SADI: Stata tools for Sequence Analysis

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`http://teaching.sociology.ul.ie/seqanal/sadihamburg.pdf`

Outline

1. What is Sequence Analysis?
2. Key SADI components
3. Worked example
4. Why plugins?
5. Further information

What is sequence analysis?

- A way of looking at time series as units
  - discrete or discretized time, usually discrete state space
  - often life-course histories
  - other longitudinal or linear structures (e.g., codings of conversations)
  - usually descriptive and exploratory
- Alternative to stochastic approaches that model the data generation process
  - Treats trajectories as wholes versus focus on hazard or transition rates, or cumulated durations, etc
- Advantage:
  - may capture structure that conventional approaches don't
  - provides a descriptive overview of complex data

How do we do sequence analysis?

- Define a similarity or distance between pairs of sequences
- We can explore the space implied by the matrix of all pairwise distances – empirical typologies
- We can compare all sequences with a small set of ideal-typical sequences
- We can compare pairs of sequences, e.g. spouses' time use; mothers' and daughters' fertility histories
- We can assess variablility of pattern within groups (e.g., destandardisation of life course across cohorts)

How do we define distance?

- Count matching elements; identity at the same time
- Hamming distance: allow state space; full or partial similarity at the same time
- Aligning methods: full or partial similarity at the same or similar time
- Optimal Matching Algorithm uses token editing (substitution, insertion, deletion) to do such alignment
- OM evangelised extensively in sociology by Andrew Abbott

Controversy and alternatives

- Controversy about OM
  - how to determine substitution costs
  - whether token sequences are a good way to represent life course data (Hollister, *SMR*, 2009; Halpin, *SMR*, 2010)
- Substitution costs make a big difference, but are intuitive in Hamming context: map state-space onto trajectory-space.
- Some alternatives
  - Dynamic Hamming (Lesnard)
  - Elzinga's combinatorial approaches
  - Time-Warp Edit Distance

SADI: Sequence Analysis DIstance measures

- For a long time, little software for SA
  - Abbott's custom programme
  - Bioinformatics software for molecular sequence analysis
- Since then, a lot of options
  - Götz Rohwer's TDA incorporated OM in mid/late 1990s
  - Kohler/Brzinsky-Fay/Luniak SQ for Stata since 2006
  - R Library Traminer since 2008
- SADI (first distributed 2007) takes a different approach to SQ
  - key difference: C-plugins rather than Mata $\Longrightarrow$ faster

SADI compared to SQ

- Plugins
  - Good: c 50X faster
  - Bad: problems of platform dependency, crashes
- Less polished!
- Deals with duplicate sequences differently: consequences for cluster analysis
- More distance measures as well as OM
  - Hamming
  - Dynamic Hamming
  - Time Warp Edit Distance
  - Some of Elzinga's combinatorial measures
- Some other utilities, graphical and otherwise
- But recommends `sqindexplot` from SQ

A worked example: mothers' labour market histories

- Data derived from BHPS work-life histories
- 6 years, mothers who have a birth at end of year 2
- Full and part-time employed, unemployed, non-employed
- Unusual in that time keyed by event in middle, not start

Data structure

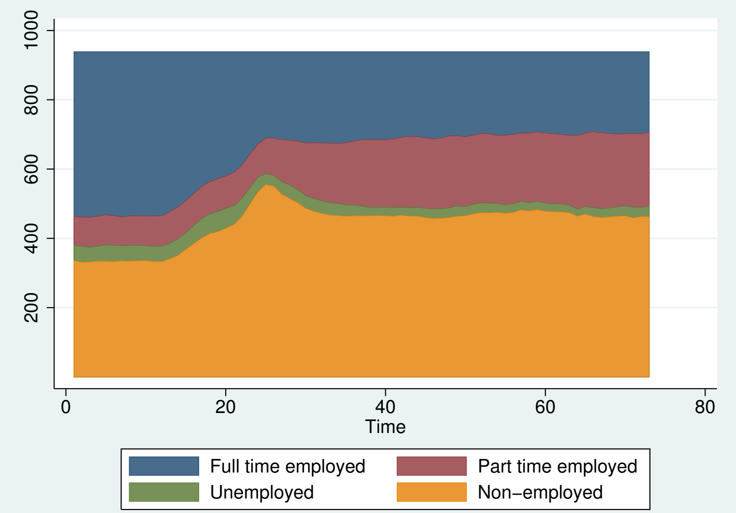
- Wide, one variable per month

```
. stripe state1-state72, gen(stripe) symbols("FPun")
. list stripe in 1/10, clean

                                                                         stripe
  1.   nnnnnnnnnnnFFuuuunnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
  2.   FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFnnn
  3.   FFFFFFFFFFFFFFFFFFFFFFnnnuuunnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
  4.   FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFPPPPPPPPPPPPPPPPPPPPPPPPPPnnnnnnnnnnnnnn
  5.   FFFFFFFFFFFFFFFFFFFFFFnnnnnnnnnnFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFnnnn
  6.   FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFnnnnnnnnnnnnnFFFFFFFFFFFF
  7.   FFFFFFFFFFFFFFFFFFFFFFFnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnPPPPPPPPPPPPPPPPPP
  8.   FFFFFFFFFFFFFFFFFnnnnnnnnnnnFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF
  9.   nnnnnnnnnnnnnnnnnnnnnnPPPPPPPPPPPPPPFFFFFFFFFFFnnnnnnnnnnnnnnnnnnnnuuuun
 10.   FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFnnnFFFFFFFFFFFFFFFFFFnnnnnnnnnnn
```

