# The Disk-Covering Method for Tree Reconstruction

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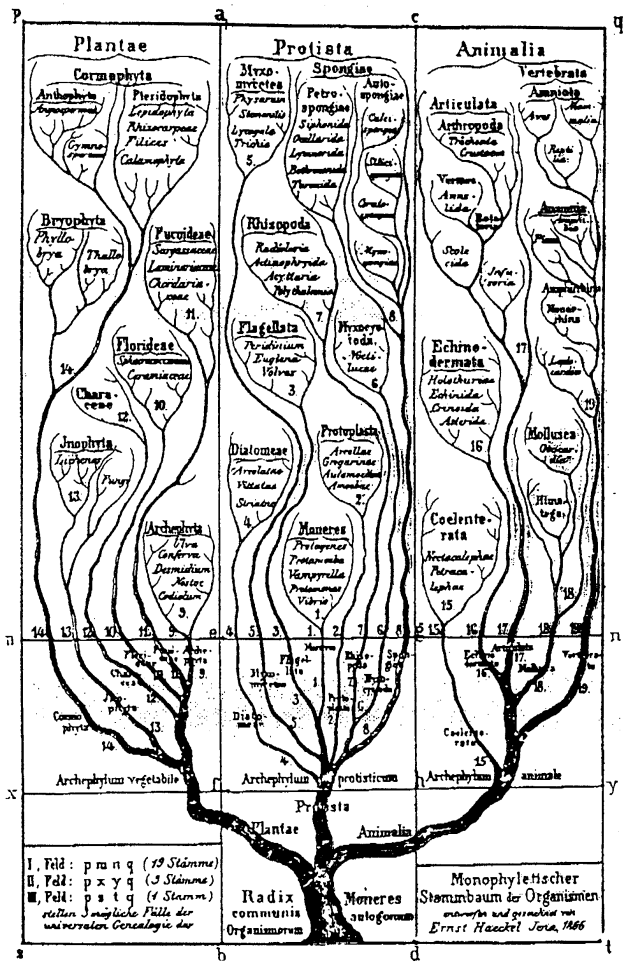
Kaikoura, 1999

# The Tree of Life




The first phylogenetic tree of life, Ernst Haeckel (1866)

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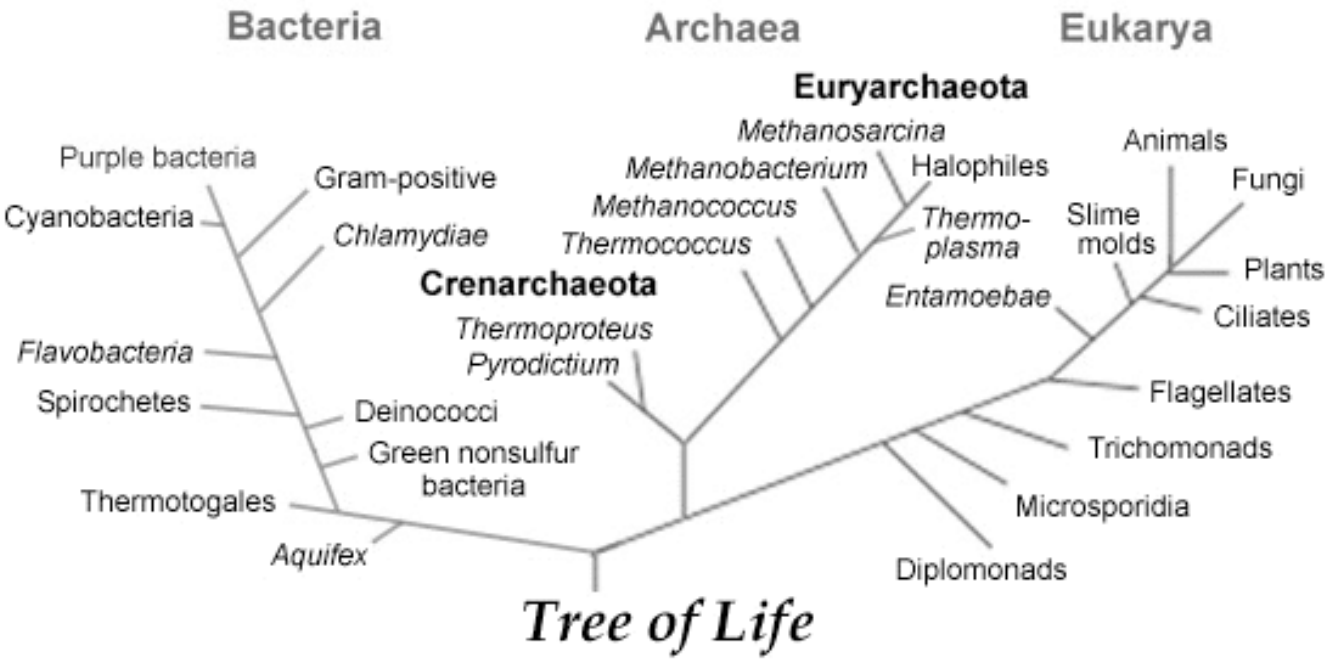


