European Doctoral School of Demography
Sequence Analysis

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Load necessary packages.

```
# Call TraMineR library
library(TraMineR)
# Call other required libraries
library(ggplot2)
library(grDevices)
library(graphics)
library(foreign)
library(cluster)
library(Hmisc)
library(TraMineRextras)
library(WeightedCluster)
library(RColorBrewer)
library(colorspace)
```

Exercise 1

1) Input the Dataset 2

[Sol.]

```
data2 <- read.csv("SFS2018_Data2.csv", na.strings=c(".",".a",".b"))
```

2) Define a sequence object with elements in data columns 2:61 and alphabet 1:6, using the following state names and labels

   1 SNP “Single, childless”,
   2 SBP “Single, child b/separat.”,
   3 SAP “Single, child a/separat.”,
   4 UNP “Union, childless”,
   5 UBP “Union, child b/separat.”,
   6 UAP “Union, child a/separat.”

[Sol.]

```
# Create a vector for the state labels
seqlab <-c("Single, childless", "Single, child b/separat.",
           "Single, child a/separat.", "Union, childless",
           "Union, child b/separat.", "Union, child a/separat.")
# Create a vector of short state names (default would be alphabet labels)
```

```r
sllist <- c("SNP","SBP","SAP","UNP", "UBP", "UAP")
# Define Color palette
color1 <-  sequential_hcl(6, palette = "SunsetDark", rev= TRUE)
# Generate sequence object
seqObj2 <- seqdef(data2, var=2:61,
                  alphabet=c(1:6), cpal=color1,
                  states=sllist, labels=seqlab)
```

3) Display (print) the first 10 sequences in extended and compact form

[Sol.]

Extended form:

```r
# Display the first 10 sequences (STS format - default)
print(seqObj2[1:10, ], format ="STS")
```

```
Sequence
1 SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-
SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-
SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP
2 SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-
SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-
SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP
3 SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-UNP-UNP-UNP-UNP-UNP-UNP-UNP-UNP-
UNP-UNP-UNP-UNP-UNP-UNP-UNP-UNP-UNP-UNP-UNP-UNP-UNP-UNP-UNP-UNP-UNP-UNP-
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UNP-UNP-UNP-UNP-UNP  4  SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-
SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-
SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-
SNP-SNP-SNP-SNP-SNP-SNP 5 SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-
SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-
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SBP-SBP-SBP-SBP-SBP-SBP 6 SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-
SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-
SBP-SBP-SBP
7 SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-
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8 SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-
SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-SBP-
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10 SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-
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SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP-SNP
```

Compact form:

```r
# Display the first 10 sequences (SPS format)
print(seqObj2[1:10, ], format ="SPS")
```

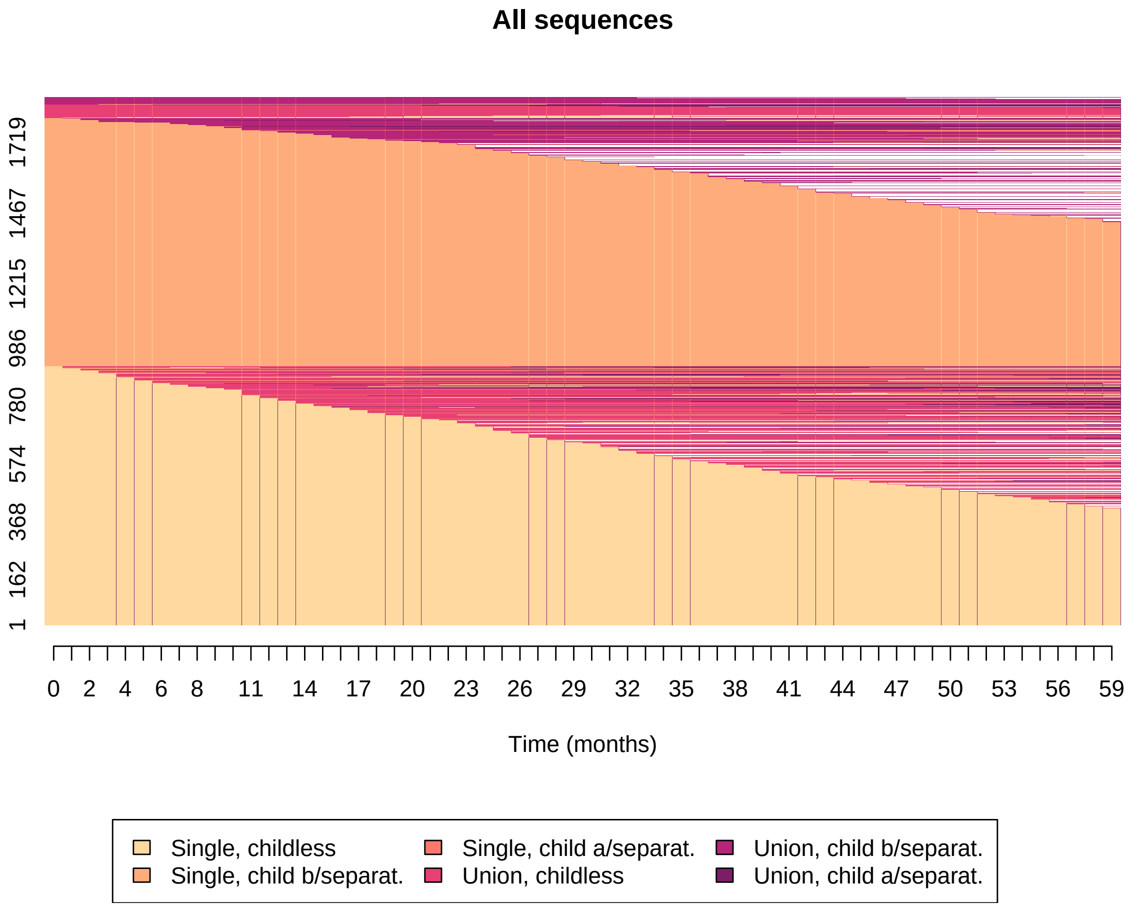
```
Sequence
1 (SBP,48)
2 (SNP,60)
```

3 (SNP,11)-(UNP,49) 4 (SNP,60)
5 (SBP,60)
6 (SBP,37)
7 (SBP,59)
8 (SBP,60)
9 (SBP,52)
10 (SNP,60)

4) Plot a full representation of sequences, and order them from the first state

[Sol.]

```
# X-axis for exercise
xtlab=seq(0,60, by=1)
# All sequences -sequence index plot (sorted - first state)
par(mfrow=c(2,1))
seqIplot(seqObj2, with.legend=TRUE, main= "All sequences",
         xtlab=xtlab, xlab="Time (months)", ylab=NA, yaxis=TRUE,
         border=NA, sortv="from.start")
```

