Sequence Analysis

Liliana Patricia Calderón Bernal
Gonzalo Daniel Garcia
Ainhoa-Elena Leger

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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)
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

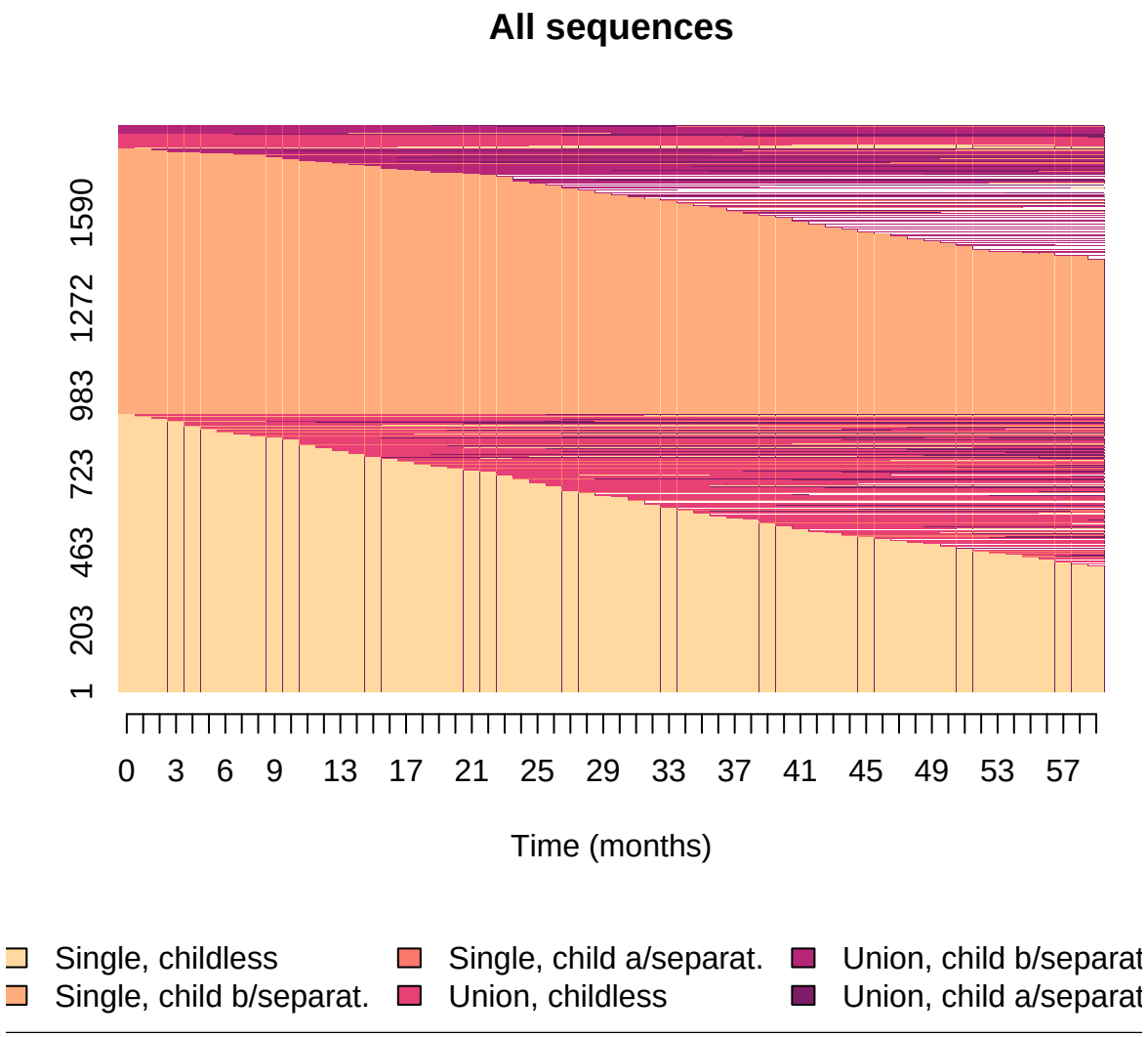
[Sol.]

```
#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.]

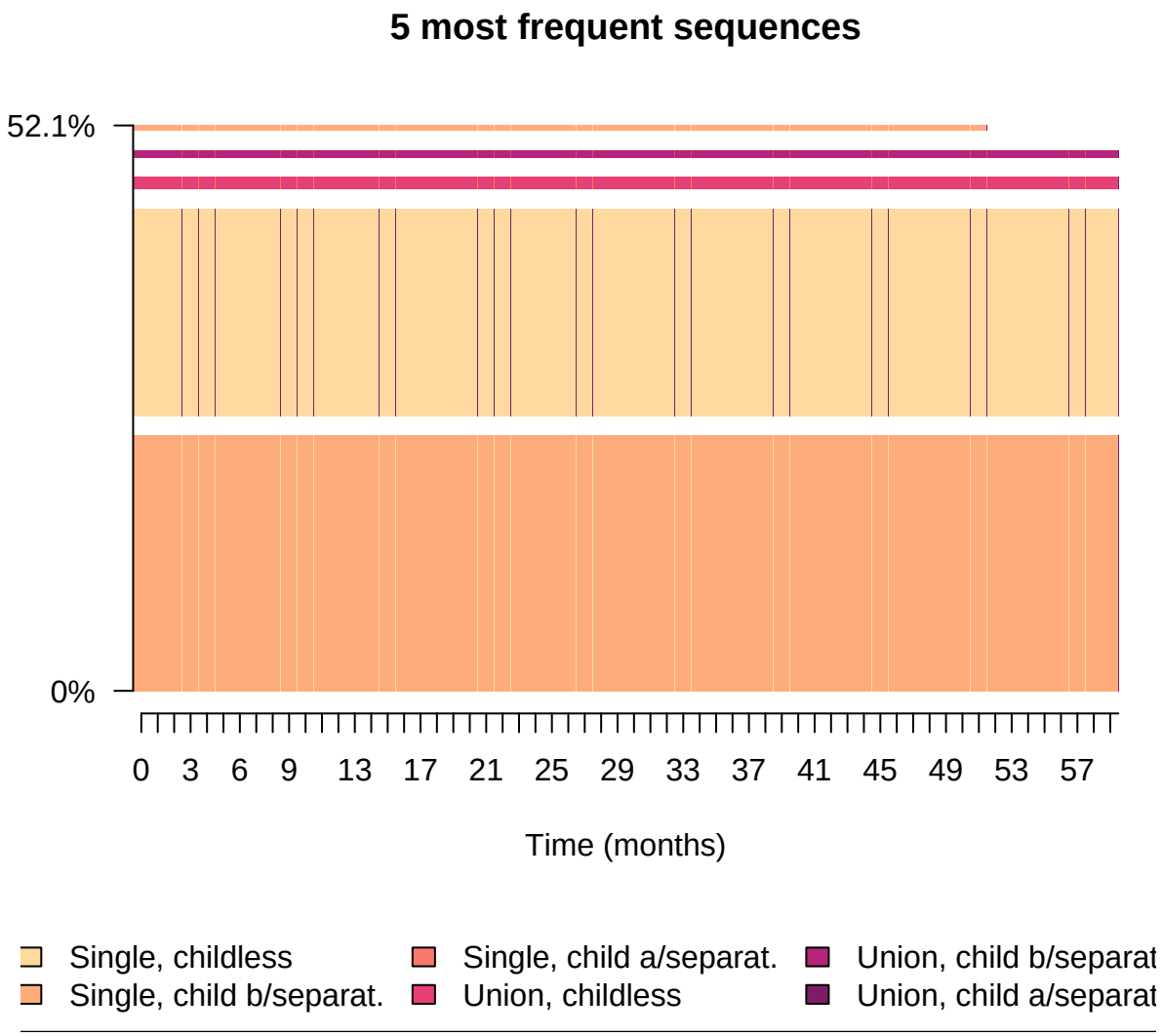
```
# X-axis for exercise
xtlab=seq(0,60, by=1)

