"Systematics is the study of biological diversity and its origins. It focuses on understanding evolutionary relationships among organisms, species, higher taxa, or other biological entities, such as genes, and the evolution of the properties of taxa including intrinsic traits, ecological interactions, and geographic distributions. An important part of systematics is the development of methods for various aspects of phylogenetic inference and biological nomenclature/classification."

-*Systematic Biology* editorial board

1

Systematics

Study of:

- the kinds and diversity of organisms

(http://www.msnbc.msn.com/id/11114156/)

- the relationships among them
- taxonomy and systems of classification

2

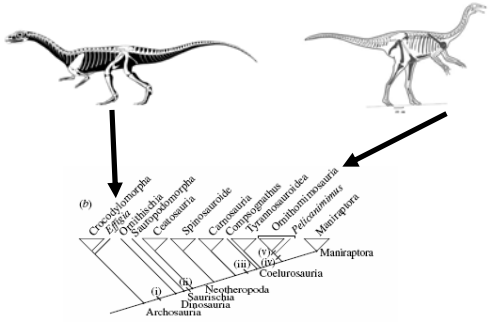
Effigia okeeffeae

Archosaur - 210 my

Harpymimus okladnikovi

Dinosaur - 120 my

3

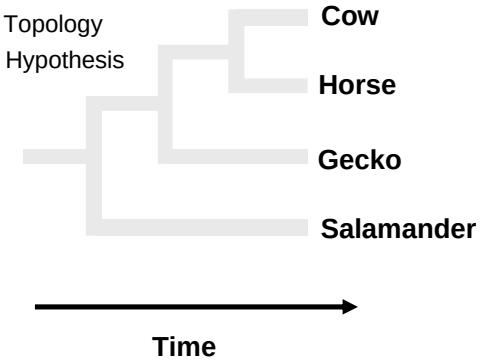


4

5

Phylogenetic Tree or cladogram

- Topology
- Hypothesis



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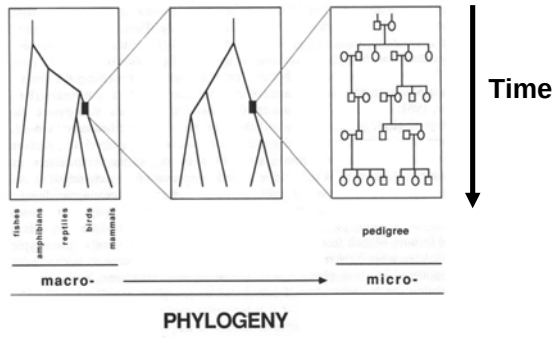
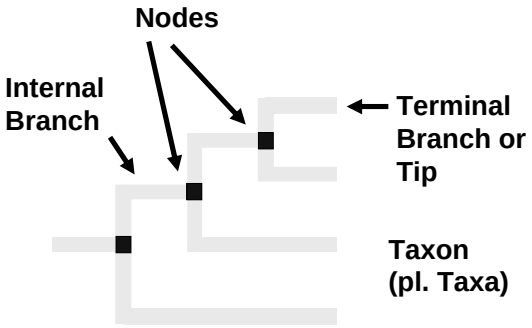


