Spectral Gerrymandering

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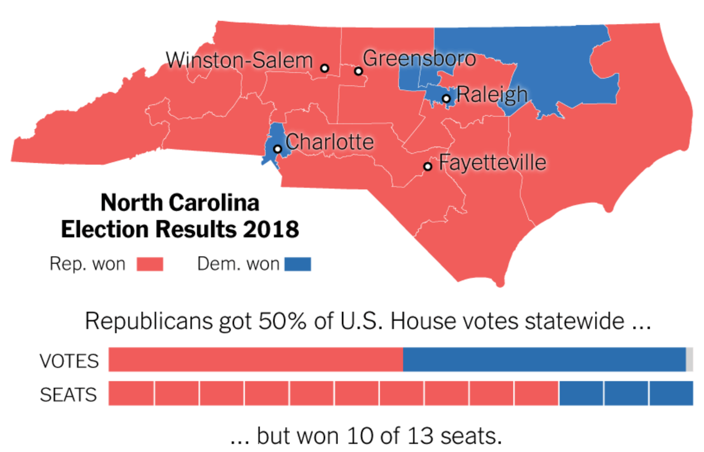
Introduction

How do you quantify the extent to which a districting plan is a gerrymander? Increasingly, researchers have used MCMC (Markov Chain Monte Carlo) methods to sample from an innumerable distribution of reasonable maps, as an empirical baseline for proposed districting plans.

But we still know very little about the properties of these dynamics.

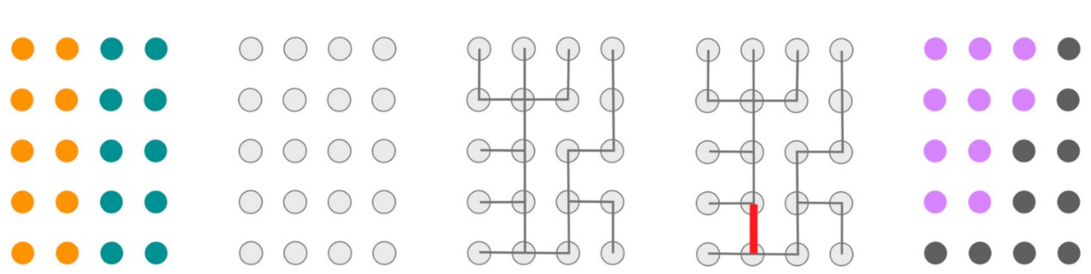


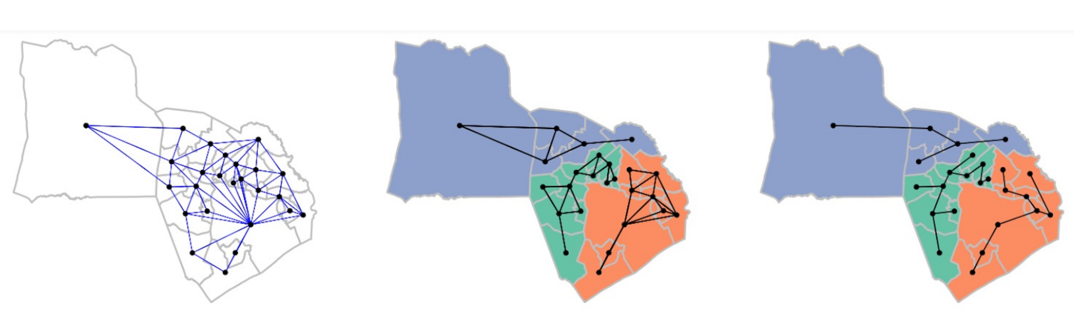
Objectives

Visualize the mixing properties for the Regular, Forest Metropolized, and Reversible Recombination algorithms.

