# Fast and accurate branch length estimation for phylogenomic trees: ERaBLE (Evolutionary Rates and Branch Length Estimation)

Manuel Binet, Olivier Gascuel, Celine Scornavacca, Emmanuel J.P. Douzery, Fabio Pardi


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## (Evolutionary Rates and Branch Length Estimation).

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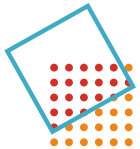
March 10, 2015



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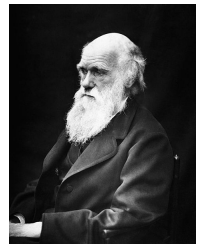
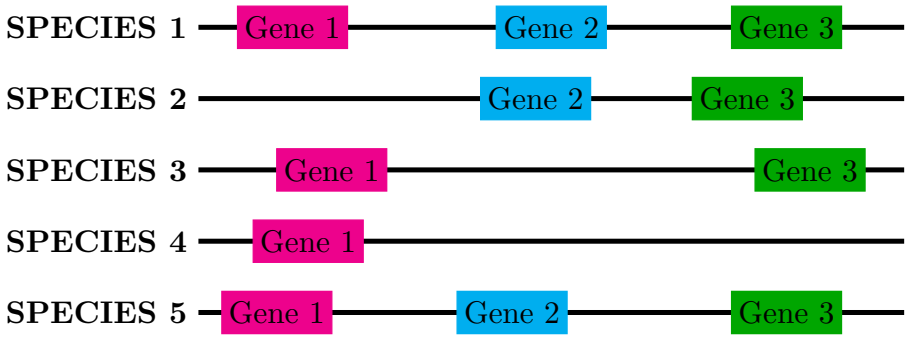
# The Phylogenomics era



Important goal: build the species tree.



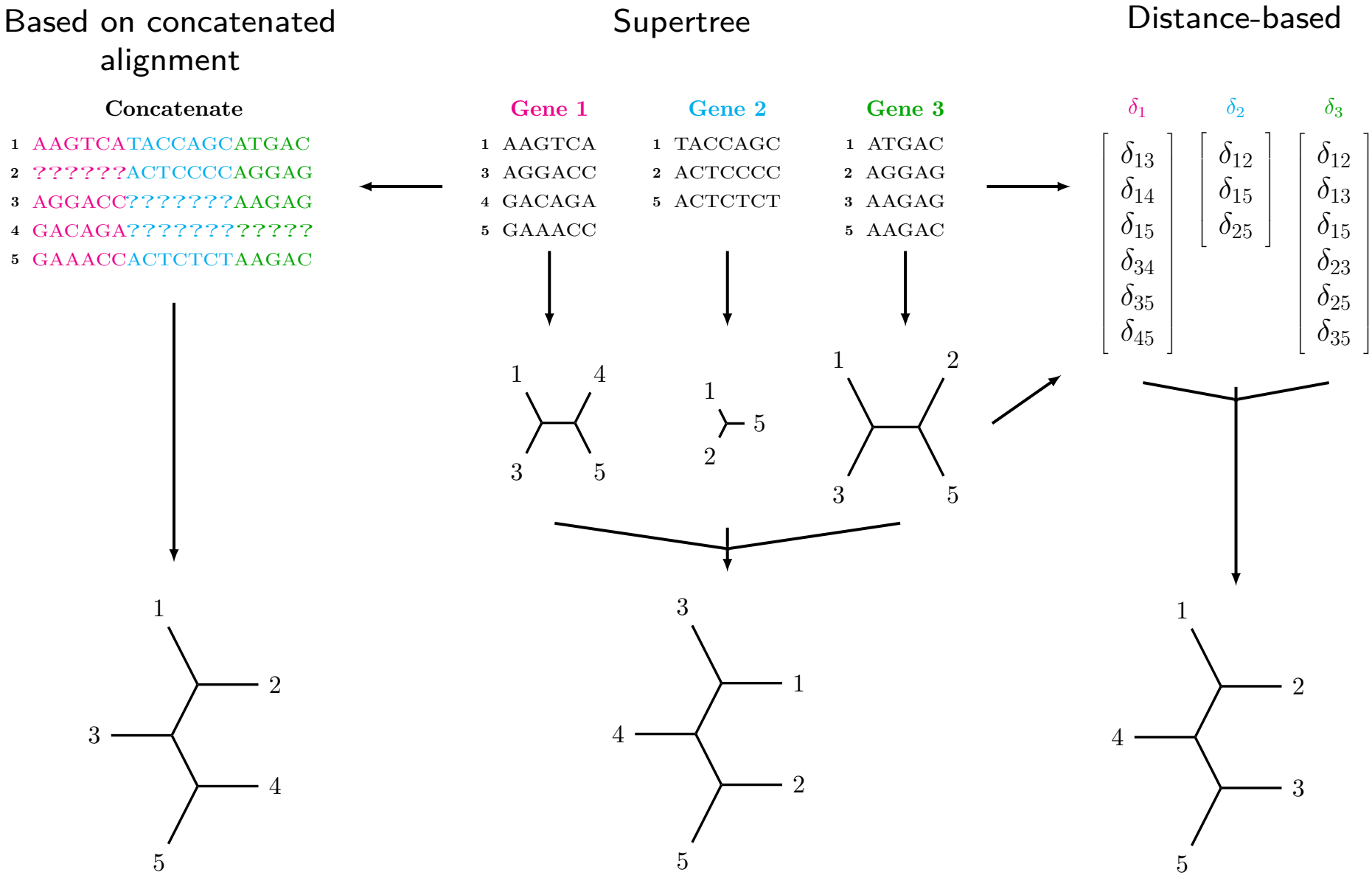

New challenges:

- Use the maximum of available data.
- Account for gene rate heterogeneity.
- Deal with conflicts in gene trees topologies.

