

PhySIC_IST: cleaning source trees to infer more informative supertrees.

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University of Montpellier II

June 16, 2008



Reconstruction of phylogenies

- INPUT: (different) source datasets

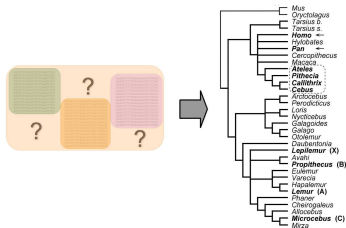
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Reconstruction of phylogenies for multiple datasets

Two main approaches

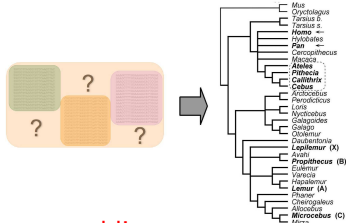
- Supermatrix approach: **assembling datasets**



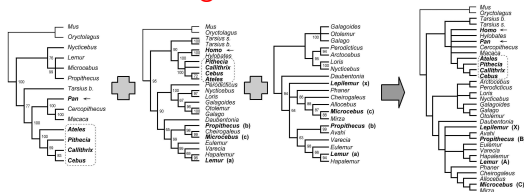
Reconstruction of phylogenies for multiple datasets

Two main approaches

- Supermatrix approach: **assembling datasets**



- Supertree approach: **assembling trees**



Interest of supertrees

Supertrees are useful for:

- Combining heterogeneous data
- Obtaining a phylogeny using several genes:
 - ▶ Avoids having to deal with too much missing data
 - ▶ Evolutionary models adapted for each gene sequence
- Pointing out problematic areas of the phylogeny
 - ▶ agreement and disagreement among input trees.
 - ▶ measuring taxon overlap

Supertree methods

VOTE vs VETO methods

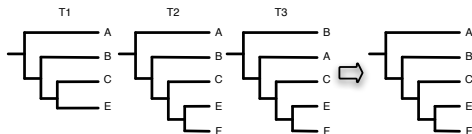
Supertree methods can be classified into two categories, depending on the way they deal with incongruent data:

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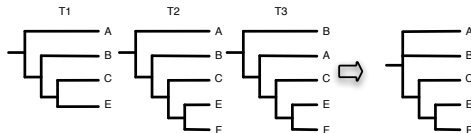
- **Vote** methods resolve conflicts, opting for the resolution that maximizes their optimization criteria.
- **worrying feature**: this approach can lead to propose clades contradicting all source trees.



Supertree methods

VOTE vs VETO methods

- Veto methods do not allow the resulting supertree to contain clades that a source tree would vote against.
 - ▶ pruning some taxa:
OR
 - ▶ proposing multifurcations
- worrying feature: this approach can lead to propose unresolved supertrees.



PhySIC

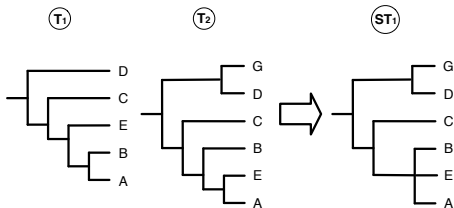
A VETO method with desirable properties

- The resulting supertree does not contain relationships contradicting the source trees (**non-contradiction** property, denoted by **PC**);

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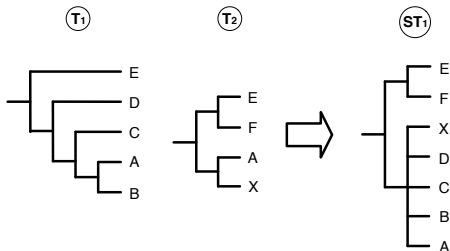
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PhySIC

