :60.00
##  NA's   :3768    NA's   :5016    NA's   :6096    NA's   :7140
##       HC8             HC9             HC10            id
##  Min.   :23.00   Min.   :17.00   Min.   :24.10   Min.   :   1.0
##  1st Qu.:35.00   1st Qu.:35.00   1st Qu.:35.00   1st Qu.: 290.8
##  Median :38.05   Median :38.50   Median :38.00   Median : 580.5
##  Mean   :38.35   Mean   :38.57   Mean   :38.49   Mean   : 580.5
##  3rd Qu.:42.00   3rd Qu.:42.00   3rd Qu.:42.00   3rd Qu.: 870.2
##  Max.   :55.00   Max.   :55.00   Max.   :54.00   Max.   :1160.0
##  NA's   :8064    NA's   :8988    NA's   :9744
##       age             male            cardio           reject
##  Min.   :15.00   Min.   :0.0000   Min.   :0.0000   Min.   :0.0000
##  1st Qu.:36.00   1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.:0.0000
##  Median :48.00   Median :1.0000   Median :0.0000   Median :0.0000
##  Mean   :46.43   Mean   :0.5741   Mean   :0.1784   Mean   :0.3164
```

```
##  3rd Qu.:57.00   3rd Qu.:1.0000   3rd Qu.:0.0000   3rd Qu.:1.0000
##  Max.   :76.00   Max.   :1.0000   Max.   :1.0000   Max.   :1.0000
##  NA's   :12
##        j            respons           time
##  Min.   : 1.00   Min.   :14.00   Min.   : 0.000
##  1st Qu.: 3.75   1st Qu.:34.00   1st Qu.: 1.750
##  Median : 6.50   Median :38.00   Median : 4.500
##  Mean   : 6.50   Mean   :38.24   Mean   : 4.625
##  3rd Qu.: 9.25   3rd Qu.:42.00   3rd Qu.: 7.250
##  Max.   :12.00   Max.   :65.00   Max.   :10.000
##                  NA's   :4362
```

```
dim(trenal)
```

```
## [1] 13920    20
```

1.2 Table structure analysis and variable understanding

The table contains observation of HC level on 1160 patients who have gone through kidney transplant. Each patient will have maximum 12 meassurements in the 12 time point $(0, 0.5, 1, 2, \cdots, 10)$ years.

if we just look at the first 12 columns, they are all Haematocrit level at the corresponding time. Thus our response variable is Haematocrit level. If we just look at first 17 columns from HC0 to reject, then the subtable looks like a wide table; If we start from column id to column time, the part of table is a long table. From now on we focus on the long table:

```
trenal.long = trenal[,13:20]
summary(trenal.long)
```

```
##        id              age             male            cardio
##  Min.   :   1.0   Min.   :15.00   Min.   :0.0000   Min.   :0.0000
##  1st Qu.: 290.8   1st Qu.:36.00   1st Qu.:0.0000   1st Qu.:0.0000
##  Median : 580.5   Median :48.00   Median :1.0000   Median :0.0000
##  Mean   : 580.5   Mean   :46.43   Mean   :0.5741   Mean   :0.1784
##  3rd Qu.: 870.2   3rd Qu.:57.00   3rd Qu.:1.0000   3rd Qu.:0.0000
##  Max.   :1160.0   Max.   :76.00   Max.   :1.0000   Max.   :1.0000
##                   NA's   :12
##      reject             j            respons           time
##  Min.   :0.0000   Min.   : 1.00   Min.   :14.00   Min.   : 0.000
##  1st Qu.:0.0000   1st Qu.: 3.75   1st Qu.:34.00   1st Qu.: 1.750
##  Median :0.0000   Median : 6.50   Median :38.00   Median : 4.500
##  Mean   :0.3164   Mean   : 6.50   Mean   :38.24   Mean   : 4.625
##  3rd Qu.:1.0000   3rd Qu.: 9.25   3rd Qu.:42.00   3rd Qu.: 7.250
##  Max.   :1.0000   Max.   :12.00   Max.   :65.00   Max.   :10.000
##                                   NA's   :4362
```

```
dim(trenal.long)
```

```
## [1] 13920     8
```

Besides the time $0, 0.5, 1, 2, 3, 4, 5, \cdots, 10$ is one-to-one correspondent to j $1, 2, 3, \cdots, 12$. But we can still leave it in the dataframe. Our response variable is the HC level(The percentage of red cells in the blood, normal levels of hermatocrit for men range from 41% to 50%, normal level for women is 36% to 48%) the explanatory variables are age, we can change the structure of the table as we are used to: Identity, time, respons, explanatory variables (time dependent), explanatory variables (time independent). The response variables are some continuous integer values? The explanatory variables have binary type: male, cardio, reject, and integer type: age

```
#install.packages("magrittr") # package installations are only needed the first time you use it
#install.packages("dplyr")    # alternative installation of the %>%
library(magrittr) # needs to be run every time you start R and want to use %>%
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
```

```
data <- trenal.long %>%
  relocate(id) %>%
  relocate(j,.after=id)%>%
  relocate(time,.after = j)%>%
  relocate(respons,.after=time)
trenal.long$id = as.factor(trenal.long$id)
trenal.long$j = as.factor(trenal.long$j)
trenal.long$male = as.factor(trenal.long$male)
trenal.long$cardio = as.factor(trenal.long$cardio)
trenal.long$reject = as.factor(trenal.long$reject)
summary(trenal.long)
```

```
##        id             age        male     cardio    reject         j
##  1      :   12   Min.   :15.00   0:5928   0:11436   0:9516   1      :1160
##  2      :   12   1st Qu.:36.00   1:7992   1: 2484   1:4404   2      :1160
##  3      :   12   Median :48.00                               3      :1160
##  4      :   12   Mean   :46.43                               4      :1160
##  5      :   12   3rd Qu.:57.00                               5      :1160
##  6      :   12   Max.   :76.00                               6      :1160
##  (Other):13848   NA's   :12                                  (Other):6960
##     respons           time
##  Min.   :14.00   Min.   : 0.000
##  1st Qu.:34.00   1st Qu.: 1.750
##  Median :38.00   Median : 4.500
##  Mean   :38.24   Mean   : 4.625
##  3rd Qu.:42.00   3rd Qu.: 7.250
##  Max.   :65.00   Max.   :10.000
##  NA's   :4362
```

```
length(unique(trenal.long$id))
```

```
## [1] 1160
```

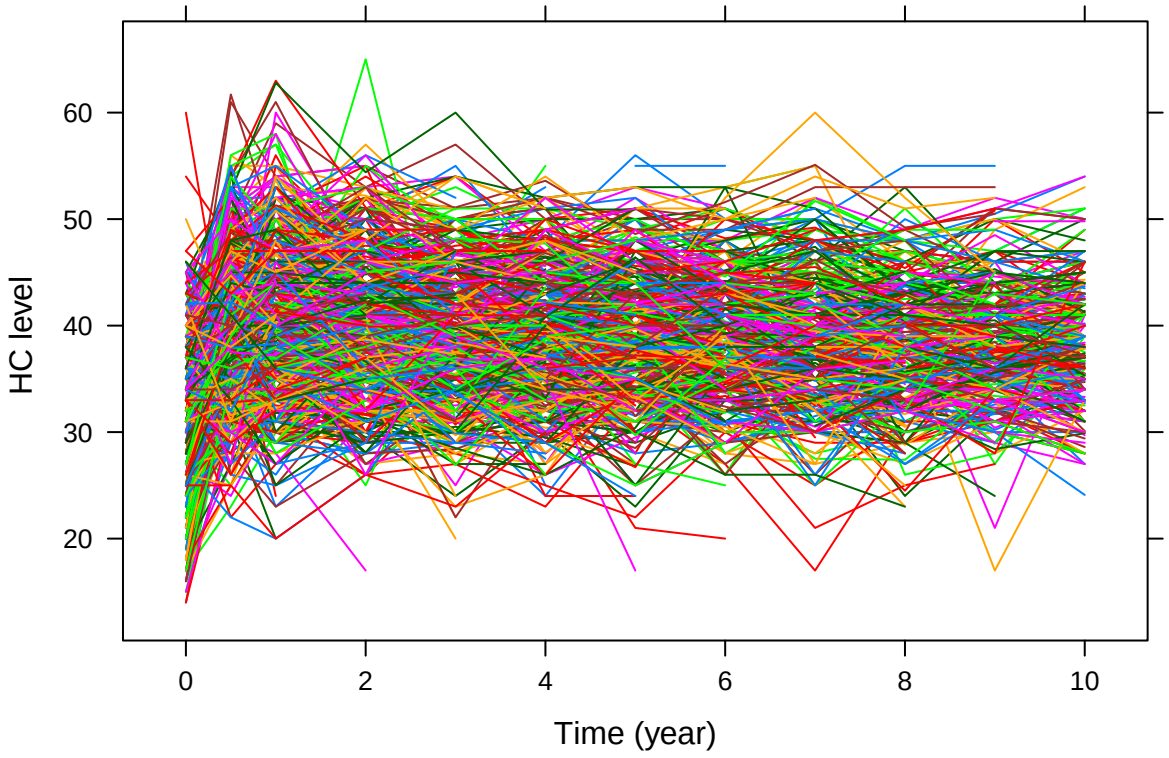
```
# Plot the raw data
#install.packages("tigerstats")
require(tigerstats)
```

```
## Loading required package: tigerstats
```

```
## Loading required package: abd
```

```
## Loading required package: nlme
```

```
##
## Attaching package: 'nlme'

## The following object is masked from 'package:dplyr':
##
##     collapse

## Loading required package: lattice

## Loading required package: grid

## Loading required package: mosaic

## Registered S3 method overwritten by 'mosaic':
##   method                           from
##   fortify.SpatialPolygonsDataFrame ggplot2

##
## The 'mosaic' package masks several functions from core packages in order to add
## additional features.  The original behavior of these functions should not be affected by this.

##
## Attaching package: 'mosaic'

## The following object is masked from 'package:Matrix':
##
##     mean

## The following object is masked from 'package:ggplot2':
##
##     stat

## The following objects are masked from 'package:dplyr':
##
##     count, do, tally

## The following objects are masked from 'package:stats':
##
##     binom.test, cor, cor.test, cov, fivenum, IQR, median, prop.test,
##     quantile, sd, t.test, var

## The following objects are masked from 'package:base':
##
##     max, mean, min, prod, range, sample, sum

## Welcome to tigerstats!
## To learn more about this package, consult its website:
##  http://homerhanumat.github.io/tigerstats
xyplot(respons ~ time, groups = id, data=data, type="l",xlab="Time (year)",ylab="HC level " )
```




```
library(ggplot2)
library(nlme)
library(lme4)
```

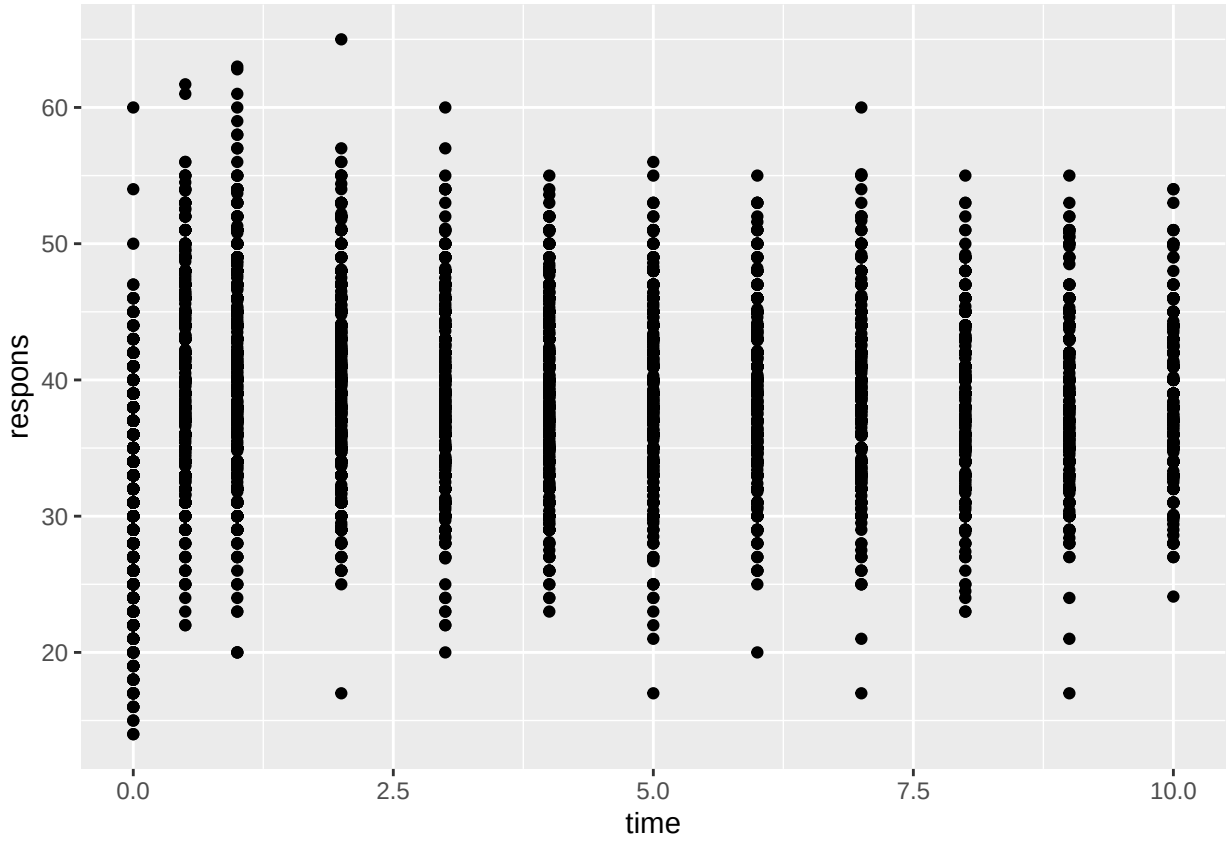
```
##
## Attaching package: 'lme4'
```

```
## The following object is masked from 'package:mosaic':
##
##     factorize
```

