STATS/CSE 780
Assignment 3

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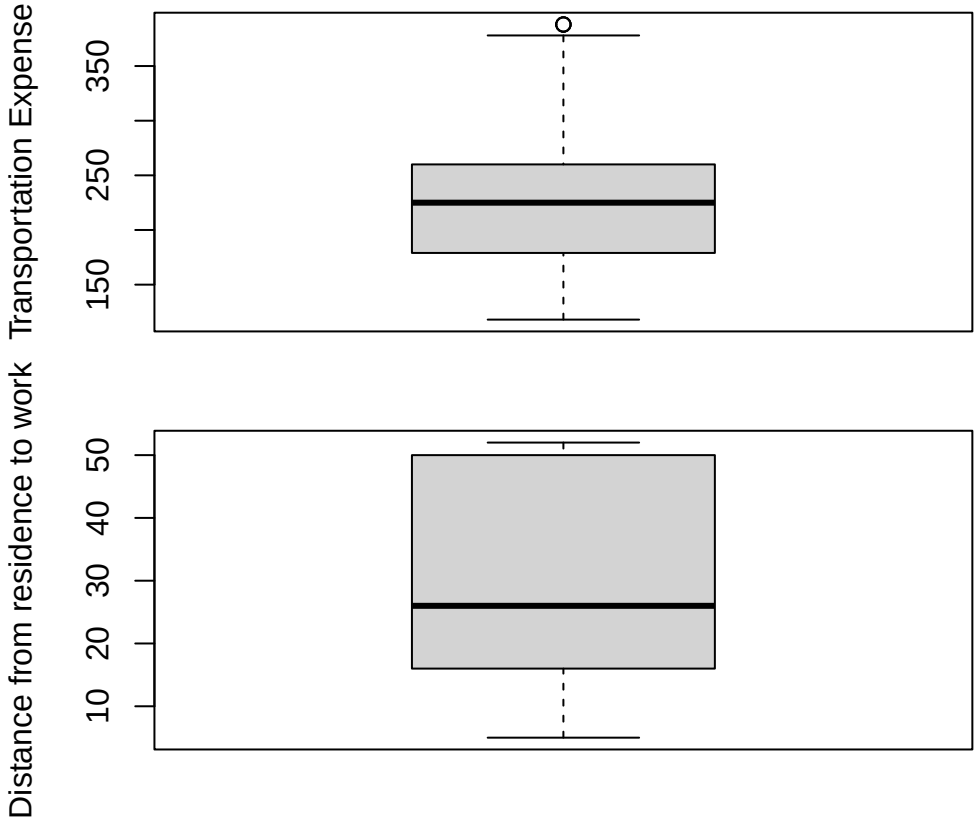
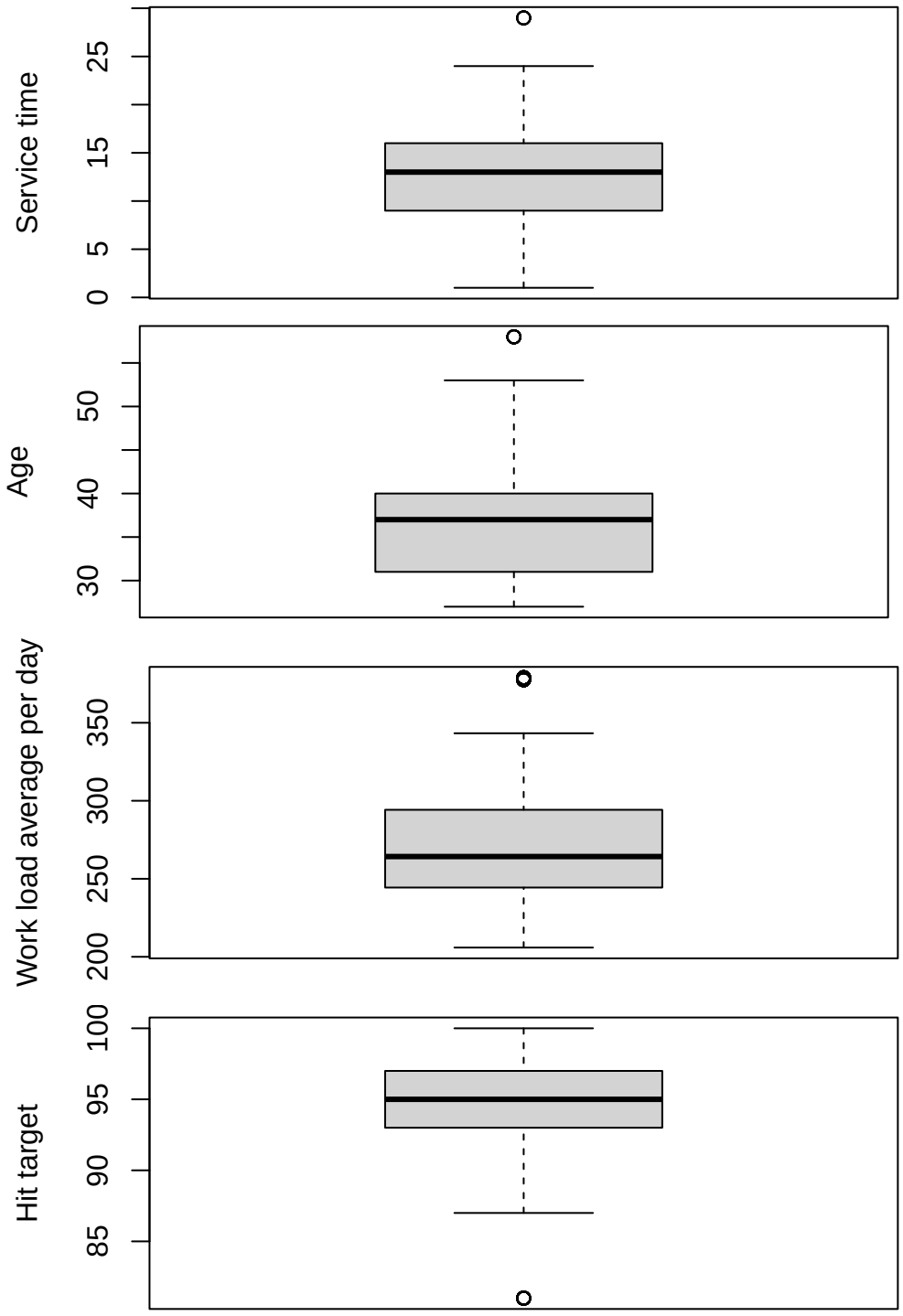
2023-11-06

	data_type	min	max	nulls_blanks
Transportation.expense	integer	118.000	388.000	0
Distance.from.Residence.to.Work	integer	5.000	52.000	0
Service.time	integer	1.000	29.000	0
Age	integer	27.000	58.000	0
Work.load.Average.day	numeric	205.917	378.884	0
Hit.target	integer	81.000	100.000	0
Son	integer	0.000	4.000	0
Pet	integer	0.000	8.000	0
Weight	integer	56.000	108.000	0
Height	integer	163.000	196.000	0
Body.mass.index	integer	19.000	38.000	0
Absenteeism.time.in.hours	integer	0.000	120.000	0

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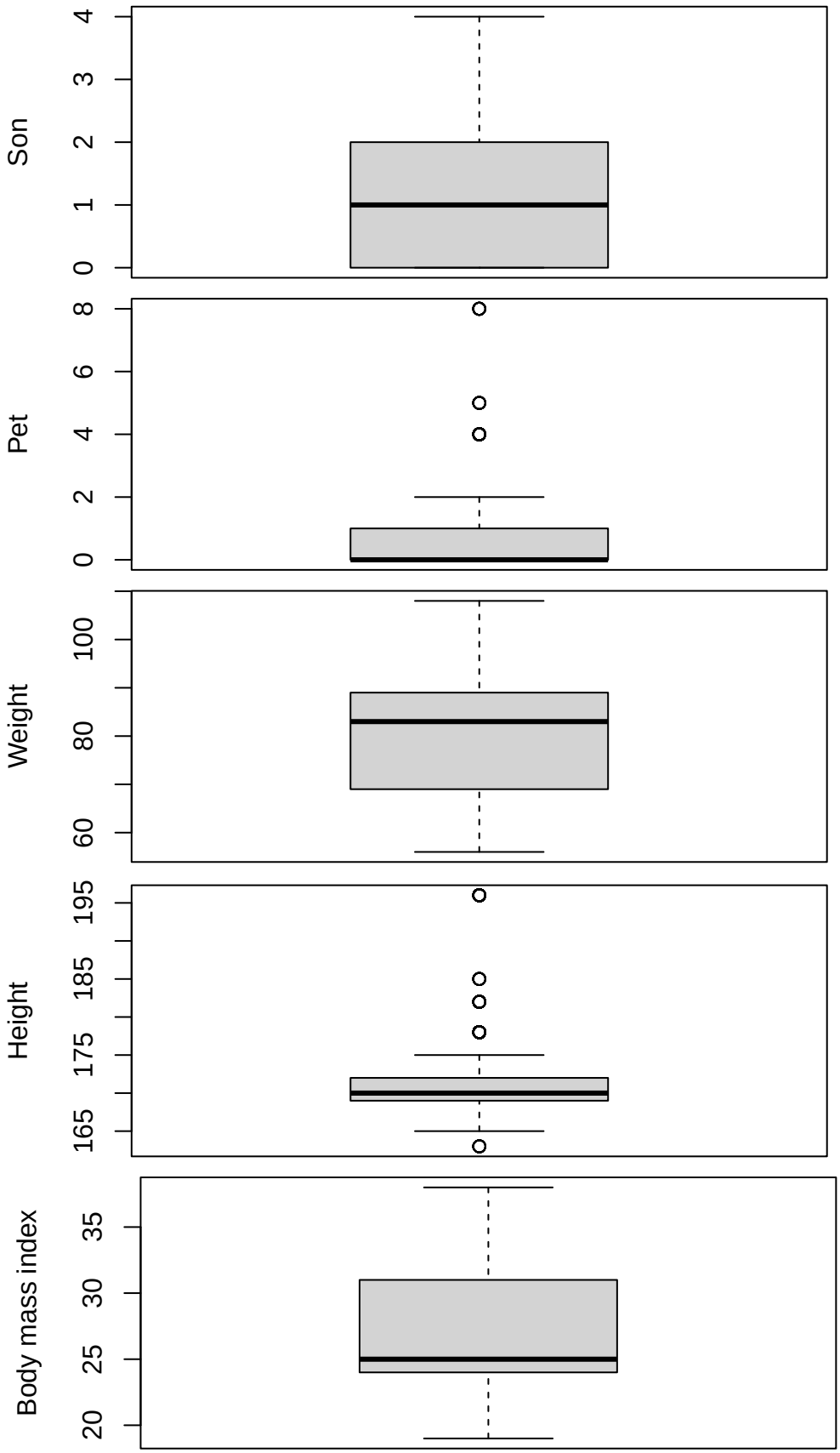
5
15
25
Age
30
40
50
Work load average per day
200
250
300
350
Hit target
85
90
95
100


