Does decompression surgery influence sagittal balance parameters in patients with spinal stenosis?

Contents

```
knitr::opts_chunk$set(
    echo = TRUE,
    message = FALSE,
    warning = FALSE
)
library(pwr)
library(tidyverse)
library(lubridate)
library(magrittr)
library(arsenal)
library(patchwork)
library(GGally)
library(ggpubr)
library(dlookr)
library(Hmisc)
library(FactoMineR)
library(factoextra)
library(clustertend)
library(irr)
library(kableExtra)
library(broom)
```

Table 1: Paired t test power calculation - n is number of pairs

n	sig.level	power
55.00992	0.05	0.8

Sample size calculation

- Primary endpoint: LL variation
- Sample size was calculated for two sided paired T-test sig. level of 0.05, power of 0.80
- Effect size calculated according to Cohen's d = (5º -> author consensus)/SD -> from this reference: doi.org/10.1007/s00586-020-06639-6
- d = 5/13
- The calculated sample size was 110 patients (55*2).

```r
ss1 <- pwr.t.test(d = 5/13, sig.level = 0.05, power = 0.80, type = "paired", alternative = "two.sided")

tidy(ss1) %>% kbl(caption = "Paired t test power calculation  - n is number of pairs") %>%
        kable_classic("hover", full_width = F)
```

Data wrangle

- To calculate the ideal spinopelvic parameters these formulas were used: ideal $LL = 0.54 \times PI + 27.6$ and ideal $PT = 0.44 \times PI - 11.4$
- The lumbar distribution index was calculated as L4-S1 lordosis/LL x 100
- Relative lumbar lordosis (RLL) and relative pelvic tilt (RPT) were the result from the following subtractions: LL – ideal LL and PT-ideal PT.
- Variation values were obtained with subtraction of the preoperative measurements from the postoperative ones

```r
data <- read_delim("data.csv", ";", escape_double = FALSE,
        col_types = cols(M.R.N. = col_character(),
          `Birth_date` = col_date(format = "%d/%m/%Y"),
          Gender = col_factor(levels = c("female", "male")),
          BMI = col_factor(levels = c("<20", "20-25", "26-30", "31-35", ">35")),
          Smoker = col_factor(levels = c("No", "Yes")),
          Levels = col_factor(
            levels = c("L2-L4", "L2-L5", "L3-L4", "L3-L5", "L3-S1", "L4-L5", "L4-S1", "L5-S1")),
          `number_of_levels` = col_factor(levels = c("1", "2", "3")),
          Approach = col_factor(levels = c("uni", "bi")),
          Odom = col_factor(levels = c("poor", "fair", "good", "excellent")),
          Complications = col_factor(levels = c("No", "Yes")),
          `Surgery_date` = col_date(format = "%d/%m/%Y")),
          trim_ws = TRUE, skip_empty_rows = T)


#Calculate ICC
#ICC two way random effects, mean of k raters, absolute agreement

PI <- data %>% select(Preop_PI_1, Preop_PI_2)
PT_pre <- data %>% select(Preop_PT_1, Preop_PT_2)
```

```r
LL_pre <- data %>% select(Preop_LL_1, Preop_LL_2)
PT_pos <- data %>% select(Postop_PT_1, Postop_PT_2)
LL_pos <- data %>% select(Postop_LL_1, Postop_LL_2)

icc_PI <- icc(PI, model = "twoway", type = "agreement", unit = "average")
icc_PT_pre <- icc(PT_pre, model = "twoway", type = "agreement", unit = "average")
icc_LL_pre <- icc(LL_pre, model = "twoway", type = "agreement", unit = "average")
icc_PT_pos <- icc(PT_pos, model = "twoway", type = "agreement", unit = "average")
icc_LL_pos <- icc(LL_pos, model = "twoway", type = "agreement", unit = "average")

ICCs <- data.frame(
  "Parameter" = c("PI", "Preop. PT", "Preop. LL", "Postop. PT", "Postop. LL"),
  "ICC value" = c(icc_PI$value, icc_PT_pre$value, icc_LL_pre$value, icc_PT_pos$value, icc_LL_pos$value)

#Use means of the 2 observers

data %<>% rowwise() %>% mutate(Preop_PI = mean(c(Preop_PI_1, Preop_PI_2))) %>%
                        mutate(Preop_PT = mean(c(Preop_PT_1, Preop_PT_2))) %>%
                        mutate(Preop_LL = mean(c(Preop_LL_1, Preop_LL_2))) %>%
                        mutate(Postop_PT = mean(c(Postop_PT_1, Postop_PT_2))) %>%
                        mutate(Postop_LL =mean(c(Postop_LL_1, Postop_LL_2)))


#New variables
## ideal and relative LL and PT

data %<>% mutate(ideal_LL_pre=0.54*`Preop_PI`+27.6) %>%
         mutate(ideal_LL_post=0.54*`Postop_PI`+27.6) %>%
         mutate(Preop_RLL=`Preop_LL`-ideal_LL_pre) %>%
         mutate(Postop_RLL=`Postop_LL`-ideal_LL_post) %>%
         mutate(ideal_PT_pre=0.44*`Preop_PI`-11.4) %>%
         mutate(ideal_PT_post=0.44*`Postop_PI`-11.4) %>%
         mutate(Preop_RPT=`Preop_PT`-ideal_PT_pre) %>%
         mutate(Postop_RPT=`Postop_PT`-ideal_PT_post) %>%
         mutate(Preop_LDI= Preop_L_L4S1/Preop_LL*100) %>% #Lordosis distribution index
         mutate(Postop_LDI= Postop_L_L4S1/Postop_LL*100)

## age

data %<>% mutate(Age = `Birth_date` %--% `Surgery_date` %/% years(1))

## delta variables

data %<>% mutate(diff_LL=`Postop_LL`- `Preop_LL`) %>%
         mutate(diff_L_L4S1=`Postop_L_L4S1`- `Preop_L_L4S1`) %>%
         mutate(diff_PT= `Postop_PT` - `Preop_PT`) %>%
         mutate(diff_seg=`Postop_seg`- `Preop_seg`) %>%
         mutate(diff_SVA= Postop_SVA - Preop_SVA) %>%
         mutate(diff_COMI= `Postop_COMI` - `Preop_COMI`) %>%
         mutate(diff_ODI= `Postop_ODI` - `Preop_ODI`) %>%
         mutate(diff_EQ5D= `Postop_EQ5D` - `Preop_EQ5D`) %>%
         mutate(diff_LDI= Postop_LDI - Preop_LDI)
```

Table 2: ICCs values for most important radiological parameters

Parameter	ICC.value
PI	0.8453484
Preop. PT	0.9169224
Preop. LL	0.8892830
Postop. PT	0.8430052
Postop. LL	0.9270249

ICCs values for most important radiological parameters

- Intraclass correlation coefficients (ICCs) estimates were calculated based on mean rating, absolute agreement, 2-way random effects model.
- Excellent reliability was achieved in inter-rater agreement analysis with ICCs ranging from 0.85 to 0.93

```
ICCs %>% kbl(caption = "ICCs values for most important radiological parameters") %>%
        kable_classic("hover", full_width = F)
```

Table of patient characteristics

- One or two levels surgery was done in 93.6% of the patients
- Unilateral approach was used in 55.8% of the cases.
- The outcome defined by the Odom criteria was good or excellent in 71.6% of the patients

```
f1 <- formulize(x=c(3, 54, 4, 5, 13, 14, 15, 16), data = data)

tab_1 <- tableby(f1, data = data,
              numeric.stats=c("meansd","medianq1q3", "Nmiss"), cat.stats = "countpct")

summary(tab_1, title = "Patient characteristics.")
```

Table 3: Patient characteristics.

	Overall (N=95)
Gender	
female	45 (47.4%)
male	50 (52.6%)
Age	
Mean (SD)	63.179 (10.671)
Median (Q1, Q3)	64.000 (56.000, 69.500)
BMI	
<20	1 (1.1%)
20-25	20 (21.1%)
26-30	46 (48.4%)
31-35	25 (26.3%)
>35	3 (3.2%)
Smoker	

	Overall (N=95)
No	89 (93.7%)
Yes	6 (6.3%)
number__of_levels	
1	52 (54.7%)
2	37 (38.9%)
3	6 (6.3%)
Approach	
uni	53 (55.8%)
bi	42 (44.2%)
Odom	
poor	7 (7.4%)
fair	20 (21.1%)
good	28 (29.5%)
excellent	40 (42.1%)
Complications	
No	85 (89.5%)
Yes	10 (10.5%)

Table of preoperative and postoperative data

- No differences between preoperative and postoperative radiological parameters, except for RLL but with a difference bellow 3º.
- For clinical scores there were significant improvements after surgery

```
#pivot_longer to automatic paired table

data_long <- data %>% pivot_longer(
  c(Preop_LL, Postop_LL, Preop_PT, Postop_PT, Preop_seg, Postop_seg, Preop_SVA, Postop_SVA,
    Preop_RLL, Postop_RLL, Preop_RPT, Postop_RPT, Preop_LDI, Postop_LDI,
    Preop_COMI, Postop_COMI, Preop_ODI, Postop_ODI, Preop_EQ5D, Postop_EQ5D),
  names_to = c("Time", ".value"),
  names_sep = "_")

tab_2 <- paired(Time ~ LL + seg + SVA + PT + RLL + RPT + LDI + COMI + ODI + EQ5D,
              data = data_long, id= M.R.N.,
              na.action = na.paired("fill"),
              numeric.stats = c("medianq1q3", "Nmiss"),
              numeric.test = "signed.rank")

summary(tab_2, title = "Preoperative and postoperative data.", pfootnote = T)
```

Table 4: Preoperative and postoperative data.