A modern view of the tree of life

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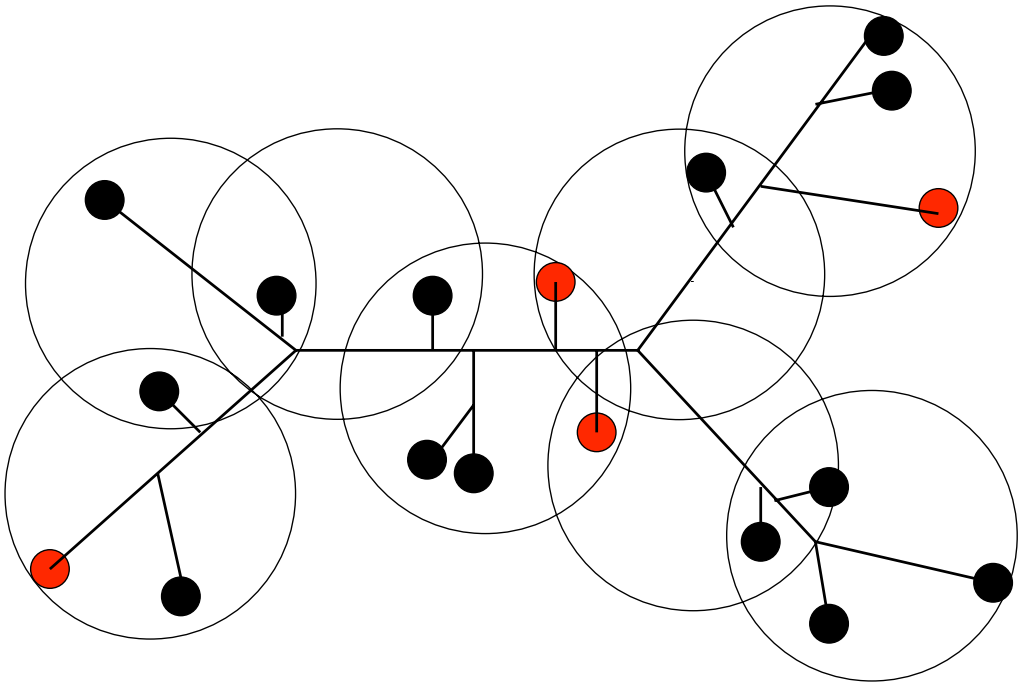
- Year-long Parsimony analyses (Rice *et al.*) of large divergent datasets are infeasible for most researchers.

# The Disk-Covering Method (DCM)



A divide-and-conquer approach based on the idea of covering given sequence data with small overlapping disks

- Each disk contains a small number of taxa.
- Taxa within a disk are very similar.
- Apply given *base-method* to subproblems.
- Use overlap to merge subtrees to obtain final tree.

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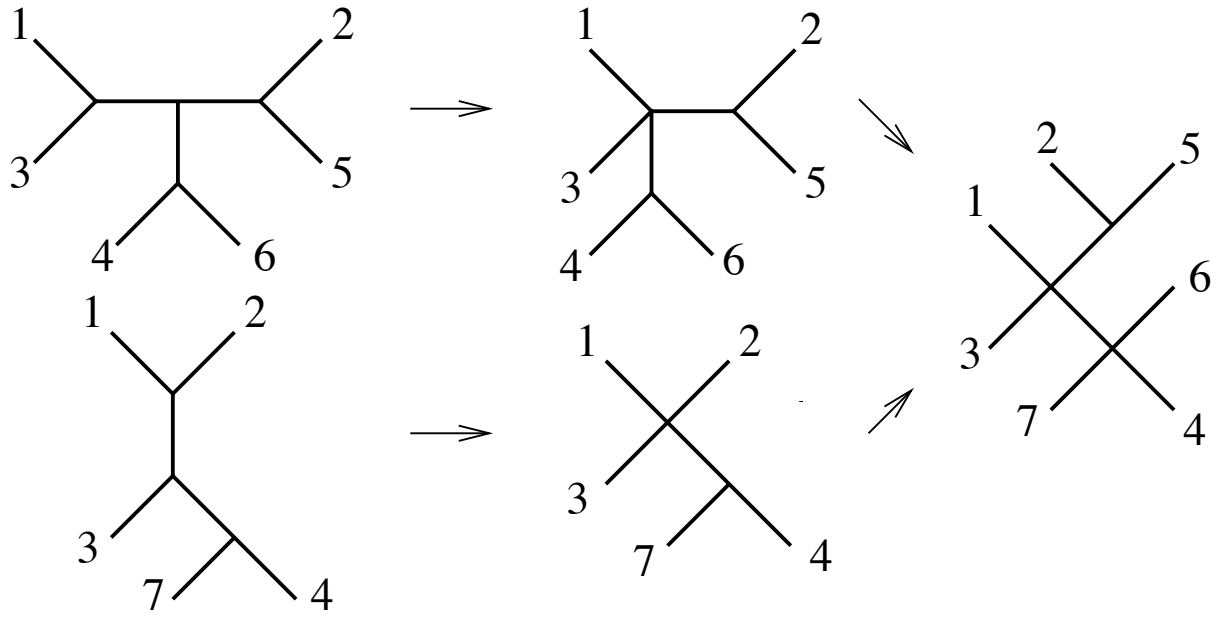
- Infer consensus of $\{T_w\}$.

# Merging Two Trees

Given trees on two overlapping sets of taxa, e.g. $\{1,2,3,4,5,6\}$ and $\{1,2,3,4,7\}$.




To merge the two trees together, first transform them (through edge contractions) so that they induce the same subtrees on their shared leaves and then combine them.

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Software: ecat, seqgen, PAUP, Phylip. Our programs in C++, LEDA.

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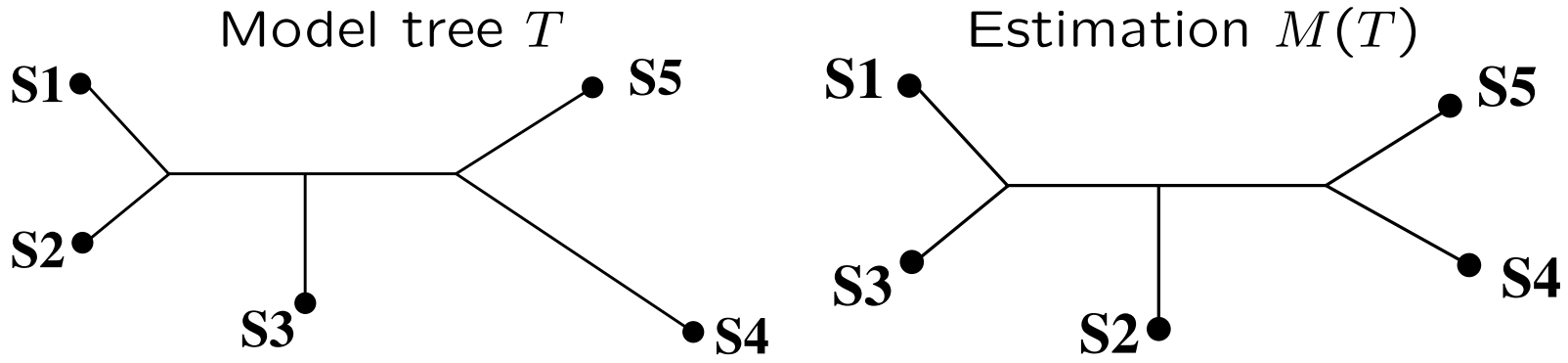

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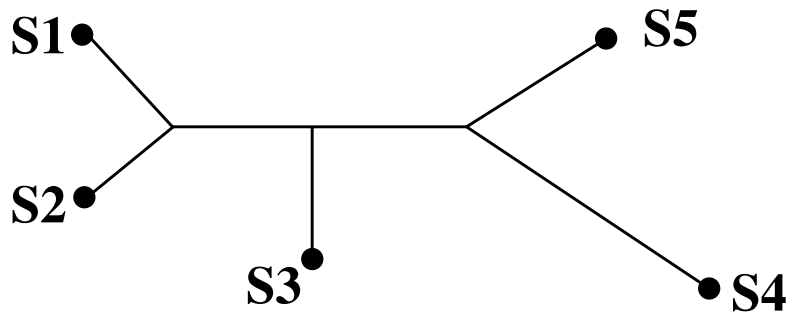
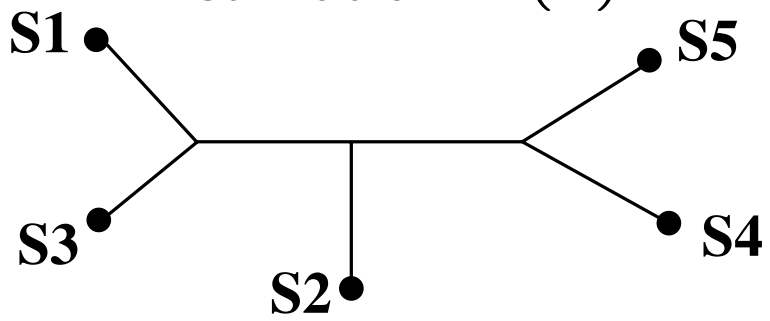
Model tree $T$

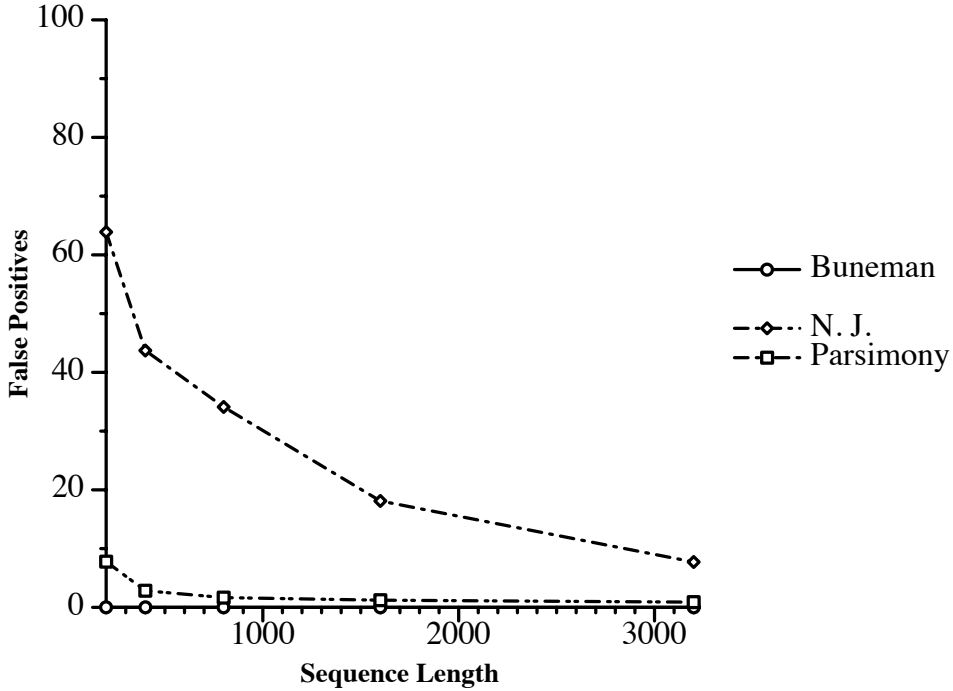



Estimation $M(T)$



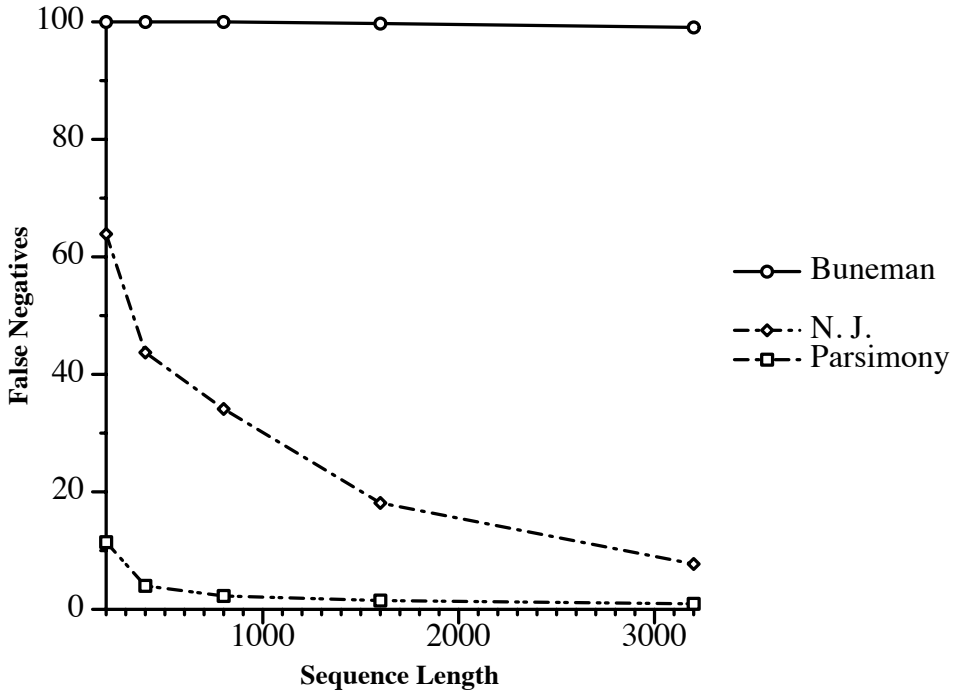

- One false positive: $\{S_1, S_3\}$ vs $\{S_2, S_4, S_5\}$
- One false negative: $\{S_1, S_2\}$ vs $\{S_3, S_4, S_5\}$

# Comparison of False Positive Rates




- 93 taxon tree (from 500 taxon *rbc*L dataset)
- maximum substitution probability $p(e)$ is 0.48
- 20 experiments per point

# Comparison of False Negative Rates

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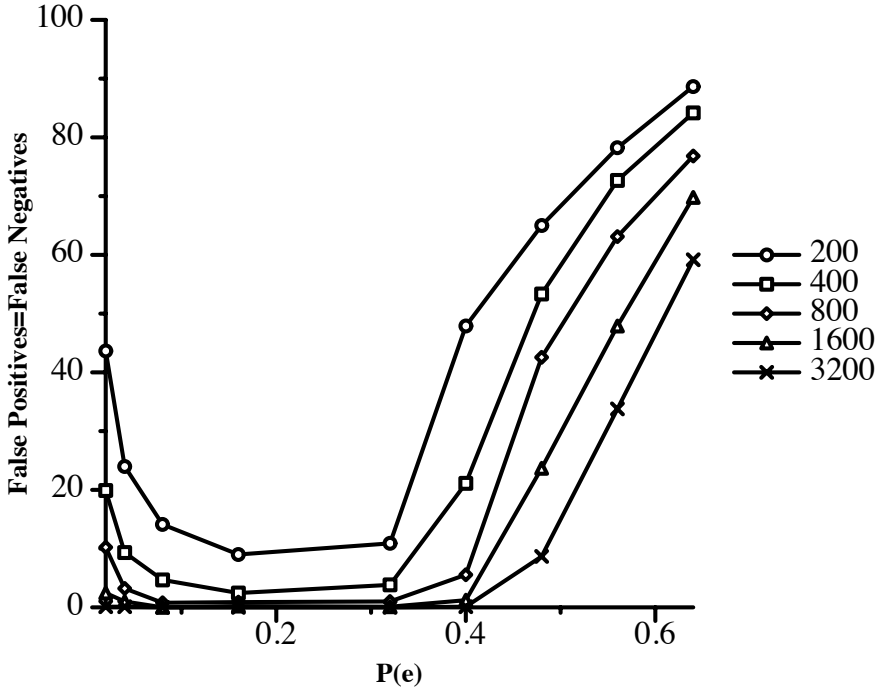
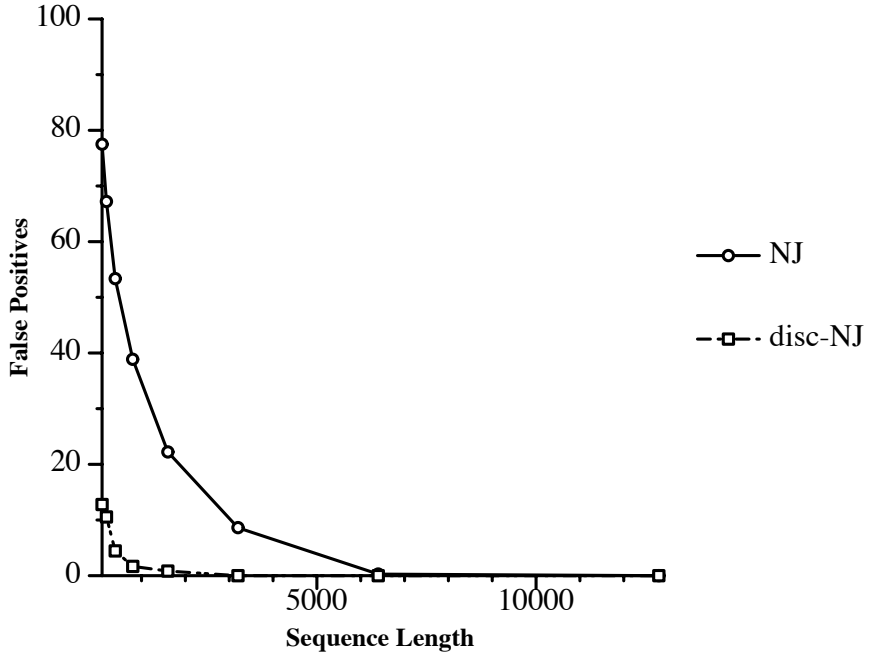
# Performance of Neighbor-Joining




P(e) vs. FP by Length

- 93 taxon tree (from 500 taxon *rbc*L dataset)
- maximum mutation probability $p(e)$ vs. FP (=FN) rate
- 20 experiments per point

# Neighbor-Joining vs DCM-NJ, **false positives**

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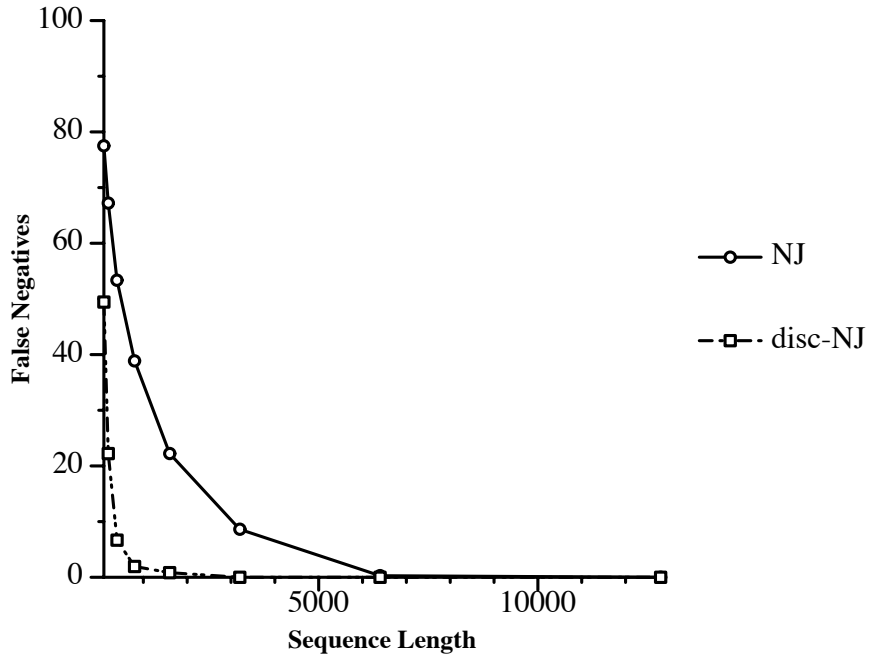


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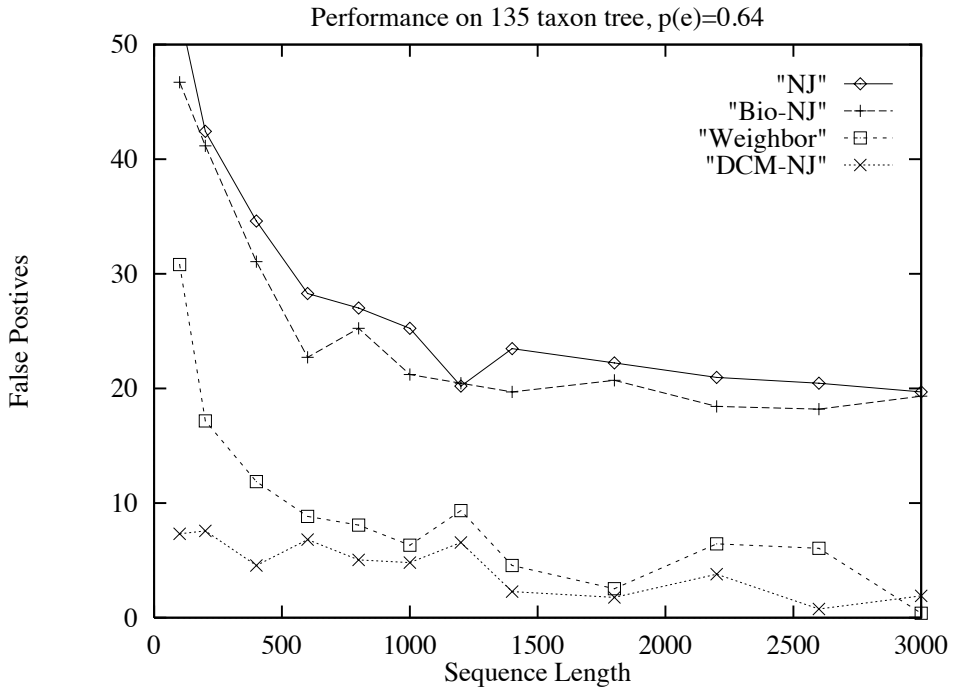
- Weighbor
  - Weighted Neighbor-Joining
  - W. Bruno, A. Halpern & N. D. Socci, 1998

# NJ, Bio-NJ, Weighbor & DCM-NJ, FP




- 135 taxon tree, maximum mutation probability $p(e) = 0.64$
- *Greedy asymmetric median tree* of a small subset of $\{T_w\}$.
- 3-5 experiments per point, work in progress. . .

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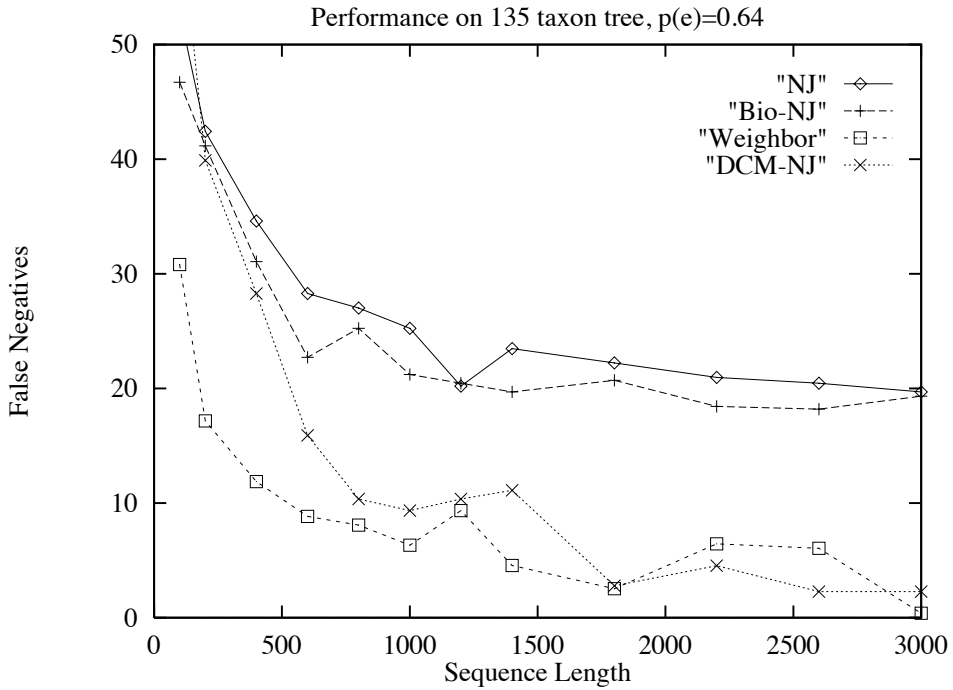


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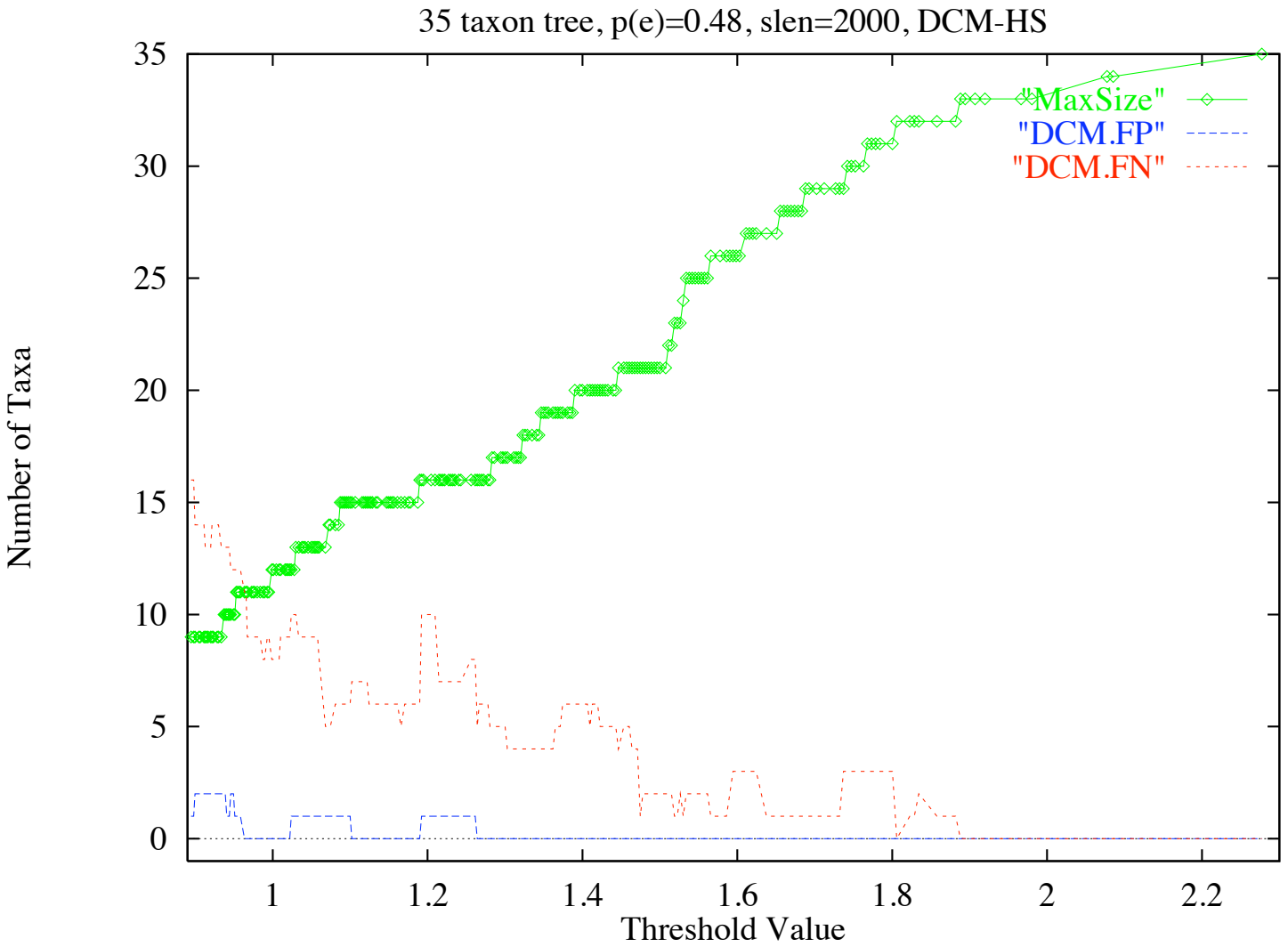
# Speeding up Parsimony and MLE



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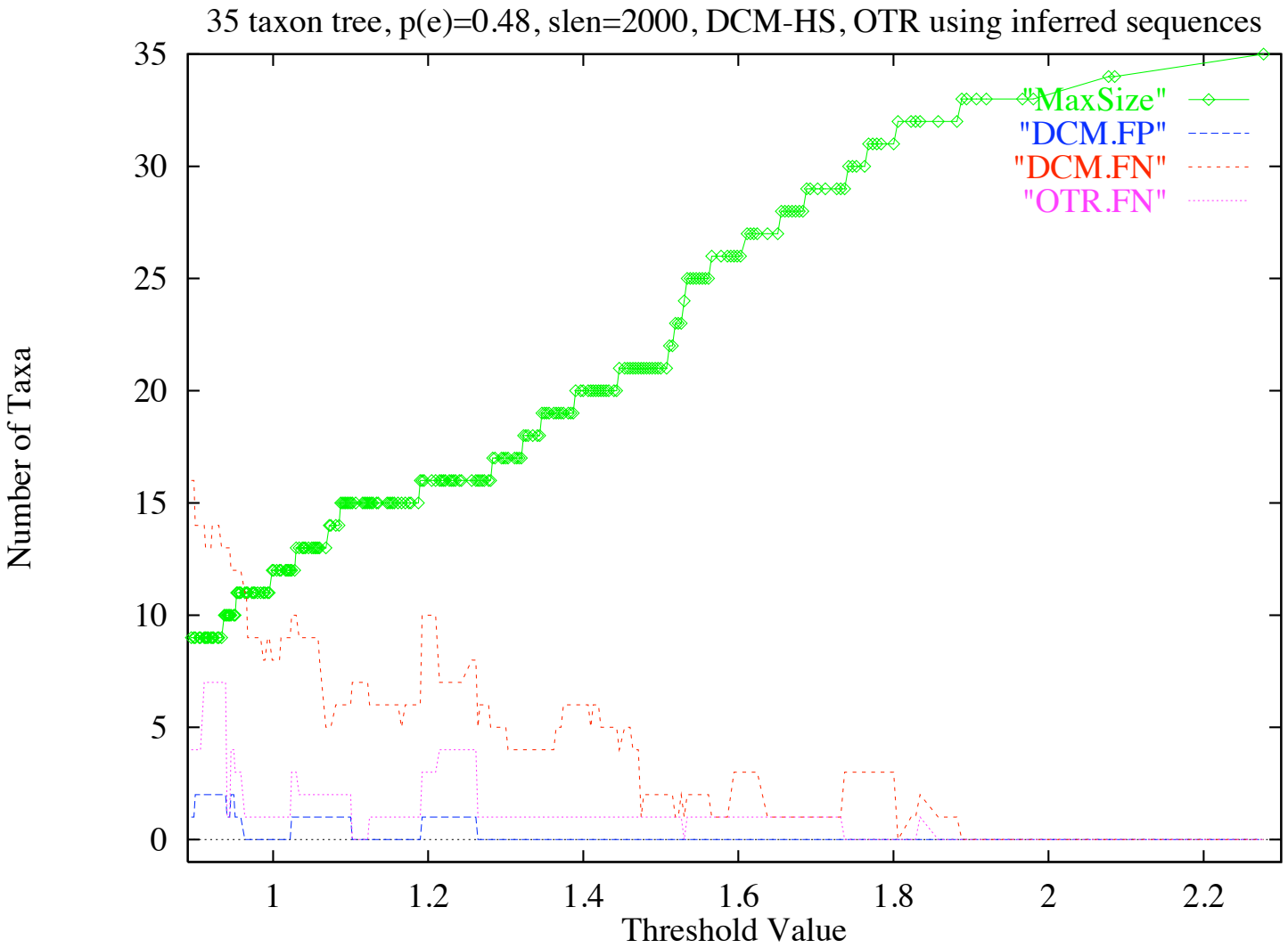
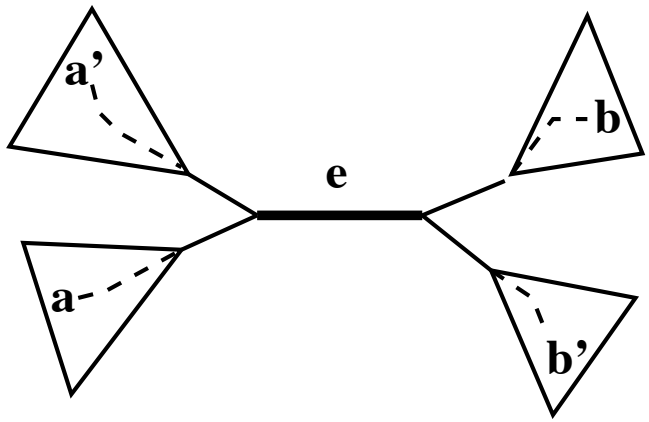


# Threshold and Merge Step

Let $T$ be a model tree and $d$ an estimated distance matrix. A *short quartet* around an internal edge $e$ is a set of four taxa $a, a', b, b'$ that lie in the four subtrees induced by $e$, of minimal width.




**Theorem** If the threshold $w$ is chosen large enough such that every short quartet induces a four-clique in $G^*$, then every merger is unique and a DCM method will recover the model tree $T$, if the base method is accurate on the base problems.

# Sequence Lengths Required for Accuracy

The length of biological sequences obtainable for phylogenetic analysis is bounded by a *few thousand* base pairs, so the question how sequence length affects performance is critical.

The sequence lengths that suffice for accuracy of distance methods such as Neighbor-Joining or the Buneman Tree grow **exponentially** in the divergence of the model tree.
(Atteson 1997, Erdös et al. 1997)

For DCM-boosted distances methods we can show:

> For almost all trees, **polylogarithmic** length suffices for accuracy with high probability, and **polynomial** length suffices for all trees with high probability.

# Conclusion and Future Research

By reduction to small and closely related-datasets, the DCM-method can substantially improve the accuracy and/or time requirements of phylogenetic tree reconstruction methods for large and divergent datasets.

Future research will focus on:

- More advanced simulations studies
- Parsimony and MLE
- exploring the application to multiple sequence alignment
- investigating performance on real datasets
- **developing a public version of the software.**

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