Sequence Analysis: Time Use Data (ATUS)

Kamila Kolpashnikova*

Introduction

Traditionally, a tool for analysing life events in social sciences, sequence analysis is becoming more and more popular for dealing with time-use data. In this tutorial, I'll walk you through the steps how to do sequence analysis with time-use data (American Time Use Survey, ATUS).

To follow this tutorial:

- change the directory to the location of cloned directory
- follow instructions in the code (R file is included)

Funding: This project has received funding from the European Union's Horizon 2020 research and innovation programme under the Marie Skłodowska-Curie grant agreement No 892101 (awardee: Kamila Kolpashnikova).

Example of Work Using Sequence Analysis

Here is an example how a published paper using sequence analysis looks like (my recent research in the Journal of Population Ageing):

Kolpashnikova, K., & Kan, M. Y. (2020). Eldercare in Japan: Cluster Analysis of daily time-use patterns of elder caregivers. Journal of Population Ageing, 1-23.

If you follow this tutorial, you will be able to recreate the analyses in the paper.

Loading Necessary Packages

```
#### Loading Necessary Packages ####
if (!require("pacman")) install.packages("pacman")

## Loading required package: pacman

library(pacman)

# load and install packages
pacman::p_load(TraMineR, TraMineRextras, downloader, cluster, RColorBrewer, devtools, haven,
               tidyverse, reshape2, WeightedCluster, nnet, plyr)
```

Load Datasets from the BLS website

Remember that in R, it's forward slashes. Here I created a function that can unzip and create dataframes from the zipped BLS ATUS files.

```
#' Download, unzip, and create a dataframe from ATUS files.
#' Note: the zipped file will be downloaded as "data" in your working directory.
#'
```

*University of Oxford

```

#' @param url A string containing a link to a zipped file from
#' the Bureau of Labor Statistics website.
#' @return The dataframe for ATUS.
#' @examples
#' zip_to_df("https://www.bls.gov/tus/special.requests/atusact-0320.zip")
#' zip_to_df("https://www.bls.gov/tus/special.requests/atusrostec-1120.zip")
zip_to_df<-function(url) {
  d <- "data"
  download(url, destfile=d)
  data <- read.table(unzip(d,
    files=paste(str_replace(str_split(tail(str_split(url,
      "/" )[[1]], 1),
      "\\." )[[1]][1], "-", "_"), ".dat", sep=""),
    header = T, sep = ",", colClasses = "character")
  return(data)
}

```

```

## download the part of ATUS that contains diaries
df <- zip_to_df("https://www.bls.gov/tus/special.requests/atusact-0320.zip")
head(df)

```

```

##          TUCASEID TUACTIONITY_N TUACTIONDUR24 TUCC5 TUCC5B TRTCCTOT_LN TRTCC_LN
## 1 20030100013280          1          60      -1      -1          -1          -1
## 2 20030100013280          2          30      -1      -1          -1          -1
## 3 20030100013280          3         600      -1      -1          -1          -1
## 4 20030100013280          4         150      -1      -1          -1          -1
## 5 20030100013280          5           5      -1      -1          -1          -1
## 6 20030100013280          6         175      -1      -1          -1          -1
##      TRTCOC_LN TUSTARTTIM TUSTOPTIME TRCODEP TRTIER1P TRTIER2P TUCC8 TUCUMDUR
## 1          -1  04:00:00  05:00:00  130124          13      1301      97         60
## 2          -1  05:00:00  05:30:00  010201           1      0102       0         90
## 3          -1  05:30:00  15:30:00  010101           1      0101       0        690
## 4          -1  15:30:00  18:00:00  120303           12     1203       0        840
## 5          -1  18:00:00  18:05:00  110101           11     1101       0        845
## 6          -1  18:05:00  21:00:00  120303           12     1203       0       1020
##      TUCUMDUR24 TUACTIONDUR TR_03CC57 TRTO_LN TRTONHH_LN TRTOHH_LN TRTHH_LN
## 1           60          60          -1          -1          -1          -1          -1
## 2           90          30          -1          -1          -1          -1          -1
## 3          690         600          -1          -1          -1          -1          -1
## 4          840         150          -1          -1          -1          -1          -1
## 5          845           5          -1          -1          -1          -1          -1
## 6         1020         175          -1          -1          -1          -1          -1
##      TRTNOHH_LN TEWHERE TUCC7 TRWBELIG TRTEC_LN TUEC24 TUDURSTOP
## 1          -1          9      -1          -1          -1          -1          -1
## 2          -1         -1      -1          -1          -1          -1          -1
## 3          -1         -1      -1          -1          -1          -1          -1
## 4          -1          1      -1          -1          -1          -1          -1
## 5          -1          1      -1          -1          -1          -1          -1
## 6          -1          1      -1          -1          -1          -1          -1

```

```

## download the part of ATUS with the information about self-reported elder caregivers
df_ec <- zip_to_df("https://www.bls.gov/tus/special.requests/atusrostec-1120.zip")
head(df_ec)