Son
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1
2
3
4
Pet
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2
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6
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Weight
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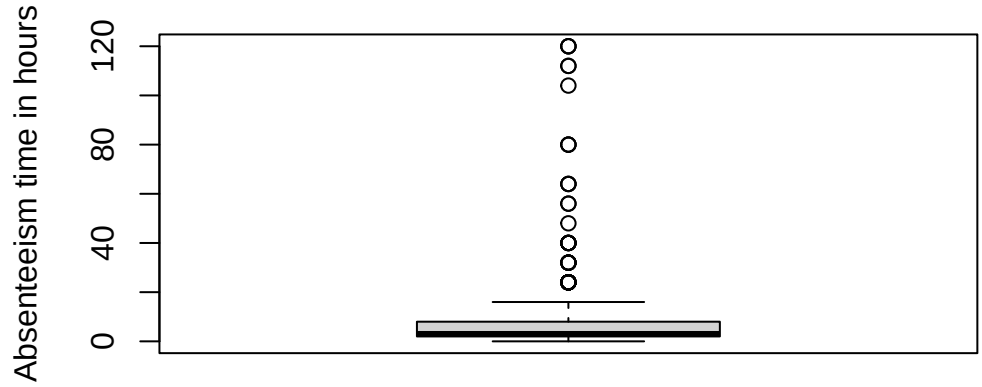
80
100
Height
165
175
185
195
Body mass index
20
25
30
35



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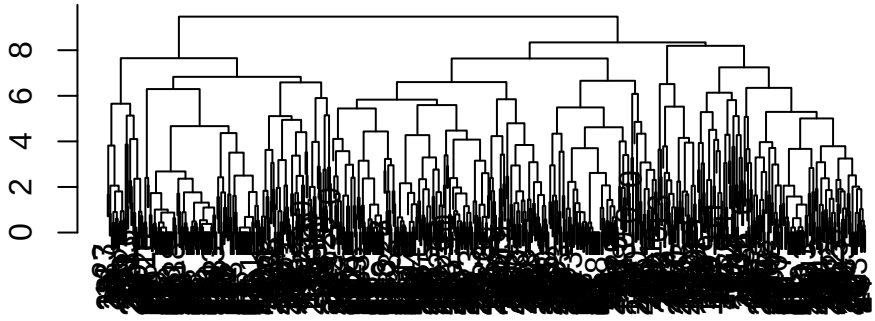

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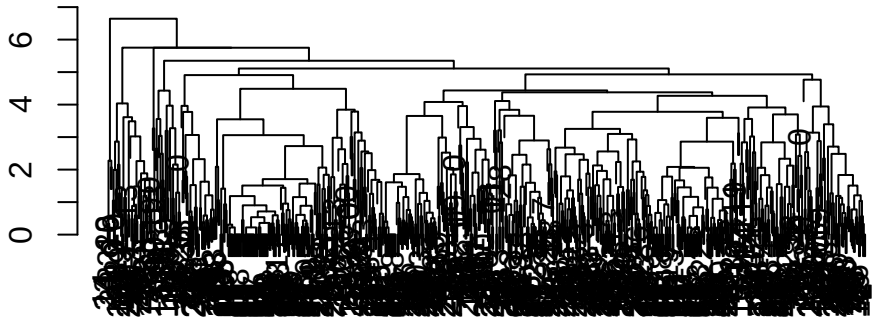

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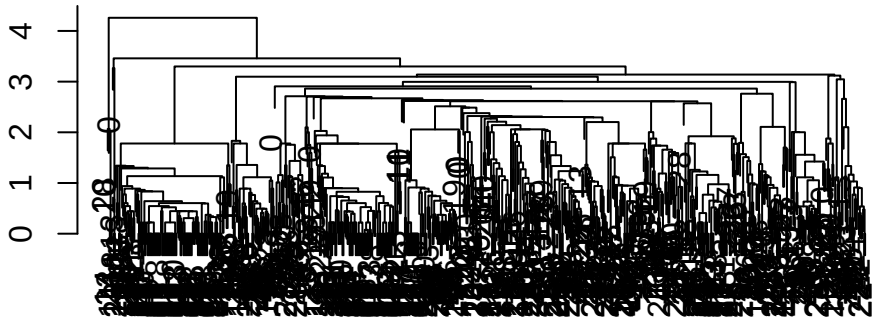

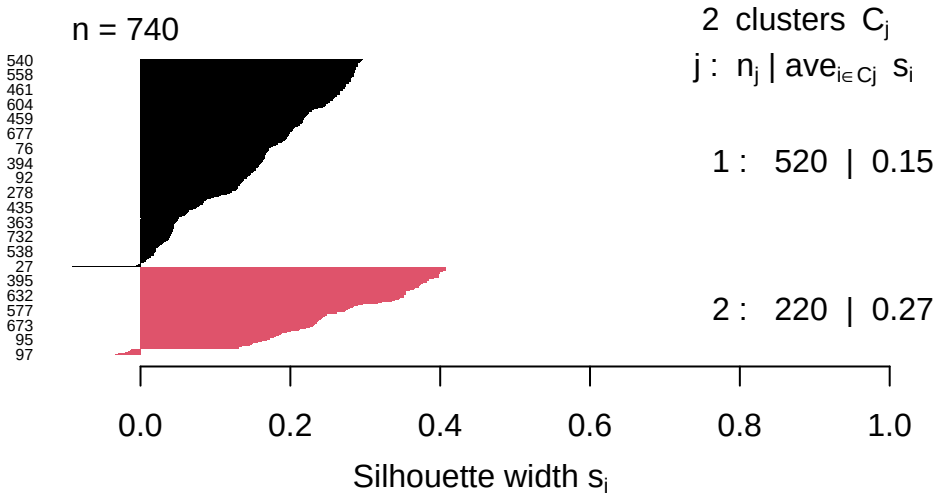

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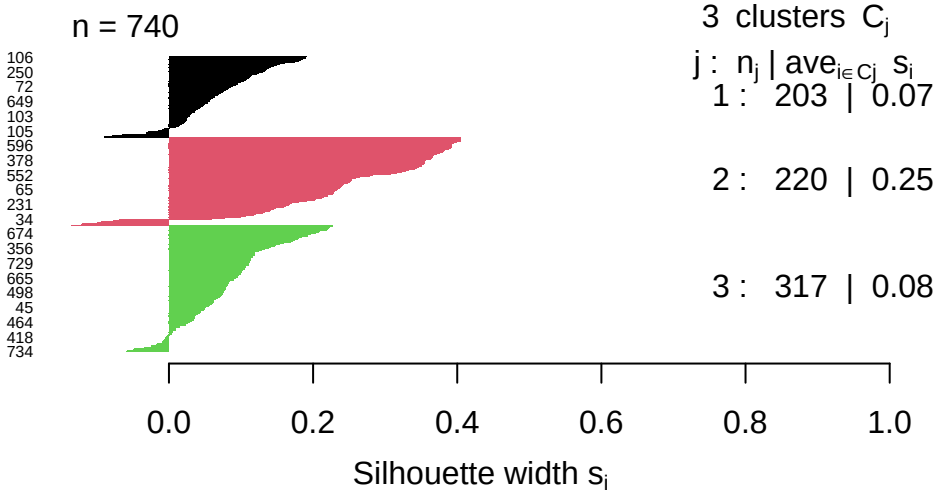

