# SEQUENCE AND CLUSTER ANALYSIS: EXPLANATIONS AND APPLICATIONS

**Amal Harrati, PhD**

**Mathematica**

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# Agenda

1) Goals and application for sequence and cluster analysis

2) Explanation of mechanics

3) Responses to readings, QA, discussion

# When to use sequence or clustering analysis?

- Long trajectories of data that are different across unit of observation.
- Lifecourse analysis; time-use data; genetic variations
- Data reduction technique

# Goal of sequence analysis

1) **Comparison:** Using distance measures (ie. optimal matching, Hamming, etc.)

2) **Grouping:** Similar sequences are grouped using cluster analysis or multidimensional scaling

3) **Application**: Use the grouped sequences are dependent or independent variables in standard statistical analysis (ie. regression, survival analysis, etc.)

Source: Brzinsky-Fay and Kohler, 2006

# Step 1: Preparation of the Data

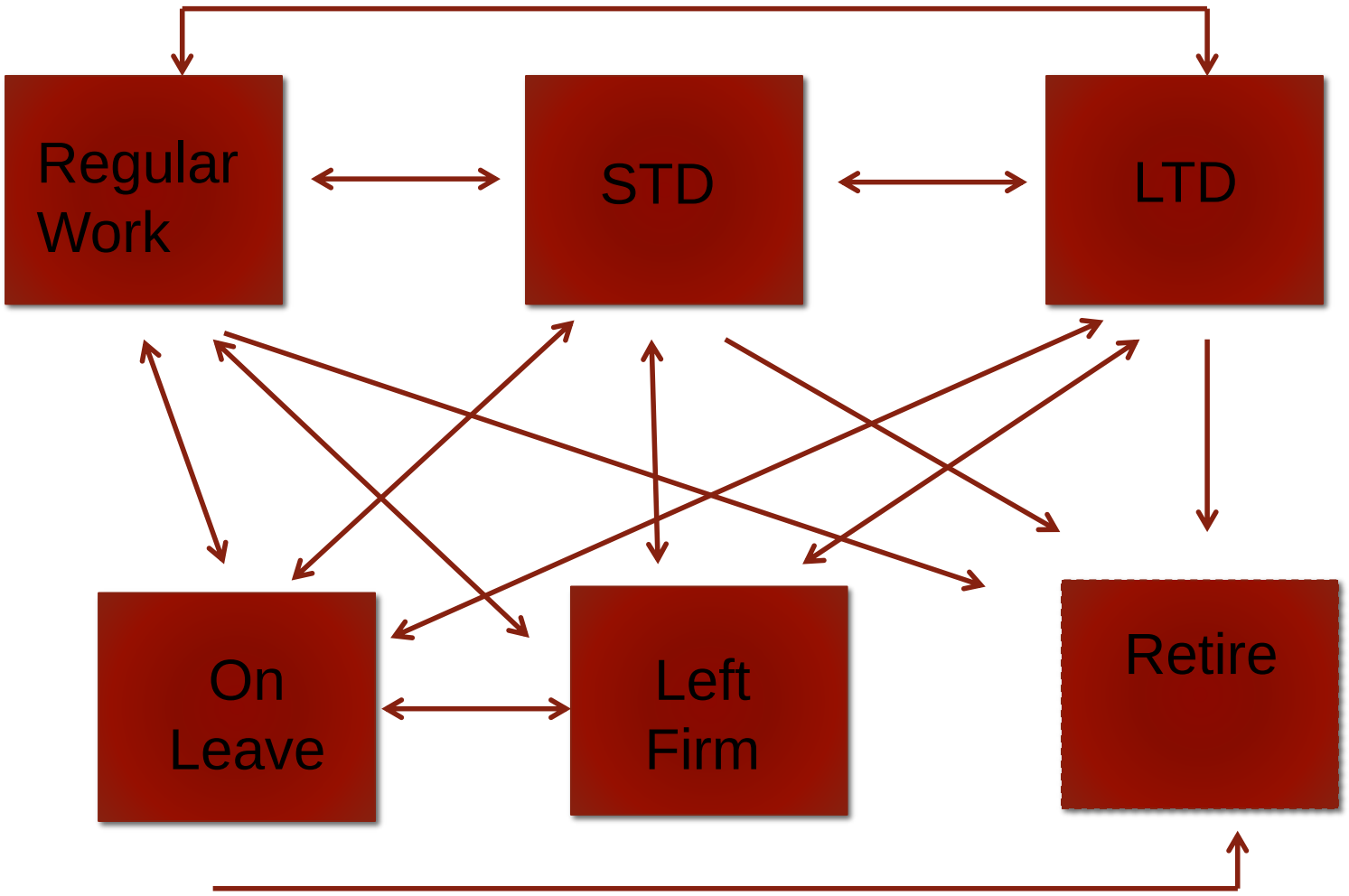
1) Consider your research question
   SA should consider not just timing, but *sequencing* and *duration*. It is largely intended to capture *trajectories, or sequences of linked states*

2) Is this a good application of the data?
   Is there enough variation in the sequence?
   Is there a long enough time period?