	Postop (N=95)	Preop (N=95)	Difference (N=95)	p value
LL				0.127[1]
Median (Q1, Q3)	53.650 (46.875, 59.850)	54.100 (48.525, 62.025)	1.300 (-3.075, 4.850)	
seg				0.060[1]

	Postop (N=95)	Preop (N=95)	Difference (N=95)	p value
Median (Q1, Q3)	20.050 (13.425, 25.900)	21.400 (13.950, 27.550)	2.000 (-3.500, 6.250)	
N-Miss	1	0	1	
SVA				0.808[1]
Median (Q1, Q3)	22.600 (9.550, 47.500)	27.200 (4.225, 48.600)	1.700 (-23.100, 25.100)	
N-Miss	20	13	28	
PT				0.213[1]
Median (Q1, Q3)	15.000 (10.675, 18.550)	14.000 (9.900, 17.525)	-0.700 (-3.700, 2.600)	
RLL				0.004[1]
Median (Q1, Q3)	-2.244 (-9.245, 2.294)	0.002 (-5.817, 4.806)	2.714 (-2.319, 6.840)	
RPT				0.532[1]
Median (Q1, Q3)	2.376 (-0.905, 7.246)	3.174 (-1.830, 7.010)	0.046 (-2.666, 3.645)	
LDI				0.273[1]
Median (Q1, Q3)	62.908 (55.090, 70.581)	63.198 (58.000, 70.159)	1.597 (-5.193, 6.249)	
COMI				< 0.001[1]
Median (Q1, Q3)	5.000 (3.000, 8.000)	8.000 (7.000, 9.000)	2.000 (0.900, 5.000)	
N-Miss	6	10	14	
ODI				< 0.001[1]
Median (Q1, Q3)	35.560 (20.000, 54.000)	48.000 (38.000, 60.000)	13.000 (3.500, 24.777)	
N-Miss	10	11	19	
EQ5D				< 0.001[1]
Median (Q1, Q3)	0.690 (0.279, 0.760)	0.516 (0.082, 0.590)	-0.164 (-0.507, 0.008)	
N-Miss	9	12	19	

1. Wilcoxon signed rank test with continuity correction

Missing imputation for PCA

- Method: multiple imputation using additive regression, bootstrapping, and predictive mean matching

```
#missing imputation

#variable selection with NAs

less_data <- data %>% select(-M.R.N., -Birth_date, -Surgery_date)

less_data2 <- less_data %>% select_if(anyNA)

f <- reformulate(colnames(less_data2))

set.seed(123)
```

Table 5: Wilcoxon signed rank test with continuity correction

statistic	p.value	alternative
2692	0.1266521	two.sided

```r
impute_arg <- aregImpute(f, data = less_data2, n.impute = 5)

## Iteration 1 Iteration 2 Iteration 3 Iteration 4 Iteration 5 Iteration 6 Iteration 7 Iteration 8
completed <- less_data

imputed <- impute.transcan (impute_arg, imputation=1, data=less_data, list.out=TRUE,
pr=FALSE, check=FALSE)

completed[names(imputed)] <- imputed
```

Primary endpoint: LL variation

- No significante differences in LL variation

```r
tidy(wilcox.test(data$Preop_LL, data$Postop_LL, paired=TRUE)) %>%
  select(-3) %>%
  kbl(caption = "Wilcoxon signed rank test with continuity correction") %>%
  kable_classic("hover", full_width = F)
```

Primary endpoint distribution

```r
plot_1 <- ggdensity(data, x = "diff_LL", fill = "#1f78b4",
   add = "mean", xlab = "LL variation", title = "Kernel density plot for LL variation")

plot_1
```

Kernel density plot for LL variation
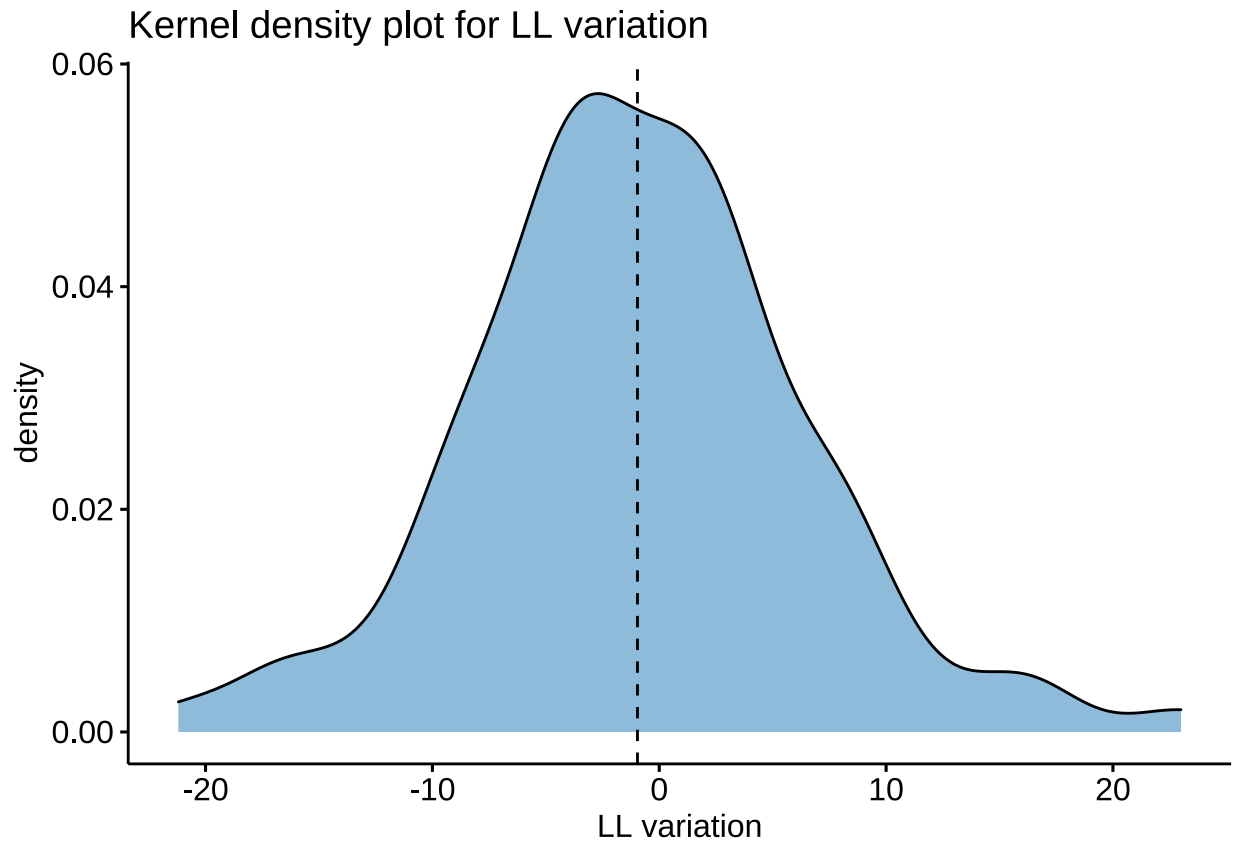
Principal component analysis

- PCA was performed after scaling of continuous variables, an eigen value >1 and a cumulative variance>80% was used as criteria to select 8 dimensions
- Graphs for cumulative variance of the dimensions, variables contribution for the first 3 dimensions, varibles distribution according to dim 1 vs dim2 and dim1 vs dim 3

```
data_cont <- completed %>% select(Age,
                                  Preop_LL, Preop_PI, Preop_PT, Preop_SVA,
                                  diff_LL, diff_PT, diff_SVA,
                                  Preop_RLL, Preop_RPT, Preop_LDI,
                                  Postop_RLL, Postop_RPT, Postop_LDI,
                                  Preop_COMI, Preop_ODI, Preop_EQ5D,
                                  diff_COMI, diff_ODI, diff_EQ5D)

res.pca <- PCA(data_cont, graph = F, scale.unit = T, ncp = 8)

eig.val <- get_eigenvalue(res.pca)

eig.val %>% kbl(caption = "Eigen values and PCAs variance percent") %>%
        kable_classic("hover", full_width = F)

#for PCA: first 8 dim to reach 80%, last dim with eigen value >1 is dim9
```

Table 6: Eigen values and PCAs variance percent

|	eigenvalue	variance.percent	cumulative.variance.percent
Dim.1	3.6655958	18.3279788	18.32798
Dim.2	2.9531295	14.7656475	33.09363
Dim.3	2.5233208	12.6166038	45.71023
Dim.4	1.9807372	9.9036858	55.61392
Dim.5	1.8834547	9.4172736	65.03119
Dim.6	1.4512533	7.2562663	72.28746
Dim.7	1.0976708	5.4883538	77.77581
Dim.8	1.0403734	5.2018668	82.97768
Dim.9	0.8408931	4.2044653	87.18214
Dim.10	0.6404951	3.2024754	90.38462
Dim.11	0.6106561	3.0532803	93.43790
Dim.12	0.4119076	2.0595382	95.49744
Dim.13	0.3006796	1.5033982	97.00083
Dim.14	0.2493594	1.2467969	98.24763
Dim.15	0.1688057	0.8440286	99.09166
Dim.16	0.1043017	0.5215083	99.61317
Dim.17	0.0773664	0.3868322	100.00000
Dim.18	0.0000000	0.0000000	100.00000
Dim.19	0.0000000	0.0000000	100.00000
Dim.20	0.0000000	0.0000000	100.00000

```
fviz_screeplot(res.pca, addlabels=T, ylim=c(0,50), title="Scree plot - explained variance for each PCA
```