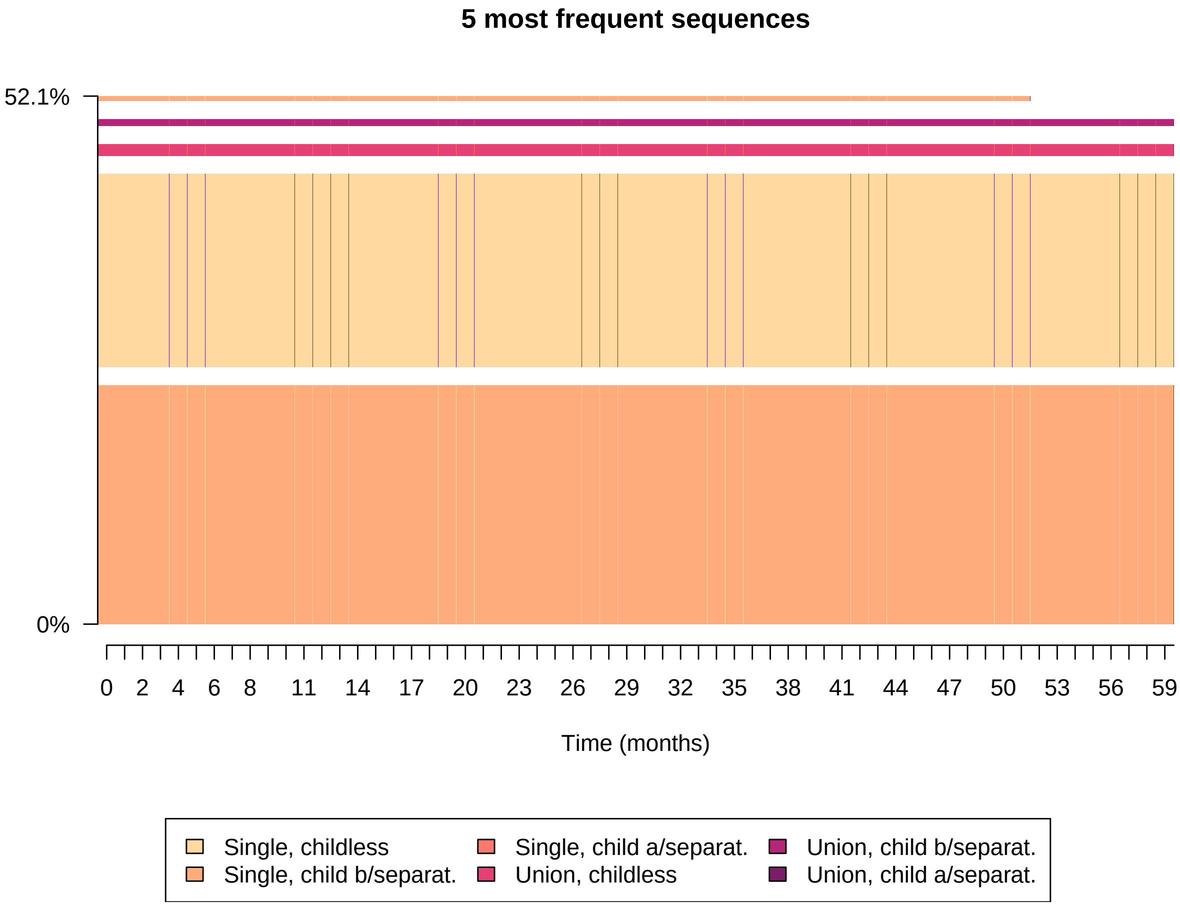


At a first glance, the majority of the individuals are single, with or without children (ligther colors) after separation. With time passing, some individuals experience unions (darker colors) and at the end of the period about half of the individuals are still single.

5) Plot the 5 most frequent sequences. Comment the plot.

[Sol.]

```
par(mfrow=c(2,1))
seqfplot(seqObj2, idxs=1:5, main="5 most frequent sequences",
         with.legend=TRUE, border=NA,
         ylab=NA, xlab="Time (months)", xtlab=xtlab)
```



The same information can be obtained as a frequency table with absolute and relative frequencies.

```
seqtab(seqObj2, idxs=1:5)
```

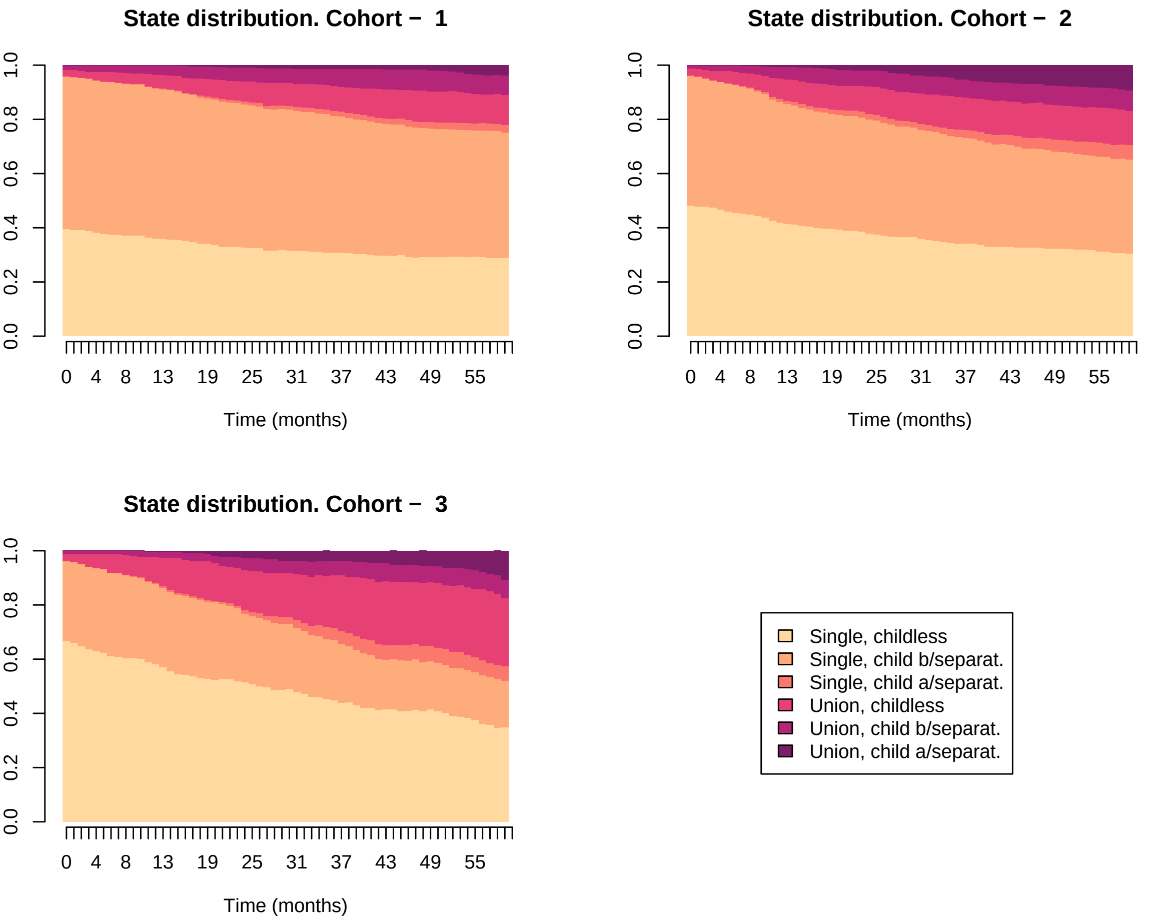
```
       Freq Percent
SBP/60  514   27.34
SNP/60  416   22.13
UNP/60   25    1.33
UBP/60   15    0.80
SBP/52   10    0.53
```

The five most frequent sequences after the separation are “Single, child b/separat.” for the 52 months (<1%), “Union, child b/separat.” for the whole period (<1%), “Union, childless” for the whole period (1%), “Single, childless” for the whole period (22%), “Single, child b/separat.” for the whole period (27%). Overall, the five most frequent sequences account for 52% of all the sequences.

6) Create a state distribution plot for each birthcohort (BIRTHCOH). What are the cross-cohort differences in the distribution of states overtime?

[Sol.]

```
seqdplot(seqObj2, group=data2$BIRTHCOH, with.legend=TRUE,
         main= "State distribution. Cohort", use.layout=FALSE,
         border=NA, xtlab=xtlab, ylab=NA, xlab="Time (months)")
```



From the plot we can observe that Cohort 1 has the bigger proportion of single who are childless or had a child before separation, with the proportion of single who are childless being lower than the proportion of single who had a child before separation. Both proportions tends to remain constant/slightly decreasing over time.

In Cohort 3, the proportion of single childless represent more than half of the whole individuals just after separation and the second more frequent state is being single with a child before separation. Both the proportions of single decrease consistently over time, in favour of the other states (in particular being in a union and childless).

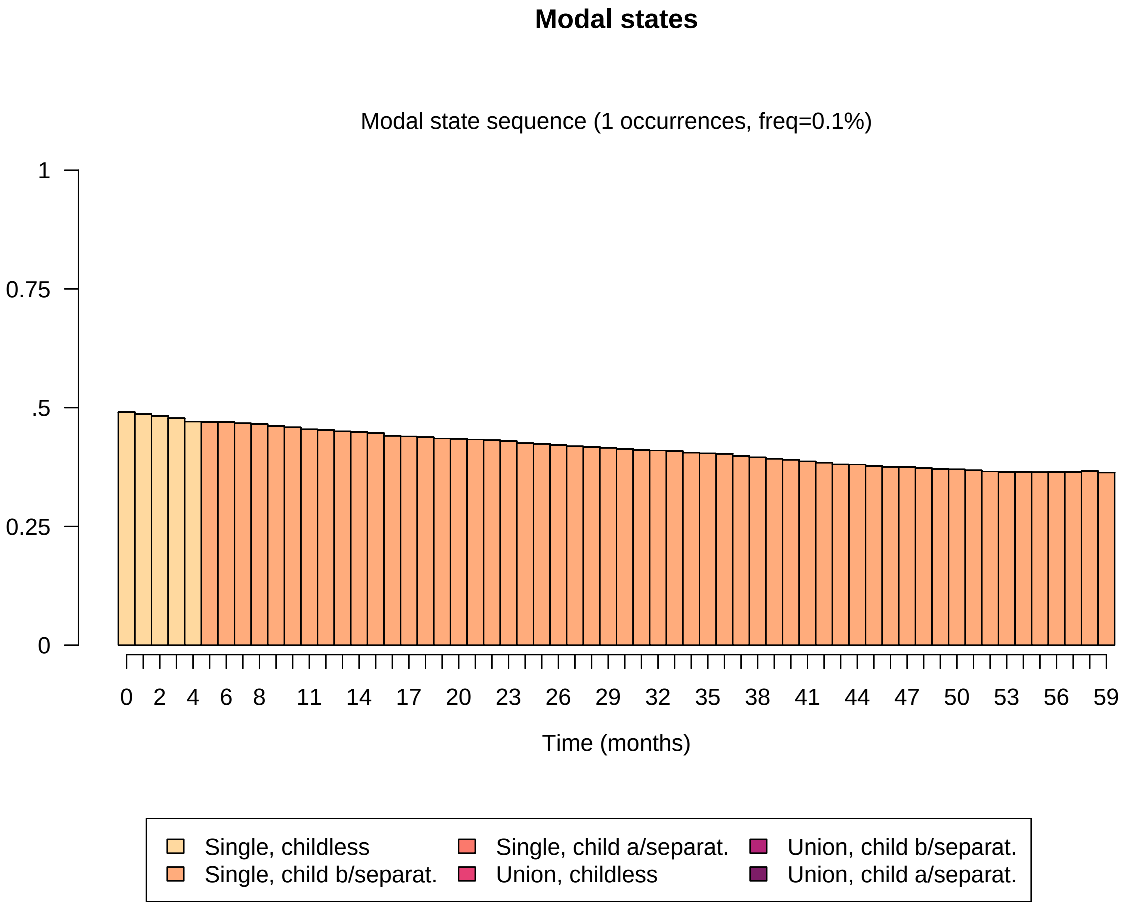
Cohort 2 can be seen as an intermediate situation.

