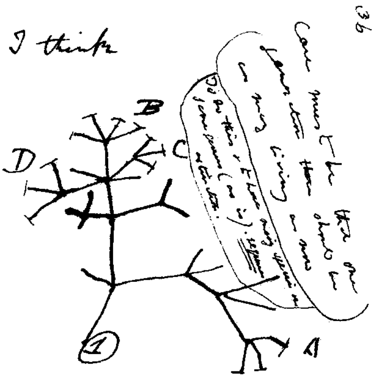
Semi-algebraic conditions for phylogenetic reconstruction

Marina Garrote-López

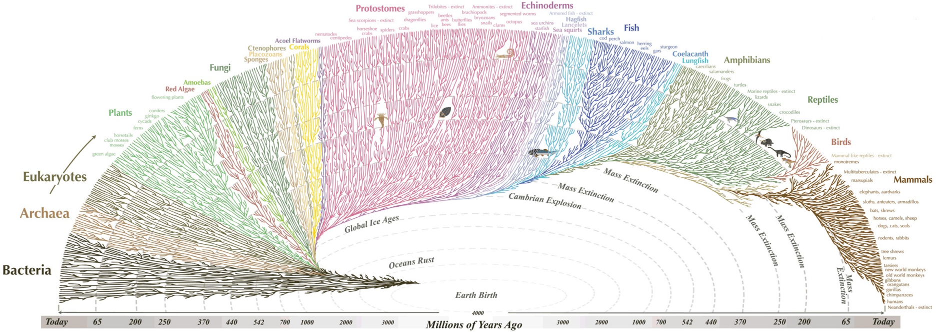
Seminari de Geometria Algebraica de Barcelona

Phylogenetics


36
I think
Case must be that one generation then should be as many living as now
To do this & to have many species in same genus (as is). requires extinction.
B
C
D
A
1

Charles Darwin, 1859

Phylogenetics



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5 SAQ: Semi-algebraic quartet reconstruction method

Phylogenetic reconstruction

Given an alignment of DNA sequences for some species,

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Human	AACGTCTATGCTCACCGATG
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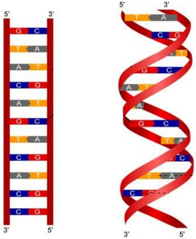
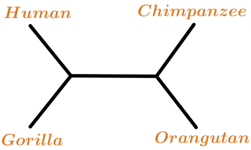
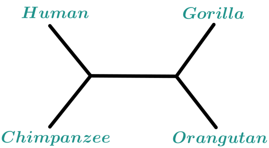
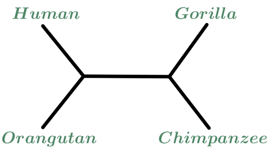


our goal is to reconstruct the topology of the phylogenetic tree that relates them.







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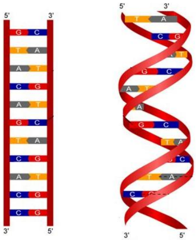

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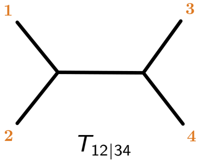
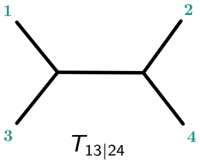
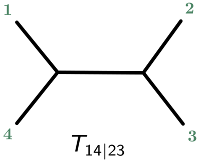


$T_{12|34}$

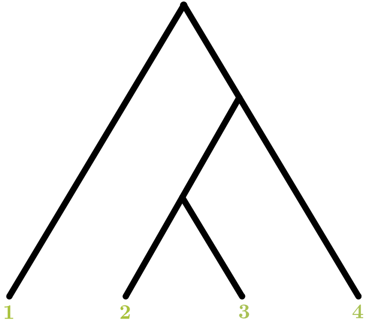


$T_{13|24}$



$T_{14|23}$

Modeling Evolution



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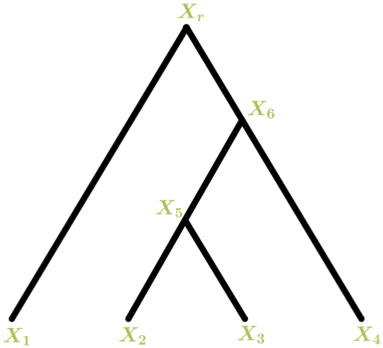

Random variables at the nodes
$X_i \in \mathcal{K} = \{\texttt{A},\texttt{C},\texttt{G},\texttt{T}\}$

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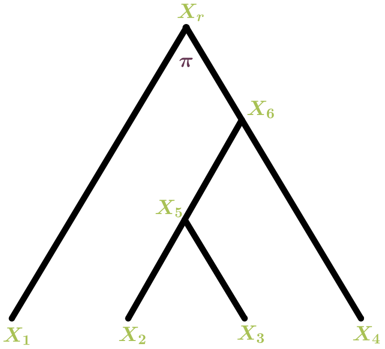

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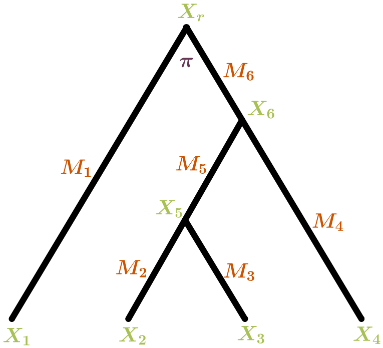

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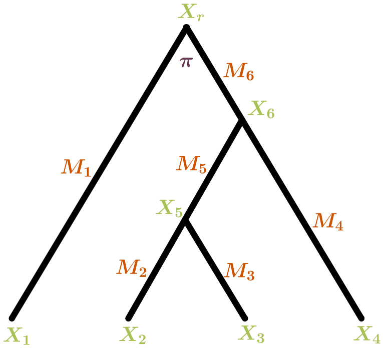

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A transition matrix is a square matrix with nonnegative entries and rows summing up to one.

Evolutionary models

Jukes Cantor Model

$$M_e = \begin{pmatrix} a_e & b_e & b_e & b_e \\ b_e & a_e & b_e & b_e \\ b_e & b_e & a_e & b_e \\ b_e & b_e & b_e & a_e \end{pmatrix},$$

where $3a_e + b_e = 1$.

