

# Portfolio 1, Study Group 10

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```
#Loading packages
pacman::p_load(sjPlot, tidyverse, broom)
```

1a

```
#importing the data.
sleep <- read.csv("sleepstudy.csv")
#selecting the data from subject 308
p308 <- subset(sleep, Subject == 308)
#making a model with the data from subject 308
m1 <- lm(Reaction ~ Days, data = p308)
summary(m1)
```

```
##
## Call:
## lm(formula = Reaction ~ Days, data = p308)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -106.397   -4.098    9.688   22.269   61.674
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    244.19      28.08   8.695 2.39e-05 ***
## Days           21.77       5.26   4.137 0.00326 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 47.78 on 8 degrees of freedom
## Multiple R-squared:  0.6815, Adjusted R-squared:  0.6417
## F-statistic: 17.12 on 1 and 8 DF,  p-value: 0.003265
```

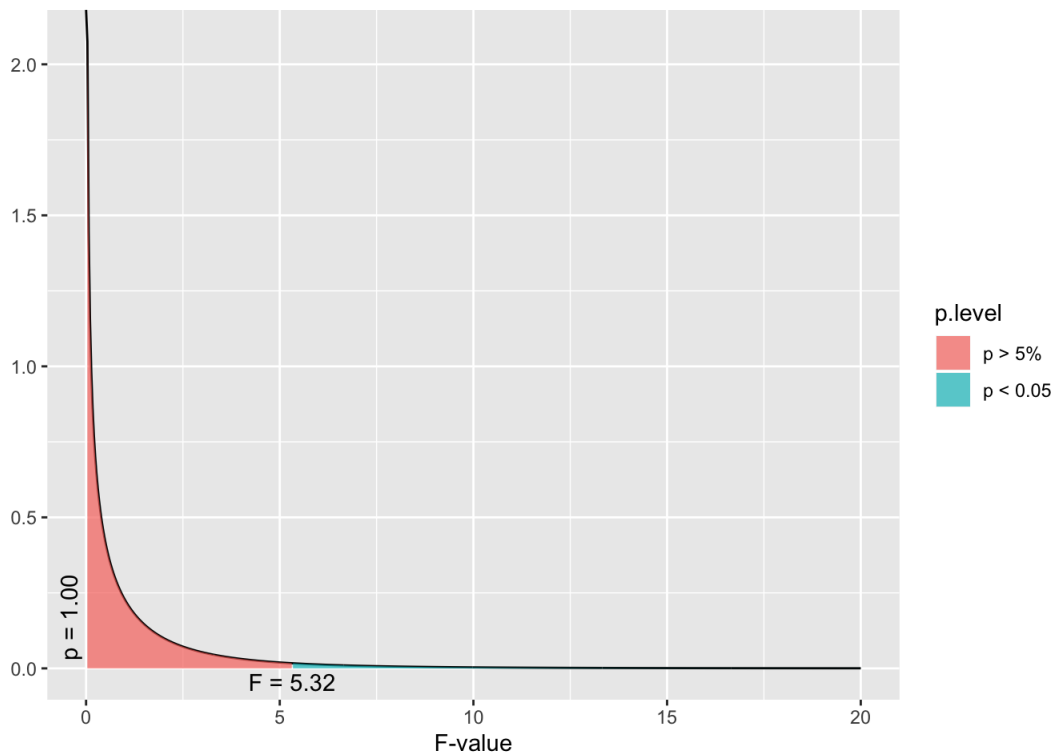
Days participant 308 was sleep deprived explained a significant proportion of variance in reaction time,  $R^2 = .64$ ,  $F(1, 8) = 17.12$ ,  $p = .003$ .

1b

As reported above the model degrees of freedom = 1 and the residual degrees of freedom = 8.

1c + 1d