```

```

##          TUCASEID TEAGE_EC TEELDUR TEELWHO TEELYRS TRELHH TUECLNO TULINENO

```

```
## 1 20110101110074      70      4      44      2      0      5      -1
## 2 20110101110156      85      4      46      2      0      5      -1
## 3 20110101110507      80      1      55     -1      0      2      -1
## 4 20110101110521      85      3      43     -1      0      3      -1
## 5 20110101110522      80      4      44      6      0      2      -1
## 6 20110101110639      64      1      38     -1      0      2      -1
```

Filter the elder caregivers and recode activities

Before we create our sequence dataframes, we need to wrangle the original data to make it usable.

```
## select ids in diaries dataframe that are in eldercare dataframe
data <- df[df$TUCASEID %in% df_ec$TUCASEID,]
head(data)
```

```
##          TUCASEID TUACTIVITY_N TUACTDUR24 TUCC5 TUCC5B TRTCCTOT_LN
## 2228592 20110101110074          1         10      0      0          0
## 2228593 20110101110074          2        300      0      0          0
## 2228594 20110101110074          3          5      0      0          0
## 2228595 20110101110074          4        525      0      0          0
## 2228596 20110101110074          5          5      0      0          0
## 2228597 20110101110074          6         30      0      0          0
##          TRTCC_LN TRTCOC_LN TUSTARTTIM TUSTOPTIME TRCODEP TRTIER1P TRTIER2P
## 2228592      -1          0  04:00:00  04:10:00  110101          11        1101
## 2228593      -1          0  04:10:00  09:10:00  020402           02        0204
## 2228594      -1          0  09:10:00  09:15:00  180482          18        1804
## 2228595      -1          0  09:15:00  18:00:00  500101          50        5001
## 2228596      -1          0  18:00:00  18:05:00  180482          18        1804
## 2228597      -1          0  18:05:00  18:35:00  010201           01        0102
##          TUCC8 TUCUMDUR TUCUMDUR24 TUACTDUR TR_03CC57 TRTO_LN TRTONHH_LN
## 2228592     97        10          10         10      -1      -1          -1
## 2228593      0       310         310        300      -1      -1          -1
## 2228594      0       315         315          5      -1      -1          -1
## 2228595      0       840         840        525      -1      -1          -1
## 2228596      0       845         845          5      -1      -1          -1
## 2228597      0       875         875         30      -1      -1          -1
##          TRTOHH_LN TRTHH_LN TRTNOHH_LN TEWHERE TUCC7 TRWBELIG TRTEC_LN TUEC24
## 2228592      -1      -1          -1          1      0      -1      -1      -1
## 2228593      -1      -1          -1          1      0      -1      -1      -1
## 2228594      -1      -1          -1         13      0      -1      -1      -1
## 2228595      -1      -1          -1          3      0      -1      -1      -1
## 2228596      -1      -1          -1         13      0      -1      -1      -1
## 2228597      -1      -1          -1        -1      0      -1      -1      -1
##          TUDURSTOP
## 2228592          -1
## 2228593          -1
## 2228594          -1
## 2228595          -1
## 2228596          -1
## 2228597          -1
```

```
## subset the data to the variables needed
data <- data[c('TUCASEID', 'TUACTIVITY_N', 'TRCODEP', 'TUACTDUR24',
               'TUSTARTTIM', 'TUSTOPTIME')]
```

```
## drop na
diary = data[complete.cases(data), ]

## rename columns to readable names
colnames(diary) <- c('caseid', 'actline', 'activity', 'duration', 'start', 'stop')
head(diary)

##
      caseid actline activity duration    start    stop
## 2228592 20110101110074      1  110101      10 04:00:00 04:10:00
## 2228593 20110101110074      2  020402     300 04:10:00 09:10:00
## 2228594 20110101110074      3  180482       5 09:10:00 09:15:00
## 2228595 20110101110074      4  500101     525 09:15:00 18:00:00
## 2228596 20110101110074      5  180482       5 18:00:00 18:05:00
## 2228597 20110101110074      6  010201      30 18:05:00 18:35:00

## create activity dictionary
## this list contains information to reducing activity coding to 11 main categories (listed below this)
## you can rename the original categories yourself, but you have to figure it out on your own
act_dict <- c("010101" = 1, "010102" = 1, "010199" = 1, "010201" = 2,
"010299" = 2, "010301" = 2, "010399" = 2, "010401" = 2, "010499" = 2,
"010501" = 2, "010599" = 2, "019999" = 2, "020101" = 3, "020102" = 3,
"020103" = 3, "020104" = 3, "020199" = 3, "020201" = 3, "020202" = 3,
"020203" = 3, "020299" = 3, "020301" = 3, "020302" = 3, "020303" = 3,
"020399" = 3, "020400" = 3, "020401" = 3, "020402" = 3, "020499" = 3,
"020500" = 3, "020501" = 3, "020502" = 3, "020599" = 3, "020600" = 3,
"020601" = 3, "020602" = 3, "020603" = 3, "020681" = 10, "020699" = 3,
"020700" = 3, "020701" = 3, "020799" = 3, "020800" = 3, "020801" = 3,
"020899" = 3, "020900" = 3, "020901" = 3, "020902" = 3, "020903" = 3,
"020904" = 3, "020905" = 3, "020999" = 3, "029900" = 3, "029999" = 3,
"030100" = 4, "030101" = 4, "030102" = 4, "030103" = 4, "030104" = 4,
"030105" = 4, "030106" = 4, "030107" = 4, "030108" = 4, "030109" = 4,
"030110" = 4, "030111" = 4, "030112" = 4, "030199" = 4, "030200" = 4,
"030201" = 4, "030202" = 4, "030203" = 4, "030204" = 4, "030299" = 4,
"030300" = 4, "030301" = 4, "030302" = 4, "030303" = 4, "030399" = 4,
"040100" = 4, "040101" = 4, "040102" = 4, "040103" = 4, "040104" = 4,
"040105" = 4, "040106" = 4, "040107" = 4, "040108" = 4, "040109" = 4,
"040110" = 4, "040111" = 4, "040112" = 4, "040199" = 4, "040200" = 4,
"040201" = 4, "040202" = 4, "040203" = 4, "040204" = 4, "040299" = 4,
"040300" = 4, "040301" = 4, "040302" = 4, "040303" = 4, "040399" = 4,
"030186" = 4, "040186" = 4, "030000" = 5, "030400" = 5, "030401" = 5,
"030402" = 5, "030403" = 5, "030404" = 5, "030405" = 5, "030499" = 5,
"030500" = 5, "030501" = 5, "030502" = 5, "030503" = 5, "030504" = 5,
"030599" = 5, "039900" = 5, "039999" = 5, "040000" = 5, "040400" = 5,
"040401" = 5, "040402" = 5, "040403" = 5, "040404" = 5, "040405" = 5,
"040499" = 5, "040500" = 5, "040501" = 5, "040502" = 5, "040503" = 5,
"040504" = 5, "040505" = 5, "040506" = 5, "040507" = 5, "040508" = 5,
"040599" = 5, "049900" = 5, "049999" = 5, "050000" = 6, "050100" = 6,
"050101" = 6, "050102" = 6, "050103" = 6, "050104" = 6, "050199" = 6,
"050200" = 6, "050201" = 6, "050202" = 6, "050203" = 6, "050204" = 6,
"050205" = 6, "050299" = 6, "050300" = 6, "050301" = 6, "050302" = 6,
"050303" = 6, "050304" = 6, "050305" = 6, "050399" = 6, "050400" = 6,
"050401" = 6, "050403" = 6, "050404" = 6, "050405" = 6, "050499" = 6,
"059900" = 6, "059999" = 6, "060000" = 6, "060100" = 6, "060101" = 6,
"060102" = 6, "060103" = 6, "060104" = 6, "060199" = 6, "060200" = 6,
```

