

# EDSD 2024-2025 Sequence Analysis Assignment

Gilbert Habaasa

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#Instructor: Nicola Barban

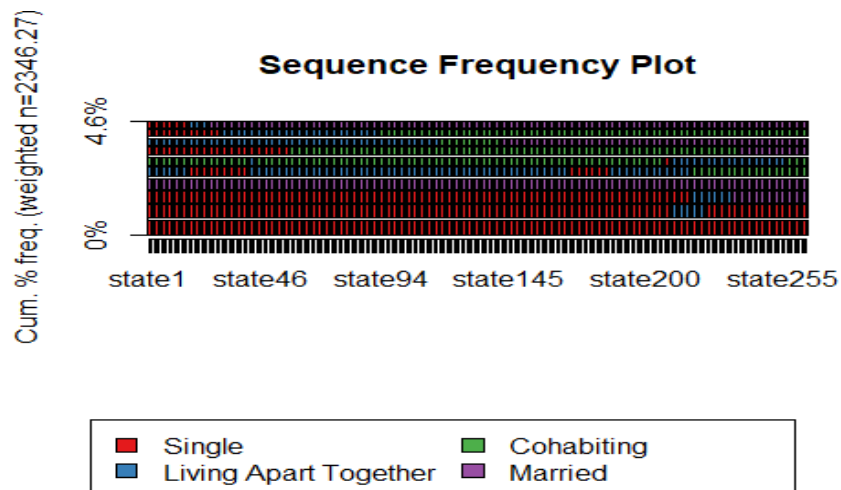
##A. Import the data in R and describe the distribution of life states using relevant sequence

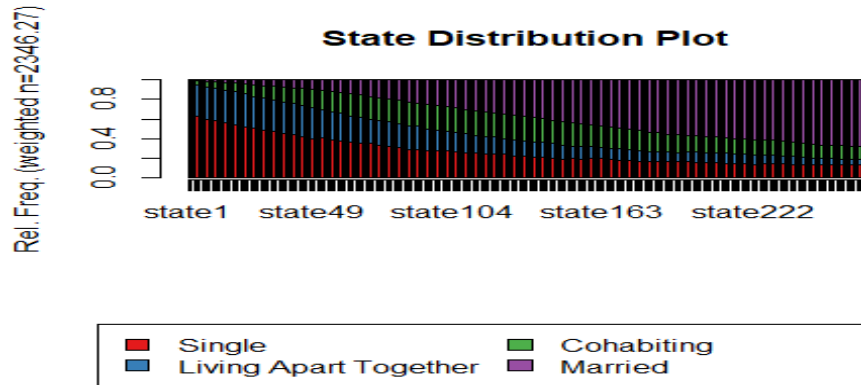
The German Family Panel (pairfam) data was imported from <https://sa-book.github.io/>. The detailed steps on importation from stata, recoding of life states, definition of state labels, codes, colours, and creation of sequence object are shown in the rmd file attached separately to the assignment. For question 2 and 3, detailed codes on mean duration in each state, plots, computation on life course dissimilarities in the data, as well as clustering methods to derive typical trajectories and describe groups are presented in rmd file indicated above.