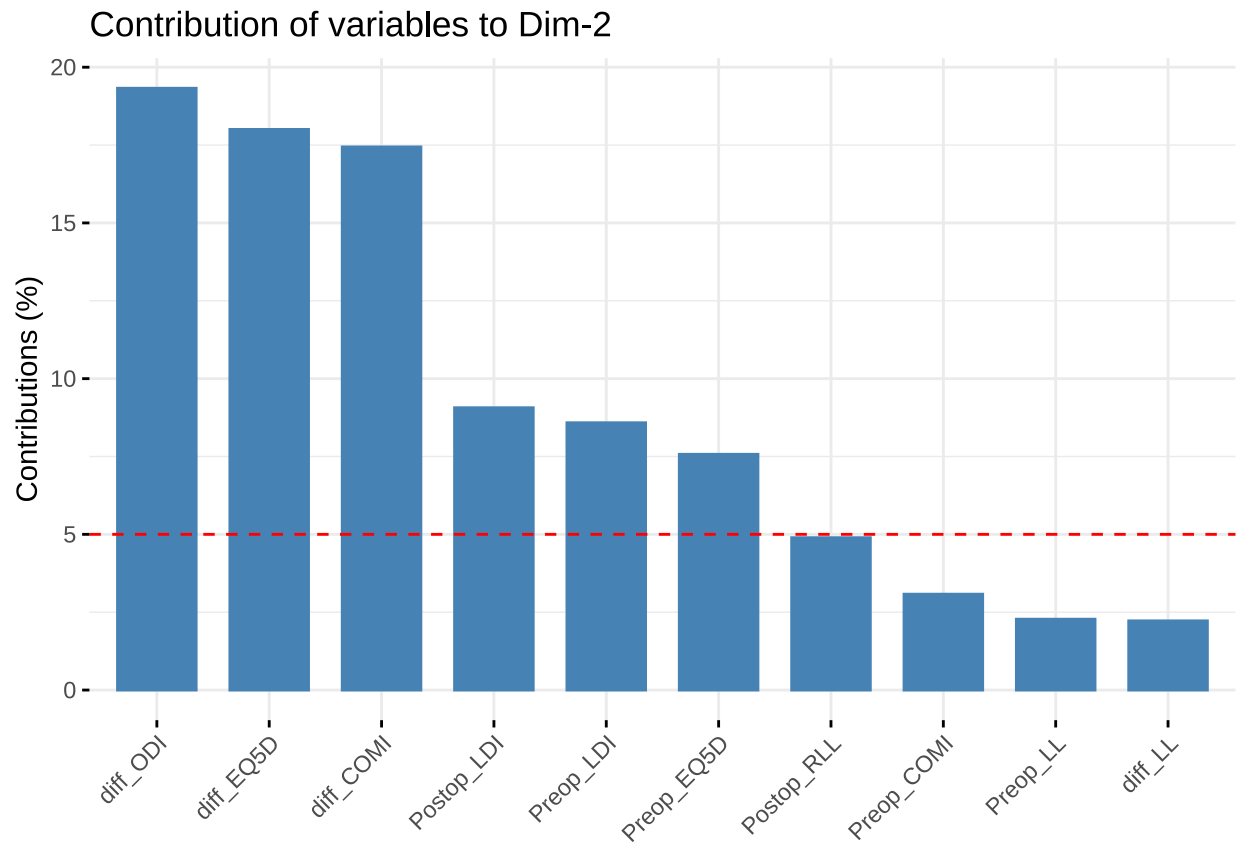## Scree plot - explained variance for each PCA dimension
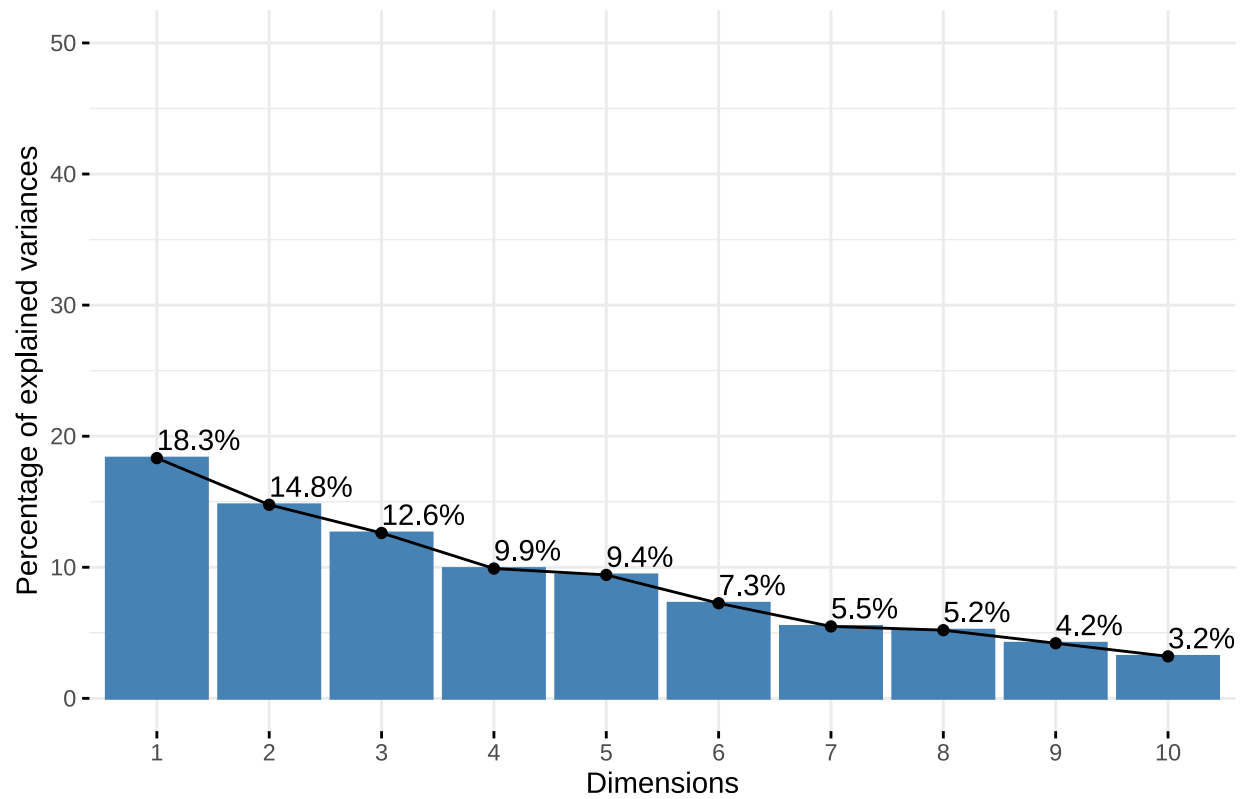

```r
#contribution for each dimension

fviz_contrib(res.pca, choice = "var", axes = 1, top = 10)
```
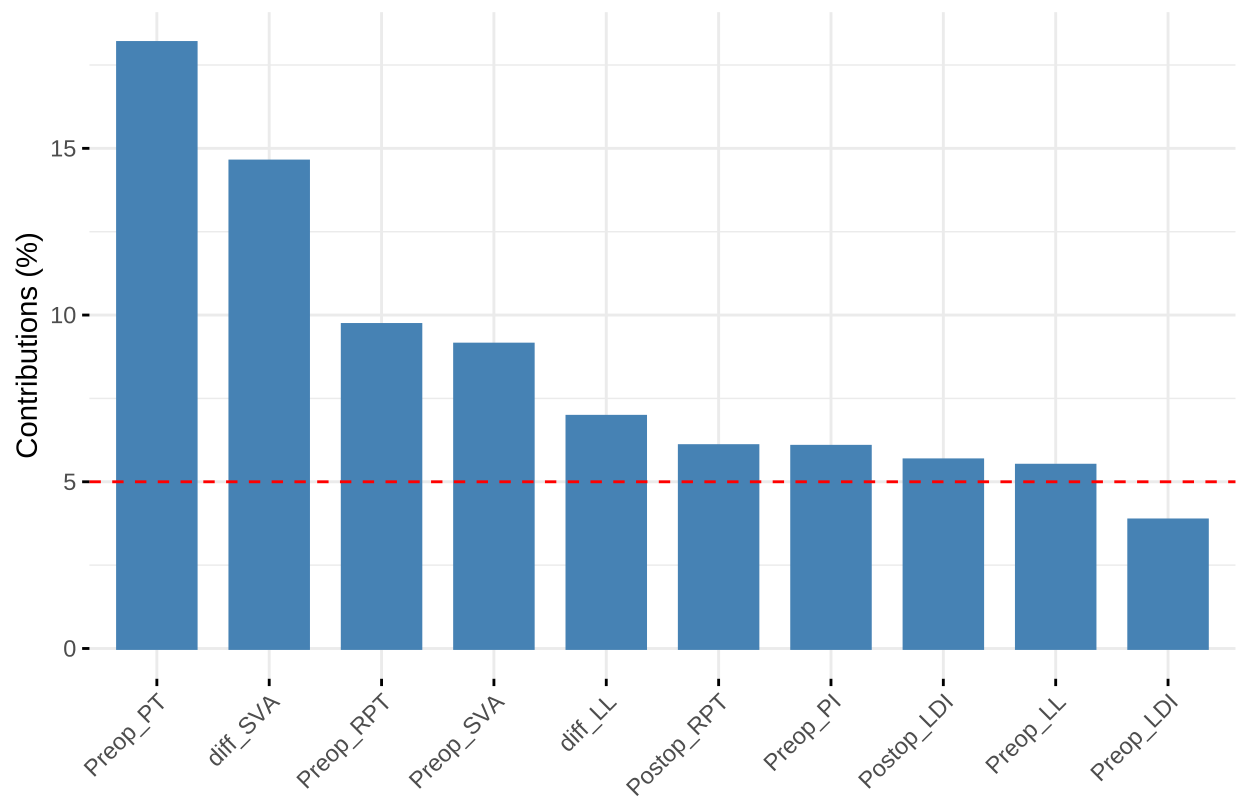
Contribution of variables to Dim-1
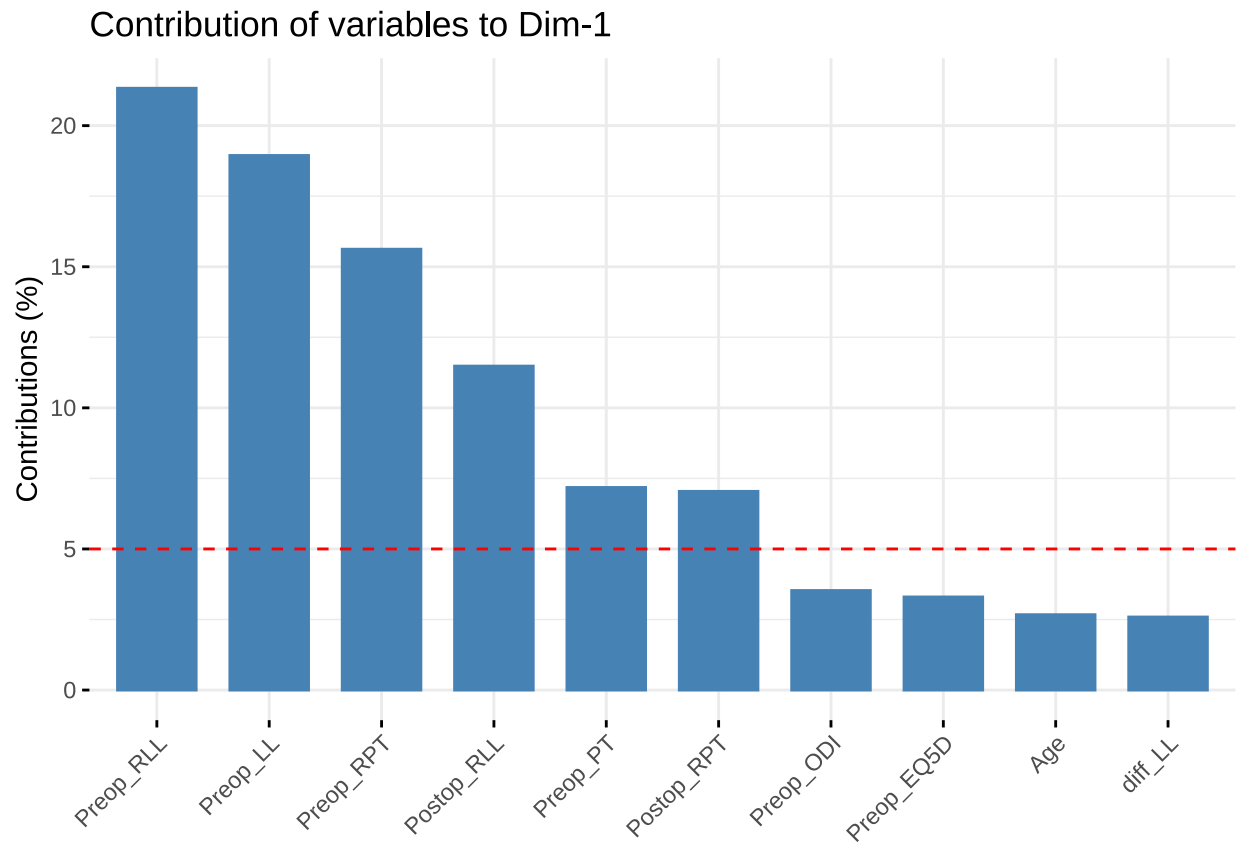

```
fviz_contrib(res.pca, choice = "var", axes = 2, top = 10)
```
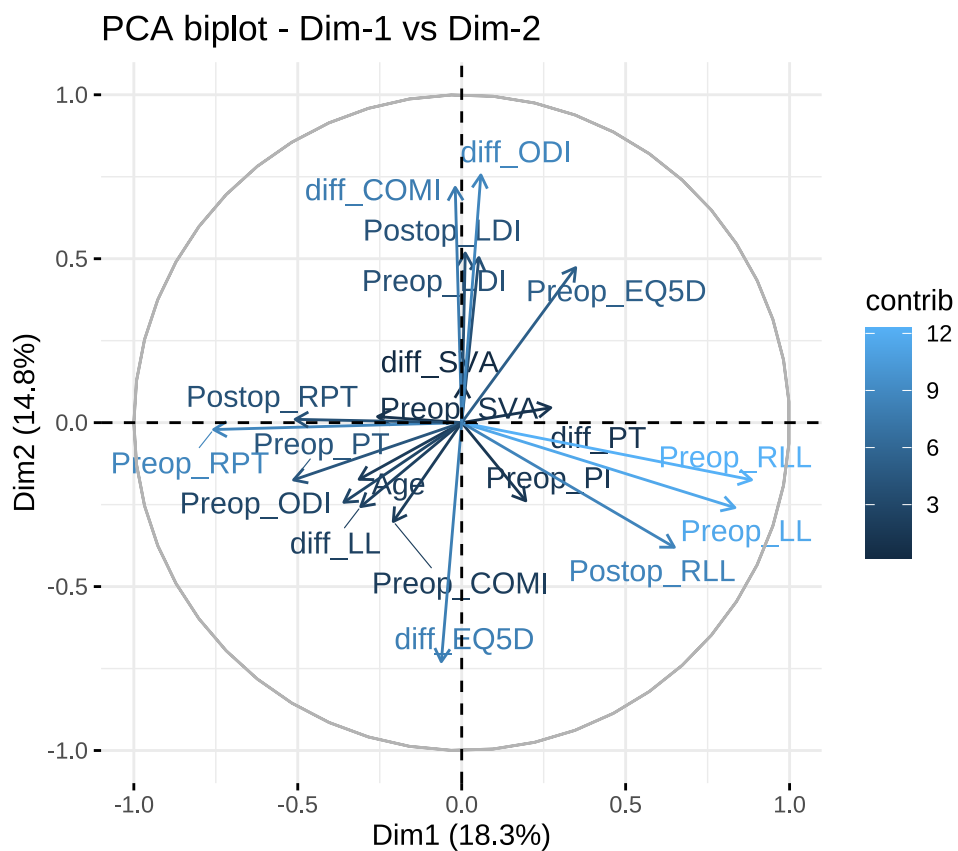
Contribution of variables to Dim-2

```
fviz_contrib(res.pca, choice = "var", axes = 3, top = 10)
```