```
dist_f(f=0, deg.fl = 1, deg.f2 = 8, xmax=20)
```



A regression with these degrees of freedom becomes statistically significant when the f-value gets above 5.32 at  $p < .05$ .

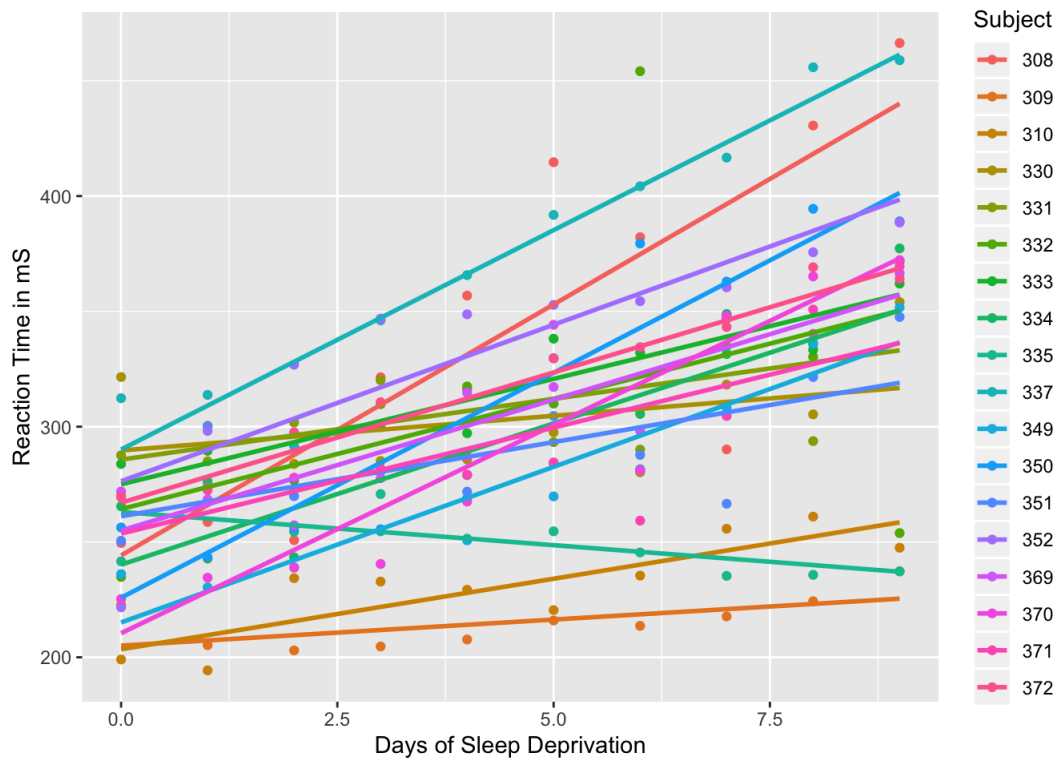
## 2a

```
#getting the coefficients (slope and intercept) for each participant:
fitted_models <- sleep %>% group_by(Subject) %>% do(model = lm(Reaction ~ Days, data = .))
#putting the data, into a tibble
m2 <- fitted_models %>% tidy(model)
m2
```

```
## # A tibble: 36 x 6
## # Groups:   Subject [18]
##   Subject term      estimate std.error statistic  p.value
##   <int> <chr>      <dbl>    <dbl>    <dbl>    <dbl>
## 1   308 (Intercept)  244.    28.1     8.70 2.39e- 5
## 2   308 Days        21.8     5.26     4.14 3.26e- 3
## 3   309 (Intercept)  205.    5.22    39.3 1.93e-10
## 4   309 Days         2.26    0.977    2.31 4.93e- 2
## 5   310 (Intercept)  203.    7.24    28.1 2.78e- 9
## 6   310 Days         6.11    1.36     4.51 1.98e- 3
## 7   330 (Intercept)  290.    13.1    22.1 1.85e- 8
## 8   330 Days         3.01    2.45     1.23 2.55e- 1
## 9   331 (Intercept)  286.    13.8    20.7 3.05e- 8
## 10  331 Days         5.27    2.58     2.04 7.55e- 2
## # ... with 26 more rows
```

## 2b

```
#making subject a factor:
sleep$Subject <- as.factor(sleep$Subject)
#plotting Reaction time as a function of days sleep deprived with each subject having their own regression
line:
ggplot(sleep, aes(Days, Reaction, colour = Subject))+geom_point()+geom_smooth(method = "lm", se=FALSE) + xlab(
  "Days of Sleep Deprivation") + ylab("Reaction Time in mS")
```



2c