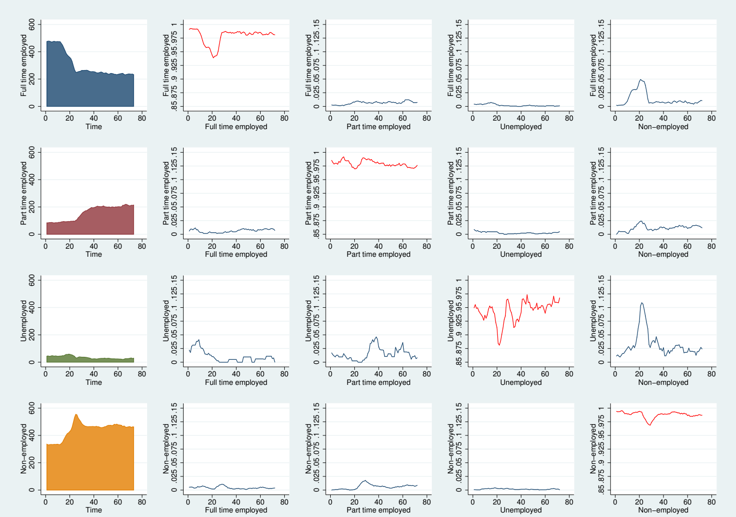
Chronogram: state distribution summary

```
. chronogram state*, id(pid)
```



trprgr: transition rate time-series

```
. trprgr state*, id(pid) gmax(575) floor(0.85) ceiling(0.15)
```

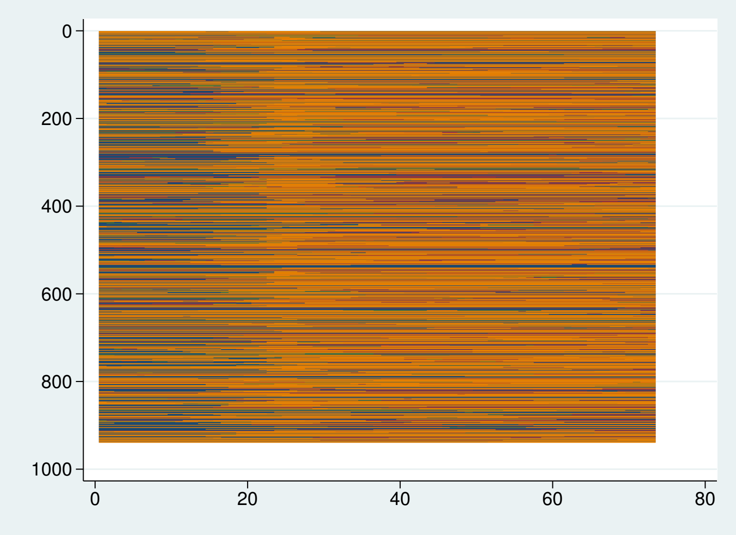


Indexplot, (SQ)

