

# 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 Haematocrit 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   :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 measurements in the 12 time point (0, 0.5, 1, 2, ..., 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, ..., 10 is one-to-one correspondent to j 1, 2, 3, ..., 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)

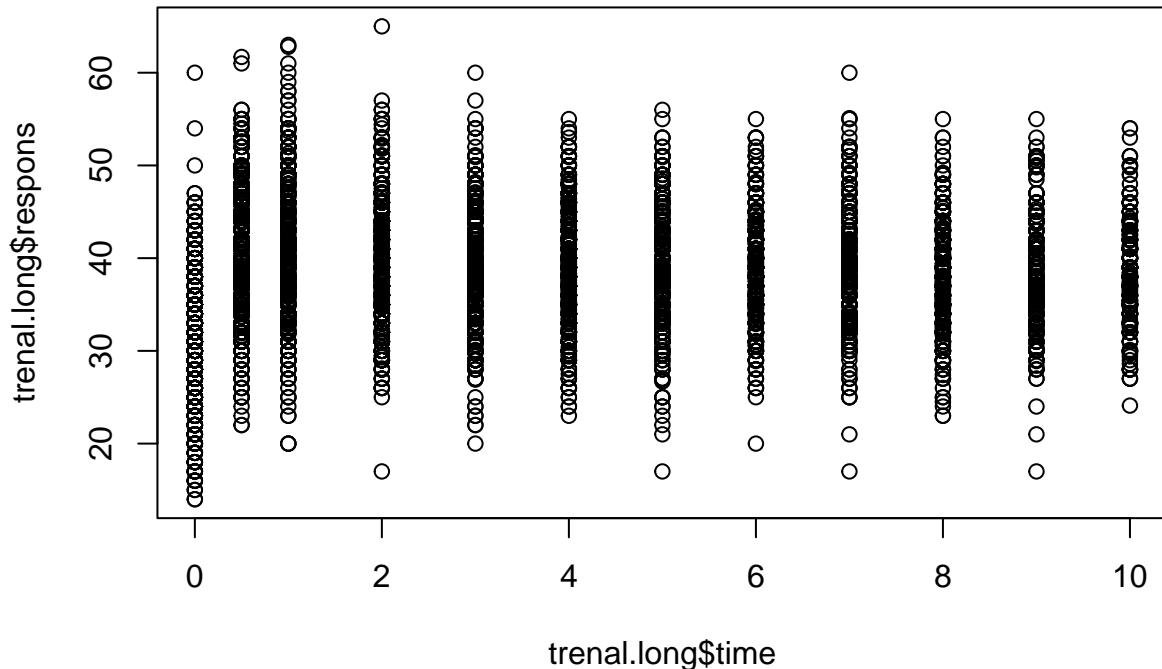
##      id          age       male   cardio   reject      j
## 1   : 12   Min.   :15.00 0:5928  0:11436  0:9516  1   :1160
## 2   : 12  1st Qu.:36.00 1:7992  1: 2484  1:4404  2   :1160
## 3   : 12 Median  :48.00           3           3           3   :1160
## 4   : 12 Mean   :46.43           4           4           4   :1160
## 5   : 12 3rd Qu.:57.00           5           5           5   :1160
## 6   : 12 Max.   :76.00           6           6           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
plot(trenal.long$time,trenal.long$respons)

```



```

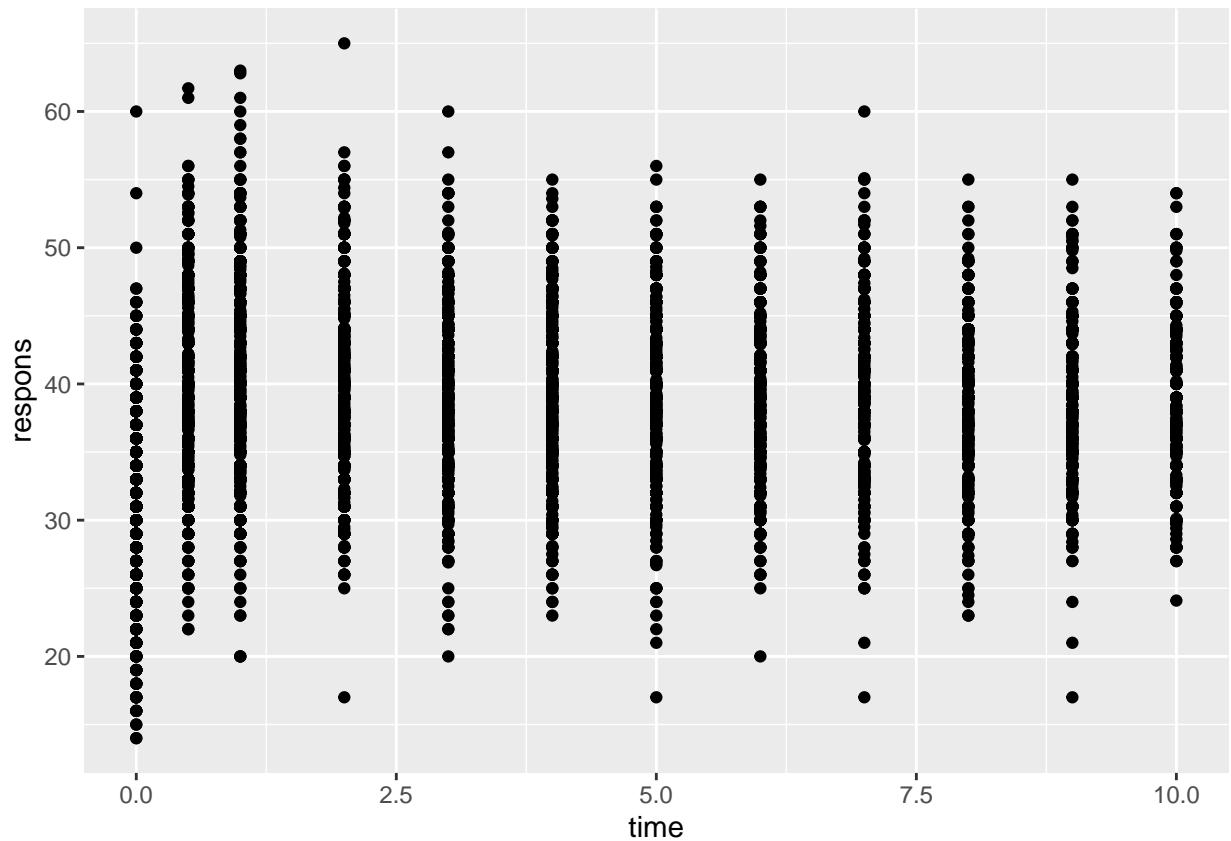
library(ggplot2)
library(nlme)

##
## Attaching package: 'nlme'
## The following object is masked from 'package:dplyr':
##     collapse
library(lme4)

## Loading required package: Matrix
##
## Attaching package: 'lme4'
## The following object is masked from 'package:nlme':
##     lmList
#Plot data
ggplot(data, aes(x=time, y=responses)) + geom_point()