```
#puting the degrees of freedom into the dataframe with the regression coefficients
m2$t.value <- m2$statistic
m2$statistic <- NULL
m2$df_model <- 1
m2$df_residual <- 8
m2
```

```
## # A tibble: 36 x 8
## # Groups:   Subject [18]
##   Subject term      estimate std.error p.value t.value df_model df_residual
##   <int> <chr>         <dbl>    <dbl> <dbl>    <dbl>    <dbl>    <dbl>
## 1 308 (Intercept)    244.    28.1 2.39e- 5  8.70      1         8
## 2 308 Days          21.8    5.26 3.26e- 3  4.14      1         8
## 3 309 (Intercept)    205.    5.22 1.93e-10 39.3      1         8
## 4 309 Days           2.26    0.977 4.93e- 2  2.31      1         8
## 5 310 (Intercept)    203.    7.24 2.78e- 9 28.1      1         8
## 6 310 Days           6.11    1.36 1.98e- 3  4.51      1         8
## 7 330 (Intercept)    290.   13.1 1.85e- 8 22.1      1         8
## 8 330 Days           3.01    2.45 2.55e- 1  1.23      1         8
## 9 331 (Intercept)    286.   13.8 3.05e- 8 20.7      1         8
## 10 331 Days          5.27    2.58 7.55e- 2  2.04      1         8
## # ... with 26 more rows
```

2d

*#We want to look at the effects sleep deprivation has on reaction time therefore we only look at the slopes. The intercepts only show the relationship between the mean reaction time and the reaction time when the participants were 0 days sleep deprived.*

```
m3 <- filter(m2, term == "Days")
```

*#We only want those that displayed a statistically significant effect from sleep deprivation:*

```
m4 <- filter(m3, p.value < 0.05)
```

```
m4
```

```