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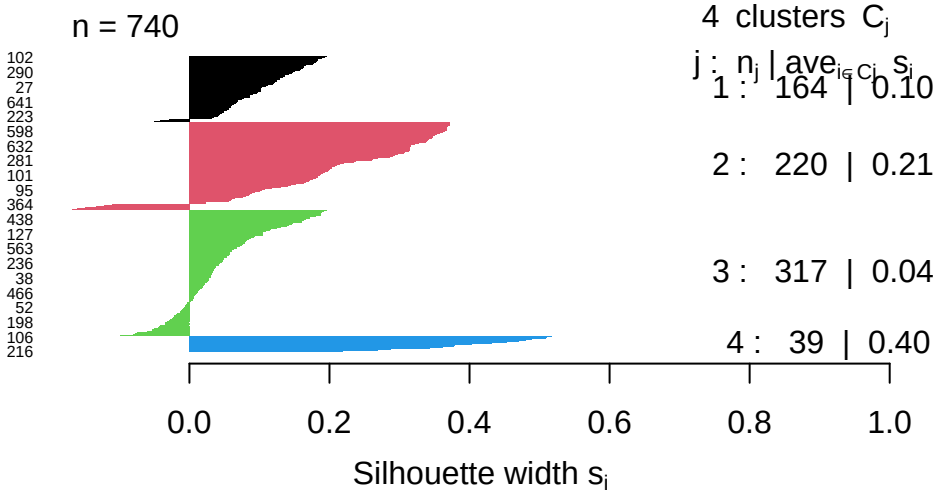

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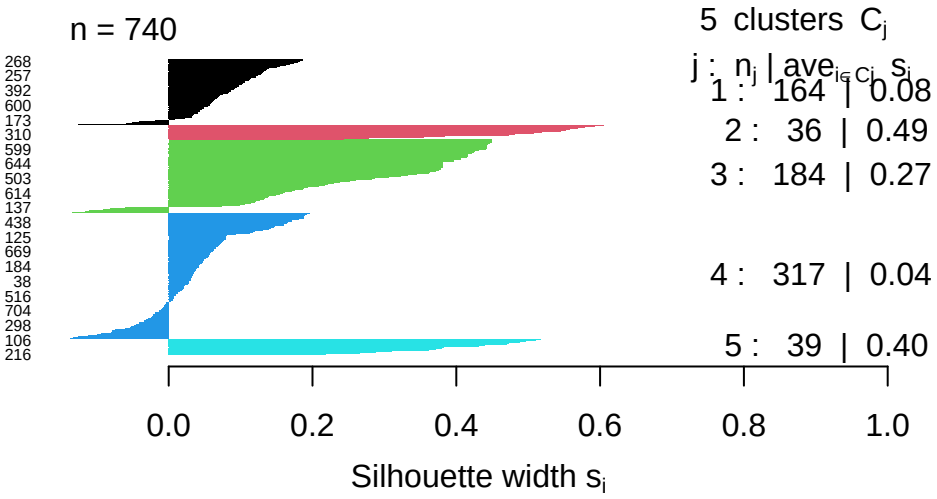

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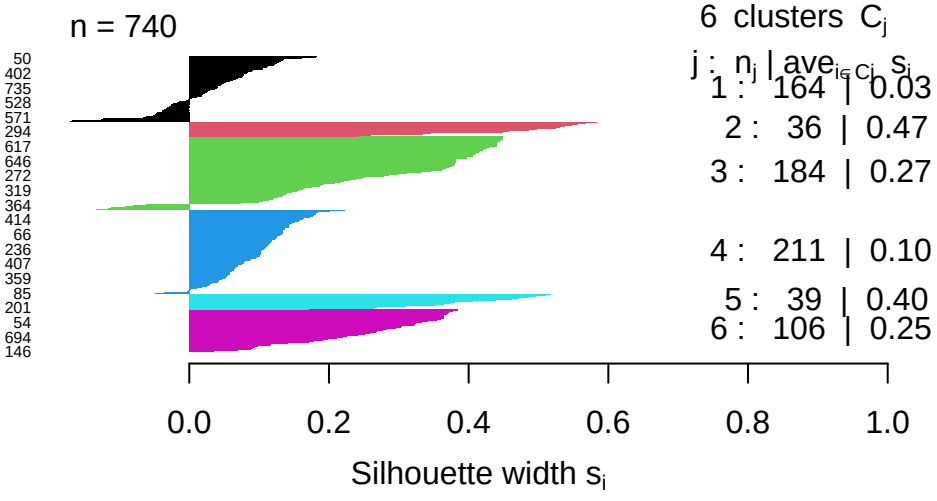

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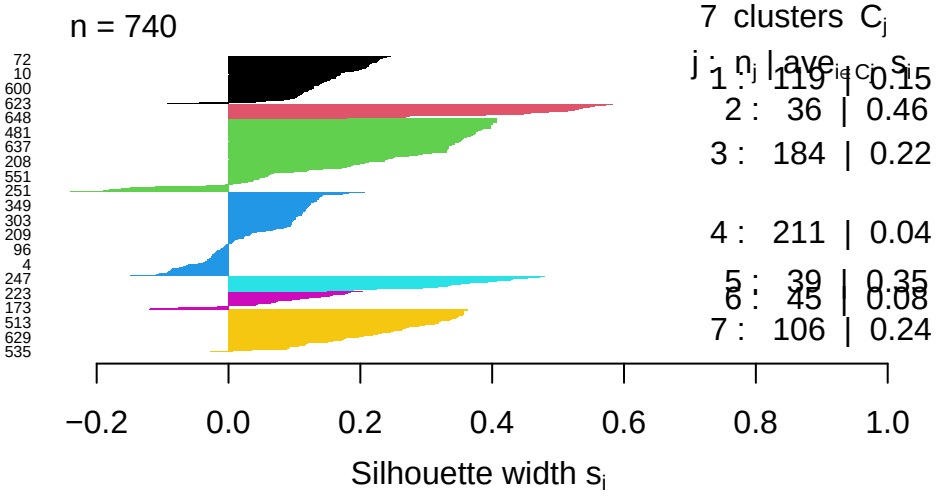

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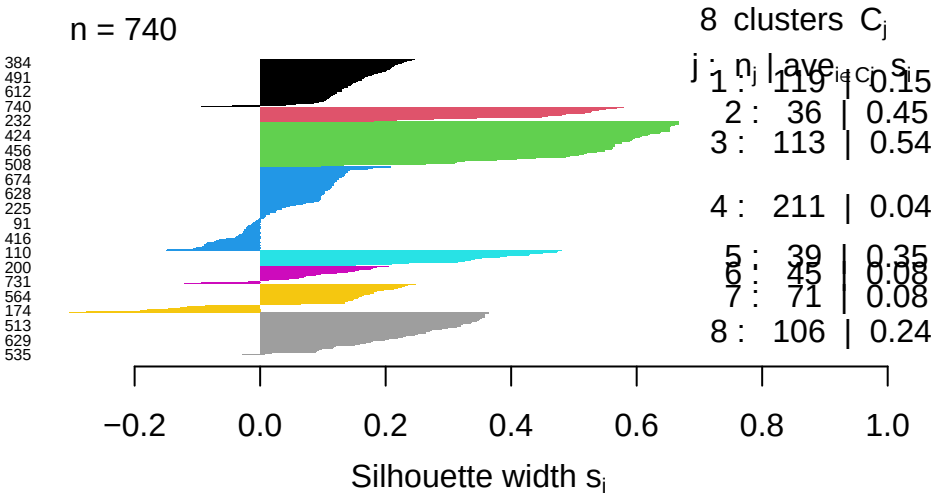

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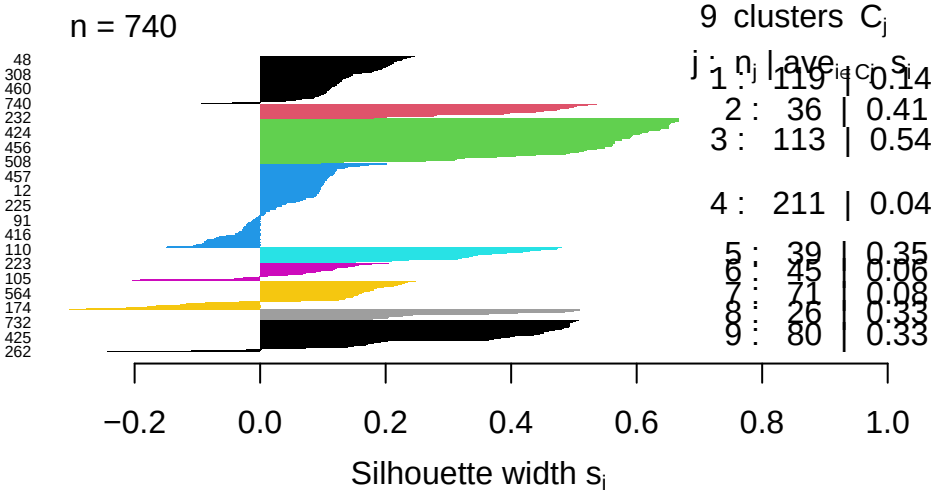