Cohort 1 is the further one in time ordering (1960/69), followed by cohort 2 (1970/79) and cohort 3 (1980/89). Therefore, we can observe that more recent cohorts tends to re-enter in an union after separation. In addition, individuals seems more more prone of having children even after the couple dissolutes.

7) What are the most frequent states one and five years after break-up? Use a modal state plot for illustration.

[Sol.]

```
par(mfrow=c(1,1))
seqmsplot(seqObj2, with.legend=TRUE, main="Modal states",
          xtlab=xtlab, ylab=NA, xlab="Time (months)")
```



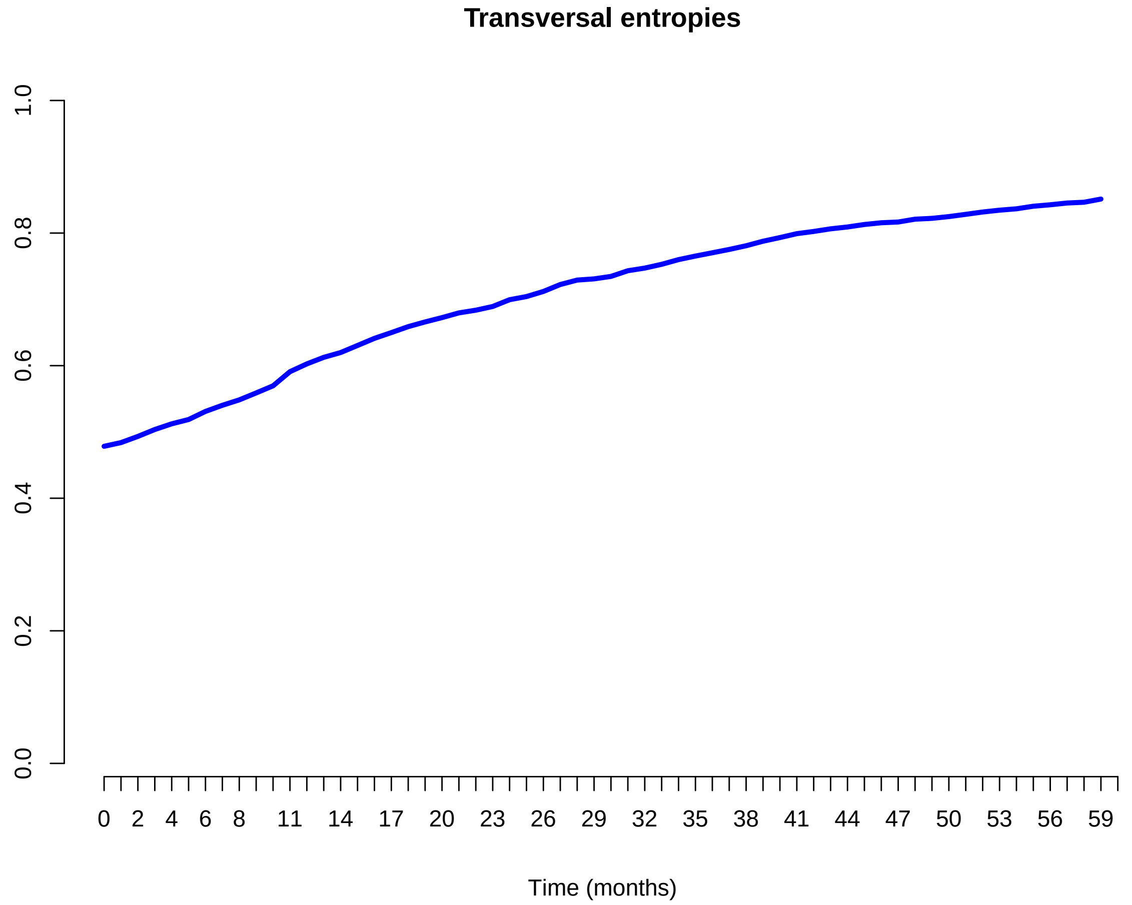
As it can be seen, “Single, childless” is the most frequent state in the first 4 months. After 4 months, “Single, child b/separat.” is the most frequent state. Therefore, one and five years after break-up the most frequent state is still “Single, child b/separat.”.

This behaviour would have been observable from a distribution plot like the one of the previous question, if considering all the cohorts combined.

8) Assess the cross-sectional state diversity plotting a measure of entropy. At what time after separation is the cross-sectional diversity of the states at its highest?

[Sol.]

```
# Plot the transversal entropies in each position of the sequence
seqHtplot(seqObj2, with.legend=FALSE, main= "Transversal entropies",
          use.layout=FALSE, border=NA,xtlab=xtlab, ylab=NA, xlab="Time (months)")
```



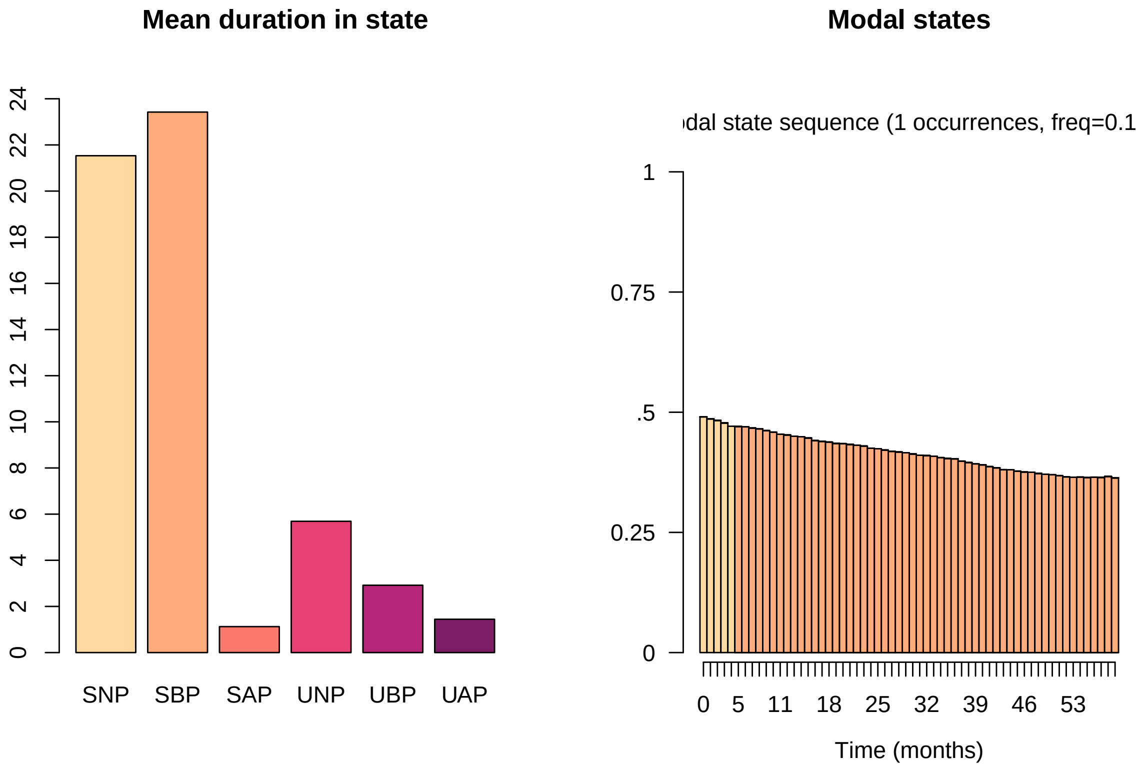
The plot shows that the entropy measure keeps increasing with time, reaching its maximum at month 60 (the end of the observation time).

