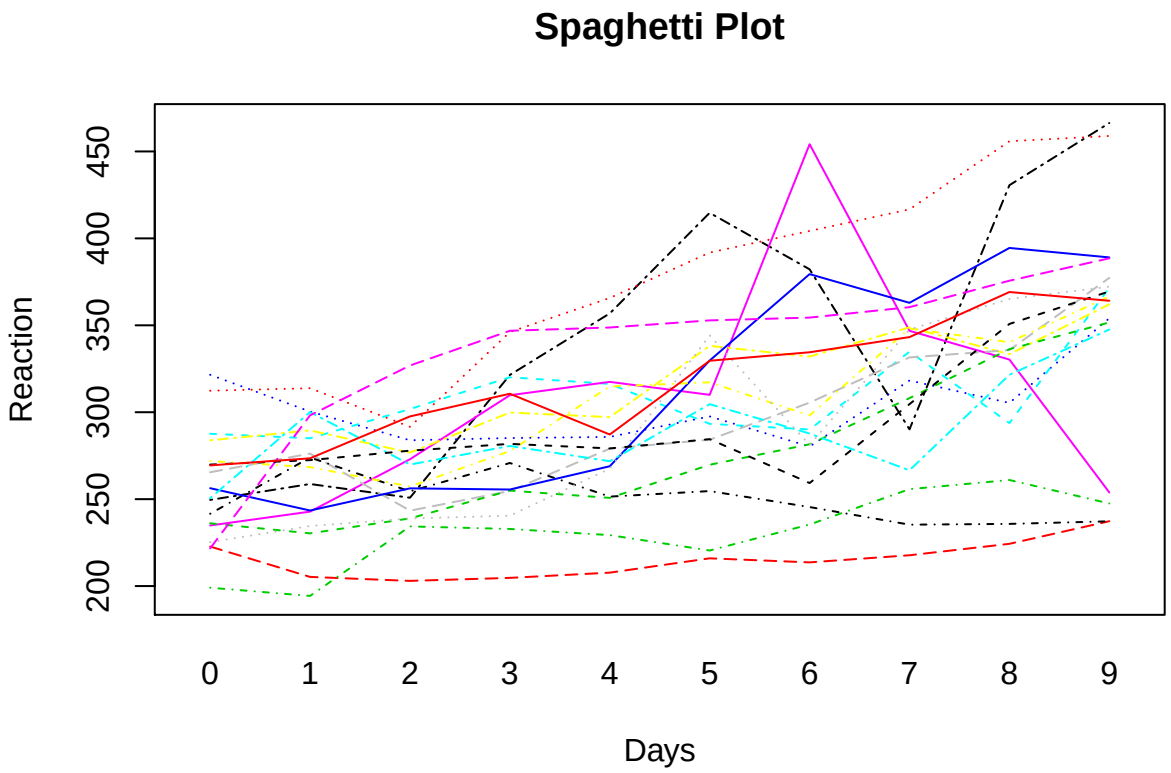
Nina_sleep

Exploratory analysis

```
sleep <- read.table('../sleep.txt')
```

Spaghetti Plot

```
n <- sleep$Subject %>% unique %>% length
interaction.plot(sleep$Days, sleep$Subject, sleep$Reaction, xlab="Days", ylab="Reaction", col=c(1:n), l
```



Already from this plot you can assume that the reaction time is increasing with increasing number of days of sleep deprivation.