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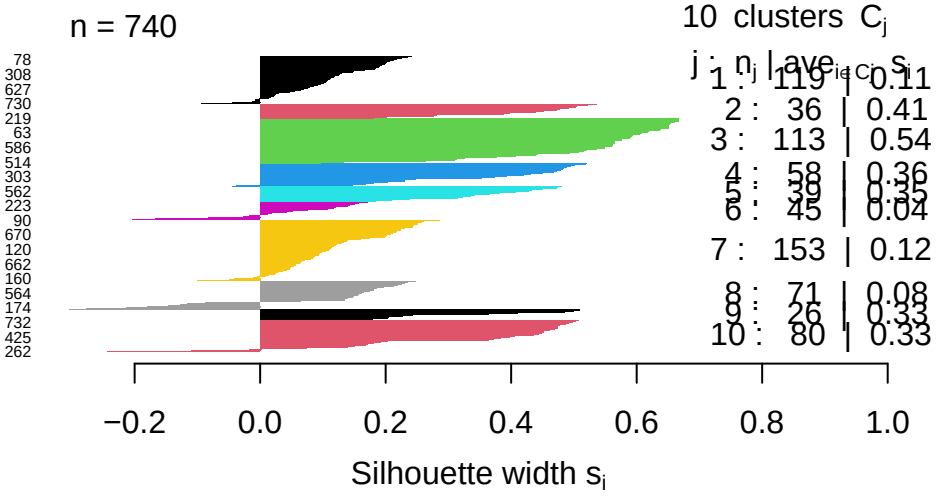

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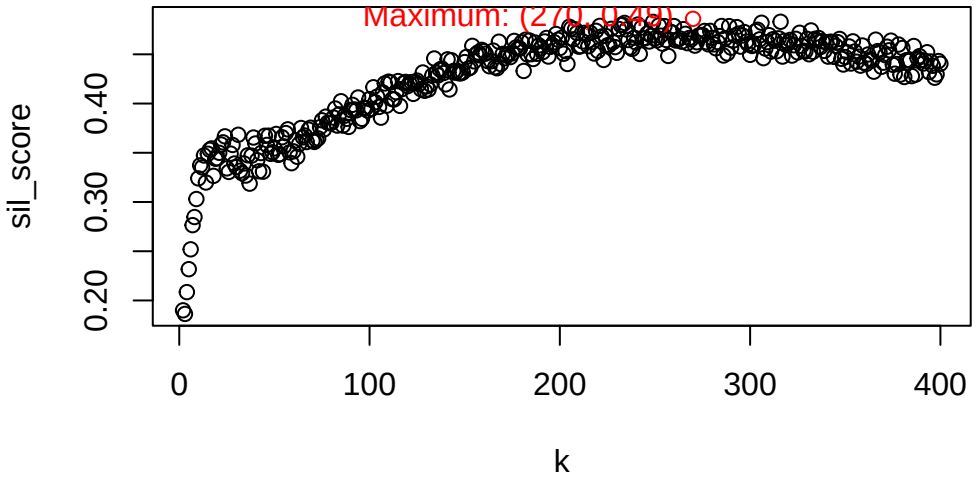

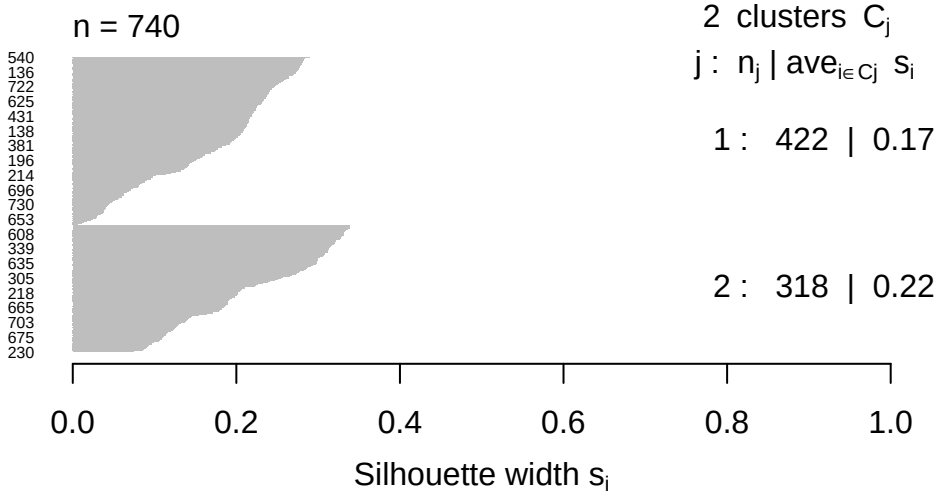

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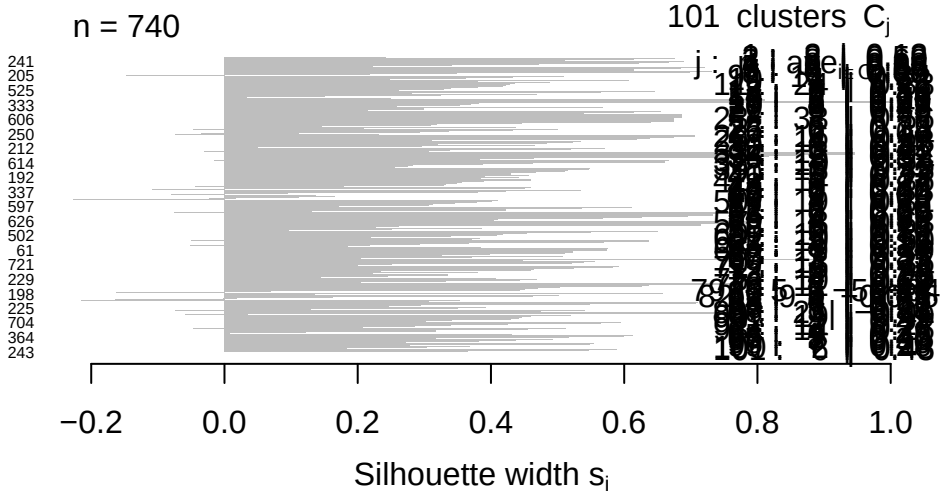

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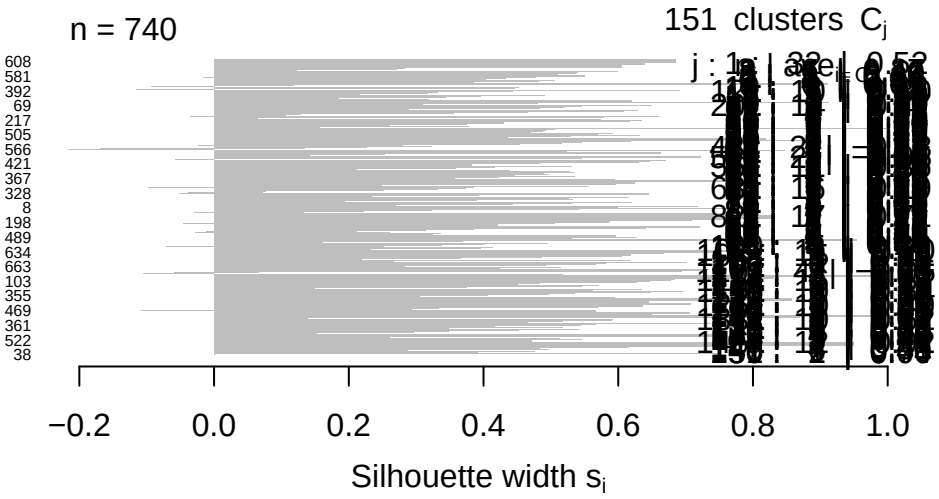

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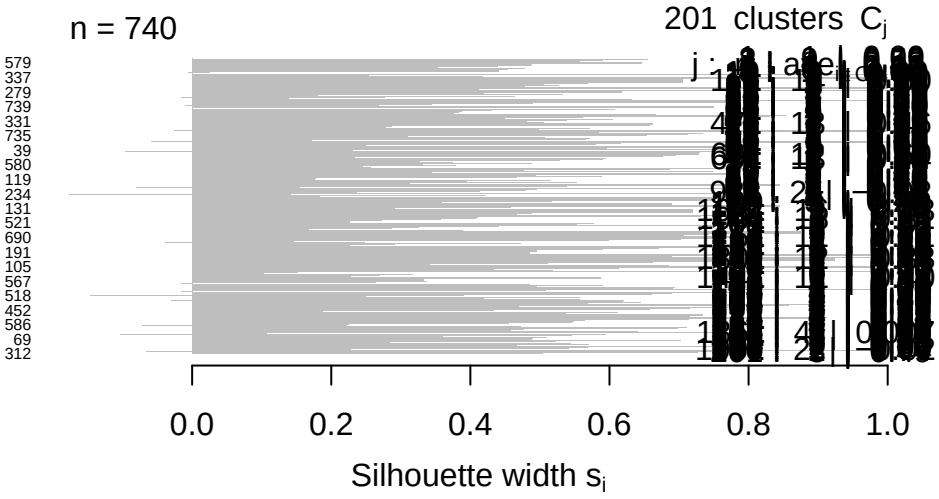

