Reconstructing Evolutionary Trees
Chapter 13

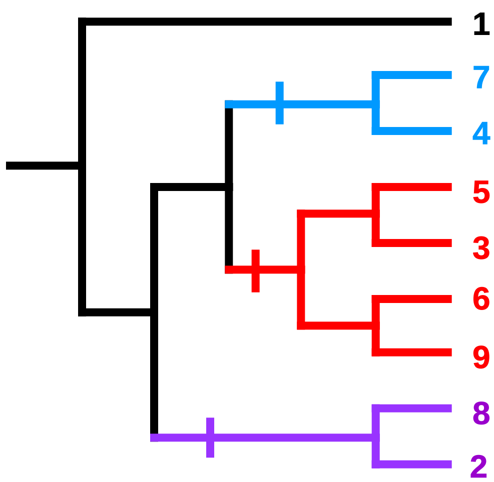
I) The Need for Classification

A) Practical – although of lesser importance, the categorization and grouping of the biological world allows standardization and organization that facilitates communication.

B) Biological – a useful classification scheme should allow the extrapolation of shared biologically significant information from one group to a related group. It would also allow the identification of uniquely varying characters among groups.

II) Cladistics versus Phenetics – two schools of thought.

A) Principle of Parsimony – Occam's razor. When given the choice between two explanations, one simple and one complex, choose the simpler one.



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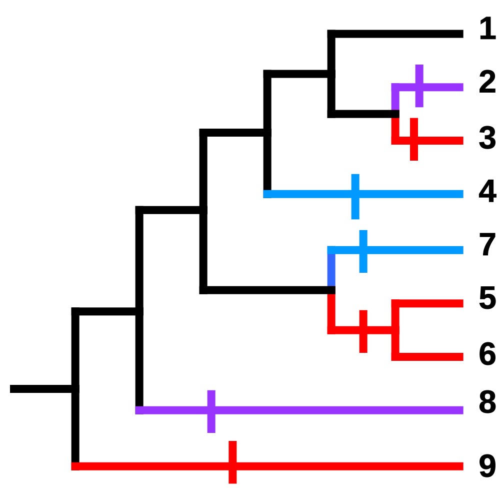

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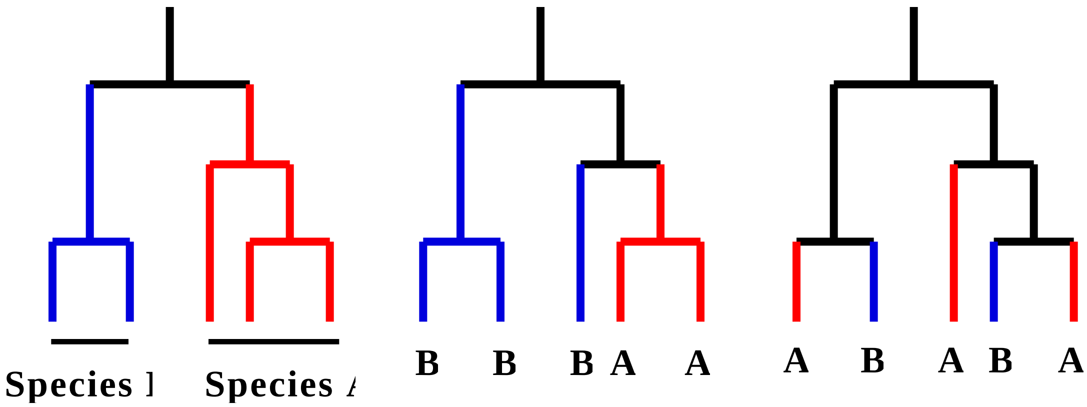
B) Cladistics – Generally thought to be begun in 1950 (and again in 1966 in English) by the German scientist, Willi Hennig (1913- 1976).