## # A tibble: 14 x 8
## # Groups:   Subject [14]
##   Subject term estimate std.error p.value t.value df_model df_residual
##   <int> <chr>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>
## 1     308 Days    21.8     5.26  0.00326    4.14     1         8
## 2     309 Days     2.26    0.977  0.0493    2.31     1         8
## 3     310 Days     6.11    1.36  0.00198    4.51     1         8
## 4     333 Days     9.14    1.37  0.000158    6.66     1         8
## 5     334 Days    12.3    2.26  0.000635    5.41     1         8
## 6     337 Days    19.0    1.80  0.00000553  10.6     1         8
## 7     349 Days    13.5    1.54  0.0000229    8.75     1         8
## 8     350 Days    19.5    2.68  0.0000862    7.27     1         8
## 9     351 Days     6.43    2.51  0.0332    2.57     1         8
## 10    352 Days    13.6    2.81  0.00131    4.83     1         8
## 11    369 Days    11.3    1.74  0.000186    6.51     1         8
## 12    370 Days    18.1    2.66  0.000138    6.80     1         8
## 13    371 Days     9.19    2.76  0.0104    3.33     1         8
## 14    372 Days    11.3    1.24  0.0000172    9.09     1         8
```

14 individuals displayed a statistically significant effect of sleep deprivation.

### 3a + 3b

We used an one tailed t-test because we were asked whether the slopes are larger than zero. there is strong theoretical background that the slopes are positive (reactiontime increases as days sleep deprived increases). Therefore it is justifiable to use a one-tailed t-test even though the risk of committing a type 1 error is increased. A t-test was used because we want to compare two means (0 and the mean of the reaction time). This test assumes normally distributed data, which is tested below with visual inspection and by using the shapiro wilks test.

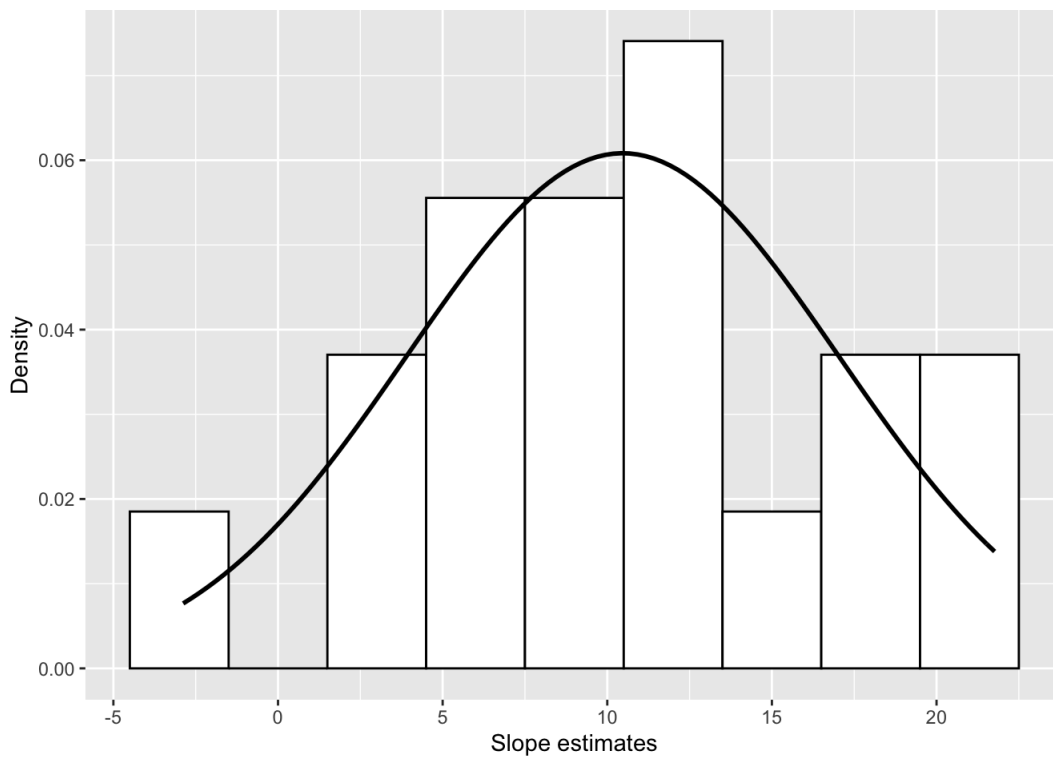
```
#first accessing the slopes from the previous exercise
est <- m3$estimate

