

Intro to Cladistic Analysis



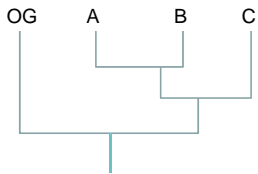
I. Overview



A. Scope

1. Ingroup vs. outgroup

e.g., angiosperms vs. non-angiosperms
e.g., primates vs. non-primates



I. Overview



A. Scope

1. Ingroup vs. outgroup
2. Taxonomic Resolution, Exemplar vs. Exhaustive Sampling

e.g., angiosperms vs. non-angiosperms

Hypothetical Analysis:

Outgroup Sampling = *Cycas* & *Pinus*

Ingroup Sampling = *Magnolia*, *Nyssa*, *Prunus*, etc.

I. Overview



B. Phylogenetic evidence

1. Morphological Characters

e.g., Phyllotaxy: 0 = alternate; 1 = opposite; 2 = whorled.

e.g., Carpel Presence: 0 = absent; 1 = present.

I. Overview



B. Phylogenetic Evidence

1. Morphological Characters

2. Molecular Characters

(e.g., DNA sequence characters)

mtDNA (e.g., cytochrome oxidase 1 or *cox1*)

cpDNA (e.g. Large subunit of RuBisCO or *rbcL*)

nrDNA (e.g. 18S or 26S)

I. Overview



B. Phylogenetic Evidence

1. Morphological Characters

2. Molecular Characters

(e.g., DNA sequence characters)

mtDNA (e.g., cytochrome oxidase 1 or *cox1*)

cpDNA (e.g. Large subunit of RuBisCO or *rbcL*)

nrDNA (e.g. 18S or 26S)

Characters = positions 1-1436 in *rbcL* gene

Character States = A; G; C; T.

I. Overview

B. Phylogenetic Evidence

1. Morphological Characters
2. Molecular Characters

3. Data

- Characters & Char. States
- Data Matrix

	Char 1	Char 2	Char 3	Char 4	etc.
<i>Cycas</i>	0	-	0	0	
<i>Pinus</i>	0	-	0	0	
<i>Nyssa</i>	1	0	1	1	
<i>Prunus</i>	1	1	1	1	
<i>Magnolia</i>	1	0	1	0	
etc.					

I. Overview

B. Phylogenetic Evidence

1. Morphological Characters
2. Molecular Characters

3. Data

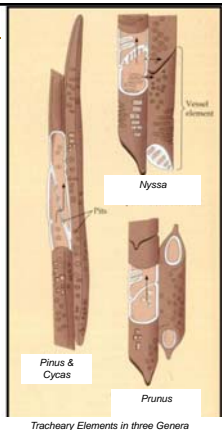
- Characters & Char. States
- Data Matrix
- 1^o Homology Assessment

Char. 1: Tracheary Element Form

<i>Cycas</i>	tracheids only (0)
<i>Pinus</i>	tracheids only (0)
<i>Nyssa</i>	vessel elements (1)
<i>Prunus</i>	vessel elements (1)
<i>Magnolia</i>	vessel elements (1)

Char. 2: Perforation Plate Form

<i>Cycas</i>	-(na)
<i>Pinus</i>	-(na)
<i>Nyssa</i>	scalariform (0)
<i>Prunus</i>	simple (1)
<i>Magnolia</i>	scalariform (0)



Tracheary Elements in three Genera

I. Overview

Char. 3: Seed Packaging

<i>Cycas</i>	gymnospermy
<i>Pinus</i>	gymnospermy
<i>Nyssa</i>	angiospermy
<i>Prunus</i>	angiospermy
<i>Magnolia</i>	angiospermy



I. Overview

Char. 3: Seed Packaging

Cycas	gymnospermy
Pinus	gymnospermy
Nyssa	angiospermy
Prunus	angiospermy
Magnolia	angiospermy

Char. 4: Pollen Type

Cycas	monoaperturate
Pinus	monoaperturate
Nyssa	triperturate
Prunus	triperturate
Magnolia	monoaperturate

Cycas pollen by Kono & Tobe (2007)

Pinus pollen by Schweinböde mann et al. (2007)

Nyssa pollen by Sun et al. (2009)