#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.]

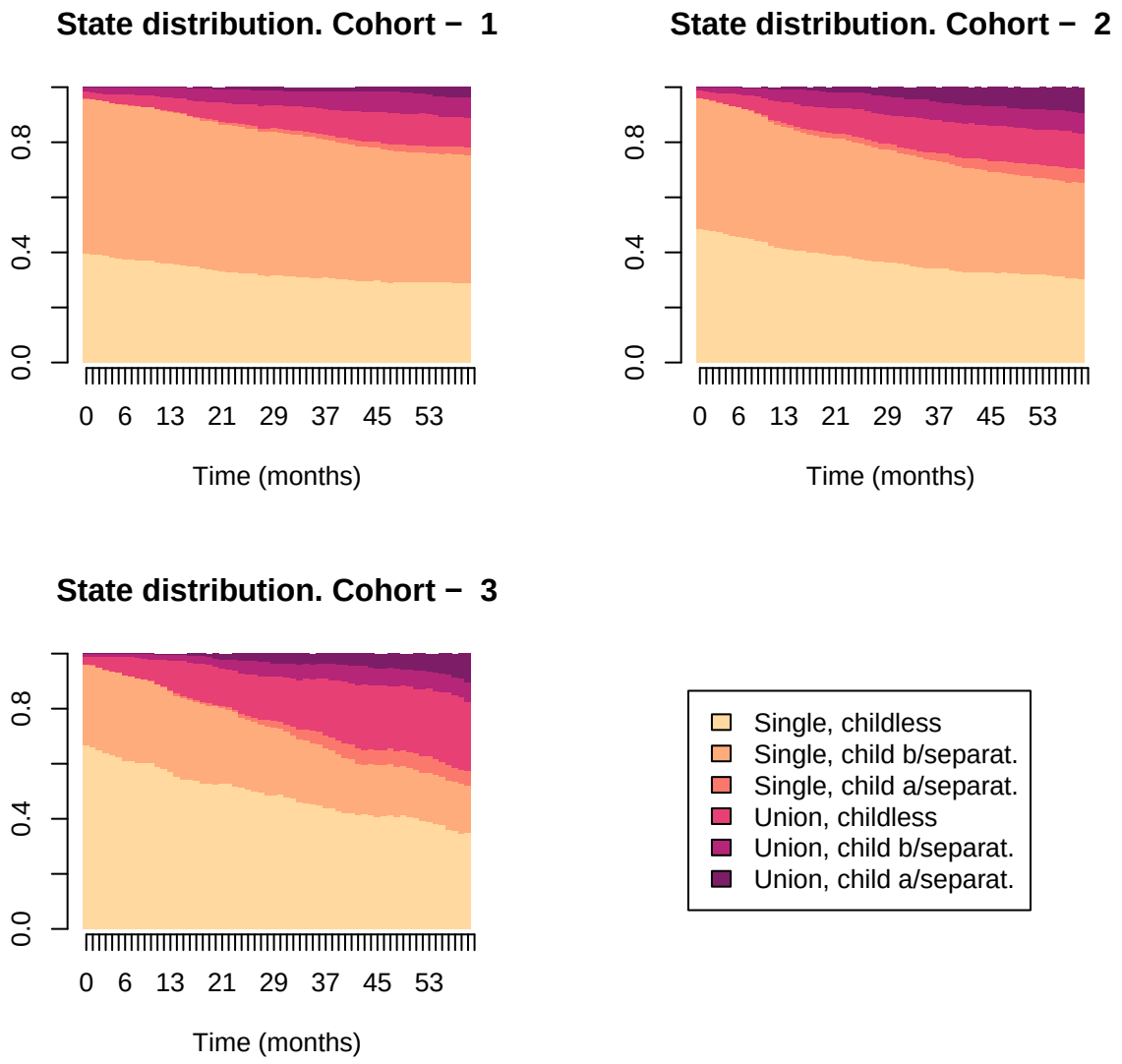
```
par(mfrow=c(2,1))
seqfplot(seqObj2, idxs=1:5, main="5 most frequent sequences",
         with.legend=TRUE, border=NA,
         ylab=NA, xlab="Time (months)", xtlab=xtlab)
```



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

[Sol.]