A VETO method with desirable properties

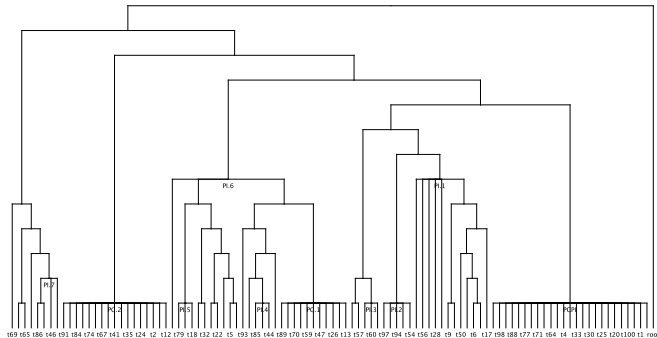
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PhySIC

A VETO method with UNdesirable proprieties

- BUT**, when \mathcal{T} contains numerous contradictions or small overlap, the supertrees built with *PhySIC* can be highly unresolved.



An improved version of *PhySIC*

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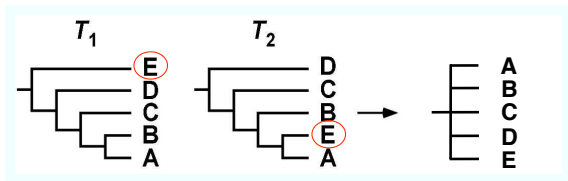
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 - AND
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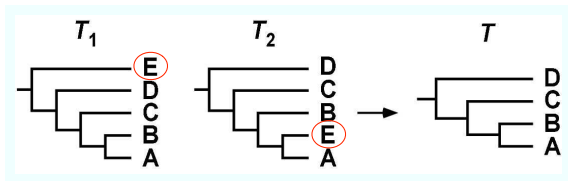
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PhySIC_IST

Outline of *PhySIC_IST*

- *PhySIC_IST* (*PHYlogenetic Signal with Induction and non-Contradiction Inserting a Subset of Taxa*) is an algorithm that operates successive insertions of taxa on a backbone tree.

PhySIC_IST

Outline of *PhySIC_IST*

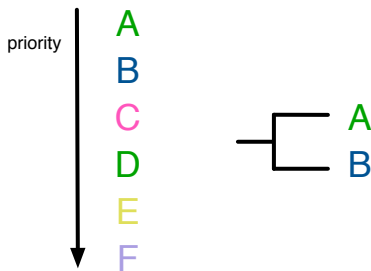
- *PhySIC_IST* (*PHYlogenetic Signal with Induction and non-Contradiction Inserting a Subset of Taxa*) is an algorithm that operates successive insertions of taxa on a backbone tree.

the order of the insertions has to be chosen carefully!

PhySIC_IST

Outline of *PhySIC_IST*

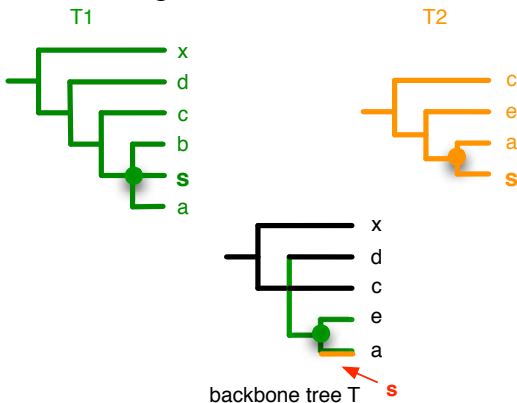
- We order taxa in decreasing priority order
- The first taxa to be inserted are those present in as much source trees as possible and involved in as few contradictions as possible
- We build the backbone tree



PhySIC_IST

Supports

- Within which region of the backbone tree can a taxon s be inserted without contradicting T_1 and T_2 ?



PhySIC_IST

Outline of *PhySIC_IST*

- one best supported position (PI) and all trees agree (PC)

PhySIC_IST

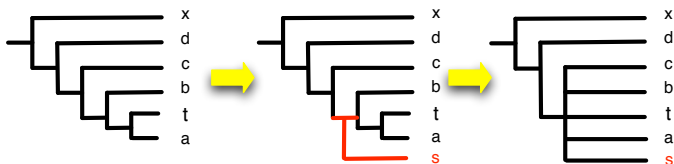
Outline of *PhySIC_IST*

- one best supported position (PI) and all trees agree (PC)
- more than one best supported position and/not all trees agree (PI and PC???)

