

# Computing medians and means of phylogenetic trees

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Max Planck Institute, Leipzig

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# Contents of the talk

- 1 Phylogenetic trees and tree space
- 2 Algorithms for computing medians and means
- 3 Applications to phylogenetic inference

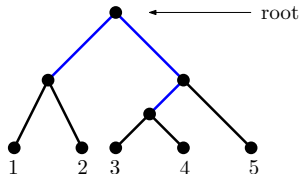
$n$ -trees

## Definition

A *metric  $n$ -tree* is a tree (connected graph with no circuit) with

- a distinguished vertex called *root*,
- $n$  vertices called *leaves* that are labeled  $1, \dots, n$ ,
- leaf and inner edges of positive length.

5-tree

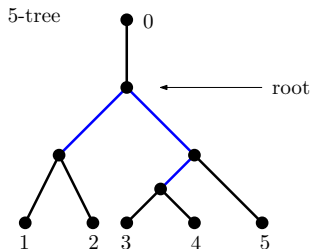


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# Need for a space of trees

We would like to

- measure distances between a given pair of trees,
- compute medians and means of a given set of trees.

We hence need a space of trees.

Construction due to **Billera, Holmes, and Vogtmann** in 2001:

**BHV Tree space:** a metric space whose points are trees.

(Metric space means we can measure distances.)

Moreover, tree space is an **Hadamard space** (i.e. it is nice).

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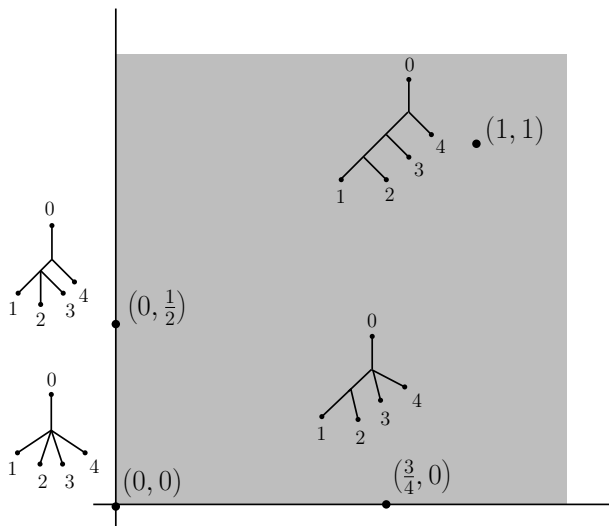
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## Orthant representation of a 4-tree



# A piece of tree space $\mathcal{T}_4$

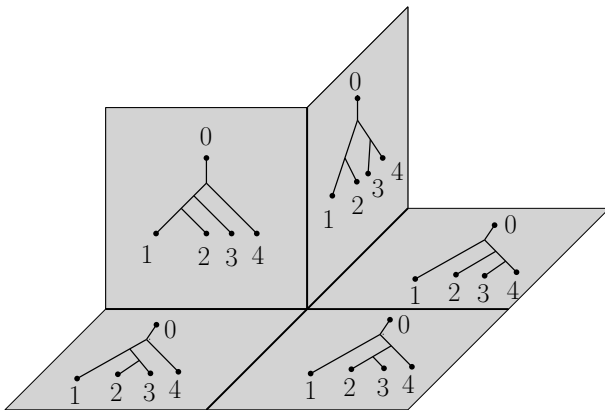


Figure : 5 out of 15 orthants of  $\mathcal{T}_4$



# Tree space

It is easy to define a metric in  $\mathcal{T}_n$  – induced by Euclidean distances.

(Hence we are able to measure distances.)

Geodesics are piecewise linear (broken line segments).

(Geodesic = shortest path between a given pair of points.)