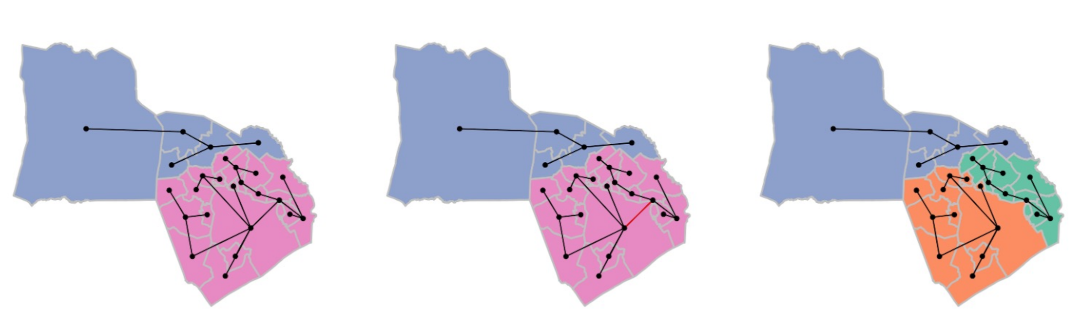
In the case of the later two dynamics, visualize these properties through the parameter space of gamma (gamma = 0.0 representing uniform on spanning trees, and gamma = 1.0 redistricting partitions).

Investigating the underlying causes of any provocative visual features.





(a) Graph (b) Graph Partition (c) Tree Partition (extended state)



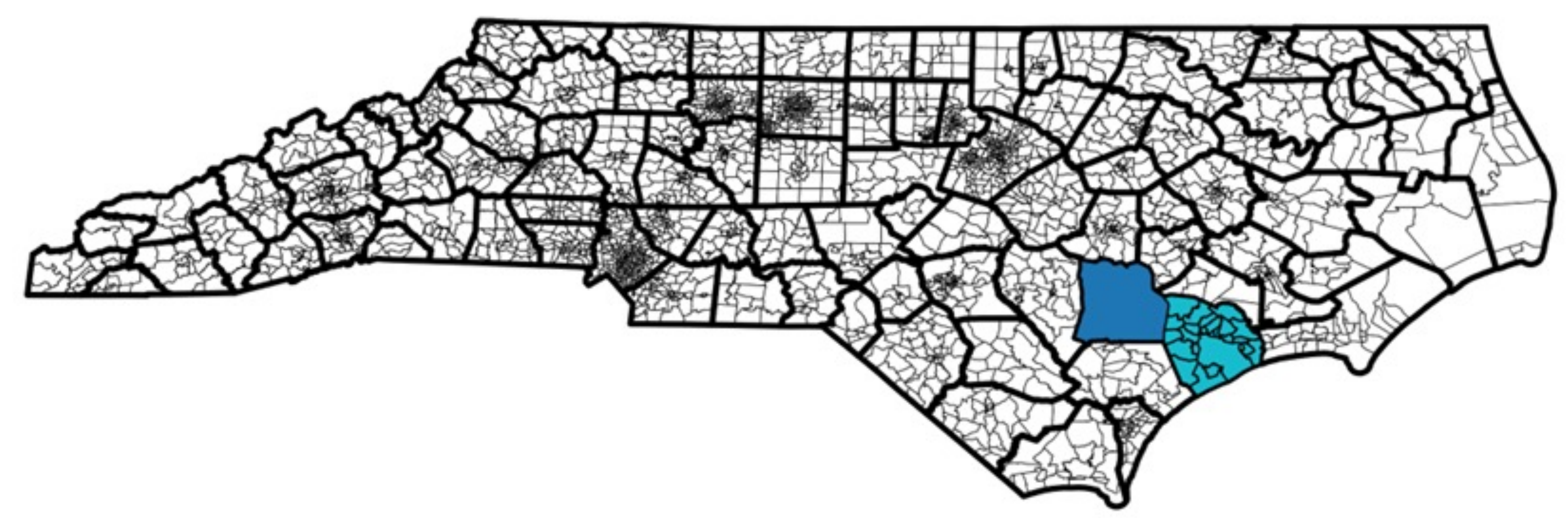
(d) Merge & Sample New Tree on Merged Subgraph (e) Find Edge to Cut (f) Split into Two Trees

Methods

Enumerated example: Duplin-Onslow County Cluster in North Carolina, illustrated below. Duplin is colored dark blue and Onslow is colored in teal.

Methodology: We model redistricting as a graph problem. We model a set of precincts in a state as a set of nodes, with edges denoting adjacencies between nodes. By simulating the three dynamics (Regular, Forest Metropolized, Reversible Recombination) on these graphs, we determine transition rates between the enumerated set of districting partitions in our county cluster example.

