# An Approach to Fitting Transmission Models to Seriations for Regional-Scale Analysis

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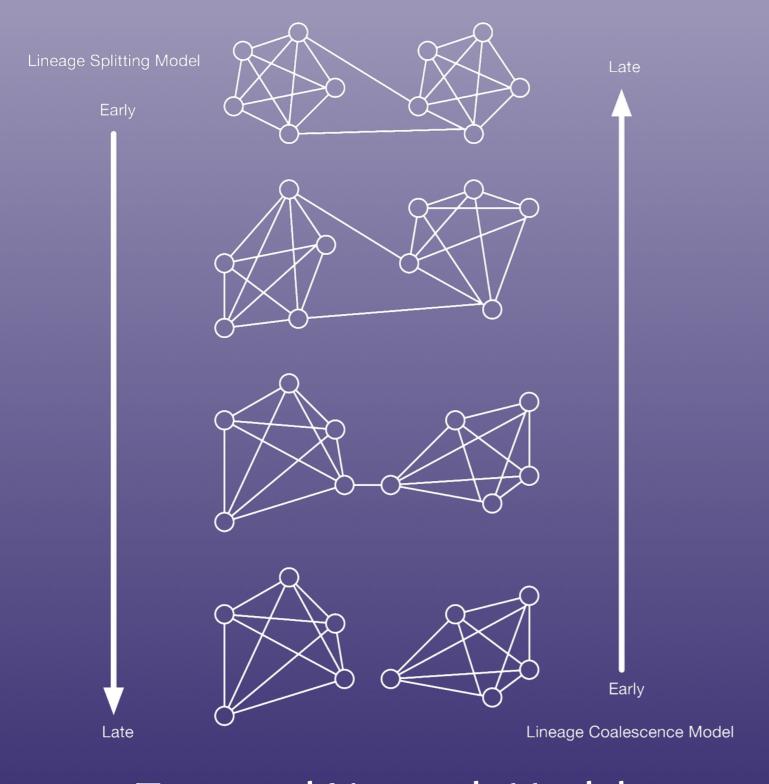




### Regional Scale CT Models

- Coarse grained compared to cognitive social learning within a population
- Finer grained compared to largest-scale phylogenetic models
- Basic question is: can we infer changing patterns of interaction within an evolving settlement system?
- THIS STUDY: can we infer the interaction pattern from time-averaged artifact class frequencies, using a diachronic tool like seriation?

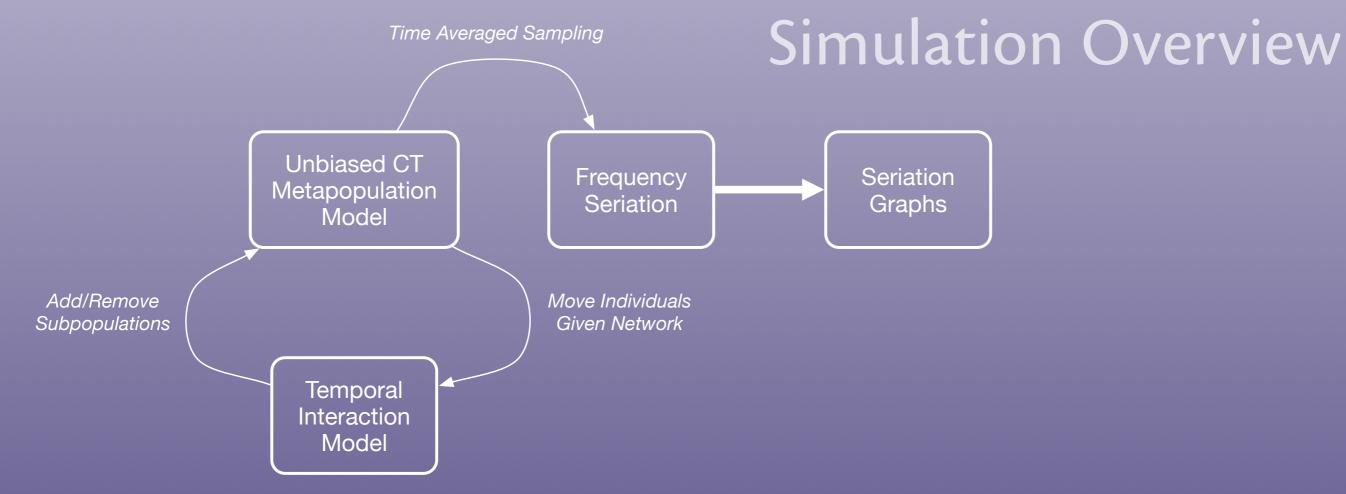
### Inferring Regional Interaction



- Links between past communities allowed flow of traits — in addition to goods and people
- Large scale changes to linkages over time creates unique trait histories
- Unique trait histories
   appear as groups of
   assemblages which can
   seriate together

