Sequence Analysis

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Load necessary packages.

```r
# 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.]

```r
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.]

```r
# 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)
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)

### Retrieve information from sequence object
summary(seqObj2)
names(seqObj2)
```

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

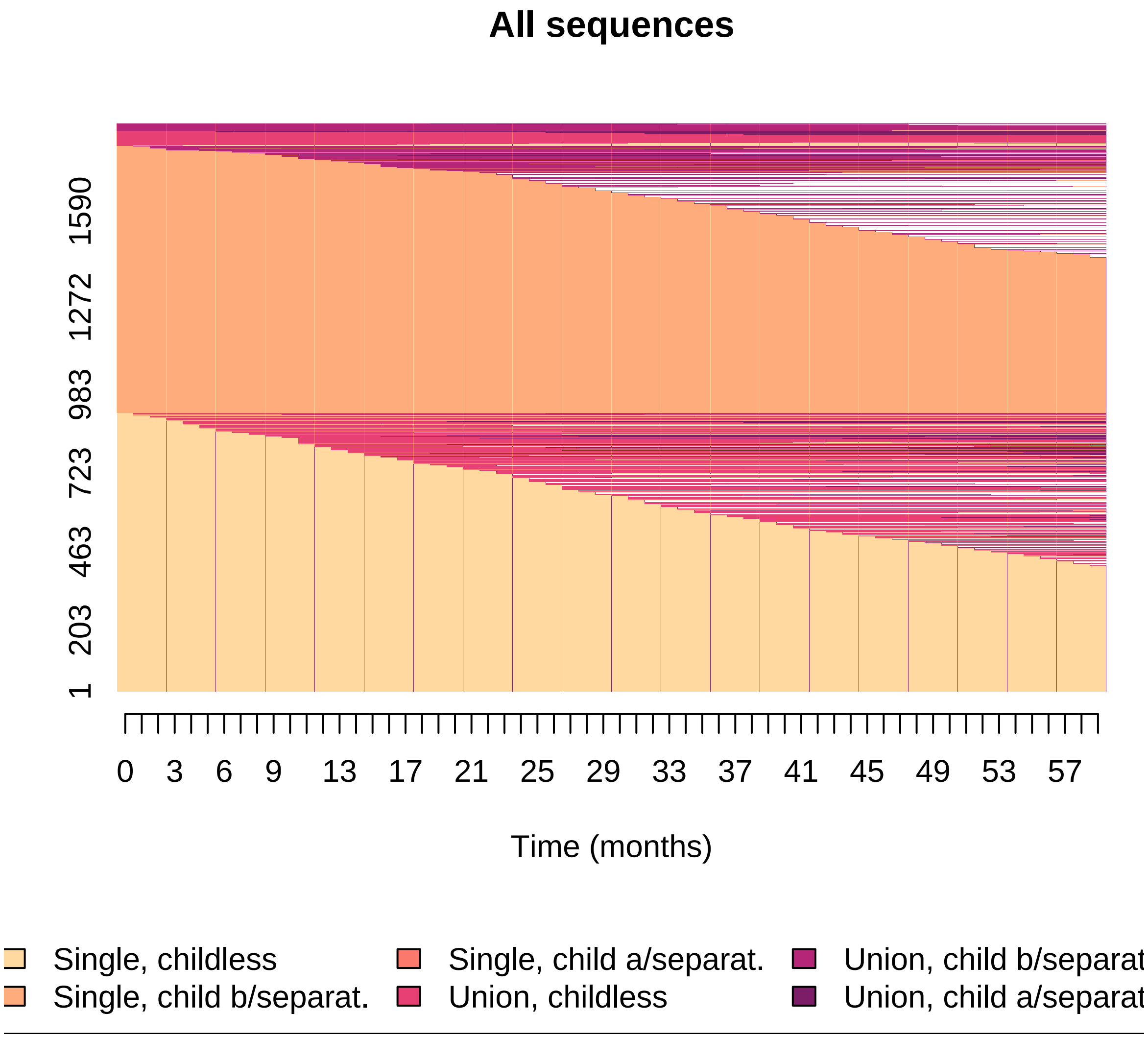
[Sol.]

```
#display the first 5 sequences, and sequence elements 1-20 (STS format - default).
print(seqObj2[1:10, ], format ="STS")
#display the first 5 sequences, and sequence elements 1-20 (SPS format)
print(seqObj2[1:10, ], format ="SPS")
```

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

[Sol.]