...

ERaBLE (Evolutionary Rates and Branch Lengths estimation).

# Categories of phylogenomics methods



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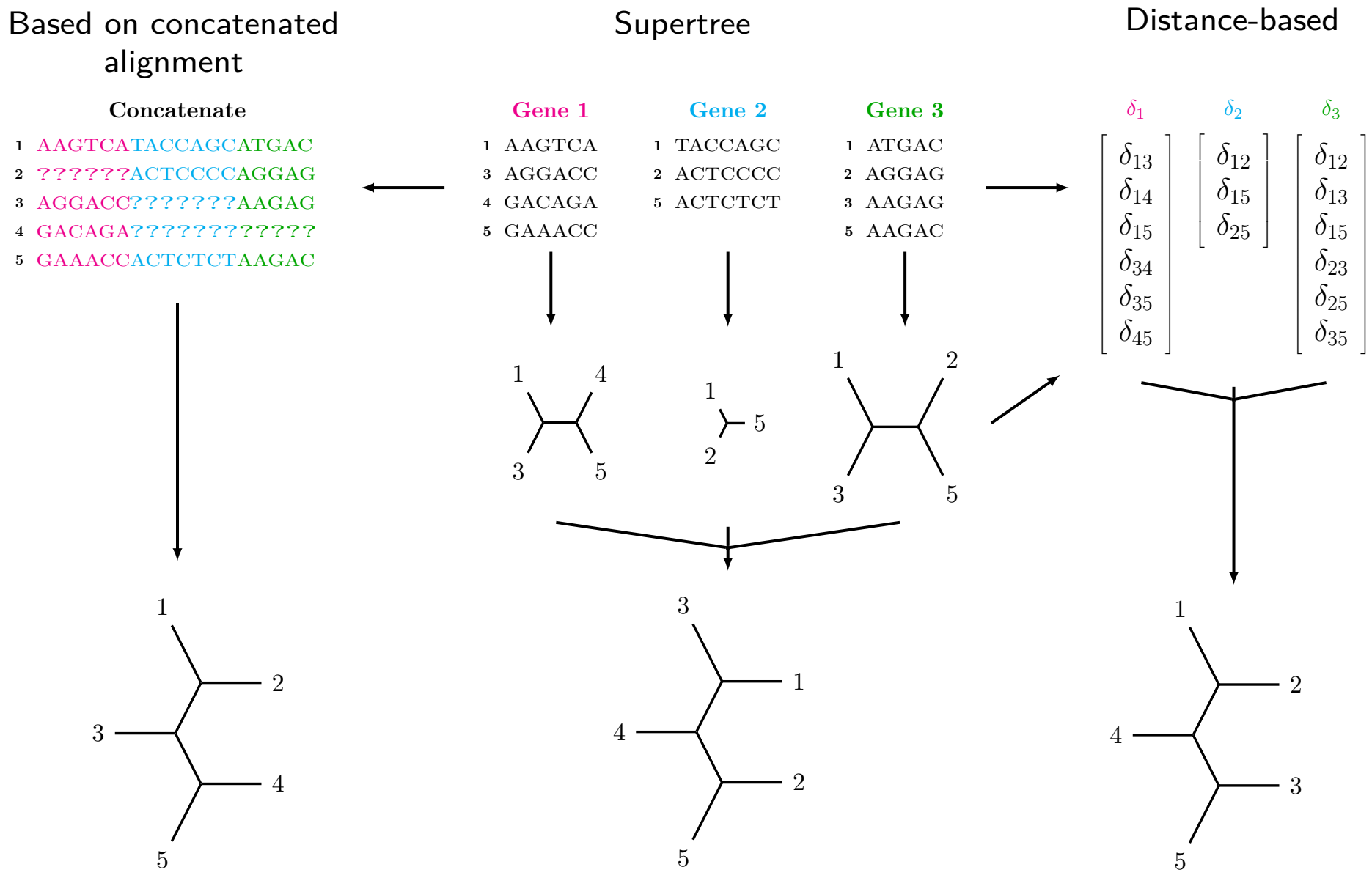



Branch lengths:

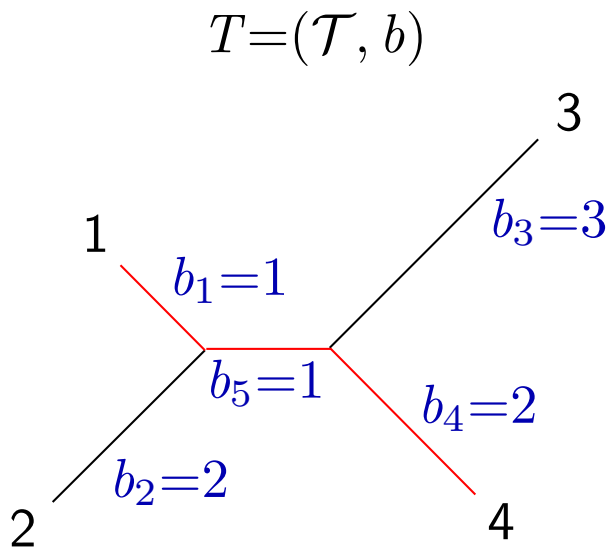
yes but computationally heavy

usually no

yes

# Tree distances

Every tree with branch lengths can be represented with a vector of tree distances by computing the distance $d_{ij}^T$ between each pair of taxa in the tree.