"060201" = 6, "060202" = 6, "060203" = 6, "060204" = 6, "060299" = 6,
 "060300" = 6, "060301" = 6, "060302" = 6, "060303" = 6, "060399" = 6,
 "060400" = 6, "060401" = 6, "060402" = 6, "060403" = 6, "060499" = 6,
 "069900" = 6, "069999" = 6, "050481" = 6, "050389" = 6, "050189" = 6,
 "060289" = 6, "050289" = 6, "070000" = 7, "070100" = 7, "070101" = 7,
 "070102" = 7, "070103" = 7, "070104" = 7, "070105" = 7, "070199" = 7,
 "070200" = 7, "070201" = 7, "070299" = 7, "070300" = 7, "070301" = 7,
 "070399" = 7, "079900" = 7, "079999" = 7, "080000" = 7, "080100" = 7,
 "080101" = 7, "080102" = 7, "080199" = 7, "080200" = 7, "080201" = 7,
 "080202" = 7, "080203" = 7, "080299" = 7, "080300" = 7, "080301" = 7,
 "080302" = 7, "080399" = 7, "080400" = 7, "080401" = 7, "080402" = 7,
 "080403" = 7, "080499" = 7, "080500" = 7, "080501" = 7, "080502" = 7,
 "080599" = 7, "080600" = 7, "080601" = 7, "080602" = 7, "080699" = 7,
 "080700" = 7, "080701" = 7, "080702" = 7, "080799" = 7, "080800" = 7,
 "080801" = 7, "080899" = 7, "089900" = 7, "089999" = 7, "090000" = 7,
 "090100" = 7, "090101" = 7, "090102" = 7, "090103" = 7, "090104" = 7,
 "090199" = 7, "090200" = 7, "090201" = 7, "090202" = 7, "090299" = 7,
 "090300" = 7, "090301" = 7, "090302" = 7, "090399" = 7, "090400" = 7,
 "090401" = 7, "090402" = 7, "090499" = 7, "090500" = 7, "090501" = 7,
 "090502" = 7, "090599" = 7, "099900" = 7, "099999" = 7, "100000" = 7,
 "100100" = 7, "100101" = 7, "100102" = 7, "100103" = 7, "100199" = 7,
 "100200" = 7, "100201" = 7, "100299" = 7, "100300" = 7, "100303" = 7,
 "100304" = 7, "100399" = 7, "100400" = 7, "100401" = 7, "100499" = 7,
 "109900" = 7, "109999" = 7, "120303" = 8, "120304" = 8, "110000" = 9,
 "110100" = 9, "110101" = 9, "110199" = 9, "110200" = 9, "110201" = 9,
 "110299" = 9, "119900" = 9, "110289" = 9, "119999" = 9, "120000" = 10,
 "120100" = 10, "120101" = 10, "120199" = 10, "120200" = 10, "120201" = 10,
 "120202" = 10, "120299" = 10, "120300" = 10, "120301" = 10, "120302" = 10,
 "120305" = 10, "120306" = 10, "120307" = 10, "120308" = 10, "120309" = 10,
 "120310" = 10, "120311" = 10, "120312" = 10, "120313" = 10, "120399" = 10,
 "120400" = 10, "120401" = 10, "120402" = 10, "120403" = 10, "120404" = 10,
 "120405" = 10, "120499" = 10, "120500" = 10, "120501" = 10, "120502" = 10,
 "120503" = 10, "120504" = 10, "120599" = 10, "129900" = 10, "129999" = 10,
 "130000" = 10, "130100" = 10, "130101" = 10, "130102" = 10, "130103" = 10,
 "130104" = 10, "130105" = 10, "130106" = 10, "130107" = 10, "130108" = 10,
 "130109" = 10, "130110" = 10, "130111" = 10, "130112" = 10, "130113" = 10,
 "130114" = 10, "130115" = 10, "130116" = 10, "130117" = 10, "130118" = 10,
 "130119" = 10, "130120" = 10, "130121" = 10, "130122" = 10, "130123" = 10,
 "130124" = 10, "130125" = 10, "130126" = 10, "130127" = 10, "130128" = 10,
 "130129" = 10, "130130" = 10, "130131" = 10, "130132" = 10, "130133" = 10,
 "130134" = 10, "130135" = 10, "130136" = 10, "130199" = 10, "130200" = 10,
 "130201" = 10, "130202" = 10, "130203" = 10, "130204" = 10, "130205" = 10,
 "130206" = 10, "130207" = 10, "130208" = 10, "130209" = 10, "130210" = 10,
 "130211" = 10, "130212" = 10, "130213" = 10, "130214" = 10, "130215" = 10,
 "130216" = 10, "130217" = 10, "130218" = 10, "130219" = 10, "130220" = 10,