```
## The following object is masked from 'package:nlme':
##
##     lmList
```

```
#Plot data
ggplot(data, aes(x=time, y=respons)) + geom_point()
```

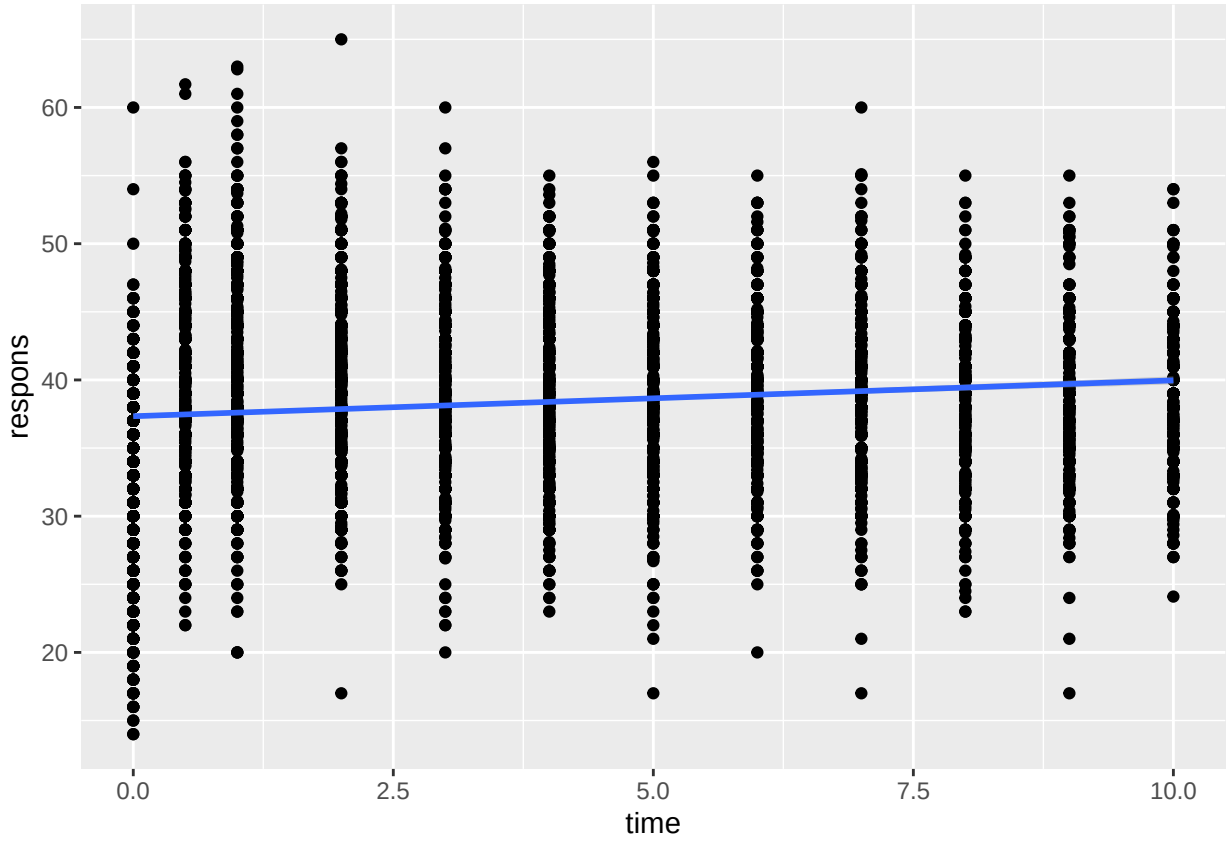
```
## Warning: Removed 4362 rows containing missing values (`geom_point()`).
```




```
#Plot data with lm line
ggplot(data, aes(x=time, y=respons)) + geom_point() + geom_smooth(method="lm")
```

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

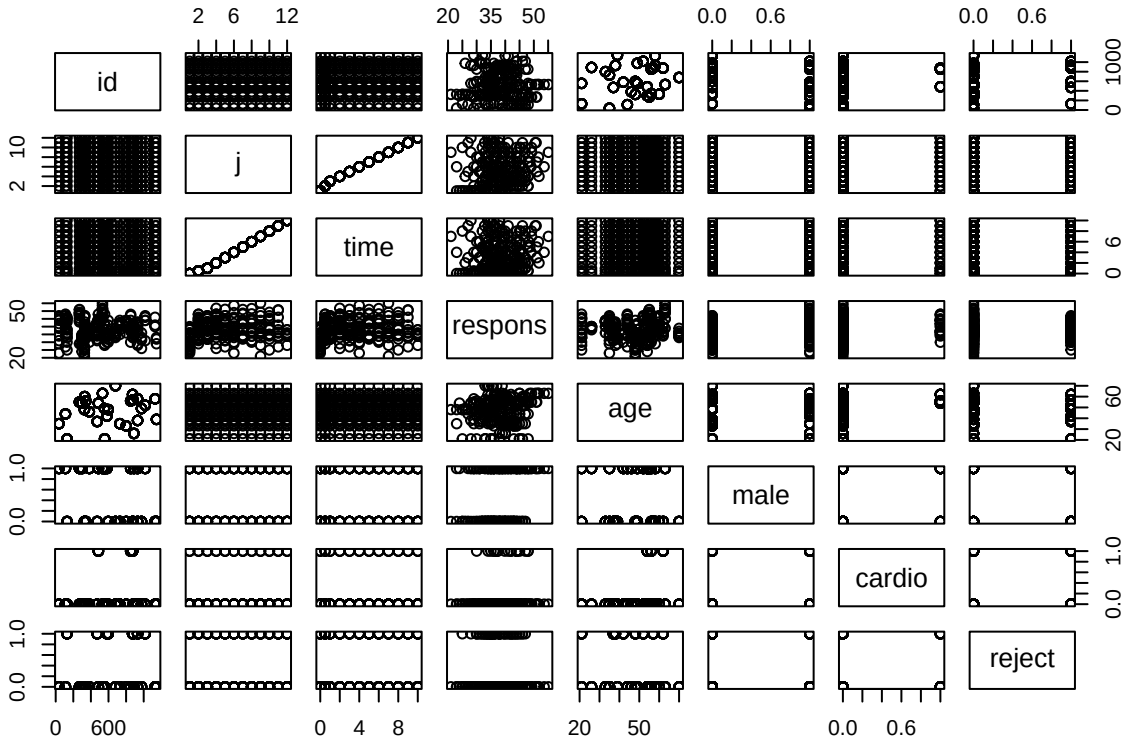
```
## Warning: Removed 4362 rows containing non-finite values (`stat_smooth()`).
## Removed 4362 rows containing missing values (`geom_point()`).
```



1.3 List of Hypotheses to be tested by the data

```
#Select a sample of data to plot
set.seed(1)
selected <- sample(1:length(unique(trenal.long$id)),30,replace=T) # random samples and permutations
#selected.vector = as.vector(selected)
data.selected = data[(data$id %in% c(selected)), ]
```

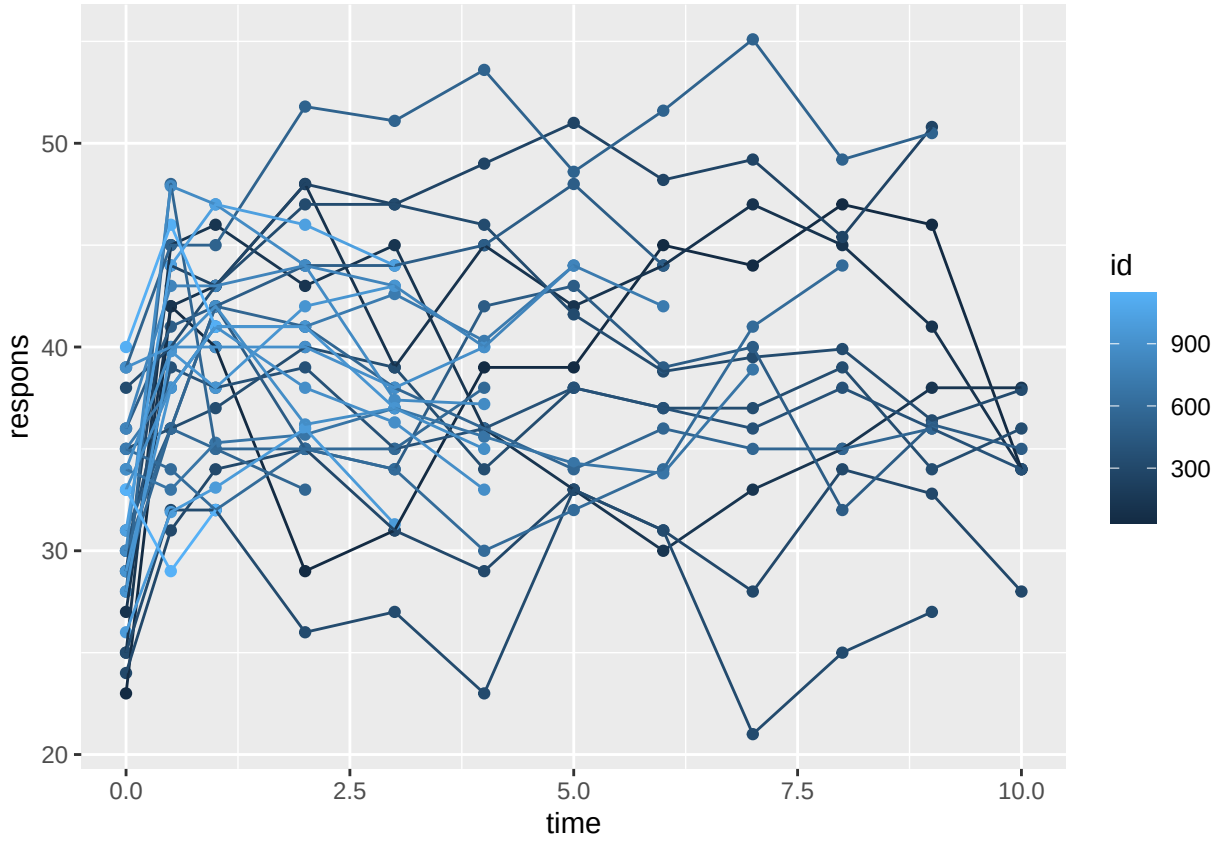
```
# Individual plots
plot(data.selected) # WHAT I WILL GET FROM THE PLOT(DATA), HOW to plot a scatter plot of HC level chang
```




```
# spaghettic plot
ggplot(data.selected,aes(x=time,y=respons,group=id,color=id))+geom_point()+ geom_line()
```

```
## Warning: Removed 106 rows containing missing values (`geom_point()`).
```

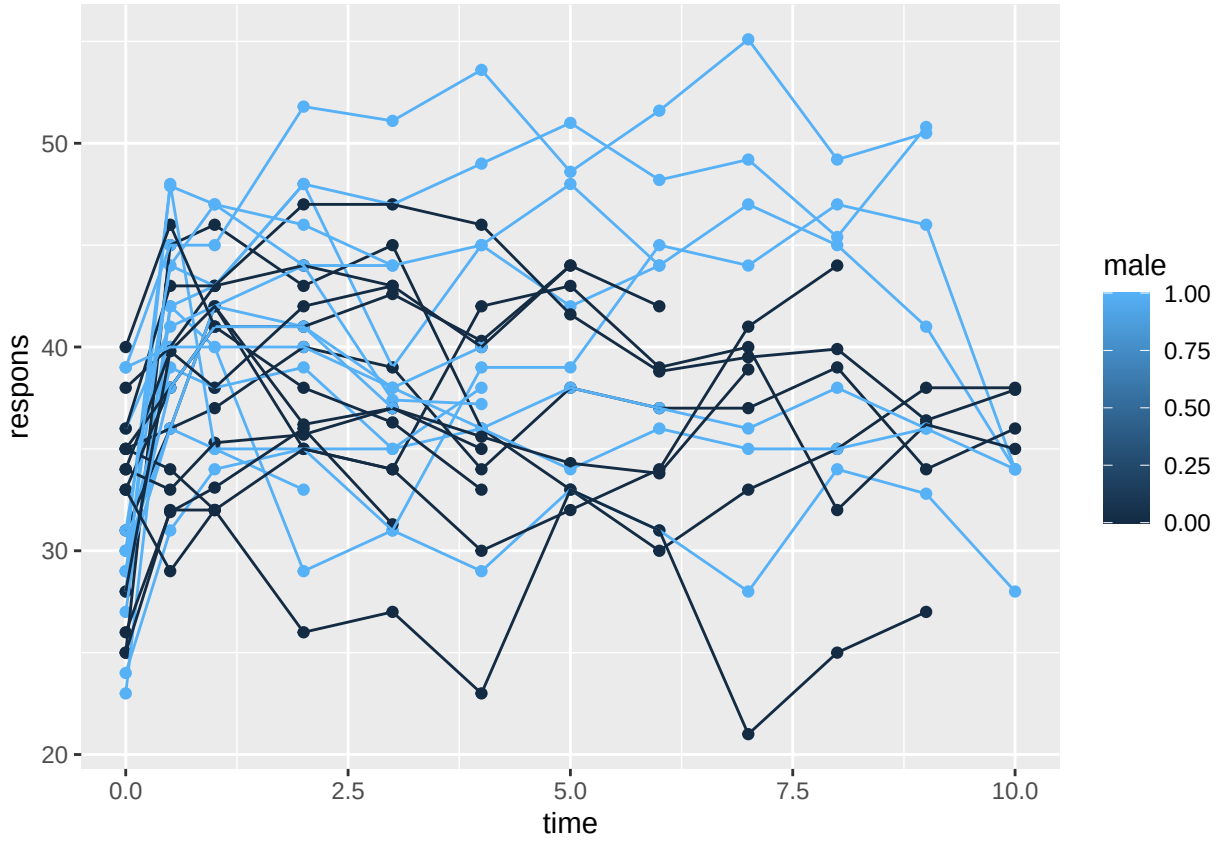
```
## Warning: Removed 106 rows containing missing values (`geom_line()`).
```




```
# Plot individual data by sex
ggplot(data.selected,aes(x=time,y= respons,group=id, color=male))+geom_point()+geom_line()
```

```
## Warning: Removed 106 rows containing missing values (`geom_point()`).
```

```
## Warning: Removed 106 rows containing missing values (`geom_line()`).
```




```
# Plot mean of male and mean of female
library(dplyr)
MEAN <- data.selected %>%
  group_by(male,age,cardio,reject) %>%
  summarise(respons = mean(respons))
```

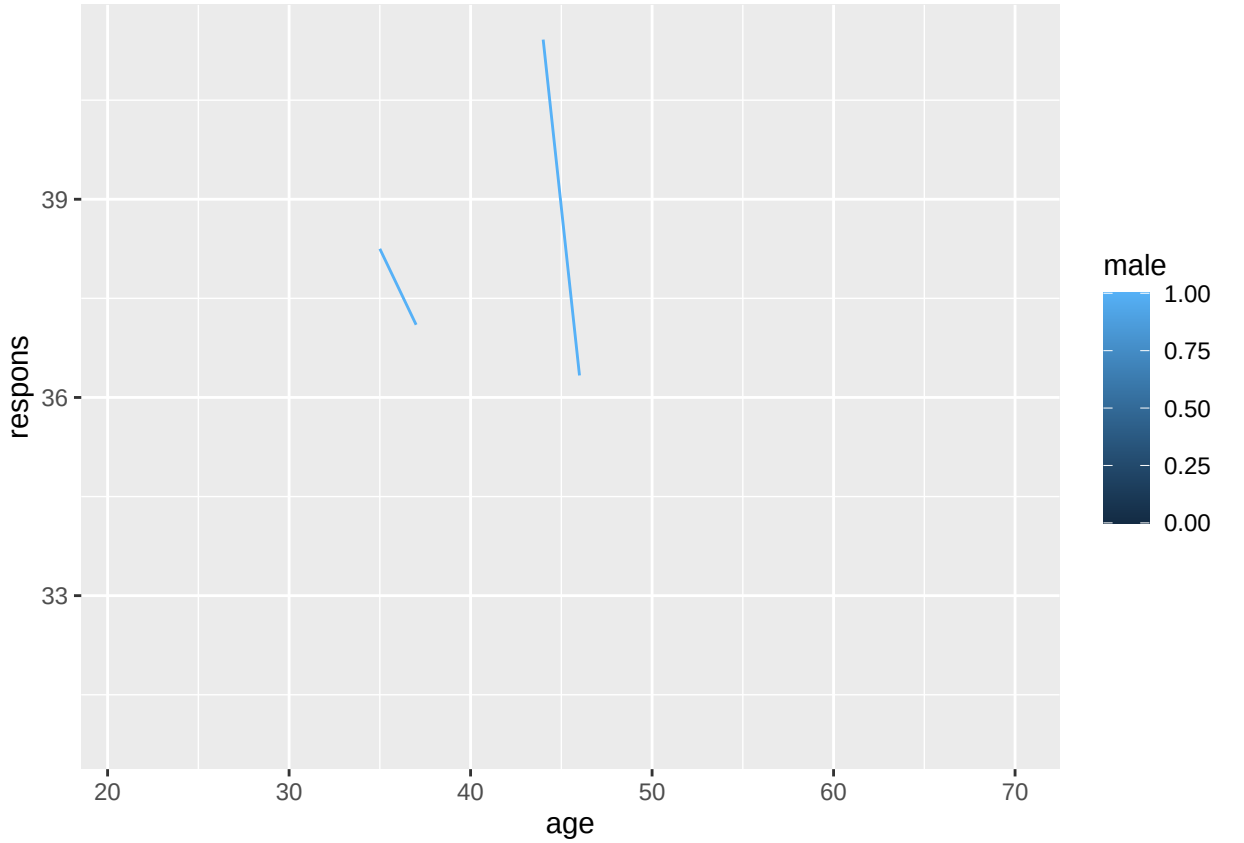
```
## `summarise()` has grouped output by 'male', 'age', 'cardio'. You can override
## using the `.groups` argument.
```