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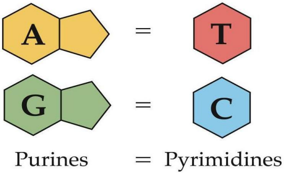

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Kimura Model

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where $a_e + b_e + c_e + d_e = 1$.

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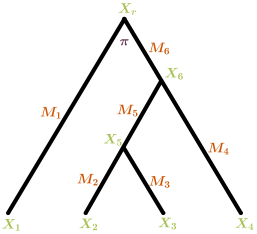
General Markov Model

$$M_e = \begin{pmatrix} a_e & b_e & c_e & d_e \\ e_e & f_e & g_e & h_e \\ j_e & k_e & l_e & m_e \\ n_e & o_e & p_e & q_e \end{pmatrix},$$

where rows sum up to 1.

Joint distribution



Definition

The **joint distribution** $p_{s_1,\dots,s_n}$ at the leaves of a rooted phylogenetic tree T, which is the probability that the random variables $X_1,\dots,X_n$ of the leaves take the states $s_1,\dots,s_n$

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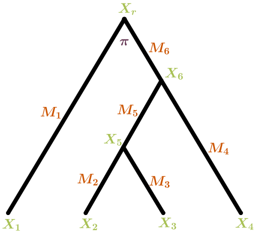

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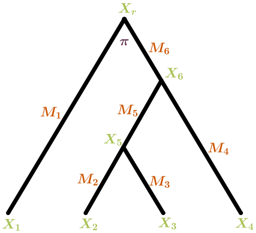
$$p_{x_1\dots x_n} = \sum_{x_v, v\in Int(T)} \pi_{x_r} \prod_{e\in E(T)} M_e(x_{pa(e)}, x_{ch(e)}),$$

Joint distribution



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$$\cdot M_2(x_5,\mathtt{T})\cdot M_3(x_5,\mathtt{C})\cdot M_4(x_6,\mathtt{C})$$

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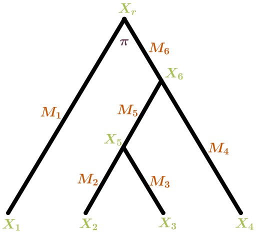

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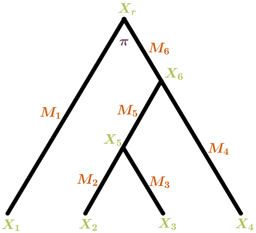

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- The entries of the joint distribution at the leaves $p^T = \left(p^T_{s_1\dots s_n}\right)_{s_1,\dots,s_n}$ can be expressed as a **polynomial** in terms of the parameters of the model.
- We can estimate p^T easily (by the relative frequencies in an alignment) but **NOT** the parameters.

Phylogenetic variety

Definition

For fixed tree T and model $\mathcal{M}$, fixed the position of the root r we use φ_T to denote the **parametrization map**,

$$\begin{array}{rcl} \varphi_T : \mathbb{R}^d & \longrightarrow & \mathbb{R}^{4^n} \\ (\pi, \{M_e\}_{e \in E(T)}) & \mapsto & P = (p_{x_1,x_1,\ldots,x_1}, p_{x_1,x_1,\ldots,x_2}, \ldots, p_{x_n,x_n,\ldots,x_n}) \end{array}$$

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The **phylogenetic algebraic variety** associated to a tree T and a model $\mathcal{M}$ is

$$\mathcal{V}_T = \overline{\operatorname{Im}\varphi_T}.$$

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Polynomials $f \in I_T$ and $f \notin I_{T'}$, with $T \neq T'$ are the **topology invariants** of T.

Using algebraic varieties in phylogenetics

- An alignment produces a point $\hat{p} = (p_{\mathtt{AA\ldots A}}, p_{\mathtt{AA\ldots C}}, \ldots, p_{\mathtt{TT\ldots T}})$ in $\mathbb{R}^{4^n}$.

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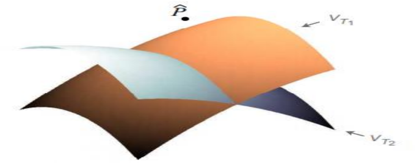
- $\hat{p}$ should be *close* to $\mathcal{V}_{T_0}$ (if the tree T_0 and model $\mathcal{M}$ fit the data).
- **Tree topology reconstruction using algebraic geometry.** For each possible topology T, evaluate elements of $I(\mathcal{V}_T)$ at $\hat{p}$: the polynomials of $I(\mathcal{V}_{T_0})$ should be ≈ 0 when evaluated at $\hat{p}$.