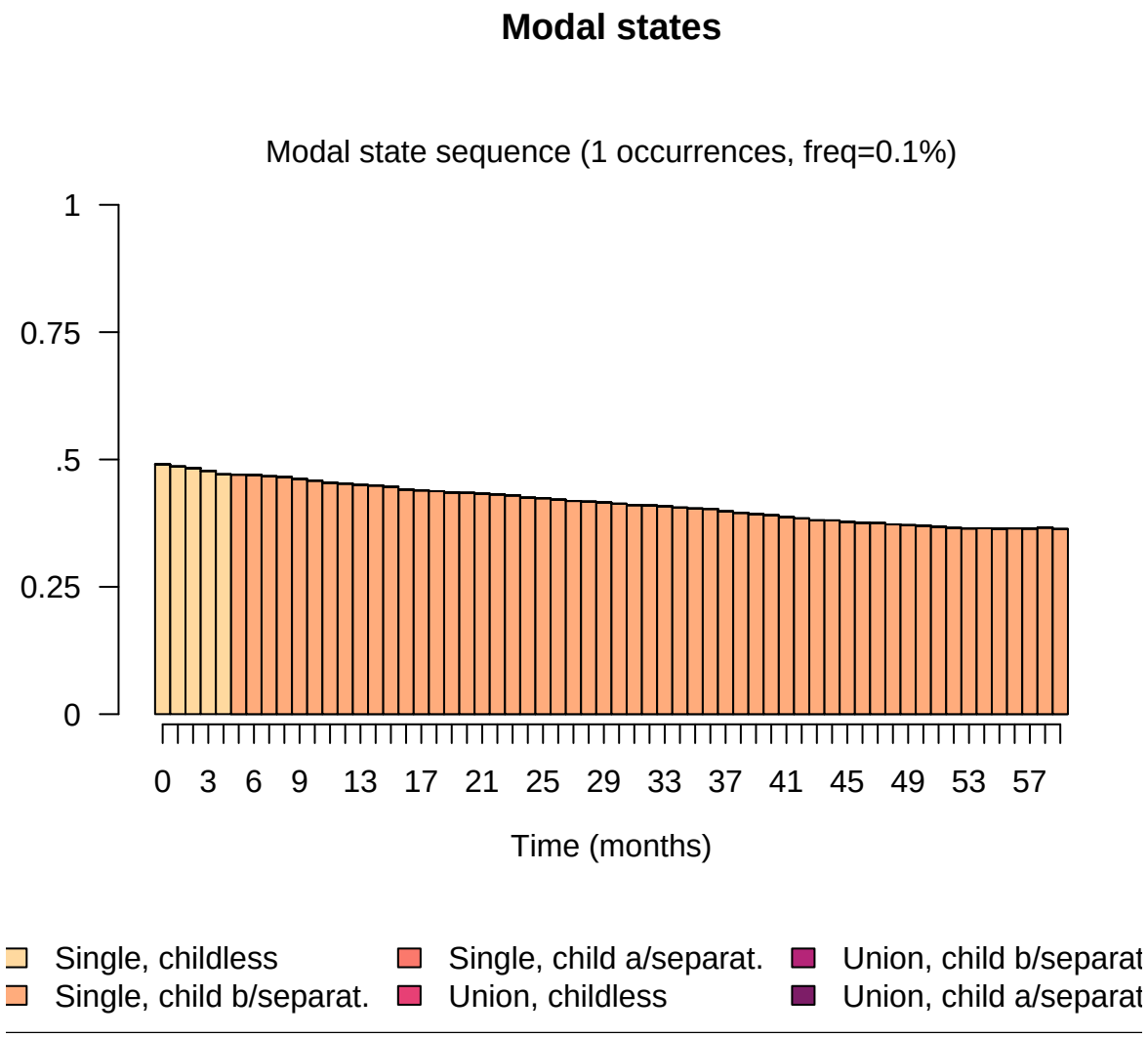
```
seqdplot(seqObj2, group=data2$BIRTHCOH, with.legend=TRUE,
         main= "State distribution. Cohort", use.layout=FALSE,
         border=NA, xtlab=xtlab, ylab=NA, xlab="Time (months)")
```



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

[Sol.]

