# Algorithmic Approaches for Biological Data, Lecture #22

Katherine St. John

City University of New York
American Museum of Natural History

27 April 2016

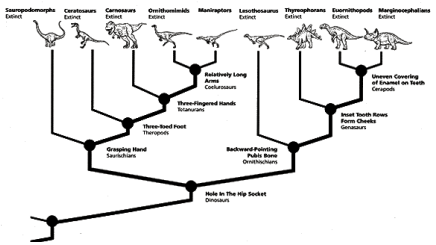
# Outline

Guest Lecturer: Dr. Eric Ford

- Fitch's Algorithm: scoring trees in linear time
- Building Trees: Wagner Builds, UPGMA, & Neighbor Joining

# Algorithm Design: Scoring Trees Under Parsimony

- How do you code this?

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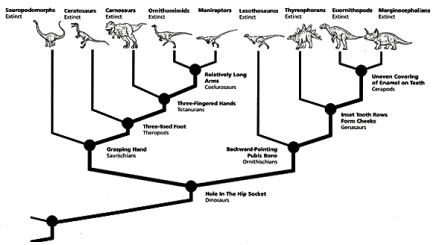


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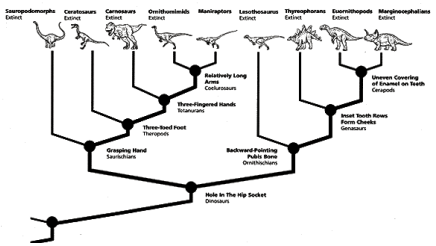


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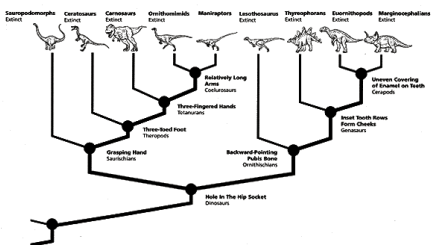


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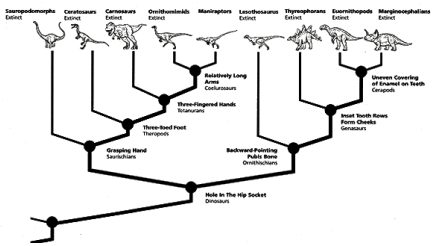


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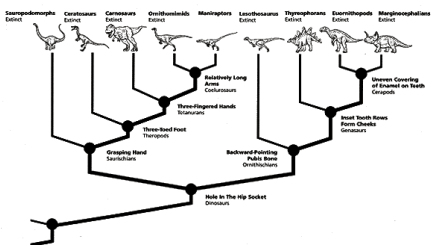


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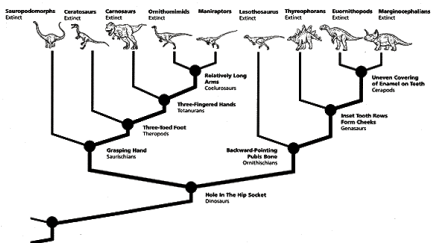


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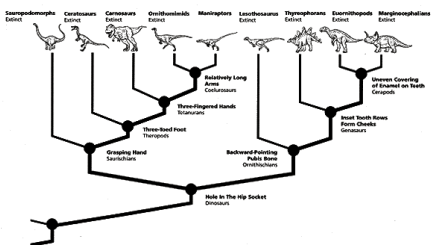


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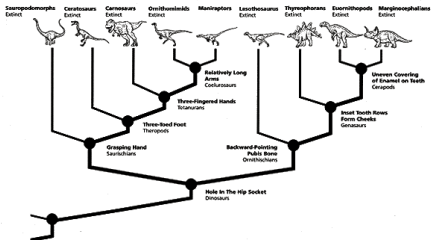


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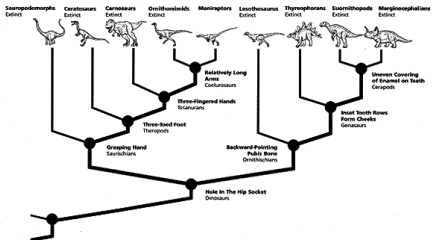


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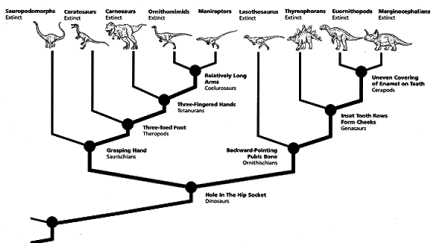


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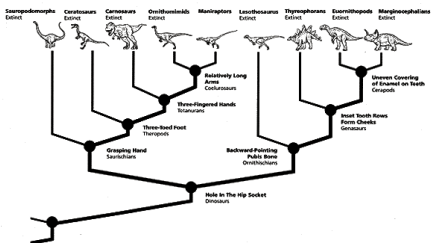


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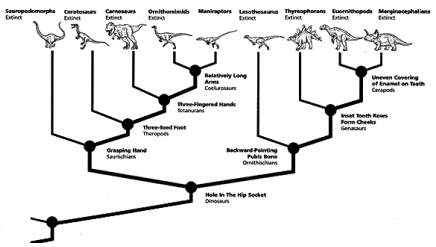


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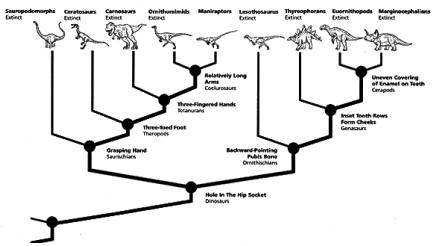


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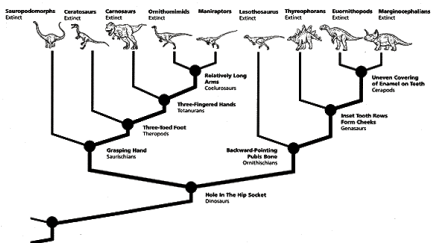


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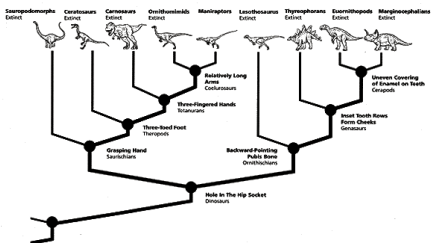


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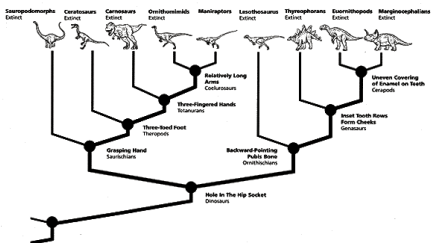


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s1 = set(l1)
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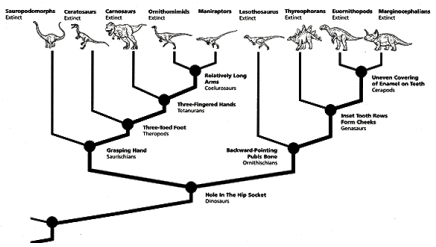


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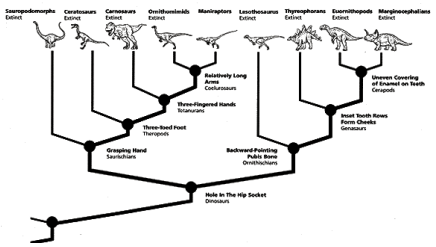

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  - Useful Python container type: `set`
    - ★ Has functions for union and intersection of sets.
    - ★ `s1 = set(l1)` set operations

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      s2 = set(l2)
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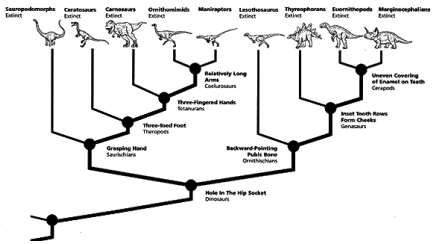


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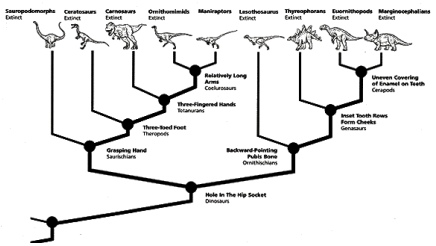


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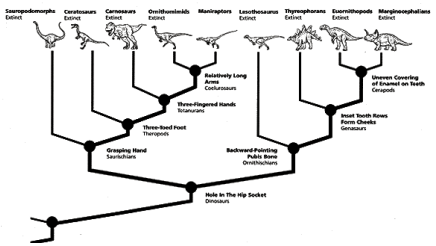


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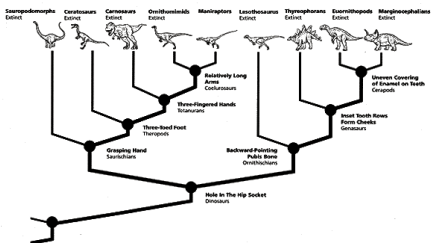


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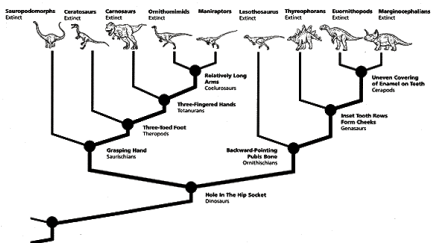


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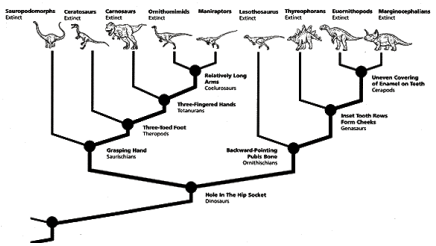


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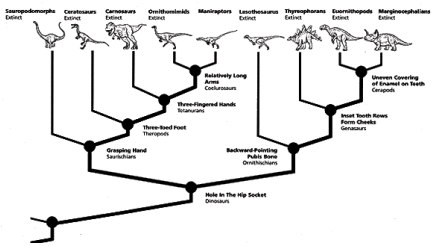


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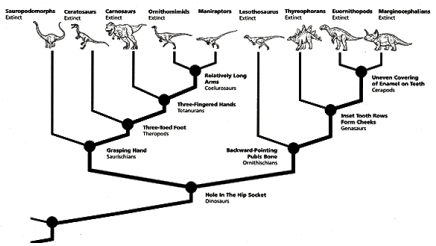


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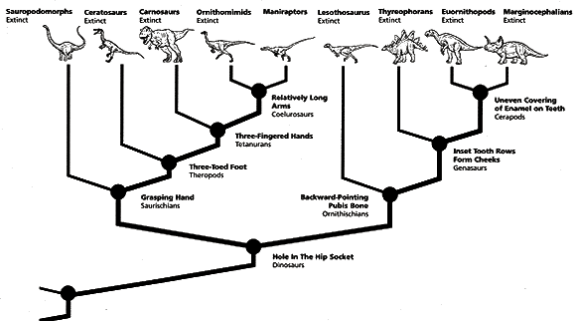


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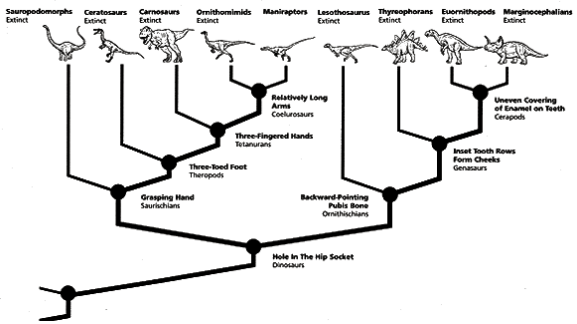


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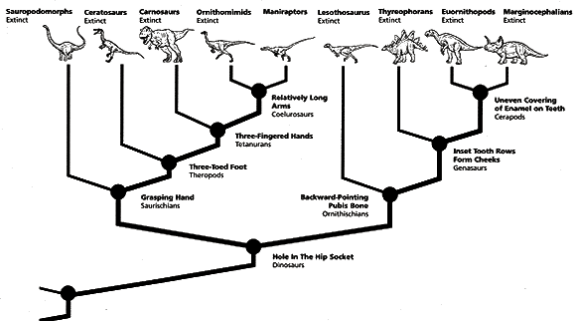


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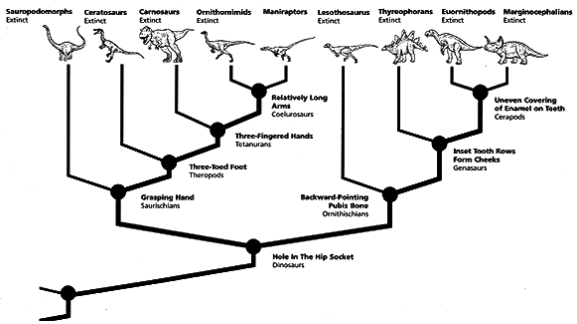


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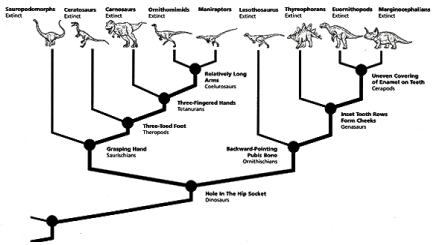
# Ways to Build Trees

- Often need a tree to start.



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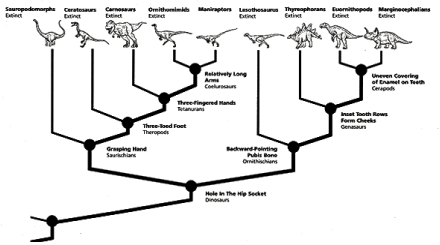


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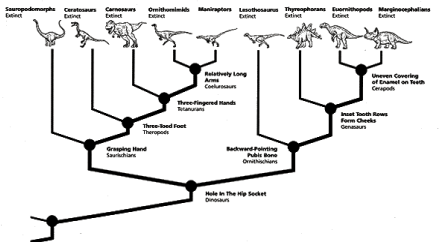


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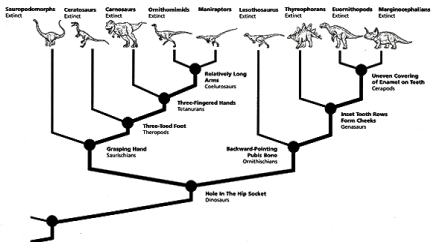


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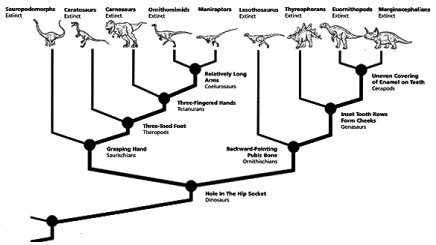


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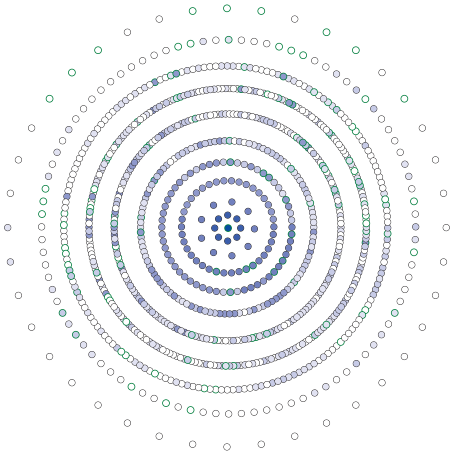
  - UPGMA: Builds clusters based on Hamming distances between sequences. Assumes an 'ultrametric' clock.
  - Neighbor Joining: Also uses distances but uses 'corrected' distances to produce better trees.

# In Pairs: Wagner Build

AACCGTTA
AACGTTAA
ACCGTTTA
CACGTTAA
AACGGTAT

1. Start with a rooted tree on the first two leaves.
2. Score (& label) the tree.
3. For each of the remaining leaves:
   - Try adding it to each edge of the tree.
   - Take the tree with the best score

# Recap



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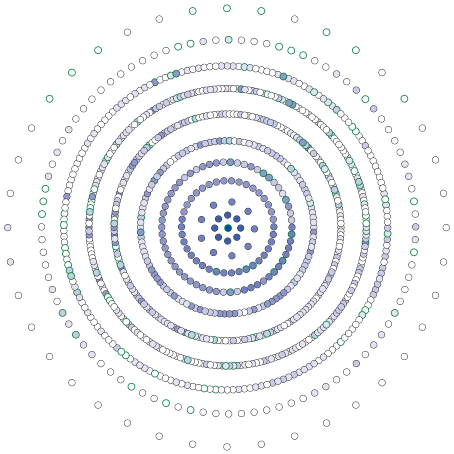

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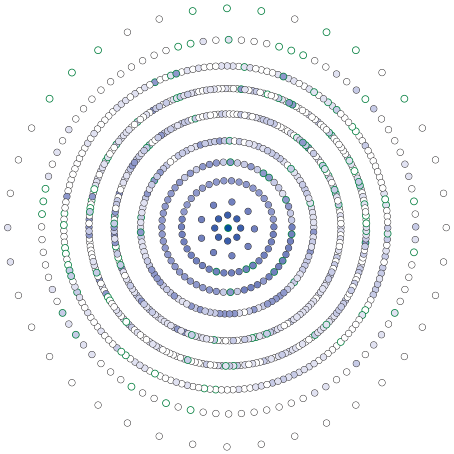

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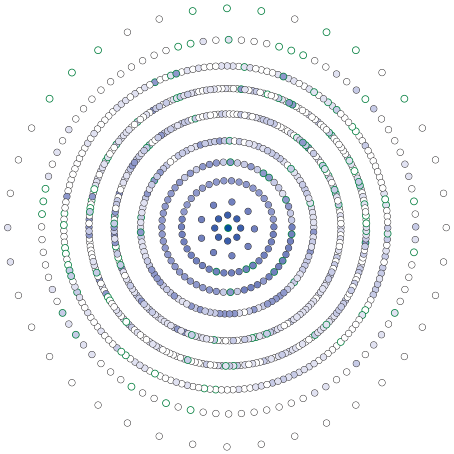

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- Challenges available at `rosalind.info`.