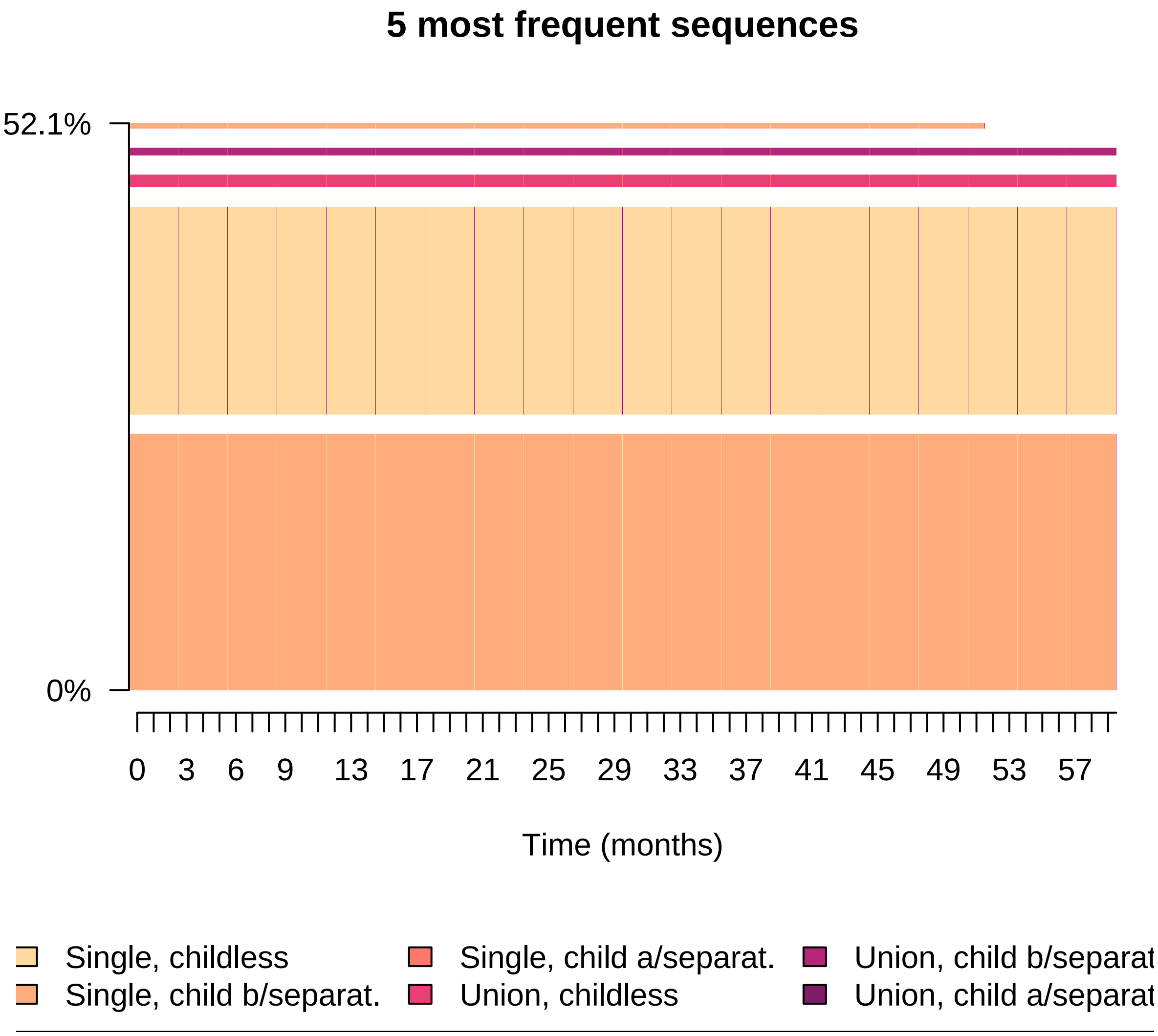
```
# X-axis for exercise
xtlab=seq(0,60, by=1)

#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")
```



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

[Sol.]

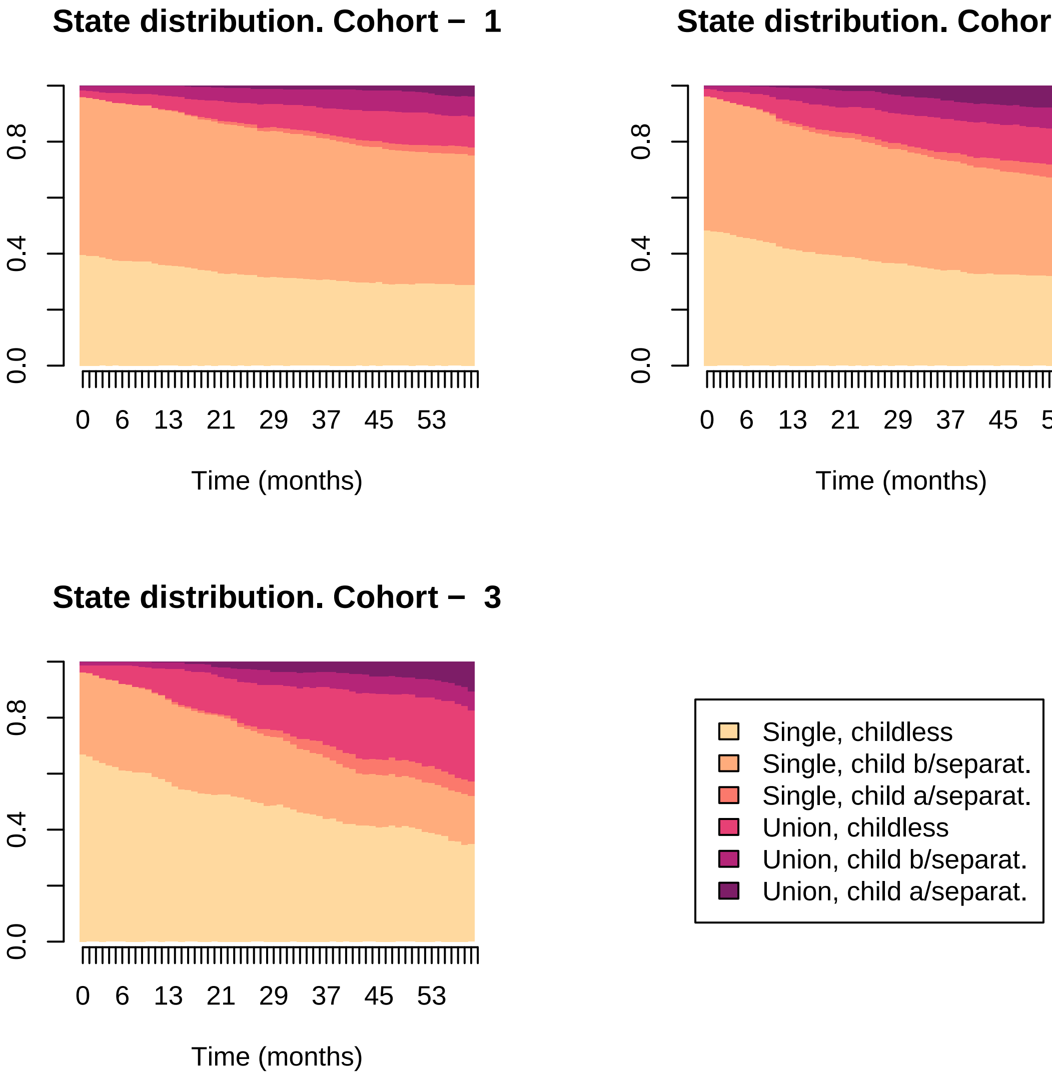
```
par(mfrow=c(2,1))
seqfplot(seqObj2, idxs=1:5, main="5 most frequent sequences",
         with.legend=TRUE, border=NA,
         ylab=NA, xlab="Time (months)", xtlab=xtlab)
```