Temporal Network Model





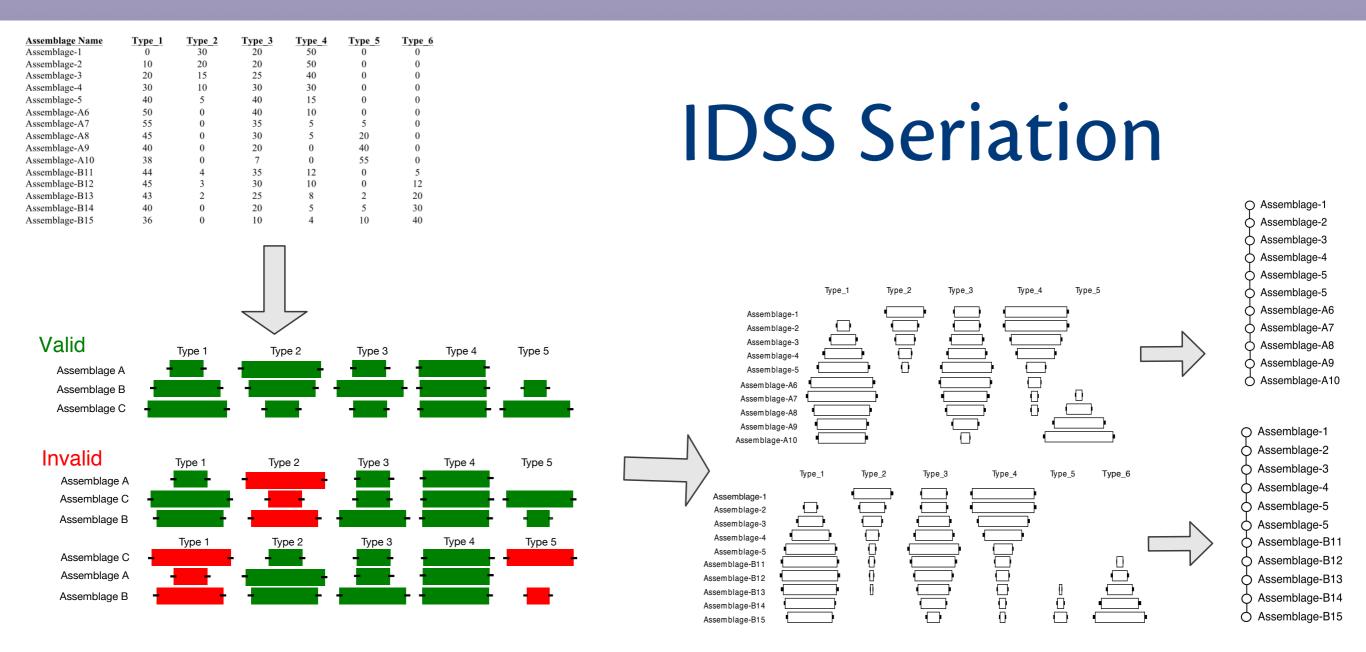
- Each community contains 100 agents
- TN model: 6-8 graph "slices" each applies for a duration
- Communities have short duration compared to run length
- Clusters of communities densely connected, sparse connections between clusters
- Unbiased copying within communities, migration according to graph slice in play, and innovation at low rates
- Samples of individuals recorded and time-averaged over community duration samples are then seriated

### IDSS Frequency Seriation

- Basic principle: not all assemblages were part of the same flow of traits, and thus will not seriate together.
- The seriation problem is thus to find all sets of assemblages that DO seriate together
- And then work out the relationship between these partial solutions

#### Core of algorithm:

- Find all valid triples
- Grow triples by combining with other assemblages
- Use bootstrap CI to determine "fit" of ordering
- Use threshold for pairwise differences to reject bad orders
- Combine partial solutions using overlaps and min summed frequency differences