Prunus pollen by S. Goring

I. Overview

Wings	
Lizard	absent
Bird	present
Human	absent
Bat	present

Bad

I. Overview

Wings	
Lizard	absent
Bird	present
Human	absent
Bat	present

Bad

Forelimb	
Lizard	wingless
Bird	plumose wing
Human	wingless
Bat	membranous wing

Better

I. Overview



C. Recognizing synapomorphies to resolve cladogram

1. Use of parsimony

Leaf shape
IG Sp. A **cordate**
IG Sp. B **cordate**
IG Sp. C **elliptic**

1 step on this tree

1 step on this tree

Problem: These are equally parsimonious

Leaf shape
IG Sp. A **cordate**
IG Sp. B **cordate**
IG Sp. C **elliptic**

1 step on this tree

1 step on this tree

Problem: These are equally Parsimonious

Which state is apomorphic and which is plesiomorphic?

I. Overview



C. Recognizing synapomorphies to resolve cladogram

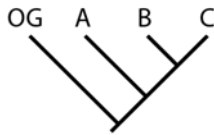
1. Use of parsimony
2. Use of outgroup method

I. Overview



C. Recognizing synapomorphies to resolve cladogram

1. Use of parsimony
2. Use of outgroup method
 - a. Root possible trees btwn OG & IG



- Leaf shape
- IG Sp. A **cordate**
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 - OG Sp. **elliptic**

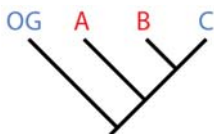


I. Overview

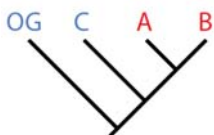


C. Recognizing synapomorphies to resolve cladogram

1. Use of parsimony
2. Use of outgroup method
 - a. Root possible trees btwn OG & IG
 - b. Score taxa



- Leaf shape
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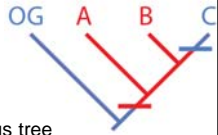


I. Overview



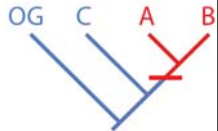
C. Recognizing synapomorphies to resolve cladogram

1. Use of parsimony
2. Use of outgroup method
 - a. Root possible trees btwn OG & IG
 - b. Score taxa
 - c. Choose most parsimonious tree



Leaf shape

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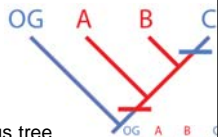


I. Overview



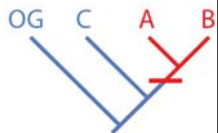
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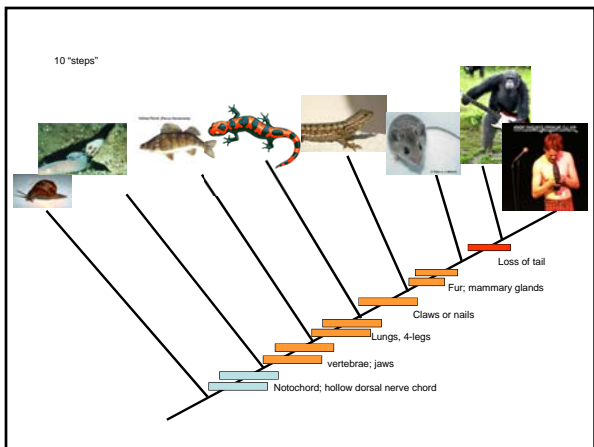
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 - b. Score taxa
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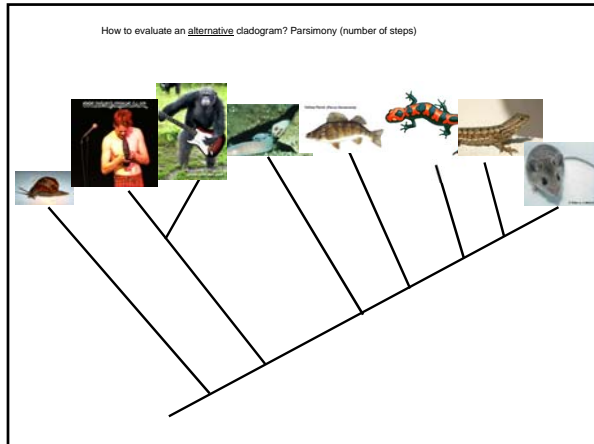