1) Major Hennigian principles are (from www.cladistics.org):

- **a) Relationships among species are to be interpreted strictly genealogically, as sister-lineages, as clade relations.**
- **b) Synapomorphies provide the only evidence for identifying common ancestry. Synapomorphies are understood to be the shared-derived (evolved, modified) features of organisms.**
- **c) Maximum conformity to evidence is sought (his auxiliary principle). Choice among competing cladistic propositions (cladograms) is decided on the basis of the greatest amount of evidence, the largest number of synapomorphies explainable as homologues.**
- **d) Whenever possible, taxonomy must be logically consistent with the inferred pattern of historical relationships. The rule of monophyly is to be followed, thereby each clade can have its unique place in the hierarchy of taxonomic names.**

2) Terminology

- **a) Synapomorphy – shared derived character. For example all mammals and only mammals have fur and lactate. The ancestor to mammals did not, therefore this is a derived trait shared by the order.**
- **b) homoplasy – similar characters (traits) in different lineages**
  - **1) convergent evolution – derived characters that evolved independently in two groups (i.e., not shared). Flippers in penguins and seals (parallel evolution).**
  - **2) reversals – synapomorphies in a clade that have been mutated back to the ancestral state.**
- **c) outgroup – organism(s) chosen to represent ancestral state(s) for characters.**
- **d) Monophyletic clade – all individuals in the group are more closely related to each other than they are to individuals in any other groups. This is the only “true” unit in cladistics.**

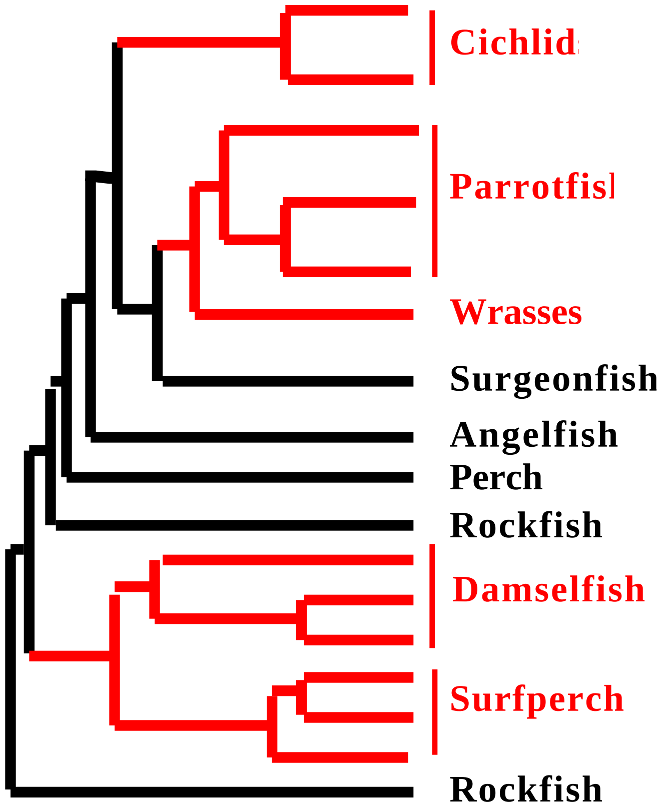


Monophyleti Paraphyleti Polyphyleti

3) Strengths
- a) Simple – only one rule: shared, derived characters
- b) Assumption “free”
- c) Resulting groups are thought to reflect evolutionary history of organisms
- d) Can be universally applied

4) Weaknesses
- a) requires considerable expertise to analyze characters
- b) Ignores a considerable amount of data (i.e., only one rule)
- c) Assumes that evolution is a bifurcating processes.
- d) Selection of outgroup is critically important.
- e) can be circular when trying to understand the evolution of characters and these same characters are the data underlying the phylogeny.

e.g., pharyngeal jawed fish – cichlids, wrasses, parrotfish, damselfish, and surfperch.



C) Phenetics – 1950 and 60s Sneath and Sokal were proponents of using all characters (as many as possible) and relying on statistical analysis to define groups.