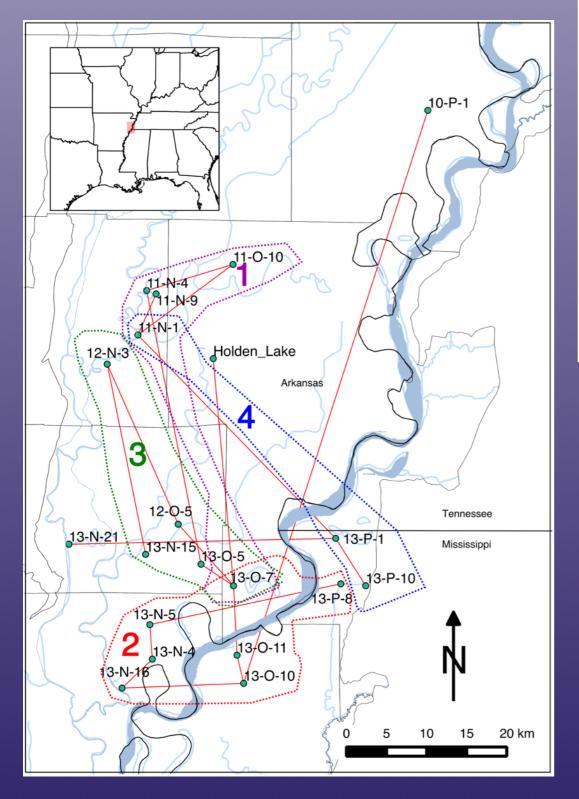
Note the compact graph representation of the solution on the right. This is useful when sets of assemblages partially overlap and diverge or coalesce

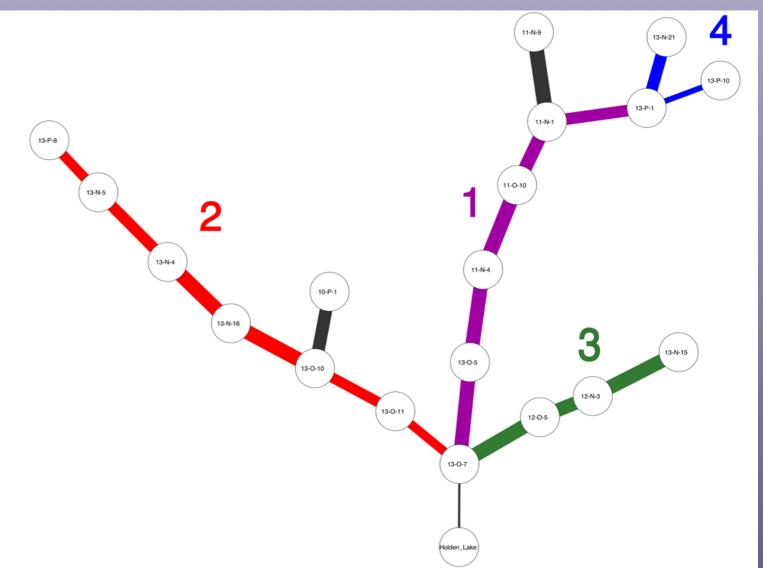
# (A10) **B**15 **A**9 **B13** B12 5 **I** 4 **I** 3 **I** 2 **I** (A10) <u>B15</u> A9 (B14) A8 B13 \_<del>A7</del> B12 B11