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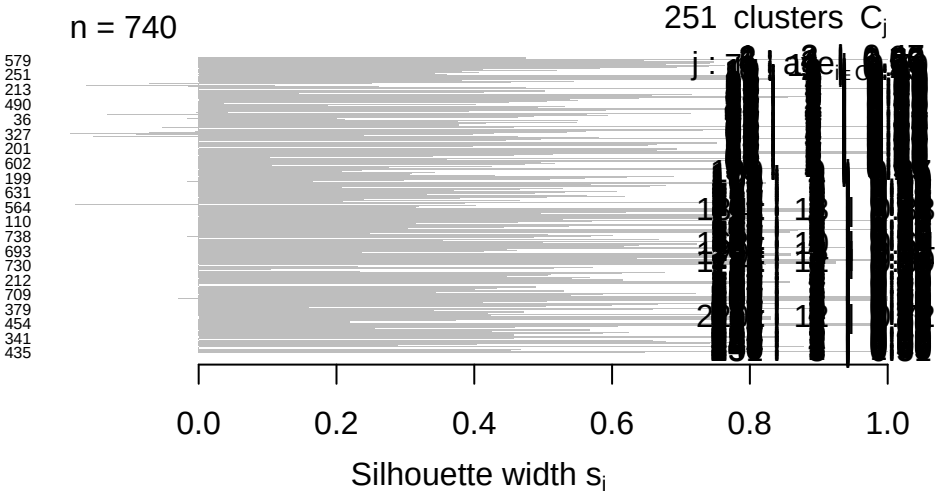

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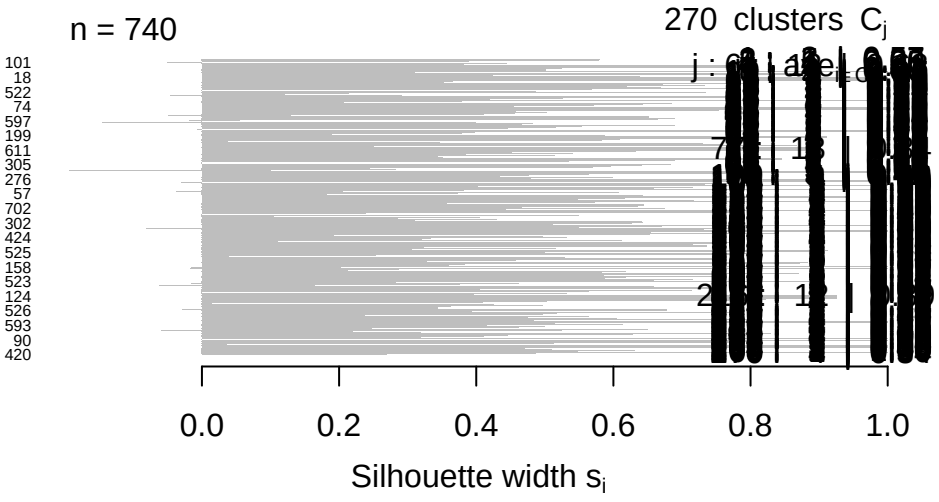

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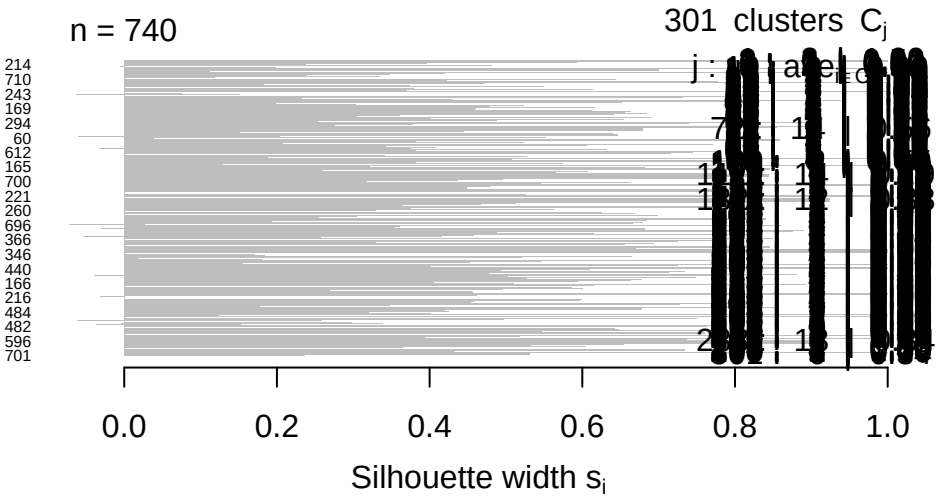

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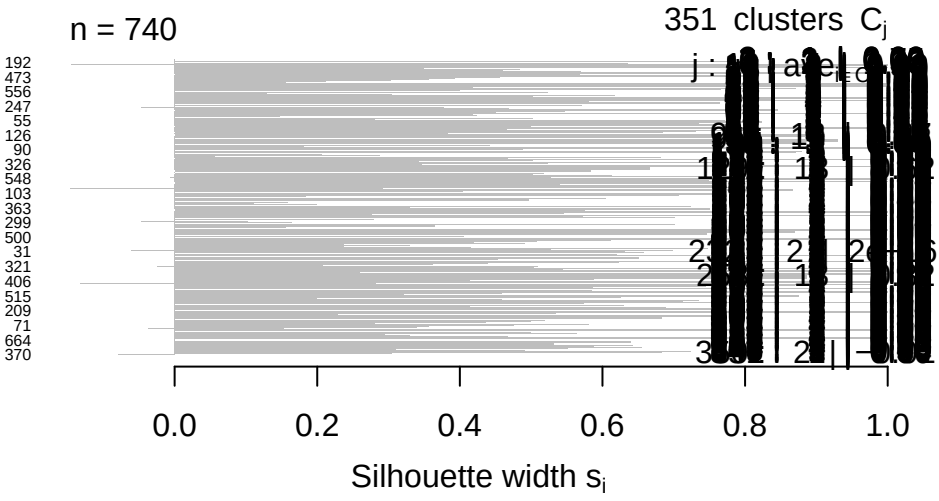

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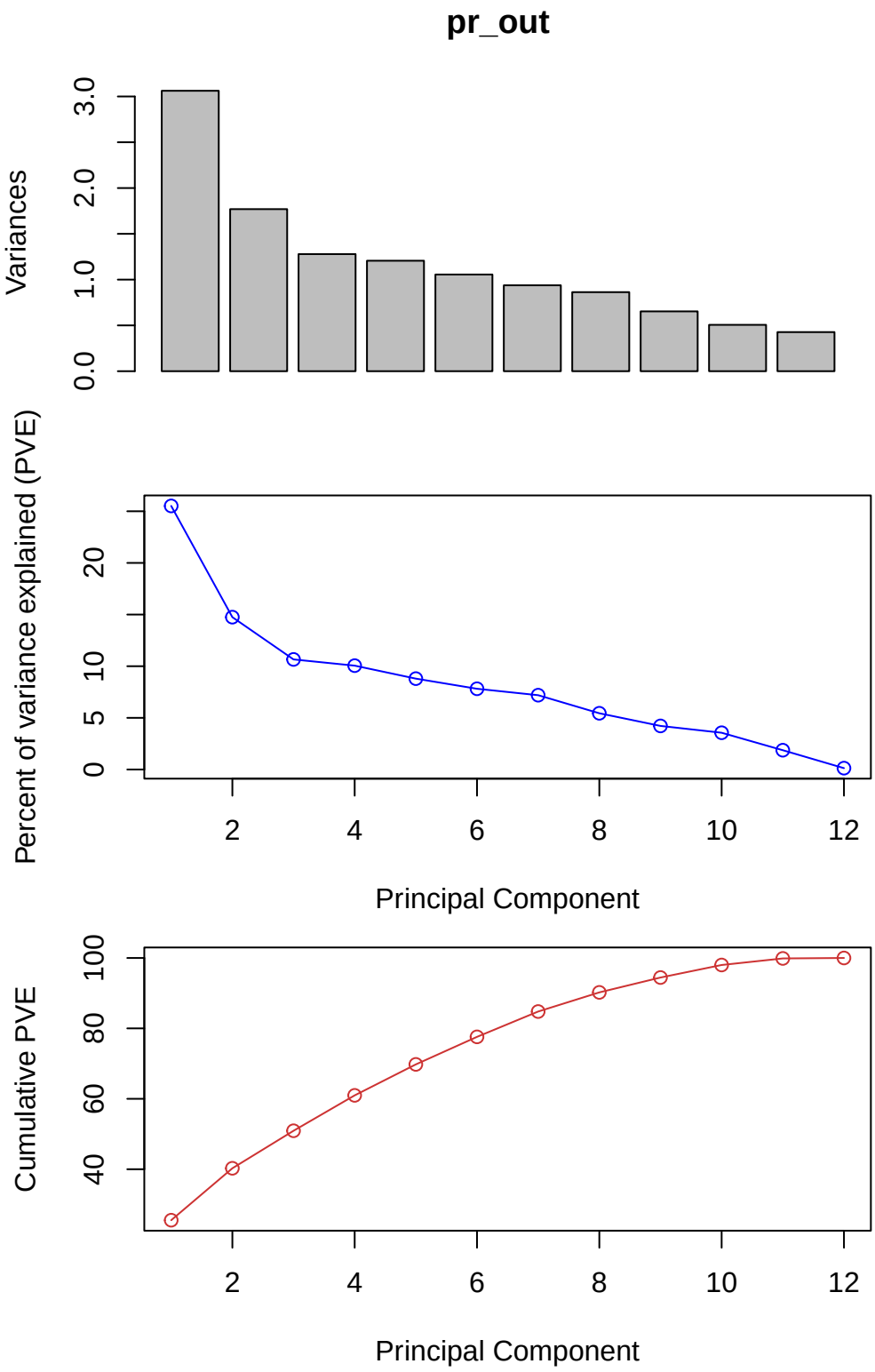