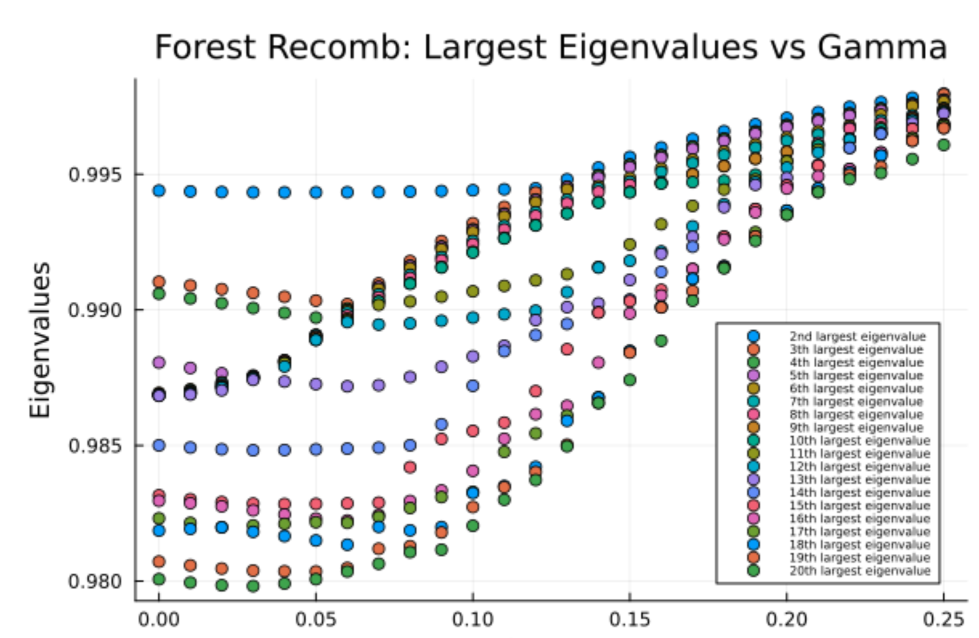
There exists tools from spectral graph theory to analyze these transition matrices. For instance, the quantity of the second largest eigenvalue of the probability transition matrix corresponds to mixing time — a higher value denotes longer mixing time.