## ## Step 1.1: Import Data from Stata

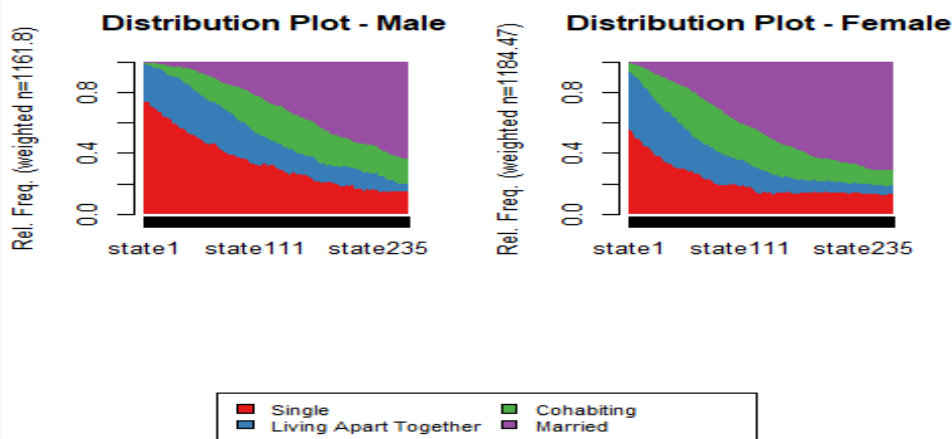
```
pairfam_raw <- read_dta("C:/Users/admin/OneDrive - London School of Hygiene and Tropical Medicine/INED 2024/Sequence analysis/Assignment/PartnerBirthbio.dta")
```

## # Step 1.5: Sequence Summary Plots: Frequency and distribution plots





# Plot distribution plots grouped by gender



## Step 1.6: Statistics and Distribution of Life States

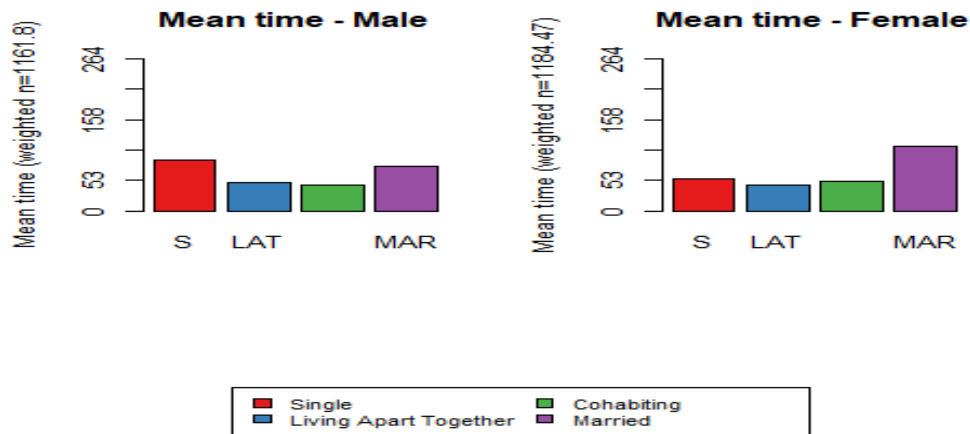
### First 10 Most Common Sequences

##		Freq	Percent
##	S/264	17.0	0.72
##	S/210-LAT/12-S/42	14.6	0.62
##	S/217-LAT/17-MAR/30	13.2	0.56
##	MAR/264	11.8	0.50
##	LAT/17-S/22-LAT/130-S/16-LAT/33-COH/46	10.2	0.43
##	COH/39-LAT/3-COH/165-S/1-LAT/46-COH/10	9.1	0.39
##	S/57-COH/180-MAR/27	9.0	0.39
##	LAT/116-COH/24-MAR/124	8.1	0.34
##	S/28-LAT/63-COH/173	7.7	0.33
##	S/15-LAT/8-MAR/241	7.3	0.31

# Computed mean durations by gender

```
## # A tibble: 2 x 5
##   sex      S    LAT    COH    MAR
##   <fct> <dbl> <dbl> <dbl> <dbl>
## 1 Male   80.1  45.7  49.8  88.4
## 2 Female 48.3  42.1  53.1 120.
```