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

[Sol.]

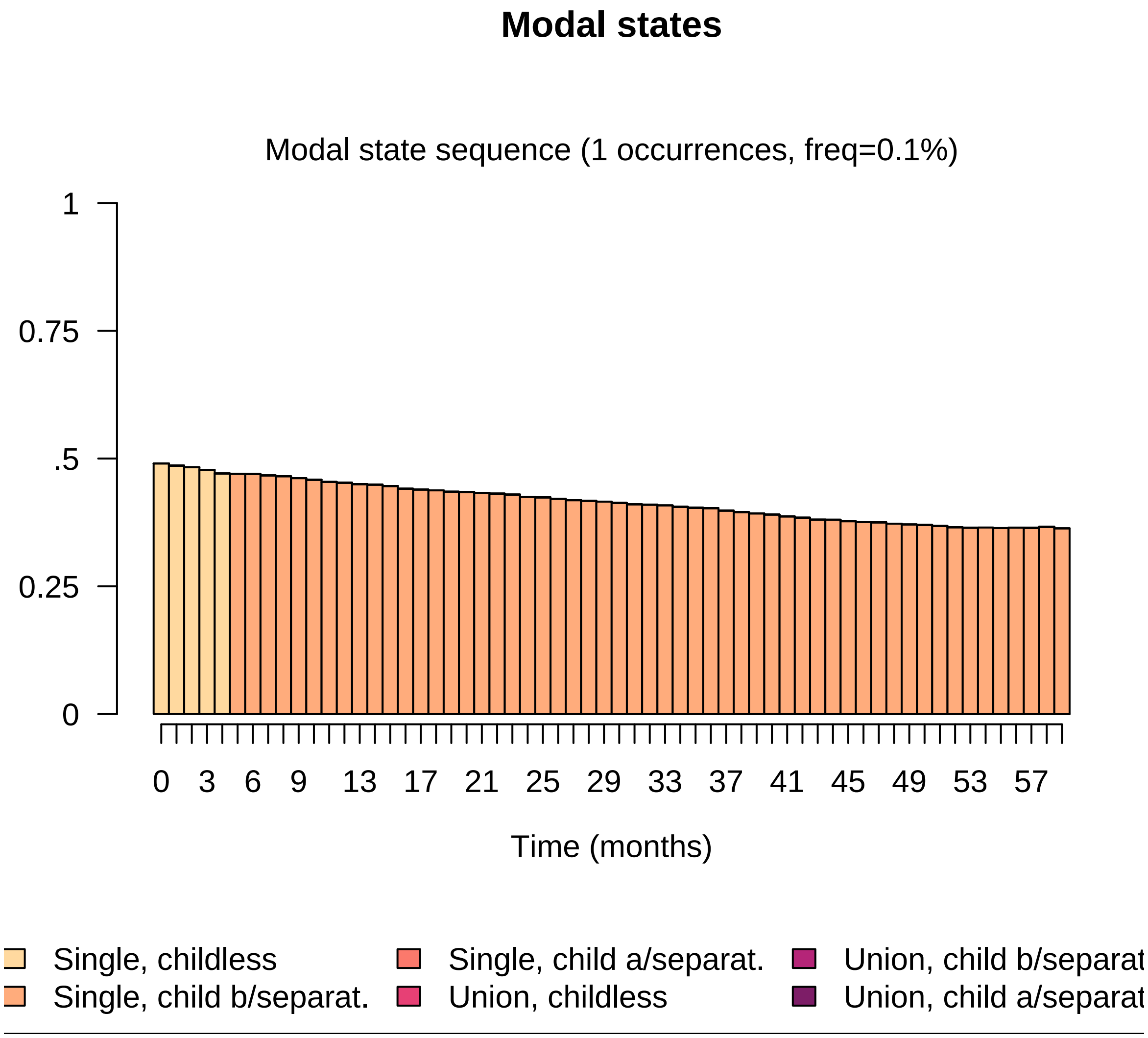
```
seqdplot(seqObj2, group=data2$BIRTHCOH, with.legend=TRUE,
         main= "State distribution. Cohort", use.layout=FALSE,
         border=NA, xtlab=xtlab, ylab=NA, xlab="Time (months)")
```



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

[Sol.]