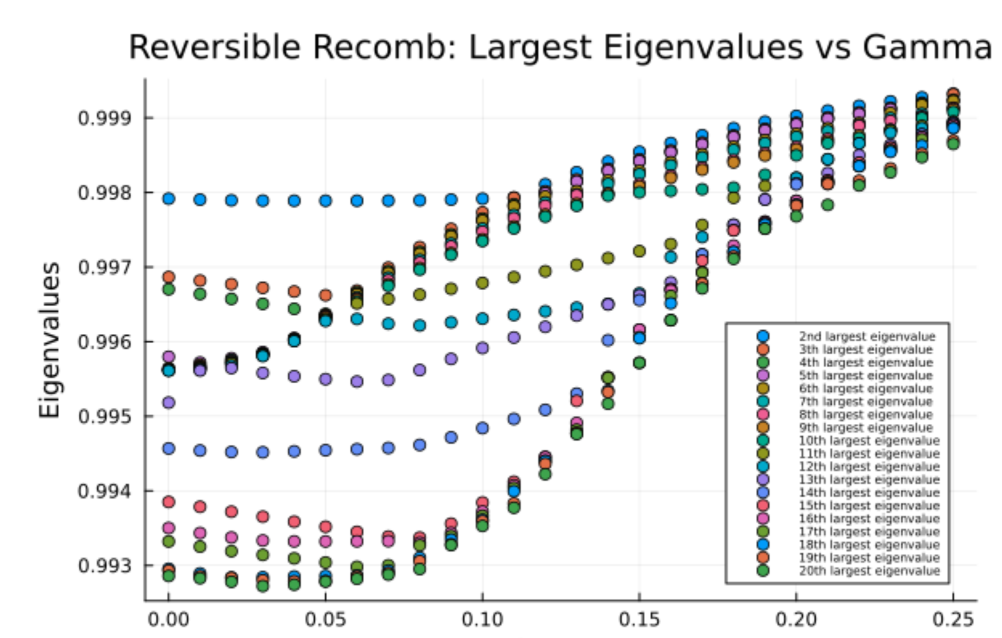


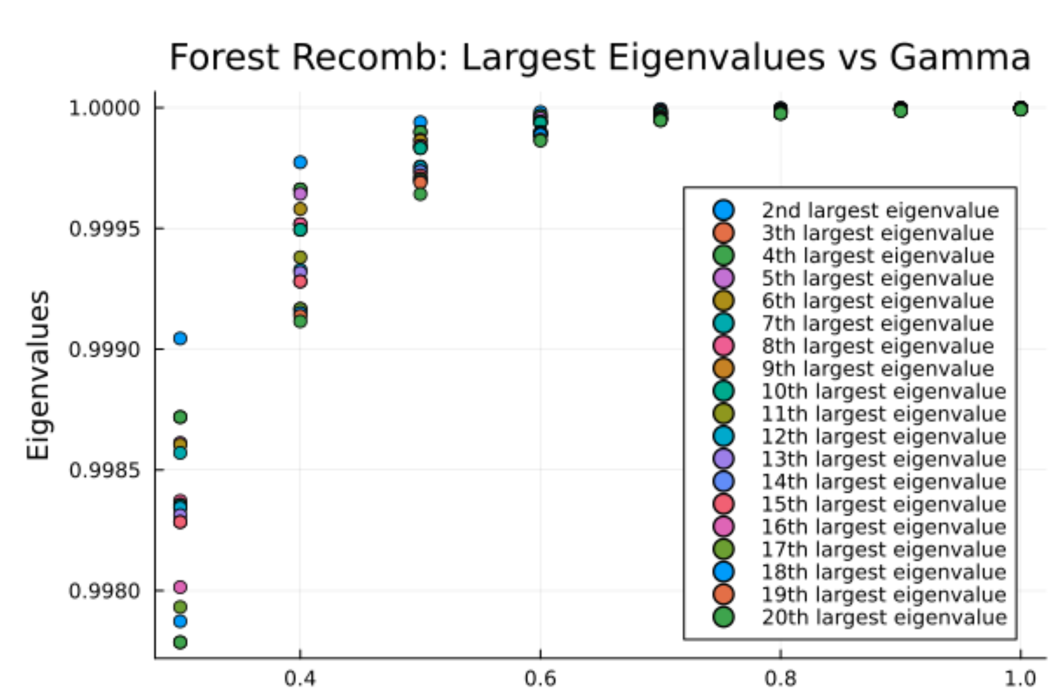
Results

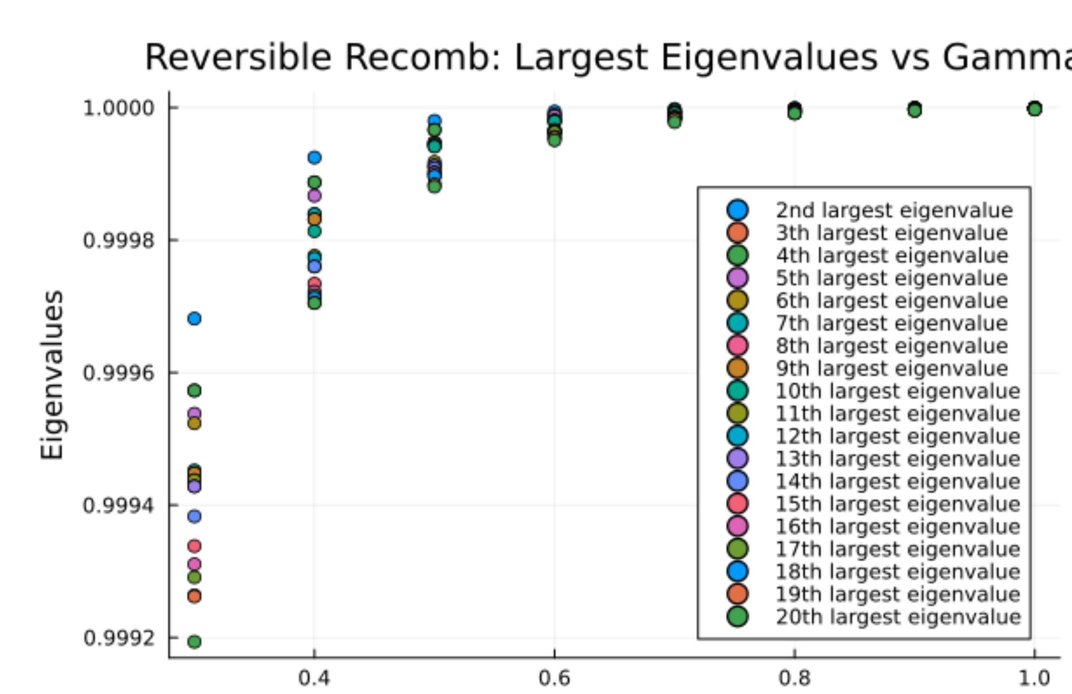
First row: visualizing the eigenvalue phase shifts. Bifurcation for 2nd largest eigenvalue occurs between gamma = 0.12 and 0.13 for Forest, 0.11 and 0.12 for Reversible