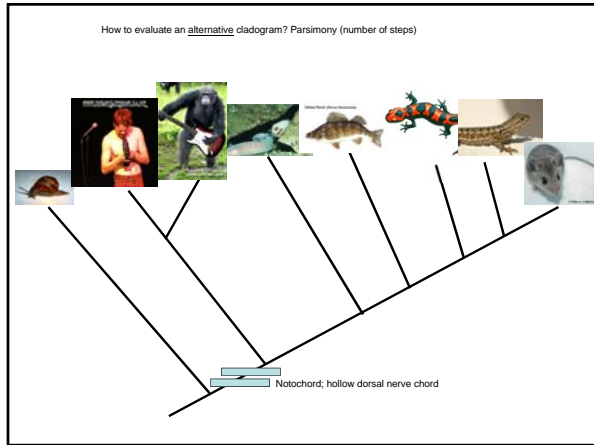
Leaf shape

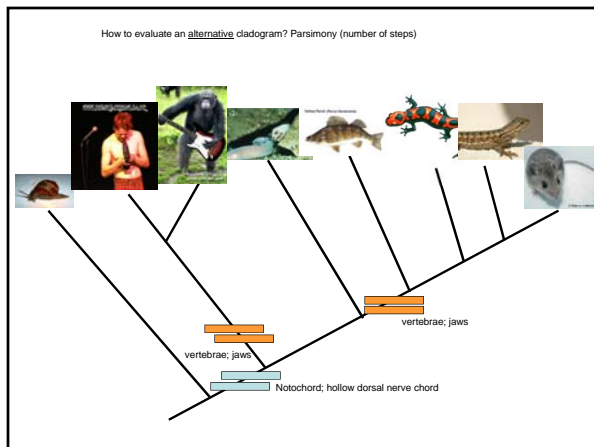
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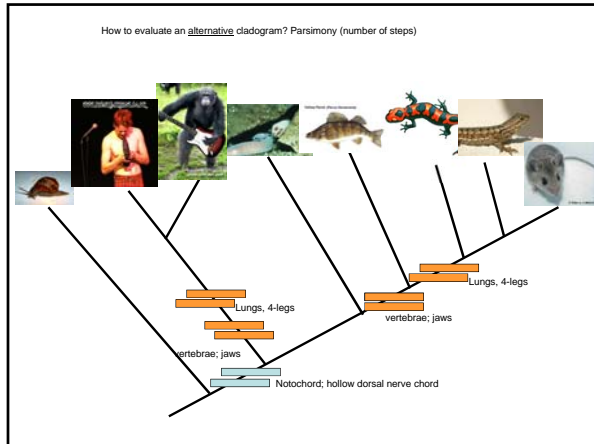