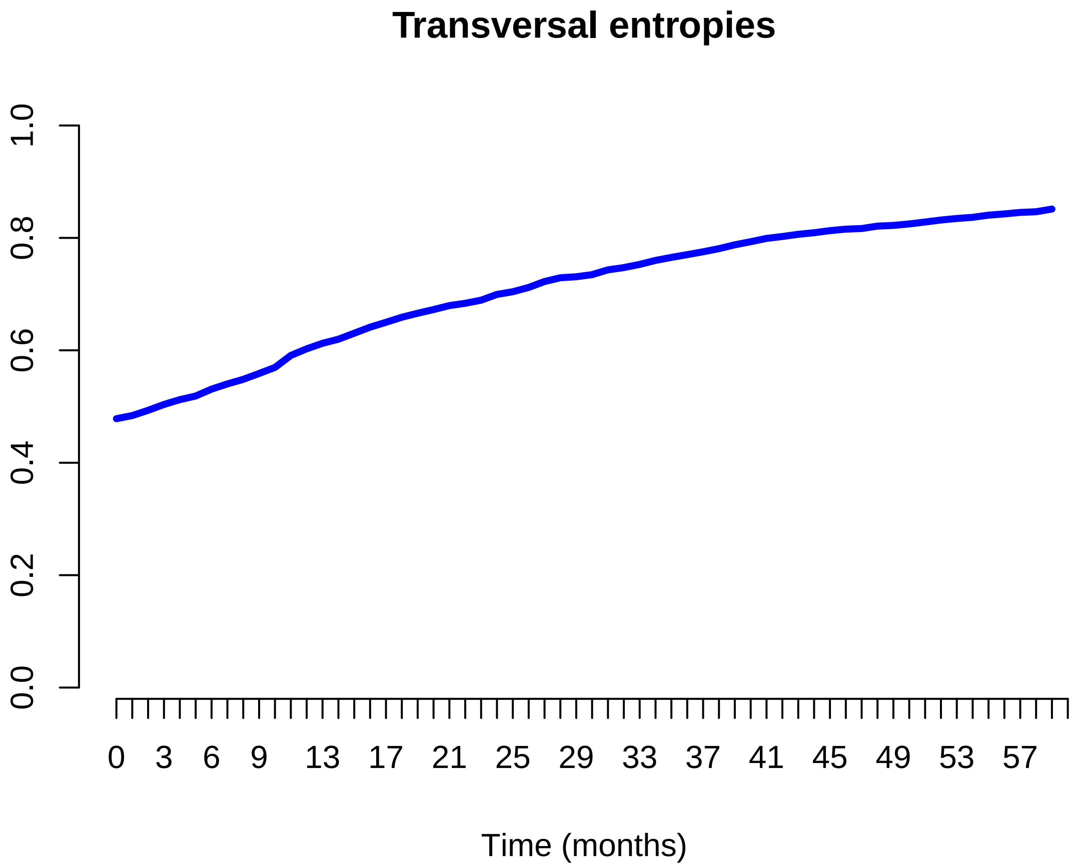
```
par(mfrow=c(1,1))
seqmsplot(seqObj2, with.legend=TRUE, main="Modal states",
          xtlab=xtlab, ylab=NA, xlab="Time (months)")
```



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.]

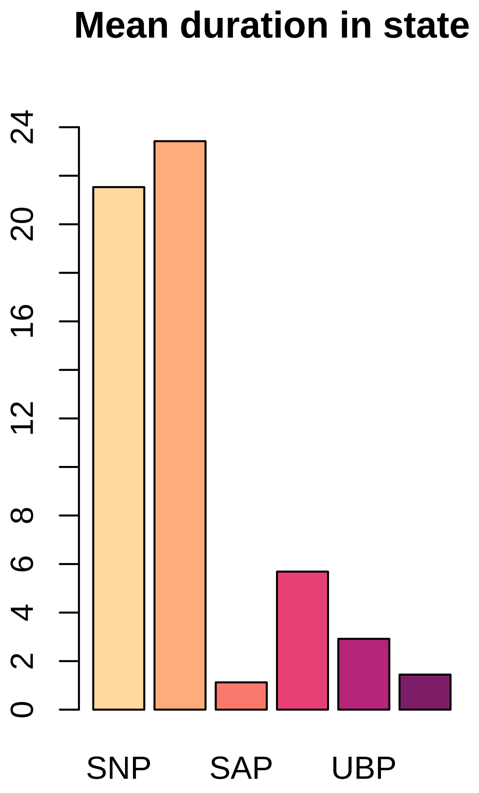
```
# Plot the transversal entropies in each position of the sequence
seqHtplot(seqObj2, with.legend=FALSE, main= "Transversal entropies",
          use.layout=FALSE, border=NA,xtlab=xtlab, ylab=NA, xlab="Time (months)")
```