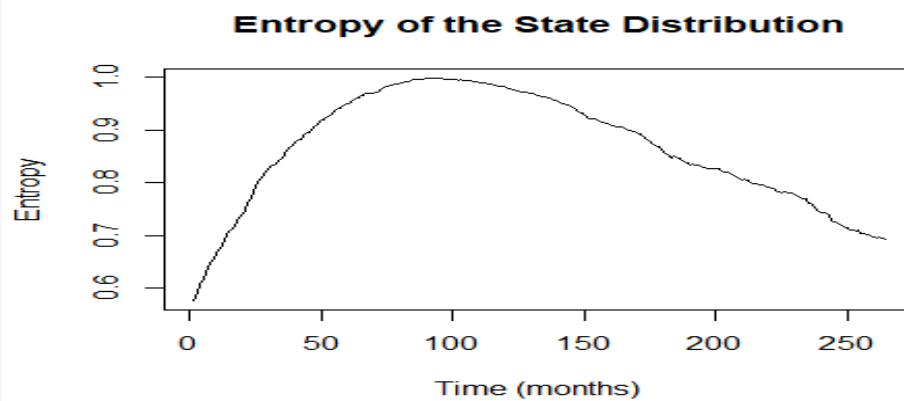
## # Mean time in each state by Gender



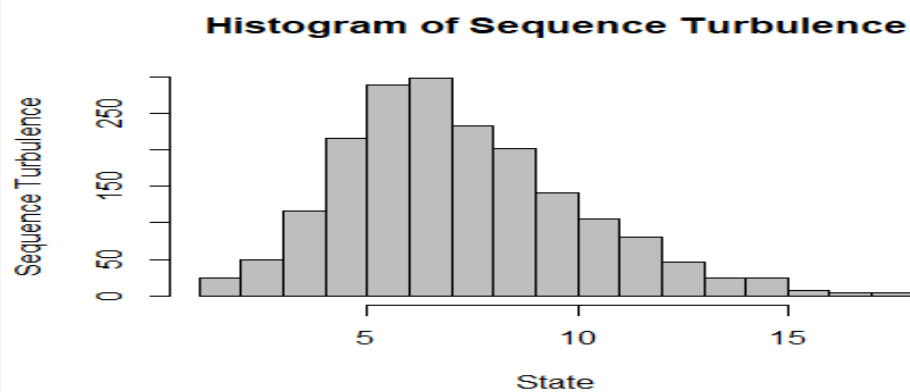
## ### Transition Matrix

```
##      [-> S] [-> LAT] [-> COH] [-> MAR]
## [S ->]    0.98    0.02    0.00    0.00
## [LAT ->]   0.02    0.96    0.02    0.00
## [COH ->]   0.00    0.00    0.98    0.01
## [MAR ->]   0.00    0.00    0.00    1.00
```

## ### Entropy Over Time



## ### Sequence Turbulence



The most common sequence is Singlehood state and is followed by sequences that start with singlehood and transition to LAT, cohabitation and marriage. On average, males spend 80.1 months in single state while females spend 48.3 months in single state. However, in marriage state, the males spend less time than females (88.4 months vs 120.0 months). On transitions, persons single have 98% chance of staying single. The 98% people stay in LAT state while 100% remain married. On the other hand, the 98% cohabiting are likely to keep in same state.

##2. Calculate life course dissimilarities in the data.

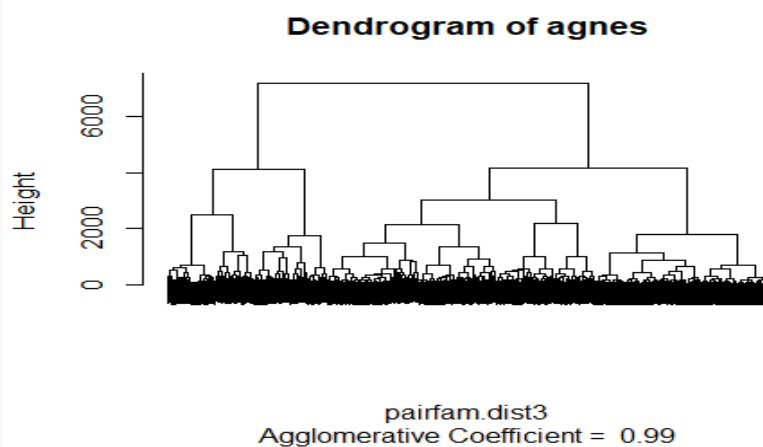
*#Step 2.6: Comparison of Dissimilarity matrices using Pairwise Correlation*