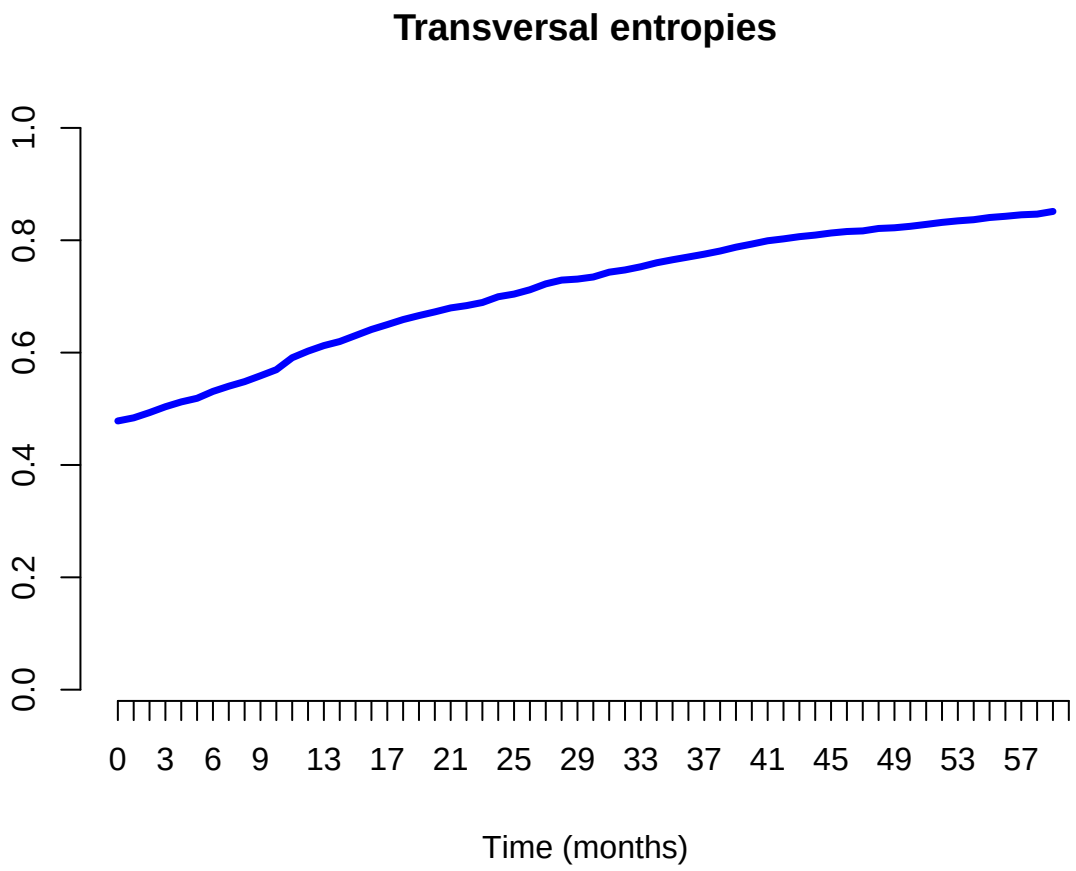
```
par(mfrow=c(1,1))
seqmsplot(seqObj2, with.legend=TRUE, main="Modal states",
          xtlab=xtlab, ylab=NA, xlab="Time (months)")
```



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.]

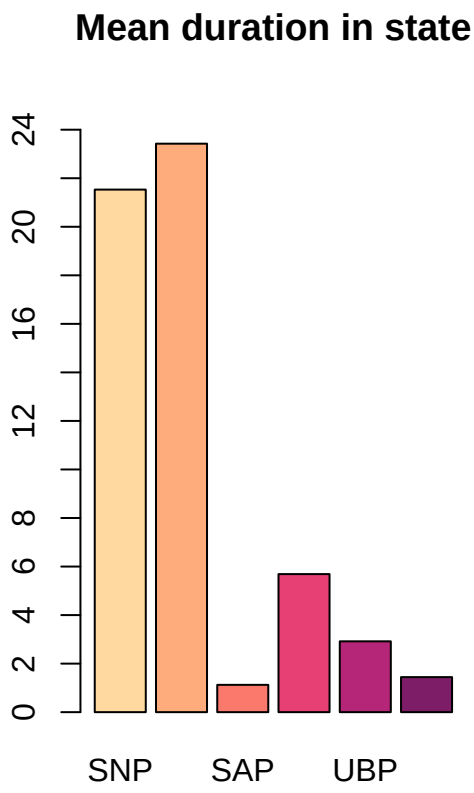
```
# Plot the transversal entropies in each position of the sequence
seqHtplot(seqObj2, with.legend=FALSE, main= "Transversal entropies",
          use.layout=FALSE, border=NA,xtlab=xtlab, ylab=NA, xlab="Time (months)")
```