$\Leftrightarrow$

$$d^T = \begin{pmatrix} d_{12} = 3 \\ d_{13} = 5 \\ \mathbf{d_{14} = 4} \\ d_{23} = 6 \\ d_{24} = 5 \\ d_{34} = 5 \end{pmatrix}$$

Vector of tree distances

$$d_{ij}^T = \sum_{e \in P_{ij}} b_e$$

# Tree distances

Every vector of tree distances is the product of the topological matrix of $T$ by the branch lengths vector of $T$. i.e. $d^T = Ab$.

$$d^T = \begin{pmatrix} d_{12}=3 \\ d_{13}=5 \\ d_{14}=4 \\ d_{23}=6 \\ d_{24}=5 \\ d_{34}=5 \end{pmatrix}$$

Vector of tree distances

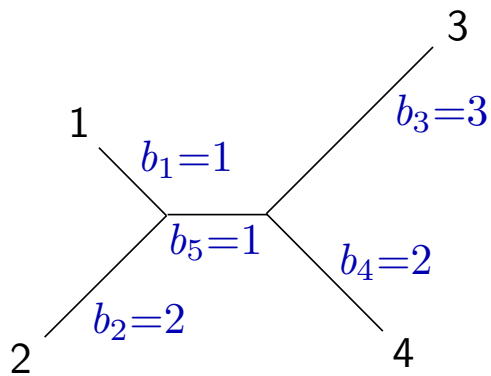
$$A = \begin{pmatrix} 1 & 1 & 0 & 0 & 0 \\ 1 & 0 & 1 & 0 & 1 \\ 1 & 0 & 0 & 1 & 1 \\ 0 & 1 & 1 & 0 & 1 \\ 0 & 1 & 0 & 1 & 1 \\ 0 & 0 & 1 & 1 & 0 \end{pmatrix}$$

Topological matrix

$$b = \begin{pmatrix} b_1=1 \\ b_2=2 \\ b_3=3 \\ b_4=2 \\ b_5=1 \end{pmatrix}$$

Branch lengths vector

$T=(\mathcal{T}, b)$



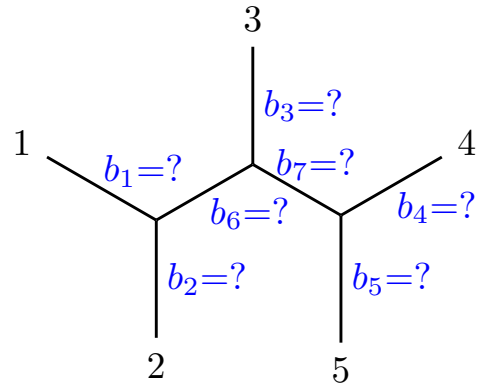

$d^T = Ab$

# A distance-based method : the weighted least square method (WLS)

Branch lengths estimation with WLS:

$$\delta = \begin{bmatrix} \delta_{12} = 0.140 \\ \delta_{13} = 0.163 \\ \delta_{14} = 0.288 \\ \delta_{15} = 0.336 \\ \delta_{23} = 0.188 \\ \delta_{24} = 0.413 \\ \delta_{25} = 0.411 \\ \delta_{34} = 0.298 \\ \delta_{35} = 0.213 \end{bmatrix}$$

input distances
(estimated from
1 gene alignment)




input topology

$$d^T = Ab$$

minimize $\sum_{ij} w_{ij}(\delta_{ij} - d_{ij}^T)^2$

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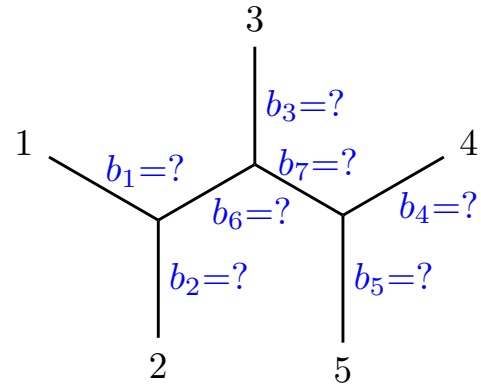