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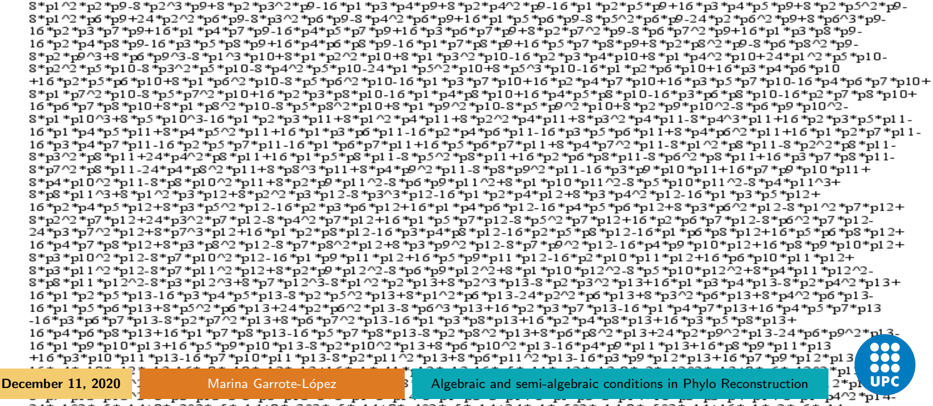

```
8*p1^2*p2*p9-8*p2^3*p9+8*p2*p3^2*p9-16*p1*p3*p4*p9+8*p2*p4^2*p9-16*p1*p2*p5*p9+16*p3*p4*p5*p9+8*p2*p5^2*p9-
8*p1^2*p6*p9+24*p2^2*p6*p9-8*p3^2*p6*p9-8*p4^2*p6*p9+16*p1*p5*p6*p9-8*p5^2*p6*p9-24*p2*p6^2*p9+8*p6^3*p9-
16*p2*p3*p7*p9+16*p1*p4*p7*p9-16*p4*p5*p7*p9+16*p3*p6*p7*p9+8*p2*p7^2*p9-8*p6*p7^2*p9+16*p1*p3*p8*p9-
16*p2*p4*p8*p9-16*p3*p5*p8*p9+16*p4*p6*p8*p9-16*p1*p7*p8*p9+16*p5*p7*p8*p9+8*p2*p8^2*p9-8*p6*p8^2*p9-
8*p2*p9^3+8*p6*p9^3-8*p1^3*p10+8*p1*p2^2*p10+8*p1*p3^2*p10-16*p2*p3*p4*p10+8*p1*p4^2*p10+24*p1^2*p5*p10-
8*p2^2*p5*p10-8*p3^2*p5*p10-8*p4^2*p5*p10-24*p1*p5^2*p10+8*p5^3*p10-16*p1*p2*p6*p10+16*p3*p4*p6*p10
+16*p2*p5*p6*p10+8*p1*p6^2*p10-8*p5*p6^2*p10-16*p1*p3*p7*p10+16*p2*p4*p7*p10+16*p3*p5*p7*p10-16*p4*p6*p7*p10+
8*p1*p7^2*p10-8*p5*p7^2*p10+16*p2*p3*p8*p10-16*p1*p4*p8*p10+16*p4*p5*p8*p10-16*p3*p6*p8*p10-16*p2*p7*p8*p10+
16*p6*p7*p8*p10+8*p1*p8^2*p10-8*p5*p8^2*p10+8*p1*p9^2*p10-8*p5*p9^2*p10+8*p2*p9*p10^2-8*p6*p9*p10^2-
8*p1*p10^3+8*p5*p10^3-16*p1*p2*p3*p11+8*p1^2*p4*p11+8*p2^2*p4*p11+8*p3^2*p4*p11-8*p4^3*p11+16*p2*p3*p5*p11-
16*p1*p4*p5*p11+8*p4*p5^2*p11+16*p1*p3*p6*p11-16*p2*p4*p6*p11-16*p3*p5*p6*p11+8*p4*p6^2*p11+16*p1*p2*p7*p11-
16*p3*p4*p7*p11-16*p2*p5*p7*p11-16*p1*p6*p7*p11+16*p5*p6*p7*p11+8*p4*p7^2*p11-8*p1^2*p8*p11-8*p2^2*p8*p11-
8*p3^2*p8*p11+24*p4^2*p8*p11+16*p1*p5*p8*p11-8*p5^2*p8*p11+16*p2*p6*p8*p11-8*p6^2*p8*p11+16*p3*p7*p8*p11-
8*p7^2*p8*p11-24*p4*p8^2*p11+8*p8^3*p11+8*p4*p9^2*p11-8*p8*p9^2*p11-16*p3*p9*p10*p11+16*p7*p9*p10*p11+
8*p4*p10^2*p11-8*p8*p10^2*p11+8*p2*p9*p11^2-8*p6*p9*p11^2+8*p1*p10*p11^2-8*p5*p10*p11^2-8*p4*p11^3+
8*p8*p11^3+8*p1^2*p3*p12+8*p2^2*p3*p12-8*p3^3*p12-16*p1*p2*p4*p12+8*p3*p4^2*p12-16*p1*p3*p5*p12+
16*p2*p4*p5*p12+8*p3*p5^2*p12-16*p2*p3*p6*p12+16*p1*p4*p6*p12-16*p4*p5*p6*p12+8*p3*p6^2*p12-8*p1^2*p7*p12+
8*p2^2*p7*p12+24*p3^2*p7*p12-8*p4^2*p7*p12+16*p1*p5*p7*p12-8*p5^2*p7*p12+16*p2*p6*p7*p12-8*p6^2*p7*p12-
24*p3*p7^2*p12+8*p7^3*p12+16*p1*p2*p8*p12-16*p3*p4*p8*p12-16*p2*p5*p8*p12-16*p1*p6*p8*p12+16*p5*p6*p8*p12+
16*p4*p7*p8*p12+8*p3*p8^2*p12-8*p7*p8^2*p12+8*p3*p9^2*p12-8*p7*p9^2*p12-16*p4*p9*p10*p12+16*p8*p9*p10*p12+
8*p3*p10^2*p12-8*p7*p10^2*p12-16*p1*p9*p11*p12+16*p5*p9*p11*p12-16*p2*p10*p11*p12+16*p6*p10*p11*p12+
8*p3*p11^2*p12-8*p7*p11^2*p12+8*p2*p9*p12^2-8*p6*p9*p12^2+8*p1*p10*p12^2-8*p5*p10*p12^2+8*p4*p11*p12^2-
8*p8*p11*p12^2-8*p3*p12^3+8*p7*p12^3-8*p1^2*p2*p13+8*p2^3*p13-8*p2*p3^2*p13+16*p1*p3*p4*p13-8*p2*p4^2*p13+
16*p1*p2*p5*p13-16*p3*p4*p5*p13-8*p2*p5^2*p13+8*p1^2*p6*p13-24*p2^2*p6*p13+8*p3^2*p6*p13+8*p4^2*p6*p13-
16*p1*p5*p6*p13+8*p5^2*p6*p13+24*p2*p6^2*p13-8*p6^3*p13+16*p2*p3*p7*p13-16*p1*p4*p7*p13+16*p4*p5*p7*p13
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16*p1*p9*p10*p13+16*p5*p9*p10*p13-8*p2*p10^2*p13+8*p6*p10^2*p13-16*p4*p9*p11*p13+16*p8*p9*p11*p13
+16*p3*p10*p11*p13-16*p7*p10*p11*p13-8*p2*p11^2*p13+8*p6*p11^2*p13-16*p3*p9*p12*p13+16*p7*p9*p12*p13
```
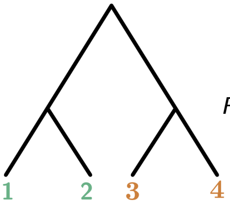