Theorem (Billera, Holmes, Vogtmann)

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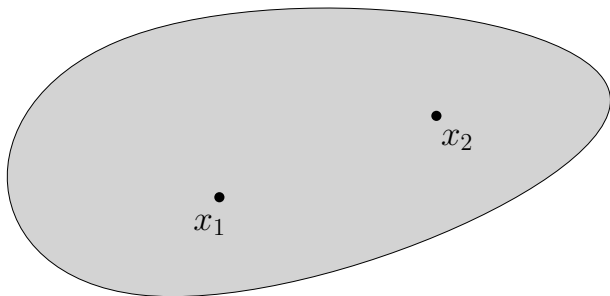
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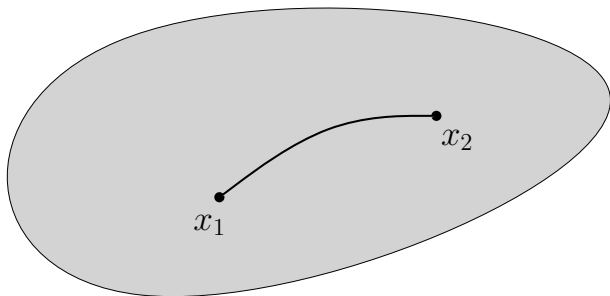
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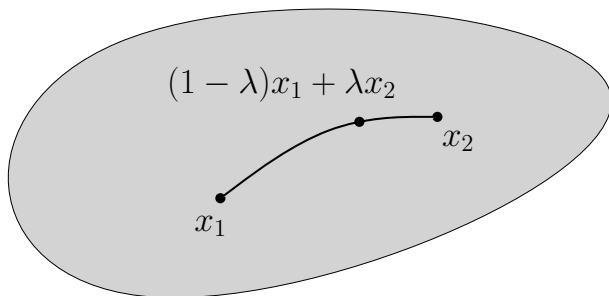
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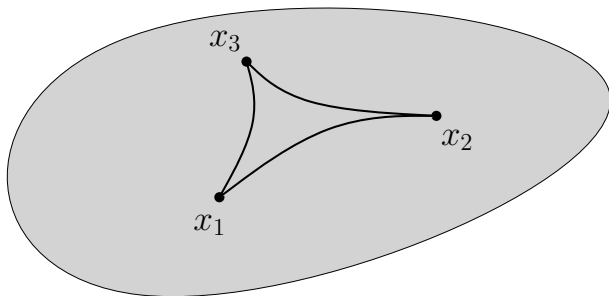
# Geodesic space



## Geodesic space



## Definition of nonpositive curvature



## The Fréchet mean

The arithmetic mean of  $x_1, \dots, x_K \in \mathbb{R}^m$  is defined as

$$\Xi(x_1, \dots, x_K) := \frac{x_1 + \dots + x_K}{K} = \frac{K-1}{K} \Xi(x_1, \dots, x_{K-1}) + \frac{1}{K} x_K.$$

We cannot directly extend this into tree space.

Theorem (Methode der kleinsten Quadrate, Gauss, 1809)

*The arithmetic mean is the unique vector in  $\mathbb{R}^m$  such that*

$$\sum_{k=1}^K d(\Xi, x_k)^2 = \min_{y \in \mathbb{R}^m} \sum_{k=1}^K d(y, x_k)^2.$$



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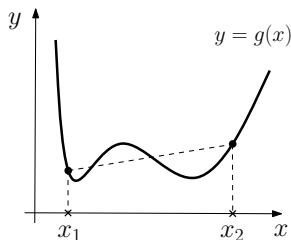
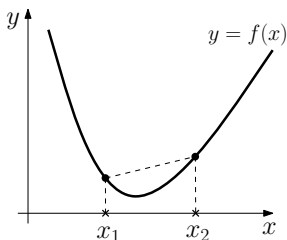
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## Convexity in tree space

### Definition (Convex function)

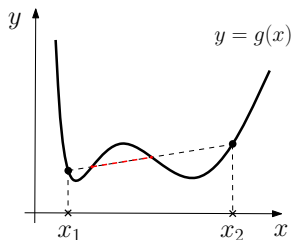
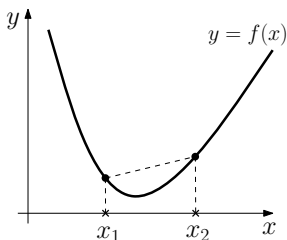
A function  $f : \mathcal{T}_n \rightarrow (-\infty, \infty]$  is *convex* if  $f \circ \gamma$  is a convex function for any geodesic  $\gamma : [0, 1] \rightarrow \mathcal{T}_n$ .