3) Creating your states

4) Consider temporality
   (Elzinga vs. Halpin)

# Example of a “state”



# Step 2: Create a difference metric

1) Optimal matching

2) Elzinga's Longest Common Subsequence

Source: Studart and Ritschard, 2016

# Optimal Matching

Three operations:

1) Insertion: one state is inserted into a sequence

2) Deletion: one state is deleted from a sequence

3) Substitution: one state is replaced by another state to into the sequence

Must assign a cost to each operation, and each suboperation.

Algorithm makes pairwise costs for all sequences and the distance is the minimal cost.

# How to compare two distinct sequences

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Sequence 1 | A | A | A | B | B | C | C | B | B | B | B | B |
| Sequence 2 | A | A | B | C | B | B | C | C | B | B | B | B |

Slide source: Ivan Mejia Guevara

# How to compare two distinct sequences

| Sequence 1 | A | A | A | B | B | C | C | B | B | B | B | B |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Sequence 2 | A | A | B | C | B | B | C | C | B | B | B | B |

- Alignment 1. Use substitution operations only:

| Sequence 1 | A | A | A | B | B | C | C | B | B | B | B | B |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Sequence 2 | A | A | B | C | B | B | C | C | B | B | B | B |
| | 0 | 0 | s | s | 0 | s | 0 | s | 0 | 0 | 0 | 0 |

Total cost = 4s

Slide source: Ivan Mejia Guevara

# How to compare two distinct sequences

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Sequence 1 | A | A | A | B | B | C | C | B | B | B | B | B |
| Sequence 2 | A | A | B | C | B | B | C | C | B | B | B | B |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Sequence 1 | A | A | A | B | B | C | C | B | B | B | B | B |
| Sequence 2 | A | A | B | C | B | B | C | C | B | B | B | B |
| | 0 | 0 | s | s | 0 | s | 0 | s | 0 | 0 | 0 | 0 |

Slide source: Ivan Mejia Guevara

# How to compare two distinct sequences

- Alignment 2. Alternatively, using insertion/deletion and substitutions:

| Sequence 1 | A | A | A | | B | B | C | C | B | B | B | B | B |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Sequence 2 | A | A | B | C | B | B | C | C | B | B | B | B | |
| | 0 | 0 | s | d | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | d |

Total Cost = s + 2D

Slide source: Ivan Mejia Guevara

# How to compare two distinct sequences

| Sequence 1 | A | A | A | B | B | C | C | B | B | B | B | B |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Sequence 2 | A | A | B | C | B | B | C | C | B | B | B | B |

- Alignment 1. Use substitution operations only:

| Sequence 1 | A | A | A | B | B | C | C | B | B | B | B | B |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Sequence 2 | A | A | B | C | B | B | C | C | B | B | B | B |
| | 0 | 0 | s | s | 0 | s | 0 | s | 0 | 0 | 0 | 0 |

Total cost = 4s

- Alignment 2. Alternatively, using insertion/deletion and substitutions:

| Sequence 1 | A | A | A | | B | B | C | C | B | B | B | B | B |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Sequence 2 | A | A | B | C | B | B | C | C | B | B | B | B | |
| | 0 | 0 | s | d | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | d |

Total cost = s + 2d

# Criticisms of Optimal Matching

- Operations imply a change in the time scale.
- If there is not a clear ranking in states, costs can be sociologically meaningless.
- Censoring creates unequal sequence length: shorter sequences have higher costs

# “Solutions to” or Alternatives to OM

Using observed transition matrix

Elzinga’s longest common subsequence

Censoring creates unequal sequence length: shorter sequences have higher costs

# Elzinga's longest common sequence

Using observed transition matrix

Elzinga's longest common subsequence

Censoring creates unequal sequence length: shorter sequences have higher costs

# Step 3: Clustering

Goal:

Provide a way of grouping sequences according to their distance metrics (similarities and dissimilarities to other sequences)