This could be a result of having different ages in the individual sequence: even though we are analyzing the data from a life-course perspective, that 60-months could represent many different ages (and stages) in a woman's life, and hence creating a bias in the plot.

9) Display side by side in a same plot area the mean times spent in each of the states and the sequence of modal states.

[Sol.]

```
par(mfrow = c(1, 2))
# Plot the mean time spent in eache state
seqmtplot(seqObj2, with.legend=FALSE, main= "Mean duration in state",
          ylab=NA, ylim=c(0,25), yaxis=F)
axis(2, at=seq(from=0, to=25, by=2))
# Plot modal states in each position of the sequence
seqmsplot(seqObj2, with.legend=FALSE, main="Modal states", xtlab=xtlab,
          ylab=NA, xlab="Time (months)")
```



The exact information on the mean times can be obtained in a table. The mean time of individuals in state “Single, child b/separat.” is 23.4 months, in “Single, childless” it is 21.5 months. In all the other states, individuals stay on average less than 6 months.

```
apply(seqistatd(seqObj2),2,mean)
```

```
      SNP       SBP       SAP       UNP       UBP       UAP
21.532447 23.424468  1.125532  5.688830  2.918085  1.443617
```

10) Compute the (overall) transition rate matrix. What is the largest transition rate between two different states?

[Sol.]

```
seqtrate(seqObj2)
```

```
             [-> SNP]     [-> SBP]     [-> SAP]     [-> UNP]     [-> UBP]
[SNP ->] 0.989975189 0.0003508684 0.0011779153 0.008445904 0.000000000
[SBP ->] 0.000000000 0.9959117681 0.0004388498 0.000000000 0.003603187
[SAP ->] 0.000000000 0.0000000000 0.9956033219 0.000000000 0.000000000
[UNP ->] 0.005545993 0.0000000000 0.0000000000 0.985848155 0.000000000
[UBP ->] 0.000000000 0.0041083100 0.0001867414 0.000000000 0.990476190
[UAP ->] 0.000000000 0.0000000000 0.0042405551 0.000000000 0.000000000
              [-> UAP]
[SNP ->] 5.012406e-05
[SBP ->] 4.619471e-05
[SAP ->] 4.396678e-03
[UNP ->] 8.605852e-03
[UBP ->] 5.228758e-03
[UAP ->] 9.957594e-01
```

The largest transition rate between two different states is the one that goes from SNP to UNP: from Single with no children to Union with no children. The second largest is the one that reverses that states from UNP to SNP. This means that going in and out from Unions is more probable than moving to other states, which relates to the fact that states where children are present are less frequent through cohorts.

11) Compute the sequence length, the number of transitions, the number of sub-sequences and the longitudinal entropy

[Sol.]

```
# Sequence length - number of elements with valid cases
length <-seqlength(seqObj2)
# Number of transitions between state episodes in each sequence
transn <-seqtransn(seqObj2)
# Number of sub-sequences contained in a sequence
subseq <- seqsubsn(seqObj2)
# Longitudinal or within-sequence entropy
entropy <- seqient(seqObj2)
```

12) Using summary(), look at the min, max, mean, median and quartiles of the distribution of each of the computed longitudinal characteristics.

[Sol.]

Summary of Sequence length:

```
summary(length)
```

```
     Length
 Min.   :23.00
 1st Qu.:60.00
 Median :60.00
 Mean   :56.13
 3rd Qu.:60.00
 Max.   :60.00
```

Summary of Number of transitions between state episodes:

```
summary(transn)
```

```
     Trans.
 Min.   :0.0000
 1st Qu.:0.0000
 Median :0.0000
 Mean   :0.4234
 3rd Qu.:1.0000
 Max.   :5.0000
```

Summary of Number of sub-sequences contained in a sequence:

```
summary(subseq)
```

```
    Subseq.
 Min.   : 2.000
 1st Qu.: 2.000
 Median : 2.000
 Mean   : 3.093
 3rd Qu.: 4.000
 Max.   :48.000
```

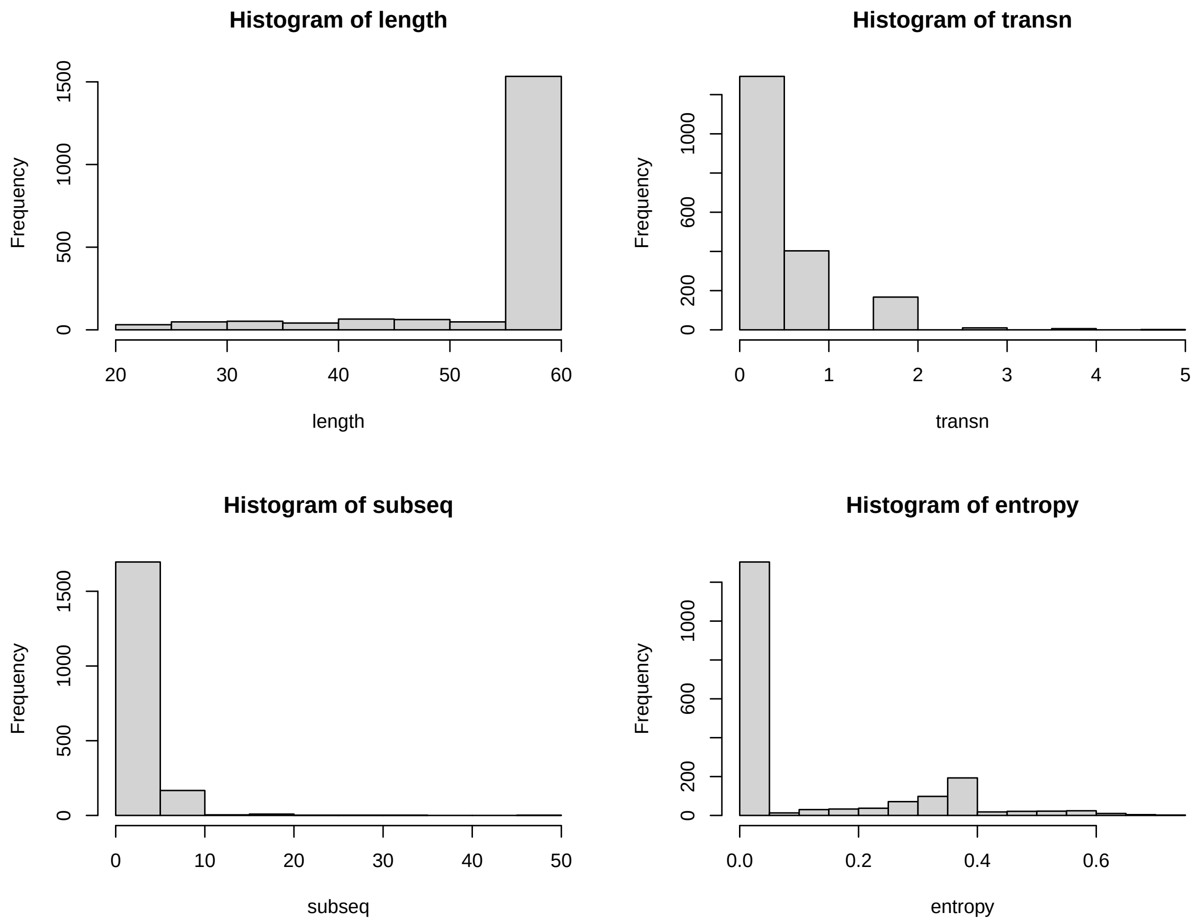
Summary of Entropy:

```r
summary(entropy)
```

```
    Entropy
 Min.   :0.0000
 1st Qu.:0.0000
 Median :0.0000
 Mean   :0.1045
 3rd Qu.:0.2359
 Max.   :0.7323
```

Looking at the histogram of these quantities, we can see that most of the sequences are concentrated on higher length, low number of transitions and sub-sequences, and low entropies.

```r
par(mfrow=c(2,2))
hist(length)
hist(transn)
hist(subseq)
hist(entropy)
```



Exercise 2

1) Input the Dataset 2

[Sol.]

```
data2 <- read.csv("SFS2018_Data2.csv", na.strings=c(".",".a",".b"))
```

2) Define a sequence object with elements in data columns 2:61 and alphabet 1:6, using the following state names and labels

   1 SNP "Single, childless",
   2 SBP "Single, child b/separat.",
   3 SAP "Single, child a/separat.",
   4 UNP "Union, childless",
   5 UBP "Union, child b/separat.",
   6 UAP "Union, child a/separat."

