## Using networks to explore, quantify, and summarize phylogenetic tree space



Jeremy M. Brown¹, Guifang Zhou², Wen Huang², Jeremy Ash¹, Melissa Marchand², Kyle Gallivan², and Jim Wilgenbusch³
${ }^{1}$ Louisiana State University, Dept. of Biological Sciences
2 Florida State University, Dept. of Mathematics
${ }^{3}$ Florida State University, Dept. of Scientific Computing

## The Team



## Overview

- Motivation
- Our network approaches
- Some applications
- Initial results
- Software


Motivation

## Summarizing Tree Sets

- Consensus trees



## Summarizing Tree Sets

- Consensus trees
- Agreement subtrees



## Summarizing Tree Sets

- Consensus trees
- Agreement subtrees
- Clustering

Statistically based postprocessing of phylogenetic analysis by clustering
Cara Stockham ${ }^{1}$, Li-San Wang ${ }^{2, *}$ and Tandy Warnow ${ }^{2}$

Report multiple consensus trees, while attempting to minimize the amount of information lost from the full distribution.

## Summarizing Tree Sets

- Consensus trees
- Agreement subtrees
- Clustering
- Dimensionality Reduction



# Networks of Trees 



## Networks of Trees



## Networks of Bipartitions



## Bipartition Covariances



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## Networks of Bipartitions



# Networks of Bipartitions 



Two Equally
Frequent Topologies

## Network Visualizations



## Network Visualizations



## Network Visualizations



## Assessing Model Fit

Using parametric bootstrapping or posterior prediction, we can compare network structures between observed and simulated datasets.

Empirical


Simulated


## Detecting Distinct Phylogenetic Signals



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Two Equally
Frequent Topologies

## Detecting Distinct Phylogenetic Signals



Two Equally
Frequent Topologies

## Network Visualizations

Completely distinct signals in two genes


## Network Visualizations

Partially overlapping signal


## Proof of Principle



Topologies used for simulating two halves of an alignment.

## Proof of Principle



Simulate


# Proof of Principle 



Majority-Rule Consensus Tree

## Proof of Principle



## Networks Detect Strong Conflict



## TreeScaper



Wen Huang. Tuesday morning iEvoBio Lightning Talk.

## Web Interface (future)

## TreeScaper Online

Input
Create Networks
Community Detection
Report Network Stats
Visualizations




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