```
MEAN
```

```
## # A tibble: 29 x 5
## # Groups:   male, age, cardio [28]
##     male   age cardio reject respons
##    <dbl> <dbl>  <dbl>  <dbl>   <dbl>
##  1     0    21      0      1    37.2
##  2     0    33      0      0    NA
##  3     0    35      0      0    NA
##  4     0    37      0      1    37.1
##  5     0    38      0      1    NA
##  6     0    39      0      0    NA
##  7     0    48      0      0    NA
##  8     0    48      0      1    NA
##  9     0    49      0      0    NA
## 10     0    56      0      0    36.8
## # ... with 19 more rows
```

```
ggplot(data.selected,aes(x=age,y=respons,color=male)) + geom_line(data=MEAN)
```

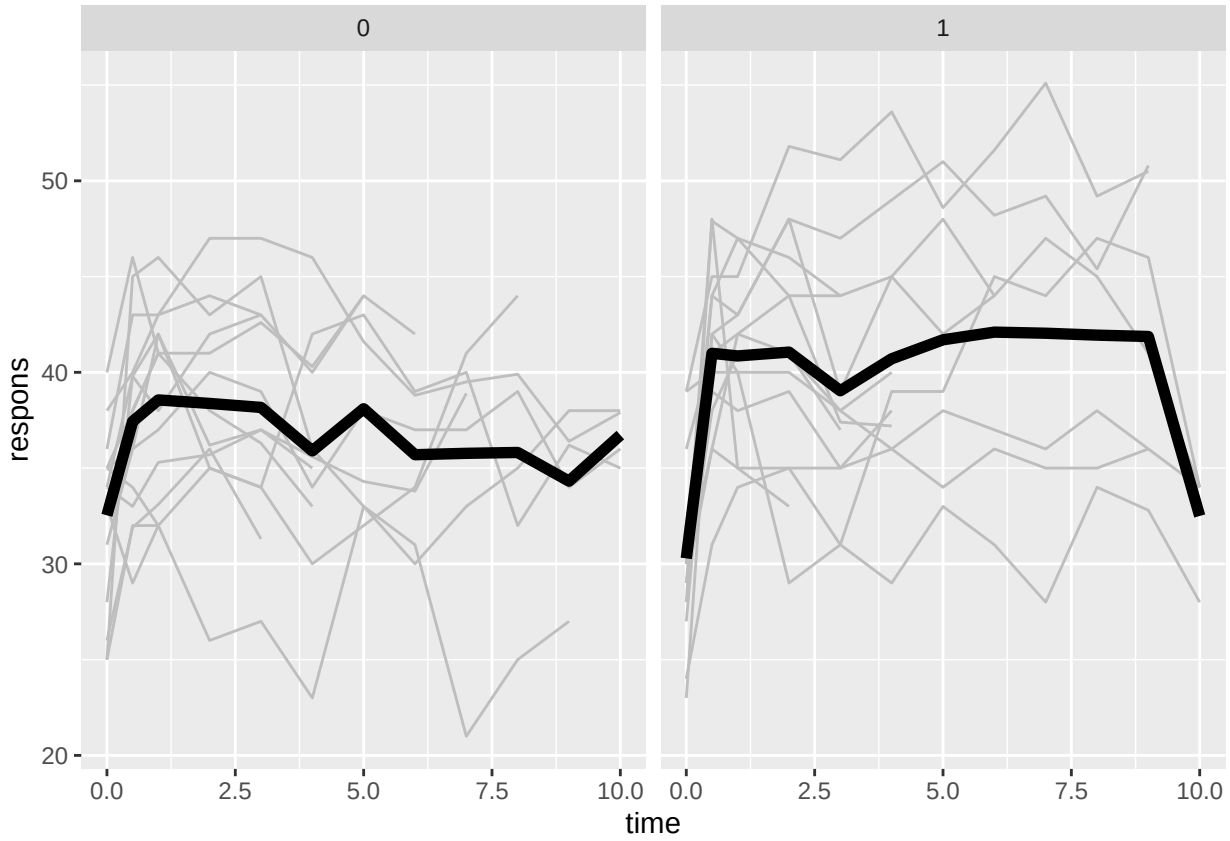
```
## Warning: Removed 3 rows containing missing values (`geom_line()`).
```




```
# Spaghetti Ggplot separated by male =1
p <- ggplot(data=data.selected,aes(x=time,y=respons,group=id))
p <- p + geom_line(col="grey")+stat_summary(aes(group=1),geom="line",fun=mean,linewidth=2)
p + facet_grid(~male)
```

```
## Warning: Removed 106 rows containing non-finite values (`stat_summary()`).
```

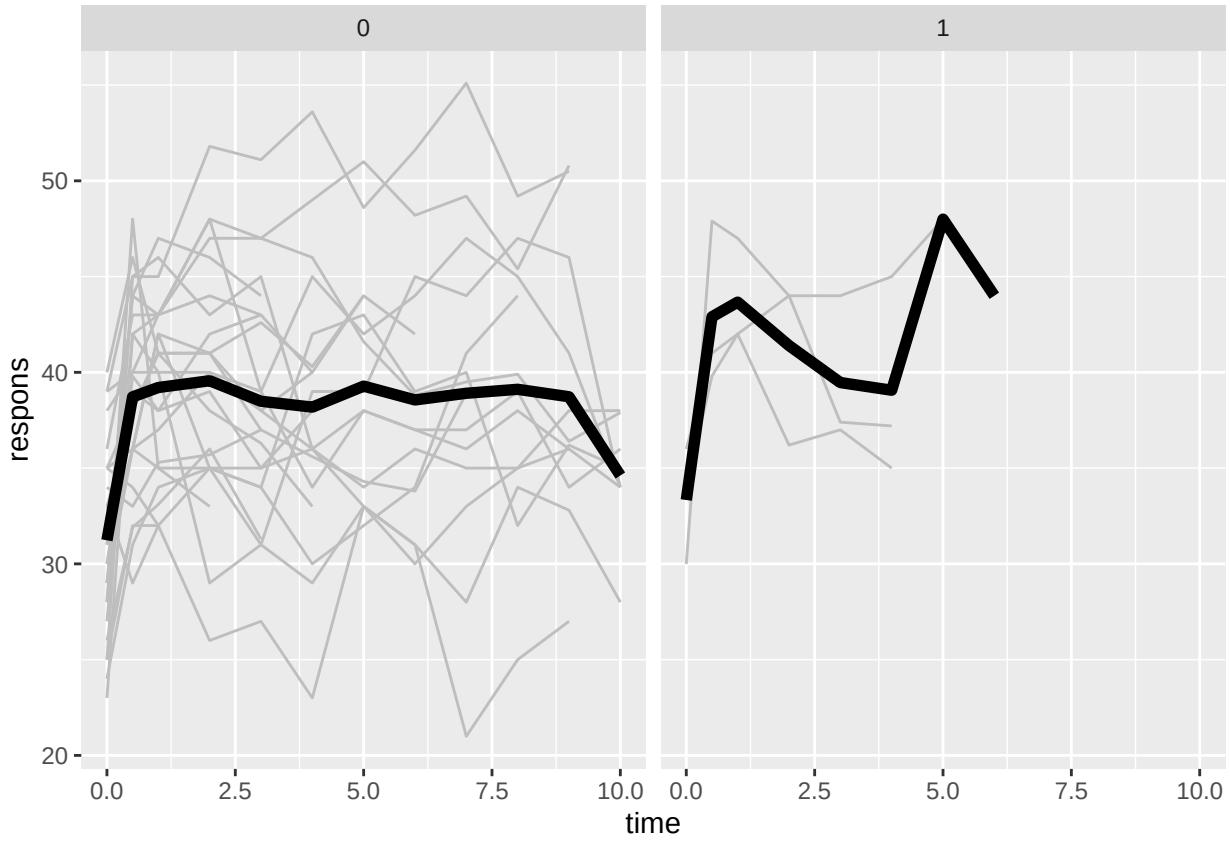
```
## Warning: Removed 106 rows containing missing values (`geom_line()`).
```




```
# Spaghetti Ggplot separated by cardio
p <- ggplot(data=data.selected,aes(x=time,y=respons,group=id))
p <- p + geom_line(col="grey")+stat_summary(aes(group=1),geom="line",fun=mean,linewidth=2)
p + facet_grid(~cardio)
```

```
## Warning: Removed 106 rows containing non-finite values (`stat_summary()`).
```

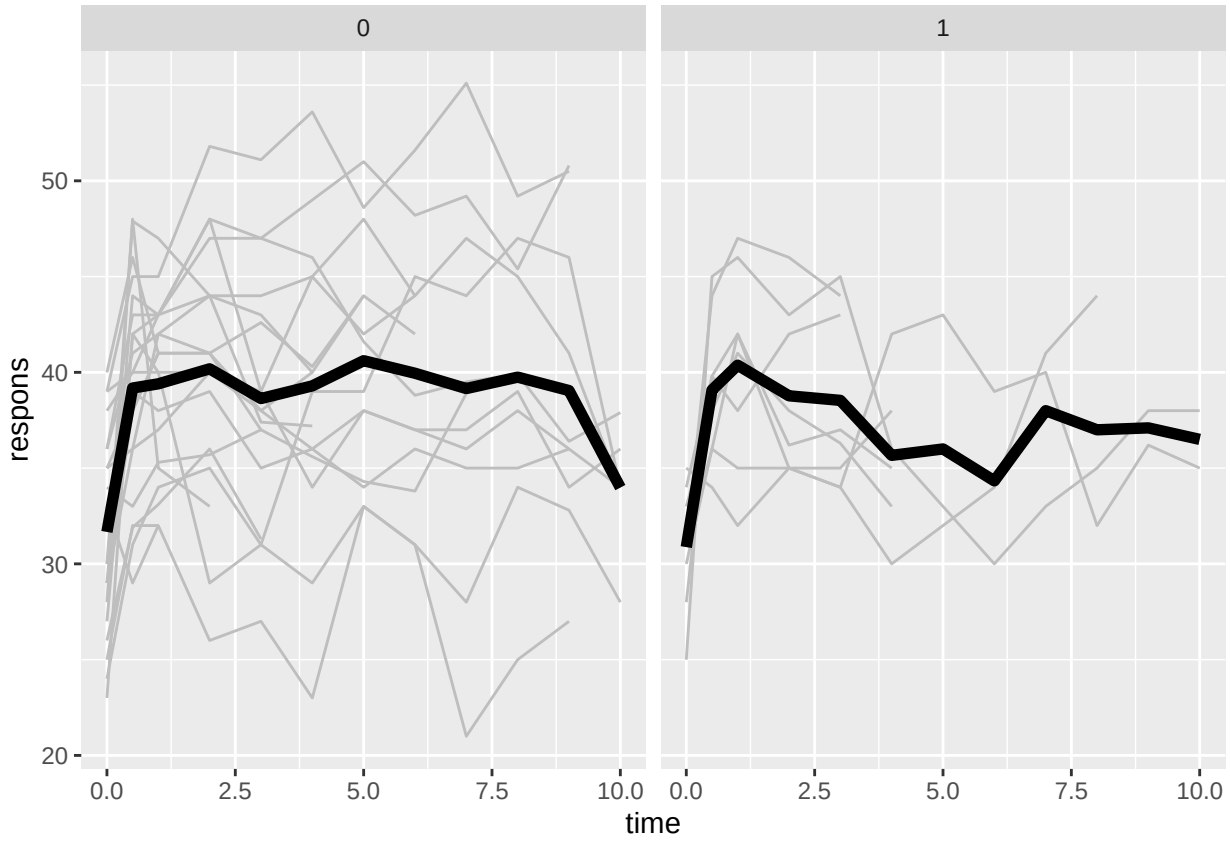
```
## Warning: Removed 106 rows containing missing values (`geom_line()`).
```




```
# Spaghetti Ggplot separated by reject =1
p <- ggplot(data=data.selected,aes(x=time,y=respons,group=id))
p <- p + geom_line(col="grey")+stat_summary(aes(group=1),geom="line",fun=mean,linewidth=2)
p + facet_grid(~reject)
```

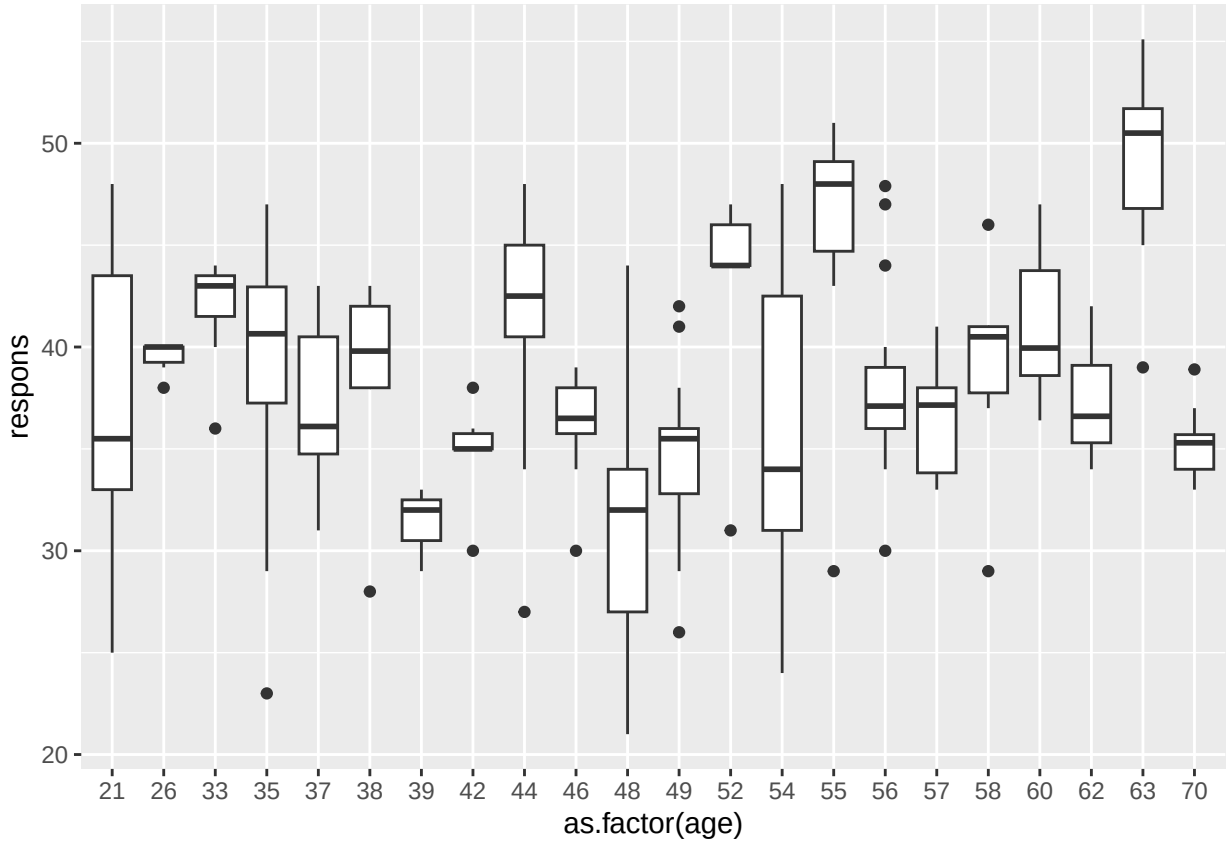
```
## Warning: Removed 106 rows containing non-finite values (`stat_summary()`).
```