#Putting them into a dataframe
estimates <- as.data.frame(est)

#testing whether the slopes are normally distributed:
shapiro.test(est)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  est
## W = 0.97881, p-value = 0.9369
```

```
ggplot(estimates, aes(est)) + geom_histogram(aes(y=..density..), colour = "black", fill = "white", binwidth
= 3) + labs(x = "Slope estimates", y = "Density") + stat_function(fun = dnorm, args = list(mean = mean(estim
ates$est), sd = sd(estimates$est)), colour= "black", size = 1)
```



As can be seen the data looks kind of normally distributed, and the shapiro wilks test is non-significant indicating that the reaction times are not significantly different from a perfect normal distribution.

One can therefore perform the t-test:

```
#Performing the t-test and telling it to perform a one-sided kind
test <- t.test(est, mu = 0, alternative = "two.sided")
test
```

```
##
## One Sample t-test
##
## data: est
## t = 6.7715, df = 17, p-value = 3.264e-06
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
## 7.205956 13.728615
## sample estimates:
## mean of x
## 10.46729
```

```
#Calculating the effect size r
r <- sqrt(test$statistic^2/((test$statistic^2)+test$parameter))
r
```

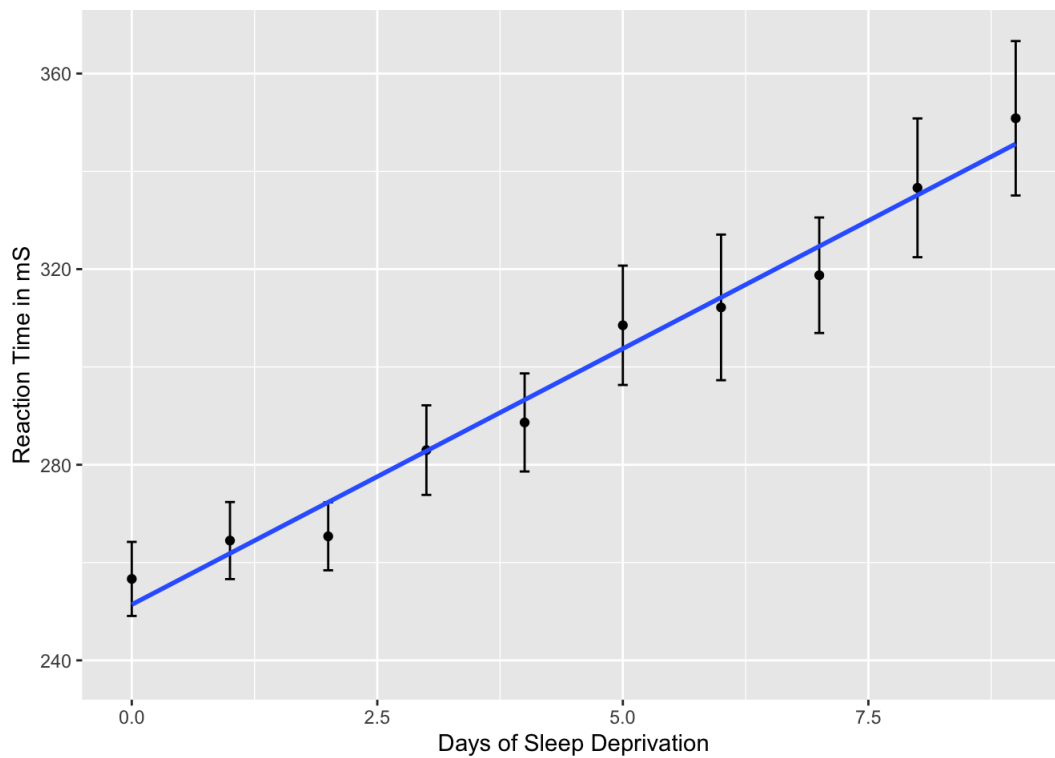
```
##          t
## 0.8541239
```

### 3c

Our slopes are shown to be statistically significantly different from 0,  $t(17)=6.77$   $p < .001$ ,  $r = 0.85$

### 3d

```
#Making a plot of Reaction time as a function of Days. And adding the mean reaction time with standard error
bars for each day
ggplot(sleep, aes(x = Days, y = Reaction))+geom_point(stat = "summary", fun.y = mean)+ stat_summary(fun.data
= mean_se, geom = "errorbar", color = 'black', width = 0.1)+geom_smooth(method = "lm", alpha=0) + xlab("Day
s of Sleep Deprivation") + ylab("Reaction Time in mS")
```



### Voluntary bonus task:

```
#Adding 10% noise.
sleep$Reaction.Noise <- sleep$Reaction+sleep$Reaction*runif(10, min = -0.05, max = 0.05)

#Getting statistics from the newly derived data
fitted_models1 <- sleep %>% group_by(Subject) %>% do(model1 = lm(Reaction.Noise ~ Days, data = .))

#putting the data, into a tibble(dataframe)
m5 = fitted_models1 %>% tidy(model1)

#Filtering out the slopes
m6 = filter(m5, term == "Days")

#We only want those that displayed a statistically significant effect from sleep deprivation:
m7 = filter(m6, p.value < 0.05)

