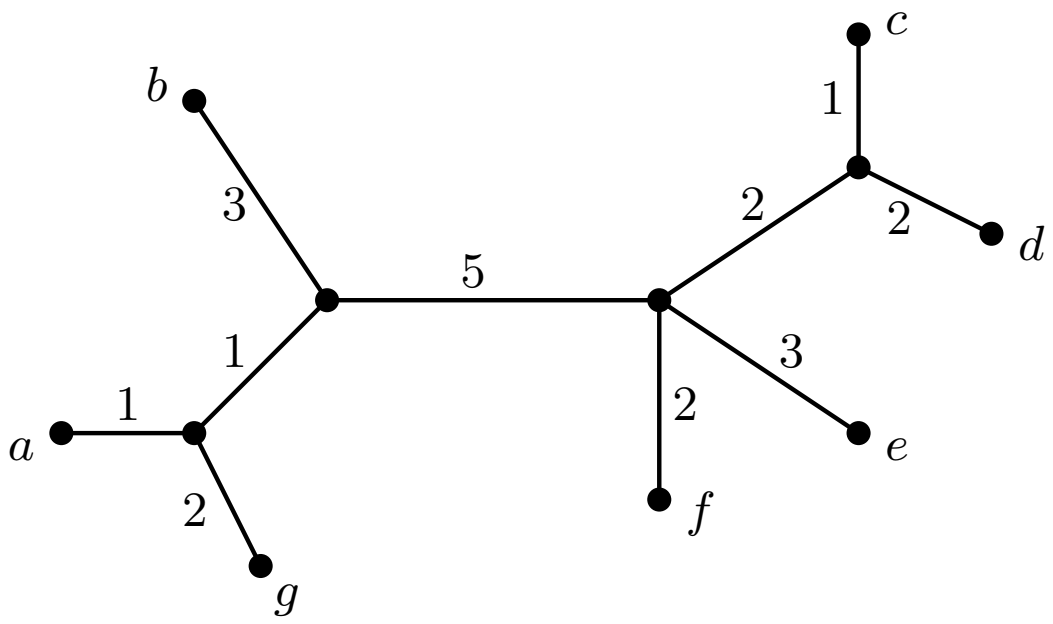
Consistency and Balanced Minimum Evolution

Newton Institute – Sept. '07

Magnus Bordewich

Joint work with O. Gascuel, K. Huber, V. Moulton

Reconstructing trees from a distance matrix



We are interested in the evolutionary history of a set of taxa X.

We are given an estimated distance matrix $\Delta = [\delta_{ij}]$.

Goal: to reconstruct the true phylogenetic tree $\mathcal{T}^*$ for the set X.

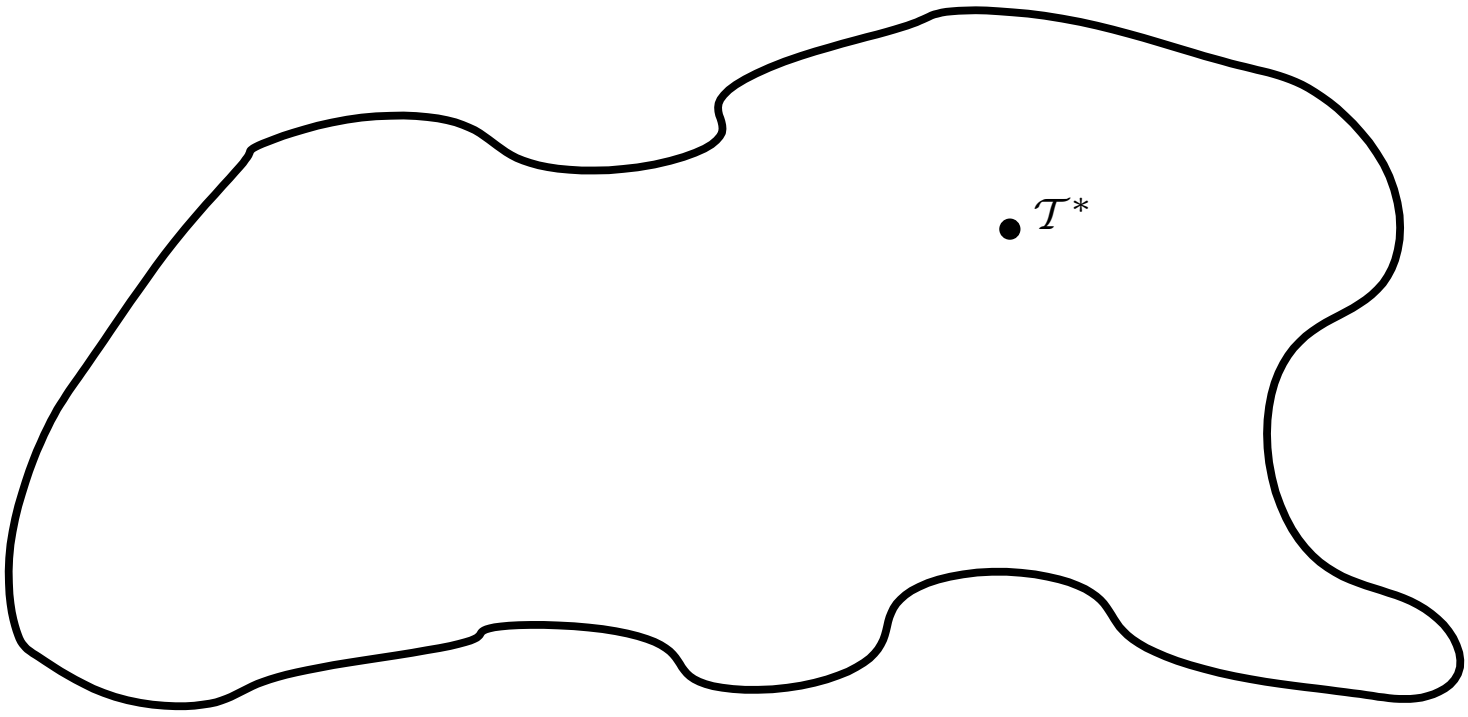
Balanced Minimum Evolution (BME) principle

BME introduced by Desper and Gascuel (2002), based on a tree length estimation scheme of Pauplin (2000).

- We are given the estimated matrix Δ.
- For a topology $\mathcal{T}$ we can estimate the branch lengths ($\hat{l}(e)$).
- We want the topology of smallest total length ($\sum_e \hat{l}(e)$).
- NJ greedily minimises this tree length.

Idea: find this minimal tree using a local topology search.