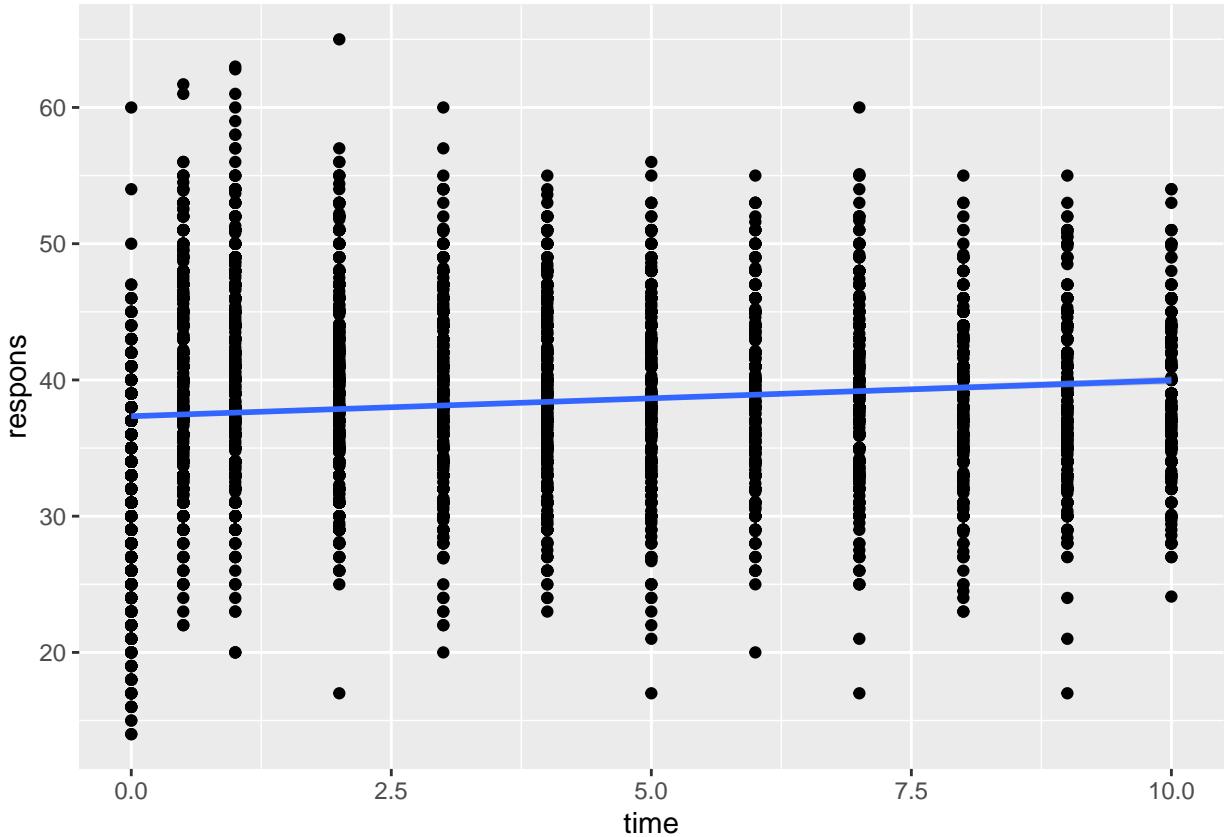
## Warning: Removed 4362 rows containing missing values (`geom_point()`).

```



```
#Plot data with lm line
ggplot(data, aes(x=time, y=responses)) + 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()`).
```



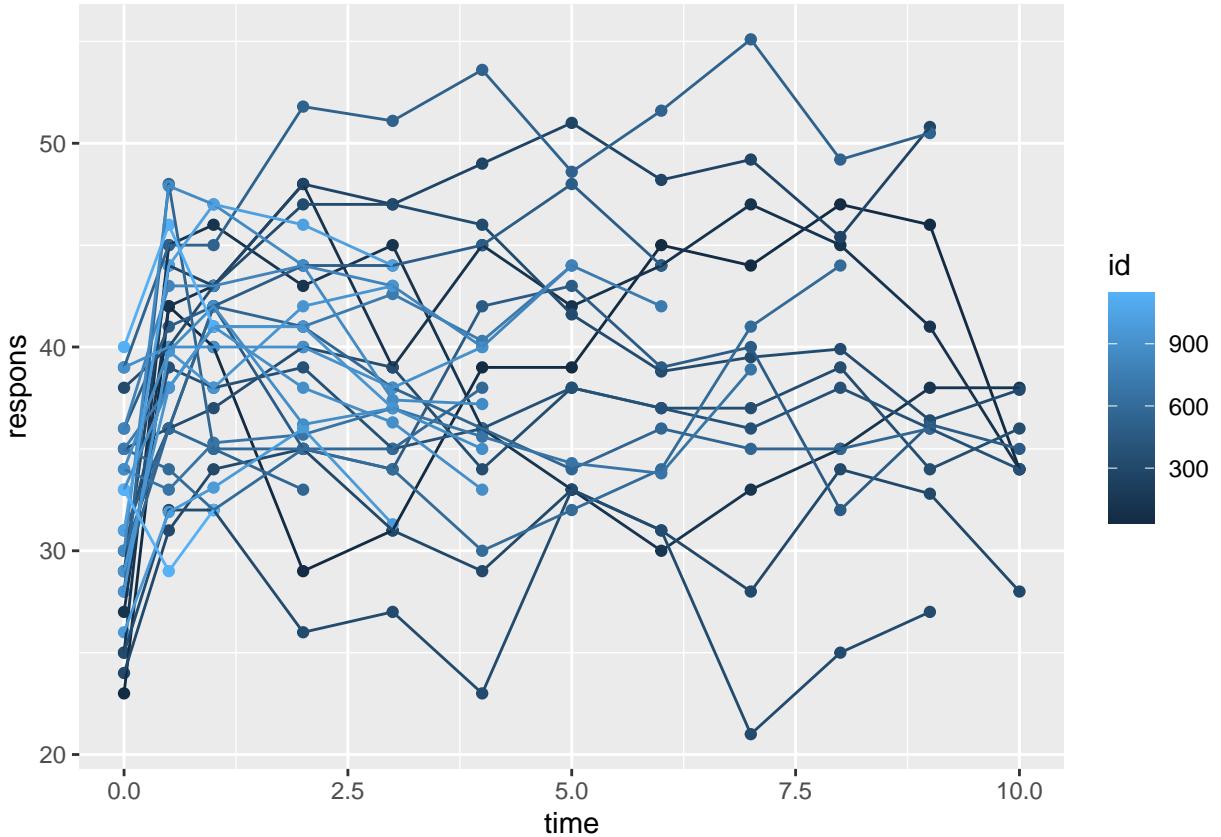
### 1.3 List of Hypotheses to be tested by the data

```
#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)), ]
```

```
#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=responses, group=id, color=id)) + geom_point() +geom_line()
```

Spaghetti Plot the response over time with the different persons

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

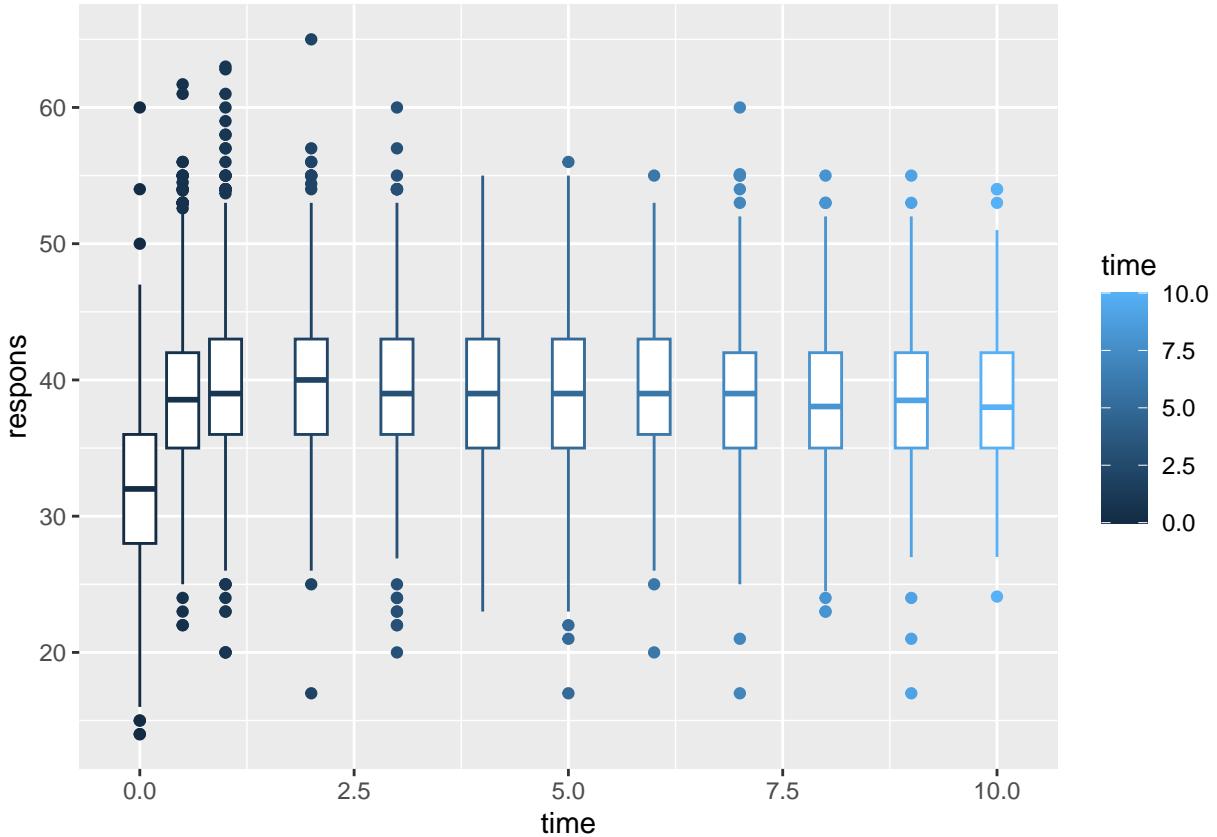