Descriptive Statistics

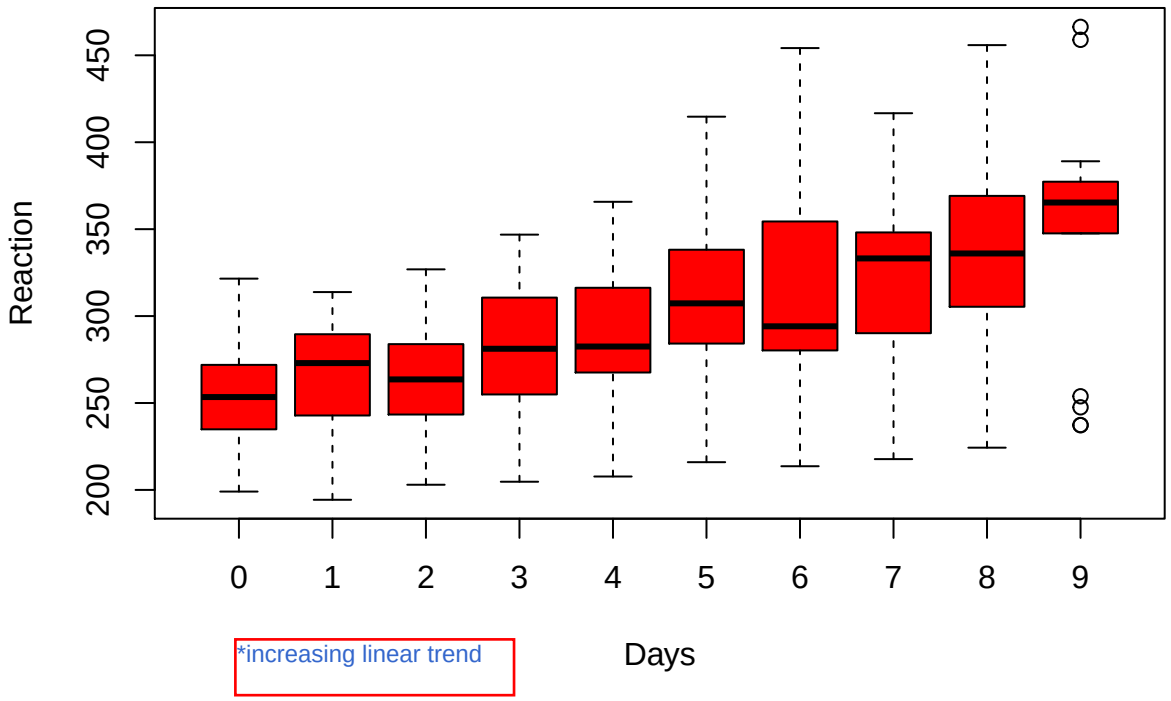
Overview

```
sleep.mean <- tapply(sleep$Reaction, list(sleep$Days), mean)
sleep.sd <- tapply(sleep$Reaction, list(sleep$Days), sd)
sleep.var <- tapply(sleep$Reaction, list(sleep$Days), var)
sleep.n <- table(sleep$Days)

overview <- cbind(c(0:9), sleep.mean, sleep.sd, sleep.var, sleep.n)
colnames(overview) <- c('Days', 'Mean', 'SD', 'Var', 'n')
round(overview, 2)
```

```
##   Days   Mean    SD     Var  n
## 0    0 256.65 32.13 1032.30 18
## 1    1 264.50 33.43 1117.59 18
## 2    2 265.36 29.47  868.68 18
## 3    3 282.99 38.86 1509.92 18
## 4    4 288.65 42.54 1809.47 18
## 5    5 308.52 51.77 2680.09 18
## 6    6 312.18 63.17 3990.92 18
## 7    7 318.75 50.10 2510.41 18
## 8    8 336.63 60.20 3624.01 18
## 9    9 350.85 66.99 4487.15 18
```

Boxplot

```
boxplot(Reaction~Days, data=sleep, xlab='Days', ylab='Reaction', col=2)
```