Flattening



$$Flatt_{12|34}(P) = \begin{array}{c} \\ \mathtt{AA} \\ AC \\ AG \\ \vdots \\ TT \end{array} \begin{array}{ccccc} \mathtt{AA} & \mathtt{AC} & \mathtt{AG} & \dots & \mathtt{TT} \\ \hline p_{\mathtt{AAAA}} & p_{\mathtt{AAAC}} & p_{\mathtt{AAAG}} & \dots & p_{\mathtt{AATT}} \\ p_{\mathtt{ACAA}} & p_{\mathtt{ACAC}} & p_{\mathtt{ACAG}} & \dots & p_{\mathtt{ACTT}} \\ p_{\mathtt{AGAA}} & p_{\mathtt{AGAC}} & p_{\mathtt{AGAG}} & \dots & p_{\mathtt{AGTT}} \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ p_{\mathtt{TTAA}} & p_{\mathtt{TTAC}} & p_{\mathtt{TTAG}} & \dots & p_{\mathtt{TTTT}} \end{array}$$

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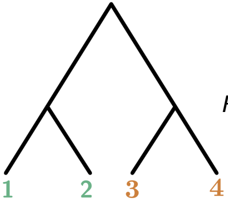

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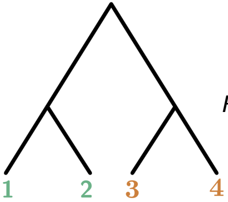
Theorem [Allman – Rhodes]

Let $P = \varphi_T(\pi, \{M_e\}_{e\in E(T)})$ where $T = T_{12|34}$. Then

$$\operatorname{rank}(Flatt_{12|34}(P)) \leq 4.$$

$Flatt_{13|24}(P)$ and $Flatt_{14|23}(P)$ have rank 16 for generic P.

Flattening



$$Flatt_{12|34}(P) = \begin{array}{c|ccccc} & \texttt{AA} & \texttt{AC} & \texttt{AG} & \dots & \texttt{TT} \\ \hline \texttt{AA} & p_{\texttt{AAAA}} & p_{\texttt{AAAC}} & p_{\texttt{AAAG}} & \dots & p_{\texttt{AATT}} \\ AC & p_{\texttt{ACAA}} & p_{\texttt{ACAC}} & p_{\texttt{ACAG}} & \dots & p_{\texttt{ACTT}} \\ AG & p_{\texttt{AGAA}} & p_{\texttt{AGAC}} & p_{\texttt{AGAG}} & \dots & p_{\texttt{AGTT}} \\ \vdots & \vdots & \vdots & \vdots & \ddots & \vdots \\ TT & p_{\texttt{TTAA}} & p_{\texttt{TTAC}} & p_{\texttt{TTAG}} & \dots & p_{\texttt{TTTT}} \end{array}$$

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Therefore 5×5 minors of $Flatt_{12|34}(P)$ are **topology invariants**.

Algebraic phylogenetic reconstruction methods

The distance of an $m \times n$ matrix M to the set

$$\mathcal{R}_k = \{m \times n \text{ matrices of rank } \leq k\}$$

can be computed easily by,

Eckart-Young Theorem

$$d_k(M) = d_F(M, \mathcal{R}_k) = \sqrt{\sum_{i \geq k+1} \sigma_i^2},$$

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Phylogenetic reconstruction methods

Compute $d_4(Flatt_{A|B}(P))$ for the tree possible bipartitions. The lower the score is, the more it is likely that the bipartition comes from an edge of T.

Stochastic phylogenetic regions

Definition

The **stochastic phylogenetic regions** is defined as

$$\mathcal{V}_T^+ = \{P \in \mathcal{V}_T \mid P = \varphi_T(s) \text{ and } s \in S \subset [0,1]^d\},$$

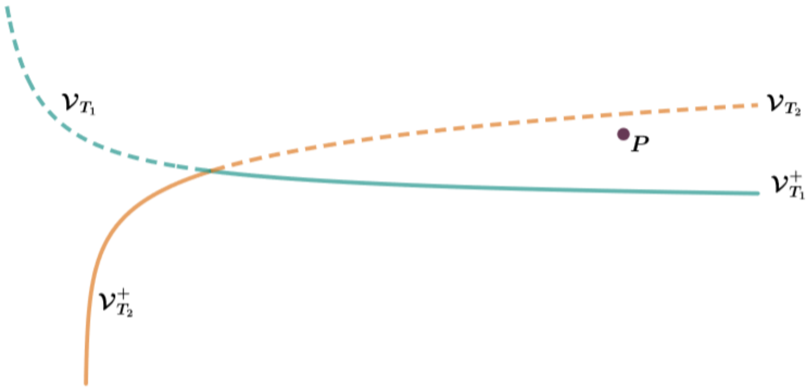
is the subset of $\mathcal{V}_T$ that contains distributions arising from stochastic parameters.

Stochastic Parameters

A vector π is stochastic iff its entries are non-negative and $\sum \pi_i = 1$.
A matrix is stochastic iff its entries are non-negative and

$$\sum_j M_e(i,j) = 1, \forall i, e$$

Could the stochastic varieties be useful for phylogenetic reconstruction?