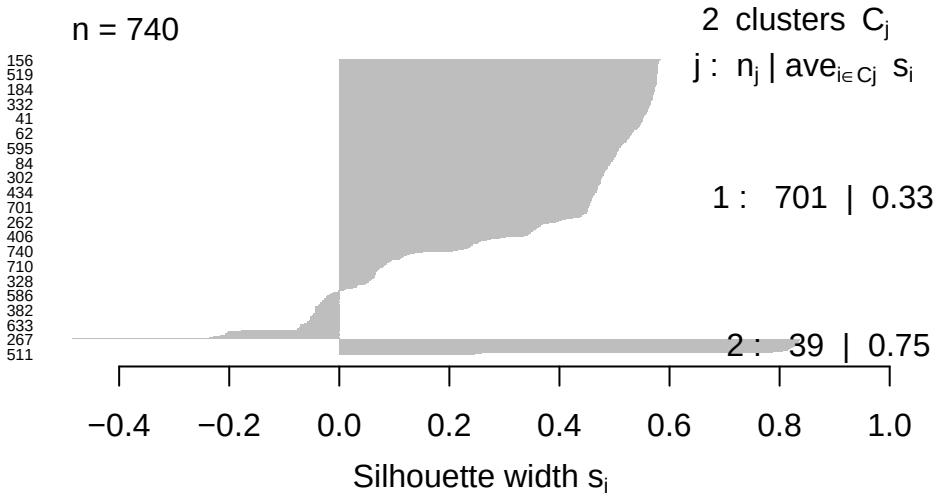

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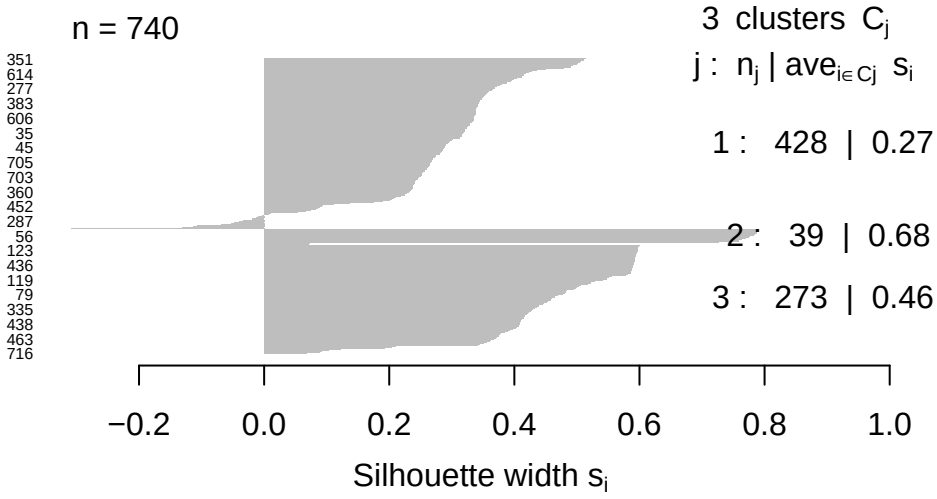

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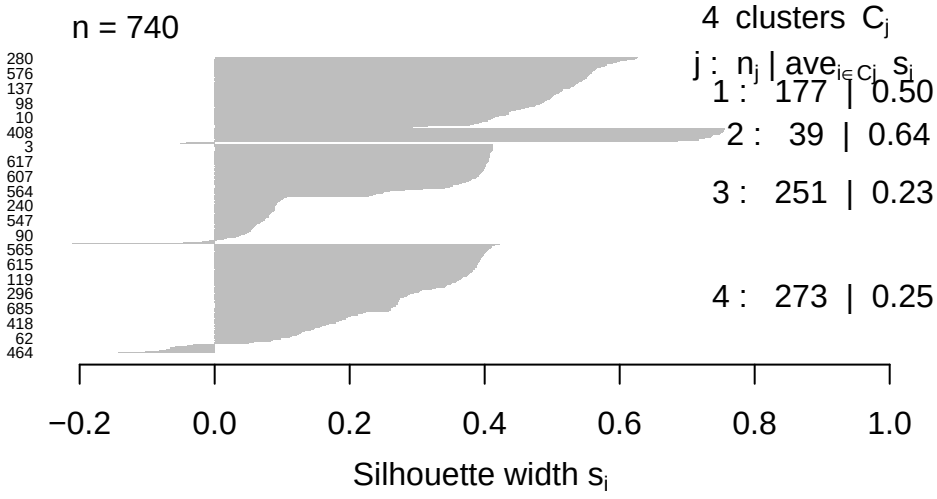

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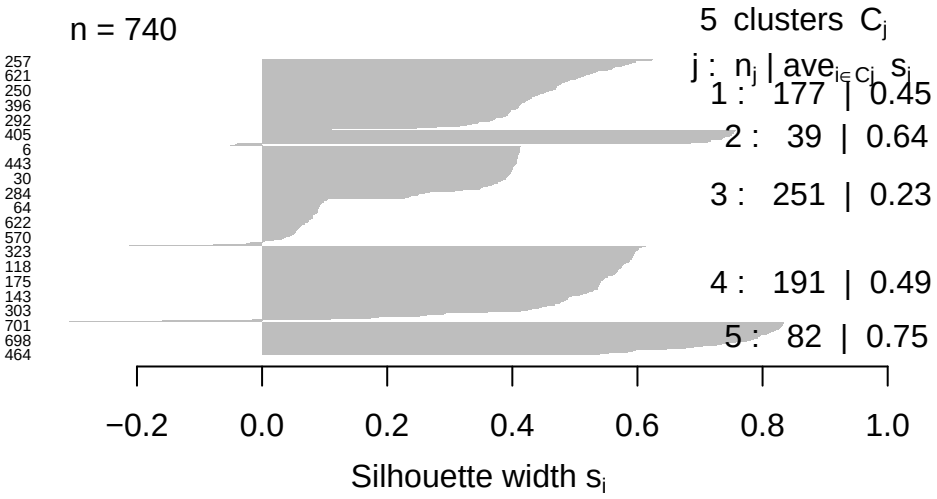

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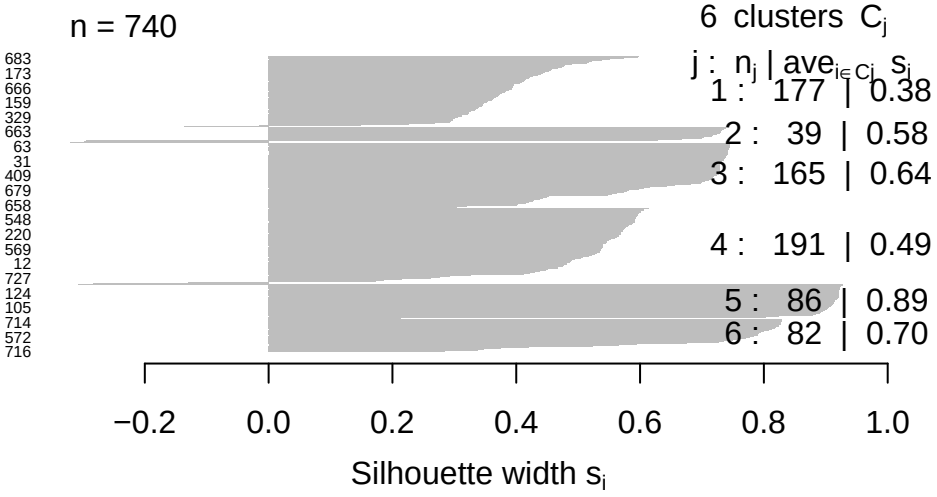

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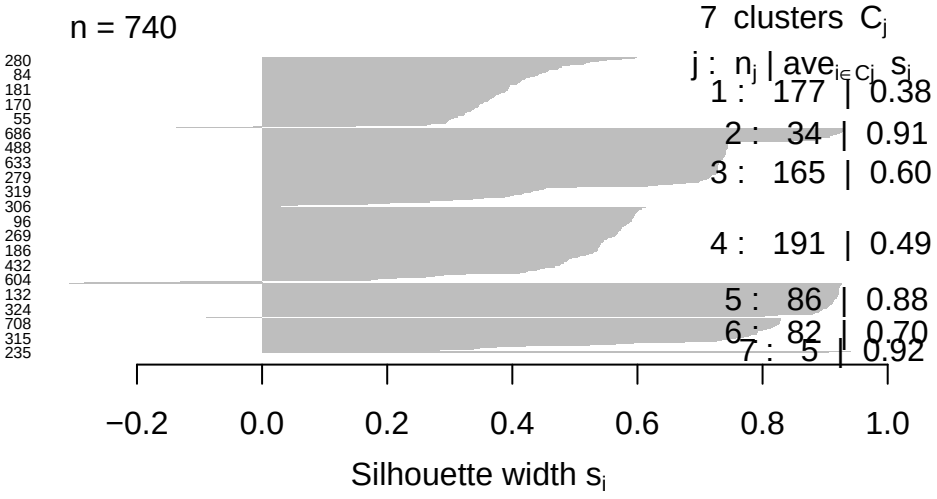