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## Definition of the Fréchet mean

Let  $T_1, \dots, T_K \in \mathcal{T}_n$ . The function

$$\xi(S) := \sum_{k=1}^K d(S, T_k)^2$$

is (strongly) convex and continuous. (**By nonpositive curvature.**)

### Theorem

- 1 There exists a unique minimizer  $\Xi \in \mathcal{T}_n$  of the function  $\xi$ .
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## Probabilistic interpretation of the mean

Let  $T_1, \dots, T_K \in \mathcal{T}_n$ . Denote the probability measure

$$\pi := \frac{1}{K} \sum_{k=1}^K \delta_{T_k}.$$

We can consider a random variable  $Y : \Omega \rightarrow \mathcal{T}_n$  with distr.  $\pi$ .

If each of the values  $T_1, \dots, T_K$  occurs with probability  $\frac{1}{K}$ , then

$$\mathbb{E}Y := \arg \min_{S \in \mathcal{T}_n} \frac{1}{K} \sum_{k=1}^K d(S, T_k)^2 = \Xi(T_1, \dots, T_K)$$

is the expectation of  $Y$ . (Also called the barycenter of  $\pi$ .)



## The law of large numbers

Given a sequence of random variables  $Y_i$  with values in  $\mathcal{T}_n$ , we define  $S_1 := Y_1$ , and

$$S_{i+1} := \frac{i}{i+1}S_i + \frac{1}{i+1}Y_{i+1},$$

Theorem (The law of large numbers, Sturm 2003)

*Let  $(Y_i)$  be a sequence i.i.d. according to  $\pi$ . Then*

$$S_i \rightarrow \Xi(T_1, \dots, T_K), \quad \text{as } i \rightarrow \infty,$$

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## Geometric median

Let  $T_1, \dots, T_K \in \mathcal{T}_n$ . Then

$$\psi(S) := \sum_{k=1}^K d(S, T_k)$$

is convex and continuous on  $\mathcal{T}_n$ .

( = the *Fermat-Weber problem* for optimal facility location)

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No explicit formula for a minimizer, only approximation algorithms, e.g. Weiszfeld's algorithm. (Compare with means.)

In  $\mathbb{R}$  it coincides with the usual definition of a median:

$$\Pr(Y \leq \mu) \geq \frac{1}{2} \quad \text{and} \quad \Pr(Y \geq \mu) \geq \frac{1}{2},$$

where  $Y : \mathbb{R} \rightarrow \mathbb{R}$  is a random variable. Then  $\mu$  is a median of  $Y$ .

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Assume  $f$  attains its minimum. How to **compute** a minimizer?

Algorithm (Proximal point algorithm)

Choose  $S_0 \in \mathcal{T}_n$  and set

$$S_{i+1} := \arg \min_{T \in \mathcal{T}_n} \left[ f(T) + \frac{1}{2\lambda_i} d(T, S_i)^2 \right],$$

for  $i \in \mathbb{N}$ .

The sequence  $S_i$  converges to a minimizer of  $f$ .

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Works also in Hadamard spaces (M.B. 2011)



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Let  $f_1, \dots, f_K$  be convex continuous and consider

$$f(T) := \sum_{k=1}^K f_k(T), \quad T \in \mathcal{T}_n.$$

Example (Median and mean)

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**Key idea:** use the PPA for  $f_1, \dots, f_K$  in a cyclic or random order.

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This is a **one-dimensional** problem!

$\implies S_{i+1}$  is a convex combination of  $T_k$  and  $S_i$ .