 "130221" = 10, "130222" = 10, "130223" = 10, "130224" = 10, "130225" = 10,
 "130226" = 10, "130227" = 10, "130228" = 10, "130229" = 10, "130230" = 10,
 "130231" = 10, "130232" = 10, "130299" = 10, "130300" = 10, "130301" = 10,
 "130302" = 10, "130399" = 10, "130400" = 10, "130401" = 10, "130402" = 10,
 "130499" = 10, "139900" = 10, "139999" = 10, "140000" = 10, "140100" = 10,
 "140101" = 10, "140102" = 10, "140103" = 10, "140104" = 10, "140105" = 10,
 "149900" = 10, "149999" = 10, "150000" = 10, "150100" = 10, "150101" = 10,
 "150102" = 10, "150103" = 10, "150104" = 10, "150105" = 10, "150106" = 10,

```

"150199" = 10, "150200" = 10, "150201" = 10, "150202" = 10, "150203" = 10,
"150204" = 10, "150299" = 10, "150300" = 10, "150301" = 10, "150302" = 10,
"150399" = 10, "150400" = 10, "150401" = 10, "150402" = 10, "150499" = 10,
"150500" = 10, "150501" = 10, "150599" = 10, "150600" = 10, "150601" = 10,
"150602" = 10, "150699" = 10, "150700" = 10, "150701" = 10, "150799" = 10,
"150800" = 10, "150801" = 10, "150899" = 10, "159900" = 10, "159999" = 10,
"160000" = 10, "160100" = 10, "160101" = 10, "160102" = 10, "160103" = 10,
"160104" = 10, "160105" = 10, "160106" = 10, "160107" = 10, "160108" = 10,
"160199" = 10, "160200" = 10, "160201" = 10, "160299" = 10, "169900" = 10,
"169999" = 10, "159989" = 10, "169989" = 10, "110281" = 10, "100381" = 10,
"100383" = 10, "180000" = 11, "180100" = 11, "180101" = 11, "180199" = 11,
"180200" = 11, "180201" = 11, "180202" = 11, "180203" = 11, "180204" = 11,
"180205" = 11, "180206" = 11, "180207" = 11, "180208" = 11, "180209" = 11,
"180280" = 11, "180299" = 11, "180300" = 11, "180301" = 11, "180302" = 11,
"180303" = 11, "180304" = 11, "180305" = 11, "180306" = 11, "180307" = 11,
"180399" = 11, "180400" = 11, "180401" = 11, "180402" = 11, "180403" = 11,
"180404" = 11, "180405" = 11, "180406" = 11, "180407" = 11, "180482" = 11,
"180499" = 11, "180500" = 11, "180501" = 11, "180502" = 11, "180503" = 11,
"180504" = 11, "180599" = 11, "180600" = 11, "180601" = 11, "180602" = 11,
"180603" = 11, "180604" = 11, "180605" = 11, "180699" = 11, "180700" = 11,
"180701" = 11, "180702" = 11, "180703" = 11, "180704" = 11, "180705" = 11,
"180782" = 11, "180799" = 11, "180800" = 11, "180801" = 11, "180802" = 11,
"180803" = 11, "180804" = 11, "180805" = 11, "180806" = 11, "180807" = 11,
"180899" = 11, "180900" = 11, "180901" = 11, "180902" = 11, "180903" = 11,
"180904" = 11, "180905" = 11, "180999" = 11, "181000" = 11, "181001" = 11,
"181002" = 11, "181099" = 11, "181100" = 11, "181101" = 11, "181199" = 11,
"181200" = 11, "181201" = 11, "181202" = 11, "181203" = 11, "181204" = 11,
"181205" = 11, "181206" = 11, "181283" = 11, "181299" = 11, "181300" = 11,
"181301" = 11, "181302" = 11, "181399" = 11, "181400" = 11, "181401" = 11,
"181499" = 11, "181500" = 11, "181501" = 11, "181599" = 11, "181600" = 11,
"181601" = 11, "181699" = 11, "181800" = 11, "181801" = 11, "181899" = 11,
"189900" = 11, "189999" = 11, "180481" = 11, "180381" = 11, "180382" = 11,
"181081" = 11, "180589" = 11, "180682" = 11, "500000" = 11, "500100" = 11,
"500101" = 11, "500102" = 11, "500103" = 11, "500104" = 11, "500105" = 11,
"500106" = 11, "500107" = 11, "509900" = 11, "509989" = 11, "509999" = 11)