```
#ggplot(data.selected, aes(x=time, y=na.pass(respons), group=id,color=id)) + geom_point() +geom_line()
```

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

### Bar plot response over time

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

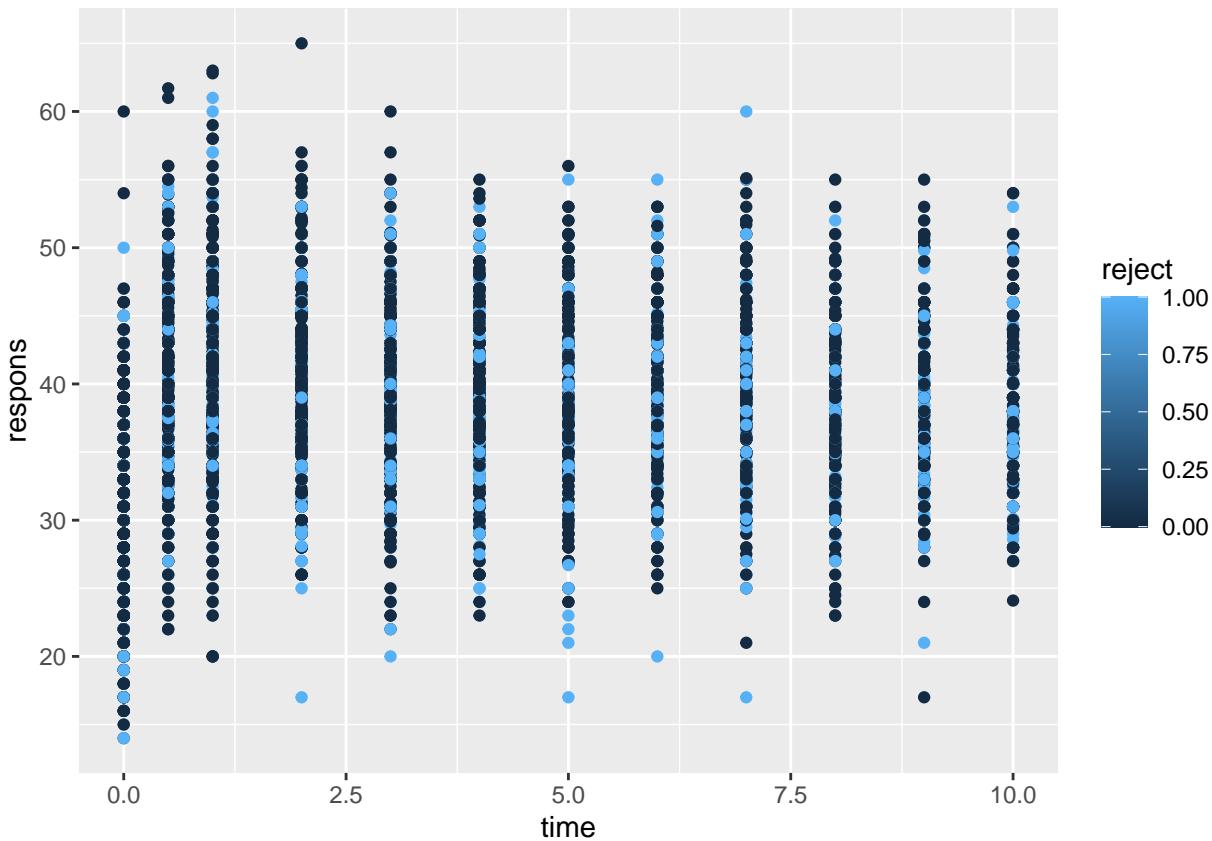


```
#### Hypothesis one HC level will change with time differently if the REJECT is different
```

```
#Plot individual data
```

```
ggplot(data, aes(x=time, y=responses, group=reject, color=reject)) + geom_point()
```

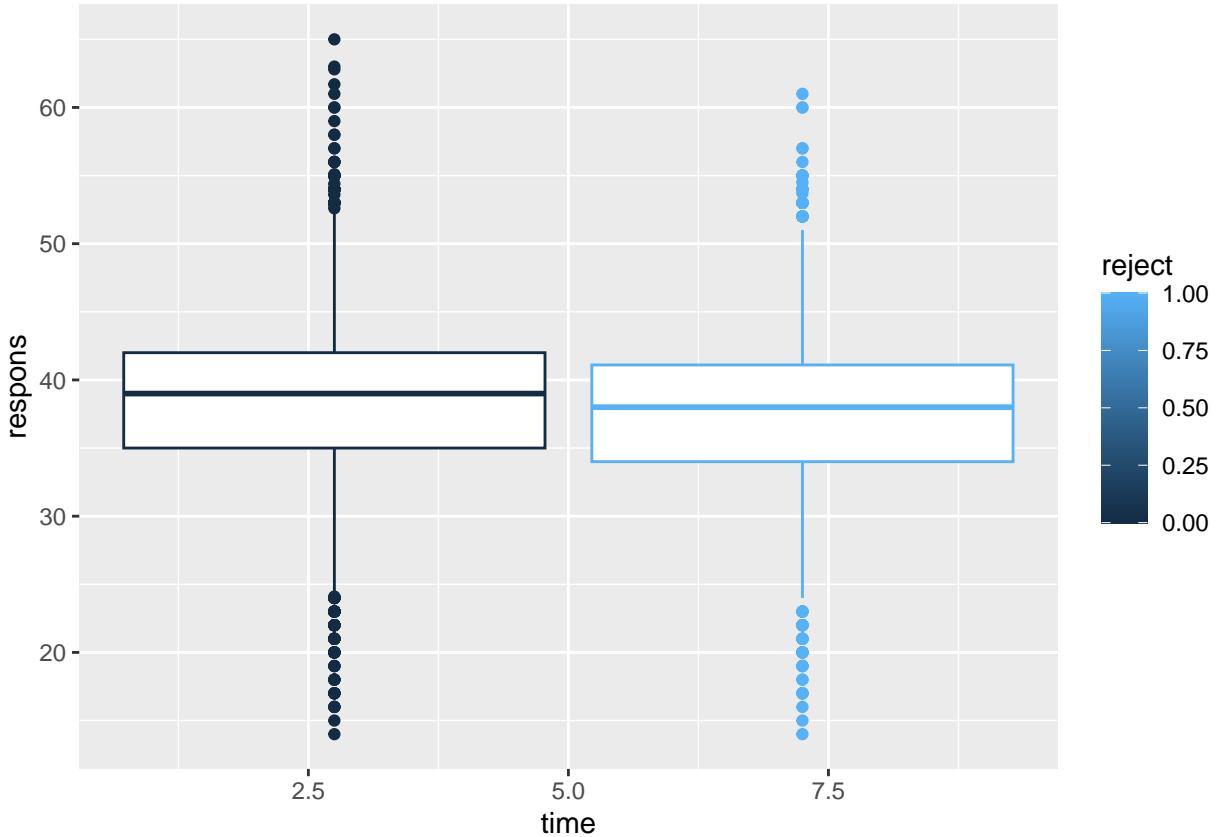
```
## Warning: Removed 4362 rows containing missing values (`geom_point()`).
```



```
##### Bar plot
```

```
# Box plot
p <- ggplot(data, aes(x=time, y=responses, 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)