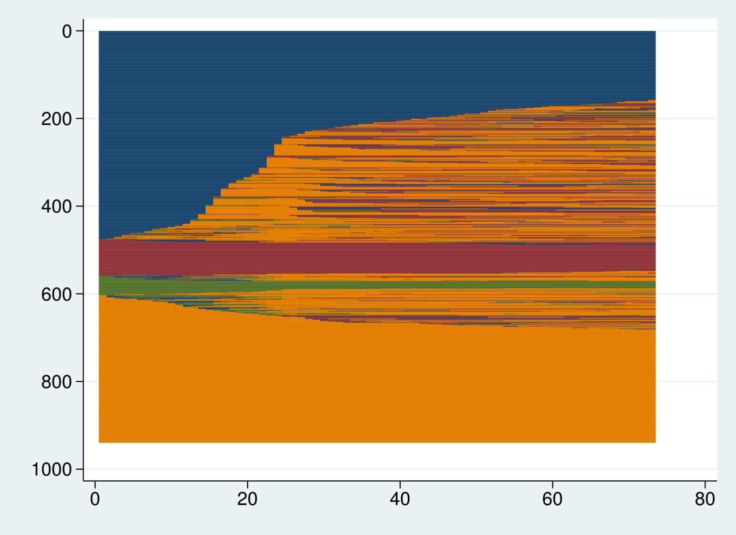
```
. reshape long state, i(pid) j(t)
. sqset state pid t
. sqindexplot, legend(off) overplot(100)
```

- This will generate a plot in "lexical" order
- Next graph is in random order, for a comparison

Indexplot, without order



Indexplot, lexically ordered



Summaries

- Foregoing summaries are useful but limited
- Indexplot is most "data-rich" but hard to read
- We can impose some order and make it easier

Optimal matching distance

- Let's define a simple state space: `F---P---u---n`
- This is represented as a substitution matrix:

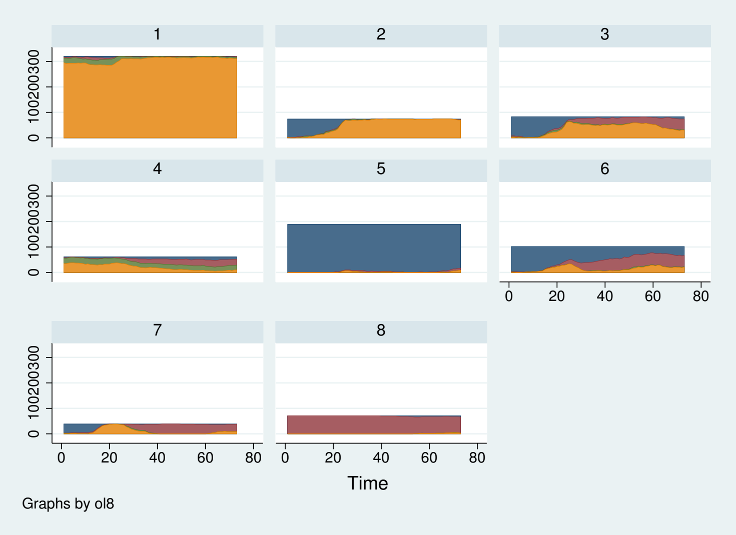
```
. matrix sm = (0,1,2,3 \ ///
               1,0,1,2 \ ///
               2,1,0,1 \ ///
               3,2,1,0)
. oma state1-state72, subs(sm) indel(1.5) pwd(oml) len(72)
Normalising distances with respect to length
(0 observations deleted)
415 unique observations
```

- *indel* cost 1.5 is half max substitution cost, as low as possible

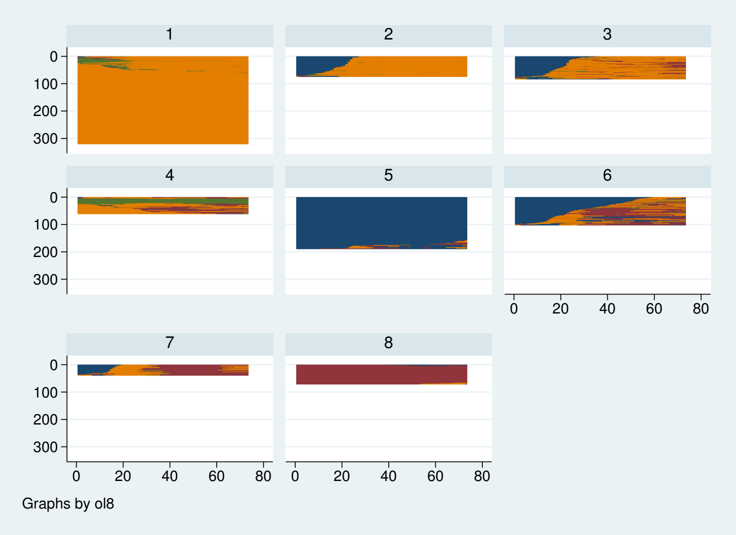
Clustering the pairwise distances

```
. clustermat wards oml, add
. cluster generate ol = groups(8 999), ties(fewer)
. tab ol8
        ol8 |      Freq.     Percent        Cum.
------------+-----------------------------------
          1 |        320       34.08       34.08
          2 |         74        7.88       41.96
          3 |         83        8.84       50.80
          4 |         61        6.50       57.29
          5 |        189       20.13       77.42
          6 |        102       10.86       88.29
          7 |         39        4.15       92.44
          8 |         71        7.56      100.00
------------+-----------------------------------
      Total |        939      100.00
```