PhySIC_IST

Outline of PhySIC_IST

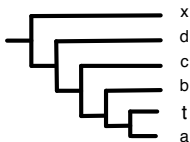
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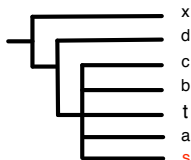
PhySIC_IST

Outline of PhySIC_IST

- one best supported position (PI) and all trees agree (PC)
- more than one best supported position and/or not all trees agree (PI and PC???)



VS



PhySIC_IST

CIC criterion

- We need to evaluate the amount of information of a tree.

PhySIC_IST

CIC criterion

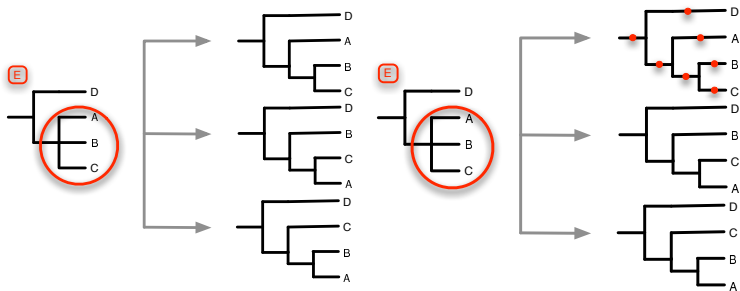
- We need to evaluate the amount of information of a tree.
- We use a variant of the CIC criterion (Thorley, Wilkinson, Charleston 1998) that also takes into account missing taxa and we define it as:

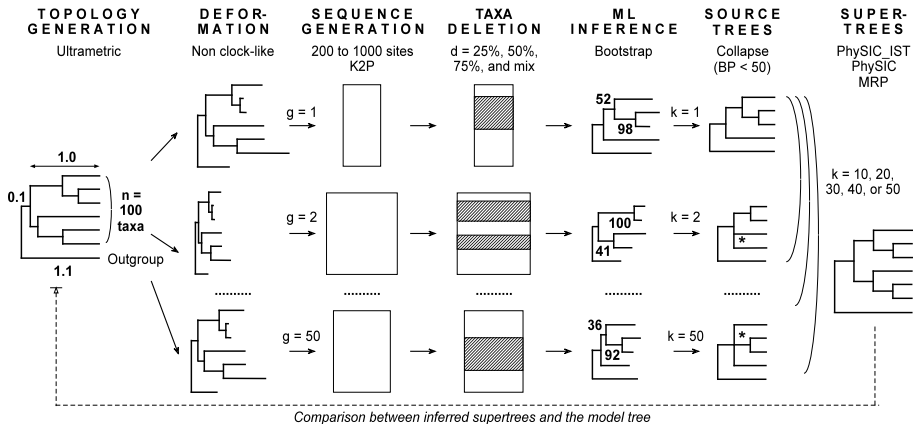
PhySIC_IST

CIC criterion

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- We use a variant of the CIC criterion (Thorley, Wilkinson, Charleston 1998) that also takes into account missing taxa and we define it as:

$$CIC(T, n) = -\lg \frac{\text{number of permitted binary trees with } n \text{ taxa}}{\text{number of possible binary trees with } n \text{ taxa}}$$

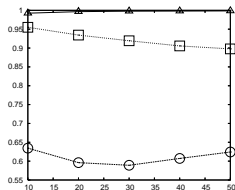




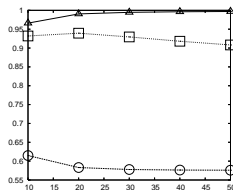
Large-scale simulations

Average *CIC* values

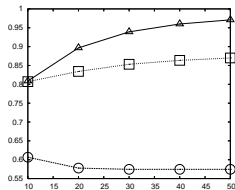
MRP \triangle , *PhySIC* \circ , *PhySIC_IST* \square