[Sol.]

```
#vector for the state labels
seqlab <-c("Single, childless", "Single, child b/separat.",
           "Single, child a/separat.", "Union, childless",
           "Union, child b/separat.", "Union, child a/separat.")
#vector of short state names (default would be alphabet labels)
sllist <- c("SNP","SBP","SAP","UNP", "UBP", "UAP")
###  Generate sequence object
seqObj2 <- seqdef(data2, var=2:61,
                  alphabet=c(1:6), cpal=color1,
                  states=sllist, labels=seqlab)
```

3) Compute the matrix of pairwise distances - OM with constant costs - between all sequences and display the results for the first 5 sequences.

[Sol.]

```
#OM with CONSTANT subcosts (OM with indel=1, subs=2)
Matrix.OM.Const <- seqdist(seqObj2, method="OM", indel=1, sm="CONSTANT")
#display matrix
print(Matrix.OM.Const[1:5,1:5])
```

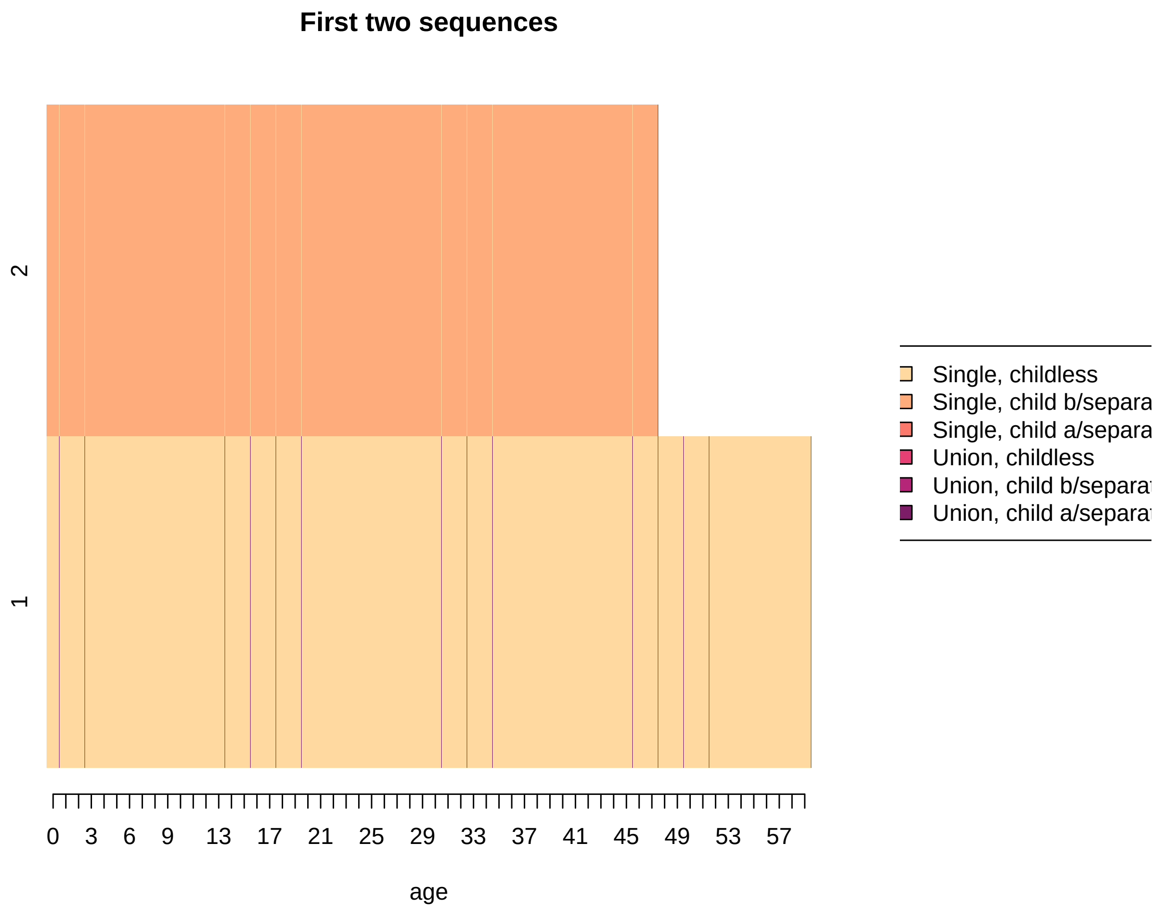
4) Plot the first 2 sequences and check that the OM distance is the number of non matching positions between them.

[Sol.]

```
#display the first 5 sequences, and sequence elements 1-20 (SPS format)
print(seqObj2[1:2, ], format ="SPS")

# Sequence
# 1 (SBP,48)
# 2 (SNP,60)

#All sequences -sequence index plot (sorted - first state)
xtlab=seq(0,60, by=1)
seqIplot(seqObj2[1:2, ], with.legend="right", main= "First two sequences",
         xtlab=xtlab, xlab="age", ylab=NA, yaxis=TRUE, sortv="from.start")
```



```
# 48*2 + 12 = 108
```

5) Check data that the LCS distance provides the same (non-normalized) distances as OM with indel=1 and a constant substitution cost of 2

[Sol.]

```
#Longest common sub-sequence
Matrix.LCS <- seqdist(seqObj2,method="LCS")
#display matrix
print(Matrix.LCS[1:5,1:5])

#Compare
print(Matrix.OM.Const[1:5,1:5])
```

6) Define a substitution cost matrix reflecting what (according to your prior knowledge) are the distances between two states (i.e. customize state-dependent substitution costs)

[Sol.]

We start by calculating the transition matrix, rounded to the 3rd decimal:

```
round(seqtrate(seqObj2),3)
```

We will try to reflect the ordinal character of this matrix by:

- setting the cost of remaining in the same state as 0

- the higher expected cost will be 10 (since dividing 1 by the transition probability would give us an `Inf`)
- the higher the probability, the lower the cost.
- for all other costs, we subtract the 3rd decimal of the transition probability to the maximum cost

We get the following state-dependent subcost matrix:

```
#OM with customized state-dependent subcosts
submatrix <- matrix(c( 0,10,9,2,10,10,
                       10,0,10,10,6,10,
                       10,10,0,10,10,6,
                       4,10,10,0,10,1,
                       10,6,10,10,0,5,
                       10,10,6,10,10,0), nrow = 6, ncol = 6, byrow = TRUE)

print(submatrix)
```

7) Compute the OM dissimilarity matrix using the previously derived substitution. Set the indel cost as half the maximum substitution cost.

[Sol.]

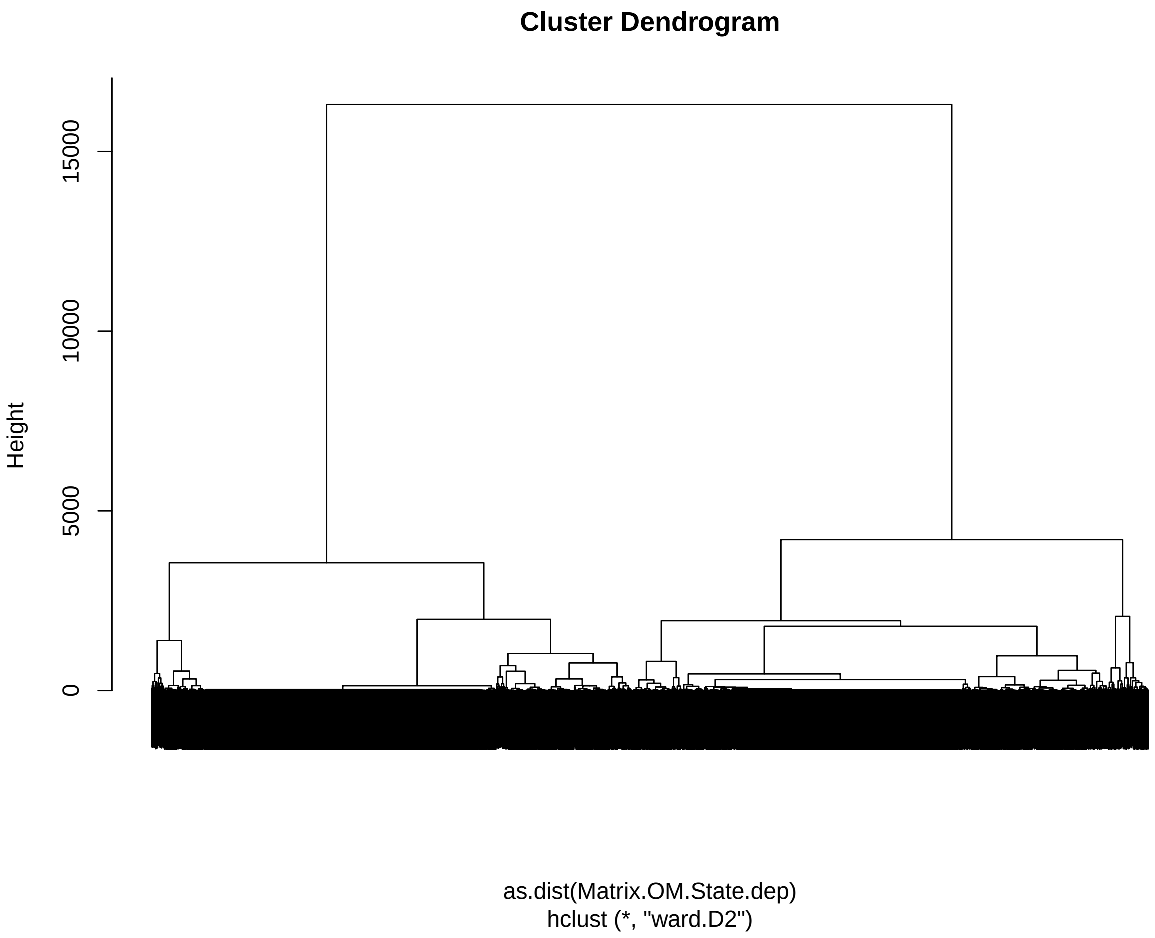
```
Matrix.OM.State.dep <- seqdist(seqObj2, method="OM", indel=5, sm=submatrix)
#display matrix
print(Matrix.OM.State.dep[1:5,1:5])
```