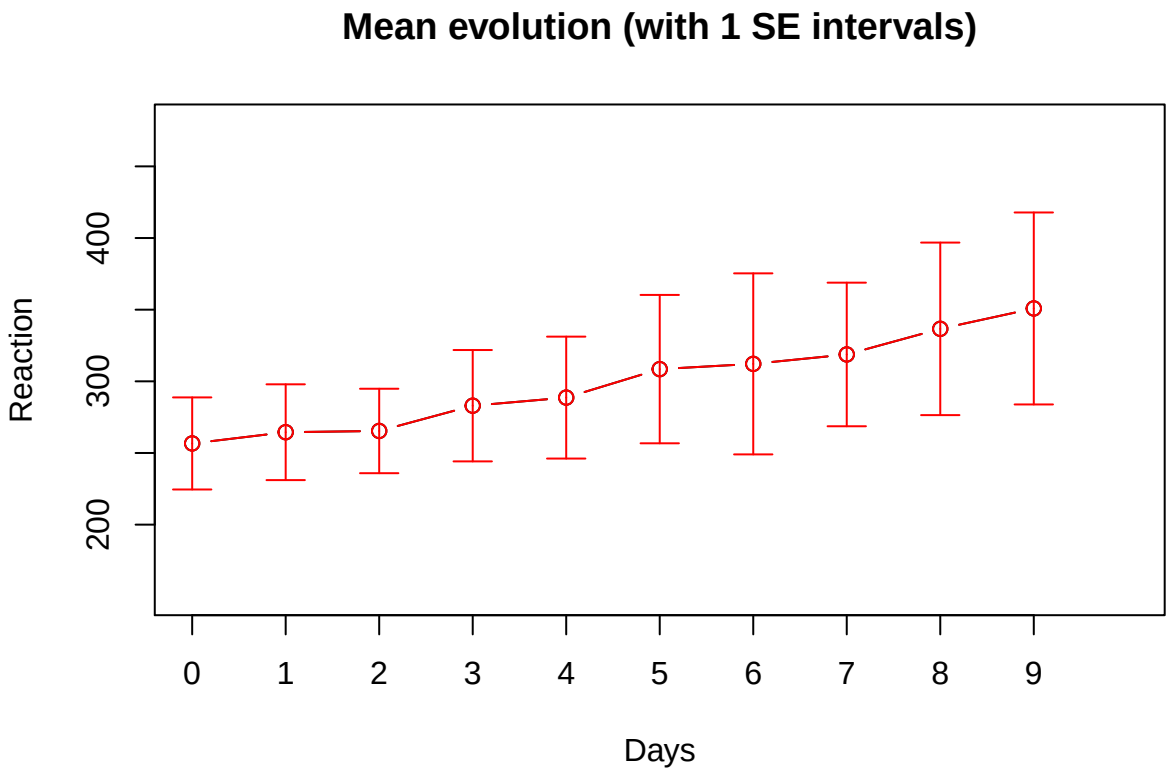
*increasing linear trend

It seems as if there's a linear trend between the number of days of sleep deprivation and the reaction time. Also the variance of the reaction time seems to increase with increasing days of sleep deprivation. (at Day 9: 5 outliers)

Mean evolution

```
# General function to plot error bars
errbar=function(x,y,height,width,lty=1,col="black"){
arrows(x,y,x,y+height,angle=90,length=width,lty=lty, col=col)
arrows(x,y,x,y-height,angle=90,length=width,lty=lty, col=col)}


## Plotting mean evolution
plot(c(0:9), overview[,2] ,type="b",xlim=c(0,10), ylim=c(150,480),xlab="Days",ylab="Reaction",axes=F, ma
axis(side=1,at=c(0:9),labels=c(0:9))
```

```
axis(side=2,at=seq(200,450,50))

box()
points(c(0:9), overview[,2],type="b",col="red")
errbar(c(0:9),overview[,2], sleep.sd, 0.1, col="red")
```



Here again you see both phenomena: The linear trend - increasing reaction time with increasing number of days. Bigger errorbars with increasing number of days.