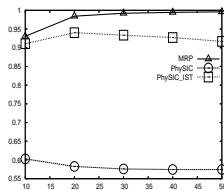
$d = 25\%$



$d = 50\%$



$d = 75\%$

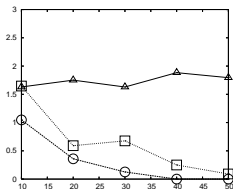


mixed d

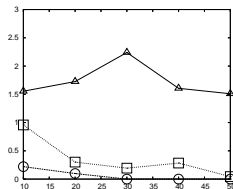
Large-scale simulations

Average percentage of type I error

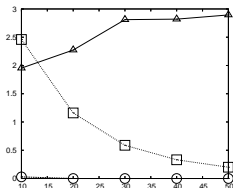
MRP \triangle , *PhySIC* \circ , *PhySIC_IST* \square



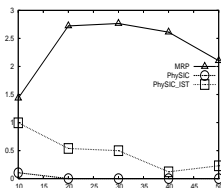
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mixed d

MRP \triangle
PhySIC \circ
PhySIC_IST \square

The improvement of *PhySIC_IST* on *PhySIC*

The improvement of *PhySIC_IST* on *PhySIC* is a consequence of three fundamental differences between them:

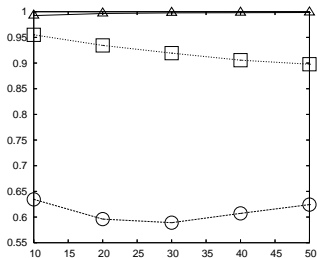
- the new version operates successive insertions of taxa on a backbone and is not based on a revised version of the Build algorithm (unlike *PhySIC*)
- the two methods do not have the same optimization criterion
 - ▶ *PhySIC* \Rightarrow nb of triplets
 - ▶ *PhySIC_IST* \Rightarrow *CIC*
- *PhySIC_IST* can propose non-plenary supertrees

- 1 Introduction
 - Combining data for phylogenetic inferences
 - Vote methods
 - Veto methods
- 2 VETO methods with desirable proprieties
 - Physic
 - *PhySIC_IST*
- 3 STC preprocess

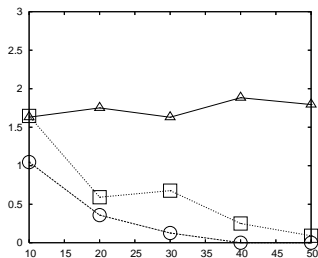
Limits of veto methods

- As the amount of available information continues to increase, the number of conflicts between source trees increases

MRP \triangle , *PhySIC* \circ , *PhySIC-IST* \square

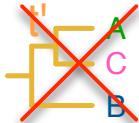
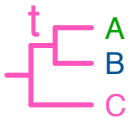
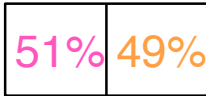


informativeness

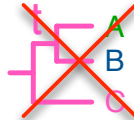
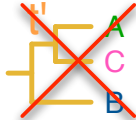
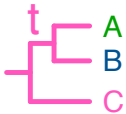


inaccuracy

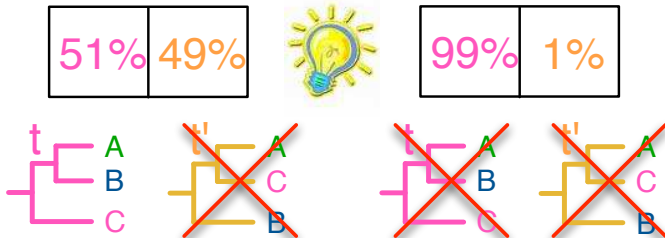
Vote VS veto methods?



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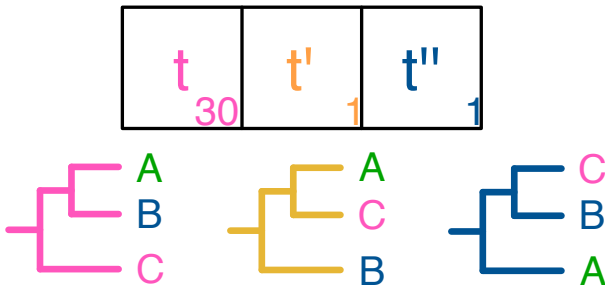
Vote VS veto methods?