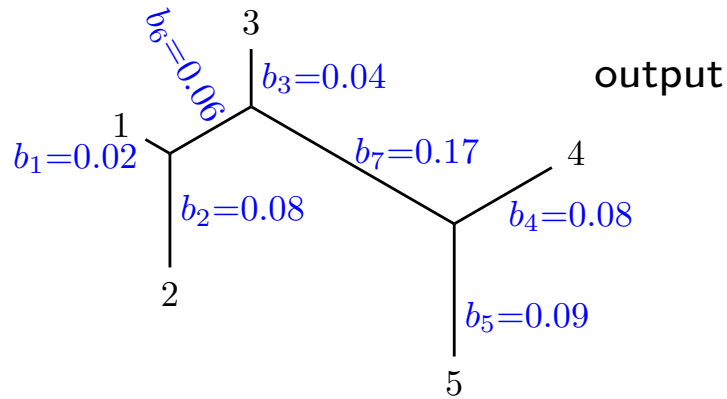

input topology

$$d^T = Ab$$

minimize $\sum_{ij} w_{ij}(\delta_{ij} - d_{ij}^T)^2$

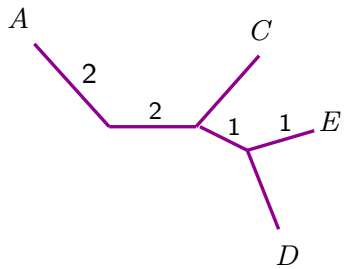
can be solved analytically in $\mathcal{O}(n^3)$

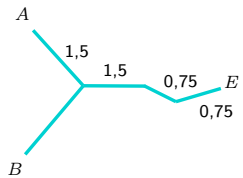
output

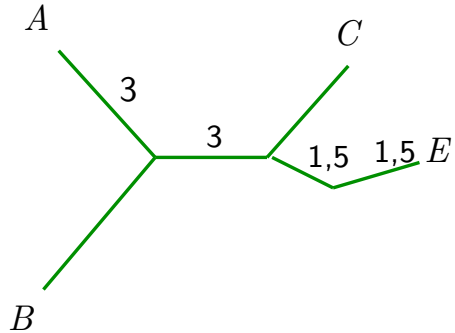


# New methode ERaBLE: Evolutionnary Rates and Branch Length Estimation

Hypothesis: Any gene $G_k$ induces approximately the same tree up to a scale factor $\alpha_k$ and the removal of a number of lineages.



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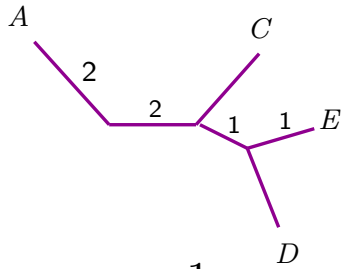
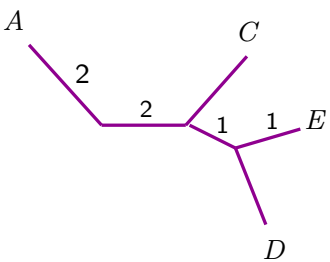
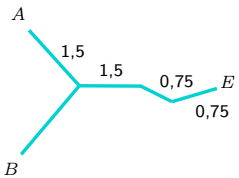