Second row: visualizing the extremely tiny spectral gap near gamma = 1.0 (uniform on partitions)



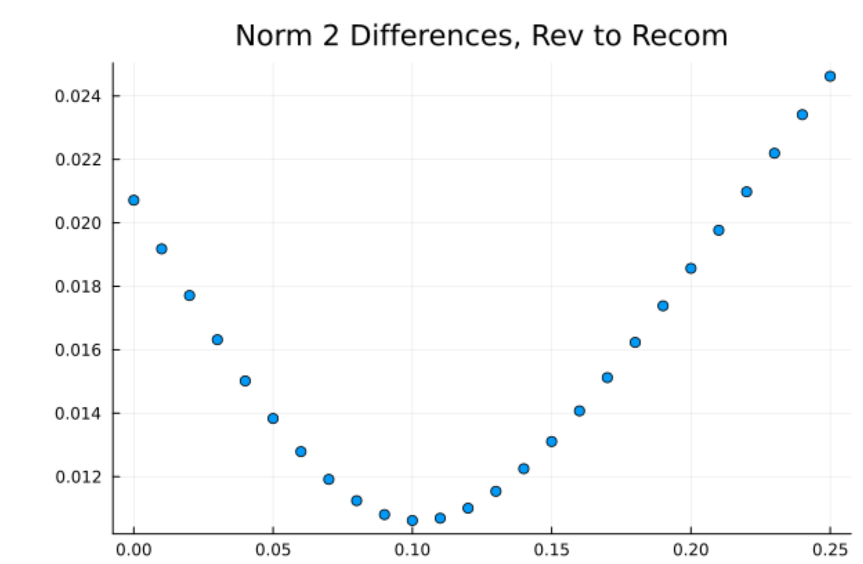






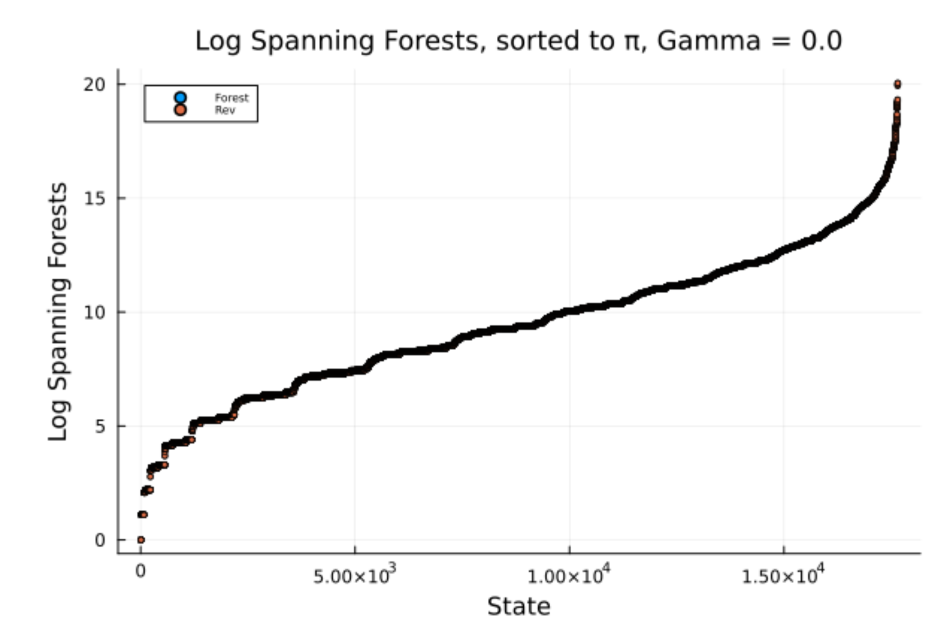
Results Cont.