8) From the previously computed OM dissimilarity matrix, create a hierarchical cluster tree object with Ward method. Display the hierarchical tree

[Sol.]

```
# cluster sequences using the OM distances with state-dependent costs and Ward method
ward.OM <- hclust(as.dist(Matrix.OM.State.dep), method = "ward.D2")

###dendogram
# plot basic dendograms
plot(ward.OM, labels=FALSE)
```



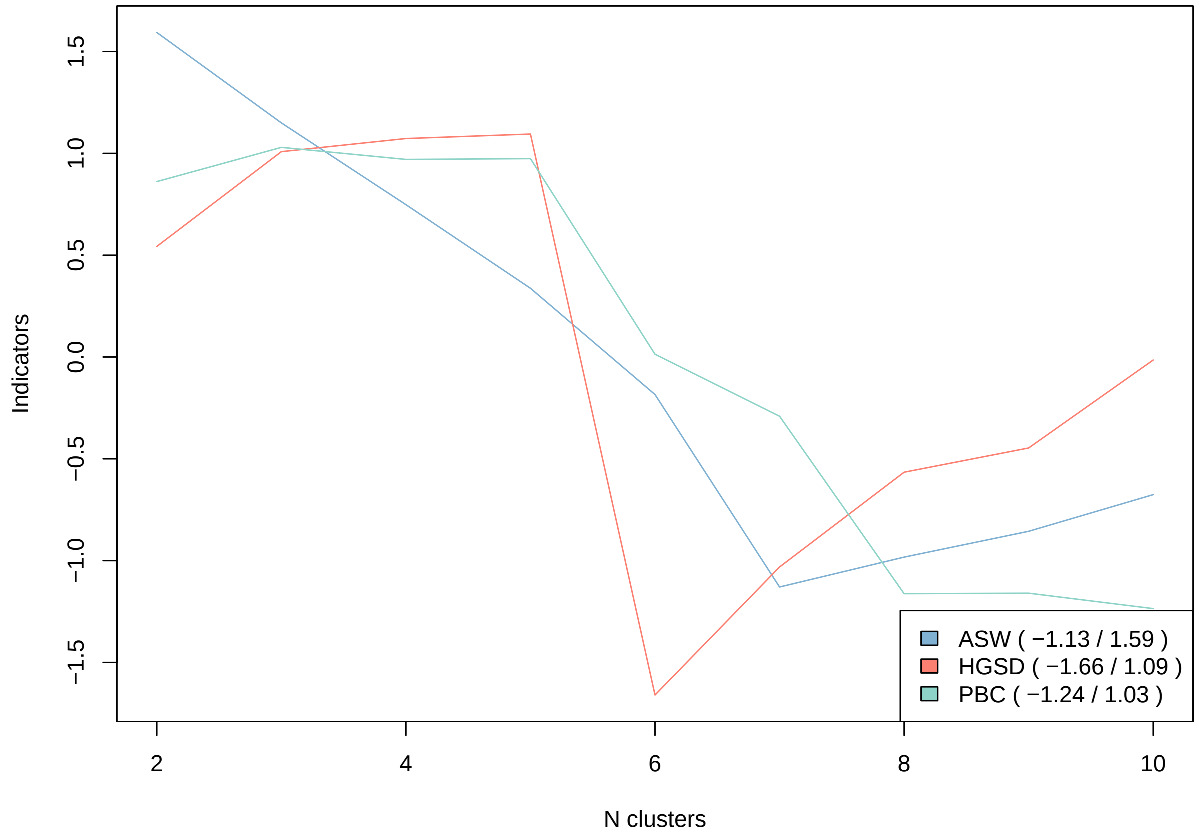
9) Calculate appropriate cluster cut-off criteria. Assess what is an empirically optimal cluster solution.

[Sol.]

```
### Generate an object with 1-10 cluster solutions for each prior anal
wardrange.OM <- as.clustrange(ward.OM, diss=Matrix.OM.State.dep, ncluster=10)

### show cluster cut-off measure values - indicate three optimal cluster solutions
summary(wardrange.OM, max.rank=3)

### plot ASW, HGSD and PBC
plot(wardrange.OM, stat=c("ASW", "HGSD", "PBC"), norm="zscore")
```

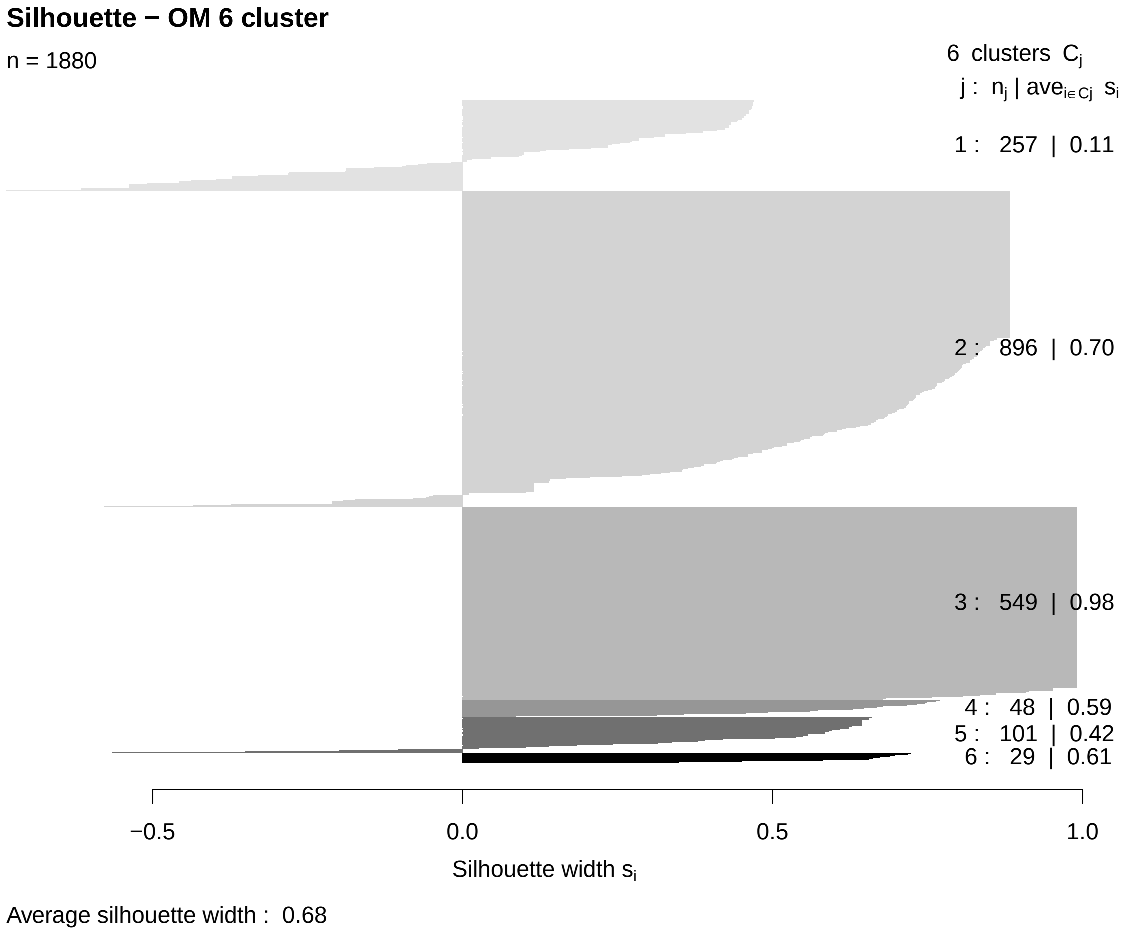


10) Select the six-cluster solution from the Ward analysis, check cluster consistency, and label the clusters by looking at the full sequence index plots (or the relative frequency version) by cluster.