Computing the distance to a Phylogenetic variety

Let $P = (p_1, \dots, p_{4^n}) \in \triangle^{4^n-1}$ be a distribution. We want to compute the distance of P to $\mathcal{V}_T^+$,

$$d(P, \mathcal{V}_T^+) = \min_{Q \in \mathcal{V}_T^+} d(P, Q)$$

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Since $Q \in \mathcal{V}_T^+$, we can write $Q = \varphi_T(x)$ with stochastic parameters $x \in \mathbb{R}^d$. Denote by $\Omega \subset \mathbb{R}^d$ the domain of stochastic parameters. Let

$$f_P(x) := d(P, \varphi_T(x)) = \sum_i^{4^n} (p_i - \varphi_i(x))^2.$$

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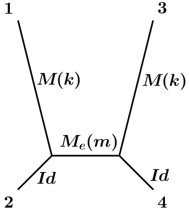
If $P^+ = \varphi_T(x^*) \in \mathcal{V}_T^+$ is such that $d(P, P^+) = d(P, \mathcal{V}_T^+)$ then

- $(P - P^+) \perp T_P \mathcal{V}_T$, i.e. x^* is a critical point of $f_P(x)$
- x^* is not a critical point of $f_P(x)$ but $P^+ \in \partial\Omega$

Long branch attraction for JC model



Let $P = \varphi_{12|34}\,(M, Id, M, Id, M_e)$.

Proposition [Casanellas – Fernández-Sánchez – G-L]

If M_e has negative off-diagonal entries and M is stochastic then $P^+ = \varphi_{12|34}(\tilde{M}, Id, \tilde{M}, Id, Id)$ is a local minimum of the distance function $d(P, \mathcal{V}_T^+)$.

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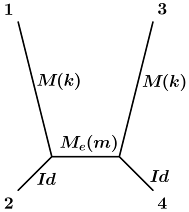

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Conjecture: Global minumum

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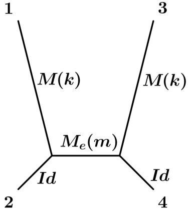

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Theorem [Casanellas – Fernández-Sánchez – G-L]

Let $P_0 = \varphi_{12|34}\,(M, Id, M, Id, M_e)$ such that $d(P_0, \mathcal{V}_T^+) = d\big(P_0, P^+\big)$ then, for any P close enough to P_0 we have

$$d(P, \mathcal{V}_T^+) \geq d(P, \mathcal{V}_{T_2}^+).$$

Computing the distance to a Phylogenetic variety

Lemma [Draisma – Horobet – Ottaviani – Sturmfels – Thomas]

For general $P \in \mathbb{C}^{4^n}$ the number of critical points of f_P on the manifold $\mathcal{V} \setminus \mathcal{V}_{sing}$ is finite and is called the **Euclidean Distance degree** of $\mathcal{V}$.

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Computations difficulties

ED degree for the Jukes Cantor model on 4-leaf trees is 290.

- $>$ 2.5 months with *Macaluay2*.
- $\approx$ 2.5 hours with *Magma*.

Numerical Algebraic Geometry Only PHCpack founds the 290 solutions.

The computations were performed on a machine with 10 *Dual Core Intel(R) Xeon(R) Silver* 64 *Processor* 4114 *(*2.20 *GHz,* 13.75*M Cache) equipped with* 256 *GB RAM running Ubuntu* 18.04.2*.*

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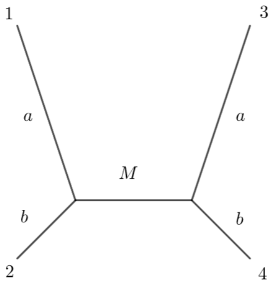
Algorithm

1. Compute the Euclidean distance degree d for the variety $\mathcal{V}_T$.
2. Compute the d critical points x such that $\nabla f(x) = 0$ and $x \in \Omega$.
3. Compute the critical points $\nabla f = 0$ at the boundaries $\partial\Omega$.
4. Choose point with the lowest value when evaluated at f.

Simulations

- We took trees with branch lengths a and b at the exterior edges. M is a JC matrix with eigenvalue $m \in [0.94, 1.06]$.
- For each set of parameters we considered 100 data points, each corresponding to 10000 independent samples from the corresponding multinomial distribution.



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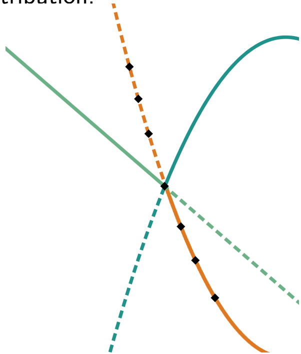
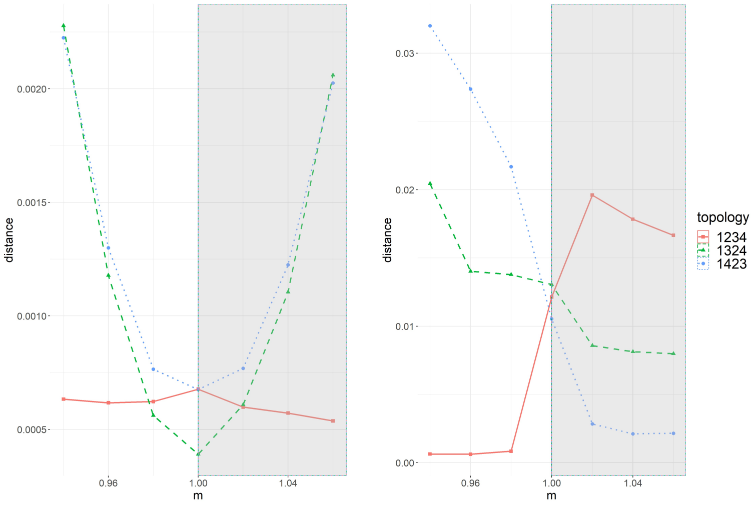
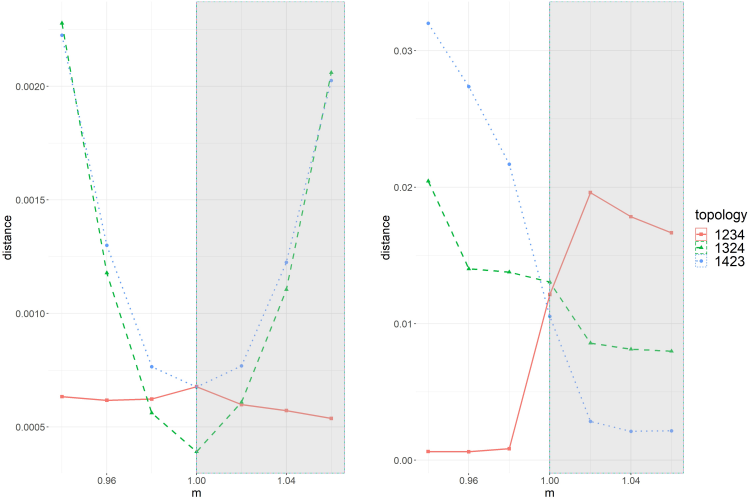