```
## Warning: Removed 106 rows containing missing values (`geom_line()`).
```



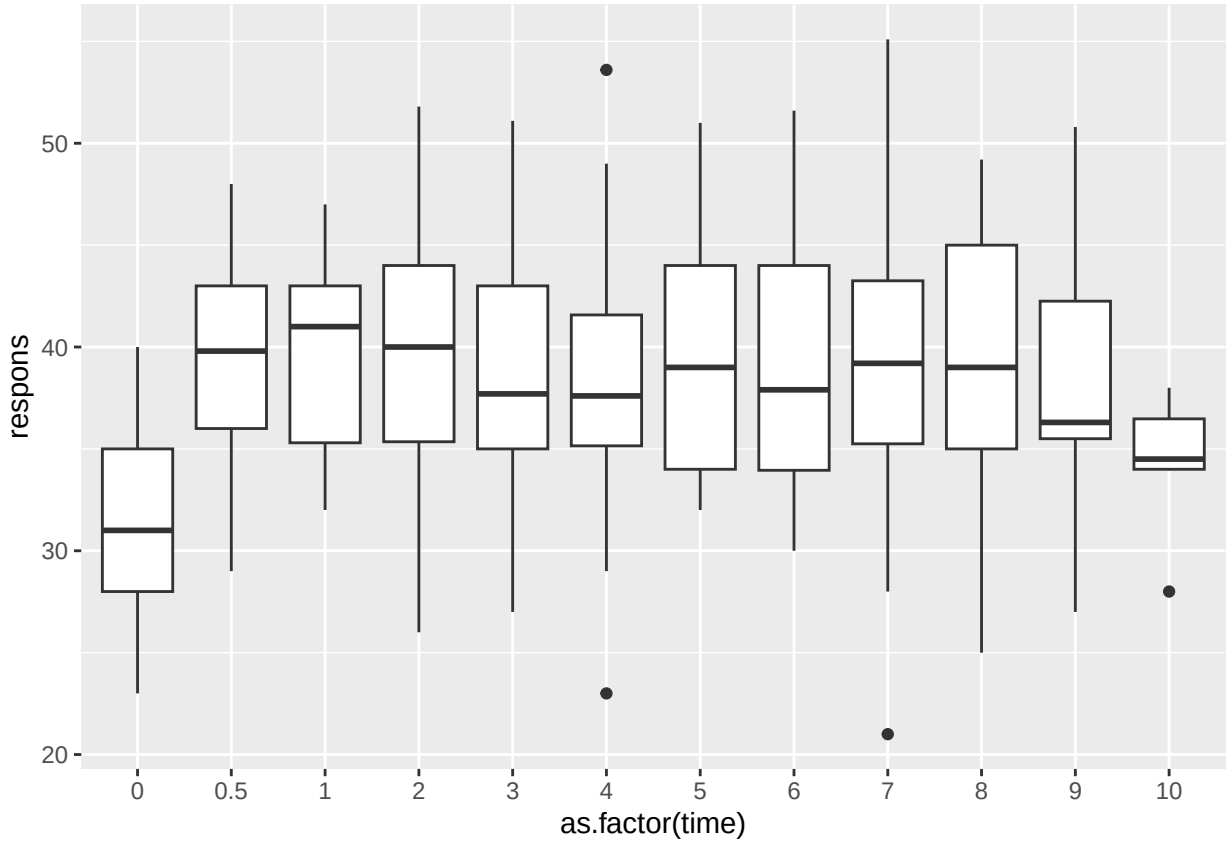

```
# BoxPlot
ggplot(data.selected,aes(x=as.factor(age),y=respons))+ geom_boxplot(position=position_dodge(1))
```

```
## Warning: Removed 106 rows containing non-finite values (`stat_boxplot()`).
```



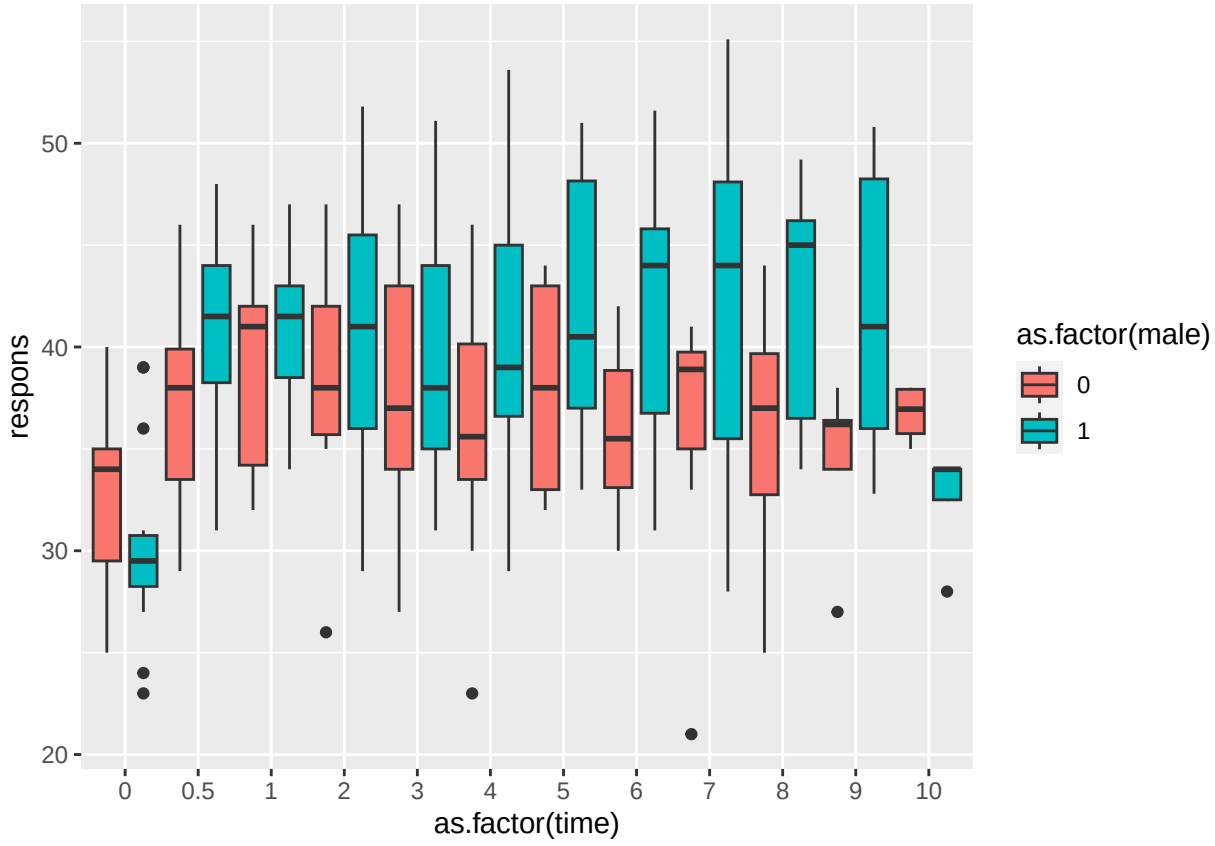

```
# BoxPlot
ggplot(data.selected,aes(x=as.factor(time),y=respons))+ geom_boxplot(position=position_dodge(1))
```

```
## Warning: Removed 106 rows containing non-finite values (`stat_boxplot()`).
```



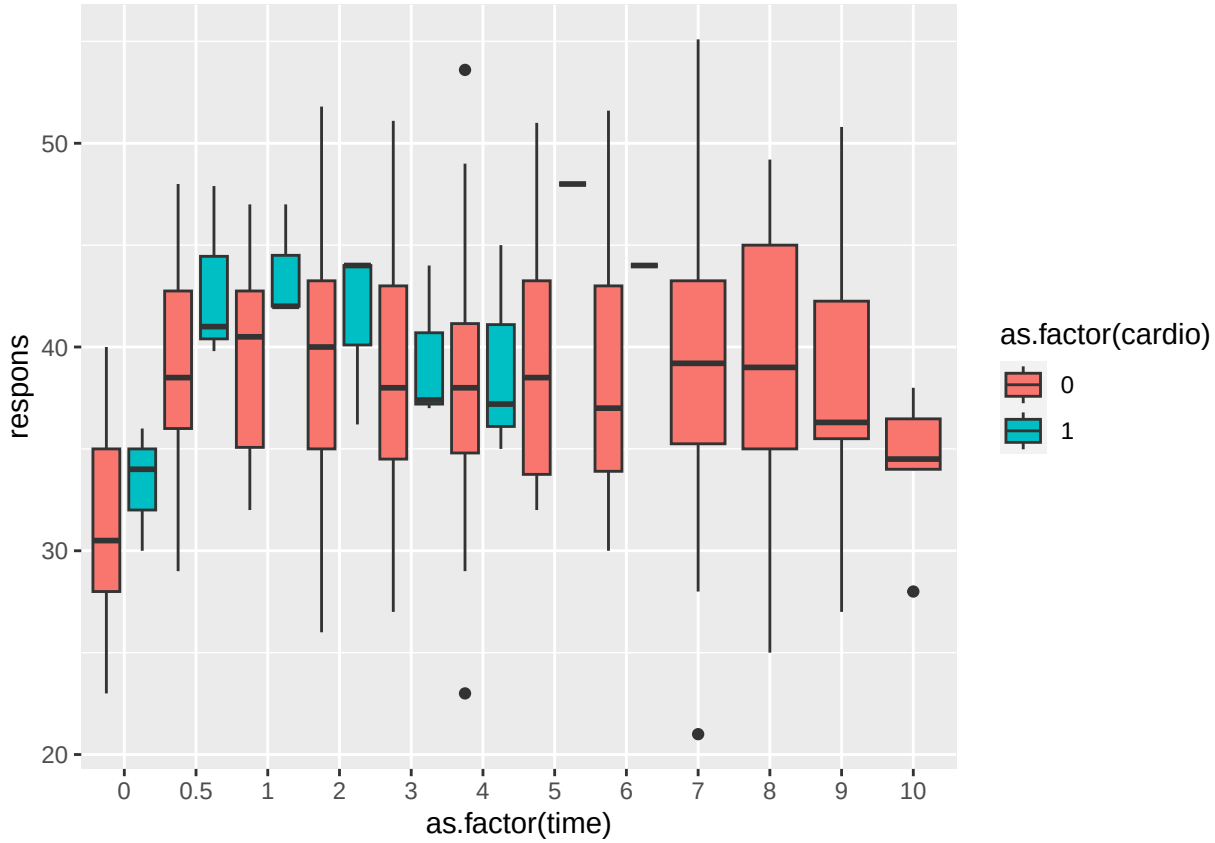

```
# Box plot by sex
ggplot(data.selected,aes(x=as.factor(time),y=respons,fill=as.factor(male)))+
  geom_boxplot(position=position_dodge(1))
```

```
## Warning: Removed 106 rows containing non-finite values (`stat_boxplot()`).
```



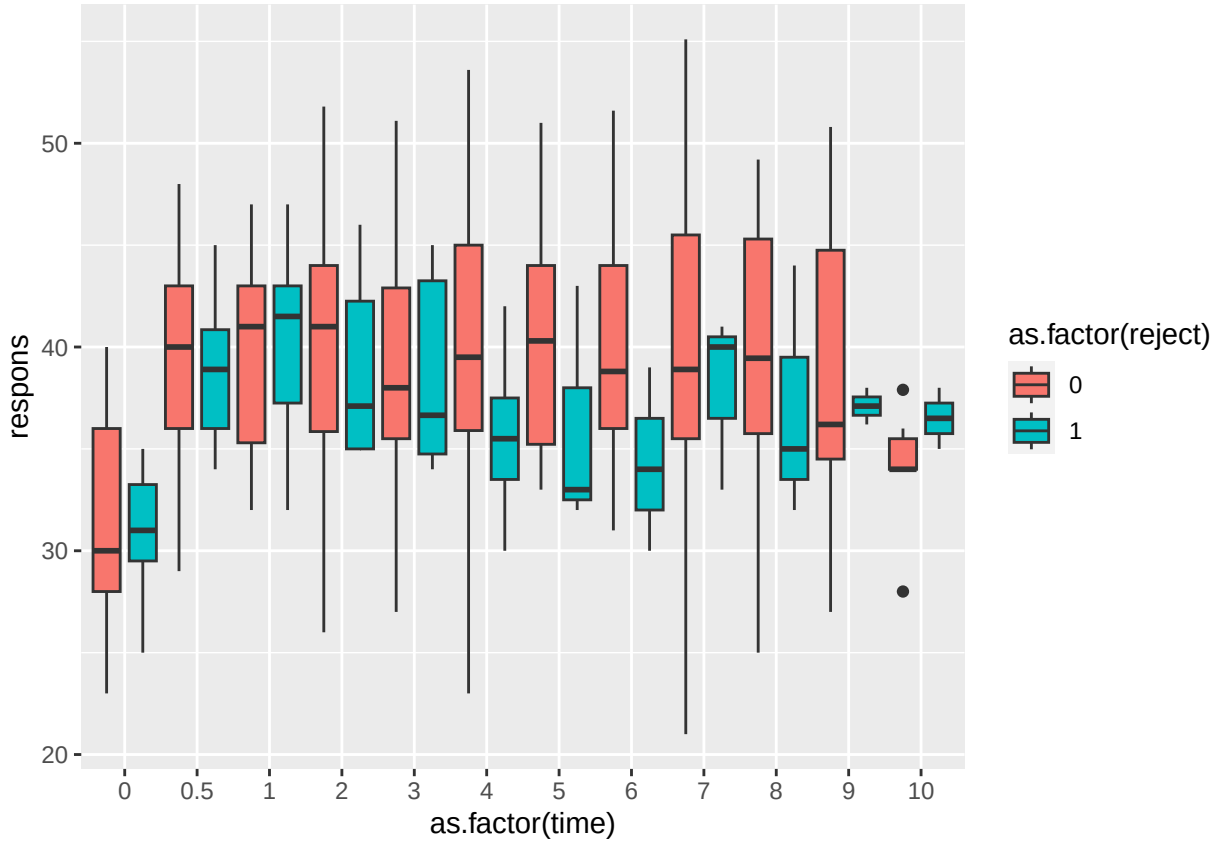

```
# Box plot by cardio
ggplot(data.selected,aes(x=as.factor(time),y=respons,fill=as.factor(cardio)))+
  geom_boxplot(position=position_dodge(1))
```

```
## Warning: Removed 106 rows containing non-finite values (`stat_boxplot()`).
```




```
# Box plot by reject
ggplot(data.selected,aes(x=as.factor(time),y=respons,fill=as.factor(reject)))+
  geom_boxplot(position=position_dodge(1))
```