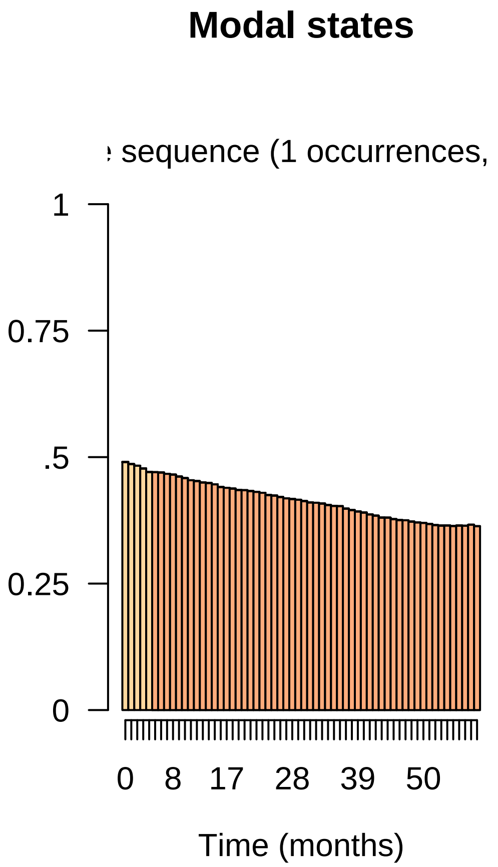


9) Display side by side in a same plot area the mean times spent in each of the states and the sequence of modal states.

[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)")
```


Mean duration in state


Modal states

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

[Sol.]

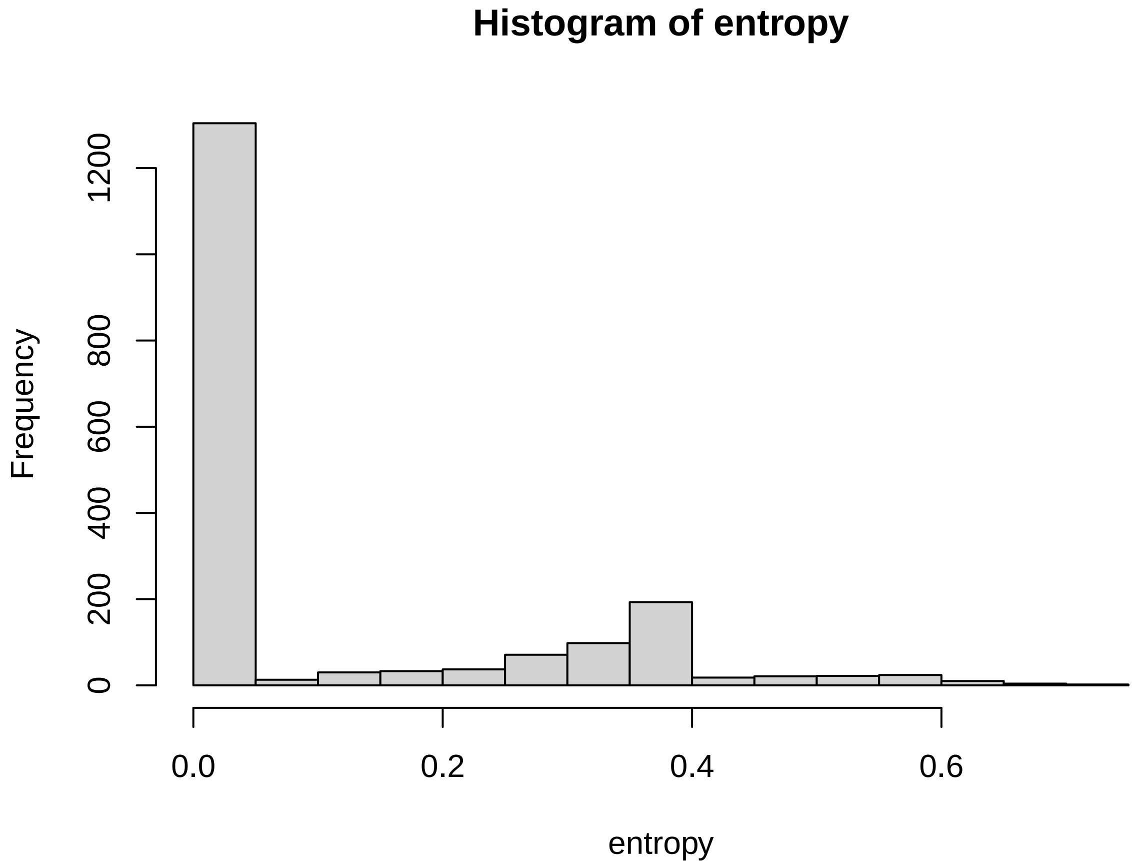
```
seqtrate(seqObj2)
```

11) Compute the sequence length, the number of transitions, the number of subsequences and the longitudinal entropy

[Sol.]

```
# Sequence lenght - number of elements with valid cases (print results for first five sequences)
length <-seqlength(seqObj2)
length[1:5]

# Number of transitions between state episodes in each sequence (print results for first five sequences
transn <-seqtransn(seqObj2)
transn[1:5]

# Number of subsequences contained in a sequence
subseq <- seqsubsn(seqObj2)
table(subseq)

# Longitudinal or within-sequence entropy
```

```r
entropy <- seqient(seqObj2)
par(mfrow=c(1,1))
hist(entropy)
```



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

[Sol.]