$\times\alpha_1=1$

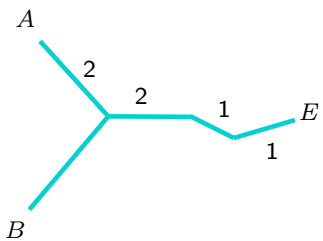
||

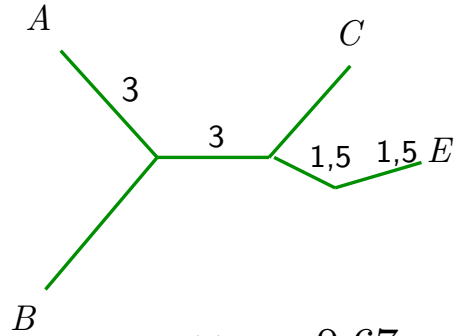



$\times\alpha_2=1.33$

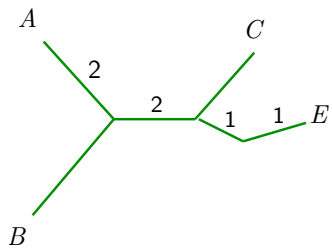
||




$\times\alpha_3=0.67$

||




After scaling

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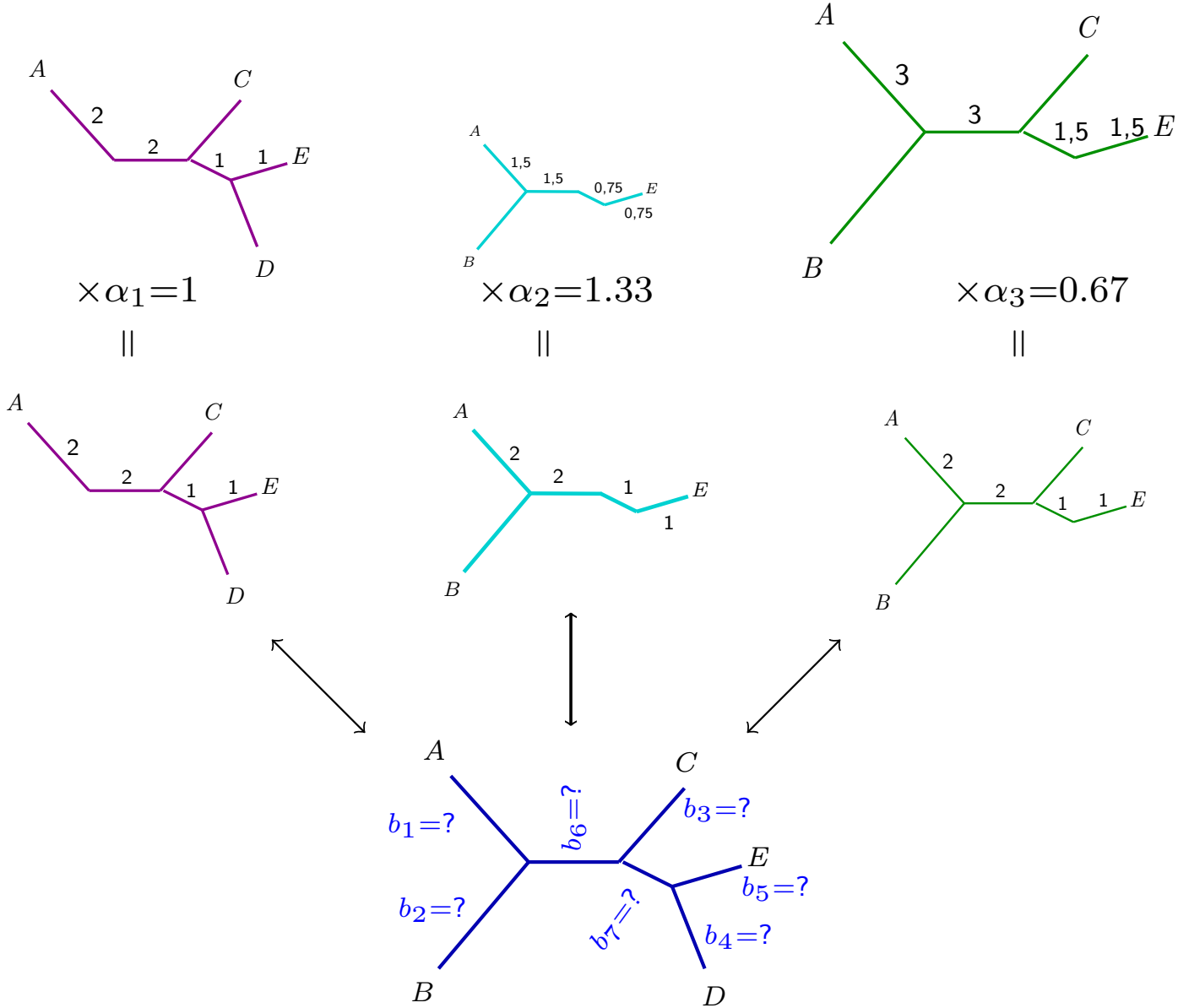


After scaling

# New methode ERaBLE: Evolutionnary Rates and Branch Length Estimation

Input data: $m$ distance vectors $\delta_1, \ldots, \delta_m$ where $\delta_k = (\delta_{ij}^{(k)})$ is defined on the taxa set $L_k$.

A given topology $\mathcal{T}$ defined on the taxa set $L = \bigcup_{k=1}^{m} L_k$.

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Objective: find

- the branch lengths $\hat{b}_1, \ldots, \hat{b}_{2n-3}$ of $\mathcal{T}$,
- the scale factors $\hat{\alpha}_1, \ldots, \hat{\alpha}_m$ of the $m$ genes,

solution of the problem:

$$\left\{ \text{minimize} \quad \sum_{k=1}^{m} \sum_{i,j \in L_k} w_{ij}^{(k)} (\hat{\alpha}_k \delta_{ij}^{(k)} - d_{ij}^{T})^2 \right.$$

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**Outputs:**

$$\hat{b}_e \quad \text{et} \quad \hat{r}_k = \frac{1}{\hat{\alpha}_k}$$

.

# Resolution of the optimization problem

The minimization problem can be solved with the method of Lagrange multipliers and leads to the linear system in $\mathcal{O}(n+m)$ equations and unknowns:

$$\begin{pmatrix} \delta_1^t W_1 \delta_1 & 0 & \cdots & 0 & [\ -\delta_1^t W_1 A_1\ ] & 1 \\ 0 & \delta_2^t W_2 \delta_2 & & \vdots & [\ -\delta_2^t W_2 A_2\ ] & 1 \\ \vdots & & \ddots & \vdots & \vdots & \vdots \\ 0 & \cdots & \cdots & \delta_m^t W_m \delta_m & [-\delta_m^t W_m A_m\ ] & 1 \\ [\ & [\ & [\ & [\ & \left[\begin{array}{c} \\ \\ \sum_{k=1}^{m} A_k^t W_k A_k \\ \\ \\ \end{array}\right] & 0 \\ -A_1^t W_1 \delta_1 & -A_2^t W_2 \delta_2 & \cdots & -A_m^t W_m \delta_m & & \vdots \\ ] & ] & ] & ] & & 0 \\ Z_1 & Z_2 & \cdots & Z_m & 0 \cdots 0 & 0 \end{pmatrix} \begin{pmatrix} \alpha_1 \\ \alpha_2 \\ \vdots \\ \alpha_m \\ b_1 \\ b_2 \\ \vdots \\ \\ \\ b_{2n-3} \\ \lambda \end{pmatrix} = \begin{pmatrix} 0 \\ \vdots \\ \vdots \\ \vdots \\ \vdots \\ \vdots \\ \vdots \\ \vdots \\ \vdots \\ 0 \\ 1 \end{pmatrix}$$