bigger errorbars -->
bigger variance

Correlations

```
## Reshaping the data into a wide form
sleep.resh <- reshape(sleep, timevar = "Days", idvar = c("Subject"), direction = "wide")
sleep.resh
```

```
##     Subject Reaction.0 Reaction.1 Reaction.2 Reaction.3 Reaction.4
## 1       308   249.5600   258.7047   250.8006   321.4398   356.8519
## 11      309   222.7339   205.2658   202.9778   204.7070   207.7161
## 21      310   199.0539   194.3322   234.3200   232.8416   229.3074
## 31      330   321.5426   300.4002   283.8565   285.1330   285.7973
## 41      331   287.6079   285.0000   301.8206   320.1153   316.2773
## 51      332   234.8606   242.8118   272.9613   309.7688   317.4629
## 61      333   283.8424   289.5550   276.7693   299.8097   297.1710
## 71      334   265.4731   276.2012   243.3647   254.6723   279.0244
## 81      335   241.6083   273.9472   254.4907   270.8021   251.4519
## 91      337   312.3666   313.8058   291.6112   346.1222   365.7324
## 101     349   236.1032   230.3167   238.9256   254.9220   250.7103
## 111     350   256.2968   243.4543   256.2046   255.5271   268.9165
```

```
## 121     351   250.5265   300.0576   269.8939   280.5891   271.8274
## 131     352   221.6771   298.1939   326.8785   346.8555   348.7402
## 141     369   271.9235   268.4369   257.2424   277.6566   314.8222
## 151     370   225.2640   234.5235   238.9008   240.4730   267.5373
## 161     371   269.8804   272.4428   277.8989   281.7895   279.1705
## 171     372   269.4117   273.4740   297.5968   310.6316   287.1726
##     Reaction.5 Reaction.6 Reaction.7 Reaction.8 Reaction.9
## 1     414.6901   382.2038   290.1486   430.5853   466.3535
## 11    215.9618   213.6303   217.7272   224.2957   237.3142
## 21    220.4579   235.4208   255.7511   261.0125   247.5153
## 31    297.5855   280.2396   318.2613   305.3495   354.0487
## 41    293.3187   290.0750   334.8177   293.7469   371.5811
## 51    309.9976   454.1619   346.8311   330.3003   253.8644
## 61    338.1665   332.0265   348.8399   333.3600   362.0428
## 71    284.1912   305.5248   331.5229   335.7469   377.2990
## 81    254.6362   245.4523   235.3110   235.7541   237.2466
## 91    391.8385   404.2601   416.6923   455.8643   458.9167
## 101   269.7744   281.5648   308.1020   336.2806   351.6451
## 111   329.7247   379.4445   362.9184   394.4872   389.0527
## 121   304.6336   287.7466   266.5955   321.5418   347.5655
## 131   352.8287   354.4266   360.4326   375.6406   388.5417
## 141   317.2135   298.1353   348.1229   340.2800   366.5131
## 151   344.1937   281.1481   347.5855   365.1630   372.2288
## 161   284.5120   259.2658   304.6306   350.7807   369.4692
## 171   329.6076   334.4818   343.2199   369.1417   364.1236
```

```
# check normality of variables Reaction.X
for (i in c(2:11)){
  print(shapiro.test(sleep.resh[,i]))
}
```

```
##
##  Shapiro-Wilk normality test
##
## data:  sleep.resh[, i]
## W = 0.97667, p-value = 0.9093
##
##
##  Shapiro-Wilk normality test
##
## data:  sleep.resh[, i]
## W = 0.94756, p-value = 0.388
##
##
##  Shapiro-Wilk normality test
##
## data:  sleep.resh[, i]
## W = 0.98688, p-value = 0.9936
##
##
##  Shapiro-Wilk normality test
##
## data:  sleep.resh[, i]
## W = 0.97738, p-value = 0.919
##
```

```
##
##  Shapiro-Wilk normality test
##
## data:  sleep.resh[, i]
## W = 0.97247, p-value = 0.8427
##
##
##  Shapiro-Wilk normality test
##
## data:  sleep.resh[, i]
## W = 0.978, p-value = 0.9271
##
##
##  Shapiro-Wilk normality test
##
## data:  sleep.resh[, i]
## W = 0.95912, p-value = 0.5847
##
##
##  Shapiro-Wilk normality test
##
## data:  sleep.resh[, i]
## W = 0.94648, p-value = 0.3724
##
##
##  Shapiro-Wilk normality test
##
## data:  sleep.resh[, i]
## W = 0.97112, p-value = 0.8186
##
##
##  Shapiro-Wilk normality test
##
## data:  sleep.resh[, i]
## W = 0.86251, p-value = 0.01342
```