```

this list is not used but it contains the codes for the 11 main activities

```

act = c("1" = "Sleep",
        "2" = "Personal Care",
        "3" = "Housework",
        "4" = "Child Care",
        "5" = "Adult Care",
        "6" = "Work and Education",
        "7" = "Shopping",
        "8" = "TV Watching",
        "9" = "Eating",
        "10" = "Leisure",
        "11" = "Travel and Other")

```

recode the activities using the activity dictionary

```

diary$lst_act <- revalue(diary$activity, act_dict)

```

The following `from` values were not present in `x`: 010199, 010599, 019999, 020400, 020500, 020600,

```
head(diary)
```

```
##               caseid actline activity duration    start    stop lst_act
## 2228592 20110101110074      1  110101      10 04:00:00 04:10:00      9
## 2228593 20110101110074      2  020402     300 04:10:00 09:10:00      3
## 2228594 20110101110074      3  180482       5 09:10:00 09:15:00     11
## 2228595 20110101110074      4  500101     525 09:15:00 18:00:00     11
## 2228596 20110101110074      5  180482       5 18:00:00 18:05:00     11
## 2228597 20110101110074      6  010201       30 18:05:00 18:35:00      2
```

```
## print out unique values for activities
```

```
unique(diary$lst_act)
```

```
## [1] "9" "3" "11" "2" "8" "1" "10" "5" "7" "4" "6"
```

```
## rename some of the activities even to fewer categories
```

```
## the activity dictionary created above gives 11 categories of activities
```

```
## in case some of the activities need to be combined
```

```
## you can follow the same logic in the following lines:
```

```
diary$lst_act = revalue(diary$lst_act, c("2" = 1, "8" = 10, "9" = 10))
```

```
unique(diary$lst_act)
```

```
## [1] "10" "3" "11" "1" "5" "7" "4" "6"
```

Then, let's create sequence dataframe, specify column names, and add ids.

```
## create sequences of activities per activity (result: long list of combined sequences)
sequences = rep(as.numeric(diary$lst_act), as.numeric(diary$duration))
```

```
## separate the long list into sequences (1440 min in each sequence)
```

```
seq = matrix(sequences, nrow=length(sequences)/1440, ncol=1440, byrow=T)
```

```
seq[1:5, 1:10]
```

```
##      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10]
## [1,]  10   10   10   10   10   10   10   10   10   10
## [2,]   1    1    1    1    1    1    1    1    1    1
## [3,]   1    1    1    1    1    1    1    1    1    1
## [4,]  10   10   10   10   10   10   10   10   10   10
## [5,]   1    1    1    1    1    1    1    1    1    1
```

```
## specify the names for the activity variables
```

```
activities<-c()
```

```
for(i in 0:1439) {
  activities<-c(activities, paste("var", i, sep = ""))
}
```

```
## transform matrix to dataframe
```

```
data <- as.data.frame(seq, row.names = unique(diary$caseid))
```

```
## used created vars names to name the columns in the dataframe
```

```
colnames(data) <-activities
```

```
## create id
```

```
data$id <- as.numeric(row.names(data))
```

Sequence Analysis

I create an object with intervals' labels. Sequences start at 04:00 AM: Depending on your own sequence intervals (if you are not using the ATUS) these labels need to be adjusted

```
t_intervals_labels <- format( seq.POSIXt(as.POSIXct("2021-11-08 04:00:00 GMT"),
      as.POSIXct("2021-11-09 03:59:00 GMT"), by = "1 min"),
      "%H:%M", tz="GMT")
```

Colour Palette

In my experience, brewing colours in R is one of the most painful experiences, especially if you have many categories of activities. Things can get even worse if you have to go grayscale if publishing articles with colour images is too expensive.

Let's brew some colours first. The number of colours is dictated by the number of states (in the alphabet). We reduced it to 8, so it won't create difficulties (difficulties arise when there are more than 12 categories).