Contribution of variables to Dim-3


```r
#Variables PCA
fviz_pca_var(res.pca, col.var = "contrib", repel=T, title="PCA biplot - Dim-1 vs Dim-2")
```

PCA biplot - Dim-1 vs Dim-2

```
fviz_pca_var(res.pca, col.var = "contrib", repel=T, axes = c(1,3), title="PCA biplot - Dim-1 vs Dim-3")
```

PCA biplot - Dim-1 vs Dim-3
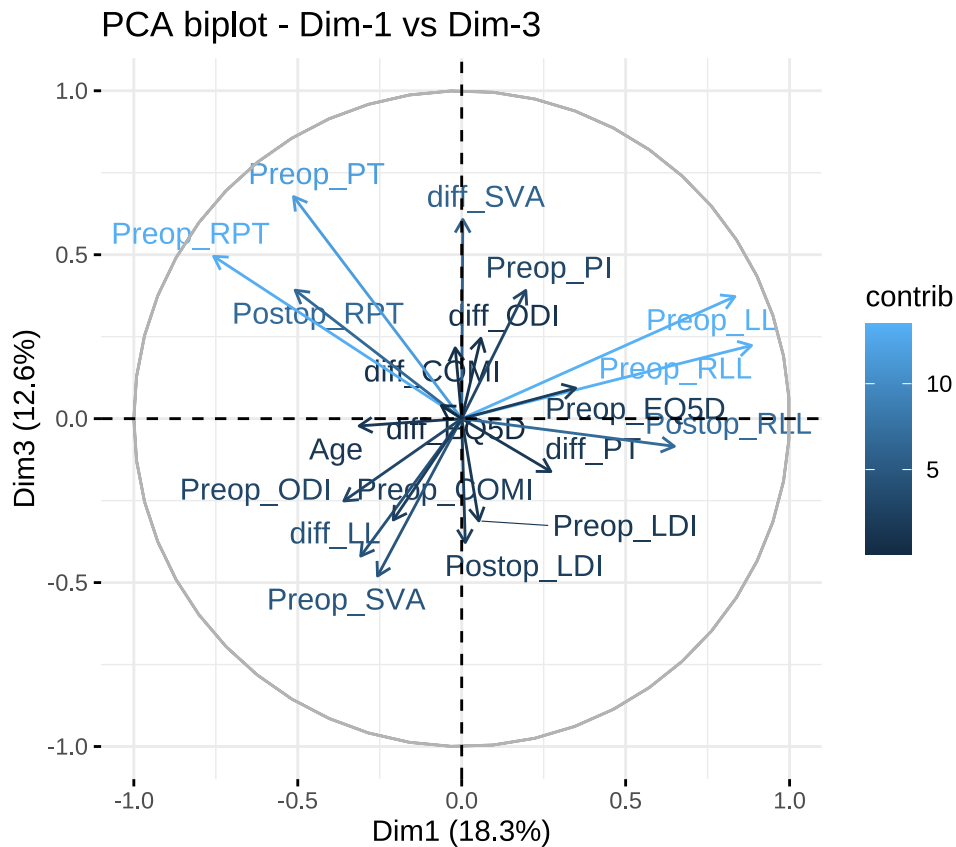
Hierarchical agglomerative clustering

- HC using Ward's criterion on the selected principal components
- 3 clusters
- Graphs for dendogram, cluster distribution according to dim 1 vs dim2 and dim2 vs dim 3

```
res.hcpc <- HCPC(res.pca, graph = F)

fviz_dend(res.hcpc, palette = "jco", rect = T, rect_fill = T, rect_border = "jco")
```

Cluster Dendrogram
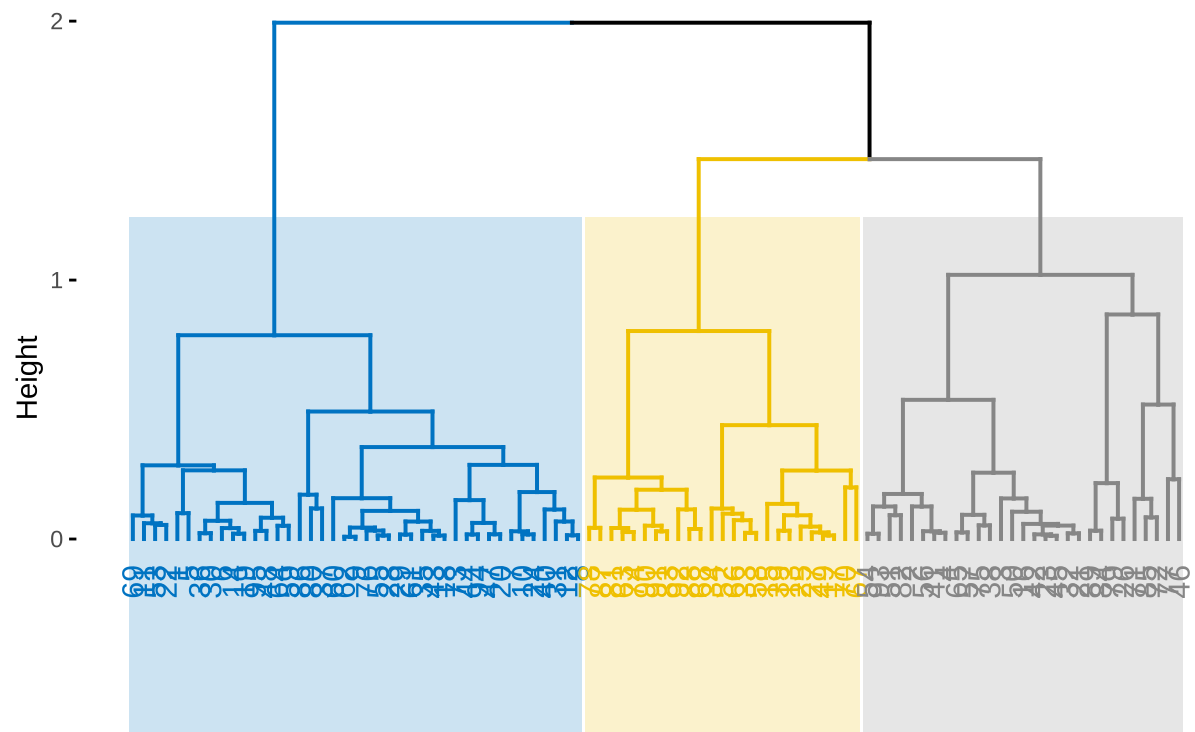

```
fviz_cluster(res.hcpc, repel = T, show.clust.cent = T, axes = c(1,2),
             palette="jco", ggtheme = theme_minimal(), title="Cluster plot according to PCA Dim-1 and D
```