- Filling the matrix and standard system solving in $\mathcal{O}((n+m)^3 + mn^4)$
- Solving in $\mathcal{O}(n^3 + mn^2)$ with our algorithms:
  - Filling the matrix in $\mathcal{O}(mn^2)$ instead of $\mathcal{O}(mn^4)$
  - Block-solving system in $\mathcal{O}(n^3)$ instead of $\mathcal{O}(n+m)^3$

$m$=# genes
$n$=# taxa

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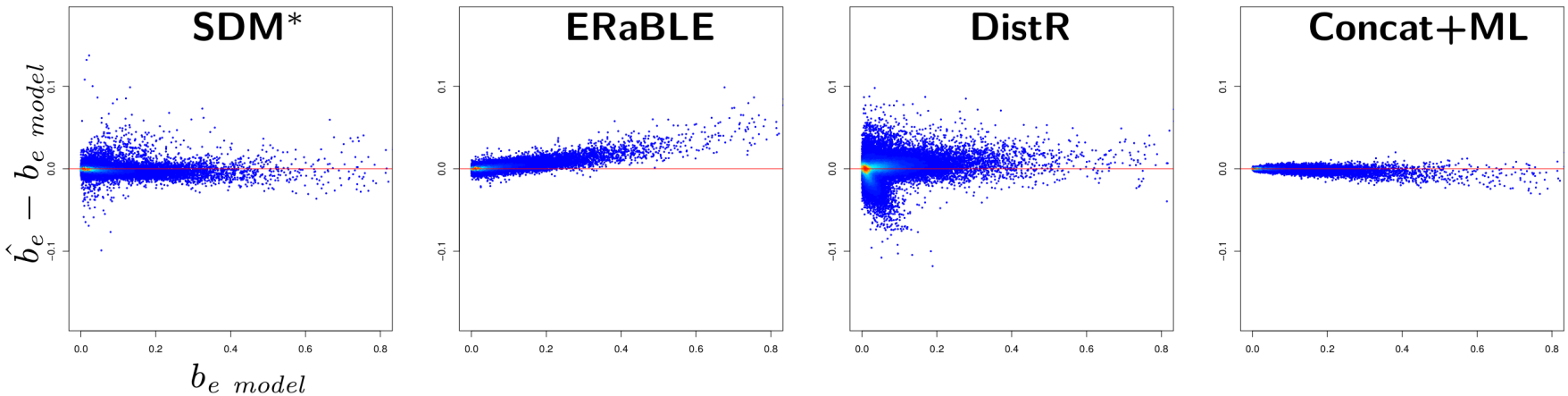
$m$=# genes
$n$=# taxa

Complexity: ERaBLE $\mathcal{O}(n^3 + mn^2)$ vs. WLS $\mathcal{O}(n^3)$

# Results on a simulated dataset

input data: $m$=500 genes defined on $n \in [4, 40]$ taxa + model topology (500 replicates).

Accuracy in the estimation of branch lengths:




Compared methods (after adaptation):

- SDM* [Criscuolo et al. 2006]. Phylogenomic distance-based method,
- DistR [Bevan et al. 2005]. Distance-based method for the estimation of gene rates,
- Concat+ML. PhyML [Guindon et al. 2010] analysis of the concatenated alignments.