# Step 3: Clustering

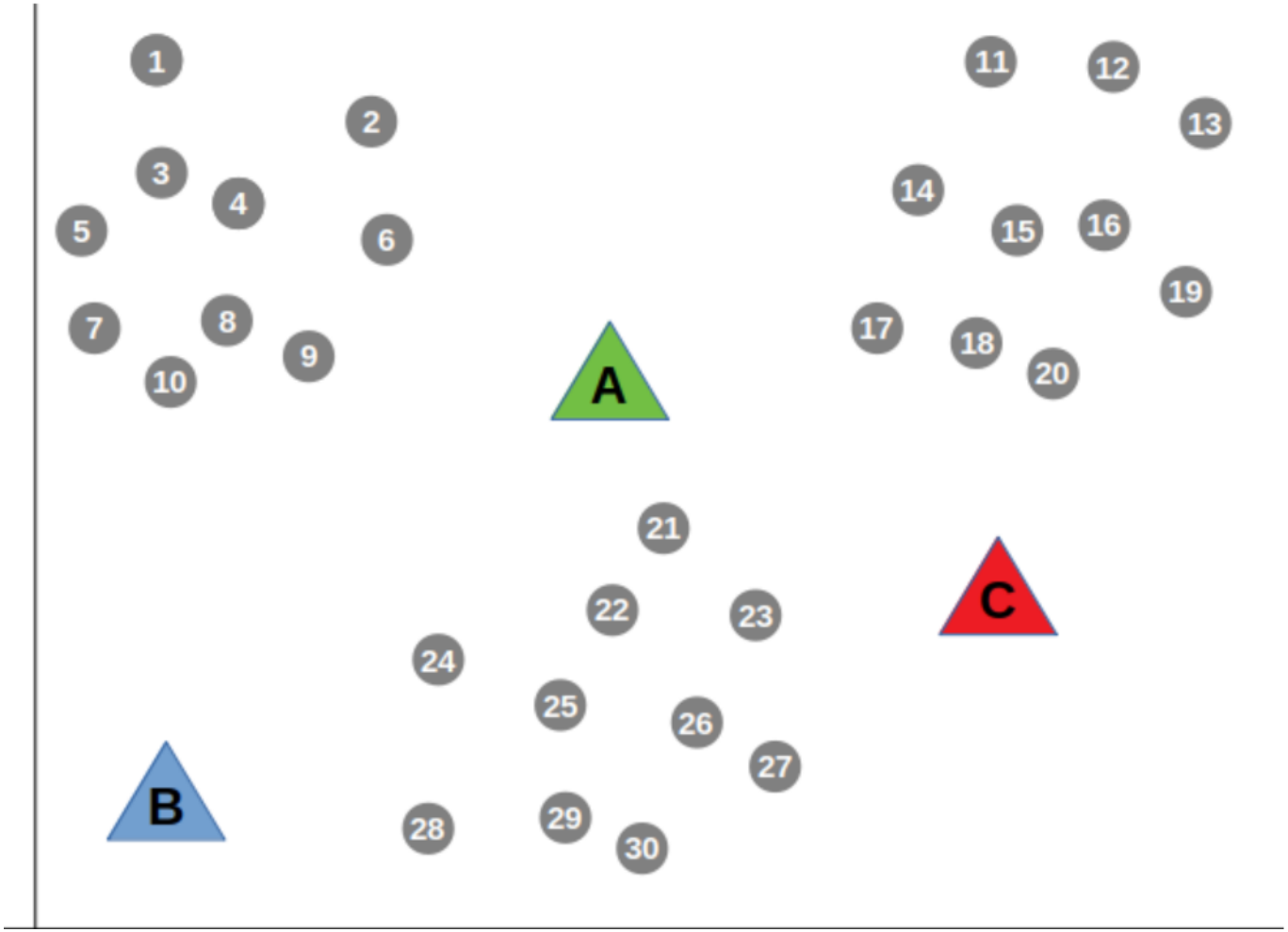
Different methods are available:

1) Ward's method
   *Minimizes total variance within clusters*

2) K-means
   *Creates centroids and minimizes mean values of centroids*

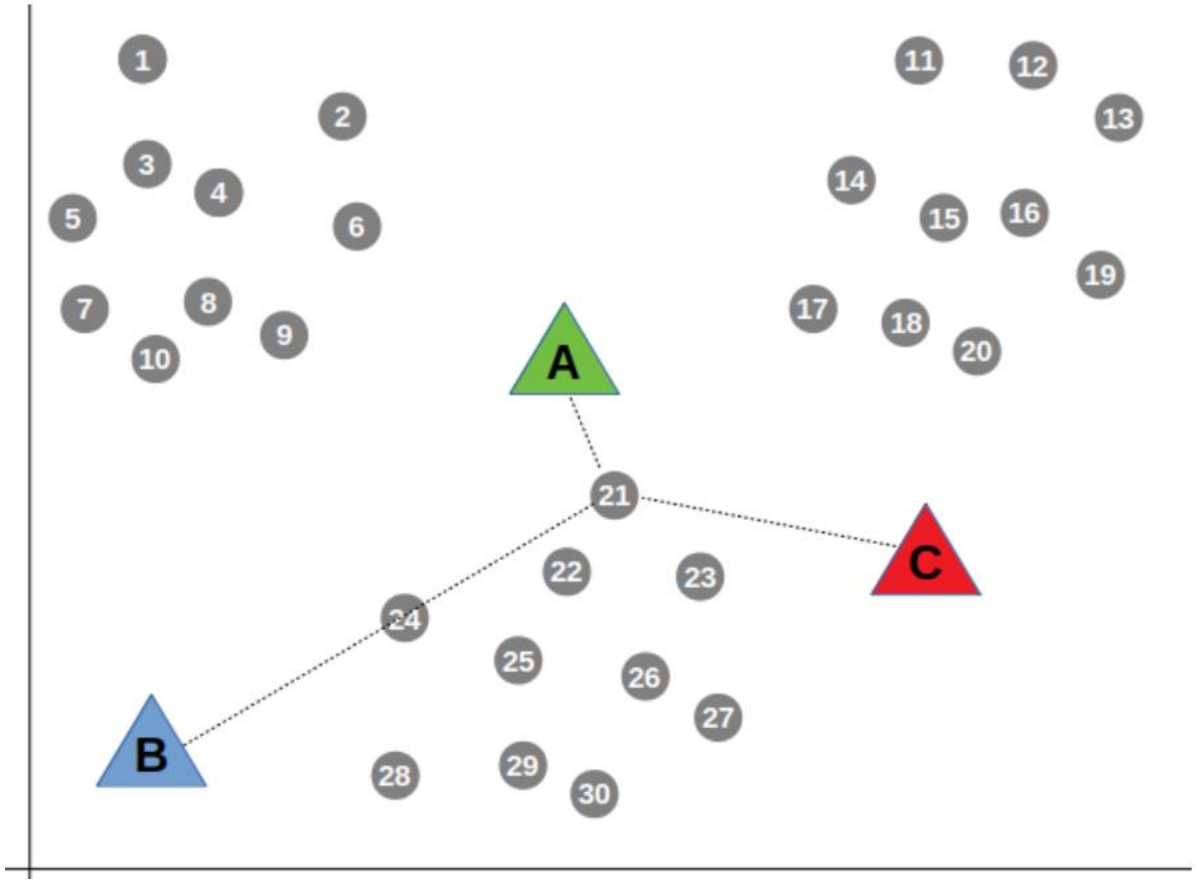
3) Partition around mediods
   Similar to k-means; splits data set into