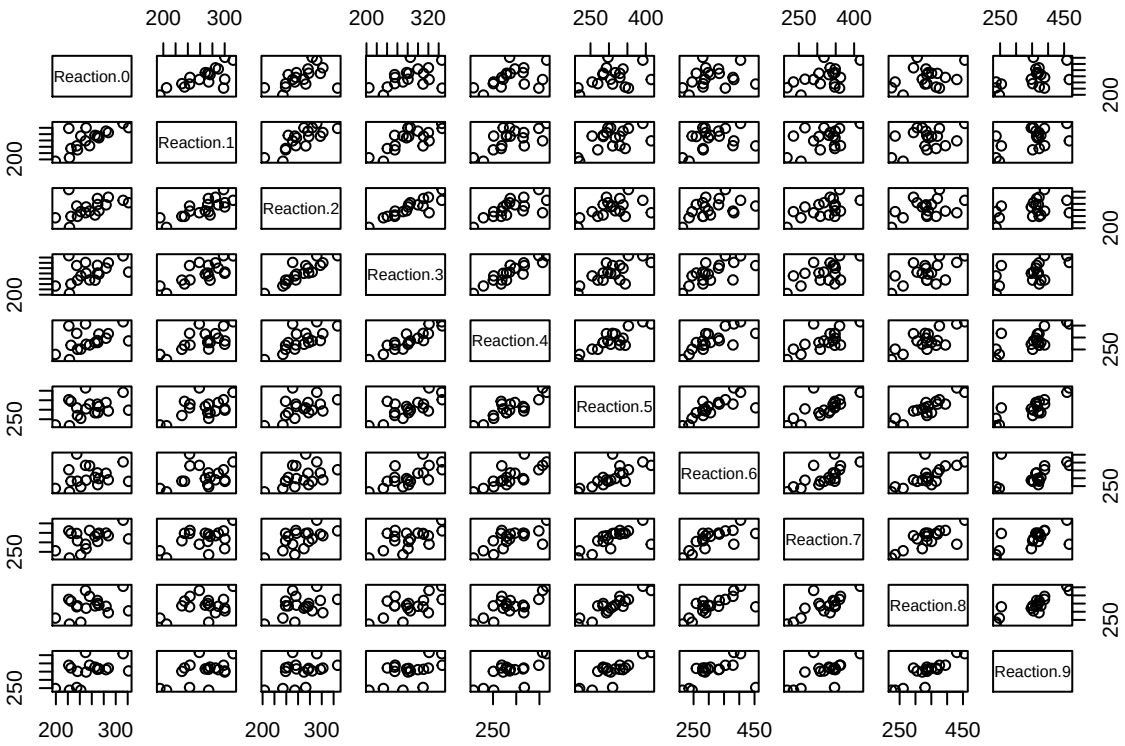
The last column (Reaction.9) is not normally distributed. So we use the 'spearman' method for correlation. (We could also use 'pearson' for all except the correlations for Reaction.9.)

```
## Correlation between the Reaction scores at different days
cor(sleep.resh[, 2:11], method='spearman')
```

```
##            Reaction.0 Reaction.1 Reaction.2 Reaction.3 Reaction.4
## Reaction.0  1.0000000  0.6594427  0.5686275  0.4179567  0.4571723
## Reaction.1  0.6594427  1.0000000  0.7461300  0.6367389  0.5562436
## Reaction.2  0.5686275  0.7461300  1.0000000  0.8534572  0.7234262
## Reaction.3  0.4179567  0.6367389  0.8534572  1.0000000  0.9133127
## Reaction.4  0.4571723  0.5562436  0.7234262  0.9133127  1.0000000
## Reaction.5  0.2239422  0.3581011  0.4344685  0.6553148  0.7296182
## Reaction.6  0.2218782  0.2920537  0.4551084  0.6759546  0.7812178
## Reaction.7  0.3457172  0.3312693  0.5087719  0.4509804  0.5789474
## Reaction.8  0.1640867  0.1496388  0.2899897  0.4654283  0.5376677
## Reaction.9  0.3106295  0.2899897  0.3168215  0.4633643  0.5933953
##            Reaction.5 Reaction.6 Reaction.7 Reaction.8 Reaction.9
## Reaction.0  0.2239422  0.2218782  0.3457172  0.1640867  0.3106295
```

```
## Reaction.1  0.3581011  0.2920537  0.3312693  0.1496388  0.2899897
## Reaction.2  0.4344685  0.4551084  0.5087719  0.2899897  0.3168215
## Reaction.3  0.6553148  0.6759546  0.4509804  0.4654283  0.4633643
## Reaction.4  0.7296182  0.7812178  0.5789474  0.5376677  0.5933953
## Reaction.5  1.0000000  0.7667699  0.7254902  0.8121775  0.7378741
## Reaction.6  0.7667699  1.0000000  0.7110423  0.6904025  0.6181631
## Reaction.7  0.7254902  0.7110423  1.0000000  0.6573787  0.6243550
## Reaction.8  0.8121775  0.6904025  0.6573787  1.0000000  0.8452012
## Reaction.9  0.7378741  0.6181631  0.6243550  0.8452012  1.0000000
```