```
## Warning: Removed 106 rows containing non-finite values (`stat_boxplot()`).
```

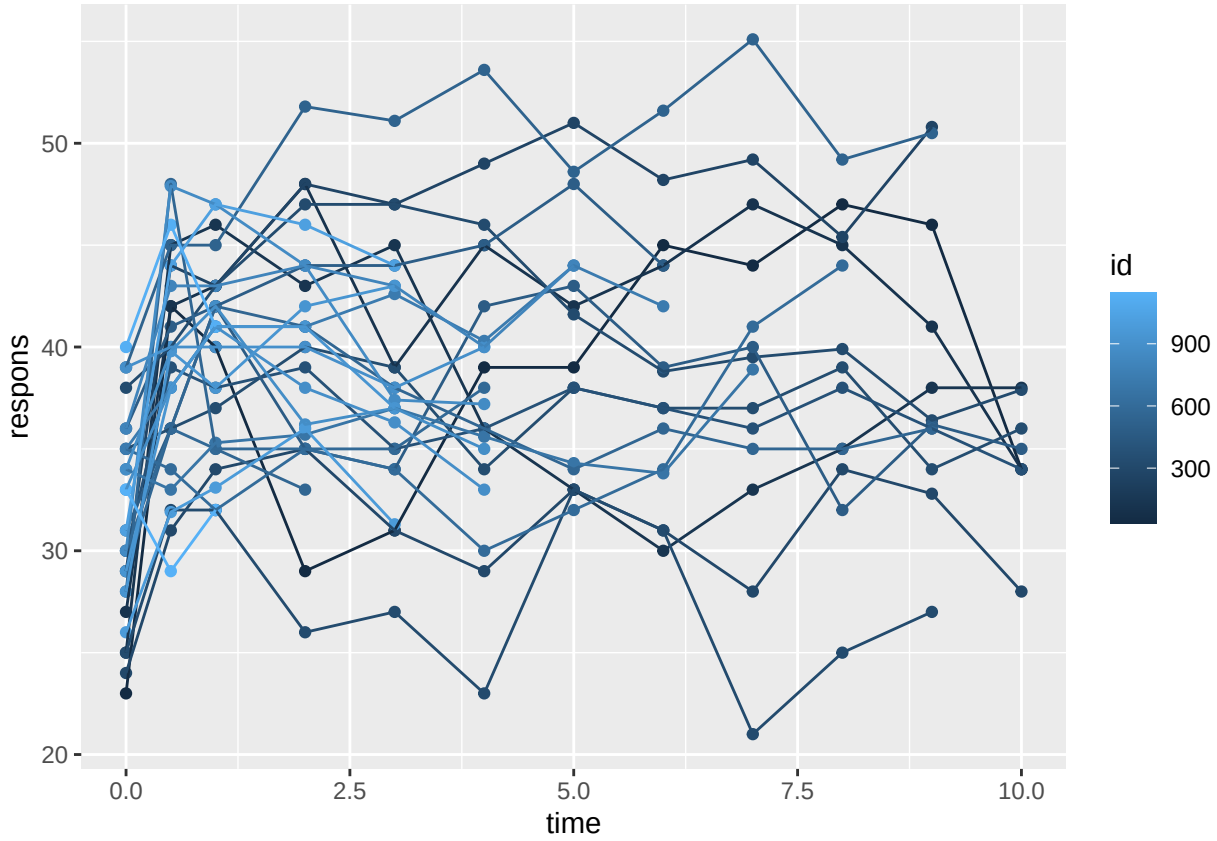


Spaghetti Plot the response over time with the different persons

```
#data.selected = data[data$id == selected.vector,]# why the dim(data.selected) = 12 x 8
# Plot the respons over time for different id
# If some responses are not available, NA
ggplot(data.selected, aes(x=time, y=respons, group=id,color=id)) + geom_point()  +geom_line()
```

```
## Warning: Removed 106 rows containing missing values (`geom_point()`).
```

```
## Warning: Removed 106 rows containing missing values (`geom_line()`).
```

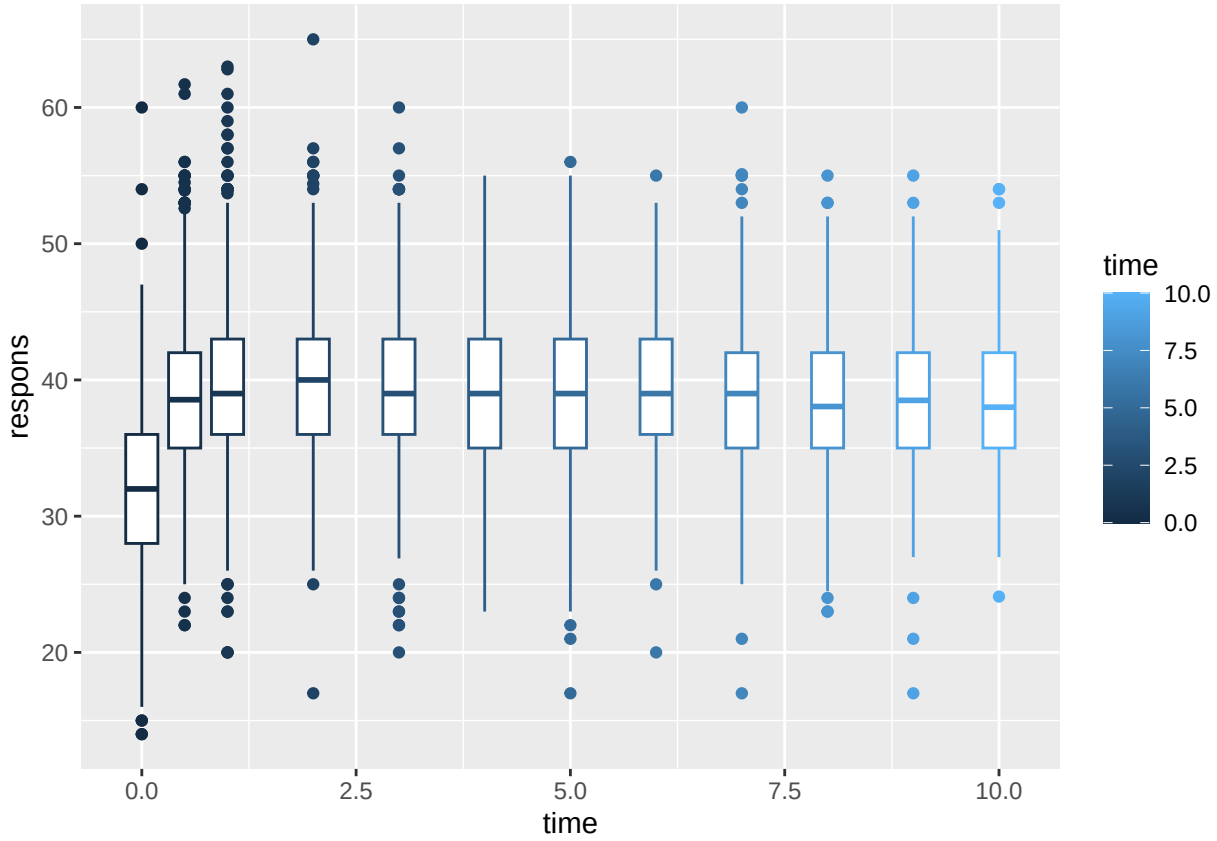



```
#ggplot(data.selected, aes(x=time, y=na.pass(respons), group=id,color=id)) + geom_point()  +geom_line()
```

```
# Box plot
p <- ggplot(data, aes(x=time, y=respons,group =time, color = time)) +
  geom_boxplot()
p
```

Bax plot response over time

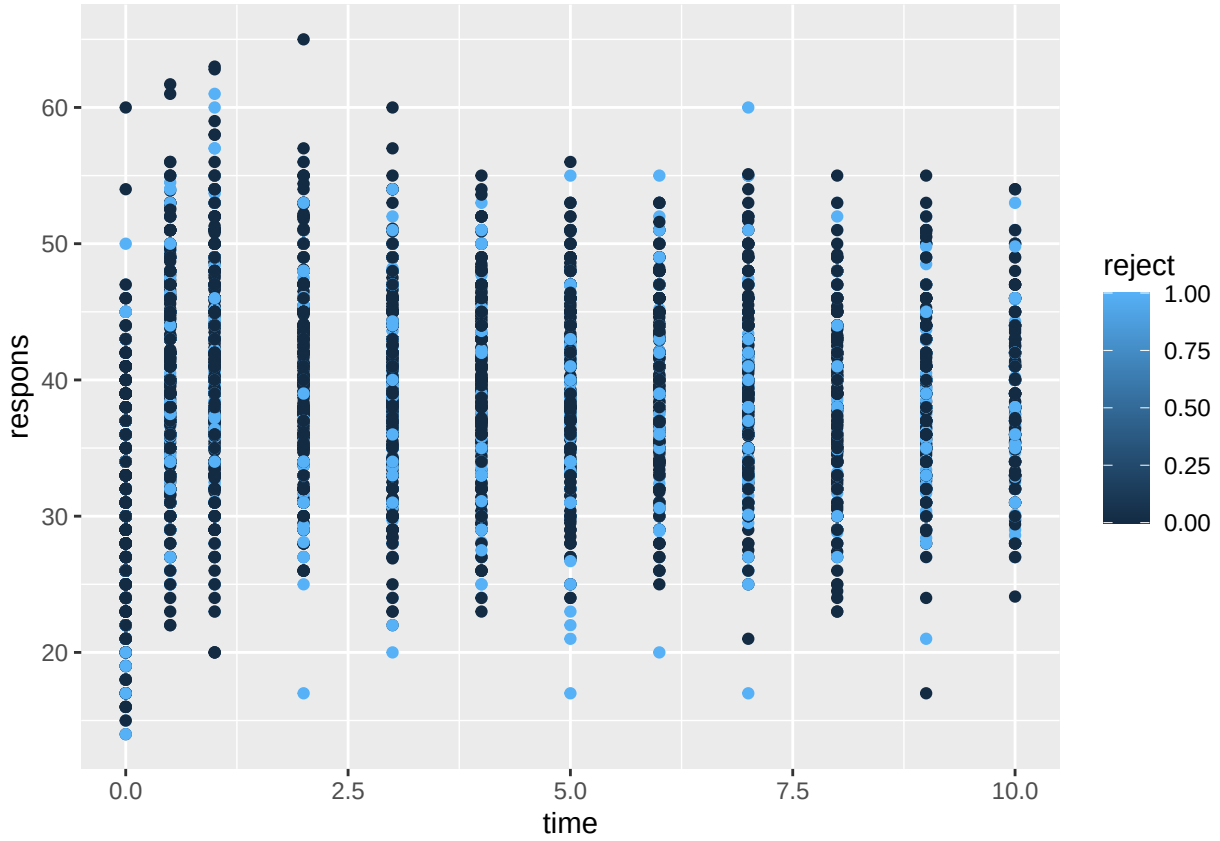
```
## Warning: Removed 4362 rows containing non-finite values (`stat_boxplot()`).
```



Hypothese one HC level will change with time differently if the REJECT is different

```
#Plot individual data
ggplot(data, aes(x=time, y=respons, group=reject,color=reject)) + geom_point()
```

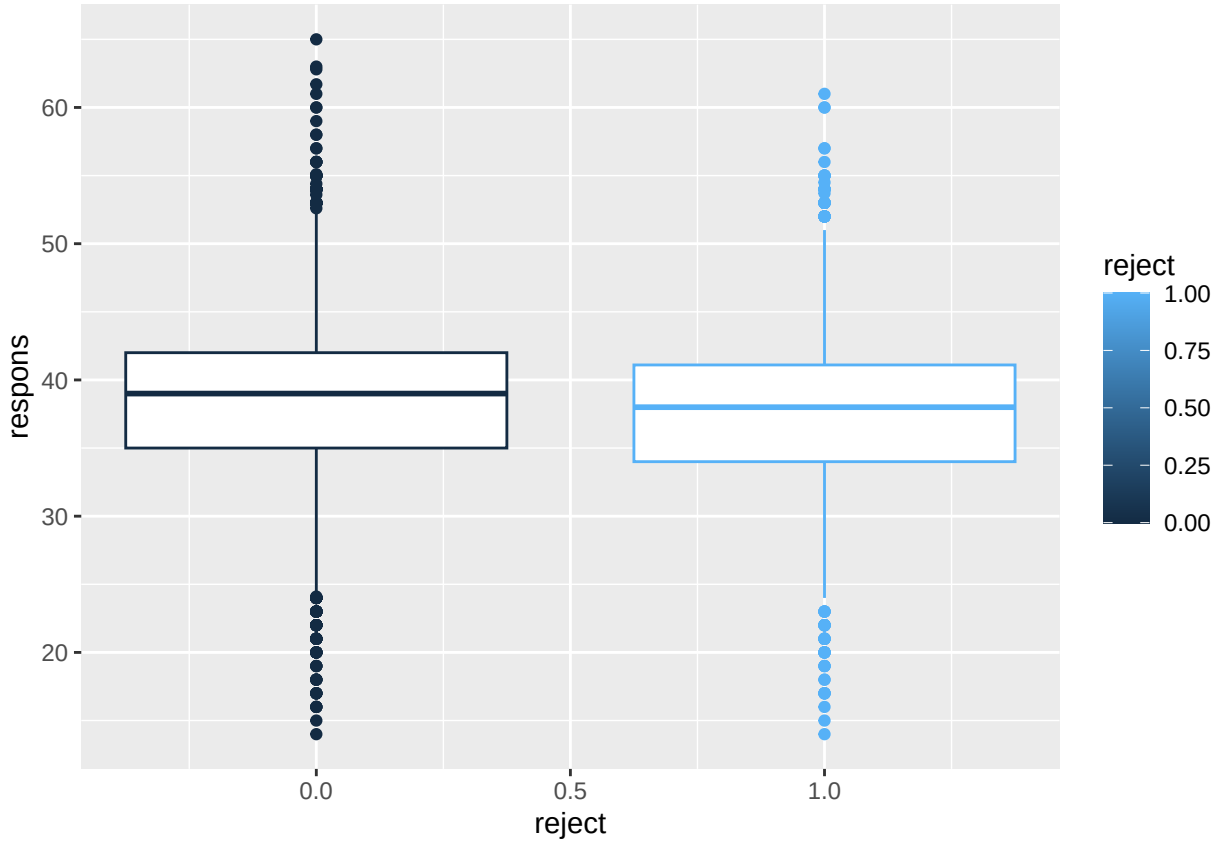
```
## Warning: Removed 4362 rows containing missing values (`geom_point()`).
```



Box plot

```
# Box plot
p <- ggplot(data, aes(x=reject, y=respons,group = reject, color = reject)) +
  geom_boxplot()
p
```