Simulations a = 0.5 & b = 0.5



Simulations a = 0.75 & b = 0.1



Stochastic conditions for the General Markov Model

Theorem [Allman – Rhodes – Taylor]

Let $P = \varphi_{\mathcal{T}}(\pi, \{M_e\}_{e\in E(\mathcal{T})})$ be a 4-tensor that arises from nonsingular real parameters for $GM(\kappa)$ model on $T_{12|34}$. If the marginalizations $P_{+\dots}$ and $P_{\dots+}$ arise from stochastic parameters and, moreover, the $\kappa^2 \times \kappa^2$ matrix

$$Flatt_{13|24}\left(P *_2 (adj(P^T_{+..+})P^T_{.+.+}) *_3 (adj(P_{.+.+})P_{.++.})\right)$$

is positive semidefinite, then P arises from stochastic parameters.

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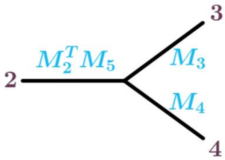

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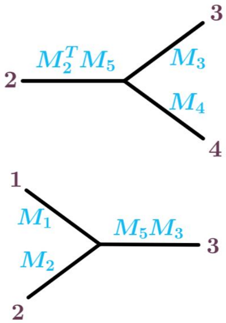

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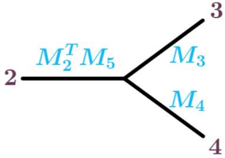

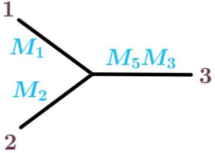

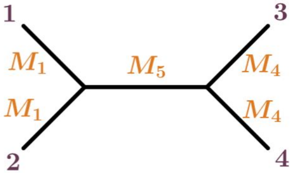

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Let $P = \varphi_{\mathcal{T}}(\pi, \{M_e\}_{e \in E(\mathcal{T})})$ be a 4-tensor for $GM(\kappa)$ model on $T_{12|34}$. Let $\tilde{P}$ be constructed as in the previous theorem. Then,

$$Flat_{13|24}(\tilde{P}) = Flat_{14|23}(\tilde{P}),$$

and

$$Flatt_{12|34}(\tilde{P}) \neq Flatt_{13|24}(\tilde{P}).$$

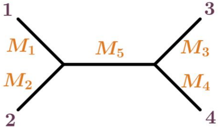
In particular

$$\begin{aligned} & det(P_{+..+})det(P_{.+.+})Flatt_{13|24}\big(P *_2 (adj(P^T_{+..+})P^T_{.+.+})) *_3 (adj(P_{.+.+})P_{.++.}))) \\ =& det(P_{+..+})det(P_{.+.+})Flatt_{14|23}\big(P *_2 (adj(P^T_{+..+})P^T_{.+.+})) *_3 (adj(P_{.+.+})P_{.++.})) \end{aligned}$$

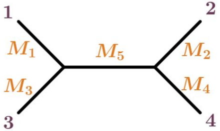
gives rise to 256 topology invariants of degree 17.

T Leaf-transformations

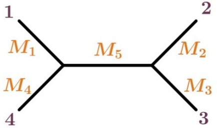
$T_{12|34}$



$T_{13|24}$

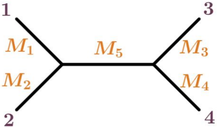


$T_{14|23}$



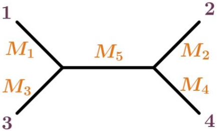
T Leaf-transformations

$T_{12|34}$



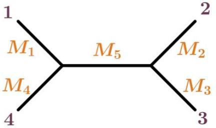
$\rightarrow \alpha_i^{12}(P_{12})$

$T_{13|24}$



$\rightarrow \alpha_i^{13}(P_{13})$

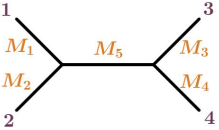
$T_{14|23}$



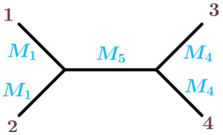
$\rightarrow \alpha_i^{14}(P_{14})$

T Leaf-transformations

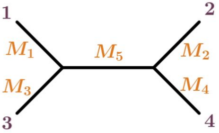
$T_{12|34}$



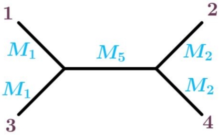
$\rightarrow \alpha_i^{12}(P_{12}) \rightarrow$



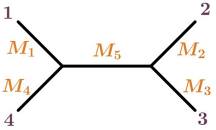
$T_{13|24}$



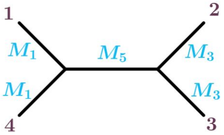
$\rightarrow \alpha_i^{13}(P_{13}) \rightarrow$



$T_{14|23}$

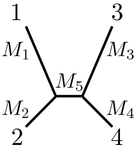


$\rightarrow \alpha_i^{14}(P_{14}) \rightarrow$

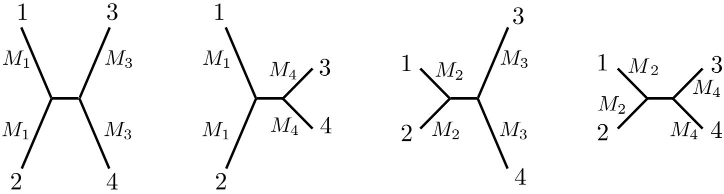


12|34 **Leaf-transformations**

Original tree T

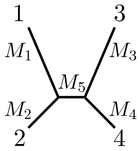


Resulting trees associated with the 12|34 leaf-transformations on the (theoretical) distribution from T