## Combining Solutions

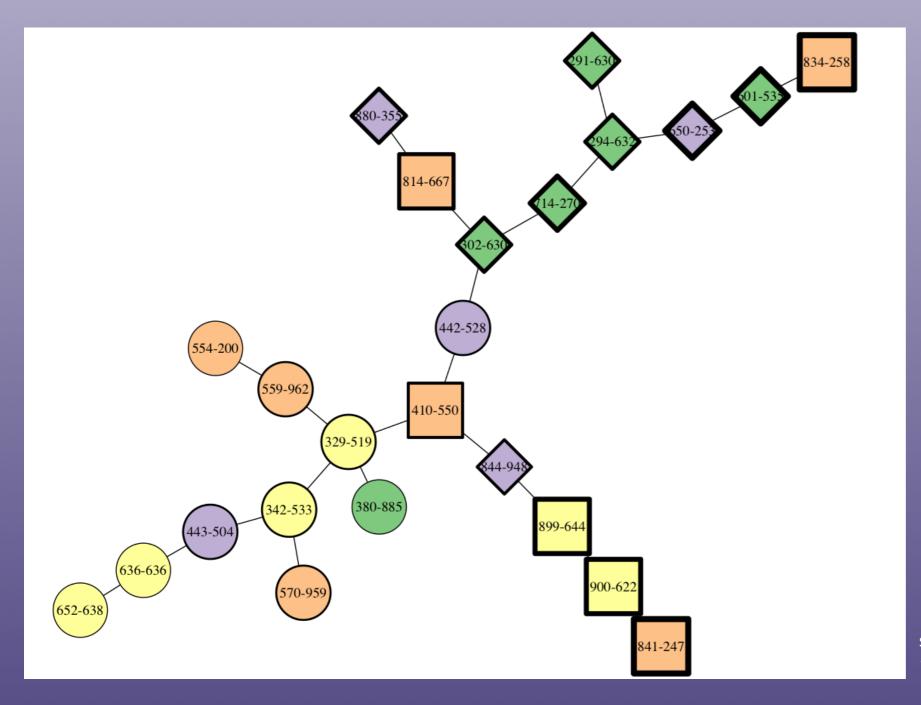
- Create a single solution using all of the vertices in the partial solutions (1-5, A6-10, B11-15)
- Edges are kept which have the smallest total frequency differences between vertices
- Creates branching points and tree-like solutions, preserving overlapping portions.
- Result is the "maximal" size solution with the "minimal" total frequency distance, hence "minmax" graph

## LMV Ceramic Seriations





- "Minmax" solution for the Memphis and St. Francis areas
- Combines 97 valid partial solutions
- Two sites (Parkin, Beck Place) link multiple spatial clusters
- Potentially shows lineage structure as well as chronology



#### Legend

Color: cluster of sites

Shape: lineage

Thickness: chronology

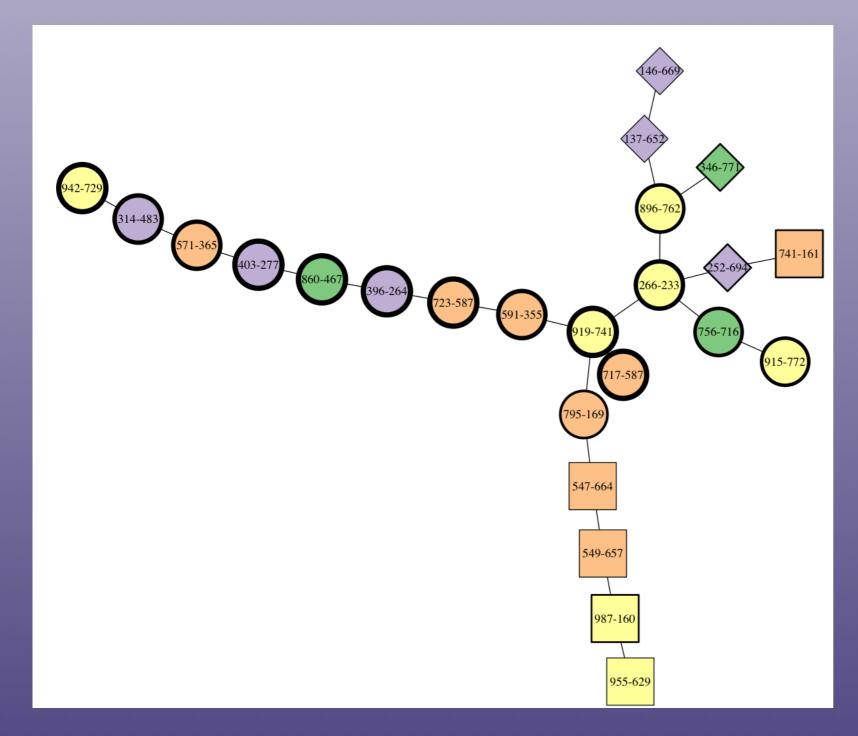
thin = early

thick = late

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### Lineage Splitting Example

- 4 clusters of 10 communities interconnected in 1 lineage
- Split into 2 lineages with 2 clusters each
- 240 possible assemblages spatially resampled to 24