```
## Warning: Removed 4362 rows containing non-finite values (`stat_boxplot()`).
```



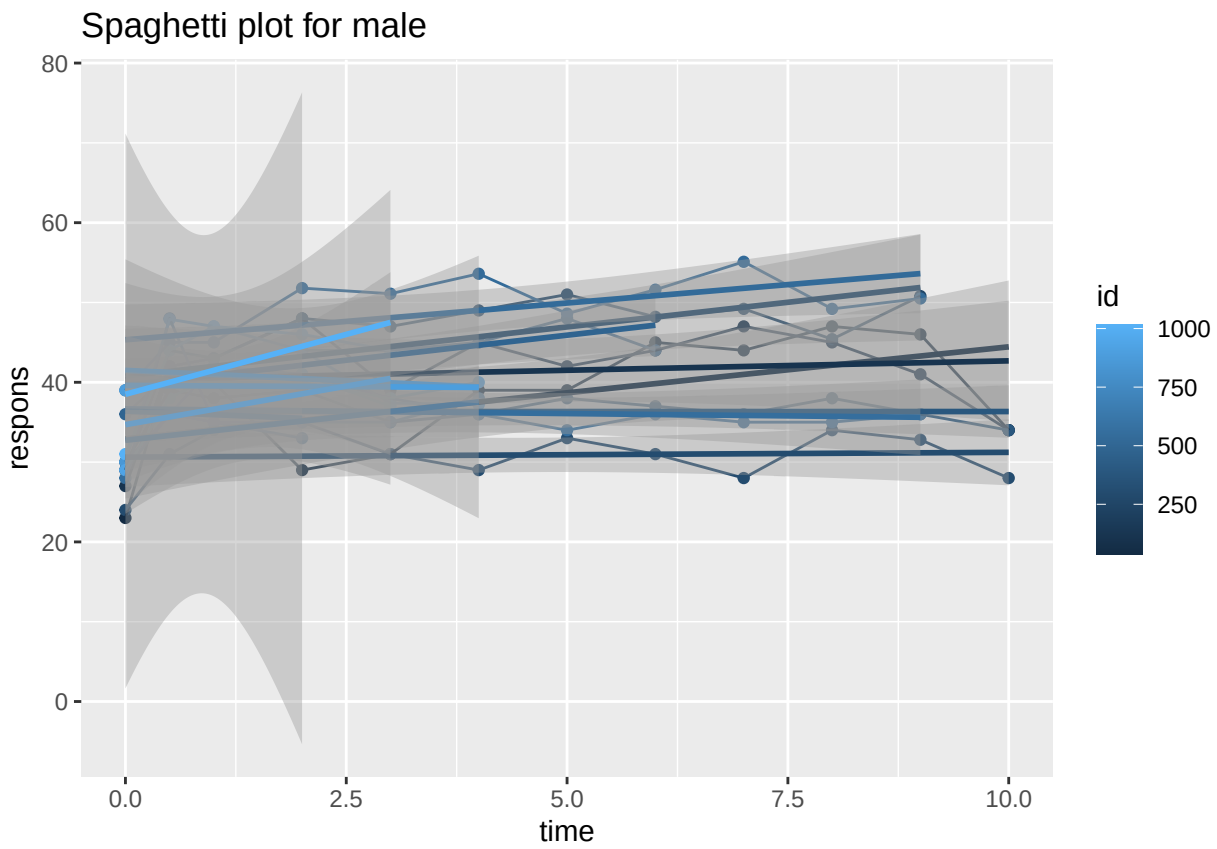
Hypothese two HC level will change with time differently if the gender is different, male (1) has generally higher HC level than female (0)

```
data.male =  data[(data$male == "1" ), ]
data.female =  data[(data$male == "0" ), ]
data.male.selected =  data[(data$male == "1" & data$id %in% c(selected)), ]
data.female.selected =  data[(data$male == "0" & data$id %in% c(selected)), ]
```

```
ggplot(data.male.selected, aes(x=time, y =respons, group=id,color=id)) + geom_point()  +geom_line()+ggt
```

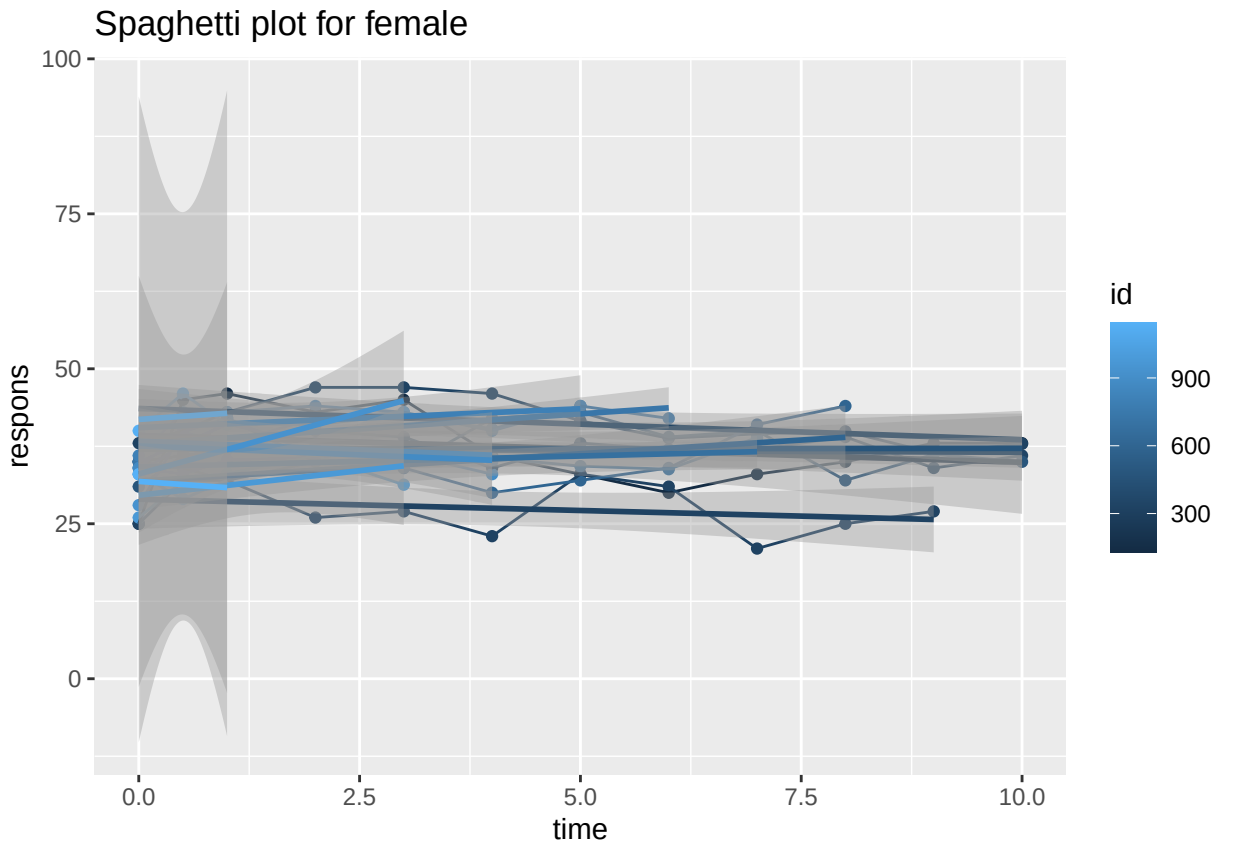
Spaghetti plots stratified by variables gender male

```
## `geom_smooth()` using formula = 'y ~ x'
## Warning: Removed 47 rows containing non-finite values (`stat_smooth()`).
## Warning: Removed 47 rows containing missing values (`geom_point()`).
## Warning: Removed 47 rows containing missing values (`geom_line()`).
```




```
ggplot(data.female.selected, aes(x=time, y= respons, group=id,color=id)) + geom_point()  +geom_line()+g
```

```
## `geom_smooth()` using formula = 'y ~ x'
## Warning: Removed 59 rows containing non-finite values (`stat_smooth()`).
## Warning: Removed 59 rows containing missing values (`geom_point()`).
## Warning: Removed 59 rows containing missing values (`geom_line()`).
```



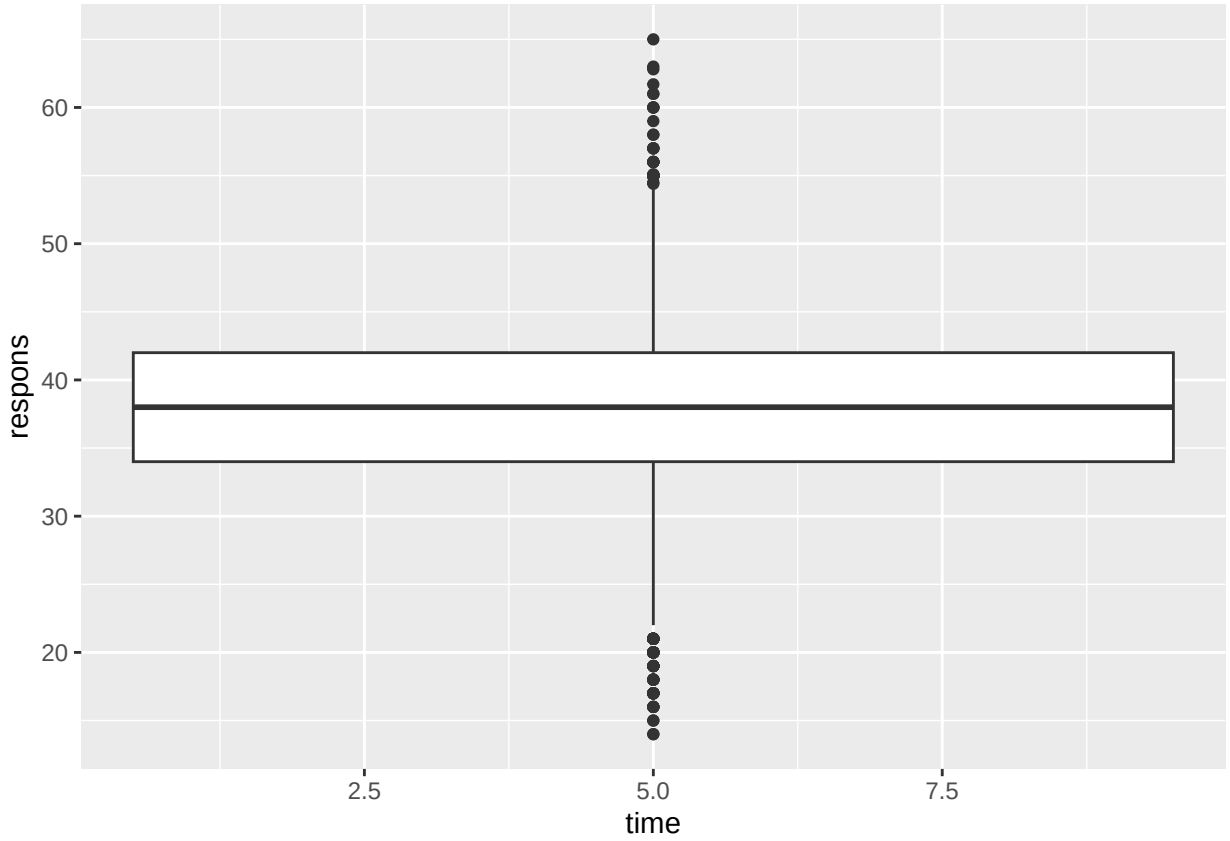
Box plot

```
p <- ggplot(data, aes(x=time, y=respons,fill= male)) +
  geom_boxplot()
p
```

```
## Warning: Continuous x aesthetic
## i did you forget `aes(group = ...)`?
```

```
## Warning: Removed 4362 rows containing non-finite values (`stat_boxplot()`).
```

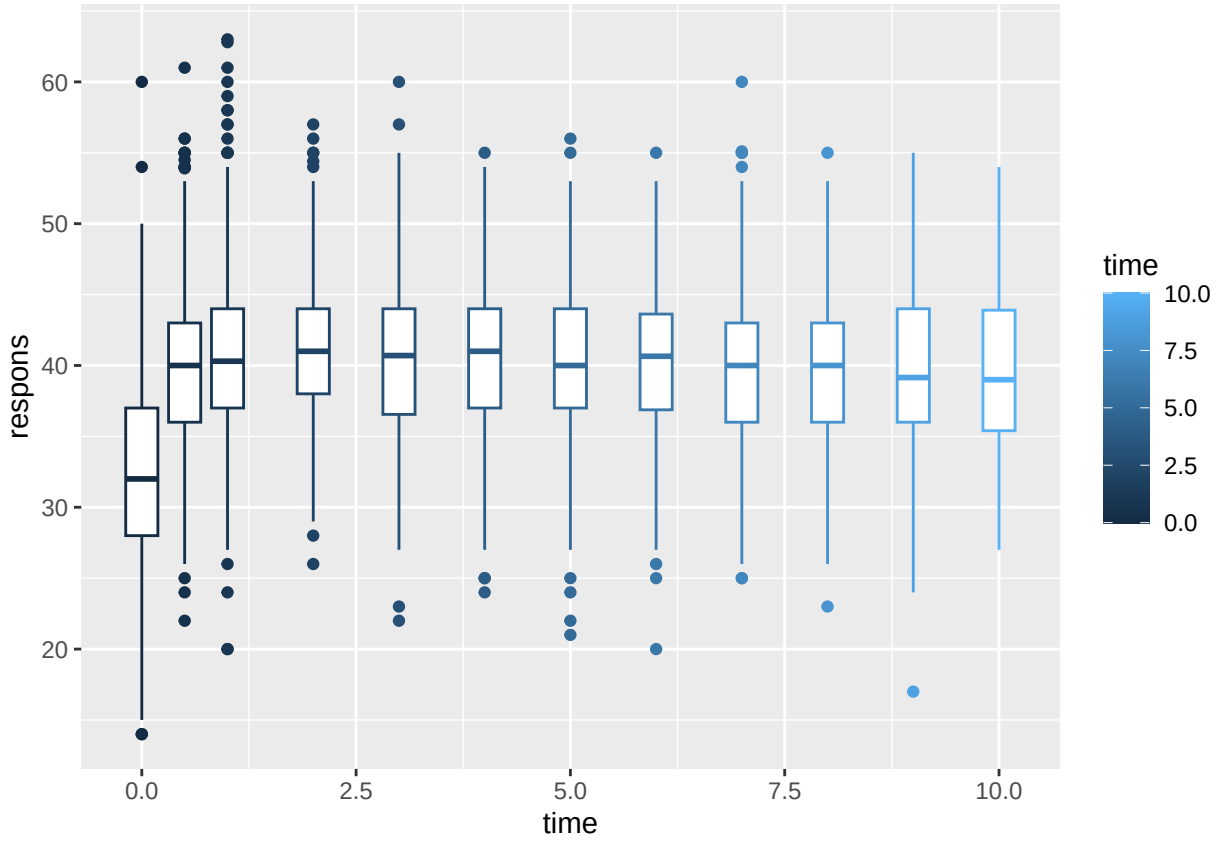
```
## Warning: The following aesthetics were dropped during statistical transformation: fill
## i This can happen when ggplot fails to infer the correct grouping structure in
##   the data.
## i Did you forget to specify a `group` aesthetic or to convert a numerical
##   variable into a factor?
```



Box plot for male and female COULD I PLOT THEM IN THE SAME FIGURE?

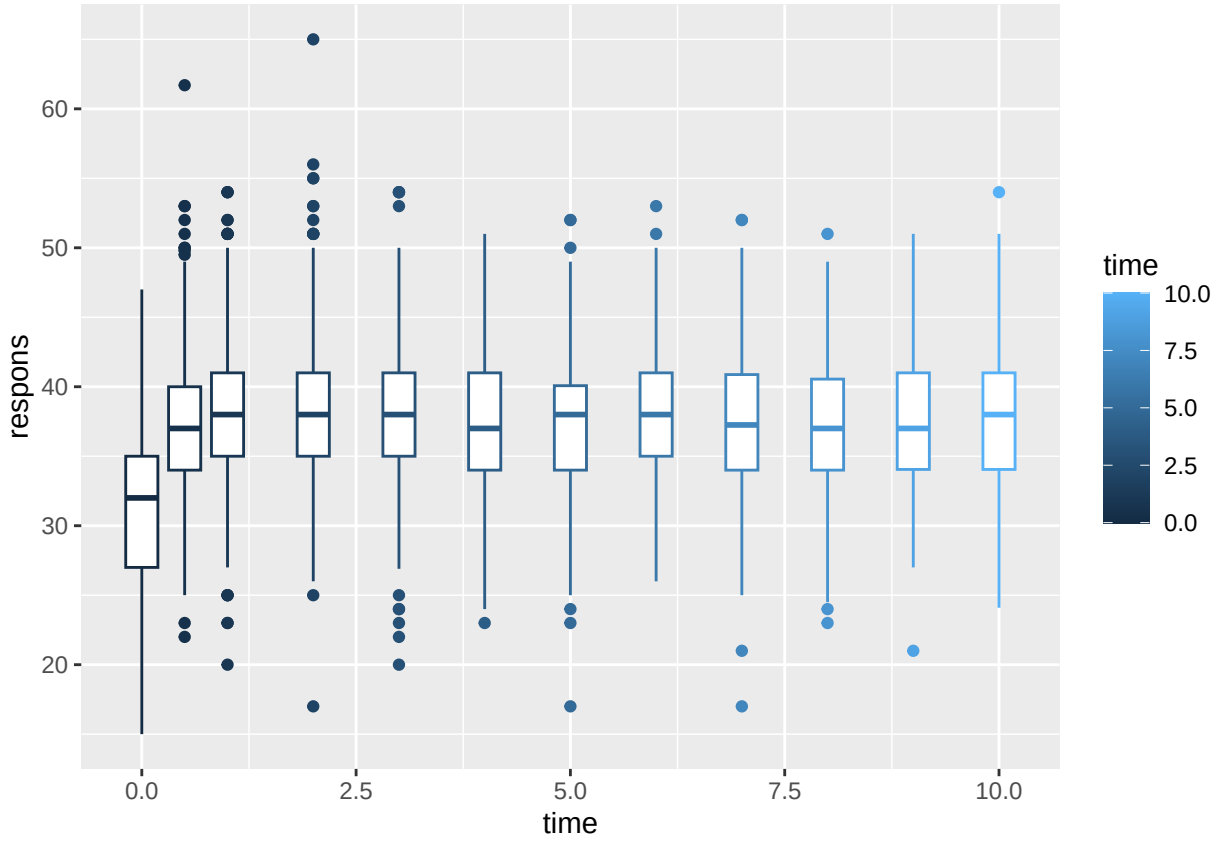
```
p.box.male <- ggplot(data.male, aes(x=time, y=respons,group = time, color = time)) +
  geom_boxplot()
p.box.male
```