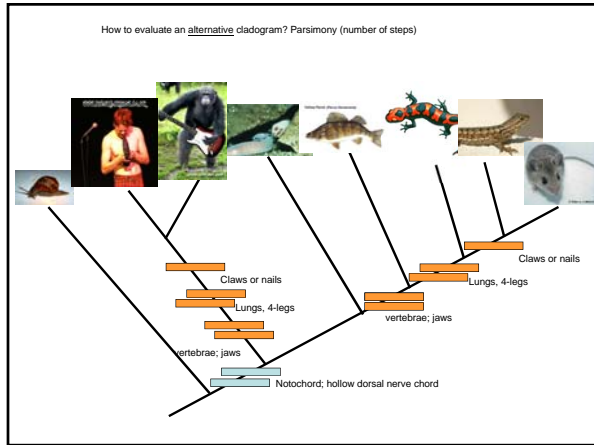


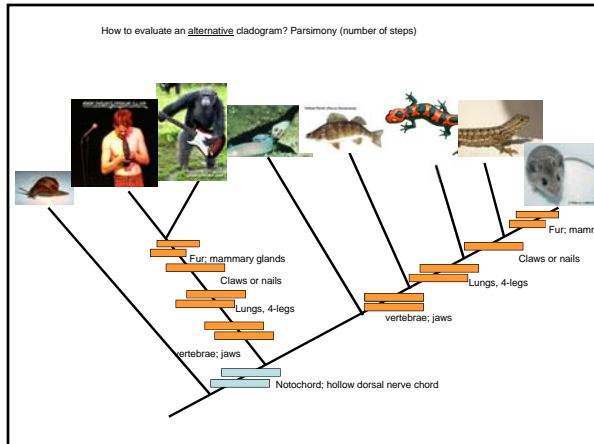


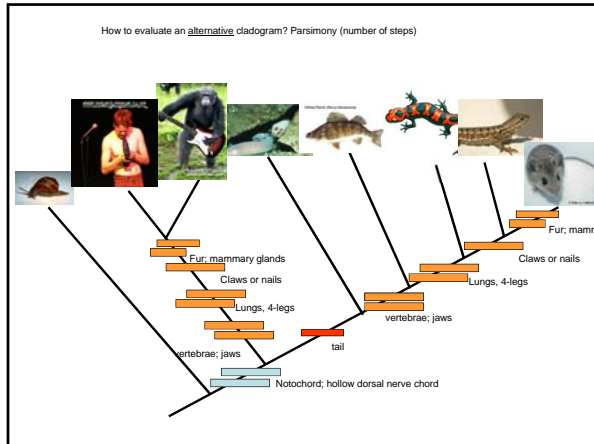


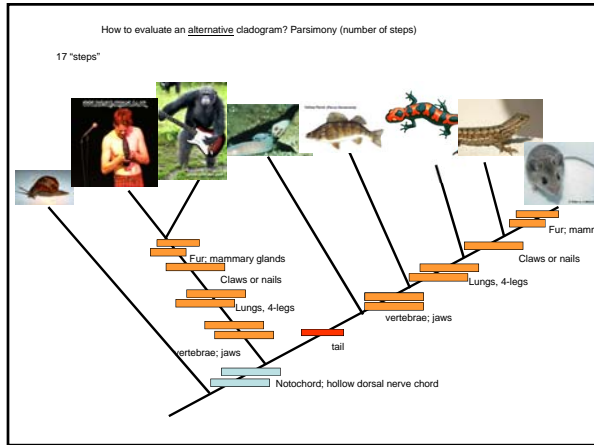


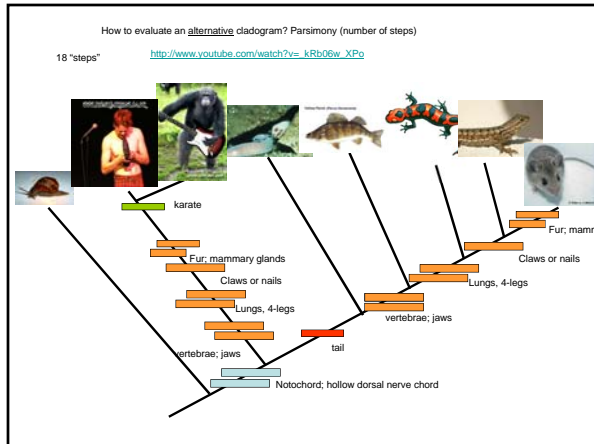












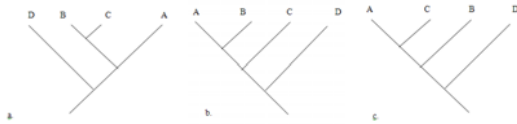
II. Cladogram Construction



A. Choose best cladogram

1. Start with all possible ingroup topologies

	char. 1	char. 2	char. 3	char. 4
Species A	0	0	1	1
Species B	1	1	0	0
Species C	1	0	1	1
Species D (outgroup)	1	1	1	0

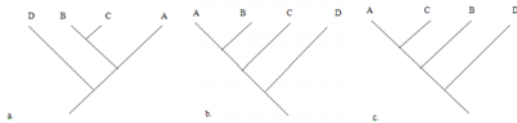


II. Cladogram Construction



2. Use parsimony to map characters

	char. 1	char. 2	char. 3	char. 4
Species A	0	0	1	1
Species B	1	1	0	0
Species C	1	0	1	1
Species D (outgroup)	1	1	1	0

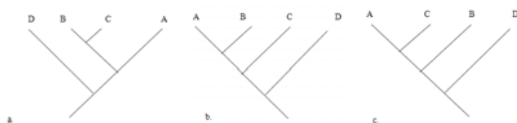


II. Cladogram Construction



3. Choose cladogram with fewest steps

	char. 1	char. 2	char. 3	char. 4
Species A	0	0	1	1
Species B	1	1	0	0
Species C	1	0	1	1
Species D (outgroup)	1	1	1	0



Dr. Chris Hardy

Tutorial:
Character State Optimization for Choosing Most Parsimonious Cladograms and Reconstructing Ancestral States.

The method we will use here is called Fitch Optimization.

1. Score terminal species for character of interest.

Downward Pass

2. Starting at the tips of the cladogram, start with two sister species and assign the intersection or union of the two to the node below them.