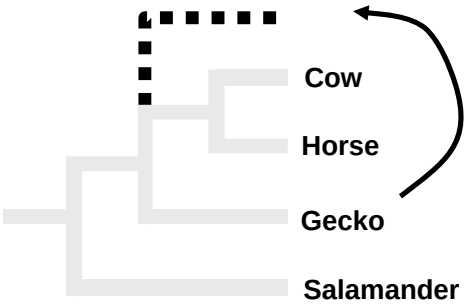
Cladogenesis **Anagenesis**

7



8

Rotation of branches

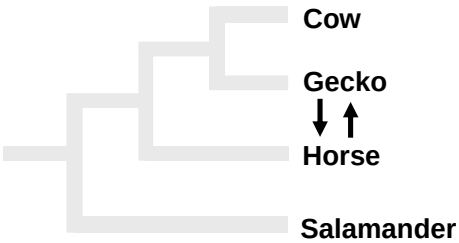


9

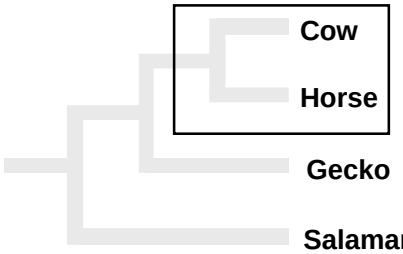
No change in topology

10

New topology

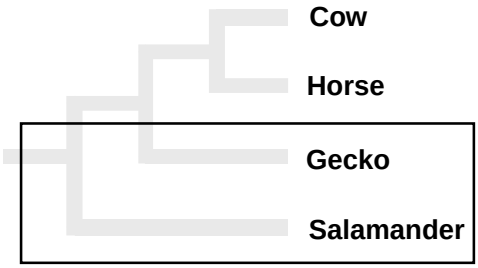


11



- **Monophyletic group**
- **Natural group**
- **Clade**

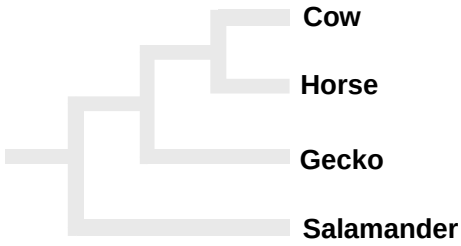
12



Herps

Paraphyletic group

13



The gecko is the *sister taxon* to the mammals in this tree.

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Steps in phylogenetic analysis

Step 1. Select characters for analysis and make data matrix.

Step 2. Select method and search for the best tree.

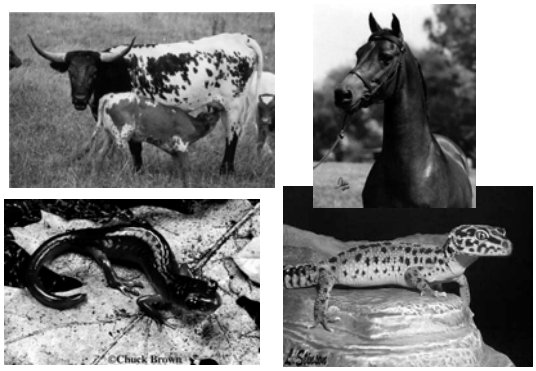
15

Steps in phylogenetic analysis

Step 1. Select characters for analysis and make data matrix.

Step 2. Select method and search for the best tree.

16



Character – any heritable attribute of an organism
Character state – any observed variation of a given character

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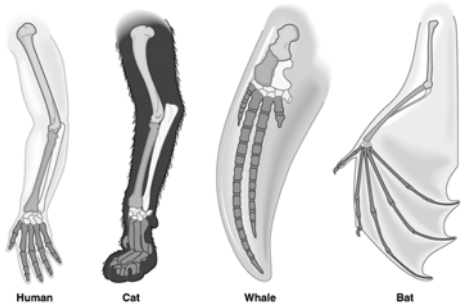


Characters must be homologous (i.e., similar because of decent from a common ancestor).

18

	1	2	3	4
	V	F	L	H
Cow	1	1	1	1
Horse	1	1	1	0
Gecko	1	0	0	0
Salamander	1	0	0	0

Data matrix

19

Steps in phylogenetic analysis

Step 1. Select characters for analysis and make data matrix.

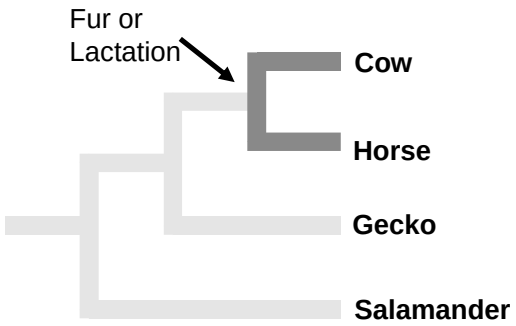
Step 2. Select method and search for the best tree.