Cluster plot according to PCA Dim-1 and Dim-2
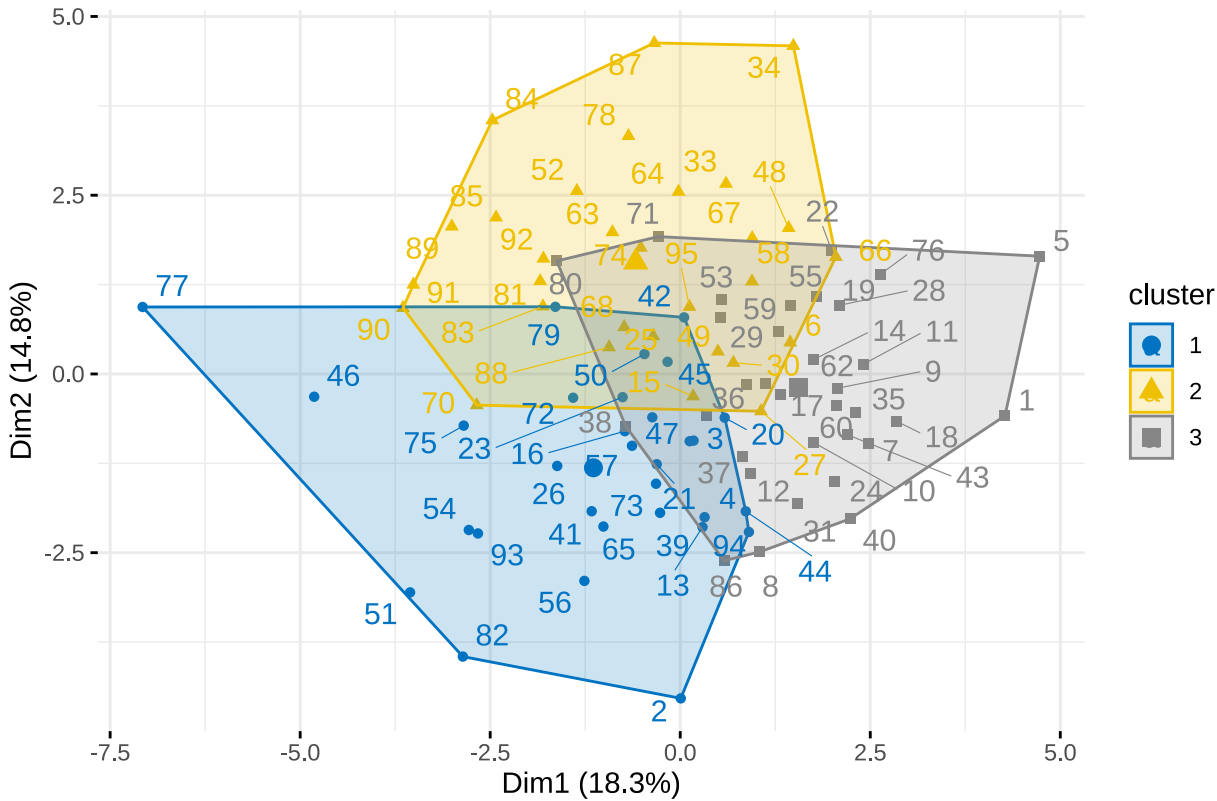

```
fviz_cluster(res.hcpc, repel = T, show.clust.cent = T, axes = c(2,3),
             palette="jco", ggtheme = theme_minimal(), title="Cluster plot according to PCA Dim-2 and D
```

Table 7: Proportion of patients for each cluster

Clusters	Freq
1	0.326
2	0.316
3	0.358

Cluster plot according to PCA Dim-2 and Dim-3
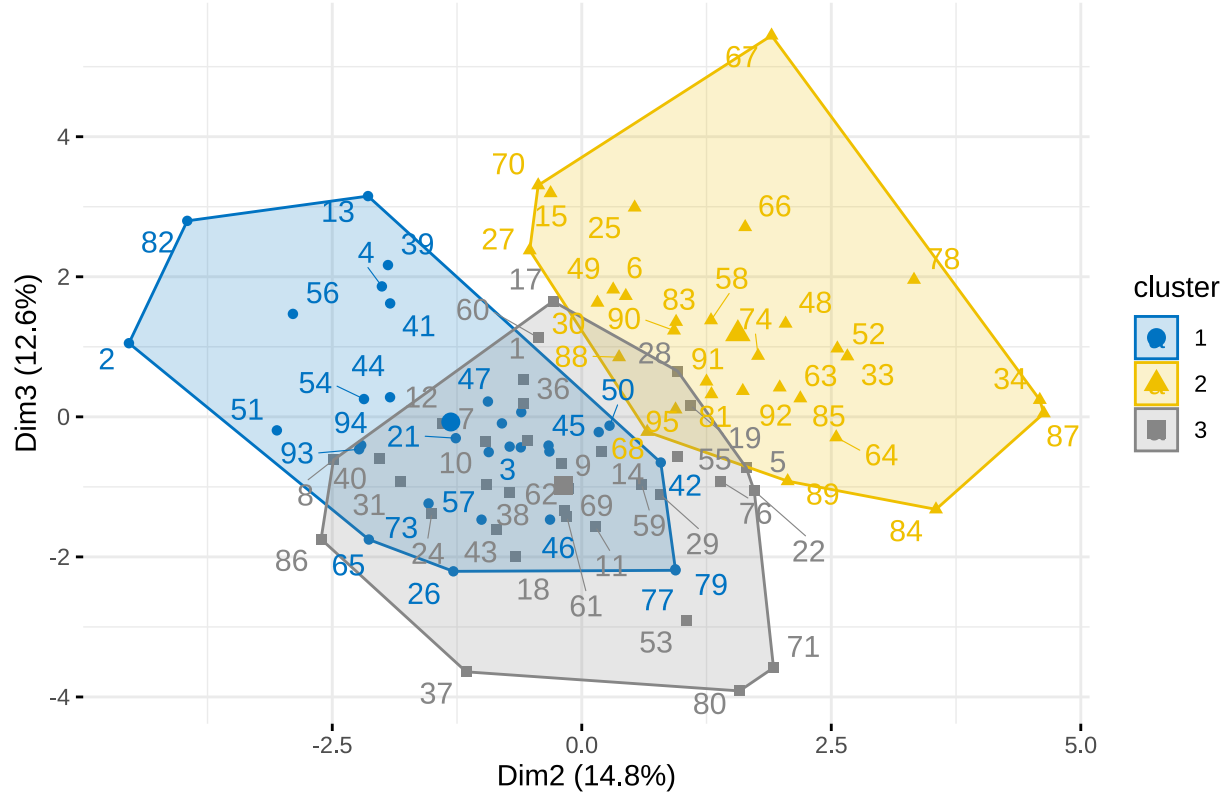

```
data_cont_clust <- res.hcpc$data.clust
```

Cluster interpretation

- cluster 1 with 31 patients (32.6%), cluster 2 with 30 patients (31.6%), cluster 3 with 34 patients (35.8%)
- Patients classified in the cluster 2 showed significant greater LL decrease (mean values for cluster 1, 2 and 3: 3.3o, -5.6 and 0.8), SVA increase after surgery (-5 mm, +25 mm and -19 mm) and no improvement of the functional status, (ODI variation: -23.1, 3.77 and -17.1)

```
round(prop.table(table(data_cont_clust$clust, dnn=c("Clusters"))), 3) %>%
    kbl(caption = "Proportion of patients for each cluster") %>%
    kable_classic("hover", full_width = F)

#1 diff LL, improvement of lordosis

plot_3 <- ggboxplot(data_cont_clust, x = "clust", y = "diff_LL",
```
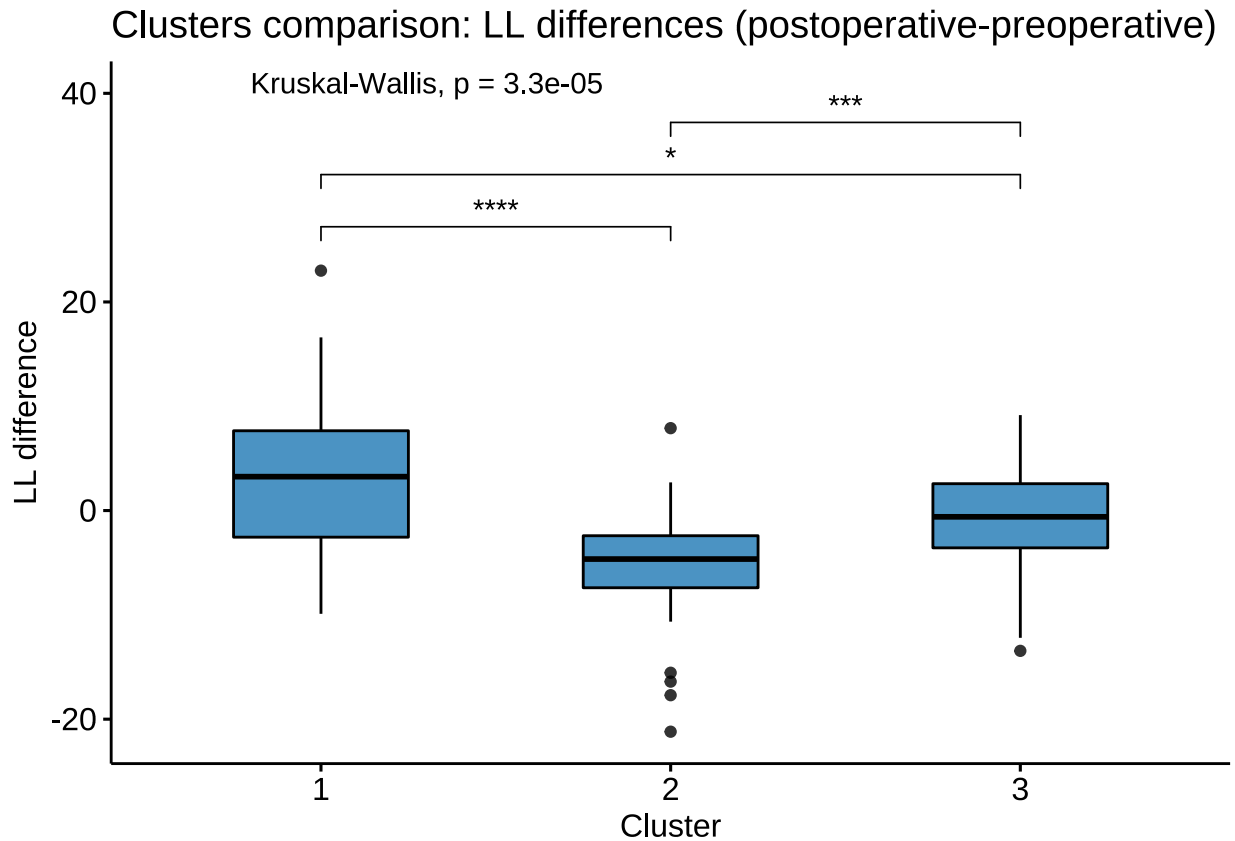
Table 8: Clusters: mean values for LL difference

clust	mean_diff_LL
1	3.3096774
2	-5.6033333
3	-0.7573529

```
        xlab = "Cluster", ylab = "LL difference",
        width=0.5, fill = "#1f78b4", alpha=0.8,
        title = "Clusters comparison: LL differences (postoperative-preoperative)") +
        stat_compare_means(aes(label = ..p.signif..),
                  comparisons = list( c("1", "2"), c("1", "3"), c("2", "3") ),
                  label.y = c(25, 30, 35))+
        stat_compare_means(label.y = 40)

plot_3
```


Clusters comparison: LL differences (postoperative-preoperative)

```
data_cont_clust %>% group_by(clust) %>% summarise(mean_diff_LL=mean(diff_LL)) %>%
    kbl(caption = "Clusters: mean values for LL difference") %>%
    kable_classic("hover", full_width = F)

#2 diff PT, the lower the value, the greater the improvement

ggboxplot(data_cont_clust, x = "clust", y = "diff_PT",
        xlab = "Cluster", ylab = "Pelvic Tilt difference",
```
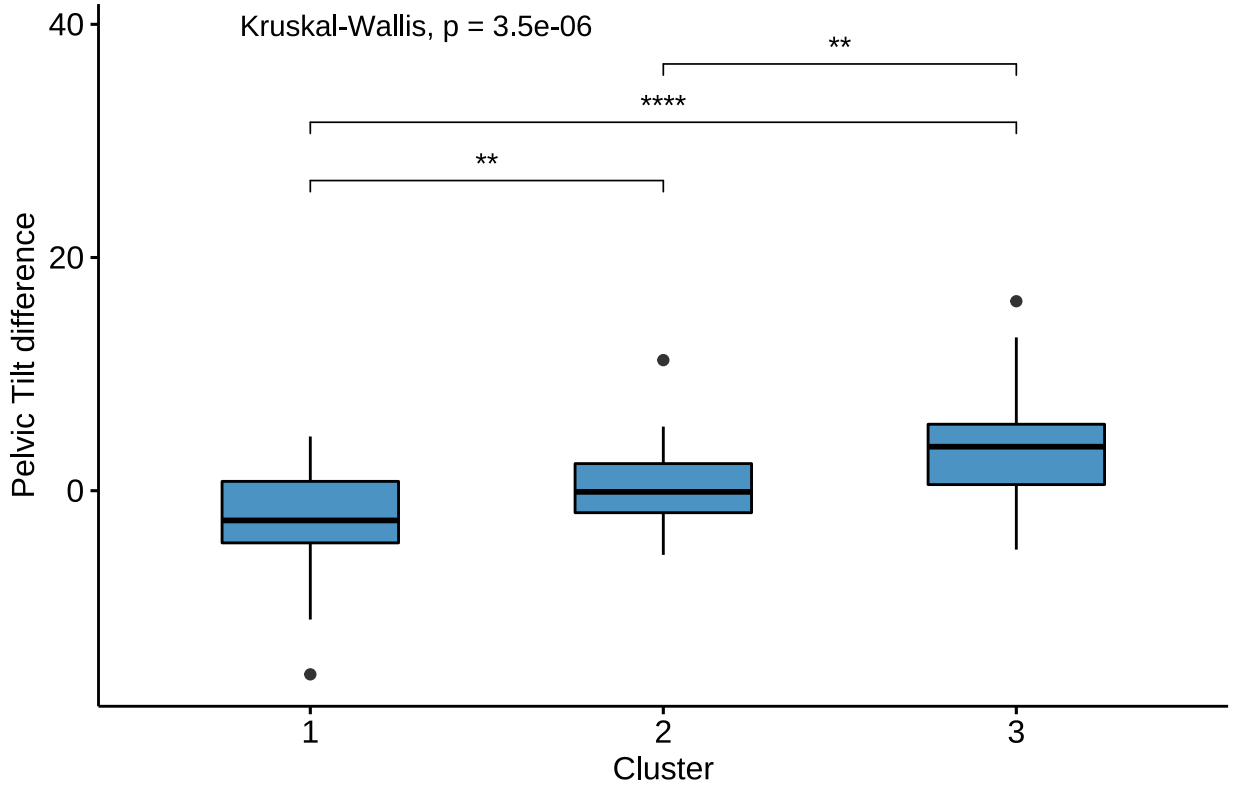
Table 9: Clusters: mean values for PT difference

clust	mean__diff__PT
1	-2.4032258
2	0.5166667
3	3.6470588

```
        width=0.5, fill = "#1f78b4", alpha=0.8,
         title = "Clusters comparison: PT differences") +
   stat_compare_means(aes(label = ..p.signif..),
                  comparisons = list( c("1", "2"), c("1", "3"), c("2", "3") ),
                  label.y = c(25, 30, 35))+
   stat_compare_means(label.y = 39)
```

Clusters comparison: PT differences


```
data_cont_clust %>% group_by(clust) %>% summarise(mean_diff_PT=mean(diff_PT)) %>%
  kbl(caption = "Clusters: mean values for PT difference") %>%
    kable_classic("hover", full_width = F)
```

```
#SVA

plot_4 <- ggboxplot(data_cont_clust, x = "clust", y = "diff_SVA",
         xlab = "Cluster", ylab = "SVA C7 difference",
         width=0.5, fill = "#1f78b4", alpha=0.8,
         title = "Clusters comparison: SVA C7 differences") +
         stat_compare_means(aes(label = ..p.signif..),
```
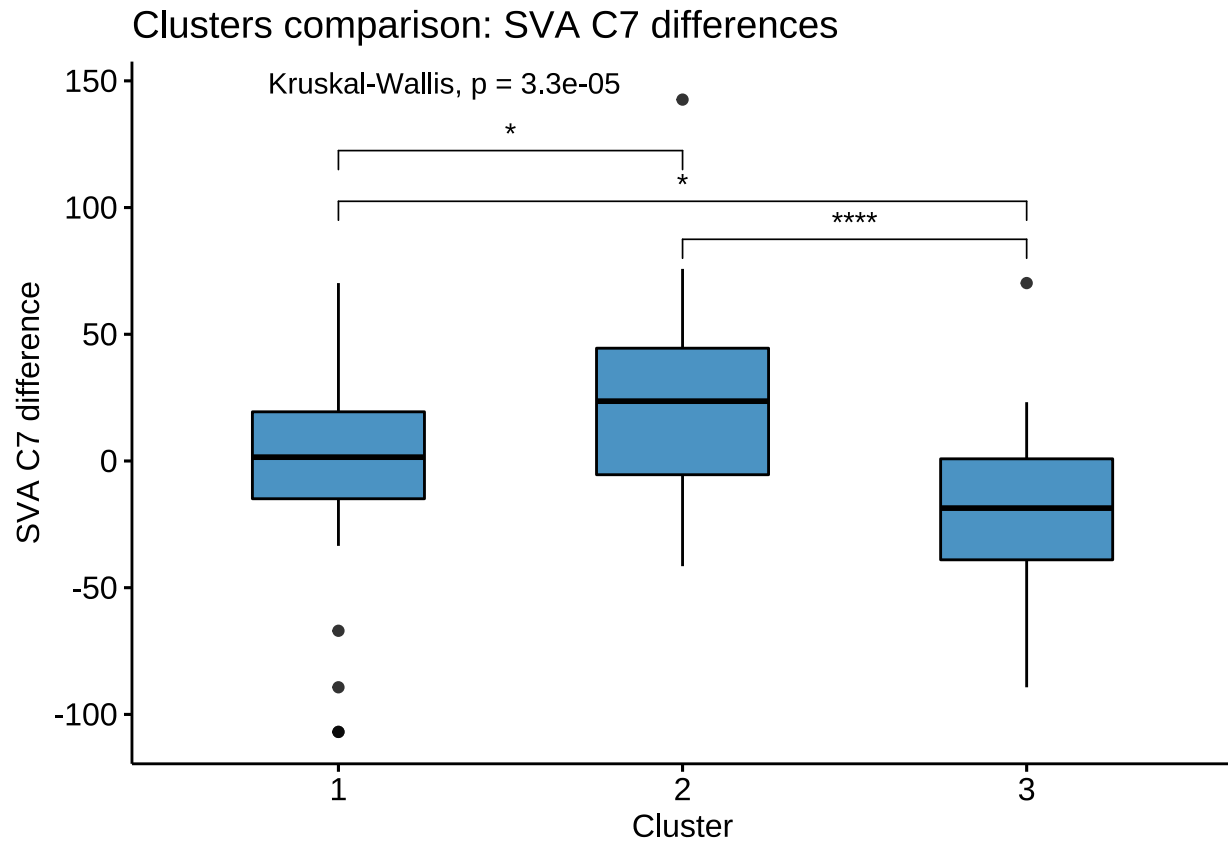
Table 10: Clusters: mean values for SVA C7 difference

clust	mean_diff_SVA
1	-4.874193
2	24.756667
3	-19.405882

```
                    comparisons = list( c("1", "2"), c("1", "3"), c("2", "3") ),
                    label.y = c(110, 90, 75))+
            stat_compare_means(label.y = 145)


data_cont_clust %>% group_by(clust) %>% summarise(mean_diff_SVA=mean(diff_SVA)) %>%
    kbl(caption = "Clusters: mean values for SVA C7 difference") %>%
    kable_classic("hover", full_width = F)
```