Local topology search



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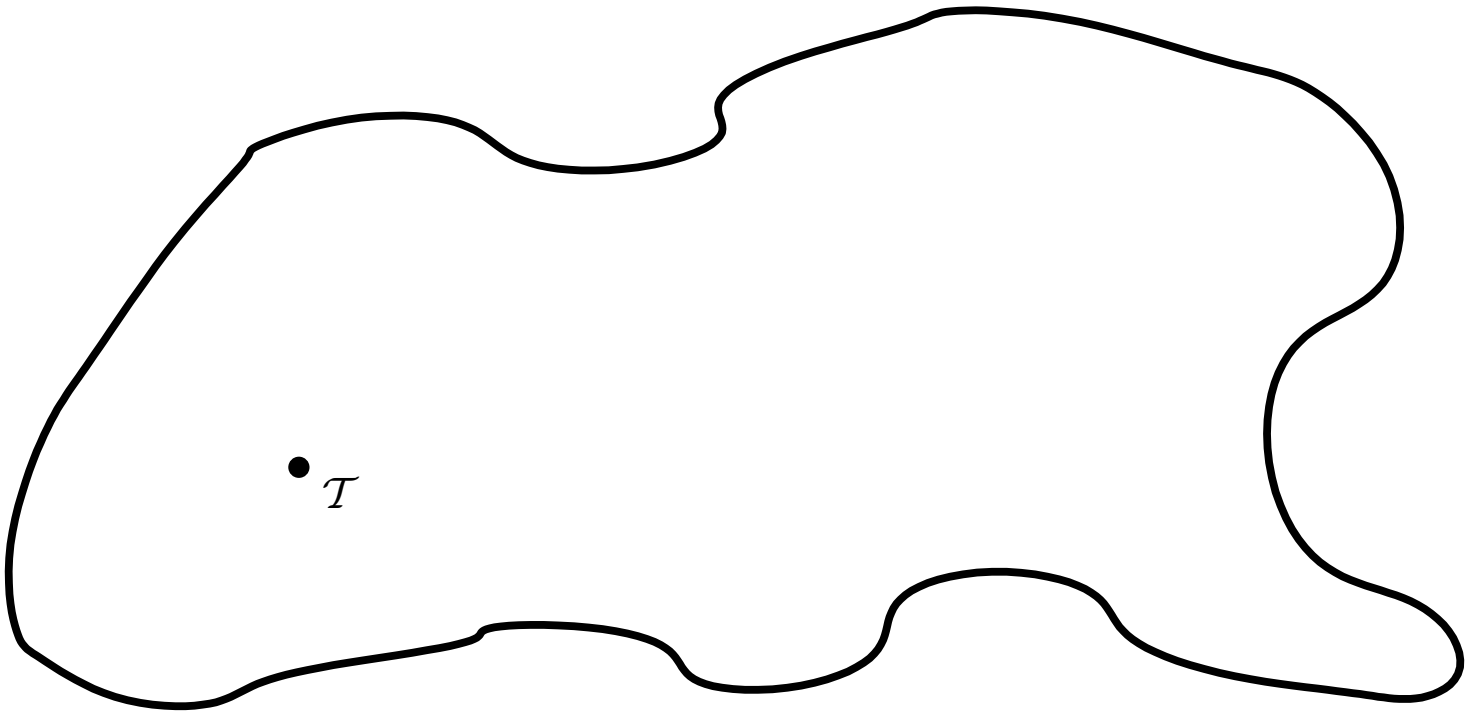

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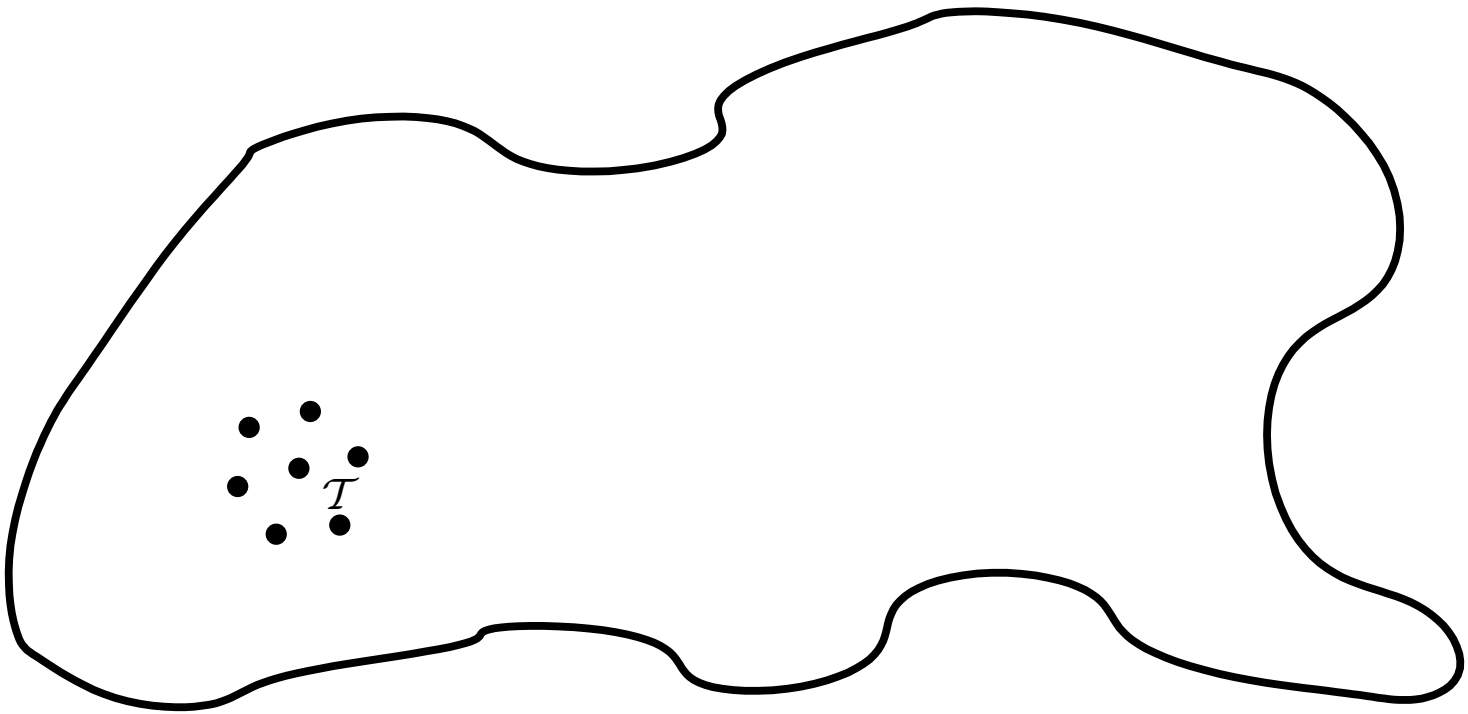