# Results on a simulated dataset

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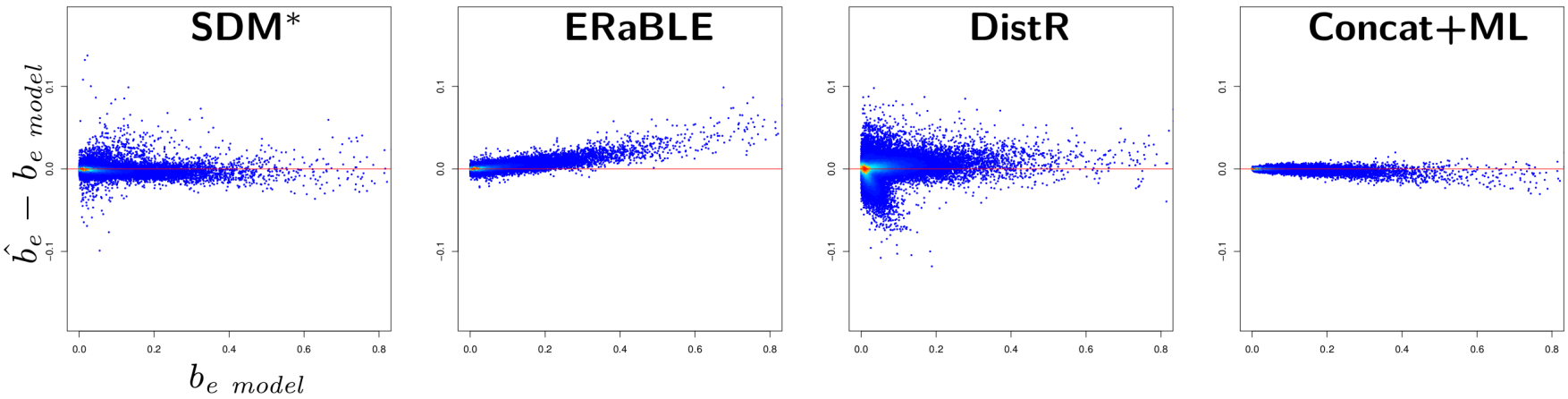
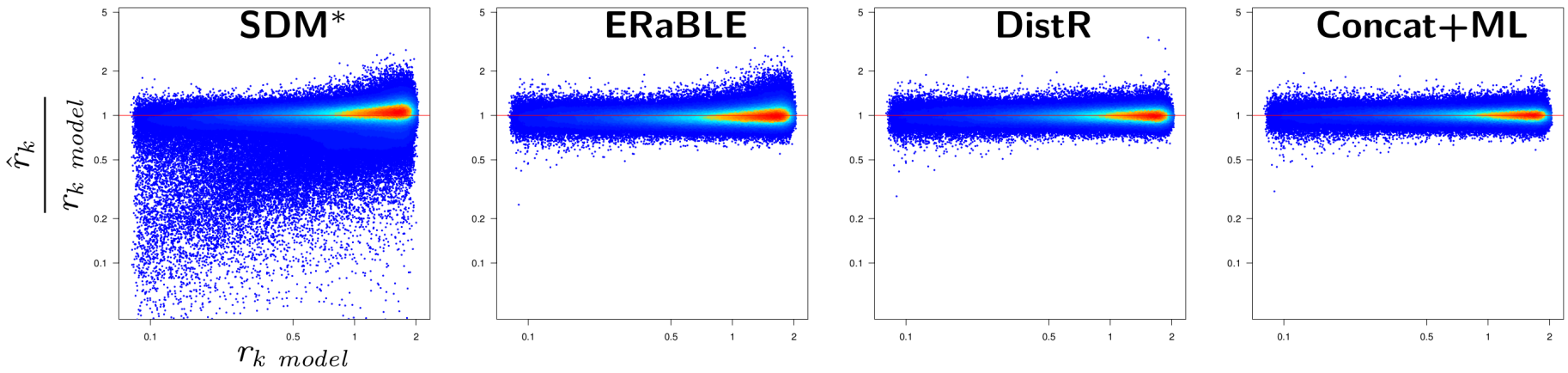