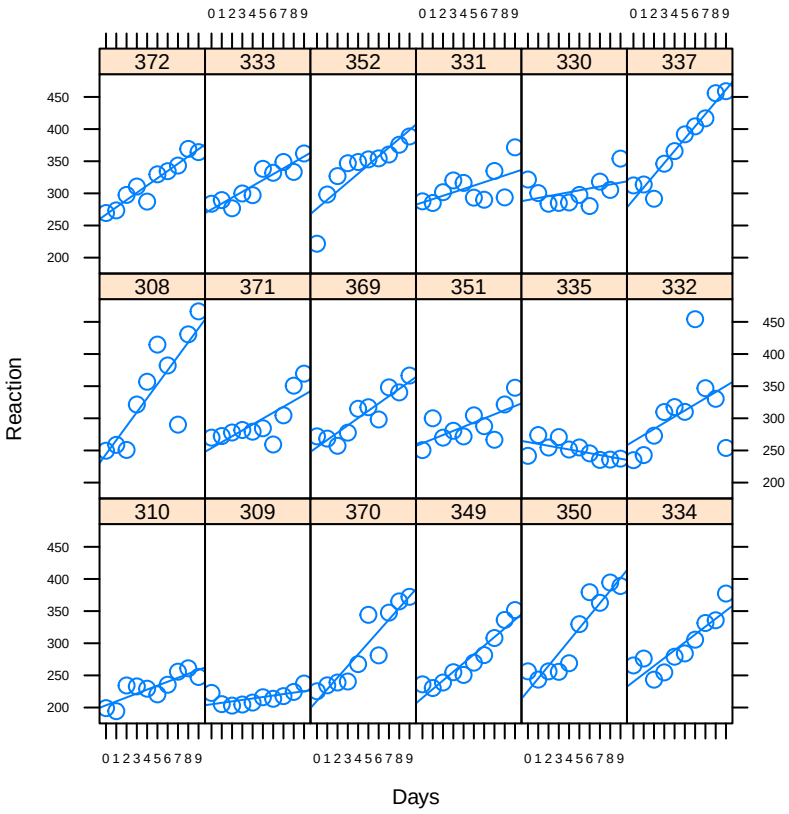
```
pairs(sleep.resh[, 2:11])
```



There seem to be high linear correlations between two following days (e.g. between Day 8 and 9, between Day 3 and 4, ...). The further the 'second' Days is apart, the lower the correlation (e.g. low correlation between Day 1 and Day 8). This appears quite 'logic', as we expect a linear trend between the number of Days and the reaction time.