```r
summary(length)
summary(transn)
summary(subseq)
summary(entropy)
```

Exercise 2

1) Input the Dataset 2

[Sol.]

```r
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.

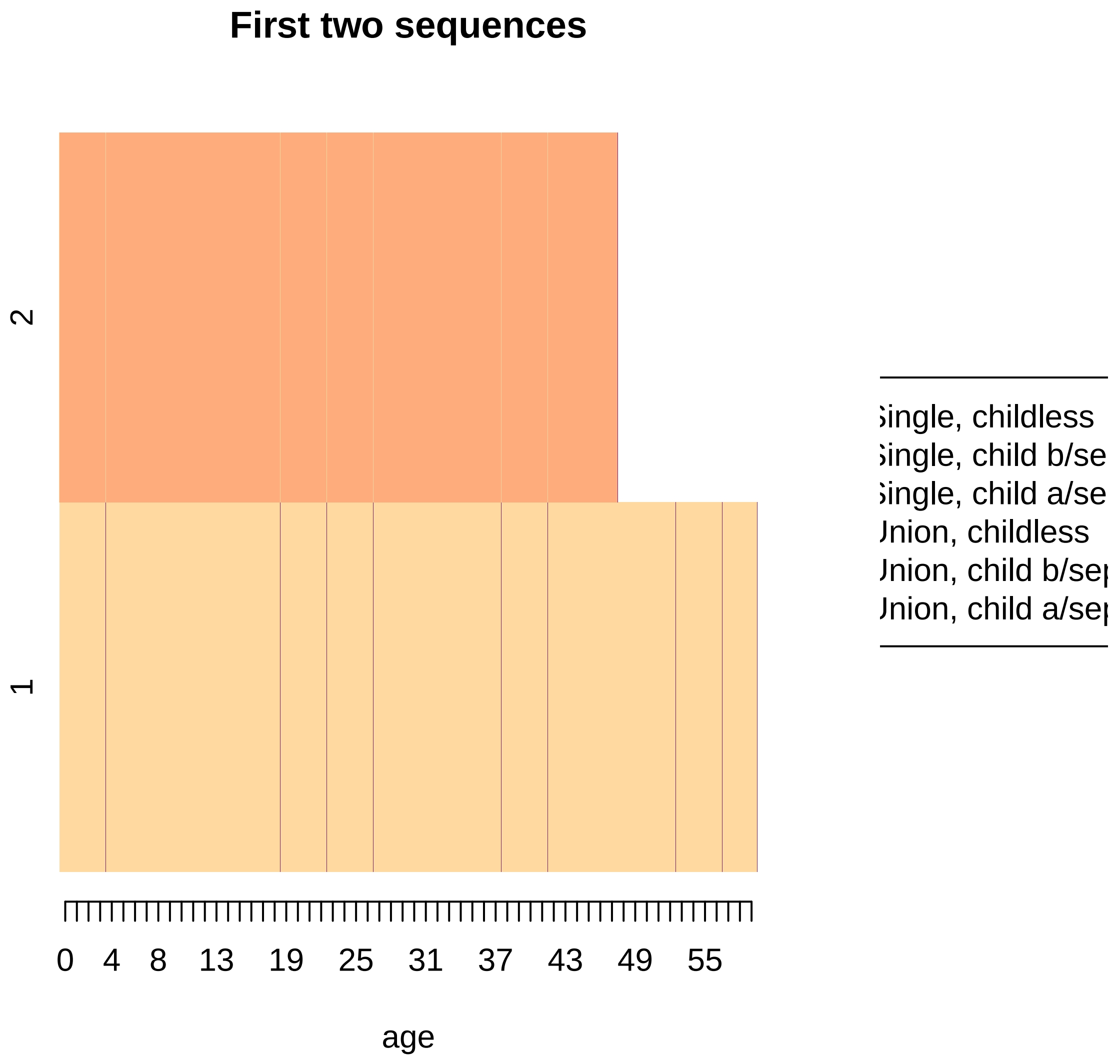
[Sol.]

```
#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 subsequence
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.]

```
seqtrate(seqObj2)