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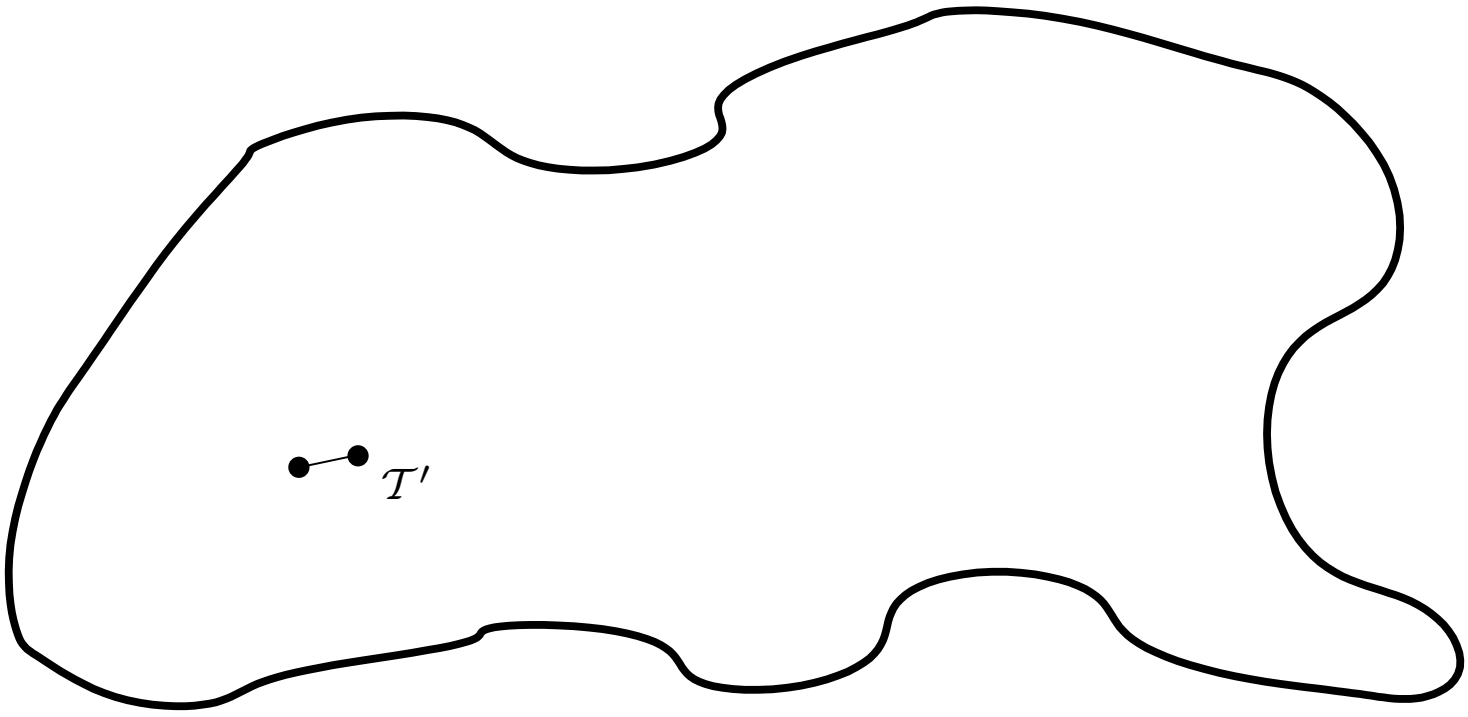

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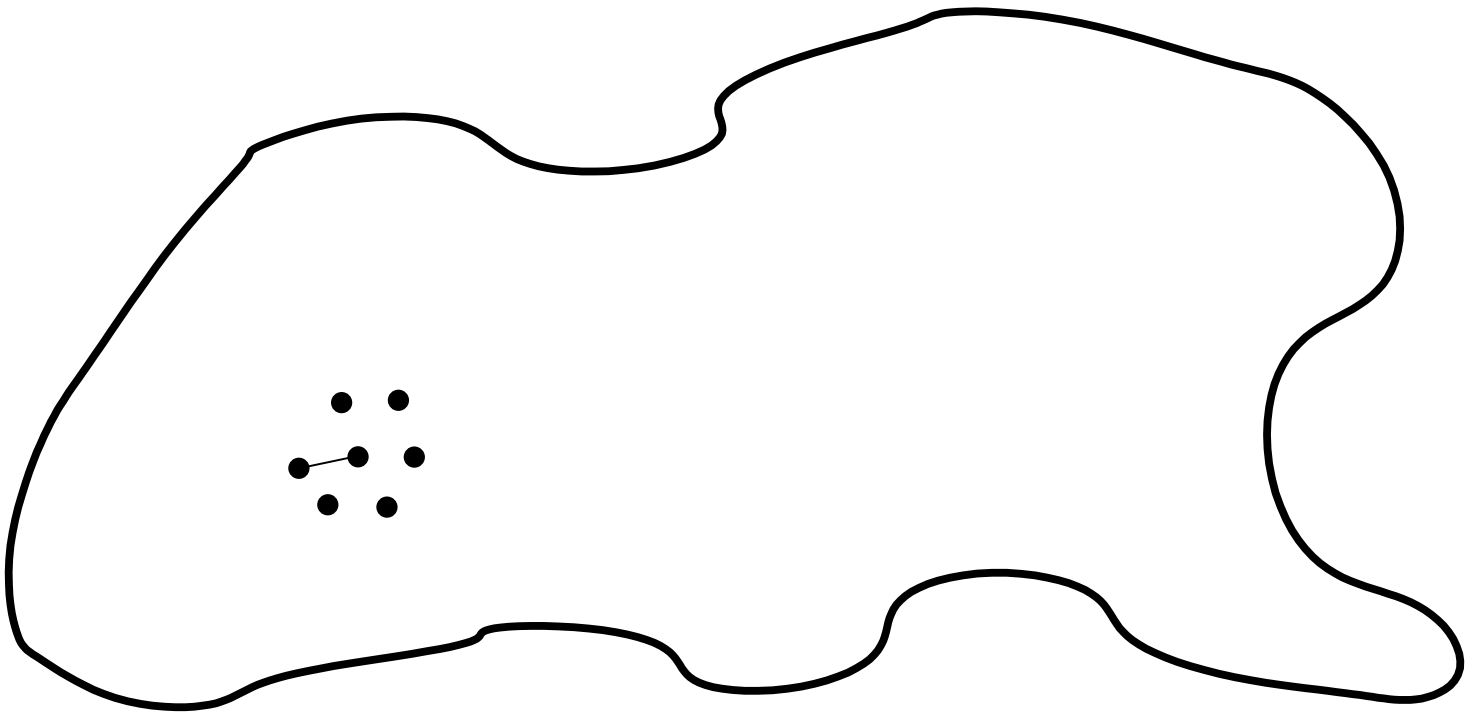