# K-means or PAM



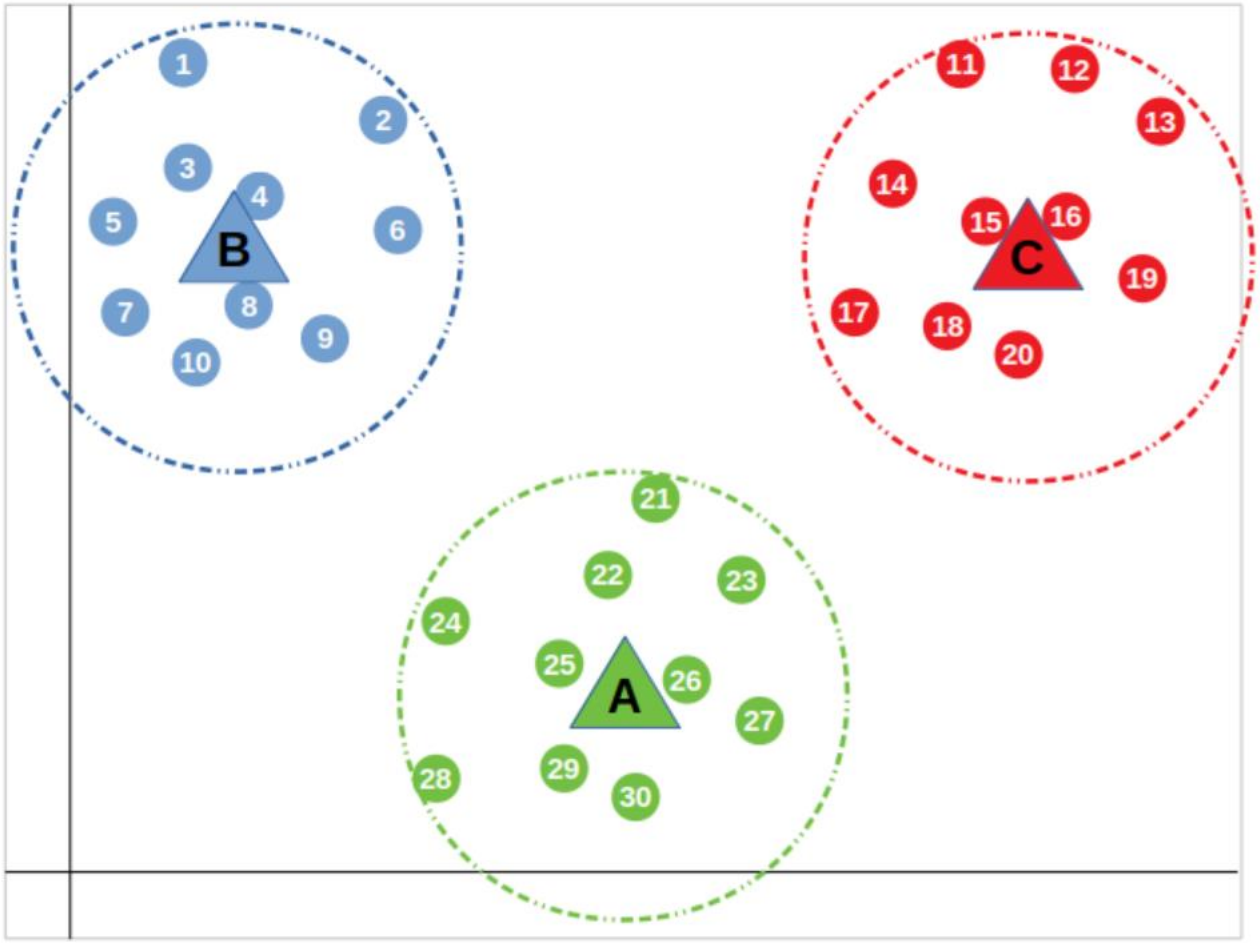

*Source: Anas Al-Masri*

# K-means or PAM




*Source: Anas Al-Masri*

# K-means or PAM




*Source: Anas Al-Masri*

# Step 3: Clustering, cont.

Diagnostics:

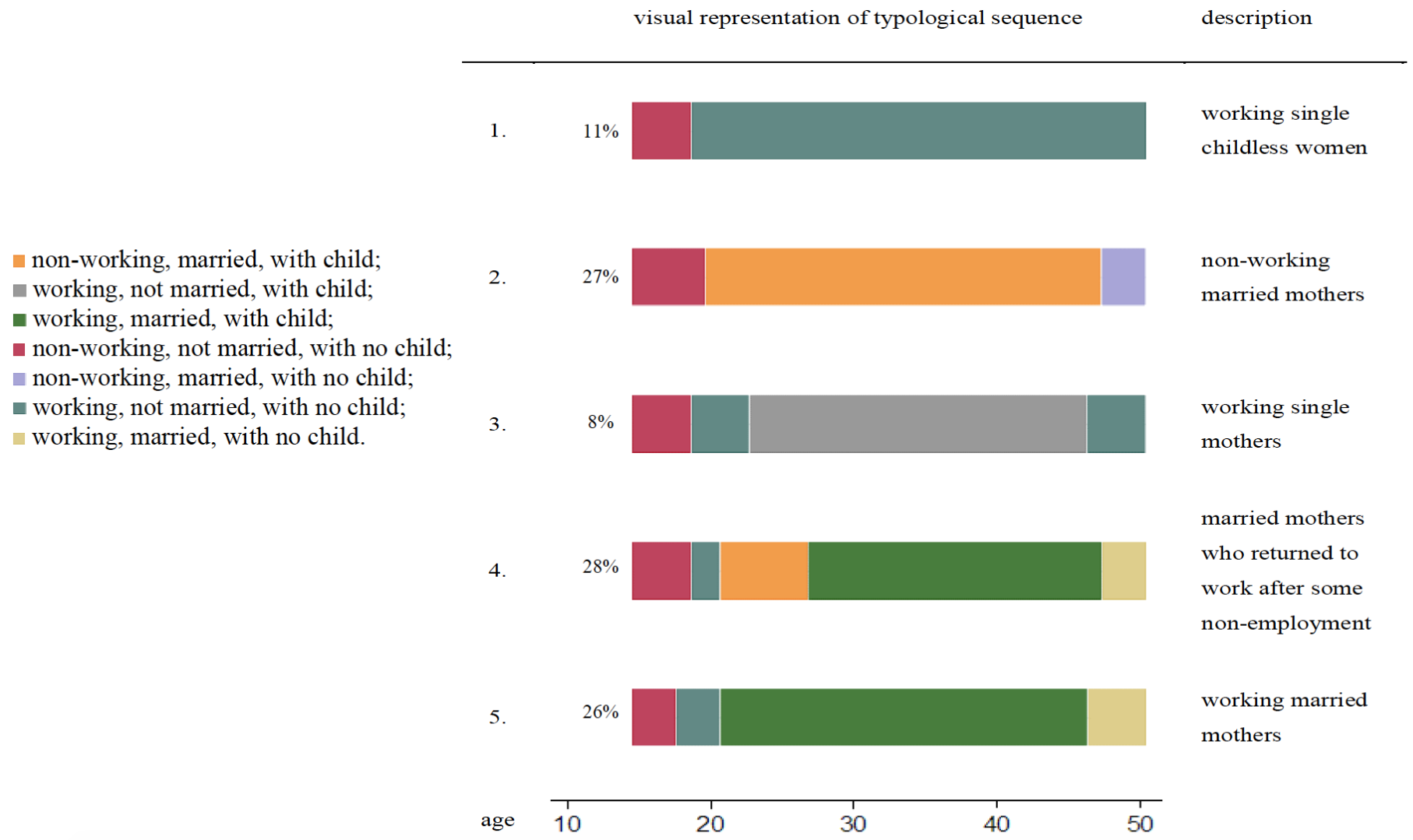
Goodness of fit tests

- Average silhouette width,
- Calinsky-Harabasz pseudo F-test

For more:  Kaufmann and Rousseeuw, 2009

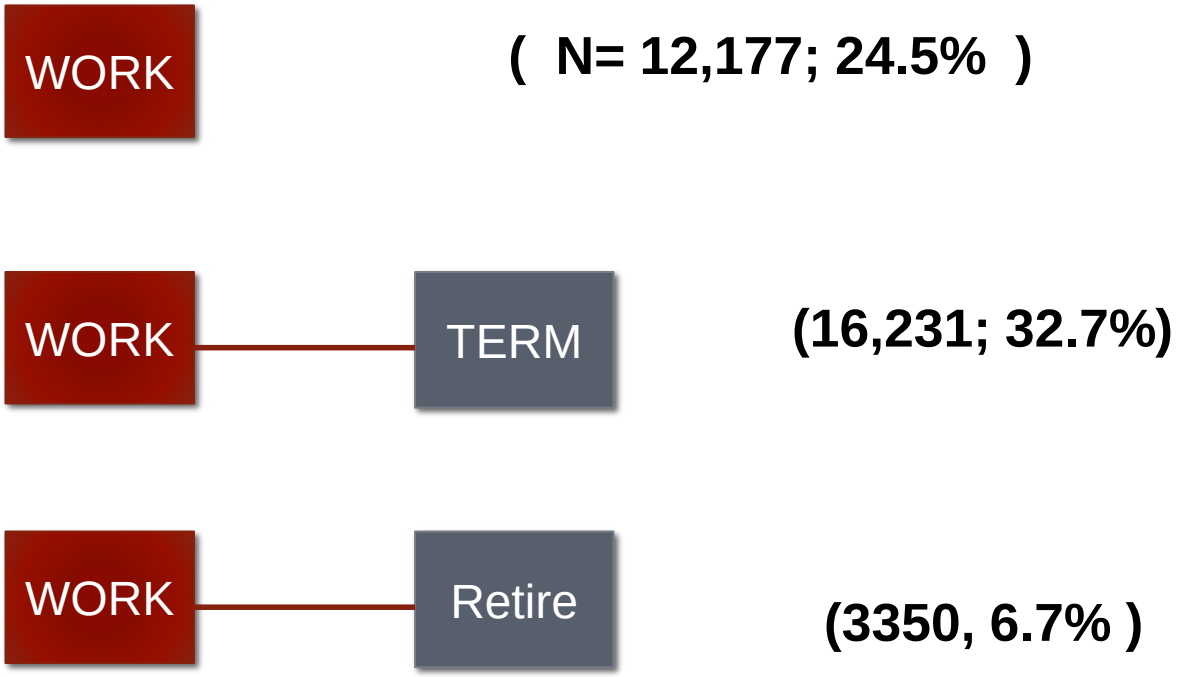
# Graphic representations for sequences and clusters