m7
```

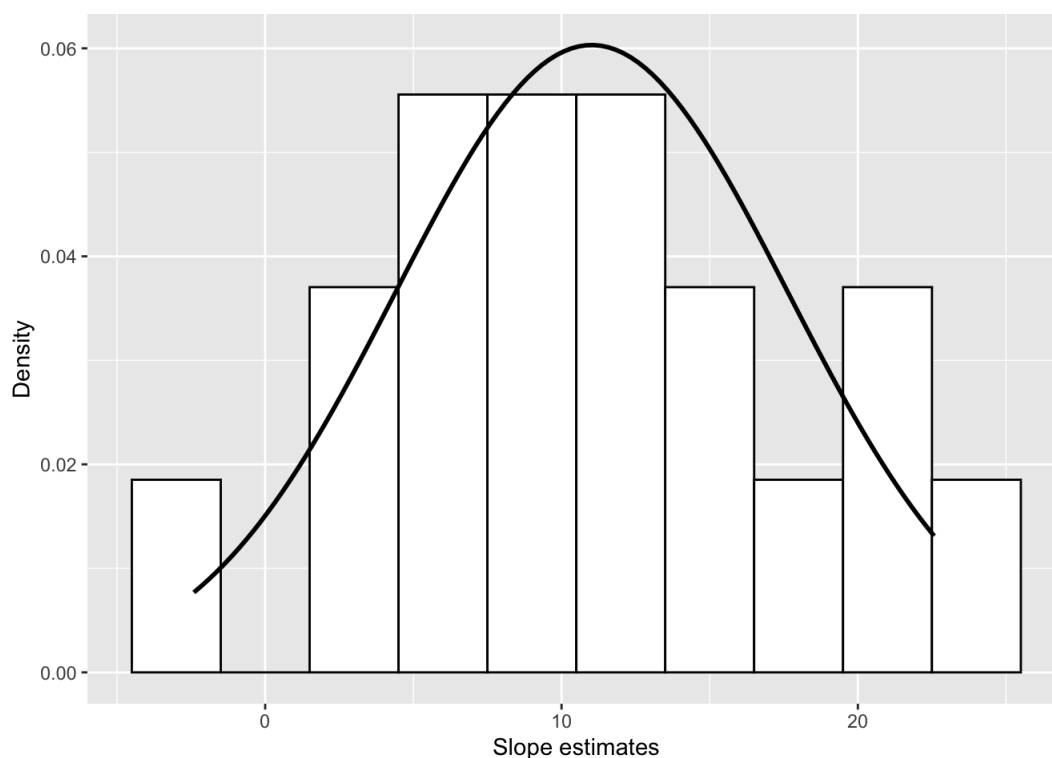
```
## # A tibble: 13 x 6
## # Groups:   Subject [18]
##   Subject term estimate std.error statistic p.value
##   <fct> <chr> <dbl> <dbl> <dbl> <dbl>
## 1 308 Days 22.6 5.75 3.93 0.00438
## 2 310 Days 6.44 1.43 4.51 0.00197
## 3 333 Days 9.73 2.01 4.83 0.00130
## 4 334 Days 12.9 2.69 4.78 0.00139
## 5 337 Days 19.7 2.13 9.26 0.0000150
## 6 349 Days 14.0 2.08 6.72 0.000149
## 7 350 Days 20.0 3.15 6.35 0.000220
## 8 351 Days 7.11 2.89 2.46 0.0391
## 9 352 Days 14.3 2.77 5.15 0.000870
## 10 369 Days 11.9 1.98 6.02 0.000316
## 11 370 Days 18.6 2.88 6.44 0.000201
## 12 371 Days 9.76 3.15 3.10 0.0146
## 13 372 Days 11.8 1.86 6.36 0.000219
```

```
#Saving the estimates and putting them into a dataframe
est1 = m6$estimate
estimates1 = as.data.frame(est1)

#Testing whether the slopes are normally distributed:
shapiro.test(est1)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  est1
## W = 0.9803, p-value = 0.953
```

```
#Plotting a histogram of the new data
ggplot(estimates1, aes(est1)) + geom_histogram(aes(y=..density..), colour = "black", fill = "white", binwidth
h = 3) + labs(x="Slope estimates", y = "Density") + stat_function(fun = dnorm, args = list(mean = mean(est
imates1$est1), sd = sd(estimates1$est1)), colour= "black", size = 1)
```



As can be seen the data looks kind of normally distributed, and the shapiro wilks test is non-significant indicating that the reaction times are not significantly different from a perfect normal distribution.

One can therefore perform the t-test with the new data:

```
#Dping a t-test and telling it to perform a one-sided type
test1 = t.test(est1, mu = 0, alternative = "two.sided")
test1
```

```
##
##  One Sample t-test
##
## data:  est1
## t = 7.0679, df = 17, p-value = 1.888e-06
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##   7.729651 14.308084
## sample estimates:
## mean of x
## 11.01887
```

```
#Calculating the effect size
r1 = sqrt(test1$statistic^2/((test1$statistic^2)+test1$parameter))
r1
```

```
##           t
## 0.8637695
```

As can be seen there is only 13 statistically significant slopes after adding 10% white noise.

The results show that adding 10% white noise can have an influence on the individual level, 13 slopes being statistically significant meaning that one person after adding the 10% noise did not seem to have their reaction time influenced by sleep deprivation, even though they seemed to be influenced by sleep deprivation without the 10% noise.

On a group level adding the 10% noise had no meaningful effect.