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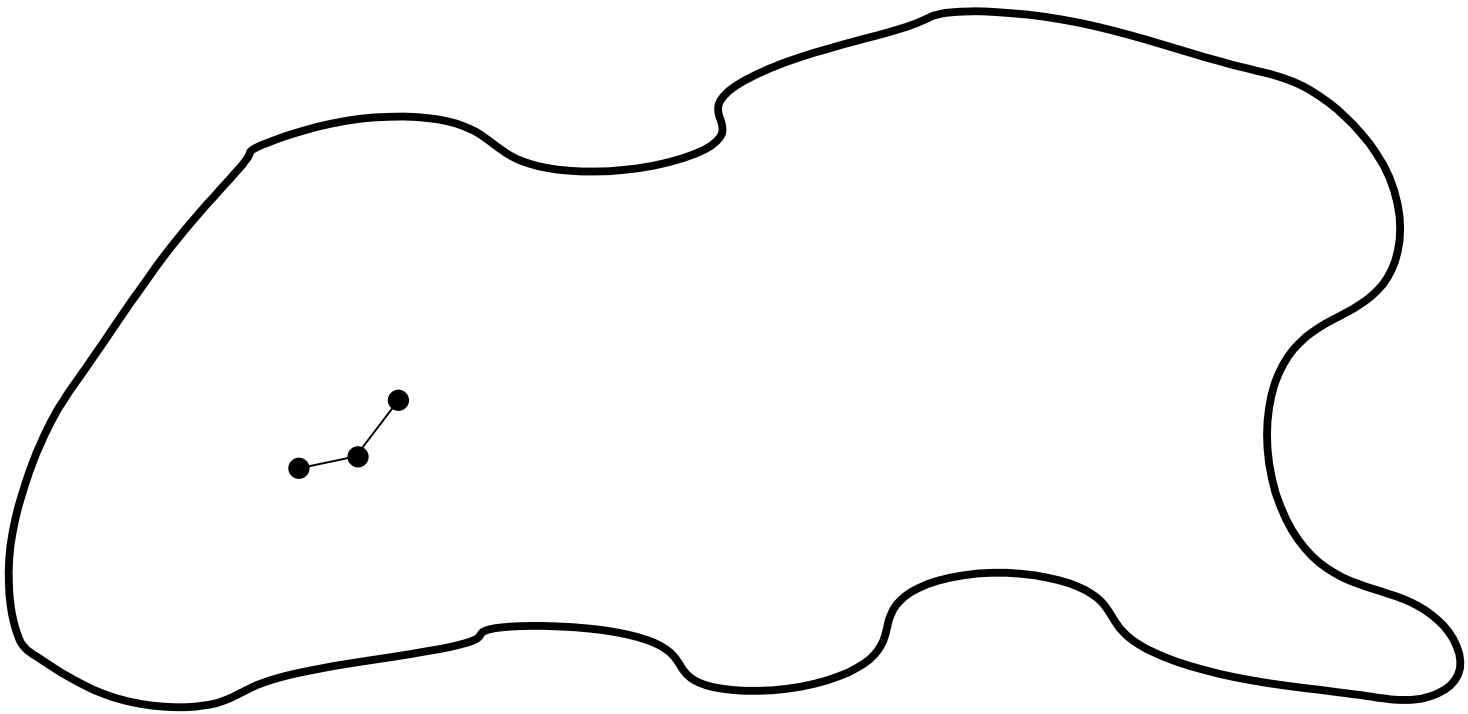