Comparison of Invariant Measures to Regular Recombination:

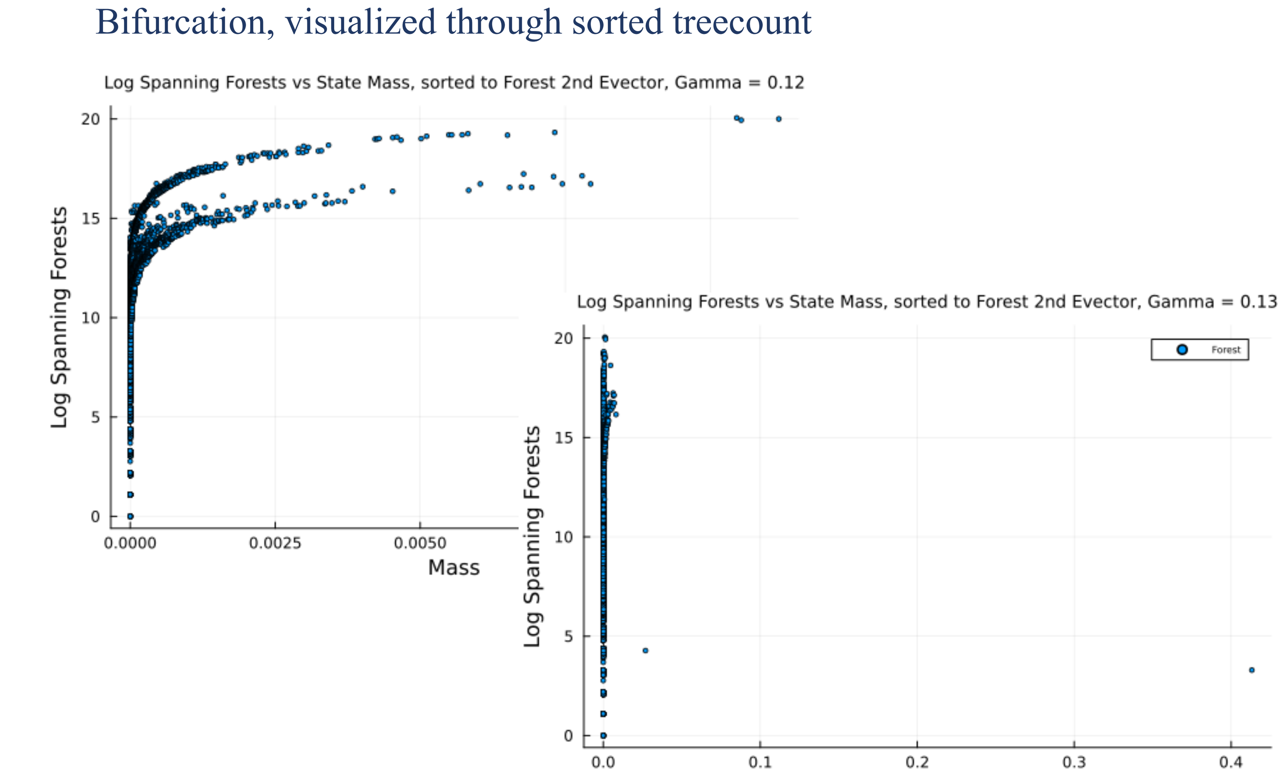


Sorted treecount by the mass of the invariant measure, at gamma = 0.0

Empirical evidence for gamma = 0.0 as uniform on spanning trees



Bifurcation, visualized through sorted treecount



Acknowledgements/References

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