```
## Warning: Removed 2647 rows containing non-finite values (`stat_boxplot()`).
```




```
p.box.female <- ggplot(data.female, aes(x=time, y=respons,group = time, color = time)) +
  geom_boxplot()
p.box.female
```

```
## Warning: Removed 1715 rows containing non-finite values (`stat_boxplot()`).
```

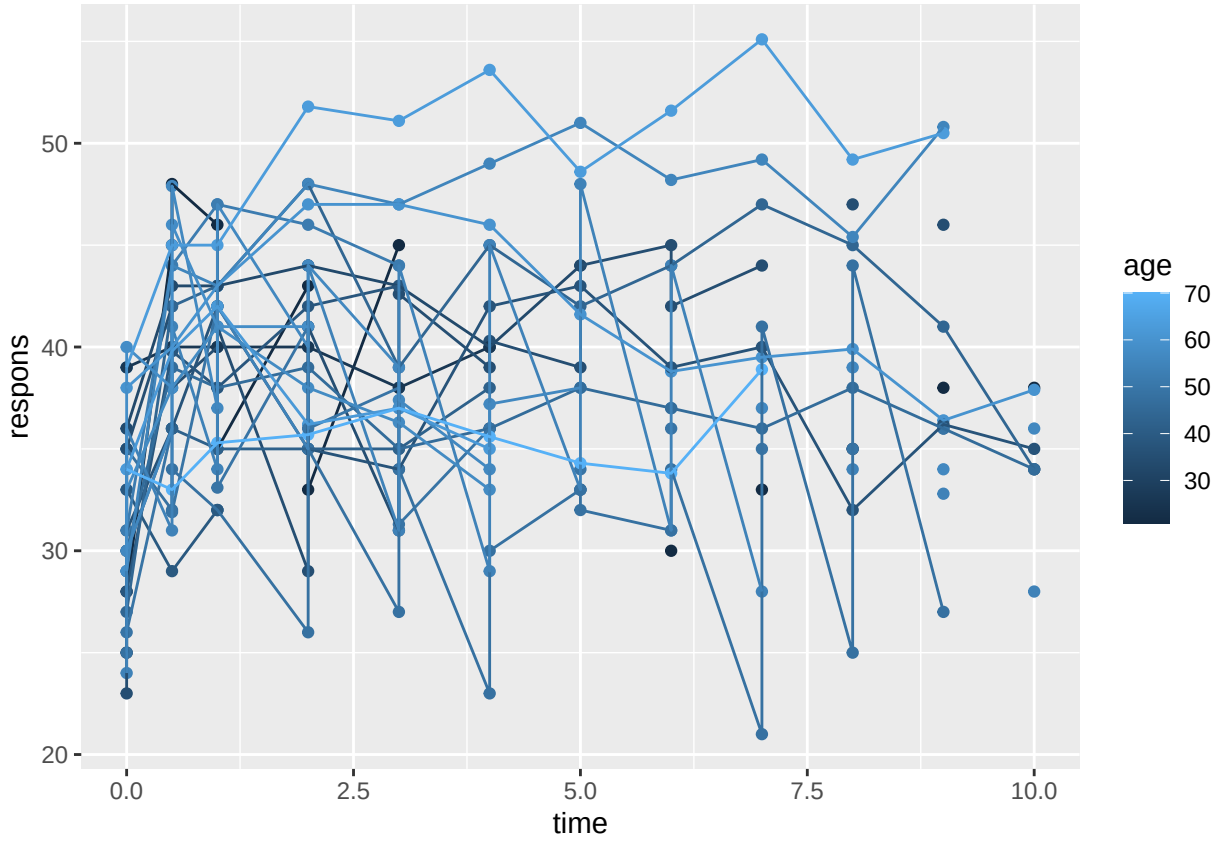


Hypothese three HC level will change with time differently if the age when performing the kidney transplant is younger

```
#Plot individual data
ggplot(data.selected, aes(x=time, y=respons, group=age,color=age)) + geom_point() +geom_line()
```

```
## Warning: Removed 106 rows containing missing values (`geom_point()`).
```

```
## Warning: Removed 82 rows containing missing values (`geom_line()`).
```




```
p <- ggplot(data, aes(x=age, y=respons,group = age, color = age)) +
  geom_boxplot()
p
```

Box plot

```
## Warning: Removed 12 rows containing missing values (`stat_boxplot()`).
```

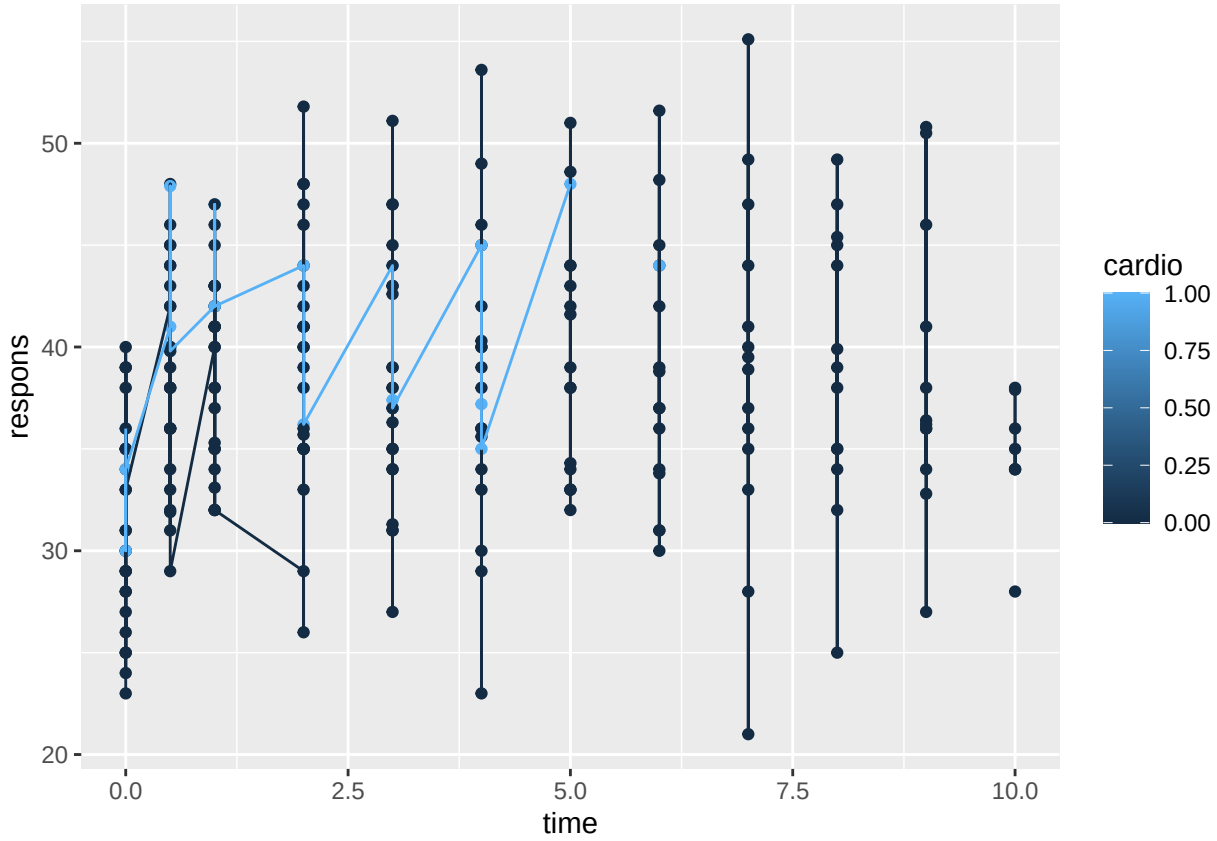
```
## Warning: Removed 4357 rows containing non-finite values (`stat_boxplot()`).
```

Hypothese four HC level will change with time differently if the patient has experienced cardio-vascular problem during the years preceding the tranplantation ##### Spathetti plot ?

```
#Plot individual data
ggplot(data.selected, aes(x=time, y=respons, group=cardio,color=cardio)) + geom_point()  +geom_line()
```

```
## Warning: Removed 106 rows containing missing values (`geom_point()`).
```

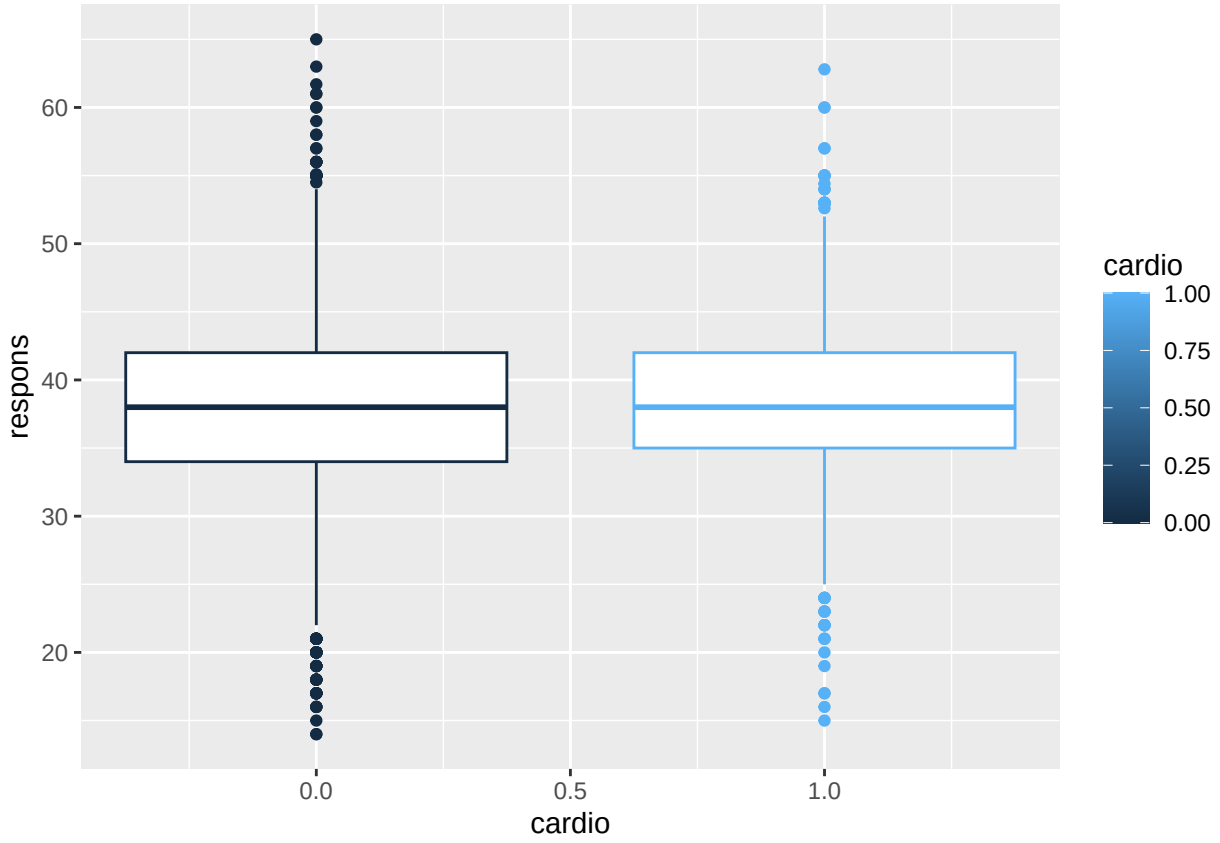
```
## Warning: Removed 30 rows containing missing values (`geom_line()`).
```



Bar plot

```
p <- ggplot(data, aes(x=cardio, y=respons,group = cardio, color = cardio)) +
  geom_boxplot()
p
```

```
## Warning: Removed 4362 rows containing non-finite values (`stat_boxplot()`).
```



Correlation analysis for different HC levels along time

For this purpose we need the wide table

```
trenal.wide = trenal[,1:17]
summary(trenal.wide)
```

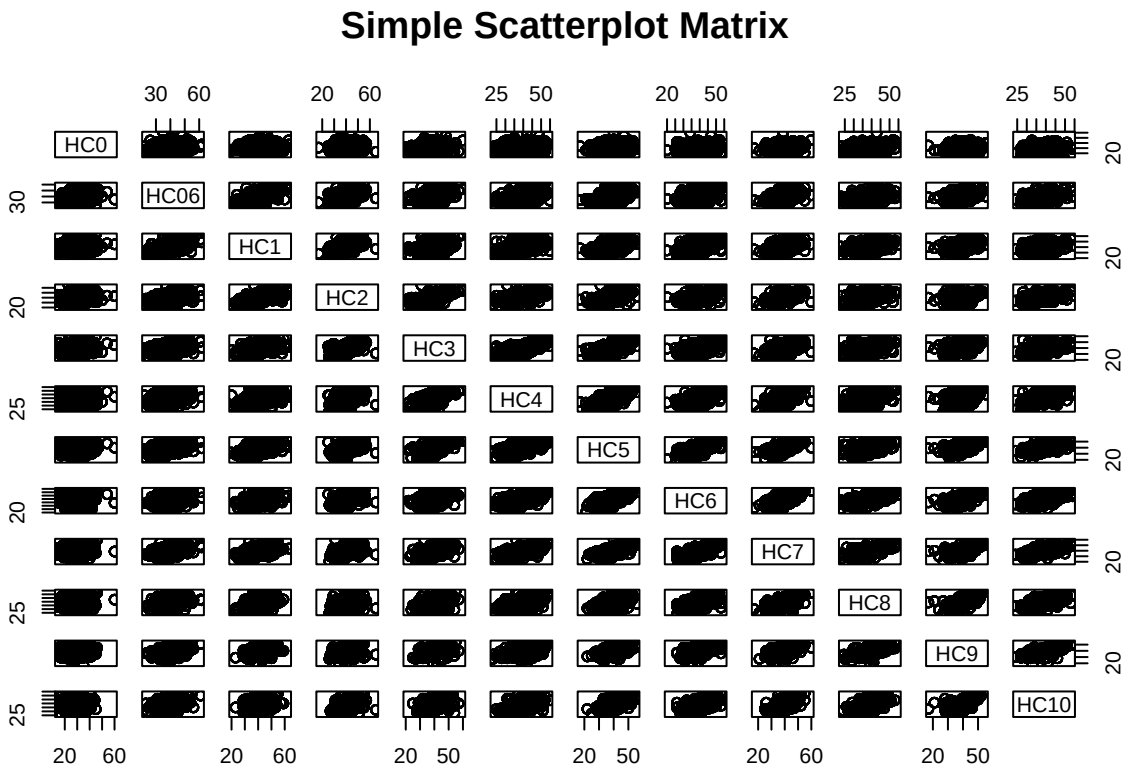
```
##       HC0             HC06            HC1             HC2             HC3
##  Min.   :14.00   Min.   :22.00   Min.   :20.00   Min.   :17.0   Min.   :20.00
##  1st Qu.:28.00   1st Qu.:35.00   1st Qu.:36.00   1st Qu.:36.0   1st Qu.:36.00
##  Median :32.00   Median :38.55   Median :39.00   Median :40.0   Median :39.00
##  Mean   :31.86   Mean   :38.83   Mean   :39.71   Mean   :39.7   Mean   :39.17
##  3rd Qu.:36.00   3rd Qu.:42.00   3rd Qu.:43.00   3rd Qu.:43.0   3rd Qu.:43.00
##  Max.   :60.00   Max.   :61.70   Max.   :63.00   Max.   :65.0   Max.   :60.00
##  NA's   :12                      NA's   :12      NA's   :1044   NA's   :2460
##       HC4             HC5             HC6             HC7
##  Min.   :23.00   Min.   :17.00   Min.   :20.00   Min.   :17.00
##  1st Qu.:35.00   1st Qu.:35.00   1st Qu.:36.00   1st Qu.:35.00
##  Median :39.00   Median :39.00   Median :39.00   Median :39.00
##  Mean   :39.16   Mean   :39.02   Mean   :39.11   Mean   :38.85
##  3rd Qu.:43.00   3rd Qu.:43.00   3rd Qu.:43.00   3rd Qu.:42.00
##  Max.   :55.00   Max.   :56.00   Max.   :55.00   Max.   :60.00
##  NA's   :3768    NA's   :5016    NA's   :6096    NA's   :7140
##       HC8             HC9             HC10            id
##  Min.   :23.00   Min.   :17.00   Min.   :24.10   Min.   :   1.0
##  1st Qu.:35.00   1st Qu.:35.00   1st Qu.:35.00   1st Qu.: 290.8
##  Median :38.05   Median :38.50   Median :38.00   Median : 580.5
```