plot_4


```
#4 ODI improvement

plot_5 <-ggboxplot(data_cont_clust, x = "clust", y = "diff_ODI",
          xlab = "Cluster", ylab = "ODI difference",
          width=0.5, fill = "#1f78b4", alpha=0.8,
          title = "Clusters comparison: ODI differences") +
          stat_compare_means(aes(label = ..p.signif..),
```
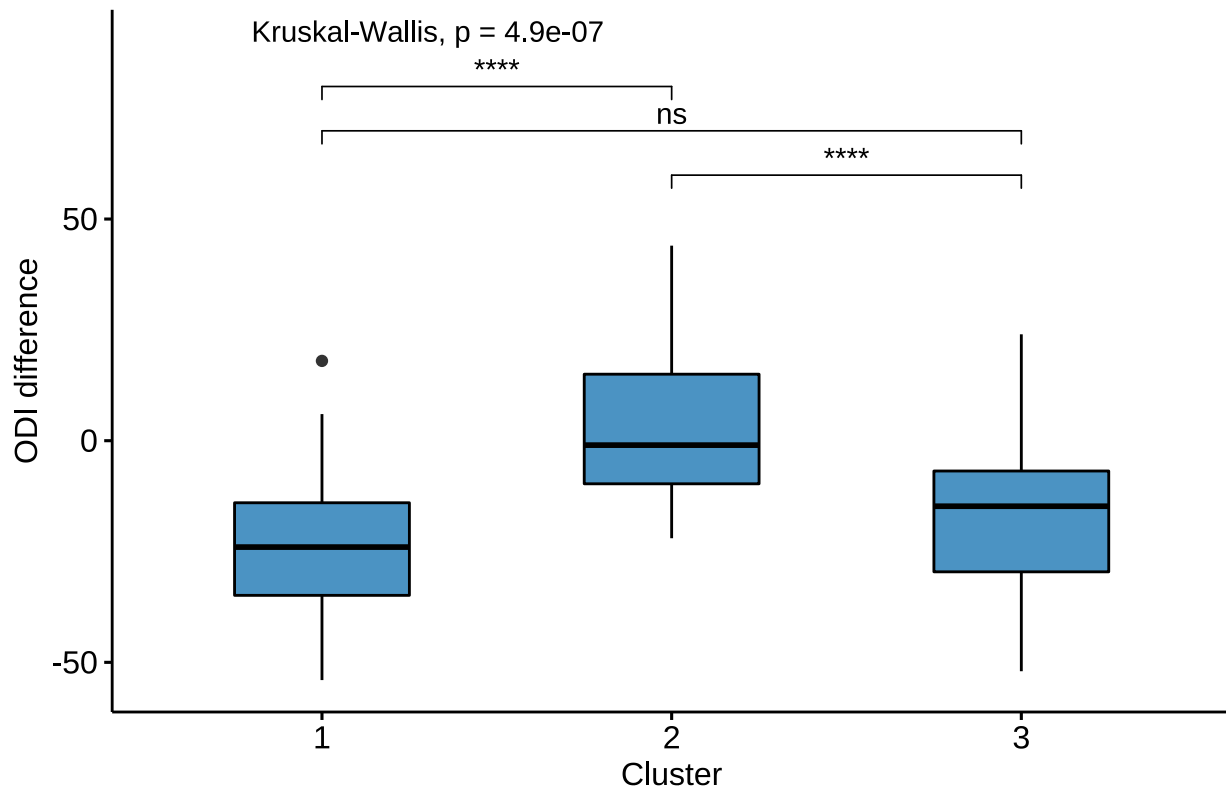
Table 11: Clusters: mean values for ODI difference

clust	mean_diff_ODI
1	-23.09258
2	3.76900
3	-17.11441

```
                    comparisons = list( c("1", "2"), c("1", "3"), c("2", "3") ),
                    label.y = c(75, 65, 55))+
          stat_compare_means(label.y = 90)

plot_5
```

Clusters comparison: ODI differences


```
data_cont_clust %>% group_by(clust) %>% summarise(mean_diff_ODI=mean(diff_ODI)) %>%
    kbl(caption = "Clusters: mean values for ODI difference") %>%
    kable_classic("hover", full_width = F)
```

## Cluster interpretation - basal state

- No remarks

Table 12: Clusters: mean values for preoperative RLL

clust	mean_RLL_pre
1	-5.1710
2	-3.0032
3	4.7045

```
#1 Preoperative RLL

data_cont_clust %>% group_by(clust) %>% summarise(mean_RLL_pre=mean(Preop_RLL)) %>%
    kbl(caption = "Clusters: mean values for preoperative RLL") %>%
  kable_classic("hover", full_width = F)
```

```
ggboxplot(data_cont_clust, x = "clust", y = "Preop_RLL",
        xlab = "Cluster", ylab = "Preoperative RLL",
        width=0.5, fill = "#1f78b4", alpha=0.8,
        title="Clusters comparison: preoperative RLL") +
  stat_compare_means(aes(label = ..p.signif..),
                    comparisons = list( c("1", "2"), c("1", "3"), c("2", "3") ),
                    label.y = c(35, 25, 20))+
  stat_compare_means(label.y = 49)
```

Clusters comparison: preoperative RLL
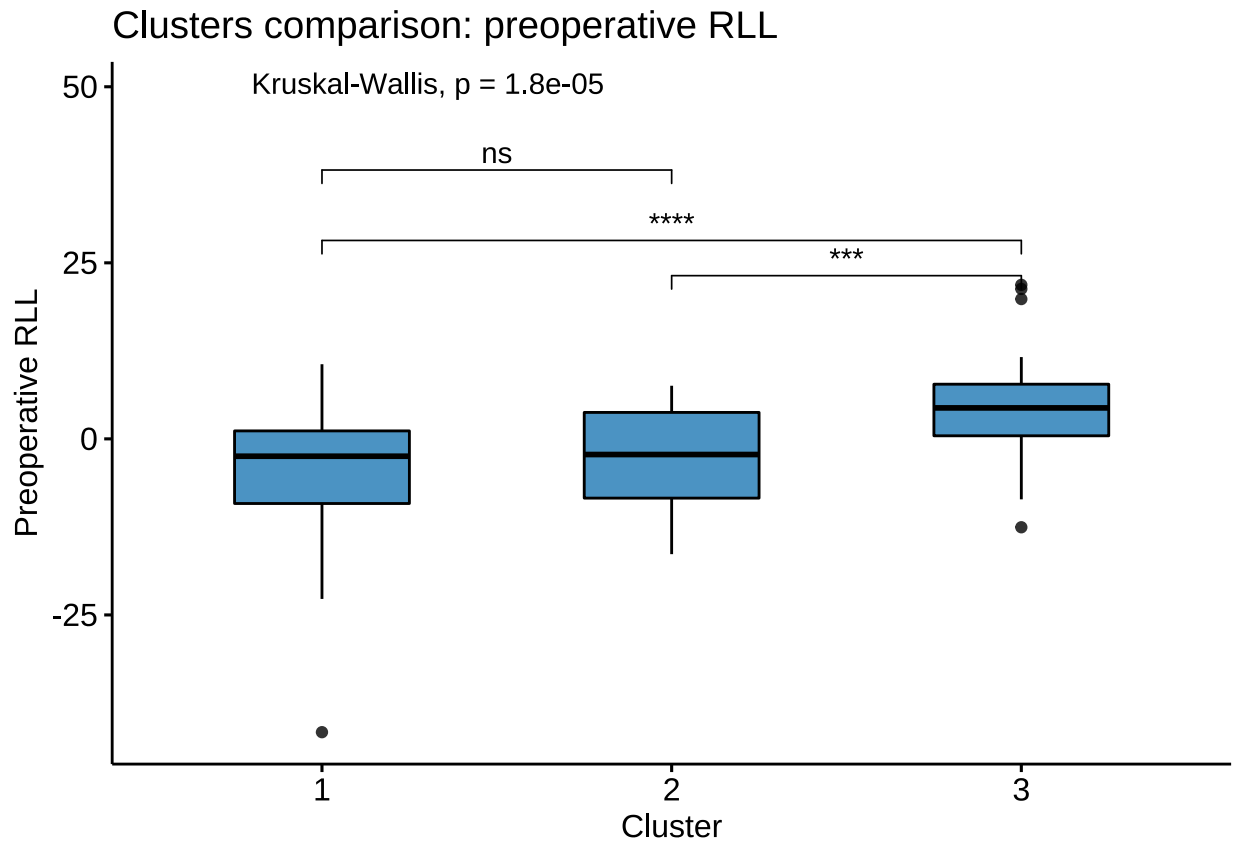

```
#2 Preoperatice RPT

ggboxplot(data_cont_clust, x = "clust", y = "Preop_RPT",
```