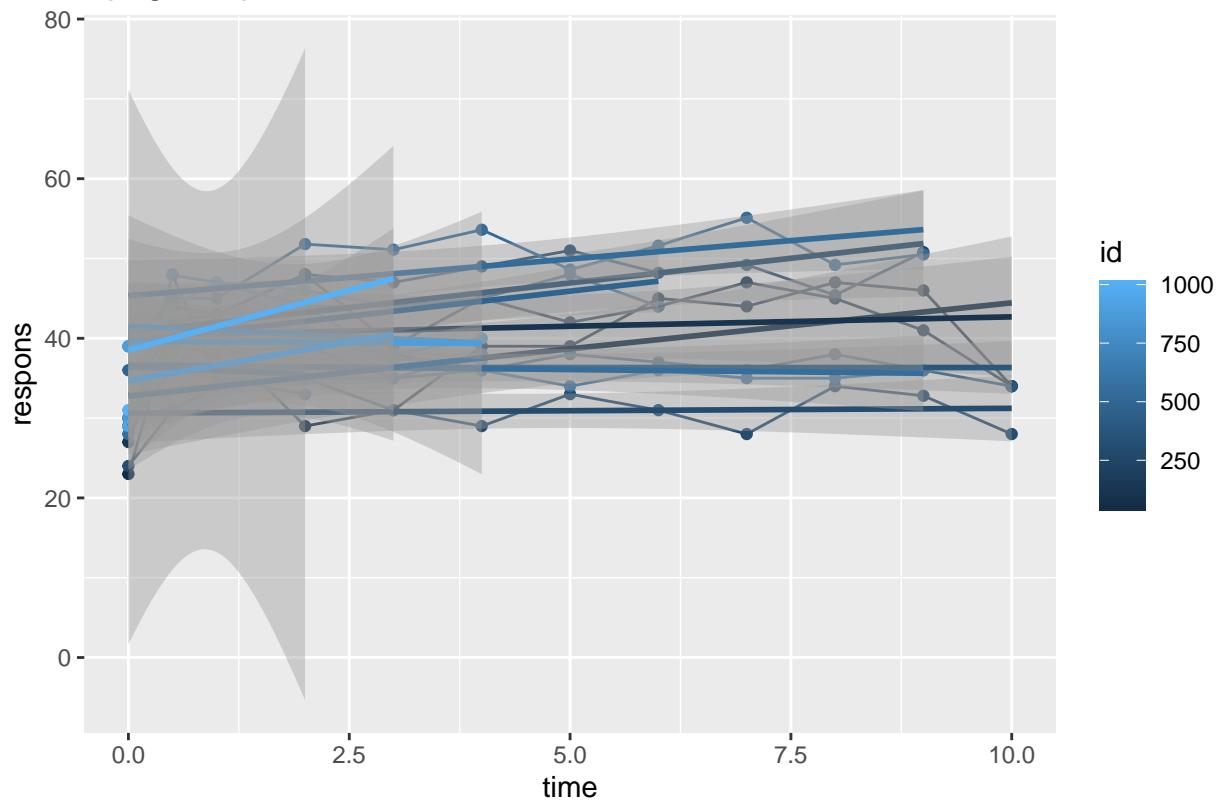
```
data.male = data[(data$male == "1"), ]
data.female = data[(data$male == "0"), ]
data.male.selected = data[(data$male == "1" & data$id %in% c(selected)), ]
data.female.selected = data[(data$male == "0" & data$id %in% c(selected)), ]
```

```
ggplot(data.male.selected, aes(x=time, y=responses, group=id, color=id)) + geom_point() + geom_line() + ggtitle("Spaghetti plot for males")
```

Spaghetti plots stratified by variables gender male

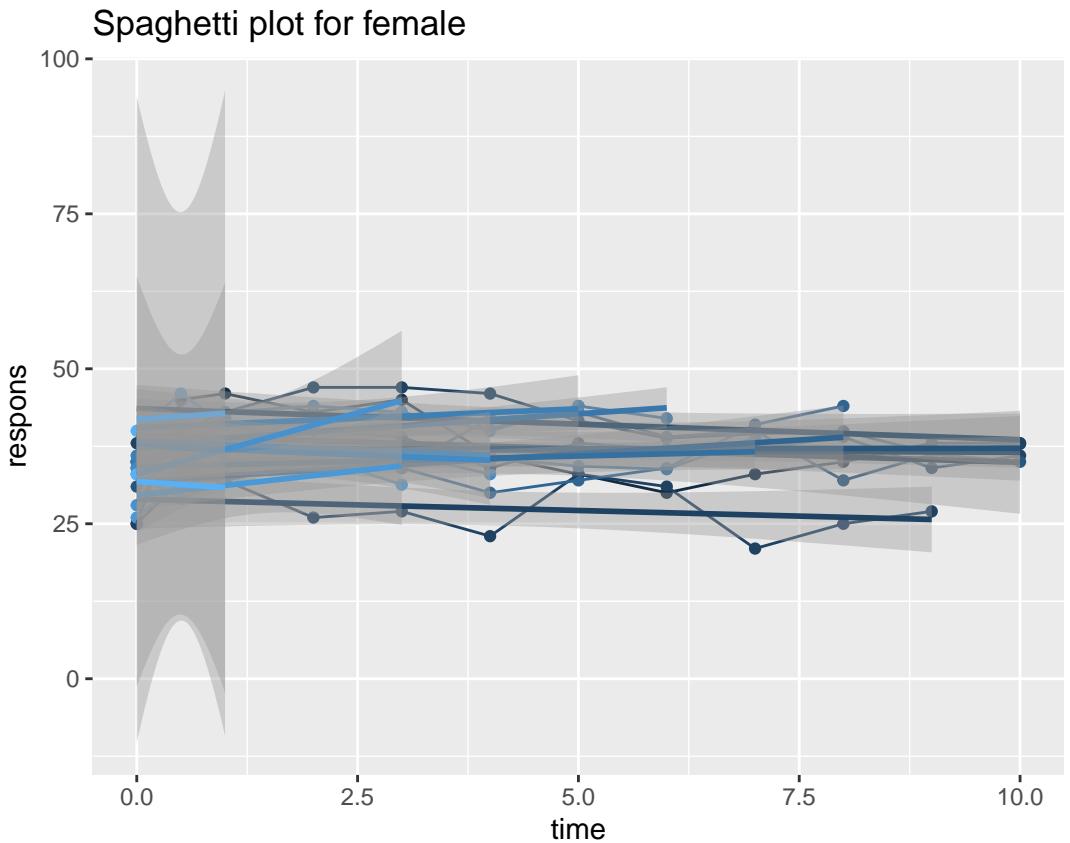
```
## `geom_smooth()` using formula = 'y ~ x'
## Warning: Removed 47 rows containing non-finite values (`stat_smooth()`).
## Warning: Removed 47 rows containing missing values (`geom_point()`).
## Warning: Removed 47 rows containing missing values (`geom_line()`).
```

Spaghetti plot for male



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

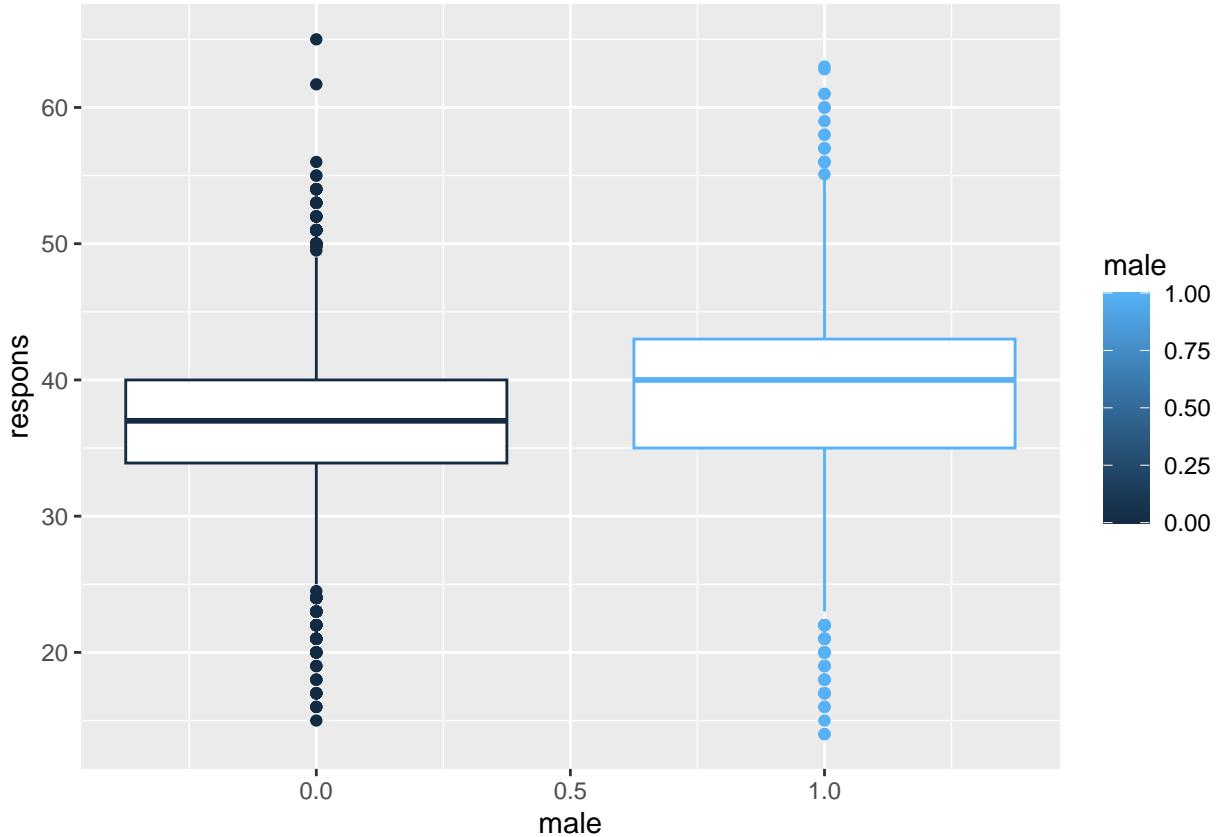
## `geom_smooth()` using formula = 'y ~ x'
## Warning: Removed 59 rows containing non-finite values (`stat_smooth()`).
## Warning: Removed 59 rows containing missing values (`geom_point()`).
## Warning: Removed 59 rows containing missing values (`geom_line()`).
```