1) Major Phenetic principles

- **a) Uses overall similarity (i.e., shared differences as well as non-changed ancestral states) to define groups**
- **b) Measure as many characters as possible and convert to overall similarity (of difference) index.**
- **c) Analyze according to standard statistical principles.**

2) Strengths

- **a) Bases relationship on a large amount of data.**
- **b) No special knowledge necessary**
- **c) Can advance with improved analytical methodology**
- **d) Does not require outgroup.**
- **e) Different approaches with different strengths and weakness can be used.**

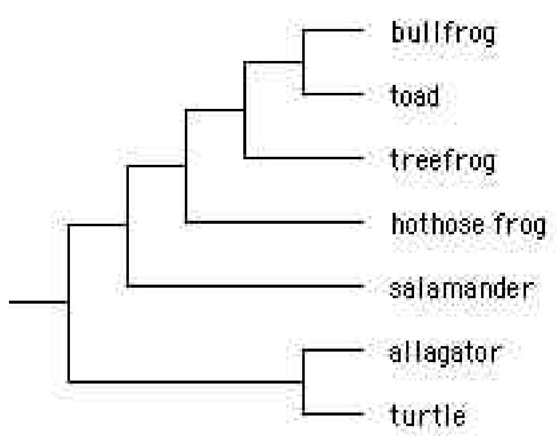
3) Weaknesses

- **a) groups may not reflect true evolutionary history due to homoplasy**
- **b) sensitive to changes in the rate of evolution**
- **c) depending on the analytical approach used, may require a considerable number of untestable assumptions**
- **d) No standard approach universally good**

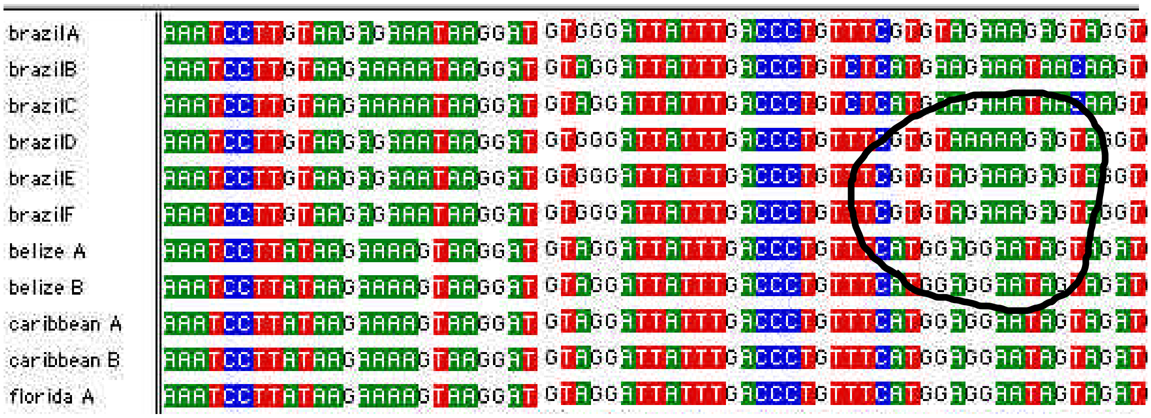
D) Data – regardless of the type of analysis, data can be in a variety of forms.

1) Morphological – using physical or behavioral attributes (meristic or metric) to determine relationship

	tympanic membrane	shelled egg	aquatic	hooded jaw
bullfrog	1	0	0	0
toad	1	0	0	0
tree frog	1	0	0/1	0
hothouse frog	1	0	0	0
salamander	1	0	1	0
alligator	0	1	1	1
turtle	0	1	1	0



2) **Molecular – can use a variety of molecular differences to determine relationships (commonly DNA)**



3) **Reliability of Results – almost any sort of data can be used to produce a tree. How well the data fit the tree, however, is a separate question**

a)Bootstrapping – data can be resampled with replacement and then the phylogenetic relationships reevaluated.

Original Data Set

	Characters											
TAXA	1	2	3	4	5	6	7	8	9	10	11	12
specie1	A	B	C	D	E	F	G	H	I	J	K	L
specie2	A	B	C	D	E	F	G	H	I	J	K	L
specie3	A	B	C	D	E	F	G	H	I	J	K	L
specie4	A	B	C	D	E	F	G	H	I	J	K	L
specie5	A	B	C	D	E	F	G	H	I	J	K	L

Data set 1

	Characters											
									1	1	1	1
TAXA	1	3	6	8	8	8	9	9	1	1	1	1
specie1	A	C	F	H	H	H	I	I	K	K	K	K
specie2	A	C	F	H	H	H	I	I	K	K	K	K
specie3	A	C	F	H	H	H	I	I	K	K	K	K
specie4	A	C	F	H	H	H	I	I	K	K	K	K
specie5	A	C	F	H	H	H	I	I	K	K	K	K