# Applications to Work-Life Trajectories



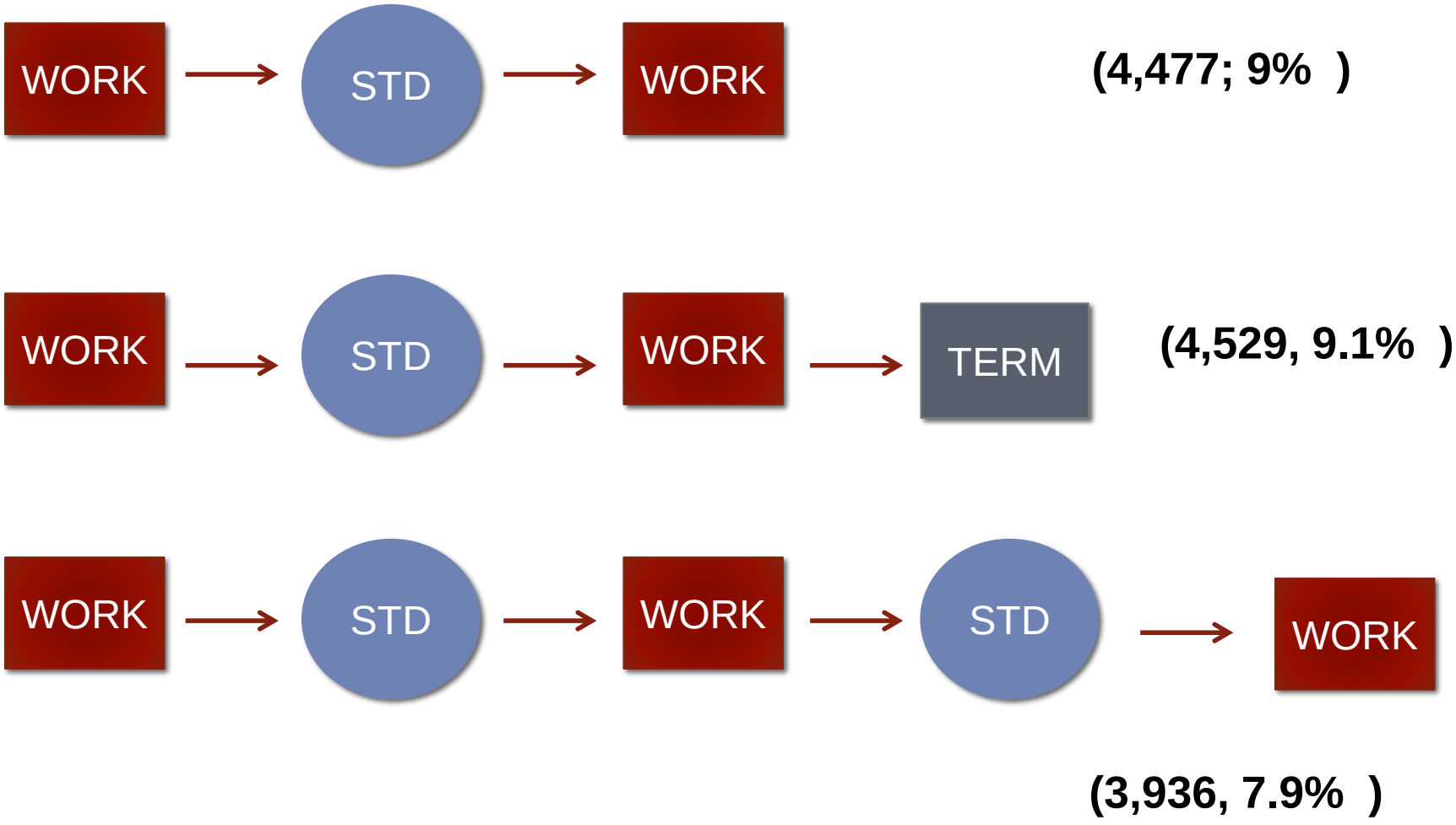

**Source:** van Hedel, Mejía-Guevara, et al. (Revise and resubmit – *American Journal of Public Health*)

# Identifying typologies: “Continuous Work”




64% (N=31,758) of the sample stays continuously employed (and/or leave Alcoa for other reasons) through sample period.

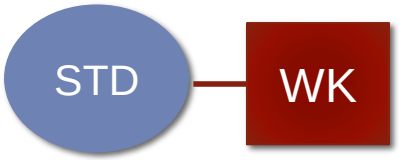
# Identifying typologies: “Minor STD”



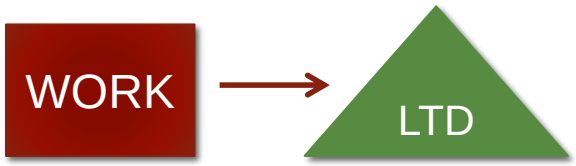
# Identifying typologies: “Disruptive”