[Sol.]

```
### store cluster solutions with best empirical fits
#OM
wardrange.OM.6 <- cutree(ward.OM , k=6)

### cluster consistency (plot silhouette widths)
#OM 5-cluster solution
silh.OM.6 <- silhouette(wardrange.OM.6, dmatrix = Matrix.OM.State.dep)
summary(silh.OM.6)
plot(silh.OM.6, main= "Silhouette - OM 6 cluster", border=NA,
     col=c("#E2E2E2", "#D3D3D3", "#B8B8B8", "#969696", "#707070", "black"))
```



11) Repeat steps 8-10 using an OM with transition rates as substitution costs, and 1 as indel costs.

[Sol.]

Since we are already using the transition rates matrix as a proxy of substitution costs, now we are lowering the indel cost from 5 to 1 and comparing results.

```
Matrix.OM.State.dep.indel1 <- seqdist(seqObj2, method="OM", indel=1, sm=submatrix)
#display matrix

# cluster sequences using the OM distances with state-dependent costs and Ward method
ward.OM.indel1 <- hclust(as.dist(Matrix.OM.State.dep.indel1), method = "ward.D2")


### Generate an object with 1-10 cluster solutions for each prior anal
wardrange.OM.indel1 <- as.clustrange(ward.OM.indel1, diss=Matrix.OM.State.dep.indel1, ncluster=10)


### store cluster solutions with best empirical fits
# OM
wardrange.OM.6.indel1 <- cutree(ward.OM.indel1 , k=6)

### cluster consistency (plot silhouette widths)
# OM 6-cluster solution
```

```
silh.OM.6.indel1 <- silhouette(wardrange.OM.6.indel1, dmatrix = Matrix.OM.State.dep.indel1)
```

12) Compare the results between the OM and the DHD approaches

[Sol.]

By lowering the indel costs, we get the following best fit for number of clusters:

```
### plot ASW, HGSD and PBC: indel cost = 5
plot(wardrange.OM, stat=c("ASW", "HGSD", "PBC"), norm="zscore")
```

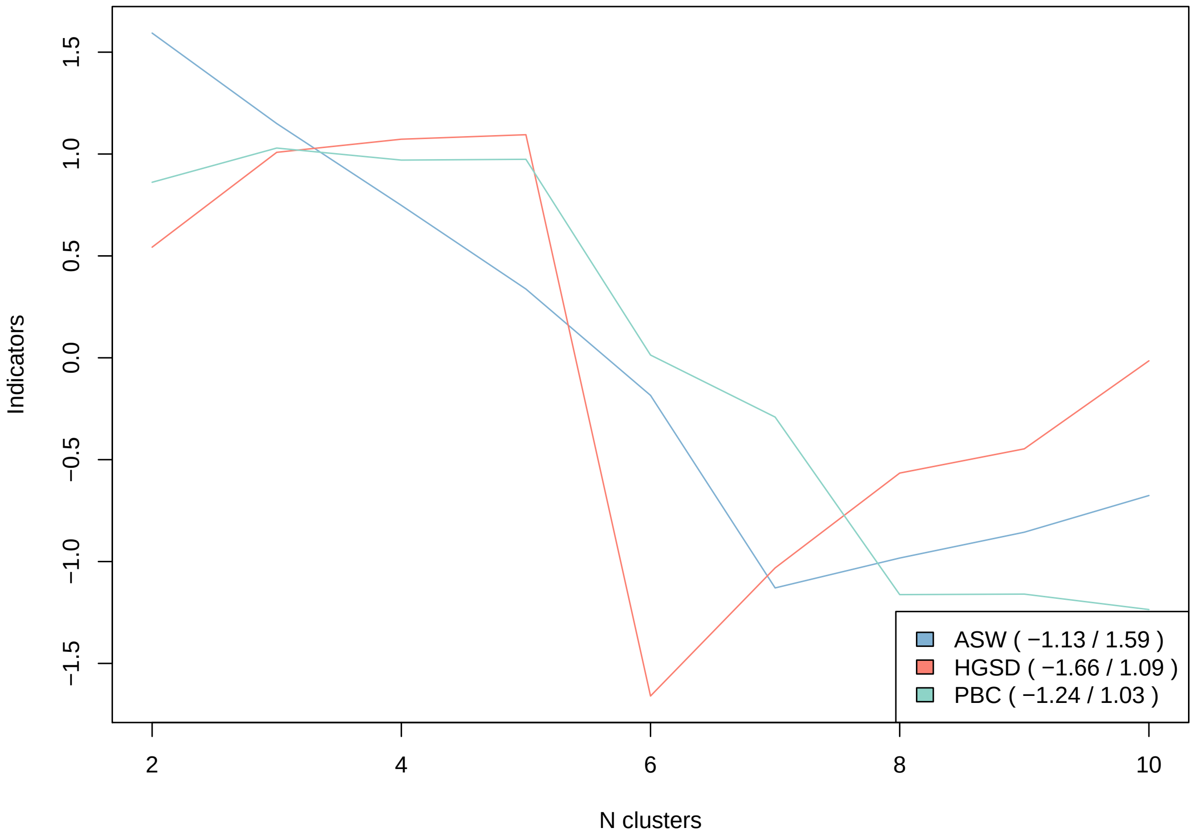


Figure 1: Indel cost = 5

```
### plot ASW, HGSD and PBC: indel cost = 1
plot(wardrange.OM.indel1, stat=c("ASW", "HGSD", "PBC"), norm="zscore")
```

When indel costs = 5 the best fit seems to be around 5 clusters, and when we lower the indel costs to 1, the best fit seems to be around 6 clusters.

If we force the solution to be a 6-cluster one, we get the following silhouette fittings:

```
### cluster consistency: indel cost = 5
plot(silh.OM.6, main= "Silhouette - OM 6 cluster, indel = 5", border=NA,
     col=c("#E2E2E2", "#D3D3D3", "#B8B8B8", "#969696", "#707070", "black"))
```