```
##### Box plot
```

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

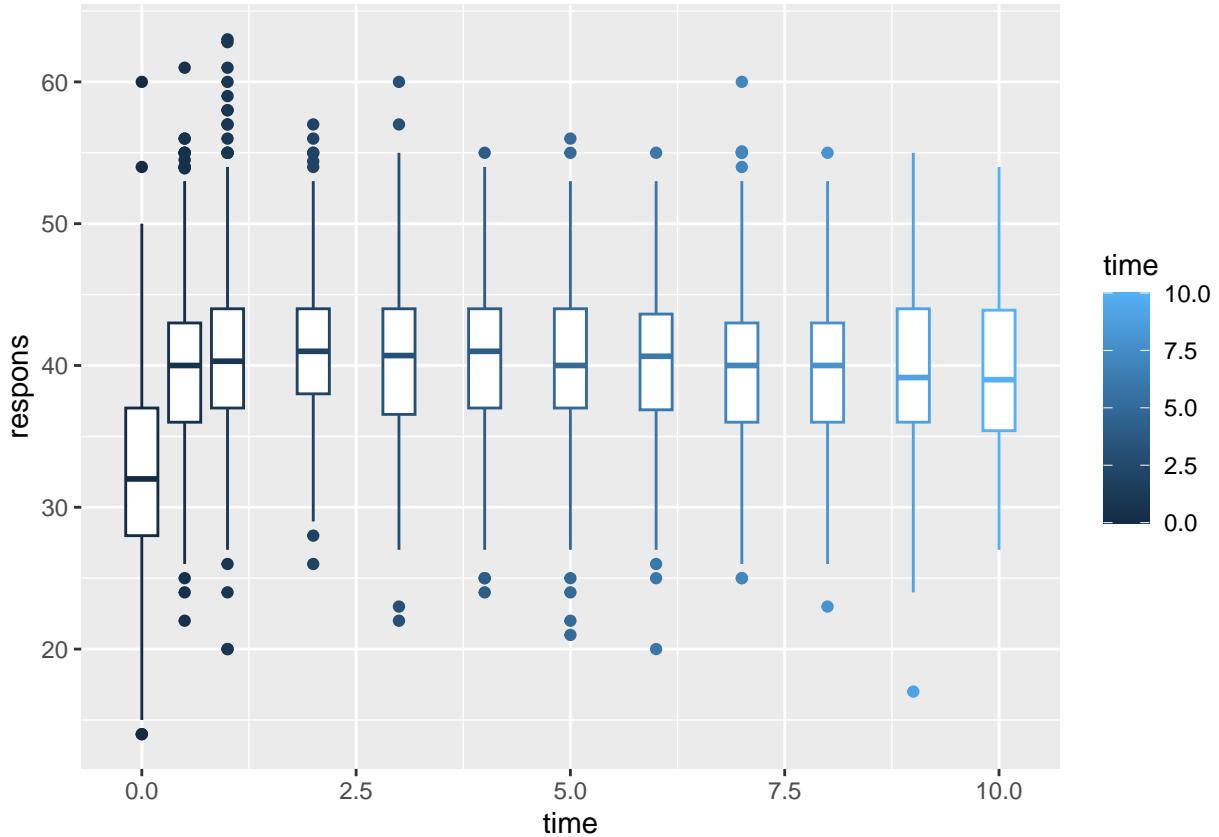
## Warning: Removed 4362 rows containing non-finite values (`stat_boxplot()`).
```



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

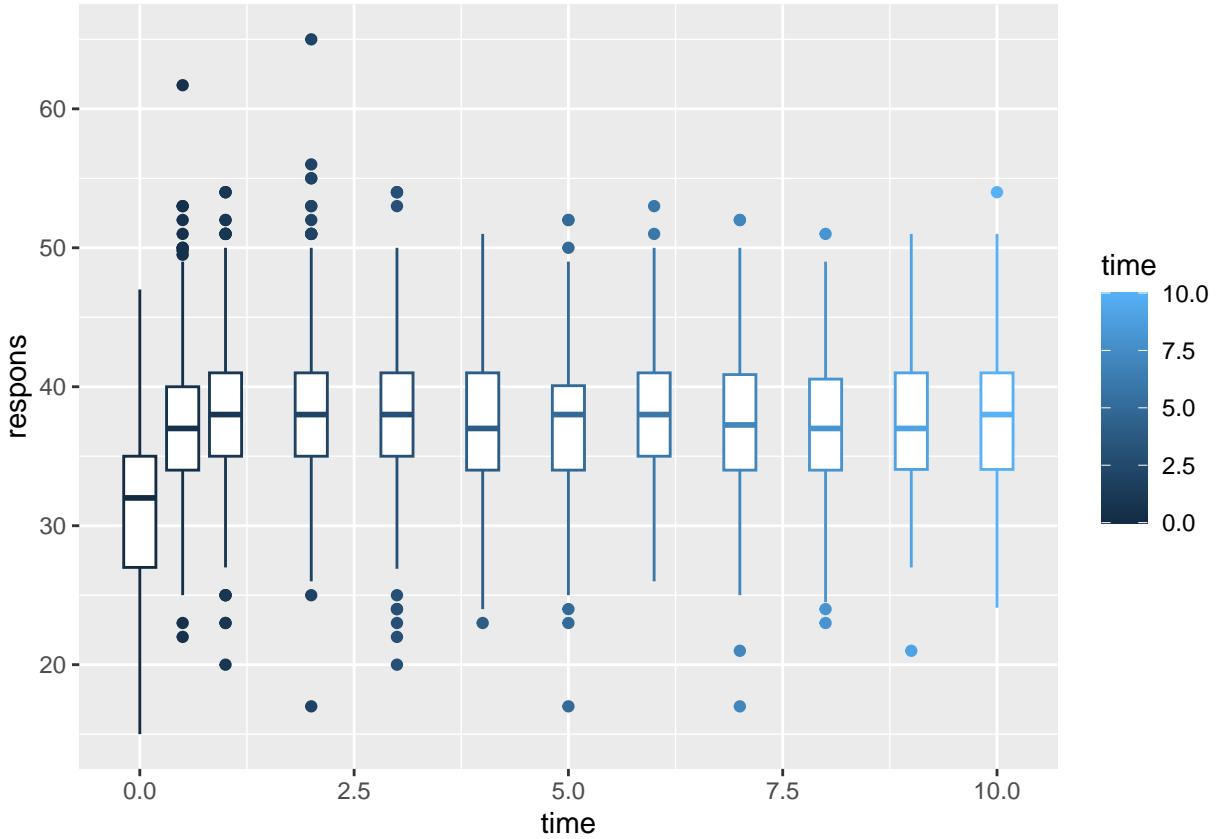
```
p.box.male <- ggplot(data.male, aes(x=time, y=responses, group = time, color = time)) +
  geom_boxplot()
p.box.male
```

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



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

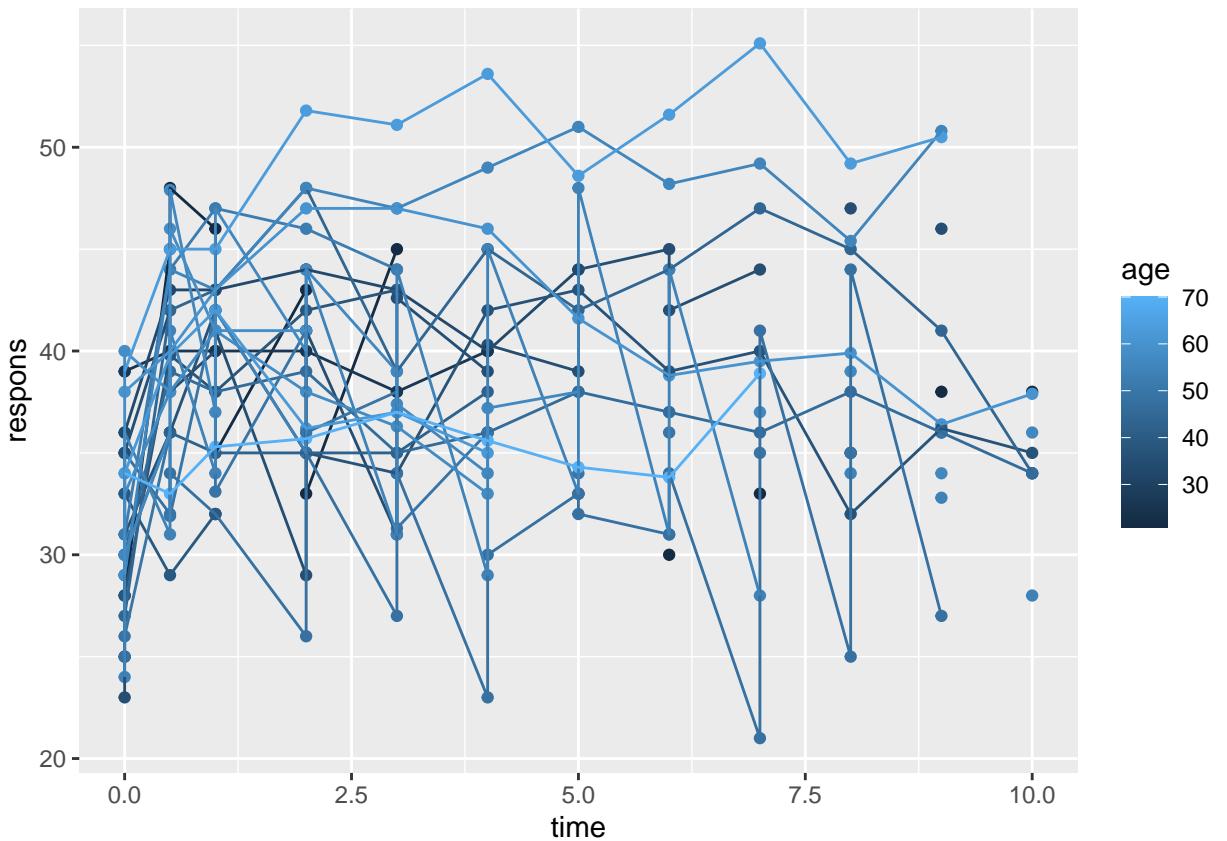
```
## Warning: Removed 1715 rows containing non-finite values (`stat_boxplot()`).
```



**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=responses, 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=responses, group = age, color = age)) +
  geom_boxplot()
p

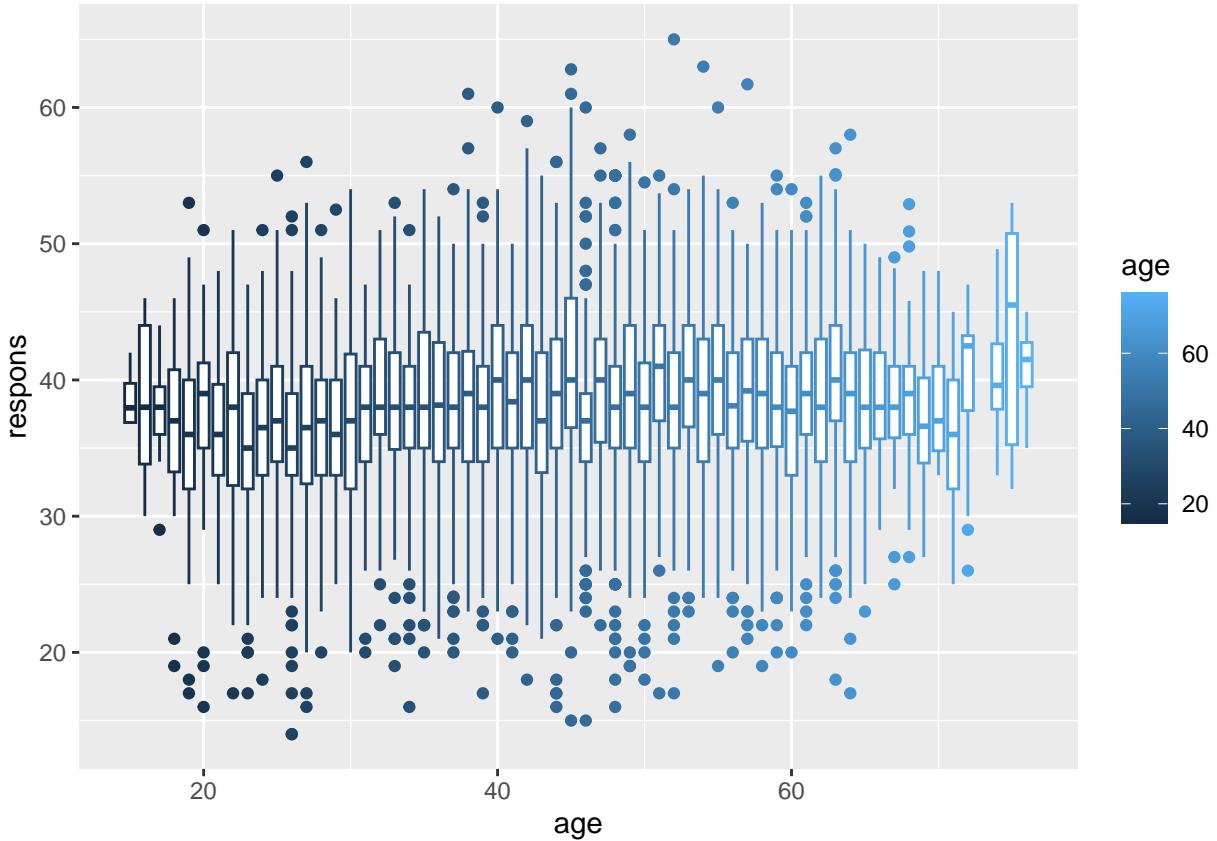
```

**Box plot**

```

## Warning: Removed 12 rows containing missing values (`stat_boxplot()`).
## Warning: Removed 4357 rows containing non-finite values (`stat_boxplot()`).