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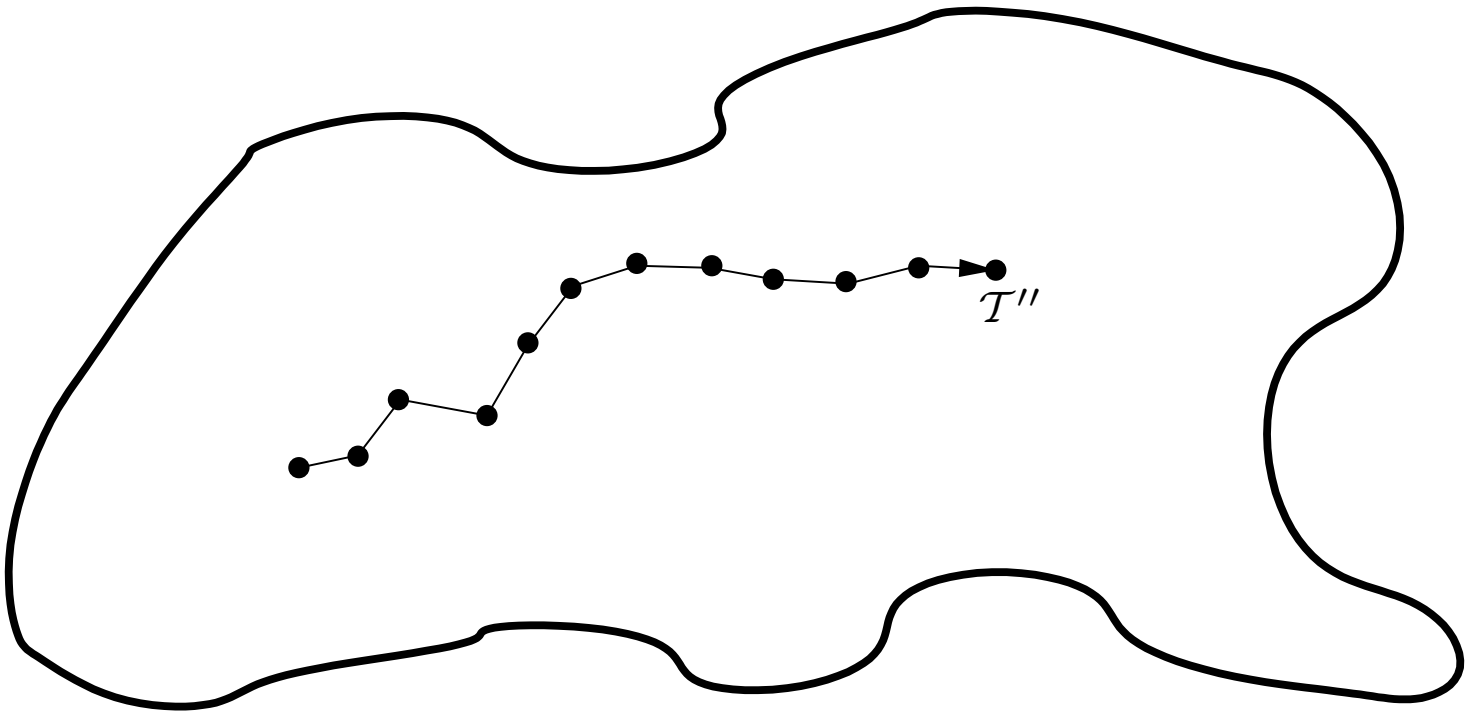
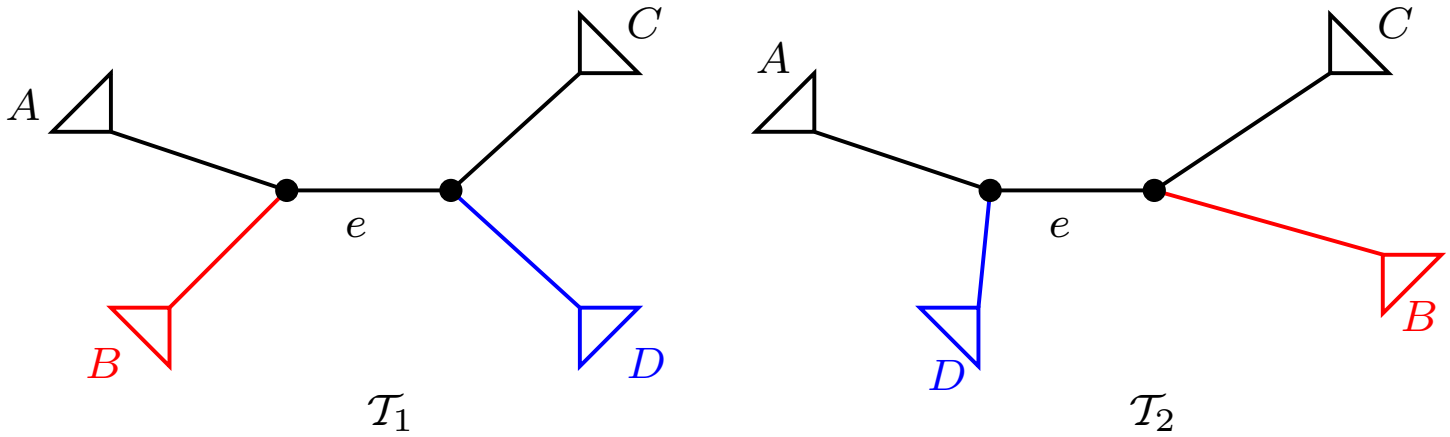
3. Output the final topology: a local minimum in tree length.

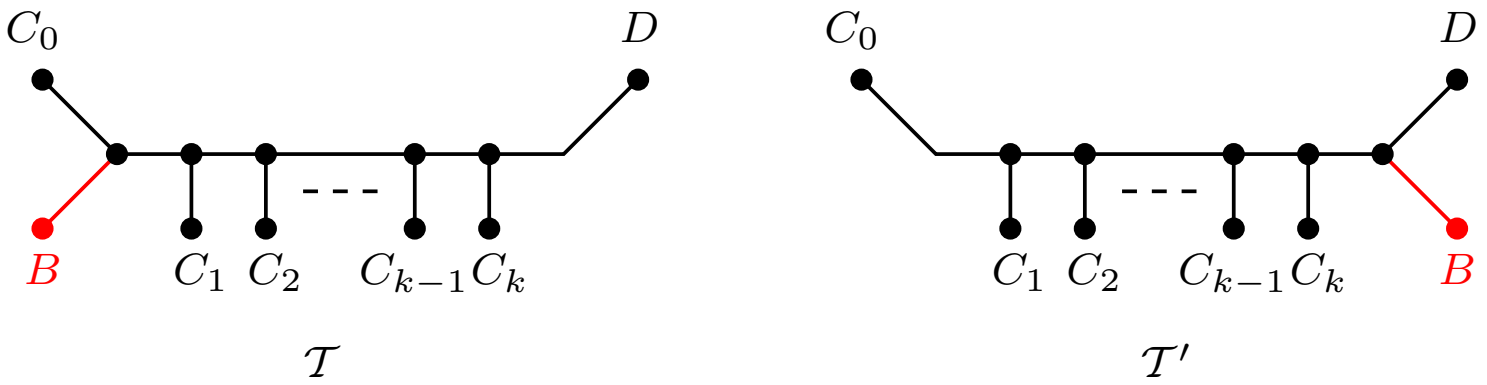


Subtree transfer operations

Nearest Neighbour Interchange (NNI):



Subtree Prune and Regraft (SPR):



FASTME

- This approach is has been programmed as FASTME, available on the web (Desper and Gasuel).
- It is extremely fast (SPR only slightly slower than NNI).
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But is it provably consistent? *I.e.* given good data do we get the correct answer?

Results

Theorem (B., Gascuel, Huber, Moulton '07)

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Theorem (B., Gascuel, Huber, Moulton '07)

From any starting tree, Balanced Minimum Evolution using an SPR local topology search has a safety radius of 1/3.

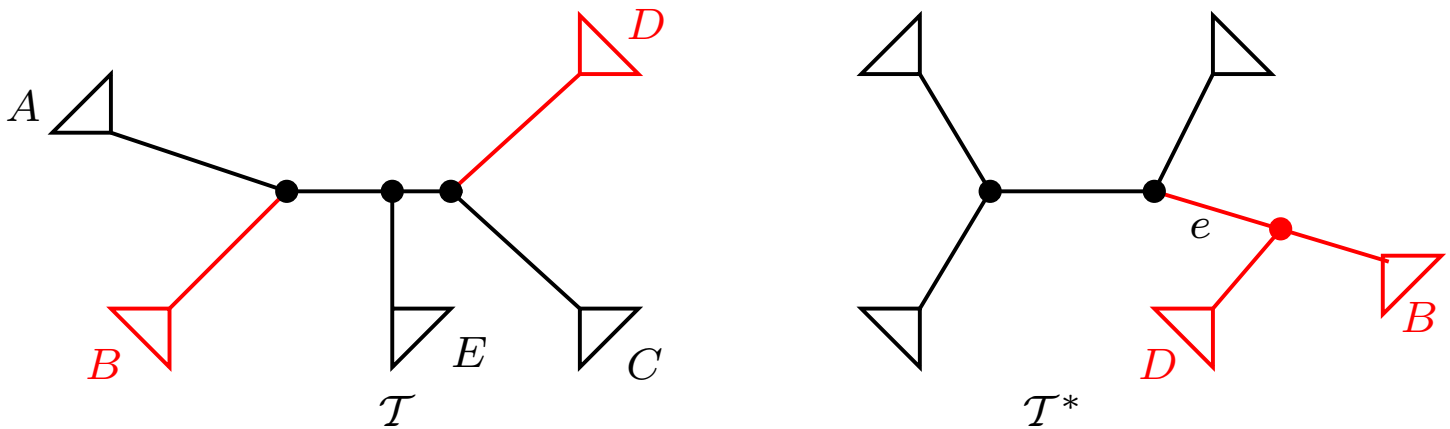
Even with small errors in the data we get to the true tree.

Robinson-Foulds distance

Lemma

For any tree $\mathcal{T} \neq \mathcal{T}^*$ there is a tree $\mathcal{T}'$ one SPR from $\mathcal{T}$ which reduces the Robinson-Foulds distance to $\mathcal{T}^*$.

We find subtrees B and D of $\mathcal{T}$ as follows



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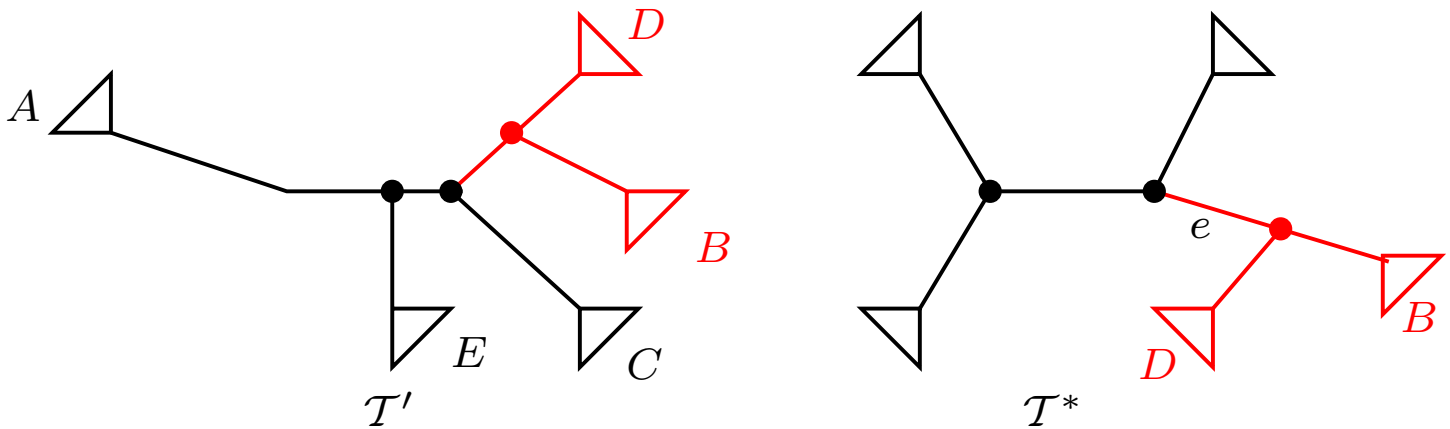

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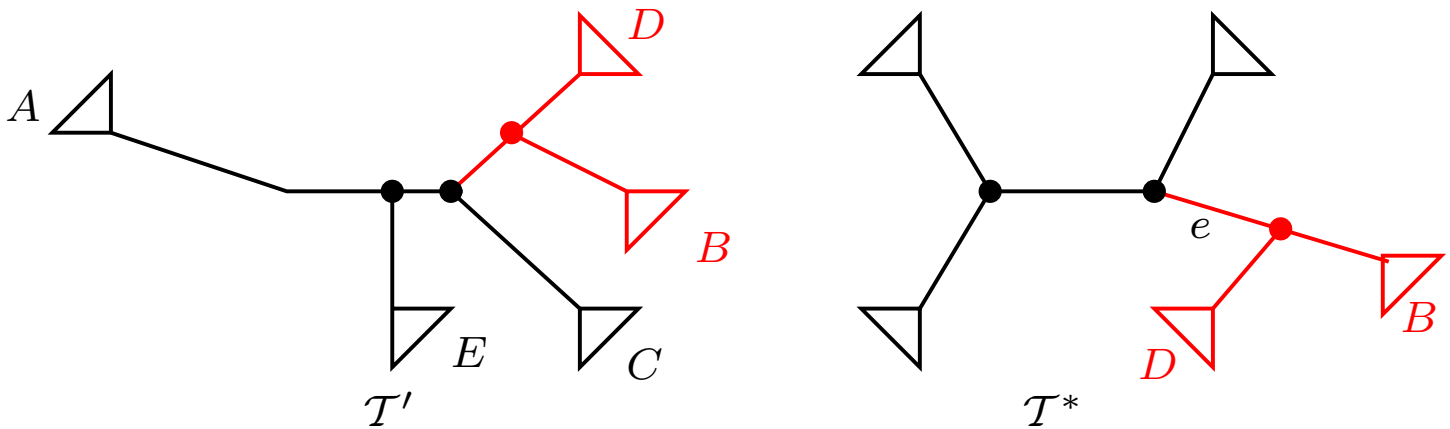

- We then form $\mathcal{T}'$ from $\mathcal{T}$ by uniting B and D.
- Split corresponding to e now appears in $\mathcal{T}'$ and $\mathcal{T}^*$.

Pauplin tree length

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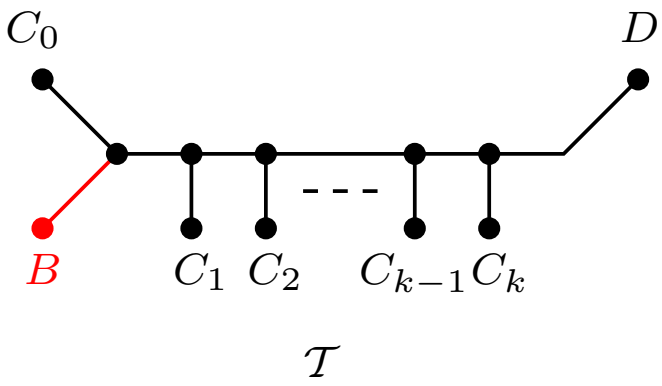
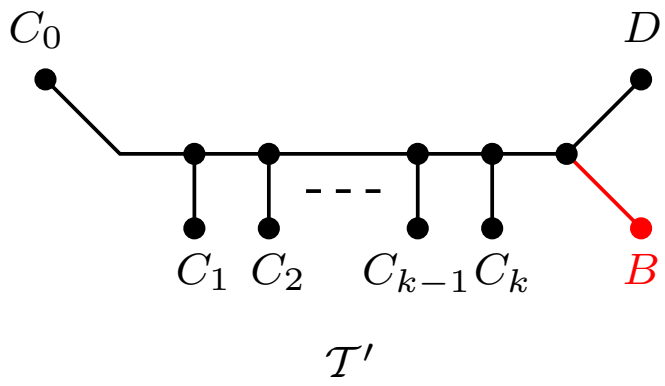
Let ϵ be the maximum error of any entry in the distance matrix Δ.