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## Computing the mean: Cyclic order version

Algorithm (M.B. 2012)

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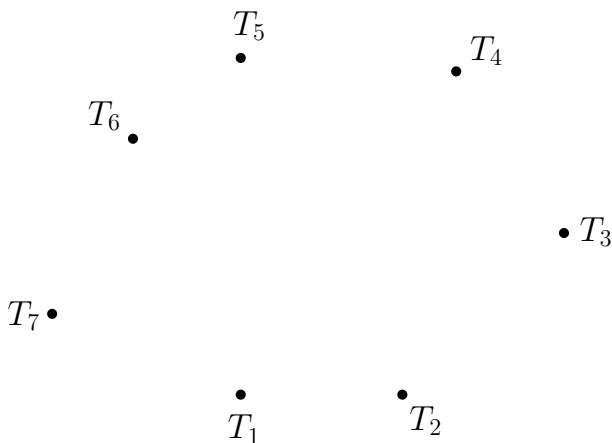
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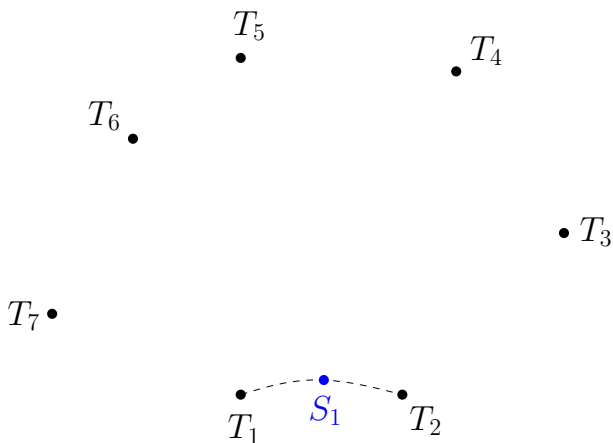
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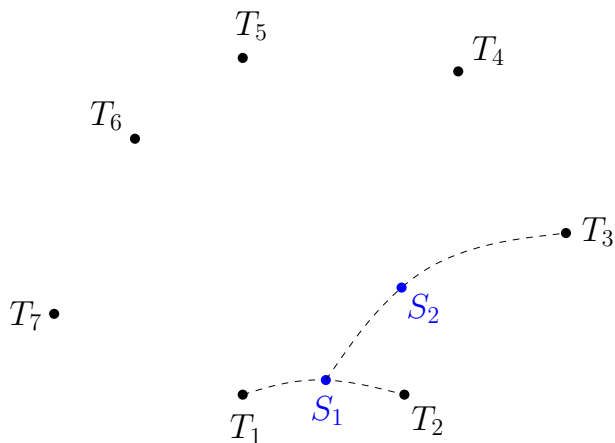
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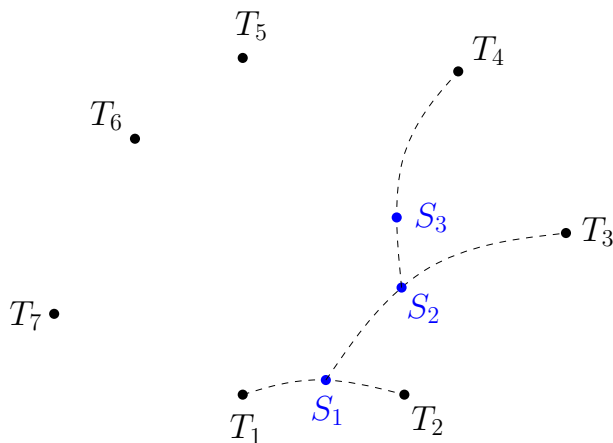