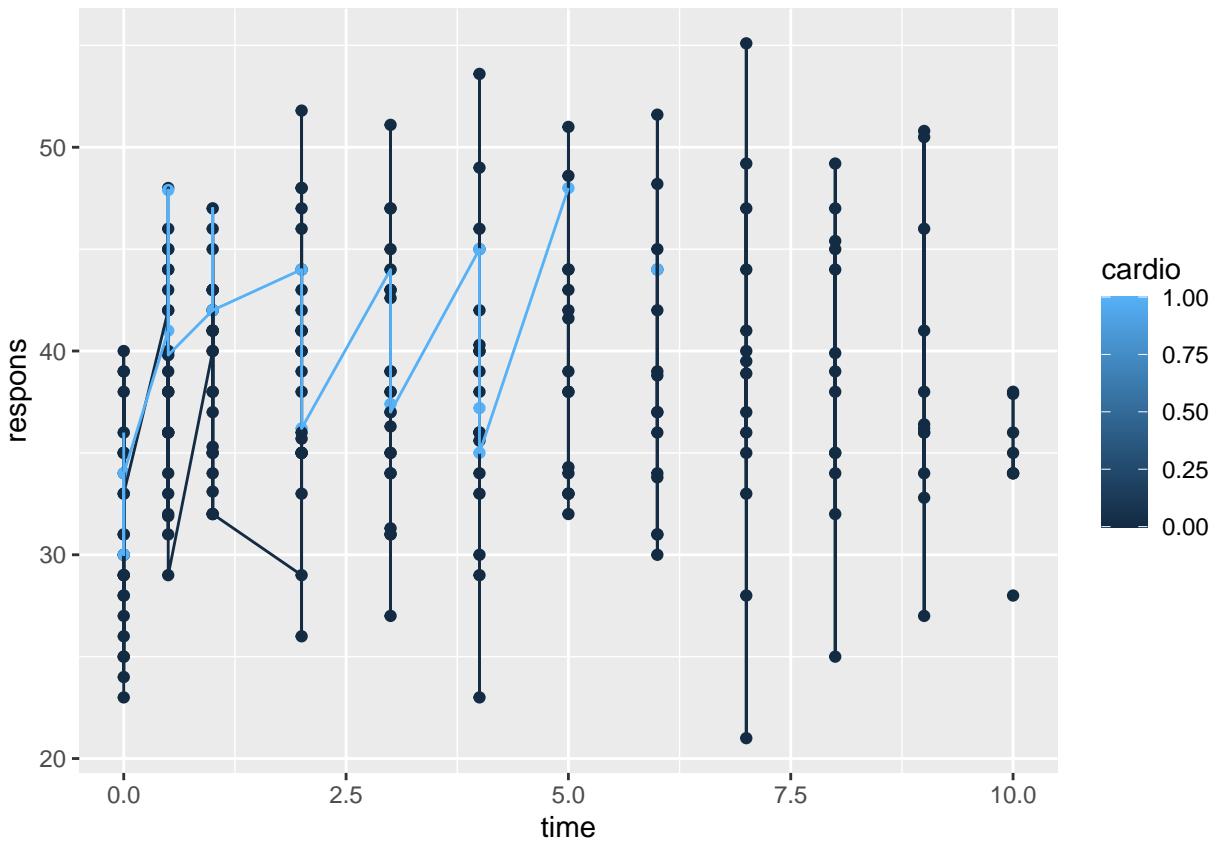
```



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

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

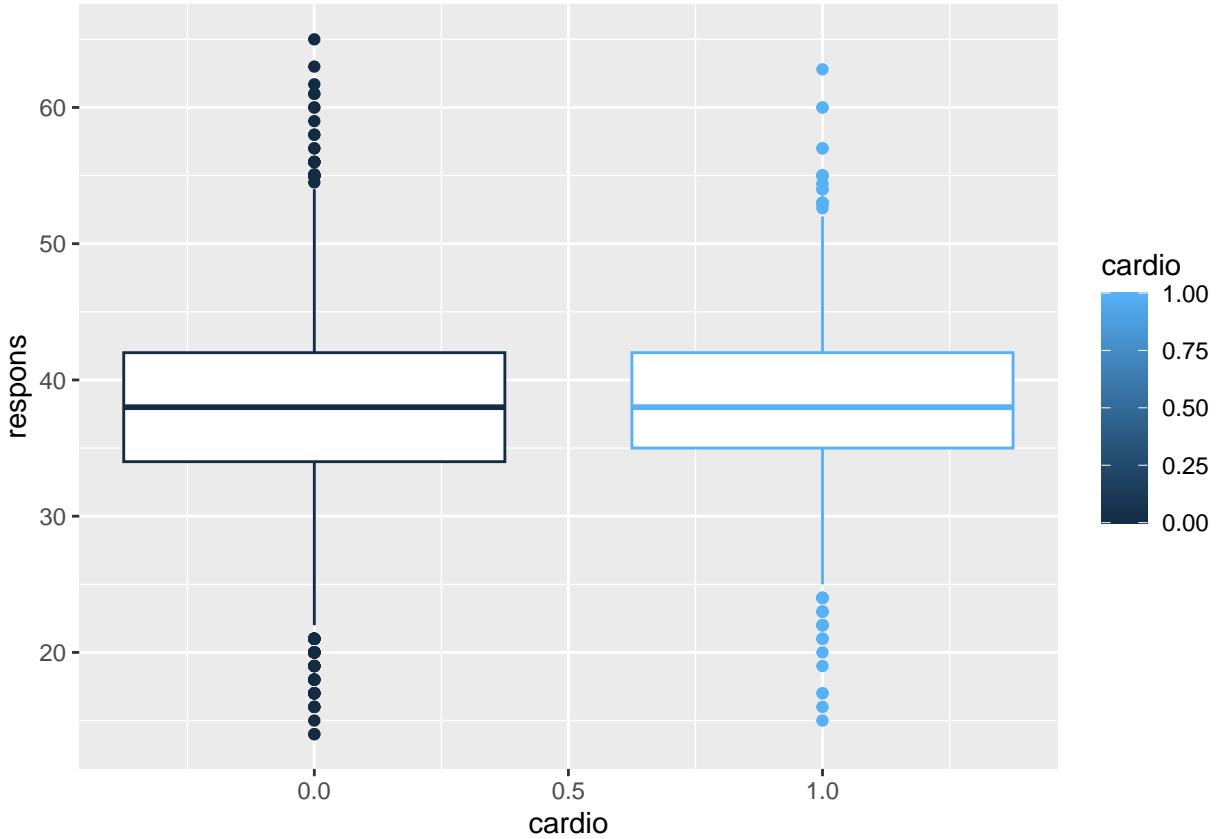
## Warning: Removed 106 rows containing missing values (`geom_point()`).
## Warning: Removed 30 rows containing missing values (`geom_line()`).
```



```
##### Bar plot
```

```
p <- ggplot(data, aes(x=cardio, y=responses, 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)
```

```
##      HCO          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    :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
##      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)

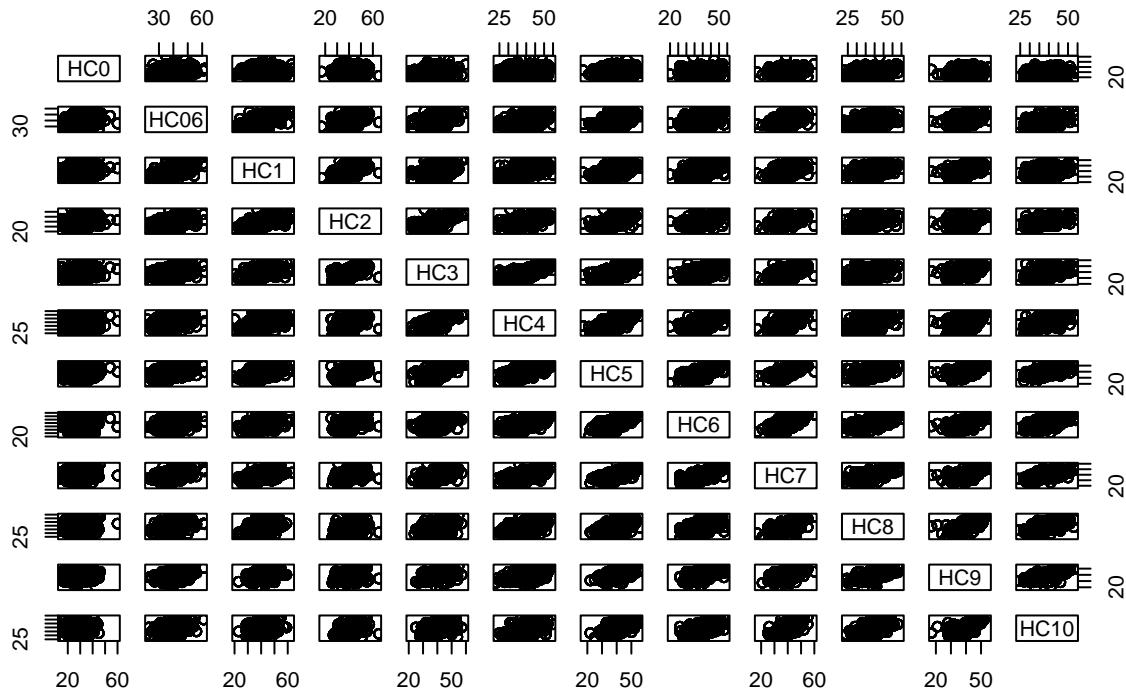
## [1] NA

# scatter plot matrix

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

```

## Simple Scatterplot Matrix



```

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

```

```

##
## Call:

```

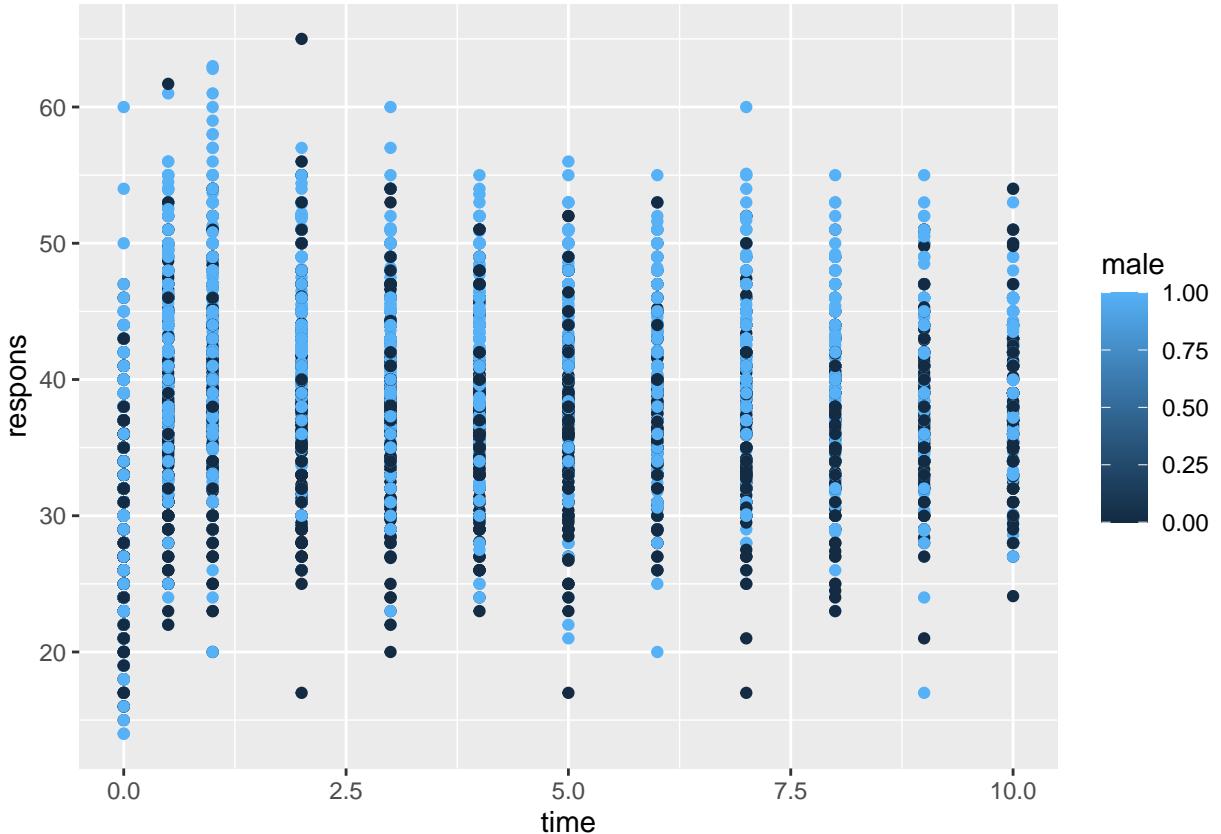
```

## 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=maale, color=maale)) + geom_point()