##	OM_constant	OM_trate	OM_seqcost	LCS	DHD
## OM_constant	1.0000000	0.9999721	0.9999736	1.0000000	0.9089094
## OM_trate	0.9999721	1.0000000	0.9999999	0.9999721	0.9098161
## OM_seqcost	0.9999736	0.9999999	1.0000000	0.9999736	0.9097426
## LCS	1.0000000	0.9999721	0.9999736	1.0000000	0.9089094
## DHD	0.9089094	0.9098161	0.9097426	0.9089094	1.0000000

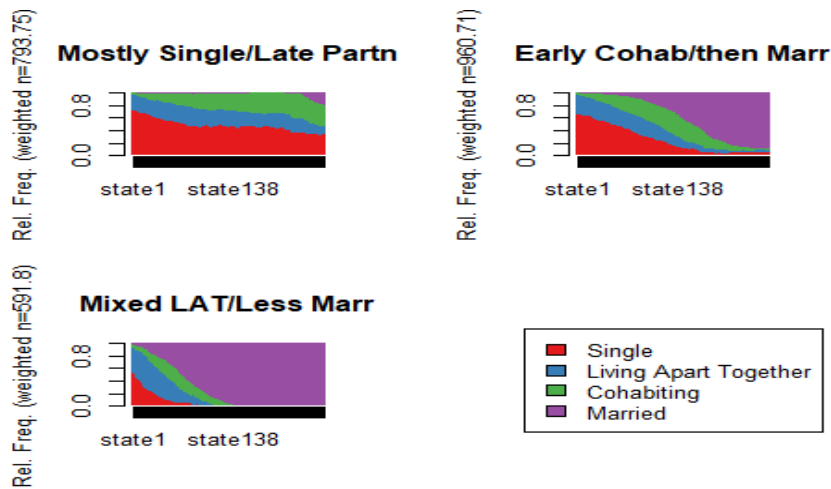
There is high correlation between OM, LCS and DHD. This implies similar results despite the method used.

##3. Use a clustering methods to derive typical trajectories and describe groups

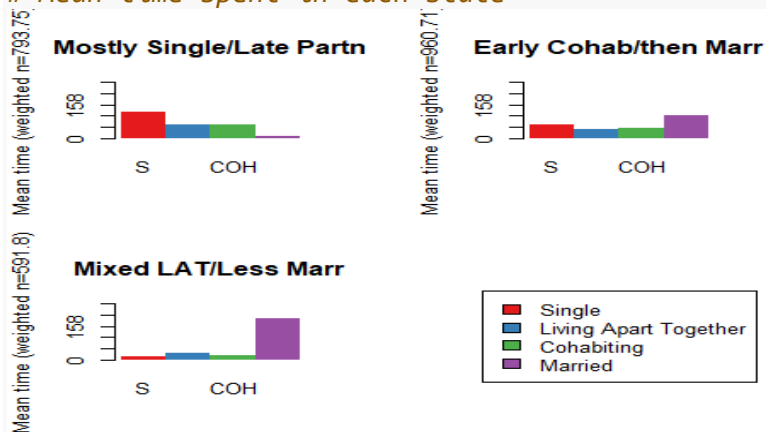
*# Step 3.1: Clustering using Ward's method*



### #Step 3.5: Generate different cluster plots



### # Mean time spent in each state



Based on 3 clusters, a diverse life course trajectory in partnership formation is observed: stable singlehood or delayed partnership; early cohabitation leading to marriage; mixed living apart together and less marriage. The first cluster is dominated by singlehood sequence. The second cluster is largely dominated by early cohabitation and marriage in the longrun. Both early cohabiting and mixed LAT report partners staying long in marriage in the long run.