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

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

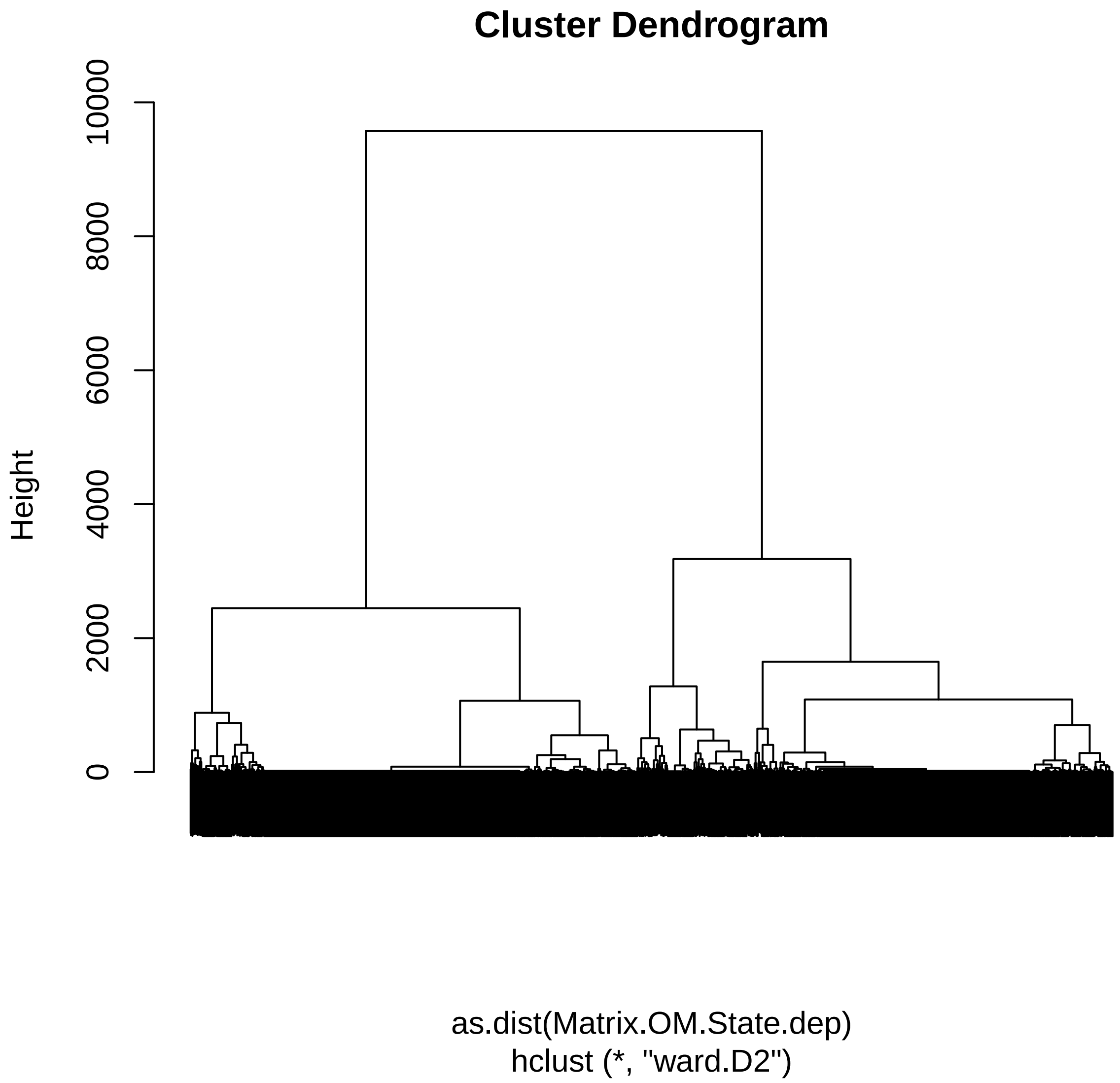
[Sol.]

```
Matrix.OM.State.dep <- seqdist(seqObj2, method="OM", indel=3, 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.]

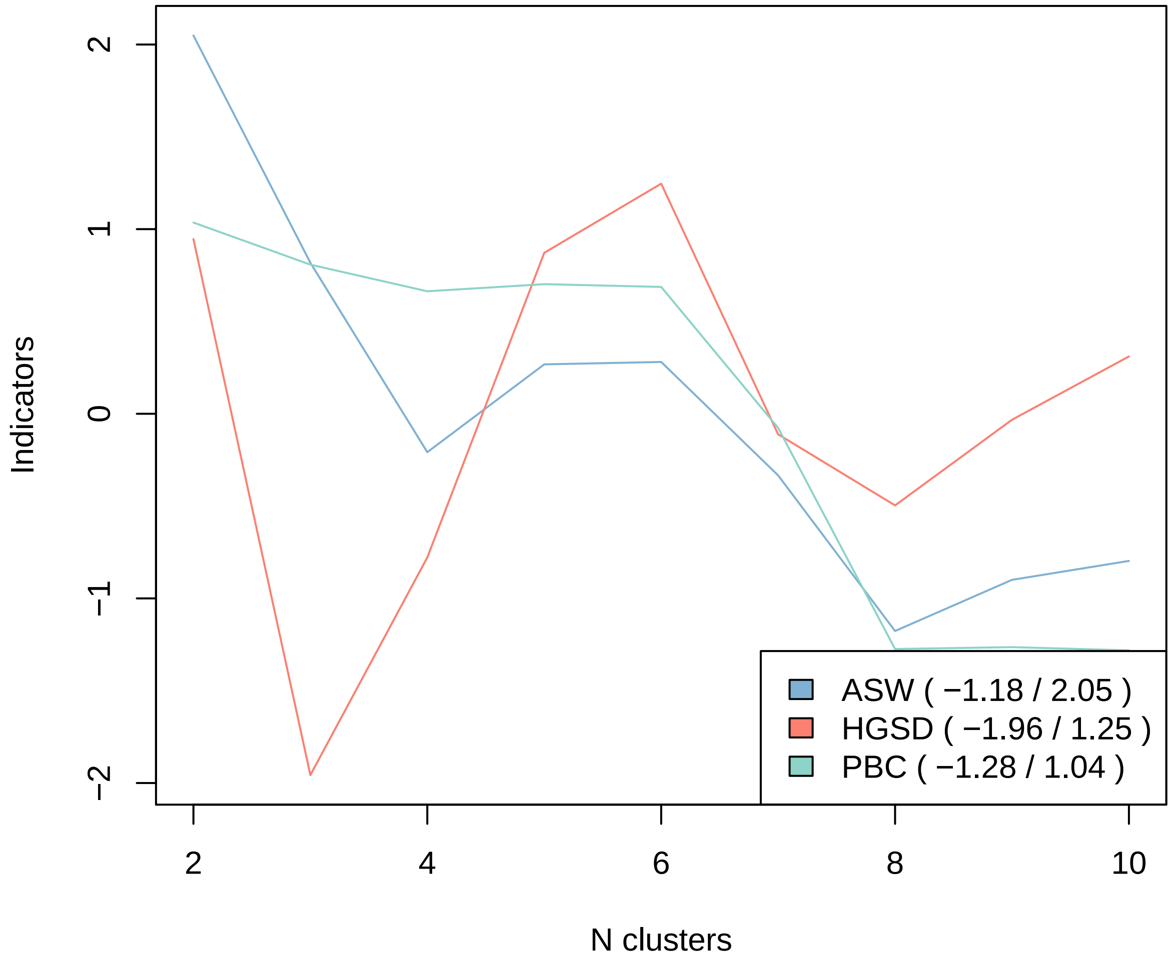
```
# cluster sequences using the OM distances with state-dependent costs and Ward method
ward.OM <- hclust(as.dist(Matrix.OM.State.dep), method = "ward.D2")

