## Statistics in BHV Tree Space

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## Overarching Goal

- many examples of tree-shaped data (phylogenies, anatomical trees, etc.)
- parameters:
- tree shape = tree topology
- edge lengths
- not Euclidean data!

Goal: develop methods for statistical analysis (i.e. mean, PCA) in a space of metric trees analogous to those for Euclidean space

## Tree Space Framework

- constructed by Billera, Holmes, and Vogtmann (2001)
- tree space $\mathbb{T}_{\mathrm{n}}=$ set of all trees with n leaves and branch lengths
- includes degenerate trees (non-binary)



## Tree Space

- represent each tree as a vector
- coordinates $=$ splits






## Tree Space

- not all sets of splits form a tree


## $\Rightarrow$ not all vectors are possible

## $\Rightarrow$ not a Euclidean space



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## Structure of ${ }^{〔} \mathbb{T}_{4}$



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## Geodesics



## Tree Space Properties

Theorem (Billera, Holmes, Vogtmann, 2001):
Tree space has global non-positive curvature.
$\Rightarrow$ unique geodesics (shortest paths)
$\Rightarrow$ well-defined mid-point tree

- BHV or geodesic distance = length of shortest path between two trees $T_{1}$ and $T_{2}$
- polynomial time algorithm to compute geodesic distance (O. and Provan, 2011)


## Mean and Variance

- weighted set $X$ in tree space:
- Fréchet mean $(X)=$ centre of mass

$$
=\underset{\mu}{\operatorname{argmin}} \sum_{x \in X} \mathrm{p}(x) \mathrm{d}(\mathrm{x}, \mu)^{2}
$$

(tree minimizing sum of square BHV distances)

- variance $(X)=\sum_{x \in X} p(x) d(x, \mu)^{2}$
- computable by algorithm based on Law of Large Numbers (Sturm 2003; Miller, O, Provan 2015; Bačák 2014)


## Experimental Results

Reference tree

| Opossum |  |
| :--- | :--- |
| Diprotodontian | Re |
|  |  |



Murphy et al., Resolution of the early placental mammal radiation using Bayesian phylogenetics. Science 294:2348-2351.

## Experimental Resulis



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## Experimental Results

Simulated DNA
sequences
500 bp $\times 10$
$1000 \mathrm{bp} \times 10$
$4000 \mathrm{bp} \times 10$

## Experimental Results

| Simulated DNA sequences | RAxML <br> bootstrap | bootstrap |
| :---: | :---: | :---: |
| $500 \mathrm{bp} \times 10$ |  |  |
|  |  | tree |
| $1000 \mathrm{bp} \times 10$ |  | distributions |
|  | MrBayes | posterior |
| $4000 \mathrm{bp} \times 10$ |  | distribution |

## Experimental Results



## Experimental Results



## Experimental Results



## Visualization vis MDS



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Bootstrap Samples


Posterior Samples


Bootstrap Samples


Posterior Samples


## Measures of Variance

- \# of different topologies in sample
- \# of different splits in sample
- sum of squared distances between trees

$$
\sum_{r=e r} \alpha(T, T)^{2}
$$








## Caveat

- Mean is sticky


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## Caveał



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## Other Statistics

- Central Limit Theorem on BHV tree space:
- special cases: Hotz, O., et al. 2012; Barden, Le, O.,

2013, 2014; Huckemann et al. 2015

- Principal Components Analysis (PCA): (Nye 2011, 2014; Feragen, O. et al. 2013; Nye et al. 2016)
- confidence regions: Willis 2016
- multiple techniques: Chakerian and Holmes 2012, Zairis et al. 2016
- and more...


## Thank You

- funding: SIMONS FOUNDATION
- webpage: http://comet.lehman.cuny.edu/owen


## Computing Mean

Theorem (Sturm, 2003): the following algorithm converges to the mean tree:

- $\mathrm{m}_{1}=\mathrm{T}_{1}$
- $i^{\text {th }}$ iteration :
- randomly choose tree $T_{i}$ from tree set with replacement
- $\mathrm{m}_{\mathrm{i}}=\frac{1}{i}$ (geodesic from $\mathrm{m}_{\mathrm{i}-1}$ to $\mathrm{T}_{\mathrm{i}}$ )


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