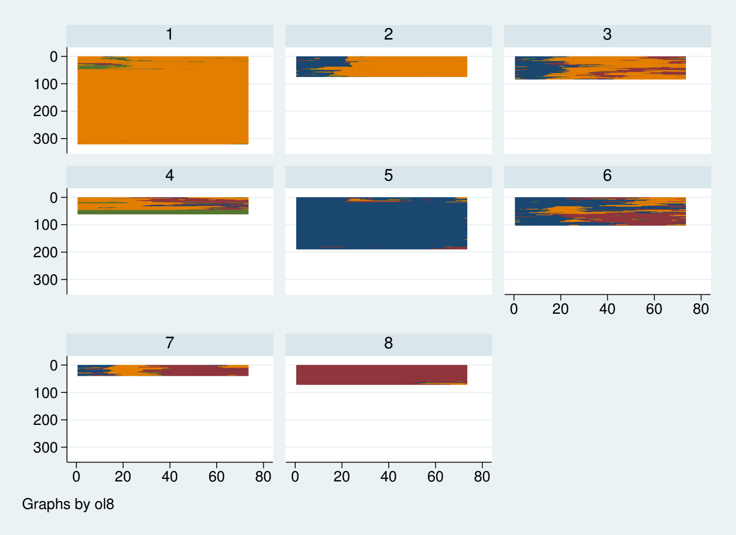
Chronogram by cluster



sqindexplot by cluster



sqindexplot by cluster with dendrogram order



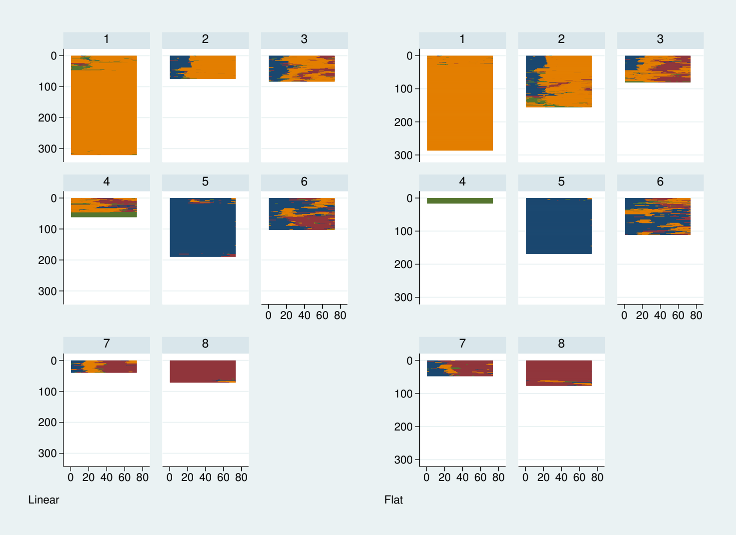
Parameterisation

- Setting substitution and *indel* costs is difficult
- No theory, somewhat controversial
- I like to understand it as mapping a perspective on state-space onto trajectory-space
- However, changing the parameters changes the results

Two contrasting cost setups

```
. matrix sm = (0,1,2,3 \ ///
               1,0,1,2 \ ///
               2,1,0,1 \ ///
               3,2,1,0)
. matrix fl = (0,1,1,1 \ ///
               1,0,1,1 \ ///
               1,1,0,1 \ ///
               1,1,1,0)
. oma state1-state72, subs(sm) indel(1.5) pwd(oml) len(72)
. oma state1-state72, subs(fl) indel(0.5) pwd(omf) len(72)
```