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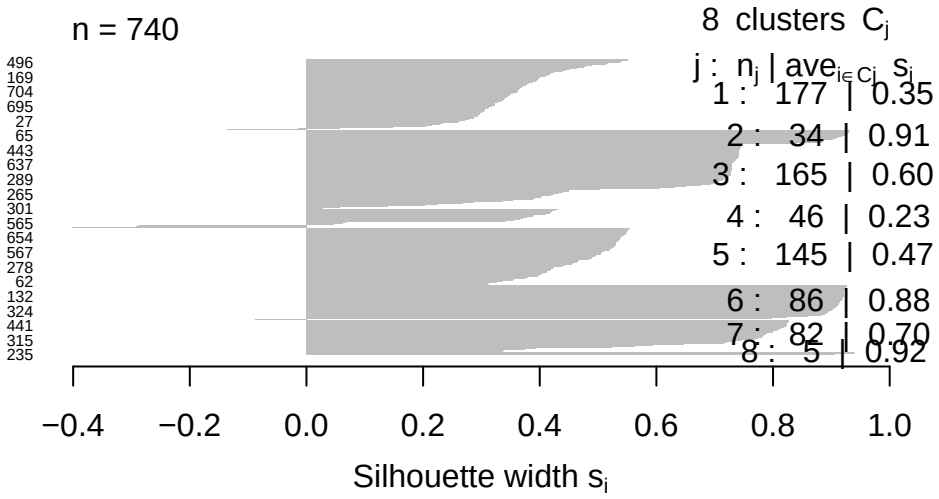

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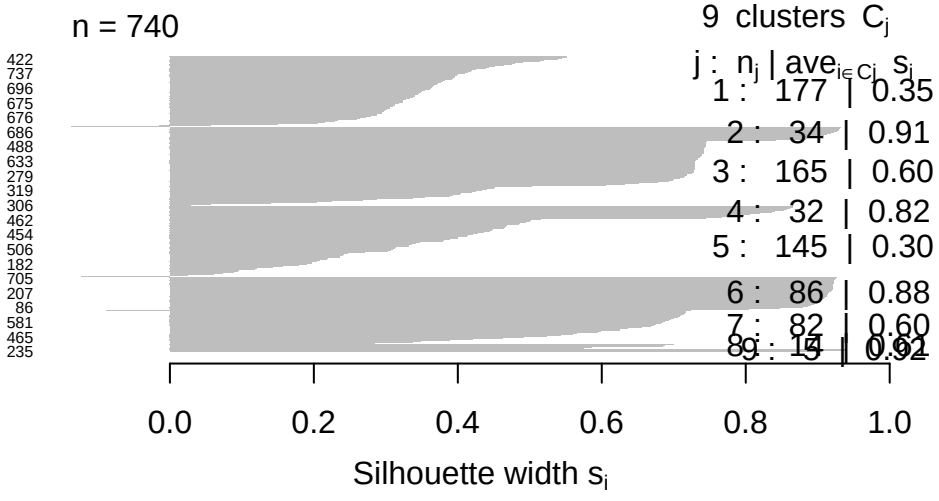

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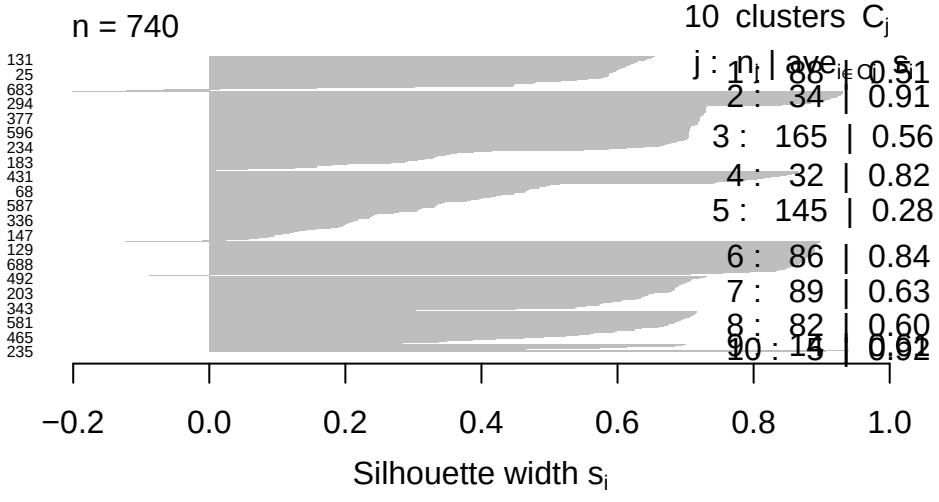

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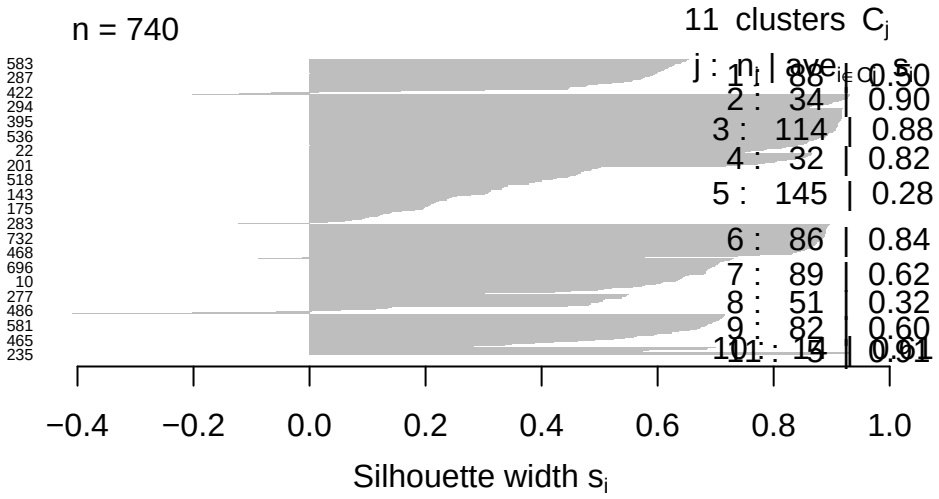

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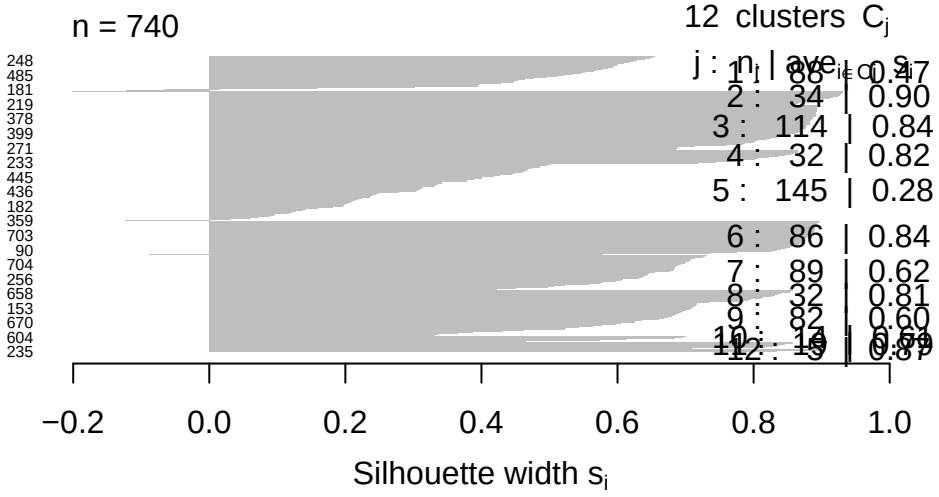

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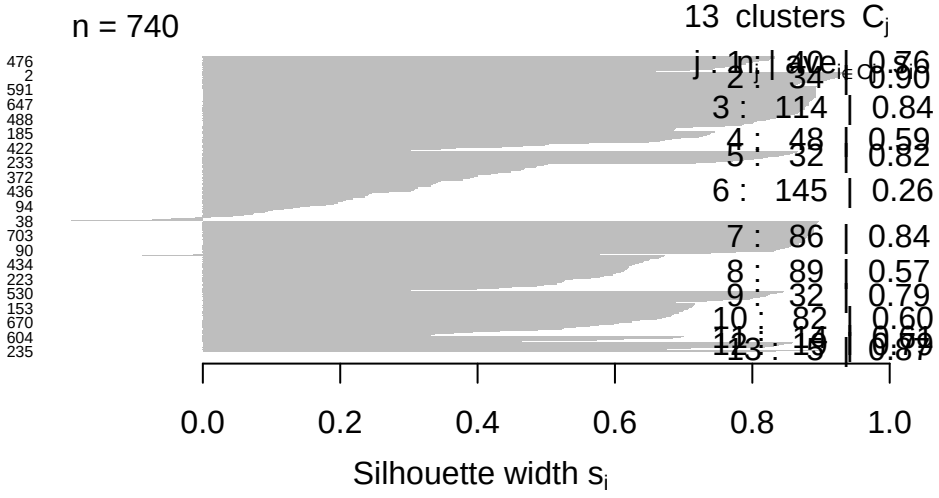