Regression per person

```
## Trellis graph
## Displaying the linear regression per person

cf <-sapply(sleep$Subject, function(x) coef(lm(Reaction~Days, data=subset(sleep, Subject==x))))

Sx <-reorder(sleep$Subject, cf[1,])
#
xyplot(Reaction ~ Days|Sx, data=sleep, type=c('p', 'r'), auto.key=T,aspect="xy", par.settings=list(axis
```



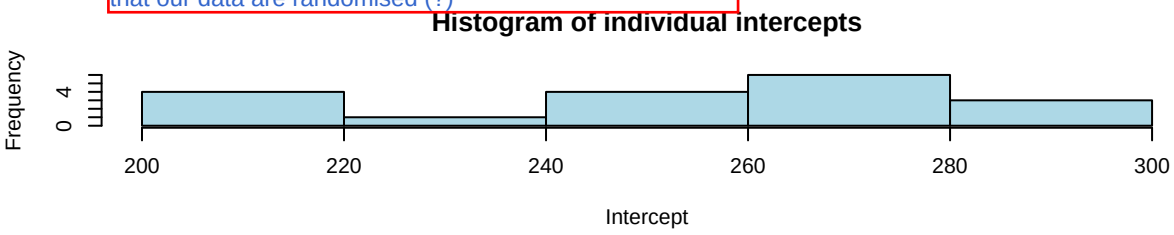
Subjects with very low reaction time at the start seem to have bigger slopes (the reaction time increases faster with increasing days of sleep deprivation).

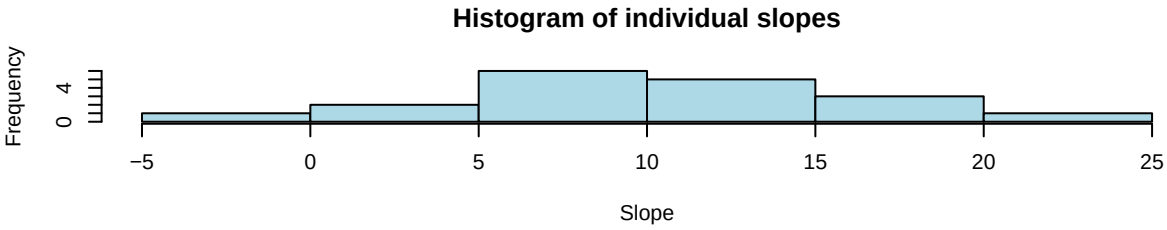
The observed slopes of the regression models show an increasing trend in the left to right, bottom to top ordering, which suggests a correlation between the initial status (intercept) and the rate of change (slope).

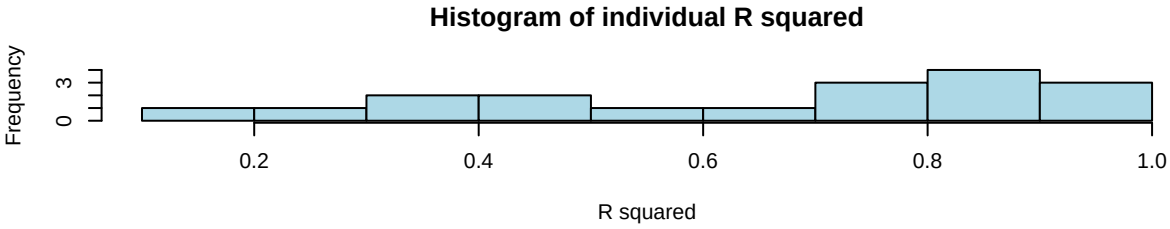
Between subject variability

```
## Linear regression per participant of Reaction on Days

## Coefficients
lin.reg.coef <- by(sleep, sleep$Subject, function(data) coef(lm(Reaction ~ Days, data=data)))
lin.reg.coef1 <- unlist(lin.reg.coef)
names(lin.reg.coef1) <- NULL
lin.reg.coef2=matrix(lin.reg.coef1,length(lin.reg.coef1)/2,2,byrow = TRUE)

## R squared
lin.reg.r.squared <- by(sleep, sleep$Subject, function(data) summary(lm(Reaction ~ Days, data=data))$r.s
lin.reg.r.squared1<- as.vector(unlist(lin.reg.r.squared))

## Histograms
par(mfrow=c(3,1))
hist(lin.reg.coef2[,1],xlab="Intercept",col="lightblue",main="Histogram of individual intercepts")
hist(lin.reg.coef2[,2],xlab="Slope",col="lightblue",main="Histogram of individual slopes")
hist(lin.reg.r.squared1,xlab="R squared",col="lightblue",main="Histogram of individual R squared")
```

The intercept corresponds to the reaction time when Day=0, the real initial status. We see from the histogram that the initial status is equally distributed, which indicates that our data are randomised (?)







