
Assignment 1

1. Starting with R and TraMineR
   - Start R and load the TraMineR library.
   - Look at the help page of the `biofam` data provided by TraMineR which you access by typing `help(biofam)` or `?biofam`. Find out which are the columns containing the sequence data.
   - Look at the first six rows of the data frame (`head(biofam)`).
   - Create the state sequence object and plot the sequences using, `seqIplot`, `seqfplot` and `seqdplot`. Comment the plots.
   - Display (`print`) the first 10 sequences in extended and compact form.
2. Describe the sequence data you plan to use by specifying:
   - What the sequences are representing and where they come from.
   - Whether there is one sequence per case or multichannel sequences? In case of multichannel sequences, specify to the following points for each channel.
   - The nature of the sequences (Categorical? Chronological? State or event sequences? ...,)
   - The alphabet (list of symbols in the sequences).
     - Is there a natural order of the symbols (ordinal variable)?
   - Size of the alphabet
     - If larger than 15, propose category mergings to reduce the size.
     - In case of numerical sequences, suggest a way to discretize the values into 15 classes or less.
   - Number of sequences.
   - Maximum and minimum sequence lengths.
   - The kind of knowledge you expect to extract from your sequences. What are you primarily interested in: sequencing, timing, duration, quantum?