Interesting resource on colors (cheatsheet):

```
## define labels first and count:
labels = c("sleep", "housework",
           "childcare", "adult care",
           "paid work", "shopping", "leisure",
           "travel")

colourCount = length(labels)
getPalette = colorRampPalette(brewer.pal(8, "Set3"))

## let's see how our colours look like
axisLimit <- sqrt(colourCount)+1
colours=data.frame(x1=rep(seq(1, axisLimit, 1), length.out=colourCount),
                  x2=rep(seq(2, axisLimit+1, 1), length.out=colourCount),
                  y1=rep(1:axisLimit, each=axisLimit, length.out=colourCount),
                  y2=rep(2:(axisLimit+1), each=axisLimit, length.out=colourCount),
                  t=letters[1:colourCount], r=labels)

## check the created palette:
ggplot() +
  scale_x_continuous(name="x") +
  scale_y_continuous(name="y") +
  geom_rect(data=colours, mapping=aes(xmin=x1, xmax=x2, ymin=y1, ymax=y2, fill=t),
           color="black", alpha=0.5) +
  geom_text(data=colours, aes(x=x1+(x2-x1)/2, y=y1+(y2-y1)/2, label=r), size=4) +
  scale_fill_manual(values = getPalette(colourCount)) + theme(legend.position = "none")
```

Defining Sequence Object

Before defining a sequence object, I reduced the dataframe to 2000 sequences. This is because I wanted for the tutorial demonstration to run faster. You can use all sequences as long as they are less than about 46000 in total. On my laptop 46000's dissimilarity matrix calculation ran for 4 hours but the cluster analysis crashed. So, I would recommend to use a random smaller sample if you have huge ones. Or, run the analyses on chunks and then combine the similar-looking clusters.

```
## subsetting is not necessary, but for the sake of efficiency
## in here I'll subset it to 2000 observations
MyData <- as_tibble(data[1:2000,])

## you want to use the full categories of states:
## (you need to change if you only focus on specific activities)
seq <- seqdef(MyData,
  var = activities,
  cnames = t_intervals_labels,
  alphabet = c("1", "3", "4", "5",
               "6", "7", "10",
               "11"),
  labels = labels,
  cpal = getPalette(colourCount),
  xtstep = 18, ##step between displayed tick-marks and labels on the time x-axis
  id = MyData$id)
## if you have weights then add ==> weights = MyData$Weight)
```

```
## check how the sequence looks like
print(seq[1:5, ], format = "STS")
```

[illegible]

Plotting Sequences

- sequence index plots

With a small `i`, the default for `idxs` is 1:10, plotting the first 10 sequences. If you set `idxs` to 0, it plots all sequences (might take a long time).

```
seqplot(seq, border = NA, with.legend = "right", legend.prop=0.4)
```

You can also use the same command with a capital I. It will plot all unless you specify `idxs` option.

```
seqIplot(seq, border = NA, with.legend = "right", legend.prop=0.4, idxs = 1:4)
```

- the most frequent sequences

Unfortunately, for time-use data, it is usually useless to plot the most frequent sequences. If you tabulate 4 frequent sequences you will see what I mean. It is because there are 1440 steps and there are barely any same sequences. This command is more useful for shorter sequences with many commonalities (as in life-course research).

```
## tabulate 4 frequent sequences:
## because there are 1440 steps there are barely any
## this is more useful for shorter sequences with many commonalities (as in life-course research)
seqtab(seq, idxs = 1:4)

##
## 1/1-10/209-1/45-11/15-10/240-11/6-7/10-11/12-1/180-3/30-4/212-10/180-1/300
## 1/1-10/60-3/30-10/110-3/35-10/10-3/150-11/20-7/60-11/20-3/150-11/5-6/249-11/5-10/110-1/425
## 1/1-10/60-3/30-10/30-3/60-11/5-10/60-11/5-1/30-11/5-7/5-11/5-7/40-11/5-7/10-11/5-7/60-10/120-11/10-1
## 1/10-3/2-10/108-1/30-11/5-5/1-11/3-10/321-11/3-5/1-11/4-6/322-11/2-10/30-11/6-10/97-1/495
##
## 1/1-10/209-1/45-11/15-10/240-11/6-7/10-11/12-1/180-3/30-4/212-10/180-1/300
## 1/1-10/60-3/30-10/110-3/35-10/10-3/150-11/20-7/60-11/20-3/150-11/5-6/249-11/5-10/110-1/425
## 1/1-10/60-3/30-10/30-3/60-11/5-10/60-11/5-1/30-11/5-7/5-11/5-7/40-11/5-7/10-11/5-7/60-10/120-11/10-1
## 1/10-3/2-10/108-1/30-11/5-5/1-11/3-10/321-11/3-5/1-11/4-6/322-11/2-10/30-11/6-10/97-1/495

##also can plot frequencies using seqfplot
seqfplot(seq, border = NA, with.legend = "right", legend.prop=0.4)
```

- tempograms

State distribution plots (aka tempogram aka chronogram) This is an easy way to plot a tempogram (compared to area plots).

```
## this is an easy way to plot a tempogram
seqdplot(seq, border = NA, with.legend = "right", legend.prop=0.4)
```