An **intersection** is where both descendants of the ancestral node have the same state; therefore, that state is assigned to the ancestral node.

A **union** is where the two descendants of the ancestral node have different states; therefore, both are temporarily assigned to the node.

3. Work the same way from another pair of taxa, down the tree until all nodes have been assigned an intersection or union.

Upward pass

4. Moving up the tree from the basal-most node (for simplicity's sake, assume that the state possessed by the most distant outgroup taxon is the state at the basal-most node), resolve any unions based upon the intersections with the lower node. If there is not intersection for a particular node on the up-pass, then your data are ambiguous for that node.

[THE STATES ASSIGNED TO NODES are one (not necessarily the only one) most parsimonious reconstruction of the state possessed by the hypothetical ancestor of that node's immediate descendants.]

II. Cladogram Construction





Table 1. Data matrix of characteristics of the sporophytes of major lineages of plants.


	Vasculature	Seeds	Flowers	Sporophyte Branching
Mosses (<i>Poltrichum</i>)	0 (absent)	0 (no)	0 (no)	0 (unbranched)
Lycopods (<i>Lycopodium</i>)	1 (present)	0 (no)	0 (no)	1 (dichotomous)
Gymnosperms (<i>Pinus</i>)	1 (present)	1 (yes)	0 (no)	2 (axillary)
Angiosperms (<i>Magnolia</i>)	1 (present)	1 (yes)	1 (yes)	2 (axillary)

II. Cladogram Construction



B. The size of the problem

1. Number of stars in the universe



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The Question
(Submitted January 15, 1997)
How many stars are there, named and un-named, known to exist?

The Answer
This is a very good question! There are too many stars for scientists to actually count one-by-one, so other methods of estimating the total number of stars are used. We believe that there are on the order of 10^{23} stars in our Universe. If you write that number out, it looks like this: 1,000,000,000,000,000,000. This is a lot of stars!

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II. Cladogram Construction



- B. The size of the problem
- 2. Number of possible trees

For 3 taxa (A, B, & C)?

II. Cladogram Construction



- B. The size of the problem
- 2. Number of possible trees

For 4 taxa (A, B, C & D)?

II. Cladogram Construction



- B. The size of the problem
- 2. Number of possible trees

For 5 taxa (A, B, C, D & E)?

II. Cladogram Construction



B. The size of the problem 2. Number of possible trees

The Number of Evolutionary Trees
Joseph Felsenstein
Systematic Zoology, Vol. 27, No. 1 (Mar., 1978), pp. 27-33.

COUNTING TREES 31

TABLE 1. THE NUMBERS OF ROOTED TREES WITH n LABELLED TIPS AND WITH UNLABELLED INTERIOR NODES.

n	Bifurcating Trees
1	1
2	1
3	3
4	15
5	105
6	945
7	10,395
8	135,135
9	2,027,025
10	34,459,425
11	654,739,075
12	13,749,310,575
13	316,234,143,225
14	7,905,853,580,625
15	213,458,048,676,575
16	6,190,283,253,639,275
17	191,898,783,962,310,625
18	6,532,690,870,762,850,625
19	221,643,695,476,699,271,575
20	8,260,794,532,837,891,659,275
21	319,830,986,772,877,270,815,625
22	13,113,070,457,697,988,903,449,625

II. Cladogram Construction



C. Major Parsimony-based cladistic programs

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II. Cladogram Construction



C. Major Parsimony-based cladistic programs

PHYLIP

A new release of PHYLIP, version 3.697, is now available as source code. This release differs in correcting the consensus tree bug that was recently pointed out, and in its license -- from version 3.695 we have had an open source license, so that PHYLIP can be distributed with other software that has commercial licenses or has a restrictive open-source license. Executables are currently at version 3.695, with the old license, but I will update them soon.

PHYLIP is a free package of programs for inferring phylogenies. It is distributed as source code, documentation files, and a number of different types of executables. These Web pages, by Joe Felsenstein of the Department of Genome Sciences, and the Department of Biology of the University of Washington, contain information on PHYLIP and ways to transfer the executables, source code and documentation to your computer.

- A general description of PHYLIP
- Executables in the PHYLIP package

II. Cladogram Construction



C. Major Parsimony-based cladistic programs



II. Cladogram Construction



C. Major Parsimony-based cladistic programs