Let k be the number of intermediate subtrees between B and D.



$\mathcal{T}$



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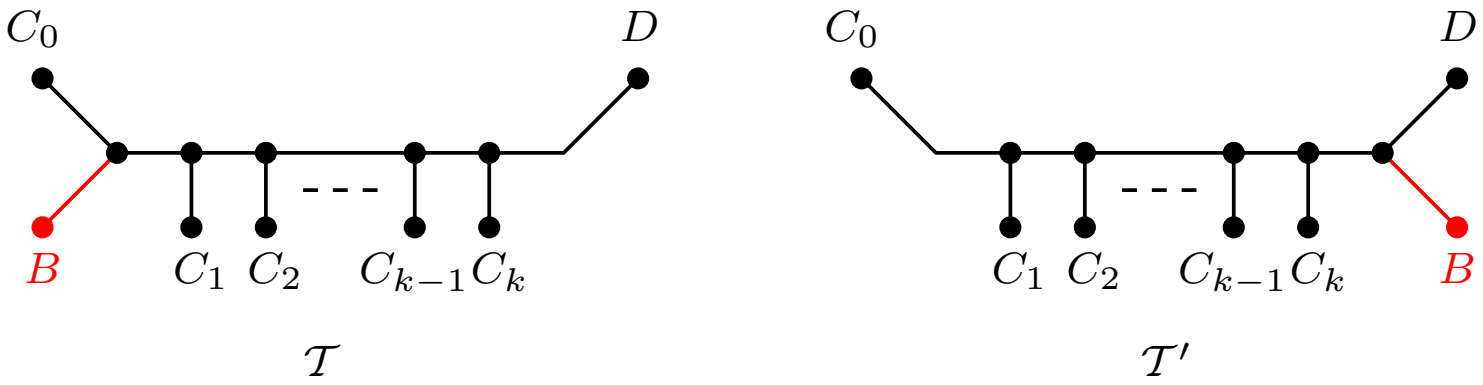

Then $\hat{l}(\mathcal{T}) - \hat{l}(\mathcal{T}') \geq (1 - 2^{-k})(l(e) - 3\epsilon)$.

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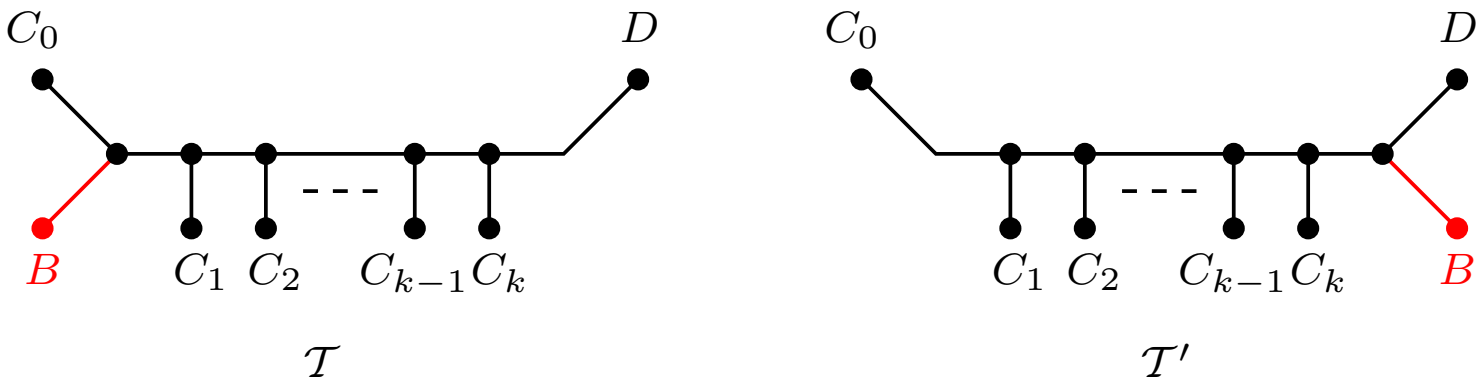

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Corollary

If $\epsilon < l_{\min}/3$, then there is no local minimum except $\mathcal{T}^*$.

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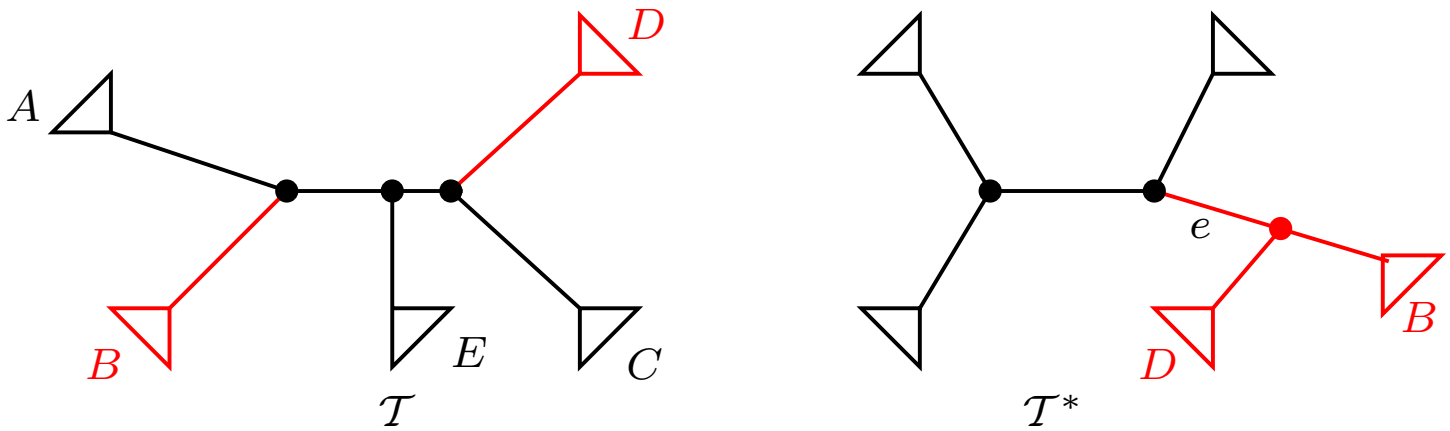