The individual intercepts don't seem to bee normally distributed. The slopes seem to follow a normal distribution. The majority of the individual models seem to fit the individual data well (high R squared), but there are also some models that don't fit the data very well.

Fitting the model - with REML

```
sleep.reml <- lmer(formula = Reaction ~ 1+Days + (1 + Days|Subject), data=sleep)
summary(sleep.reml)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: Reaction ~ 1 + Days + (1 + Days | Subject)
##    Data: sleep
##
## REML criterion at convergence: 1743.6
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.9536 -0.4634  0.0231  0.4633  5.1793
##
## Random effects:
##  Groups   Name        Variance Std.Dev. Corr
##  Subject  (Intercept) 611.90   24.737
##           Days         35.08    5.923   0.07
##  Residual             654.94   25.592
## Number of obs: 180, groups:  Subject, 18
##
## Fixed effects:
```

Linear Mixed Model (LMM)
- Hierarchical Model:
Yij = π0i + π1i * Days + εij
π0i : The intercept of subject i at Dayij = 0
π1i: The slope of subject i
εij: error term ~N (0, σε^2)

π0i = γ00 + b0i
π1i = γ10 + b1i
declare the distributions that follow b0i,b1i

? do i have to write the marginal model as well?
because this is the one that I use to do the R calculations ?
(On the marginal model we do not explicitly assume the presence of random effects representing the natural heteroginity between subjects)

Marginal model:
α: a vector of all variance components in D and Σi.
In most cases α is not known and needs to be replaces by an estimate a.

Since there is no model comparison and n (sample size) is not big enough as compared to p(number of mean parameters), the REML is used for having unbiased estimates of the variance parameters

δες διαφ. 128 για να γράψεις τελικό μοντέλο

```
##             Estimate Std. Error t value
## (Intercept)  251.405      6.824  36.843
## Days          10.467      1.546   6.771
##
## Correlation of Fixed Effects:
##      (Intr)
## Days -0.138
```

Fixed effects

x_n $\sigma\Sigma$

Testing fixed effects

```
confint(sleep.reml,  par=5:6, method='Wald', oldNames=F)
```

```
##                  2.5 %    97.5 %
## (Intercept) 238.030755 264.77945
## Days          7.437264  13.49731
```

```
confint(sleep.reml, method='boot', boot.type='perc', oldNames=F, nsim=500)
```

```
## Computing bootstrap confidence intervals ...
```

```
##
## 2 message(s): boundary (singular) fit: see ?isSingular
## 176 warning(s): Model failed to converge with max|grad| = 0.0020048 (tol = 0.002, component 1) (and
```

```
##                                    2.5 %      97.5 %
## sd_(Intercept)|Subject        12.1564045  35.6005653
## cor_Days.(Intercept)|Subject  -0.4965451   0.9999935
## sd_Days|Subject                3.1799954   8.4428738
## sigma                         22.7086308  28.4618110
## (Intercept)                  237.6105652 265.1712914
## Days                           7.4440523  13.3762388
```

```
confint(sleep.reml, level=0.95, method='profile',   oldNames=F)
```

requires the models to be fit with ML

```
## Computing profile confidence intervals ...
```

```
##                                    2.5 %      97.5 %
## sd_(Intercept)|Subject        14.3821019  37.7137452
## cor_Days.(Intercept)|Subject  -0.4814998   0.6849868
## sd_Days|Subject                3.8011759   8.7540501
## sigma                         22.8982726  28.8579976
## (Intercept)                  237.6806976 265.1295138
## Days                           7.3586543  13.5759173
```