Transitions

```
# transitions from state to state (in probabilities)
trate <- seqtrate(seq)
```

```
## [>] computing transition probabilities for states 1/3/4/5/6/7/10/11 ...
round(trate, 2)
```

```
##      [-> 1] [-> 3] [-> 4] [-> 5] [-> 6] [-> 7] [-> 10] [-> 11]
## [1 ->]      1  0.00  0.00  0.00  0.00  0.00  0.00  0.00
## [3 ->]      0  0.98  0.00  0.00  0.00  0.00  0.01  0.00
## [4 ->]      0  0.00  0.97  0.00  0.00  0.00  0.01  0.01
## [5 ->]      0  0.00  0.00  0.98  0.00  0.00  0.00  0.01
## [6 ->]      0  0.00  0.00  0.00  0.99  0.00  0.00  0.00
## [7 ->]      0  0.00  0.00  0.00  0.00  0.97  0.00  0.03
## [10 ->]     0  0.00  0.00  0.00  0.00  0.00  0.99  0.00
## [11 ->]     0  0.01  0.00  0.00  0.00  0.01  0.02  0.95
```

```
## heatmap of the transitions matrix
```

```
heatTrate=melt(trate)
```

```
head(heatTrate)
```

```
##      Var1  Var2      value
## 1 [1 ->] [-> 1] 9.962543e-01
## 2 [3 ->] [-> 1] 2.178463e-03
## 3 [4 ->] [-> 1] 3.259718e-03
## 4 [5 ->] [-> 1] 1.190891e-03
## 5 [6 ->] [-> 1] 3.979046e-04
## 6 [7 ->] [-> 1] 6.193964e-05
```

```
## plot the heatmap
```

```
ggplot(heatTrate, aes(Var2, Var1)) +
  geom_tile(aes(fill = value)) +
  geom_text(aes(label = round(value, 2))) +
  scale_fill_continuous(high = "#132B43", low = "#56B1F7", name="Transitions")
```

Changing Granularity (Minutes to Hours, etc.)

TraMineR made it very easy to change the number of steps in a sequence. *seqgranularity* is the command that will help you do it.

To use the first state to represent all, use `method = "first"`, the last = `"last"`, or the most frequent = `"mostfreq"`.

In the following chunk of code, `tspan = 15` means to transform the step to every 15 min (instead of every minute).

```
time15_seq <- seqgranularity(seq, tspan=15, method="mostfreq")
```

```
## plot the tempogram
```

```
seqdplot(time15_seq, border = NA, with.legend = "right", legend.prop=0.4)
```

You can see on the tempograms that the granularity decreased and now each step is a 15-minute slot.

Modal states sequence

```
#seqplot(time15_seq, type="ms", with.legend = "right", legend.prop=0.4)
```

```
## same as
```

```
seqmsplot(time15_seq, with.legend = "right", legend.prop=0.4, main="Modal Sequences")
```

Modal Sequences

Embrace entropy

The higher the value, the more diverse are activities at that time.

```
#transversal entropy of state distributions
#the number of valid states and the Shannon entropy of the transversal state distribution
# shows the measure of 'chaos' (diversity of activities) in the diaries
seqHtplot(time15_seq, with.legend = "right", legend.prop=0.4)
```

Calculating Dissimilarities

Substitution Cost Matrix

We need to define the substitution cost for all the transitions (it can be a constant or user-defined).

```
# seqdist() = for pairwise dissimilarities
# seqsubm() = to compute own substitution matrix
#"TRATE" option, the costs are determined from the estimated transition rates
scost <- seqsubm(time15_seq, method = "TRATE")

## [>] creating substitution-cost matrix using transition rates ...
## [>] computing transition probabilities for states 1/3/4/5/6/7/10/11 ...
round(scost, 3)

##      1->  3->  4->  5->  6->  7-> 10-> 11->
## 1->  0.000 1.962 1.953 1.984 1.992 1.995 1.927 1.956
## 3->  1.962 0.000 1.929 1.970 1.987 1.963 1.824 1.904
## 4->  1.953 1.929 0.000 1.995 1.988 1.990 1.906 1.906
## 5->  1.984 1.970 1.995 0.000 1.995 1.991 1.934 1.898
## 6->  1.992 1.987 1.988 1.995 0.000 1.993 1.952 1.919
## 7->  1.995 1.963 1.990 1.991 1.993 0.000 1.949 1.729
## 10-> 1.927 1.824 1.906 1.934 1.952 1.949 0.000 1.769
## 11-> 1.956 1.904 1.906 1.898 1.919 1.729 1.769 0.000

## calculated in this way, all are close to 2 anyway (for this dataset) 2 is default
## or we can use the usual default one of constant 2:
ccost <- seqsubm(time15_seq, method="CONSTANT", cval=2)

## [>] creating 8x8 substitution-cost matrix using 2 as constant value
round(ccost, 3)

##      1-> 3-> 4-> 5-> 6-> 7-> 10-> 11->
## 1->    0  2  2  2  2  2  2  2
## 3->    2  0  2  2  2  2  2  2
## 4->    2  2  0  2  2  2  2  2
## 5->    2  2  2  0  2  2  2  2
## 6->    2  2  2  2  0  2  2  2
## 7->    2  2  2  2  2  0  2  2
## 10->   2  2  2  2  2  2  0  2
## 11->   2  2  2  2  2  2  2  0
```