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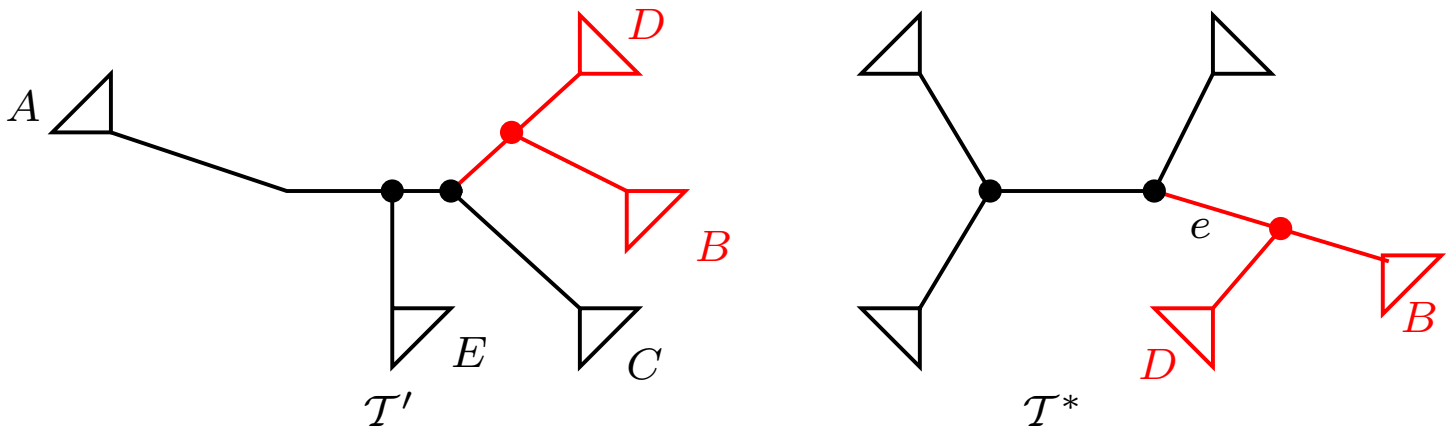

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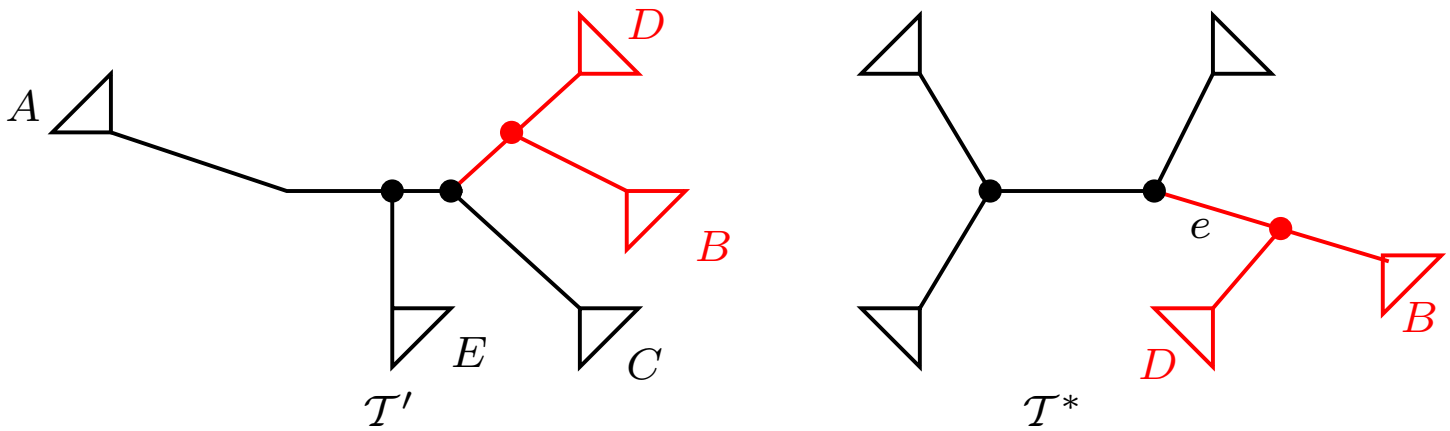

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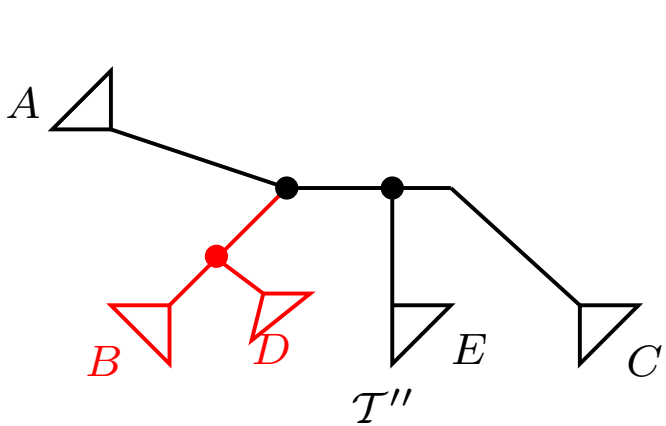

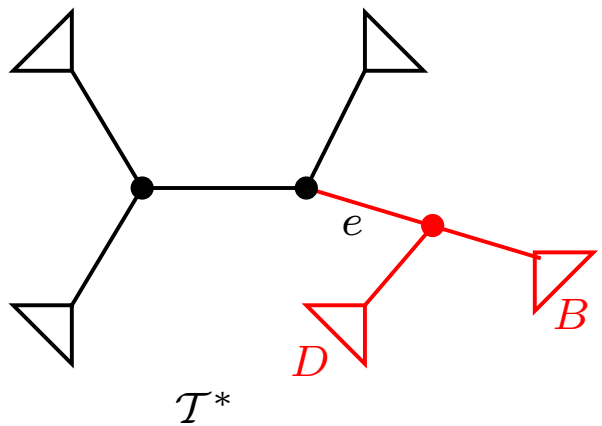

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- Can we prove other forms of robustness?

- Do any of the results hold for an NNI based local search?

  Note: NNI is more commonly used in practice, and empirically appears as good as SPR.