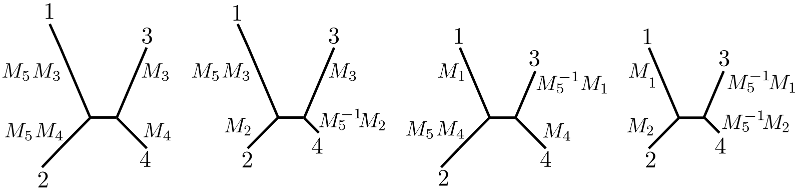


13|24 **Leaf-transformations**

Original tree T

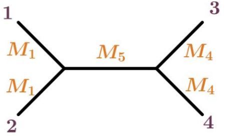


Resulting trees associated with some 13|24 leaf-transformations on the (theoretical) distribution from T

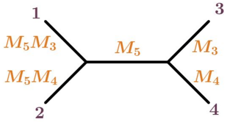


Leaf-transformations on distributions of $T = 12|34$

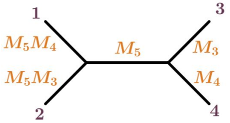
$\alpha_i^{12}(P)$



$\alpha_i^{13}(P)$

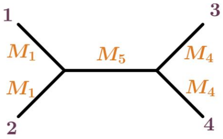


$\alpha_i^{14}(P)$



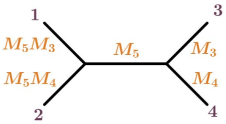
Leaf-transformations on distributions of $T = 12|34$

$\alpha_i^{12}(P)$



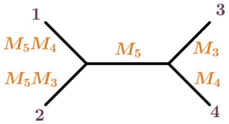
$$\Rightarrow \begin{cases} Flatt_{12|34}(\alpha_i^{12}(P)) & \rightarrow \quad \text{rank} \leq 4 \ \checkmark \\ Flatt_{13|24}(\alpha_i^{12}(P)) & \rightarrow \quad \text{rank} \leq 4 \ \text{✗} \\ Flatt_{14|23}(\alpha_i^{12}(P)) & \rightarrow \quad \text{rank} \leq 4 \ \text{✗} \end{cases}$$

$\alpha_i^{13}(P)$



$$\Rightarrow \begin{cases} Flatt_{13|24}(\alpha_i^{13}(P)) & \rightarrow \quad \text{rank} \leq 4 \ \text{✗} \\ Flatt_{12|34}(\alpha_i^{13}(P)) & \rightarrow \quad \text{rank} \leq 4 \ \checkmark \\ Flatt_{14|32}(\alpha_i^{13}(P)) & \rightarrow \quad \text{rank} \leq 4 \ \text{✗} \end{cases}$$

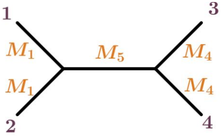
$\alpha_i^{14}(P)$



$$\Rightarrow \begin{cases} Flatt_{14|23}(\alpha_i^{14}(P)) & \rightarrow \quad \text{rank} \leq 4 \ \text{✗} \\ Flatt_{12|43}(\alpha_i^{14}(P)) & \rightarrow \quad \text{rank} \leq 4 \ \checkmark \\ Flatt_{13|42}(\alpha_i^{14}(P)) & \rightarrow \quad \text{rank} \leq 4 \ \text{✗} \end{cases}$$

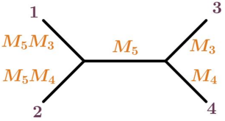
Leaf-transformations on distributions of $T = 12|34$

$\alpha_i^{12}(P)$



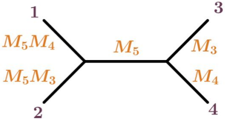
$$\Rightarrow \begin{cases} Flatt_{12|34}(\alpha_i^{12}(P)) & \rightarrow \quad \text{PSD ✗} \\ Flatt_{13|24}(\alpha_i^{12}(P)) & \rightarrow \quad \text{PSD ✓} \\ Flatt_{14|23}(\alpha_i^{12}(P)) & \rightarrow \quad \text{PSD ✓} \end{cases}$$

$\alpha_i^{13}(P)$



$$\Rightarrow \begin{cases} Flatt_{13|24}(\alpha_i^{13}(P)) & \rightarrow \quad \text{PSD ✗} \\ Flatt_{12|34}(\alpha_i^{13}(P)) & \rightarrow \quad \text{PSD ✗} \\ Flatt_{14|32}(\alpha_i^{13}(P)) & \rightarrow \quad \text{PSD ✗} \end{cases}$$

$\alpha_i^{14}(P)$



$$\Rightarrow \begin{cases} Flatt_{14|23}(\alpha_i^{14}(P)) & \rightarrow \quad \text{PSD ✗} \\ Flatt_{12|43}(\alpha_i^{14}(P)) & \rightarrow \quad \text{PSD ✗} \\ Flatt_{13|42}(\alpha_i^{14}(P)) & \rightarrow \quad \text{PSD ✗} \end{cases}$$

SAQ: semi-algebraic quartet reconstruction method

Theorem [Casanellas – Fernández-Sánchez – G-L]

The rank of the *psd* approximation of a real matrix M is less than or equal to $rank(M)$.

SAQ: semi-algebraic quartet reconstruction method

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The rank of the *psd* approximation of a real matrix M is less than or equal to $rank(M)$.

Lemma [Casanellas – Fernández-Sánchez – G-L]

Let P be the theoretical distribution from a 3-parameter Kimura process on the quartet tree $T = 12|34$. Then, the rank of the *psd* approximation of the flattening matrix $Flat_{T'}(\alpha^{T'}(P))$ is grater than 4 for $T' \neq T$.