Similar but non-identical cluster result



Utilities to compare distances and cluster results

- SADI contains a number of utilities for comparing different algorithms and parameterisations
- Compare cluster solutions:
  - `permtab`: Permute solutions to maximise and assess agreement
  - `ari`: Adjusted Rand Index
- Compare distance matrices
  - `corrsqm`: Correlation between pairwise distance matrices

Unlabelled classifications

- Cluster solutions are "unlabelled classifications": the identity of groups is only given by their membership
- Cluster solutions agree to the extent that membership matches
- The Adjusted Rand Index is a score based on the extent to which pairs of cases in the same group in one solution are also in the same group in the other
- `permtab` permutes one classification to maximise agreement (as Cohen's κ), and tabulates result
- For cluster sizes much above 8 permutation is very slow, so `permtabga` calculates an approximate solution (using genetic algorithm)

Permuting linear and flat solutions

- Command: `permtab ol8 of8`

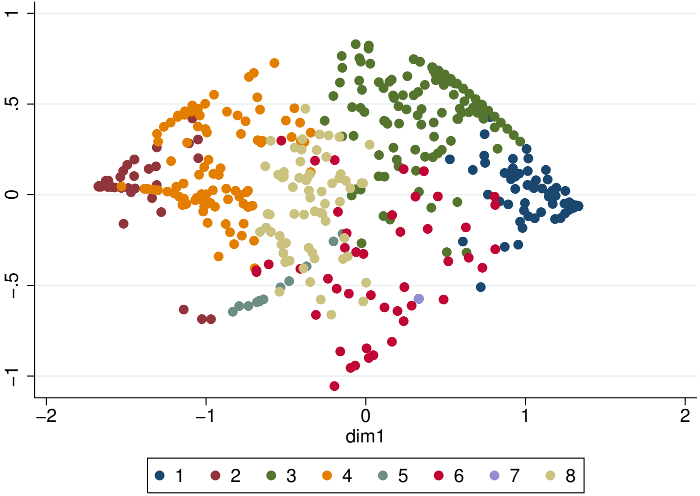
```
                Kappa max: 0.7742
Permutation
  vector        Permuted table:
     1                   1     2     3     4     5     6     7     8
  +-----+              +-----------------------------------------------+
1 |  1  |            1 | 293    26     1     0     0     0     0     0 |
2 |  2  |            2 |   1    72     1     0     0     0     0     0 |
3 |  3  |            3 |   0     3    76     0     0     2     2     0 |
4 |  7  |            4 |   5     0     0    16     0    14    24     2 |
5 |  4  |            5 |   0     0     0     0   180     9     0     0 |
6 |  5  |            6 |   0     0    10     0    39    21    32     0 |
7 |  6  |            7 |   0     0     0     0     0     1    38     0 |
8 |  8  |            8 |   0     0     0     0     0     0     0    71 |
  +-----+              +-----------------------------------------------+
```

Correlations of distances

- Summary based on `corrsqm` *mat1 mat2*, `nodiag`

```
Hamming linear 1.000  0.855  0.995  0.850  0.860  0.855  0.045
Hamming flat   0.855  1.000  0.850  0.987  0.998  1.000  0.094
OM linear      0.995  0.850  1.000  0.859  0.852  0.850  0.031
OM flat        0.850  0.987  0.859  1.000  0.980  0.987  0.066
TWED linear    0.860  0.998  0.852  0.980  1.000  0.998  0.127
TWED flat      0.855  1.000  0.850  0.987  0.998  1.000  0.093
X/t            0.045  0.094  0.031  0.066  0.127  0.093  1.000
```

Is clustering robust? Check with MDS



Discrepancy

- Studer et al's "discrepancy" measure gives us an alternative to cluster analysis
- Analogy to ANOVA and R-squared
  - TSS is the distance to the centre of gravity of the whole matrix
  - RSS is the distance to the centre of gravity of the partition
- Simple way to test for association between distance and a categorical variable

By Date of Birth, OM and X/t

```
. discrepancy dob, distmat(oml) id(pid) niter(5000)

Discrepancy based R2 and F, 5000 permutations for p-value

             | pseudo R2   pseudo F    p-value
-------------+-------------------------------------
         dob |  .1439802   52.42148      .0002

. discrepancy dob, distmat(xts) id(pid) niter(5000)

Discrepancy based R2 and F, 5000 permutations for p-value

             | pseudo R2   pseudo F    p-value
-------------+-------------------------------------
         dob |  .0693522   23.22551      .0658
```