#### Legend

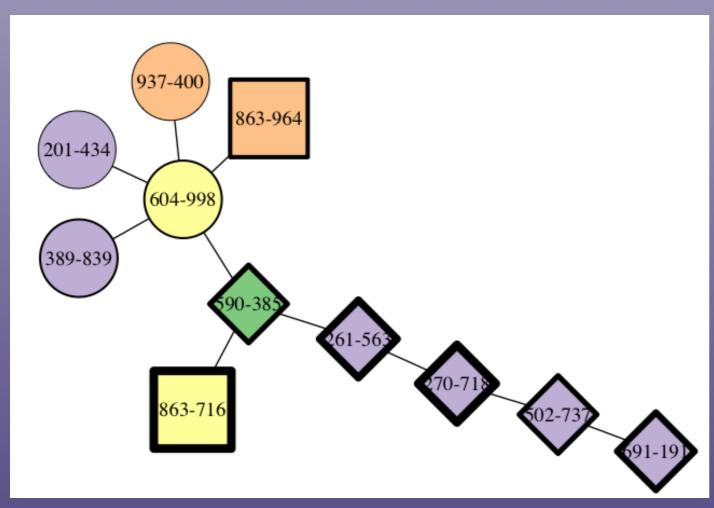
Color: cluster of sites
Shape: lineage
Thickness: chronology
thin = early
thick = late

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### Lineage Merging Example

- Same temporal network as lineage split, except...
- Begin with 2 lineages of 2 clusters each
- Merge into a single regional lineage

#### Observations



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- Examples with clear lineage structure and chronology seem to have lower migration and innovation rates
- Previous slide migration rate: 0.09
- Previous slide innovation rate: 0.00008

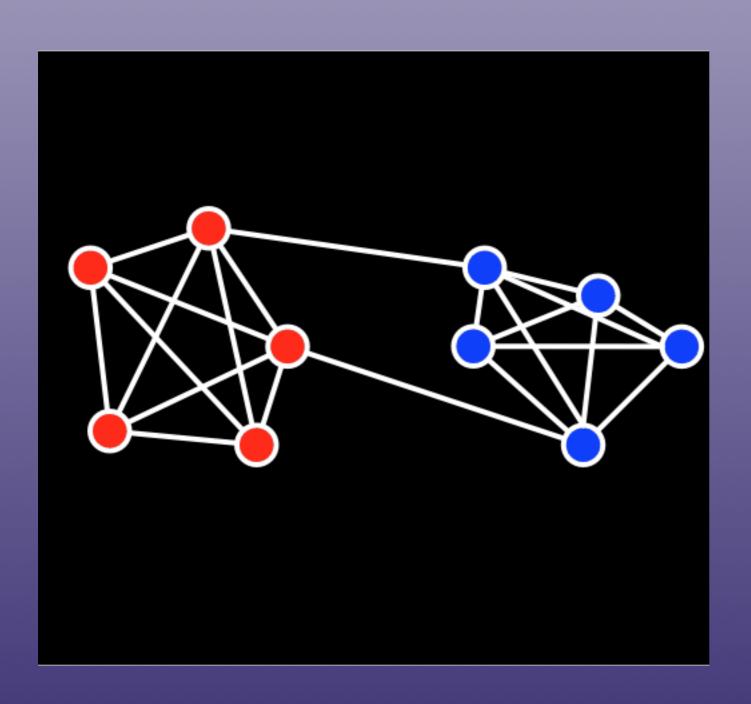
- Good chronology, no lineage structure
- Migration rate: 0.14
- Innovation: 0.0003

# For more information

- Simulation: <a href="https://github.com/mmadsen/seriationct">https://github.com/mmadsen/seriationct</a> (rel v1.2)
- Seriation: <a href="https://github.com/clipo/idss-seriation">https://github.com/clipo/idss-seriation</a> (rel v2.1)

- Analysis: <a href="https://github.com/mmadsen/experiment-seriationct">https://github.com/mmadsen/experiment-seriationct</a>
   and <a href="https://github.com/mmadsen/experiment-seriationct-2">https://github.com/mmadsen/experiment-seriationct-2</a>
- Notes: <a href="http://notebook.madsenlab.org">http://notebook.madsenlab.org</a>

### Lineage "Split" Animation



- One lineage
- Two clusters of sites
- Start with weak links between clusters
- Between cluster links go away
- Yielding separate
   evolutionary histories
   after split