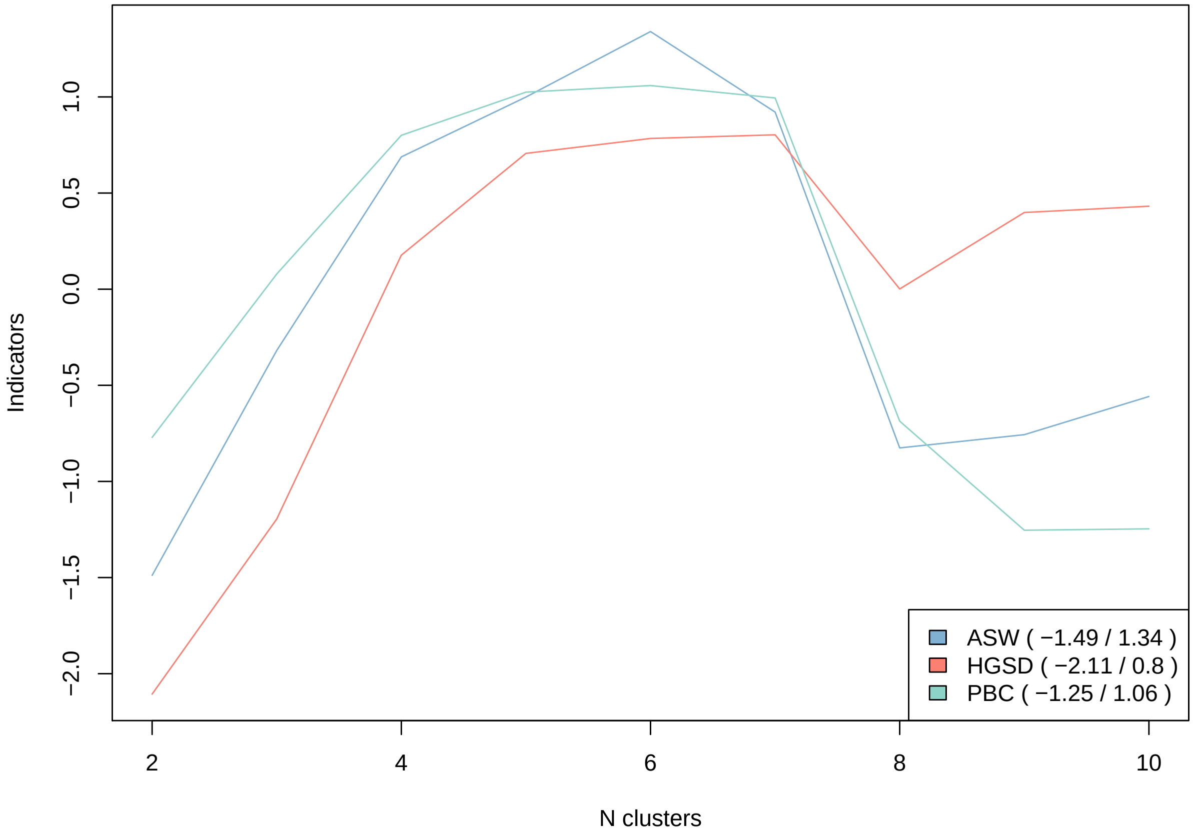
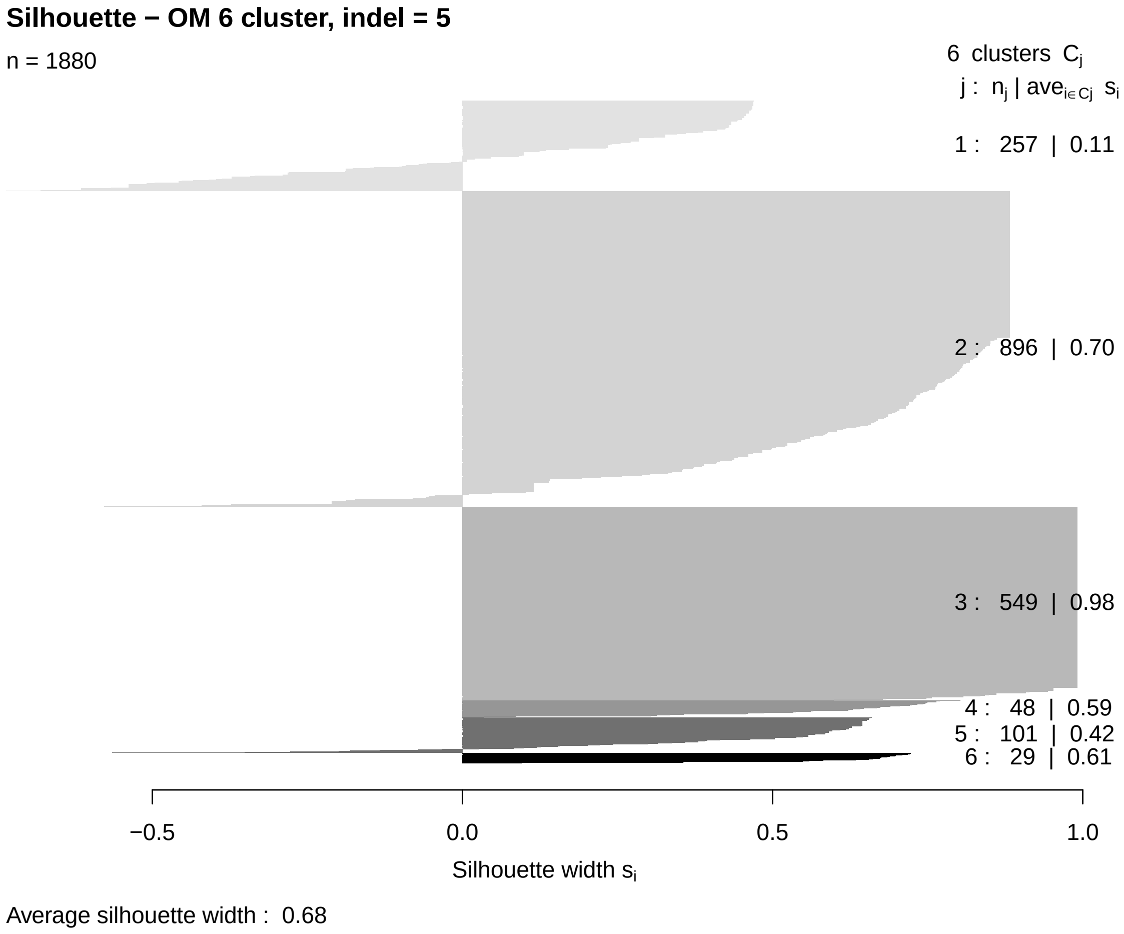


Figure 2: Indel cost = 1



```
### cluster consistency: indel cost = 1
plot(silh.OM.6.indel1, main= "Silhouette - OM 6 cluster, indel = 1", border=NA,
     col=c("#E2E2E2", "#D3D3D3", "#B8B8B8", "#969696", "#707070", "black"))
```

When we have indel costs = 5, the first cluster does not have the best fitting. But when we lower the costs down to 1, the 6-cluster solution is a much better fitting.

We understand that if we use the transition rates matrix as a substitution matrix cost, we need lower indel costs than usual to have better fitting for clustering.

References

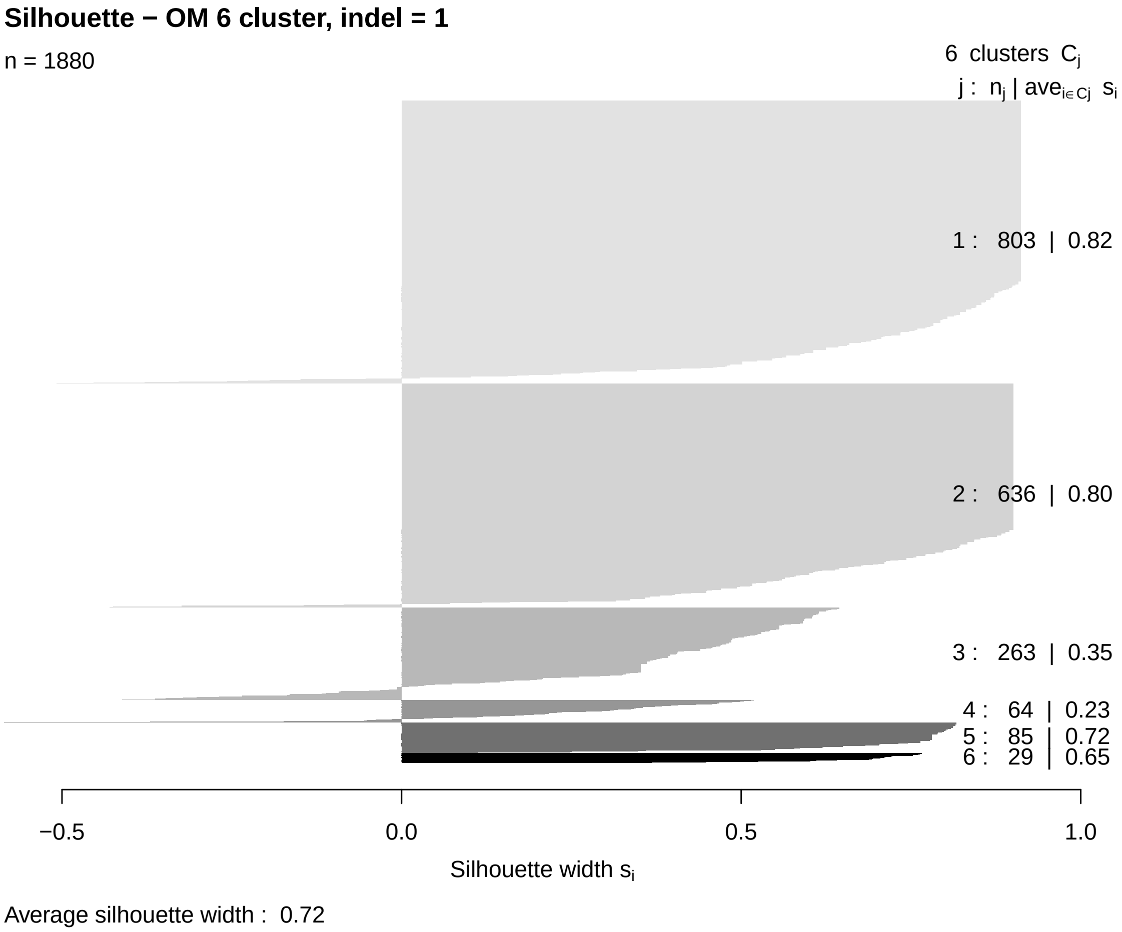


Figure 3: Silhoutte Indel cost = 1