Data set 2

	Characters											
								1	1	1	1	1
TAXA	1	1	2	7	7	7	8	9	0	1	2	2
specie1	A	A	B	G	G	G	H	I	J	K	L	L
specie2	A	A	B	G	G	G	H	I	J	K	L	L
specie3	A	A	B	G	G	G	H	I	J	K	L	L
specie4	A	A	B	G	G	G	H	I	J	K	L	L
specie5	A	A	B	G	G	G	H	I	J	K	L	L

Data Set 3

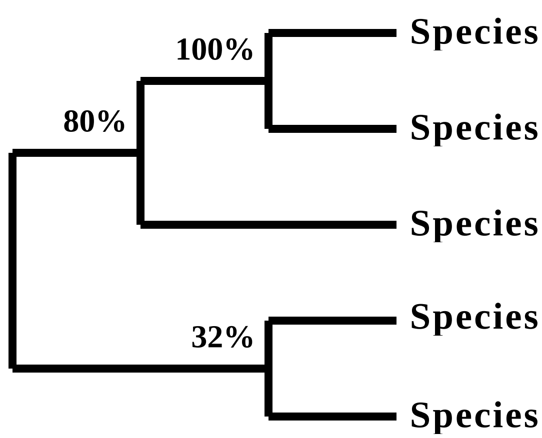
	Characters											
								1	1	1	1	1
TAXA	1	3	4	5	7	9	9	1	2	2	2	2
specie1	A	C	D	E	G	I	I	K	L	L	L	L
specie2	A	C	D	E	G	I	I	K	L	L	L	L
specie3	A	C	D	E	G	I	I	K	L	L	L	L
specie4	A	C	D	E	G	I	I	K	L	L	L	L
specie5	A	C	D	E	G	I	I	K	L	L	L	L

Data Set 4

	Characters											
										1	1	1
TAXA	2	2	3	4	7	7	8	9	9	1	1	2
specie1	B	B	C	D	G	G	H	I	I	K	K	L
specie2	B	B	C	D	G	G	H	I	I	K	K	L
specie3	B	B	C	D	G	G	H	I	I	K	K	L
specie4	B	B	C	D	G	G	H	I	I	K	K	L
specie5	B	B	C	D	G	G	H	I	I	K	K	L

Number OVERALL:

Character	Frequency
A	4
B	3
C	3
D	2
E	1
F	1
G	6
H	5
I	7
J	1
K	8
L	7



4) Solving discrepancies among phylogenies

a) Invoke special knowledge or expertise

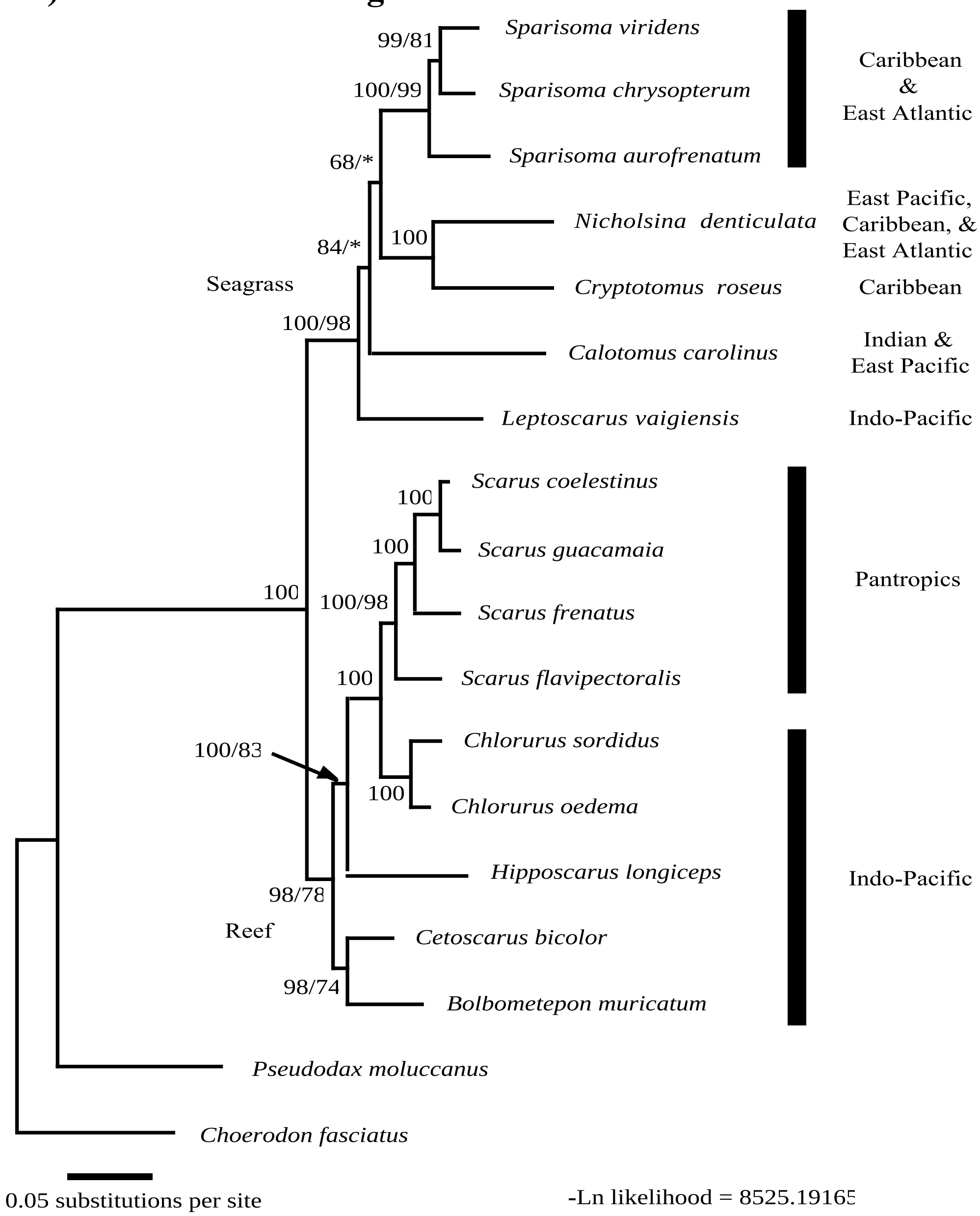
b) Wait for more data

c) Use several different types of characters and analytical approaches and leave ambiguous unresolved differences

III) Phylogenetic Trees for Evolutionary Understanding

A) Character Mapping – understanding the evolutionary history of important biological, behavioral, or morphological characters

1) Evolution of feeding mode in fish



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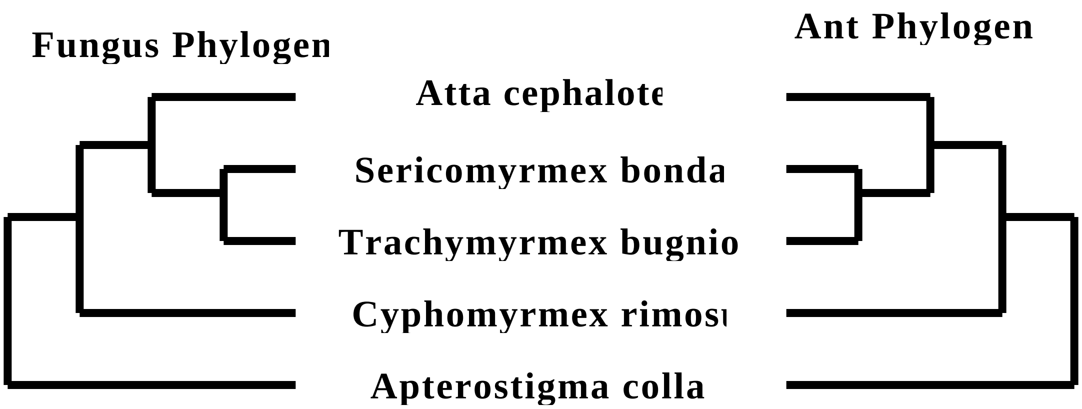
2) Understanding Coevolution in Ants and Fungi – some species of ants farm fungi for food.



3) Identifying Species (or not)