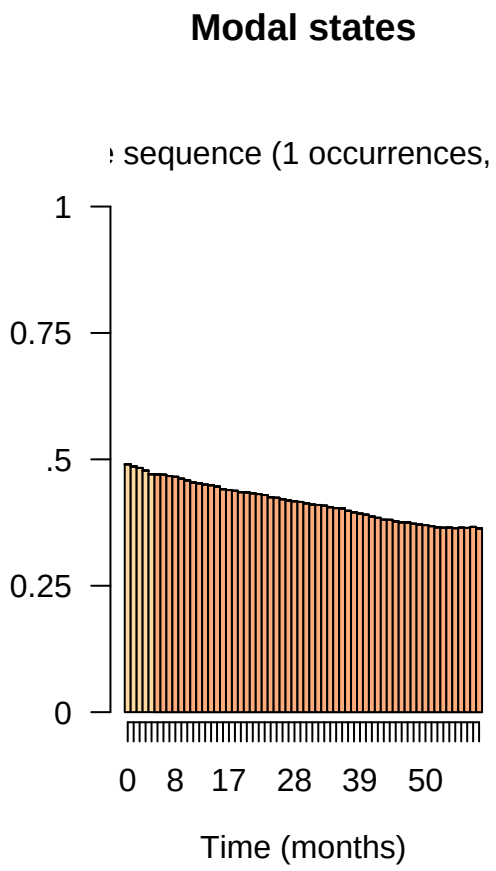


9) Display side by side in a same plot area the mean times spent in each of the states and the sequence of modal states.

[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)")
```





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

[Sol.]

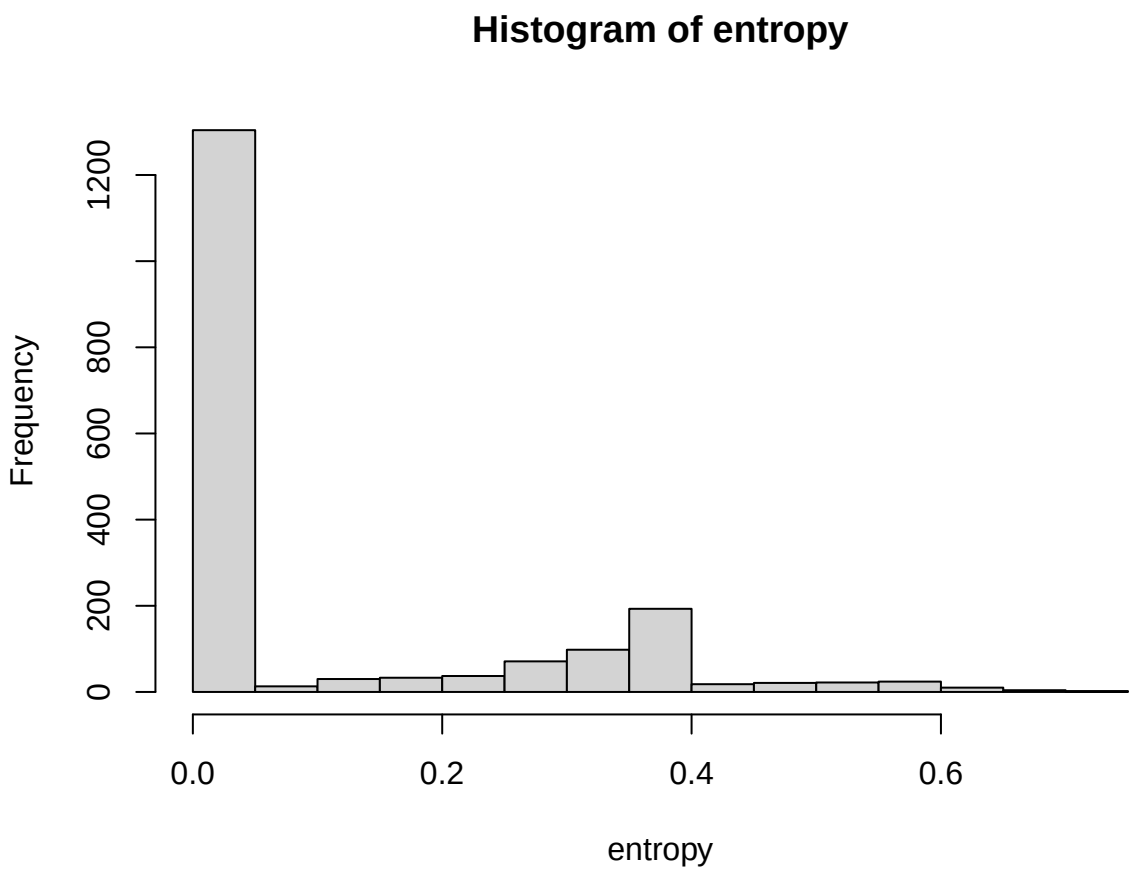
```
seqtrate(seqObj2)
```

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

[Sol.]

[Sol.]

References