Optimal Matching

Optimal matching for calculating dissimilarities between sequences need the specification of both substitution and indel costs. The algorithm is developed by Needleman and Wunsch (1970). For the illustration how the algorithm works please link to my explanation of optimal matching

If the sequence file is heavy, calculate only the upper part of the matrix by `full.matrix = FALSE` The usual default is that substitution cost is twice the indel cost, and default indel cost is 1.

```
om_time <- seqdist(time15_seq, method = "OM", indel = 1, sm = scost)

## [>] 2000 sequences with 8 distinct states
## [>] checking 'sm' (size and triangle inequality)
## [>] 2000 distinct sequences
```



```
## [>] min/max sequence lengths: 96/96
## [>] computing distances using the OM metric
## [>] elapsed time: 28.864 secs
## this results in a dissimilarity matrix which you can look at using:
round(om_time[1:10, 1:10], 1)
```

```
##      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10]
## [1,]  0.0 72.6 102.9 87.5 86.5  93.1 86.3 95.7 106.2  63.8
## [2,] 72.6  0.0 46.4 67.4 48.6 102.1 46.0 49.1  70.4  53.0
## [3,] 102.9 46.4  0.0 51.2 39.5  93.8 72.9 36.1  72.7  81.3
## [4,] 87.5 67.4 51.2  0.0 64.2  93.7 99.0 63.4 100.3  88.5
## [5,] 86.5 48.6 39.5 64.2  0.0  97.3 73.2 50.3  58.3  66.0
## [6,] 93.1 102.1 93.8 93.7 97.3  0.0 116.3 86.9 111.2 100.6
## [7,] 86.3 46.0 72.9 99.0 73.2 116.3  0.0 66.4  87.1  45.1
## [8,] 95.7 49.1 36.1 63.4 50.3  86.9 66.4  0.0  66.4  68.0
## [9,] 106.2 70.4 72.7 100.3 58.3 111.2 87.1 66.4  0.0  87.9
## [10,] 63.8 53.0 81.3 88.5 66.0 100.6 45.1 68.0 87.9  0.0
```

Cluster Analysis

Let's run cluster analysis on our dissimilarity matrix

Other common methods are:

- “average”,
- “single”,
- “complete”

The “average” and “single” options do not work well for time-use data (check). The “complete” option is a possibility (check).

```
## run cluster analysis on the calculated dissimilarity matrix
clusterward <- agnes(om_time, diss = TRUE, method = "ward")
## other common methods are "average", "single", "complete" (instead of "ward")
## "average" and "single" do not work well for time-use data (check if you want)
## "complete" can be an option
## "ward" is the "industry standard"

# Convert hclust into a dendrogram and plot
hcd <- as.dendrogram(clusterward)

# plot the dendrogram
plot(hcd, type = "rectangle", ylab = "Height")
```

How good is our clustering?

Let's inspect the splitting tree branches:

```
#inspect the splitting steps
ward.tree <- as.seqtrees(clusterward, seqdata = time15_seq,
                        diss = om_time,
                        ncluster = 25)

## plot the tree of tempograms to check how it splits the diaries
seqtreedisplay(ward.tree, type = "d", border = NA, show.depth = TRUE)
```

There are many possible tests for the cluster solution quality: - Point Biserial Correlation (PBC). - Hubert's Gamma (HG). - Hubert's Gamma (Somers'D) (HGSD). - Average Silhouette Width (ASW). - Average Silhouette Width (weighted) (ASWw). - Calinski-Harabasz index (CH). - R2. - Calinski-Harabasz Index squared (CHsq). - R2sq. - Hubert's C coefficient (HC).

```
#test cluster solution quality
wardtest <- as.clustrange(clusterward,
                        diss = om_time,
                        ncluster = 25)

#plot the quality criteria
plot(wardtest, stat = c("ASW", "HC", "PBC"), norm = "zscore", lwd = 4)
```

Let's say that our solution is pretty good for 8 clusters.

1. Cut the tree

```
c8 <- cutree(clusterward, k = 8)
```

```
## bind with the dataset
```

```
MyData<-cbind(MyData, c8)
```

2. Plot the cluster solution (will save in the working directory)

```
#plot cluster solution
```

```
png("plot_clusters.png", 1200, 800)
```

```
seqdplot(time15_seq, group = c8, border = NA)
```

```
dev.off()
```

```
## pdf
```

```
## 2
```

How to plot a cluster

```
# subset data by cluster
```

```
cl1<-(time15_seq[MyData$c8 == "1",])
```

```
# plot the selected cluster
```

```
par(mfrow=c(1,1))
```

```
seqdplot(cl1, main = "",
```

```
  cex.main = 1.7,
```

```
  with.legend = FALSE,
```

```
  yaxis = FALSE,
```

```
  cpal = getPalette(colourCount),
```

```
  ylab = "",
```

```
  border = NA)
```

```
## write new data to csv if needed  
#write.csv(MyData, "clustered_EC.csv")
```