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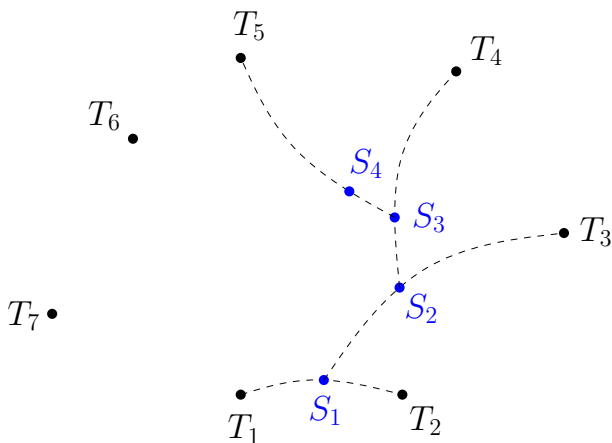
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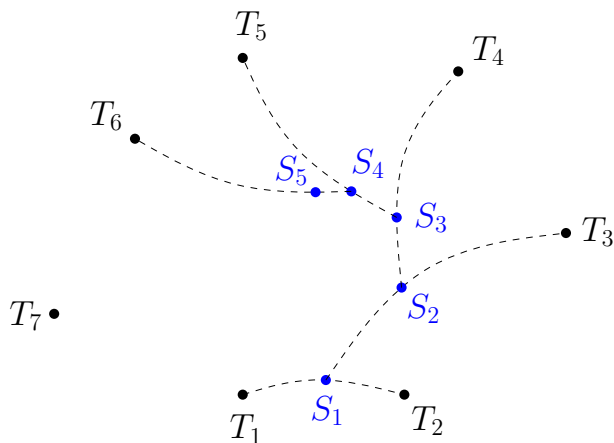
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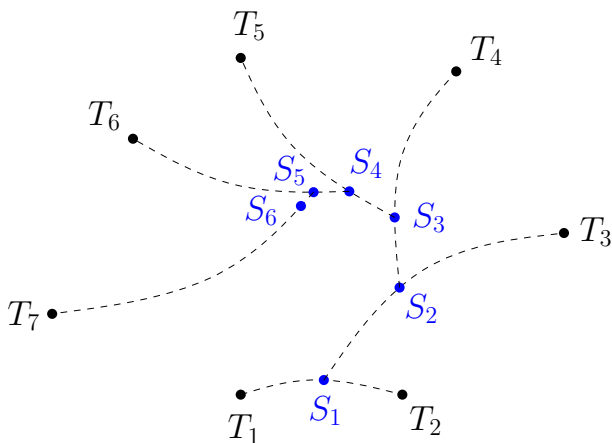
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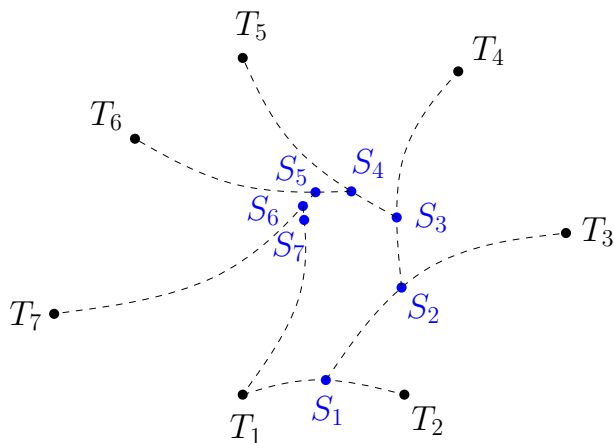
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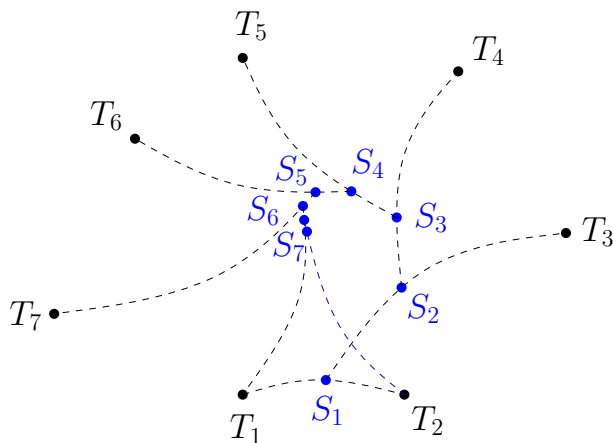