```
##  Mean   :38.35   Mean   :38.57   Mean   :38.49   Mean   : 580.5
##  3rd Qu.:42.00   3rd Qu.:42.00   3rd Qu.:42.00   3rd Qu.: 870.2
##  Max.   :55.00   Max.   :55.00   Max.   :54.00   Max.   :1160.0
##  NA's   :8064    NA's   :8988    NA's   :9744
##       age             male            cardio           reject
##  Min.   :15.00   Min.   :0.0000   Min.   :0.0000   Min.   :0.0000
##  1st Qu.:36.00   1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.:0.0000
##  Median :48.00   Median :1.0000   Median :0.0000   Median :0.0000
##  Mean   :46.43   Mean   :0.5741   Mean   :0.1784   Mean   :0.3164
##  3rd Qu.:57.00   3rd Qu.:1.0000   3rd Qu.:0.0000   3rd Qu.:1.0000
##  Max.   :76.00   Max.   :1.0000   Max.   :1.0000   Max.   :1.0000
##  NA's   :12
```

```
cor(trenal.wide$HC0,trenal.wide$HC06)
```

```
## [1] NA
```

```
# scatter plot matrix

pairs(~HC0+HC06+HC1+HC2+HC3+HC4+HC5+HC6+HC7+HC8+HC9+HC10,data=trenal.wide,
   main="Simple Scatterplot Matrix")
```



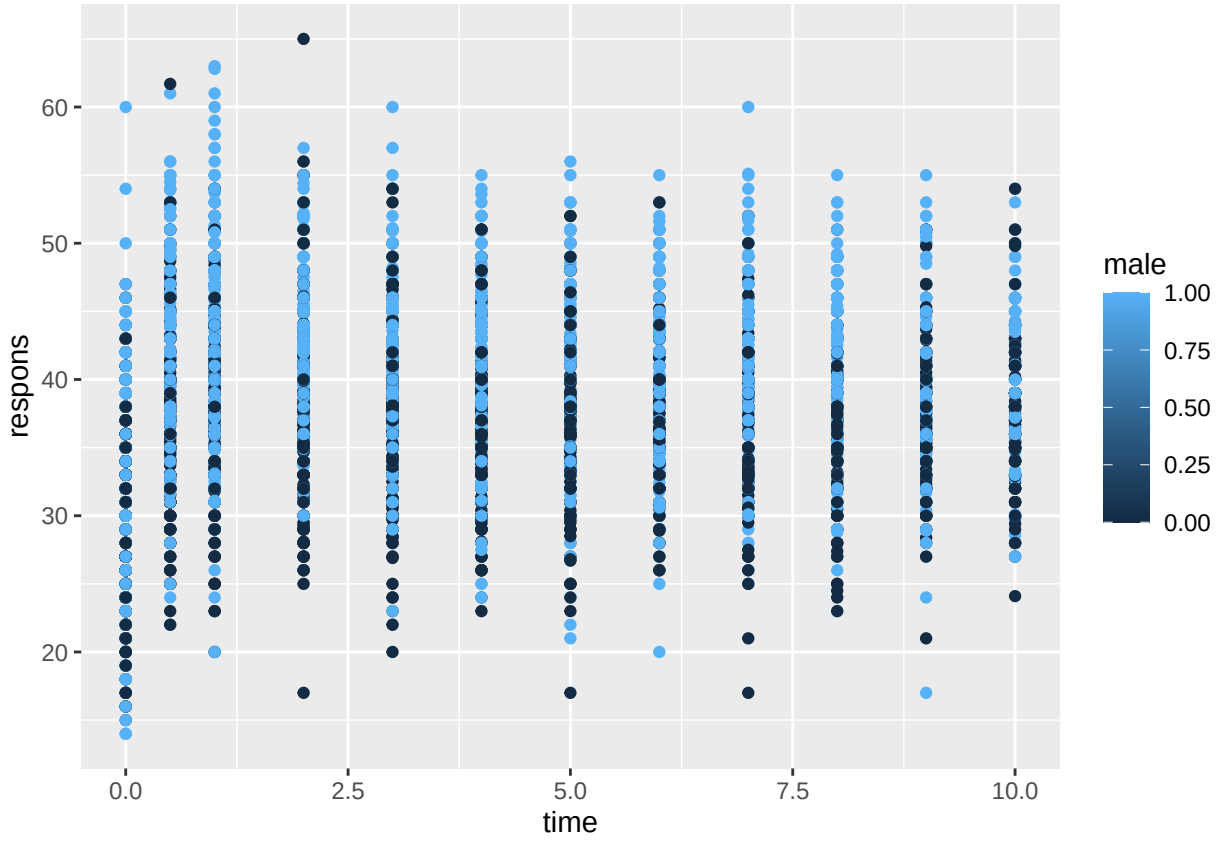

```
#Lm
lm<-lm(respons~time,data=data)
summary(lm)
```

```
##
## Call:
```

```
## lm(formula = respons ~ time, data = data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -23.3368  -3.8633   0.0393   3.8206  27.1367
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 37.33685    0.09410   396.8   <2e-16 ***
## time         0.26322    0.02073    12.7   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 6.023 on 9556 degrees of freedom
##   (4362 observations deleted due to missingness)
## Multiple R-squared:  0.01659,    Adjusted R-squared:  0.01648
## F-statistic: 161.2 on 1 and 9556 DF,  p-value: < 2.2e-16
```

```
#Plot individual data
ggplot(data, aes(x=time, y=respons, group=male,color=male)) + geom_point()
```

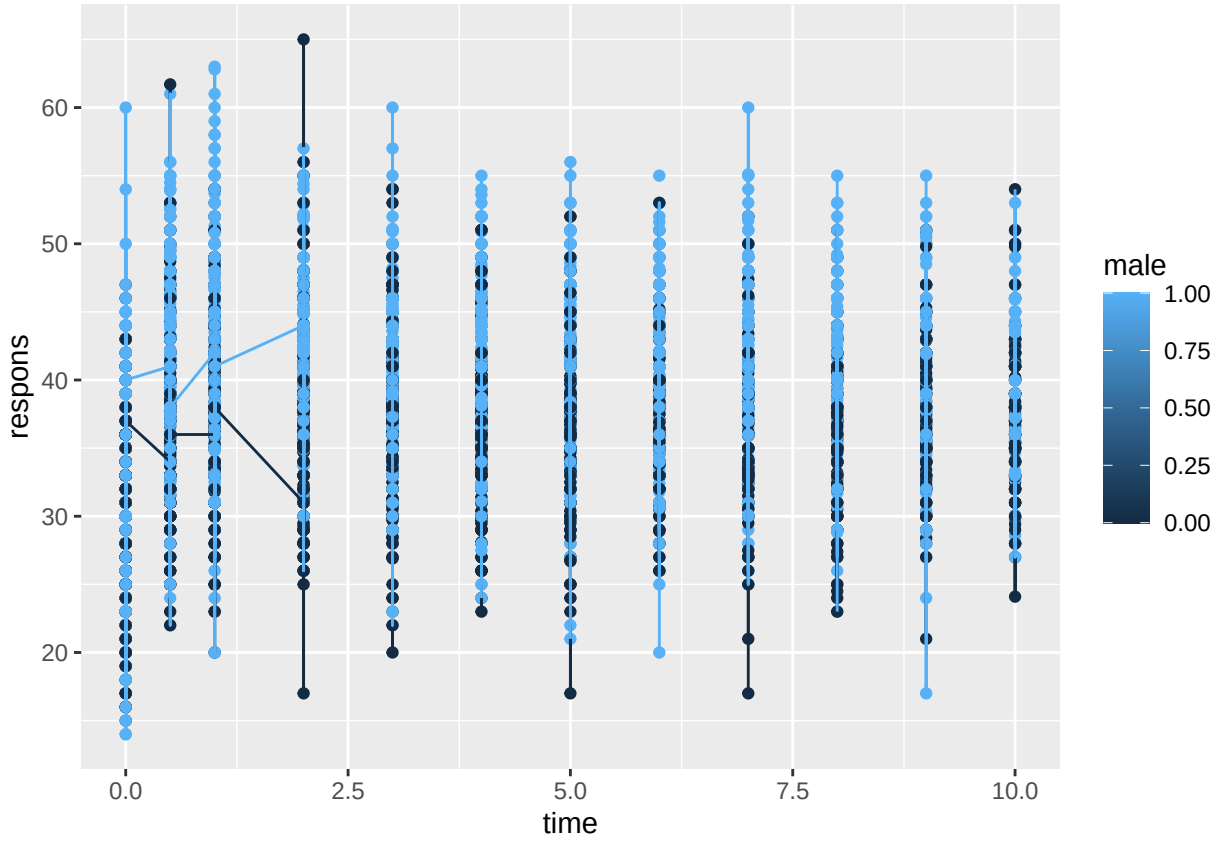
```
## Warning: Removed 4362 rows containing missing values (`geom_point()`).
```




```
#Spaghetti Plot
ggplot(data, aes(x=time, y=respons, group=male,color=male)) + geom_point() +geom_line()
```

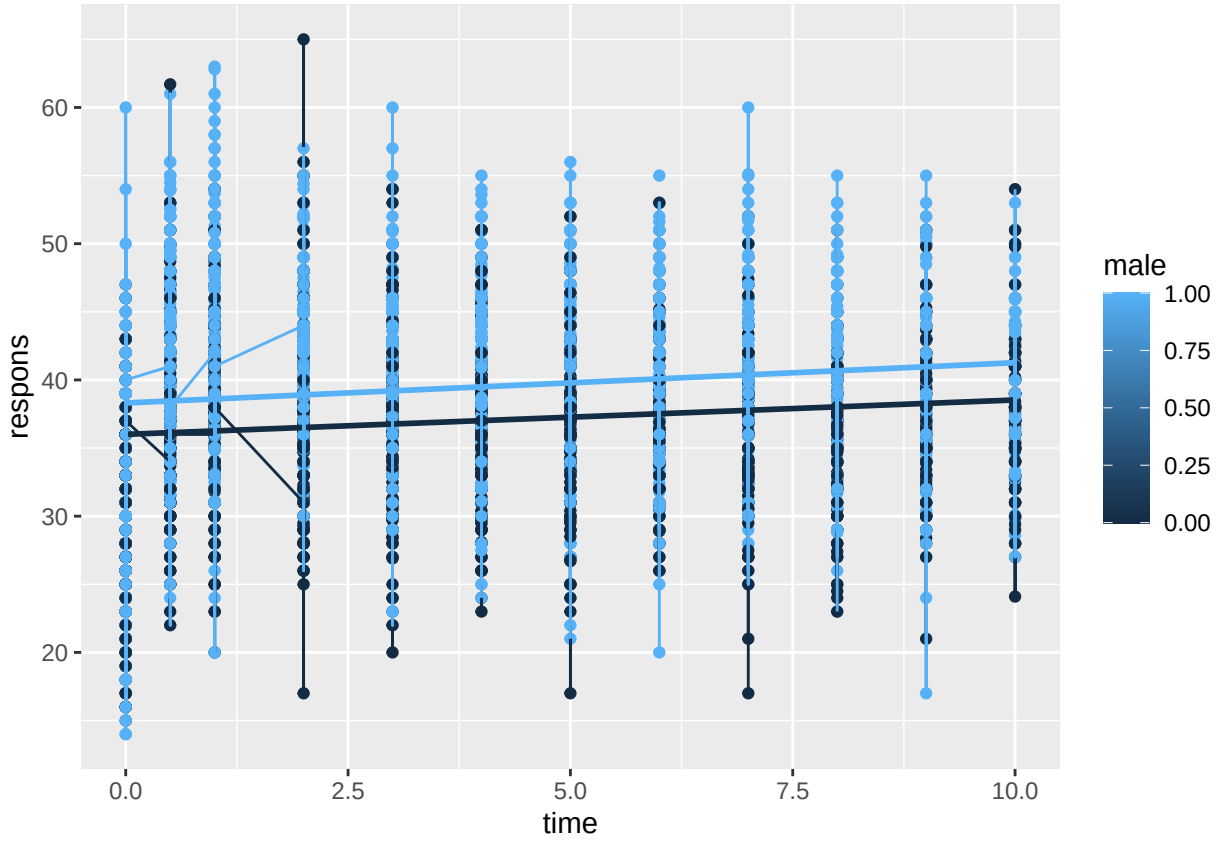
```
## Warning: Removed 4362 rows containing missing values (`geom_point()`).
```

```
## Warning: Removed 638 rows containing missing values (`geom_line()`).
```




```
#Spaghetti with fitted lines
ggplot(data, aes(x=time, y=respons, group=male,color=male)) + geom_point()+ geom_smooth(method="lm",se=
```

```
## `geom_smooth()` using formula = 'y ~ x'
## Warning: Removed 4362 rows containing non-finite values (`stat_smooth()`).
## Warning: Removed 4362 rows containing missing values (`geom_point()`).
## Warning: Removed 638 rows containing missing values (`geom_line()`).
```



Linear mixed effect model Fixed effect could be time, gender, age, reject, cardio Random effect could be

```
#lme
#data = trenal.long
#lme <- lme(repsons ~ time + age ,data=data)
#lme<-lme(respons~time+age+male+reject+cardio,data=data)
#summary(lme)

#newdata<-data.frame(ID=c(1,2,3,4,5),week=c(3,3,3,3,3))
#newdata$prediction<-predict(lm,newdata=newdata)
#newdata
#predict(lme,newdata=newdata,level=0:1)
```