###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.]

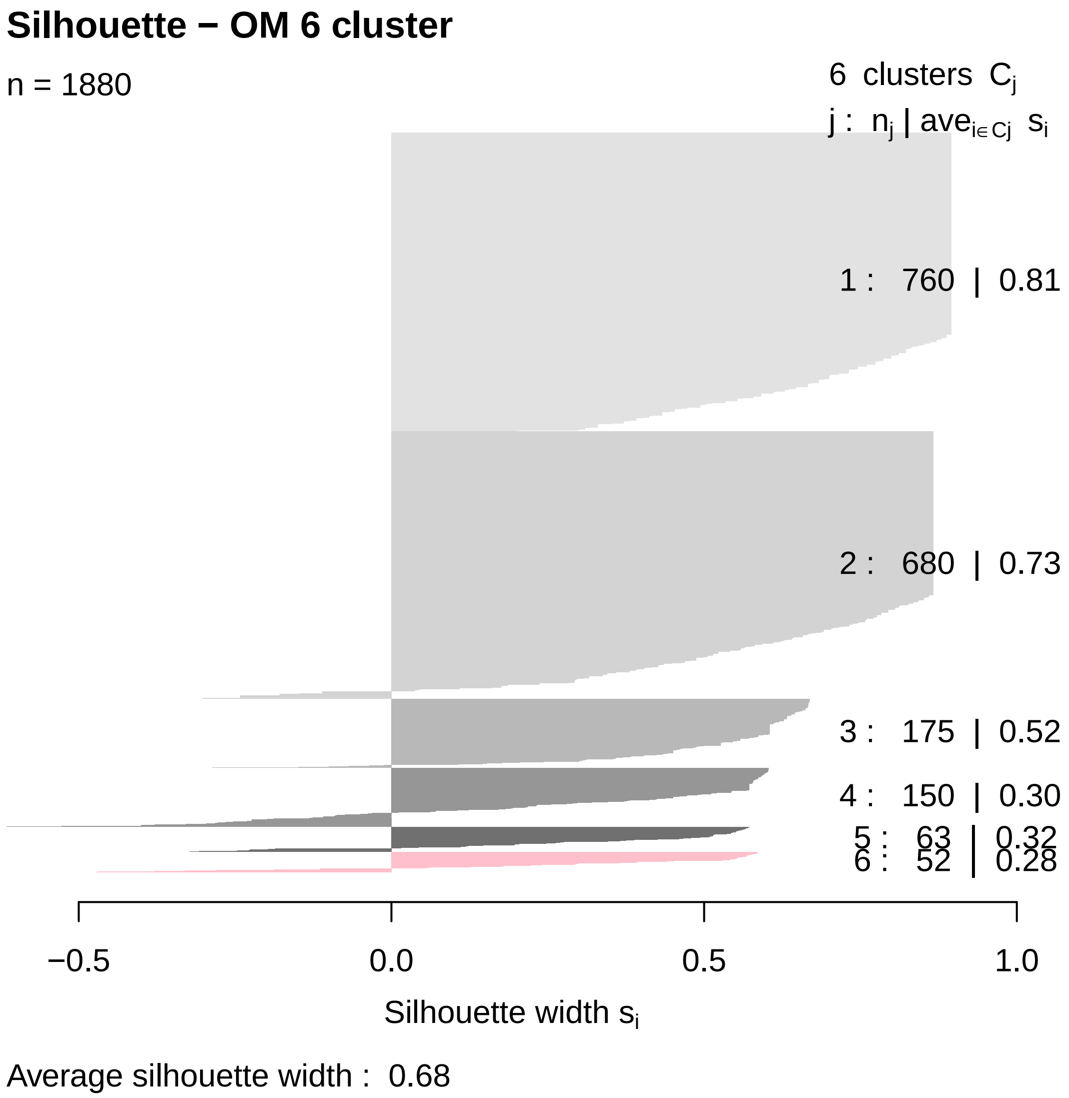
```
### Generate an obseject with 1-10 cluster solutions for each prior anal
wardrange.OM <-as.clustrange(ward.OM, diss=Matrix.OM.State.dep, ncluster=10)

### 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", "pink"))
```



11) Repeat steps 8-10 using a DHD dissimilarity matrix

[Sol.]

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

[Sol.]

References