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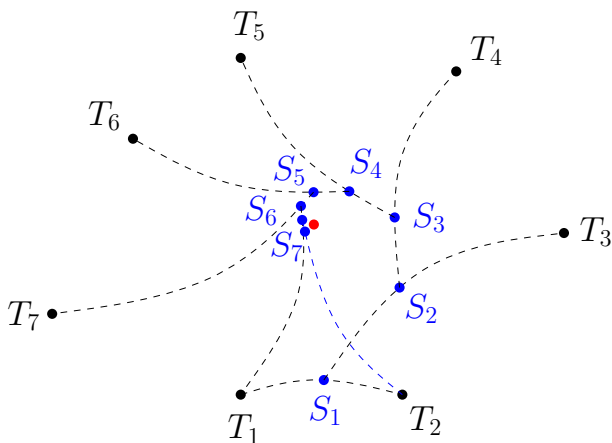




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The Owen-Provan algorithm (2011)

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## Statistical model (see Philipp Benner's poster for details)

We start with multiple sequence alignments  $\rightsquigarrow$

### Posterior distribution is defined:

- first on each orthant  $\mathcal{O}_i$  of tree space (fixed tree topology)  
 $\implies \mu_i$
- posterior distribution on the whole tree space  $\mathcal{T}_n$  :

$$\mu := \sum_{i=1}^{(2n-3)!!} w_i \mu_i.$$

### Difficulties:

- the weights  $w_i$  require to compute a complicated integral
- the number of orthants (tree topologies) is **big**:  $(2n - 3)!!$

## Statistical model (see Philipp Benner's poster for details)

We start with multiple sequence alignments  $\rightsquigarrow$

### Posterior distribution is defined:

- first on each orthant  $\mathcal{O}_i$  of tree space (fixed tree topology)  
 $\implies \mu_i$
- posterior distribution on the whole tree space  $\mathcal{T}_n$  :

$$\mu := \sum_{i=1}^{(2n-3)!!} w_i \mu_i.$$

### Difficulties:

- the weights  $w_i$  require to compute a complicated integral
- the number of orthants (tree topologies) is **big**:  $(2n - 3)!!$



## Statistical model - continued

We'll therefore give point estimates of posterior distribution  $\mu$ :

- median:

$$\arg \min_{S \in \mathcal{T}_n} \int_{\mathcal{T}_n} d(S, T) \, d\mu(T)$$

- mean:

$$\arg \min_{S \in \mathcal{T}_n} \int_{\mathcal{T}_n} d(S, T)^2 \, d\mu(T)$$

Markov chain Monte Carlo (MCMC) methods yield samples of posterior distribution:

$$\rightsquigarrow T_1, \dots, T_K \in \mathcal{T}_n \quad \rightsquigarrow \pi := \frac{1}{K} \sum_{k=1}^K \delta_{T_k} \quad (\pi \approx \mu)$$

Median and mean of  $\pi$  are computed with the above algorithms.

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## Real data experiments (see Philipp Benner's poster)

We used ribosomal subunit rRNA sequence alignment:

- number of species: 12
- number of trees: 20,000
- number of iterations:  $10^7$

### Conclusion:

- computations took less than 5 minutes
- very good speed of convergence (no theory though)
- random-order versions seem to be better

More computational studies certainly **needed** in the future!

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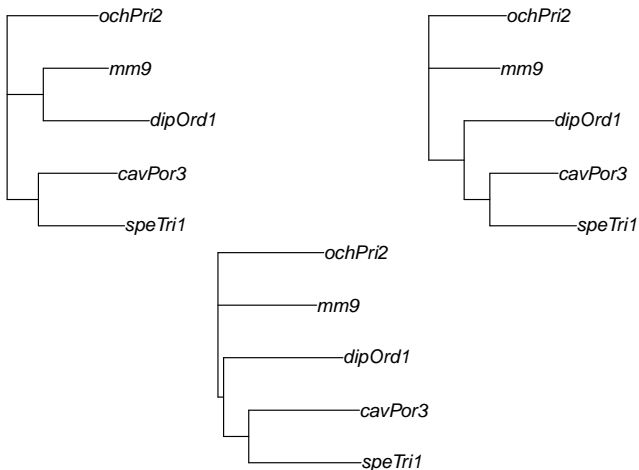
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## Real data experiments - continued



## Summary:

- The BHV Tree space has nice geometrical properties.
- ... it is rather “big”, but that doesn't seem to be an issue.
- The median and mean are well-defined and behave nicely.
- One can compute distances in polynomial time.
- There are rigorous approximation algorithms for medians and means.
- We used all that in phylogenetic inference and **would like to hear your opinion!**

## References

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