**( 2,931; 5.9% )**

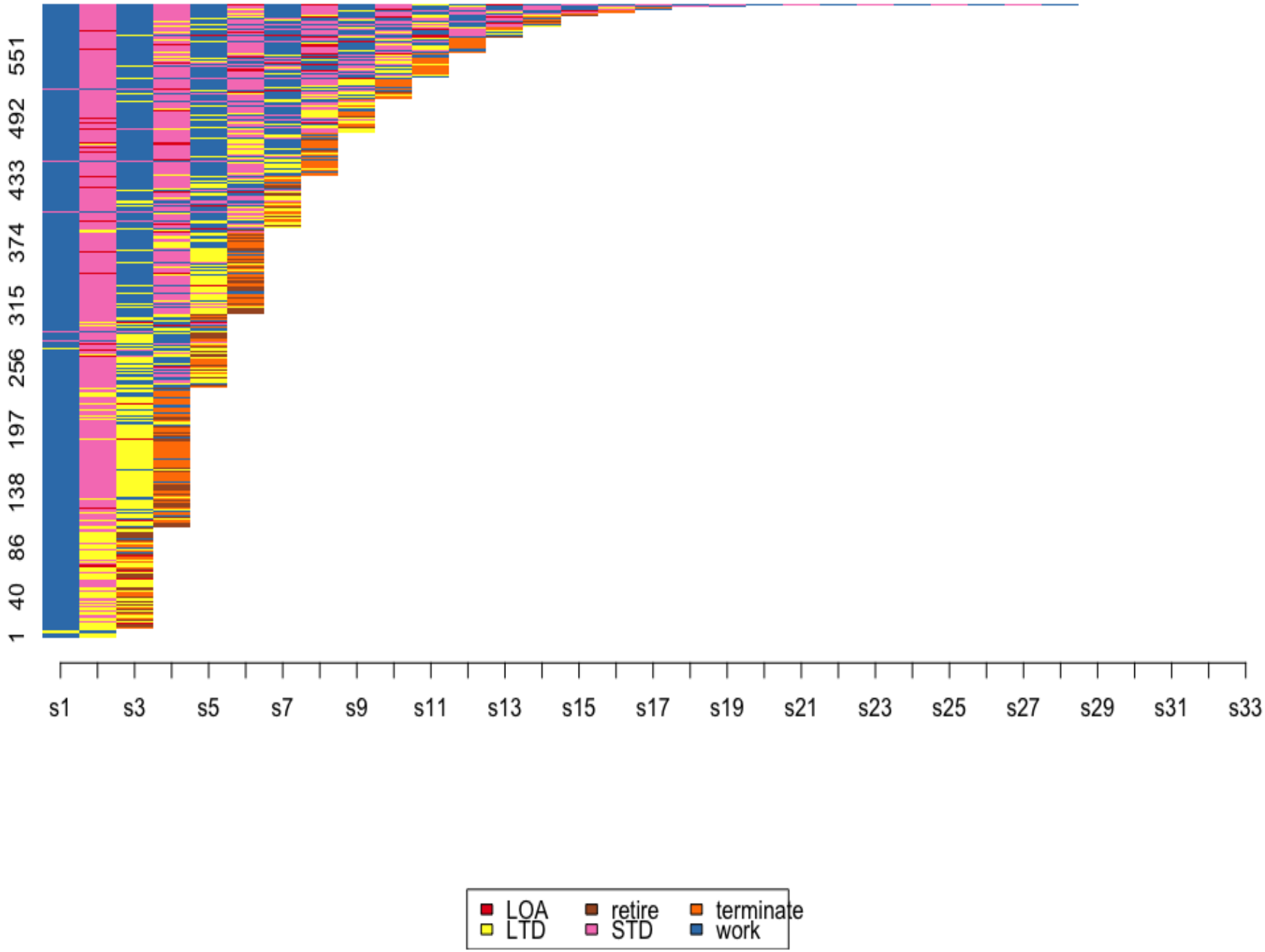

**( 1,262; 2.5% )**



# Identifying typologies: “Ever LTD”




**( 1.4% )**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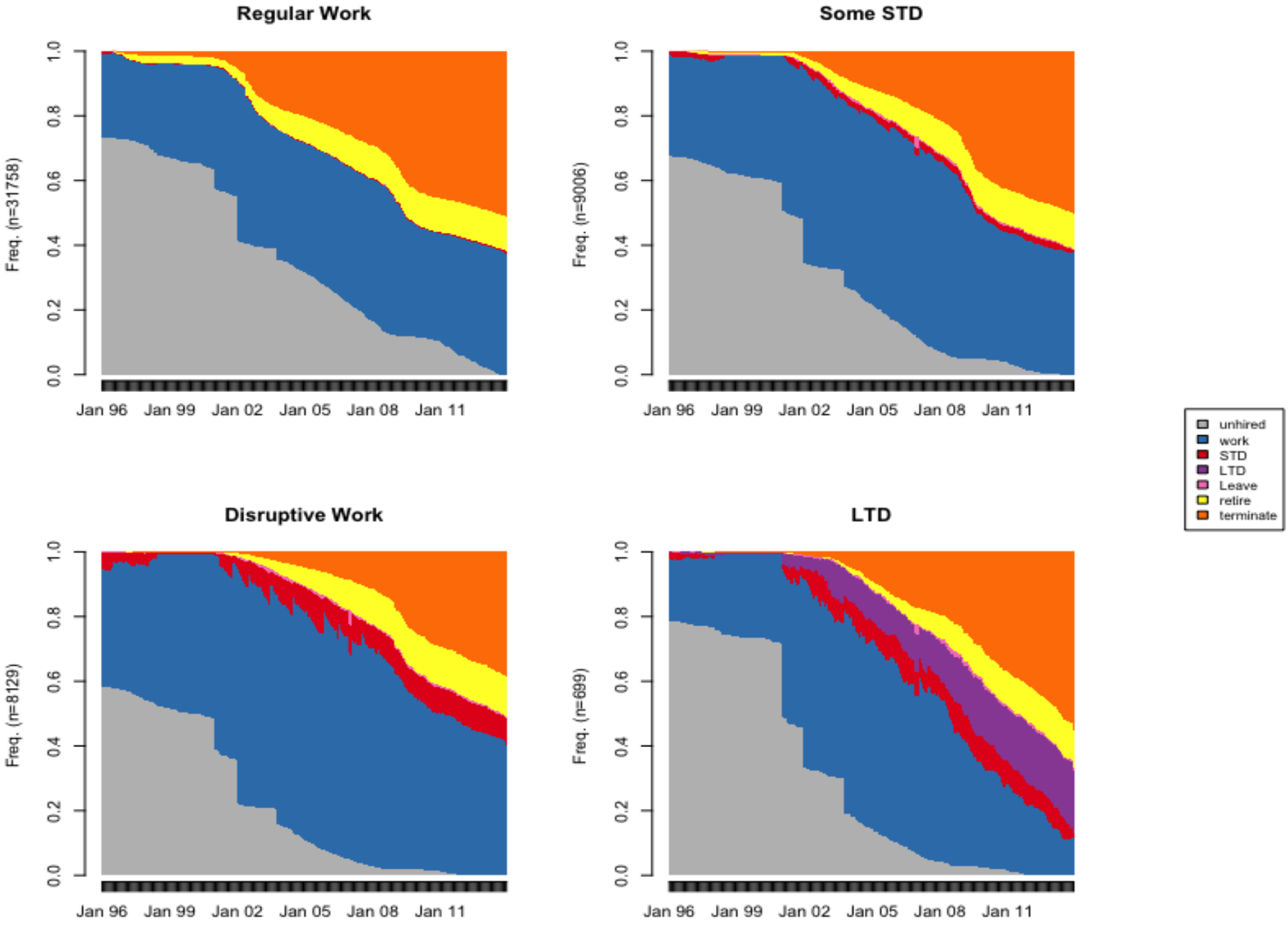
LOA
LTD
retire
STD
terminate
work


Regular Work
Some STD
Disruptive Work
LTD
Freq. (n=31758)
Freq. (n=9006)
Freq. (n=8129)
Freq. (n=699)
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Jan 99
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Jan 05
Jan 08
Jan 11
unhired
work
STD
LTD
Leave
retire
terminate

# Reflections on the readings, QA, discussion

# Thank you!

Questions?

aharrati@mathematica-mpr.com