Average silhouette width : 0.64

```
[1] 0.171699
```

Introduction

Methods

Discussion

Supplementary material

```
# ----- SETUP ----- #
# Load packages
packages <- c("knitr", "tidyverse", "ggplot2", "cluster", "fossil")
lapply(packages, library, character.only = TRUE)

# Read data, extract labels, and keep only quantitative data
absentData_raw <- read.csv("Absenteeism_at_work.csv", sep = ";")
absentData_lab <- absentData_raw$`Reason.for.absence`
absentData <- absentData_raw %>%
  select(-c("Reason.for.absence","ID","Month.of.absence","Day.of.the.week","Seasons",
            "Disciplinary.failure","Education","Social.drinker","Social.smoker"))
# ----- DATA EXPLORATION ----- #
# Check data types, min, max, and missing data
data_type <- sapply(absentData,class)
min <- sapply(absentData, function(col){min(col,na.rm=TRUE)})
max <- sapply(absentData, function(col){max(col,na.rm=TRUE)})
nulls <- sapply(absentData, function(col){sum(is.na(col))})
blanks <- sapply(absentData,
                 function(col){ifelse(is.na(sum(col == "")), 0, sum(col == ""))})
data_summary <- data.frame(row.names = names(nulls), data_type=data_type,
                           min=min, max=max, nulls_blanks=nulls+blanks)
kable(data_summary)

# Create box plots to check for outliers
b01 <- boxplot(absentData$Transportation.expense, ylab = "Transportation Expense")
b02 <- boxplot(absentData$Distance.from.Residence.to.Work,
               ylab = "Distance from residence to work")
b03 <- boxplot(absentData$Service.time, ylab = "Service time")
b04 <- boxplot(absentData$Age, ylab = "Age")
b05 <- boxplot(absentData$Work.load.Average.day, ylab = "Work load average per day")
```

```r
b06 <- boxplot(absentData$Hit.target, ylab = "Hit target")
b07 <- boxplot(absentData$Son, ylab = "Son")
b08 <- boxplot(absentData$Pet, ylab = "Pet")
b09 <- boxplot(absentData$Weight, ylab = "Weight")
b10 <- boxplot(absentData$Height, ylab = "Height")
b11 <- boxplot(absentData$Body.mass.index, ylab = "Body mass index")
b12 <- boxplot(absentData$Absenteeism.time.in.hours, ylab = "Absenteeism time in hours")

# ----- DATA CLEANSING -----
# Handle outliers by capping them using interquartile range
cap <- function(val, bplot) {
  lower_fence <- bplot$stats[2]-(1.5*(bplot$stats[4]-bplot$stats[2])) #Q1-1.5*IQR
  upper_fence <- bplot$stats[4]+(1.5*(bplot$stats[4]-bplot$stats[2])) #Q3+1.5*IQR
  val <- ifelse(val < lower_fence, lower_fence, val)
  val <- ifelse(val > upper_fence, upper_fence, val)
  val
}
absentData <- absentData %>%
  mutate(Transportation.expense = cap(val=Transportation.expense, bplot=b01),
         Service.time = cap(val=Service.time, bplot=b03),
         Age = cap(val=Age, bplot=b04),
         Work.load.Average.day = cap(val=Work.load.Average.day, bplot=b05),
         Hit.target = cap(val=Hit.target, bplot=b06),
         Pet = cap(val=Pet, bplot=b08),
         Height = cap(val=Height, bplot=b10),
         Absenteeism.time.in.hours = cap(val=Absenteeism.time.in.hours, bplot=b12))

# ----- AGGLOMERATIVE HIERARCHICAL CLUSTERING ----- #
# Compare linkage types
absentData_sd <- scale(absentData)
absentData_dist <- dist(absentData_sd)
```

```r
plot(hclust(absentData_dist), xlab = "", sub = "", ylab = "",
     labels = absentData_lab, main = "Complete Linkage")
plot(hclust(absentData_dist, method = "average"),
     labels = absentData_lab, main = "Average Linkage",
     xlab = "", sub = "", ylab = "")
plot(hclust(absentData_dist, method = "single"),
     labels = absentData_lab, main = "Single Linkage",
     xlab = "", sub = "", ylab = "")

# Choose k using goodness-of-clustering
set.seed(780)
plotHeirSilK <- function(k){
  hc_out <- hclust(dist(absentData_sd))
  hc_clusters <- cutree(hc_out, k)
  sil <- silhouette(hc_clusters, dist(absentData_sd))
  plot(sil, nmax= 800, cex.names=0.5, main = "", col=1:k, border=NA)
}
plotHeirSilK(2)
plotHeirSilK(3)
plotHeirSilK(4)
plotHeirSilK(5)
plotHeirSilK(6)
plotHeirSilK(7)
plotHeirSilK(8)
plotHeirSilK(9)
plotHeirSilK(10)

# Perform hierarchical clustering using k=2
set.seed(780)
hc_out <- hclust(dist(absentData_sd))
adj.rand.index(cutree(hc_out, k = 2), as.numeric(as.factor(absentData_lab)))
```

```r
# ----- K-MEANS CLUSTERING ----- #
# Functions to get silhouette and plot for a k value
set.seed(780)
silK <- function(k){
  x_k <- kmeans(absentData_sd, k, nstart = 20)
  silhouette(x_k$cluster, dist(absentData_sd))
}
plotSil <- function(sil){
  plot(sil, nmax= 800, cex.names=0.5, main = "", border=NA)
}

# Choose k using goodness-of-clustering
k <- c(2:400)
sil_k <- lapply(k, silK)
sil_score <- sapply(sil_k, function(x) {mean(x[,"sil_width"])})
sil_max <- max(sil_score)
sil_max_k <- match(sil_max, sil_score)+min(k)-1
plot(x=k, y=sil_score, col=ifelse(sil_score==sil_max, "red", "black"))
text(x=sil_max_k, y=sil_max, pos=2, col="red",
     labels= c(paste0("Maximum: (",sil_max_k,", ",round(sil_max,2), ")")))

# Plot some of the silhouettes
plotSil(sil_k[[1]])
plotSil(sil_k[[100]])
plotSil(sil_k[[150]])
plotSil(sil_k[[200]])
plotSil(sil_k[[250]])
plotSil(sil_k[[sil_max_k-1]])
plotSil(sil_k[[300]])
plotSil(sil_k[[350]])
```

```r
# Perform k-means clustering with best k value
set.seed(780)
km_out <- kmeans(absentData, sil_max_k, nstart = 20)
km_clusters <- km_out$cluster

# Compare the k-means clusters with the given labels.
# Compute the rand index between the labels and k-means clustering.
rand.index(km_clusters, as.numeric(as.factor(absentData_lab)))
adj.rand.index(km_clusters, as.numeric(as.factor(absentData_lab)))

# ----- K-MEANS CLUSTERING AFTER PCA ----- #
# Principal component analysis (PCA)
pr_out <- prcomp(absentData, scale = TRUE)

# Proportion of variance explained
plot(pr_out)

pve <- 100 * pr_out$sdev^2 / sum(pr_out$sdev^2)
plot(pve, type = "o",
xlab = "Principal Component", col = "blue", ylab = "Percent of variance explained (PVE)")

plot(cumsum(pve), type = "o", ylab = "Cumulative PVE",
     xlab = "Principal Component", col = "brown3")

# Choose k using goodness-of-clustering
plotPCAHeirSilK <- function(k){
  hc_out <- hclust(dist(dist(pr_out$x[, 1:2])))
  hc_clusters <- cutree(hc_out, k)
  sil <- silhouette(hc_clusters, dist(pr_out$x[, 1:2]))
  plot(sil, nmax= 800, cex.names=0.5, main = "", border=NA)
}
```

```
plotPCAHeirSilK(2)
plotPCAHeirSilK(3)
plotPCAHeirSilK(4)
plotPCAHeirSilK(5)
plotPCAHeirSilK(6)
plotPCAHeirSilK(7)
plotPCAHeirSilK(8)
plotPCAHeirSilK(9)
plotPCAHeirSilK(10)
plotPCAHeirSilK(11)
plotPCAHeirSilK(12)
plotPCAHeirSilK(13)

hc_out <- hclust(dist(dist(pr_out$x[, 1:2])))
hc_clusters <- cutree(hc_out, 11)
adj.rand.index(hc_clusters, as.numeric(as.factor(absentData_lab)))
```

References

R Core Team. (2023). *R: A language and environment for statistical computing*. R Foundation for Statistical Computing. https://www.R-project.org/