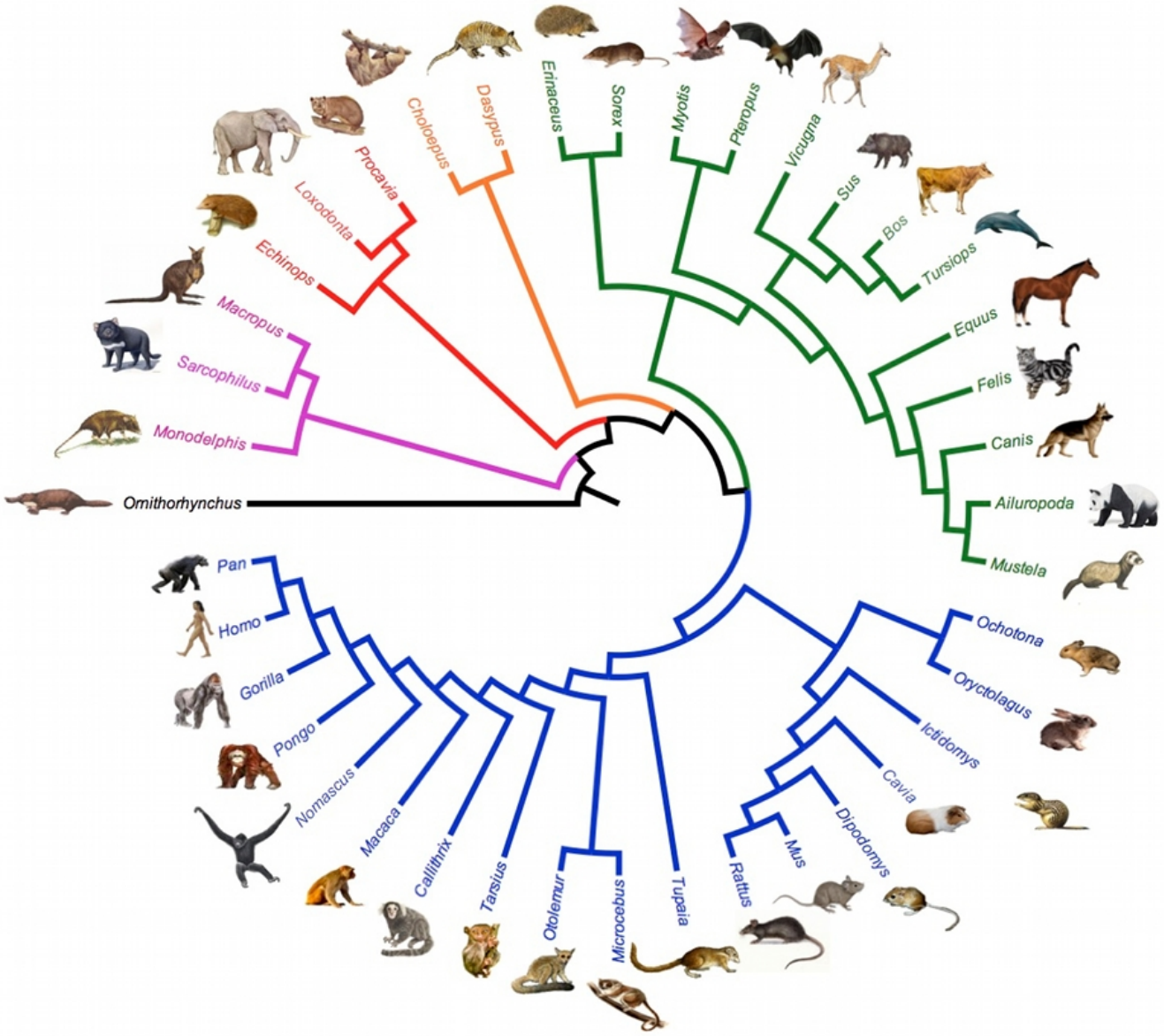

Accuracy in the estimation of gene rates (logarithmic scale):



# Results on the OrthoMaM dataset [Douzery et al. 2014]

input data: $m$=6953 nucleotide exon alignments over $n$=4 to 40 mammals.

input topology: the topology of the 40 mammals present in OrthoMaM:

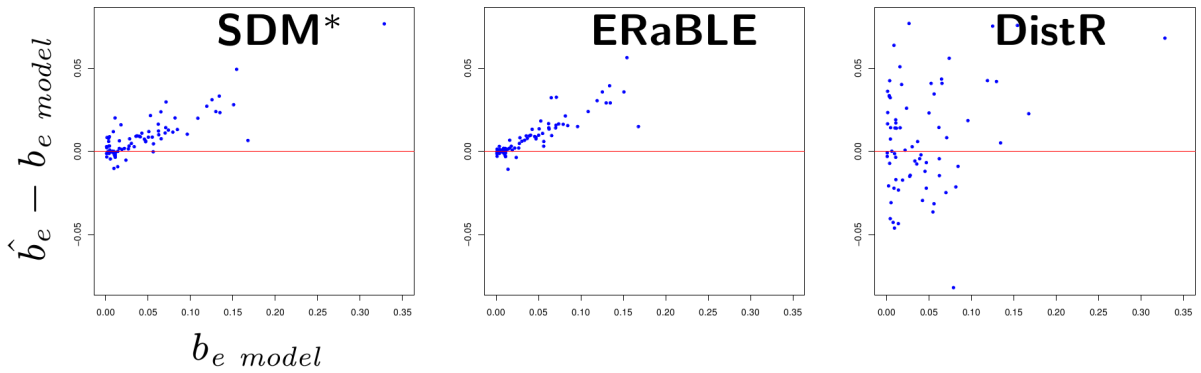


# Results on the OrthoMaM dataset

| | SDM* | ERaBLE | DistR | Concat+ML |
|---|---|---|---|---|
| Running times | 8h33m⋆ | 7s⋆ | 2h8m⋆ | 41h16m |
| RAM | 1.2 GB | 221 MB | 3 GB | 488 GB |

⋆ add 2min46s for the 6953 input distances estimation

Accuracy in the estimation of branch lengths:




Concat+ML as model

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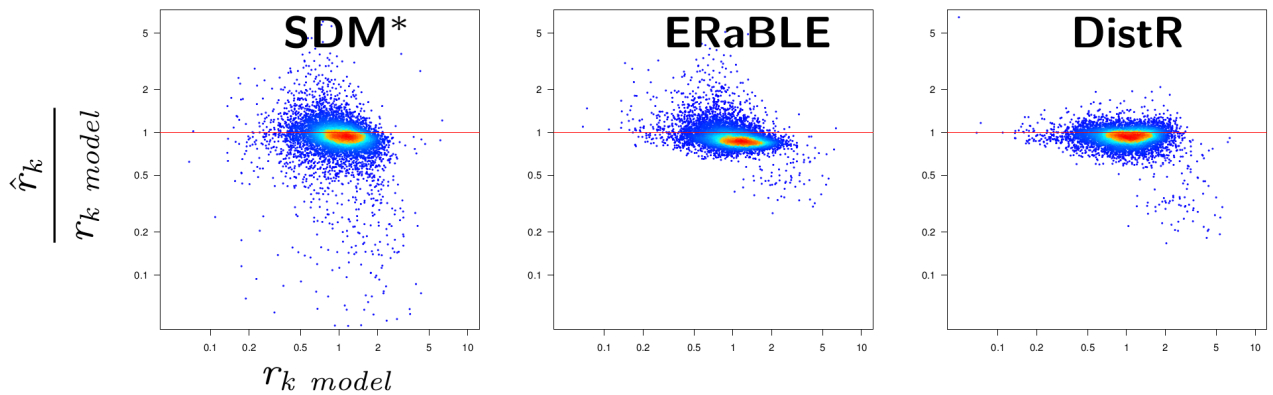


Concat+ML as model

# Conclusion

ERaBLE gives branch lengths to phylogenomic trees (e.g. estimated with supertree methods).

ERaBLE is relatively accurate in the estimations of branch lengths and of gene rates.

ERaBLE is fast with a complexity in $\mathcal{O}(n^3 + mn^2)$ (linear in $m$).

# Thank you for your attention.

Any questions?

Fundings: