Introduction to Phylogeny

Lecture Notes for 9 October 2003
CMP 464/788: Introduction to Computational Biology

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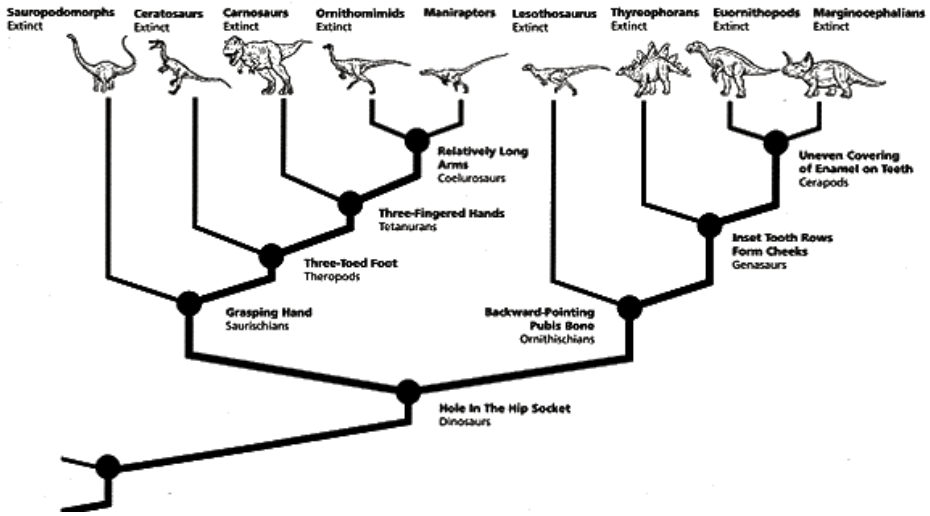
Goal: Reconstruct the Evolutionary History



(www.amnh.org/education/teacherguides/dinosaurs)

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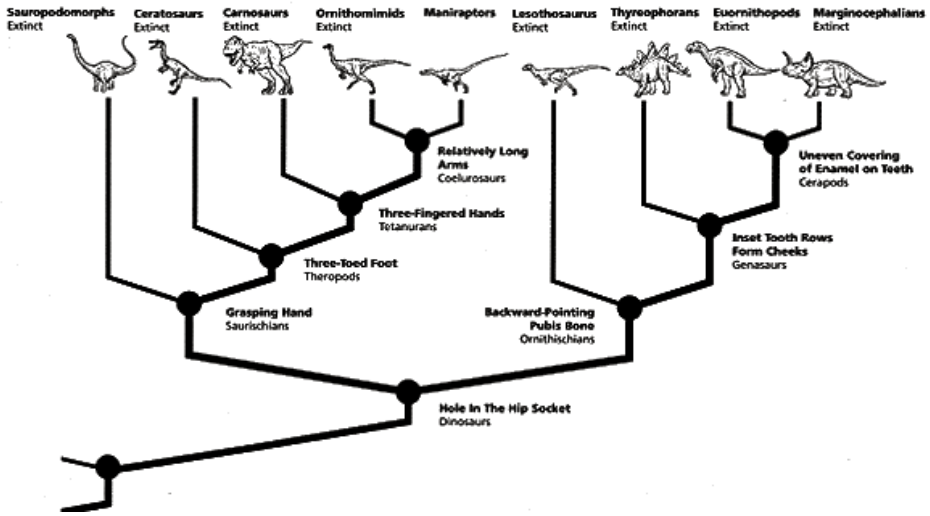

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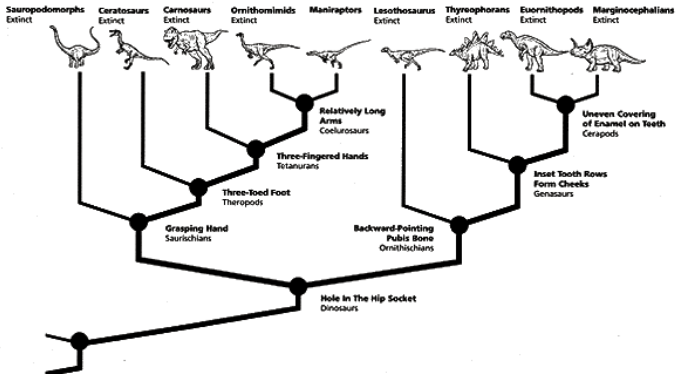
The evolutionary process not only determines relationships among taxa, but allows prediction of structural, physiological, and biochemical properties.

Process for Reconstruction: Input Data

Start with information about the taxa. For example:

Morphological
Characters



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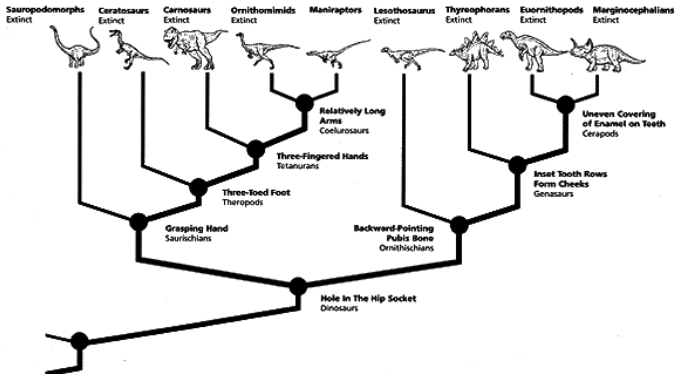

Biomolecular Sequences

A	GTTAGAAGGCGGCCAGCGAC. . .
B	CATTTGTCCTAACTTGACGG. . .
C	CAAGAGGCCACTGCAGAATC. . .
D	CCGACTTCCAACCTCATGCG. . .
E	ATGGGGCACGATGGATATCG. . .
F	TACAAATACGCGCAAGTTCG. . .

Process for Reconstruction

Process for Reconstruction

Input

Data

A	GTTAGAAGGC...
B	CATTTGTCCT...
C	CAAGAGGCCA...
D	CCGACTTCCA...
E	ATGGGGCACG...
F	TACAAATACG...

Process for Reconstruction

Input Data			Reconstruction Algorithms
A	GTTAGAAGGC...	$\longrightarrow$	Maximum Parsimony
B	CATTTGTCCT...		Maximum Likelihood
C	CAAGAGGCCA...		Distance Methods: NJ,
D	CCGACTTCCA...		Quartet-Based,
E	ATGGGGCACG...		Fast Convering,
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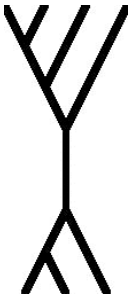
Process for Reconstruction

Input Data		Reconstruction Algorithms	Output Tree
A	GTTAGAAGGC...	Maximum Parsimony	
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- determining origins of HIV infection
- origin of other virus and bacteria strains

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  This is not feasible for more than 20 taxa.

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    (use clever ways to limit the number of trees checked, while still sampling much of "tree-space")
  - Polynomial-time methods, based on the distance between taxa

Distance-Based Methods

- These methods calculate the distance between taxa:

	B	D	A	C	F	E
B	0	0.496505	0.496505	0.444519	0.375798	0.268166
D	0.496505	0	0.496505	0.375798	0.275673	0.279728
A	0.496505	0.496505	0	0.362124	0.323812	0.496505
C	0.444519	0.375798	0.362124	0	0.496505	0.496505
F	0.375798	0.275673	0.323812	0.496505	0	0.496505
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- One way to calculate distance is to take differences divided by the length (the normalized Hamming distance).

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- Many of these methods have good performance empirically, and some can be proven to have nice accuracy properties.

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- Simulation is used instead to evaluate methods, given a model of evolution.

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