```

## Warning: Removed 4362 rows containing missing values (`geom\_point()`).



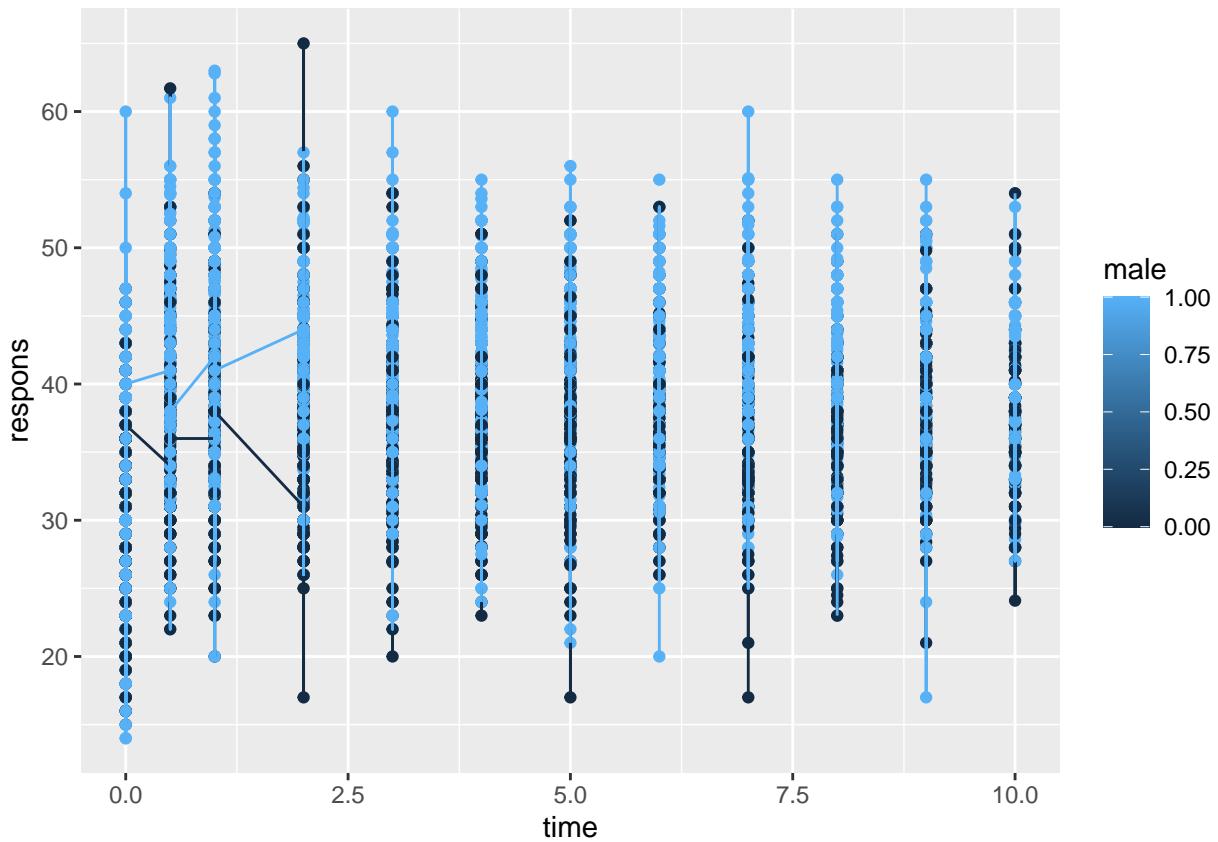
```

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

```

## Warning: Removed 4362 rows containing missing values (`geom\_point()`).

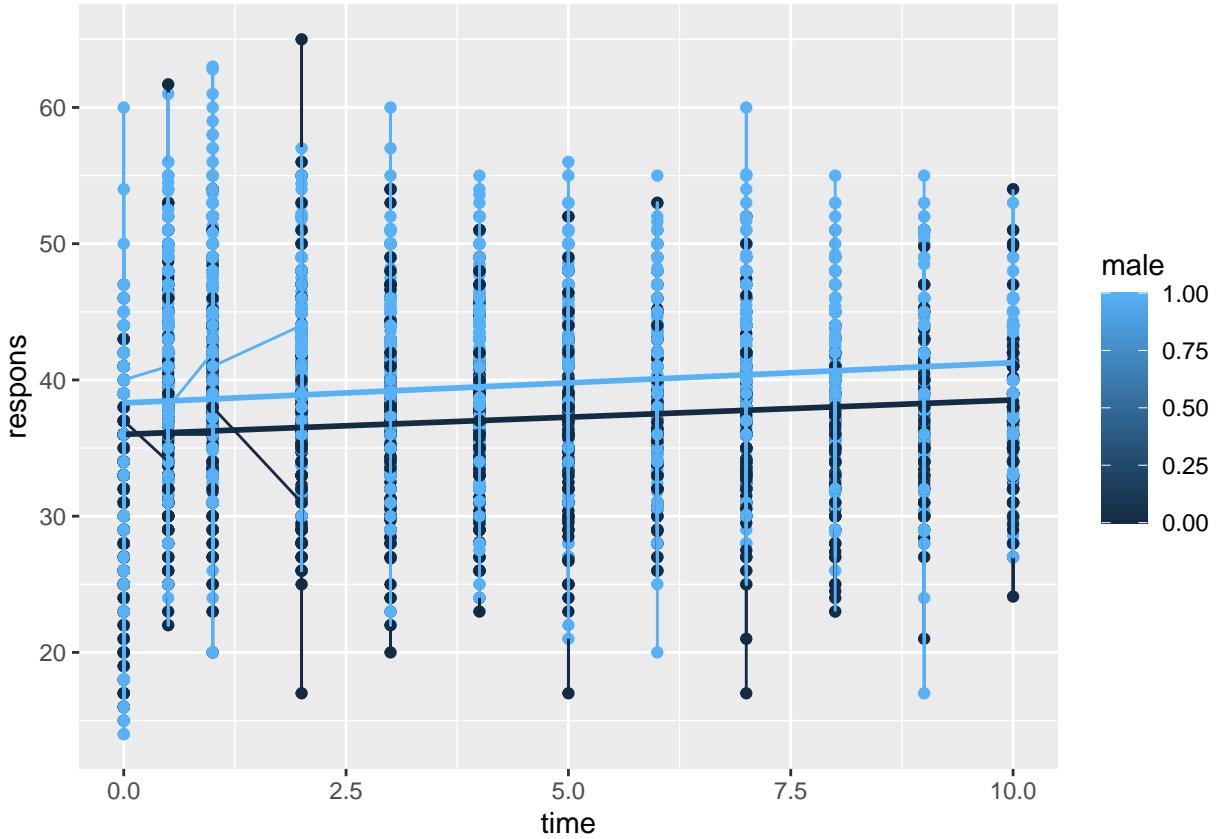
```
## Warning: Removed 638 rows containing missing values (`geom_line()`).
```



#Spaghetti with fitted lines

```
ggplot(data, aes(x=time, y=responses, 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)
```