Table 13: Clusters: mean values for preoperative RPT

clust	mean_RPT_pre
1	5.455290
2	6.579800
3	-1.682118

```
        xlab = "Cluster", ylab = "Preoperative RPL",
        width=0.5, fill = "#1f78b4", alpha=0.8,
        title = "Clusters comparison: preoperative RPT") +
  stat_compare_means(aes(label = ..p.signif..),
                    comparisons = list( c("1", "2"), c("1", "3"), c("2", "3") ),
                    label.y = c(25, 20, 15))+
  stat_compare_means(label.y = 30)
```
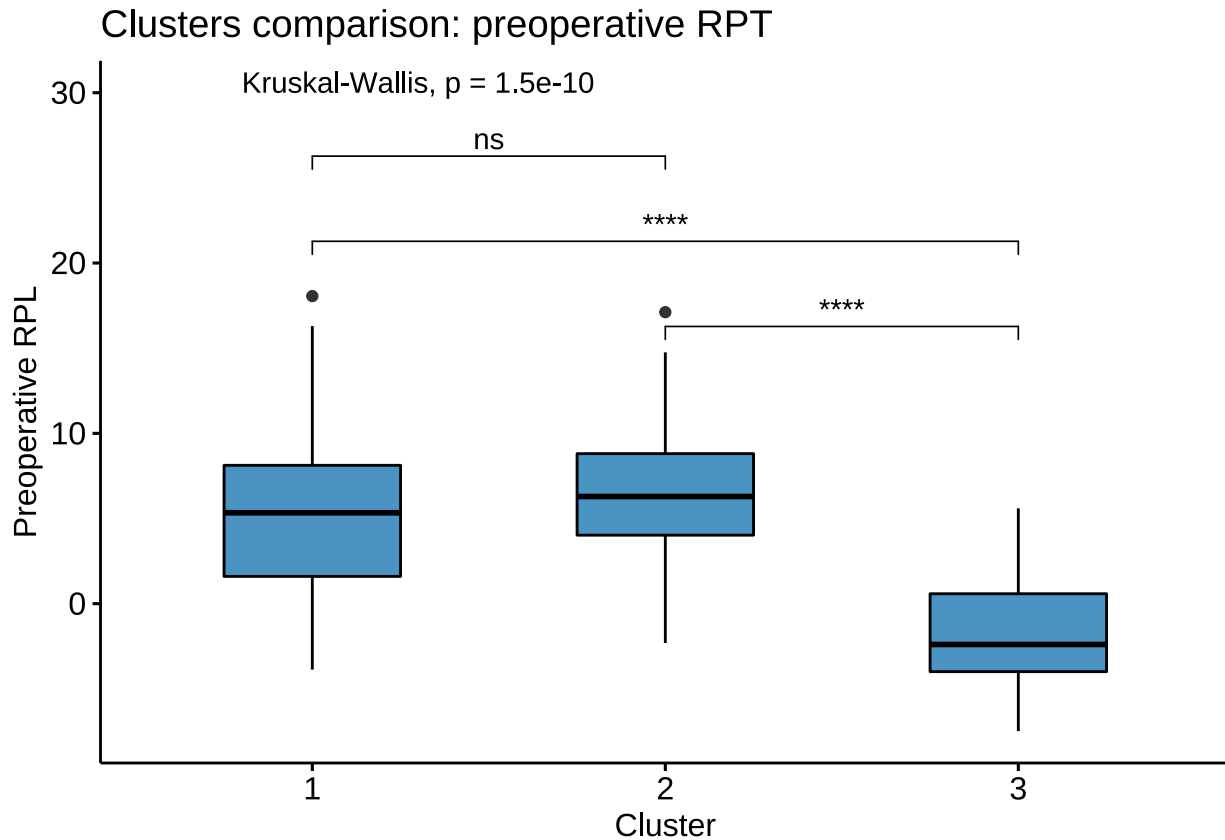


```
data_cont_clust %>% group_by(clust) %>% summarise(mean_RPT_pre=mean(Preop_RPT)) %>%
    kbl(caption = "Clusters: mean values for preoperative RPT") %>%
  kable_classic("hover", full_width = F)
```

```
#3 Preoperative ODI

ggboxplot(data_cont_clust, x = "clust", y = "Preop_ODI",
        xlab = "Cluster", ylab = "Preoperative ODI",
        width=0.5, fill = "#1f78b4", alpha=0.8,
        title = "Clusters comparison: preoperative ODI") +
```
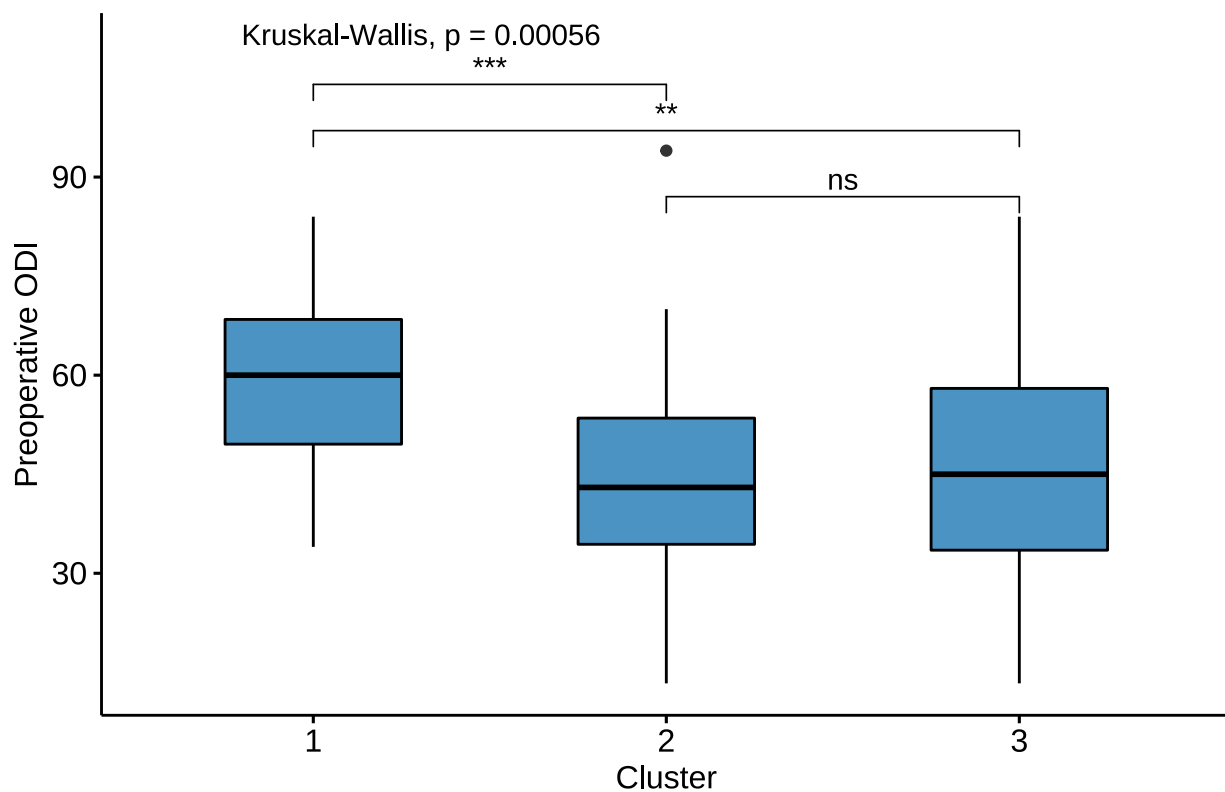
Table 14: Clusters: mean values for preoperative ODI

clust	mean_Preop_ODI
1	59.20774
2	44.67433
3	45.94088

```
    stat_compare_means(aes(label = ..p.signif..),
                       comparisons = list( c("1", "2"), c("1", "3"), c("2", "3") ),
                       label.y = c(100, 93, 83))+
    stat_compare_means(label.y = 110)
```


Clusters comparison: preoperative ODI

```
data_cont_clust %>% group_by(clust) %>% summarise(mean_Preop_ODI=mean(Preop_ODI)) %>%
    kbl(caption = "Clusters: mean values for preoperative ODI") %>%
    kable_classic("hover", full_width = F)
```

```
#4 Age

ggboxplot(data_cont_clust, x = "clust", y = "Age",
         xlab = "Cluster", ylab = "Age",
         width=0.5, fill = "#1f78b4", alpha=0.8,
         title = "Clusters comparison: Age") +
    stat_compare_means(aes(label = ..p.signif..),
                       comparisons = list( c("1", "2"), c("1", "3"), c("2", "3") ),
                       label.y = c(100, 90, 85))+
```

Table 15: Clusters: mean values for Age

clust	mean_Preop_Age
1	67.51613
2	62.86667
3	59.50000

```
    stat_compare_means(label.y = 110)
```

Clusters comparison: Age

Kruskal-Wallis, p = 0.0075
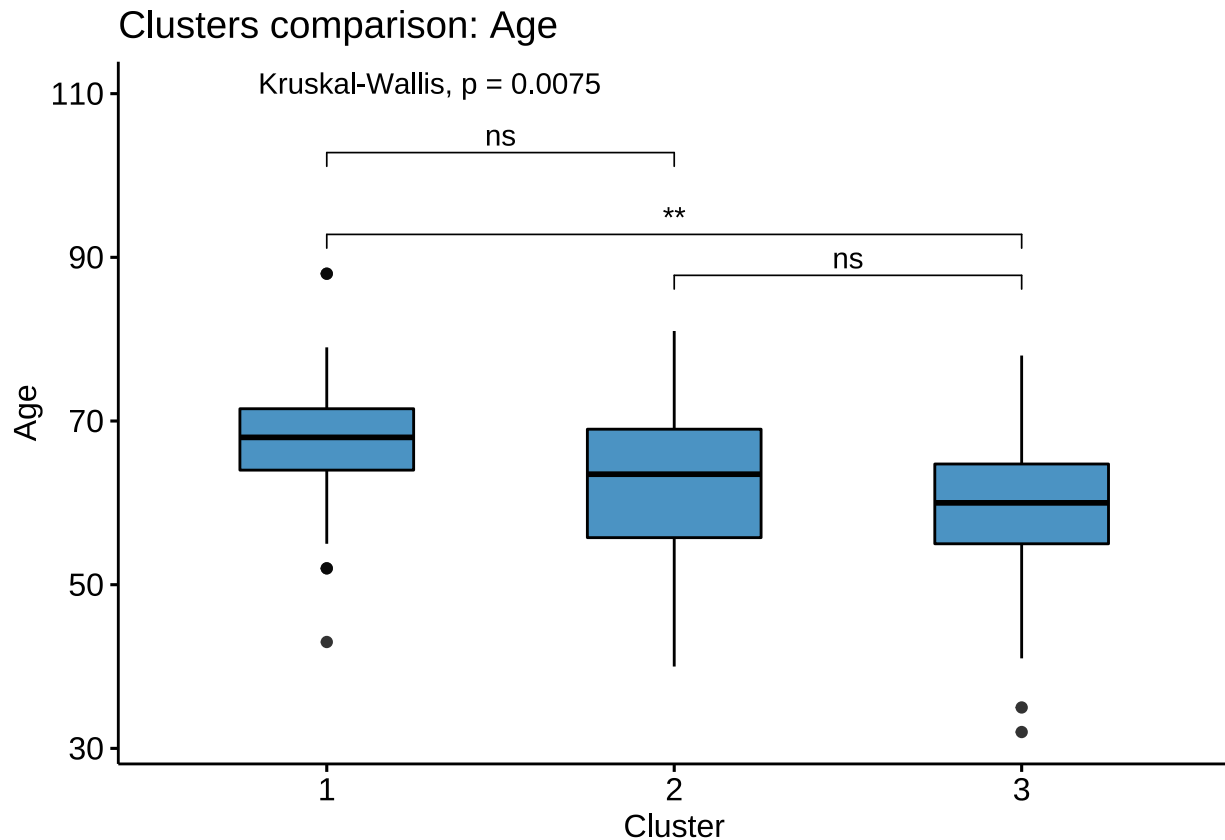

```
data_cont_clust %>% group_by(clust) %>% summarise(mean_Preop_Age=mean(Age)) %>%
      kbl(caption = "Clusters: mean values for Age") %>%
    kable_classic("hover", full_width = F)
```

Clinical correlation

- Moderate correlation between LL improvement and ODI decrease

```
tidy(cor.test(data$diff_LL, data$diff_ODI)) %>%
  select(-4, -7) %>%
  kbl(caption = "Pearson's product-moment correlation") %>%
  kable_classic("hover", full_width = F)
```

Table 16: Pearson's product-moment correlation

estimate	statistic	p.value	conf.low	conf.high	alternative
-0.3330923	-3.038907	0.0032804	-0.5195323	-0.1163763	two.sided

```
plot2 <- ggscatter(data, x = "diff_ODI", y = "diff_LL",
               add = "reg.line",
               add.params = list(color = "#1f78b4", fill = "lightgray"), # Customize reg. line
               conf.int = TRUE,
               xlab = "ODI variation", ylab = "LL variation")

plot_2 <- plot2 + stat_cor(method = "pearson", label.x = 3, label.y = 30)

plot_2
```