SAQ: semi-algebraic quartet reconstruction method

SAQ method

Let P be a data point obtained from an alignment, then the score for $T = 12|34$ is:

$$s^{i}_{12|34} := \frac{\min\left\{\delta_4\left(psd\left(Flatt_{13|24}\left(\alpha_i^{12}(P)\right)\right)\right), \delta_4\left(psd\left(Flatt_{14|23}\left(\alpha_i^{12}(P)\right)\right)\right)\right\}}{\delta_4\left(psd\left(Flatt_{12|34}\left(\alpha_i^{12}(P)\right)\right)\right)}$$

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$$\text{and } s_{12|34} := \text{mean}_i\{s^i_{12|34}\}$$

SAQ: semi-algebraic quartet reconstruction method

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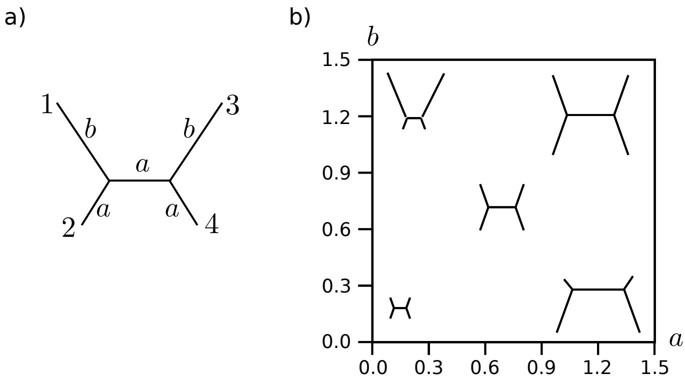
$$\text{and } s_{12|34} := \text{mean}_i\{s^i_{12|34}\}$$

$$\mathtt{SAQ}(P) := \frac{1}{s_{12|34}(P) + s_{13|24}(P) + s_{14|23}(P)}\left(s_{12|34}(P), s_{13|24}(P), s_{14|23}(P)\right).$$

If $Q \in \mathbb{R}^{256}$ is a distribution that tends to P generated on the tree $12|34$ with generic stochastic parameters, then

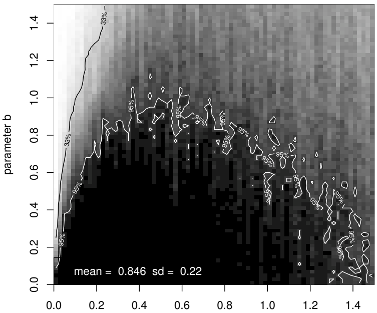
$$\lim_{Q \to P} \mathtt{SAQ}(Q) = \mathtt{SAQ}(P) = (1, 0, 0).$$

Simulations: Tree Space

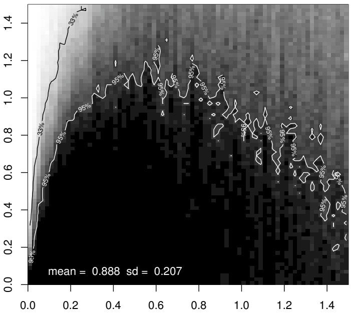


Simulations: Tree Space

GM; length 500 bp



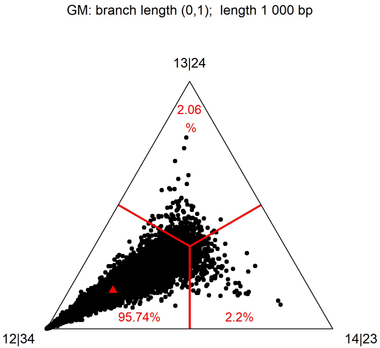
GM; length 1 000 bp



base pairs	SAQ	Erik+2	NJ	ML
500	84.6	72.4	72.5	72.1
1 000	88.8	80.3	79.7	73.6

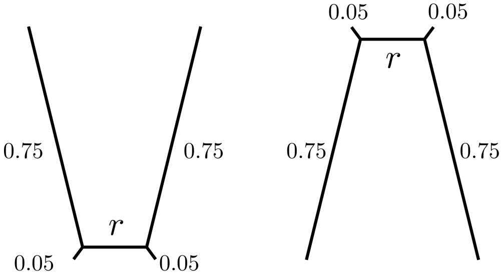
Simulations: Random branch lengths

A total of 10 000 alignments are considered, obtained from 4-taxa trees with random branch lengths uniformly distributed in the interval (0,1), and generated according to the General Markov substitution model.

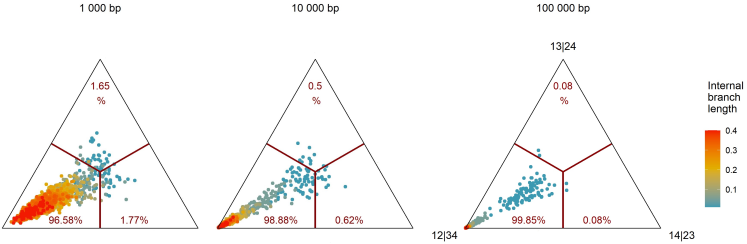


Simulations: Mixture models

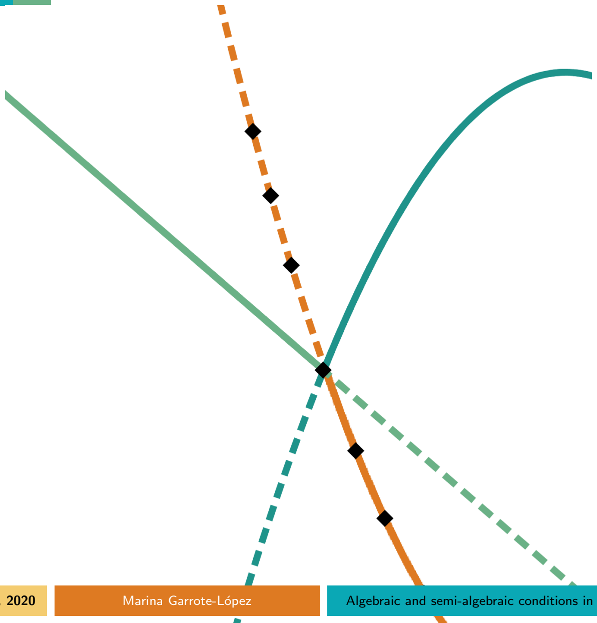
Mixture data



Simulations: Mixture models



internal branch length	0.01	0.05	0.1	0.2	0.3
SAQ	37	83	96	100	100
Erik+2 (2)	12	35	60	86	96
MP	0	2	19	76	99
ML(GTR+2 Γ)	0	4	14	77	95



Thanks for your attention!