- **IDEA:** flexible liberal(voting) preprocessing of the input trees before a veto approach.

Source Tree Correction (STC) preprocess

We want to drop the statistically less supported alternative(s), if any exists.



STC preprocess

- After that, the STC preprocess modifies the source trees (*PhySIC_IST*), forcing them not to contain the dropped resolutions.

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- Each modified tree may contain either new multifurcations, or lack some of its former taxa.

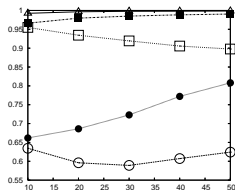
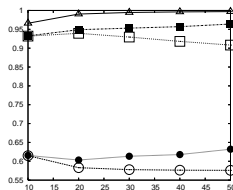
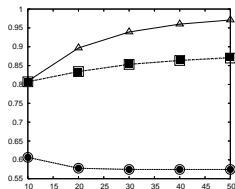
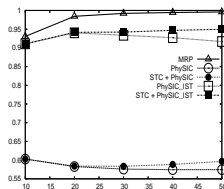
STC preprocess

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- A threshold α is chosen by the user.

VOTE

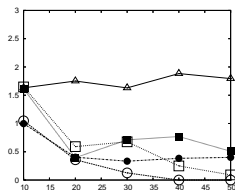
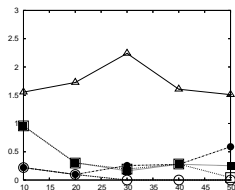
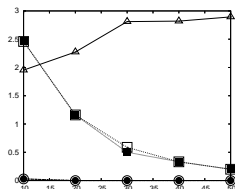
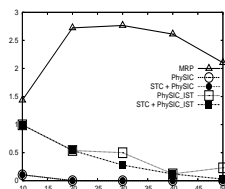
VETO



Large-scale simulations ($\alpha = 0.05$)Average *CIC* valuesMRP \triangle , *PhySIC* \circ , *PhySIC_IST* \square , STC+ *PhySIC* \bullet and STC+ *PhySIC_IST* \blacksquare  $d = 25\%$  $d = 50\%$  $d = 75\%$ mixed d

Large-scale simulations ($\alpha = 0.05$)

Average percentage of type I error

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Conclusions

- *PhySIC_IST*: new version of *PhySIC*
 - ▶ more informative but still reliable supertrees
- STC: a statistical preprocess of the source trees to detect and correct artifactual positions of taxa
- This approach has the advantage of separating the liberal resolution of conflicts in the data from the assemblage of the supertree.
 - ▶ feedback of the source trees
- Test STC+ *PhySIC_IST* on biological datasets

Conclusions

- http://www.atgc-montpellier.fr/physic_ist/

The screenshot shows the PhysIC_IST server interface. At the top, there is a header with the ATGC logo and the ISEM logo. Below the header, the text reads "LIRMM Montpellier bioinformatics platform ISEM". The main content area is titled "PhysIC_IST server: healing source trees to infer healthy supertrees." and includes the following information:

- Authors: Scornavacca C., Berry V., Douzery E.J.P., Ranwez V.
- Submitted to BMC Bioinformatics.
- Please cite THIS paper if you use PhysIC_IST.

The interface also features a "PhysIC_IST online execution" section with the following fields and options:

- Source tree file: File Example file
- Backbone tree file (optional):
- Outgroup file (optional):
- File format: UNIX Windows Mac
- Bootstrap threshold for source clade selection: 0
- Correction threshold used by STC: 0.9
- Your name:

A left sidebar contains a navigation menu with the following items: Home, Organization, Citations & Statistics, Online programs, PhysIC_IST, PhysIC_IST Downloads, Online execution, Papers & contacts, User's guide, Binaries, Databases, and Datasets.

Thanks

- Olivier Gascuel and Vincent Lefort
- Céline Brochier, Vincent Daubin and Férédric Delsuc