Crosstab

- With date of birth (decade)

```
         Pearson chi2(21) = 557.4917   Pr = 0.000
           |                    dob
       ol8 |         2          3          4          5 |     Total
-----------+--------------------------------------------+----------
         1 |       160         44         47         69 |       320
         2 |         0          8         40         26 |        74
         3 |         0          4         36         43 |        83
         4 |         2          6         22         31 |        61
         5 |        23         54         85         27 |       189
         6 |         0          7         53         42 |       102
         7 |         0          0         25         14 |        39
         8 |         3         17         37         14 |        71
-----------+--------------------------------------------+----------
     Total |       188        140        345        266 |       939
         Pearson chi2(21) = 399.1509   Pr = 0.000
           |                    dob
       xt8 |         2          3          4          5 |     Total
-----------+--------------------------------------------+----------
         1 |         0          7         78         93 |       178
         2 |         2         25        106         99 |       232
         3 |         3         15         31          9 |        58
         4 |         0          1         25         27 |        53
         5 |         0          0          1          1 |         2
         6 |         0          0          0          1 |         1
         7 |        23         48         68         18 |       157
         8 |       160         44         36         18 |       258
-----------+--------------------------------------------+----------
     Total |       188        140        345        266 |       939
```

Good and bad of plugins

- Statacorp doesn't encourage plugins, for good reasons pushes Mata
- But sometimes plugins are preferable
    - faster when doing loop-intensive calculations (x50)
    - access existing external code and libraries
    - implement algorithms and data structures not available (or slow) in Mata
        - e.g. recursive enumeration of subsequences
        - hashtable data structure in same problem
- Downsides
    - need to compile separately for numerous platforms
    - can crash Stata
    - C can be a nightmare!

Compiling for multiple platforms

- The main platforms for Stata seem to be:
  - Windows 64-bit
  - Windows 32-bit
  - MacOS (Intel CPU)
  - Linux 64-bit
  - Linux 32-bit
- From Linux64 it is possible to cross compile for Windows and Linux, 32 and 64 bit
- Cross comiplation for Mac is difficult, but may be possible
- Compiling on Mac and on other Unix is straightforward

Cross-compilation on 64-bid Debian

- Load these packages (other distributions are analogous)

```
apt-get install mingw32
apt-get install mingw-w64
apt-get install libc6-dev-i386
```

- Then compile:

```
# Linux 32
gcc -m32 -fPIC -shared -DSYSTEM=OPUNIX stplugin.c myplugin.c
# Linux 64
gcc -m64 -fPIC -shared -DSYSTEM=OPUNIX stplugin.c myplugin.c
# Windows 32
i586-mingw32msvc-cc -shared -DSYSTEM=STWIN stplugin.c myplug
# Windows 64
x86_64-w64-mingw32-gcc -shared -DSYSTEM=STWIN stplugin.c myp
```

MacOS

- On Mac, using gcc

```
gcc -bundle -DSYSTEM=APPLEMAC stplugin.c myplugin.c -o myplugin.plugin
```

(thanks to Glenn Hoetker, Arizona, for help compiling for Mac)

Installation

- For SADI

```
net from http://teaching.sociology.ul.ie/sadi
net install sadi
```

- SADI requires `moremata`

```
ssc install moremata
```

- For SQ, for indexplots

```
ssc install sq
```

Further reading

- Halpin, 2014, *SADI: Sequence Analysis Tools for Stata*, WP2014-03, Dept of Sociology, University of Limerick, `http://www.ul.ie/sociology/pubs/wp2014-03.pdf`
- Halpin, 2014, Three narratives of sequence analysis, in Bühlmann et al (eds), *Advances in Sequence Analysis*, Springer
- Halpin, 2012, *Sequence analysis of life-course data: a comparison of distance measures*, WP2012-02, Dept of Sociology, University of Limerick `http://www.ul.ie/sociology/pubs/wp2012-02.pdf`
- Studer et al., 2011, Discrepancy Analysis of State Sequences, *Sociological Methods and Research*, 40(3)
- Studer, 2012, *Étude des inégalités de genre en début de carrière académique*, Ch 2 "Comparaison des mesures de distance", `http://archive-ouverte.unige.ch/unige:22054`

This document

- This document is available at `http://teaching.sociology.ul.ie/seqanal/sadihamburg.pdf`