20

Maximum parsimony (Cladistics)

- Simpler explanations are preferred over more complex ones.
- Chooses the tree with the fewest evolutionary steps as best estimate of phylogeny.
- Minimizes confusing effects of homoplasy (convergent or analogous characters)

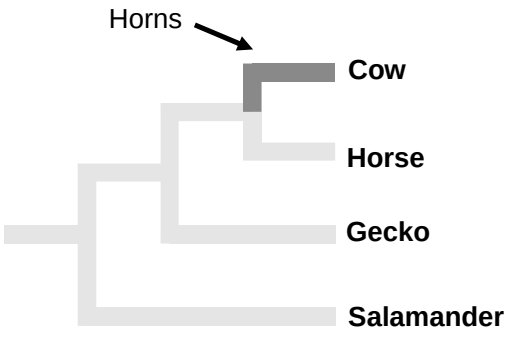
21



Apomorphy – derived character state

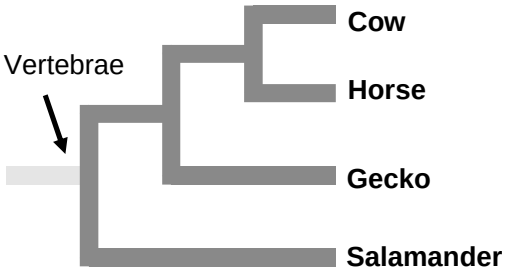
Synapomorphy – shared derived character state

22



Autapomorphy – unshared derived character state

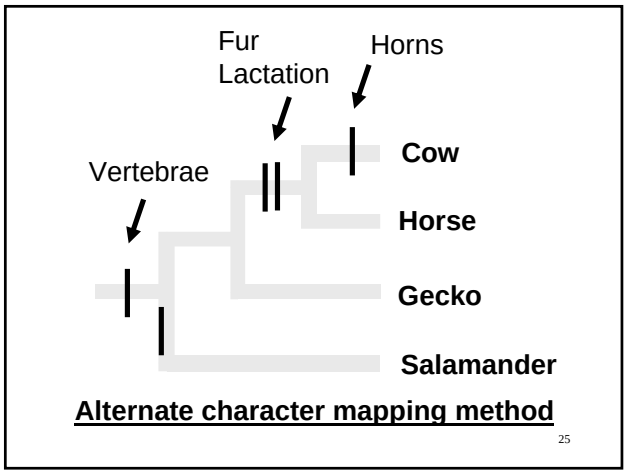
23



Plesiomorphy - ancestral character state

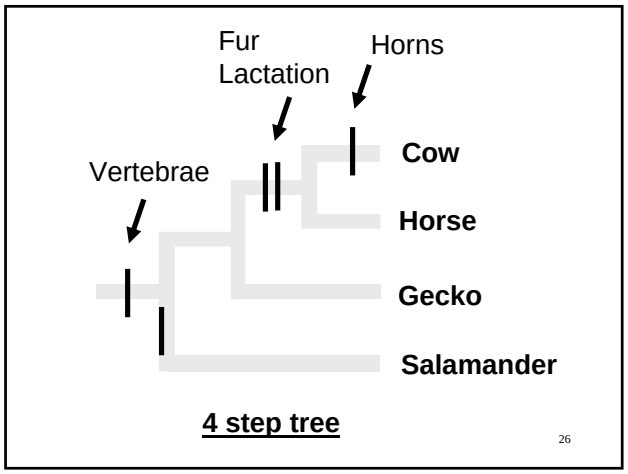
Symplesiomorphy – shared ancestral character state

24



Alternate character mapping method

25



4 step tree

26

No. taxa	No. rooted trees
2	1
3	3
4	15
5	105
10	3×10^{7}
50	3×10^{77}
1000	$4 \times 10^{2,864}$

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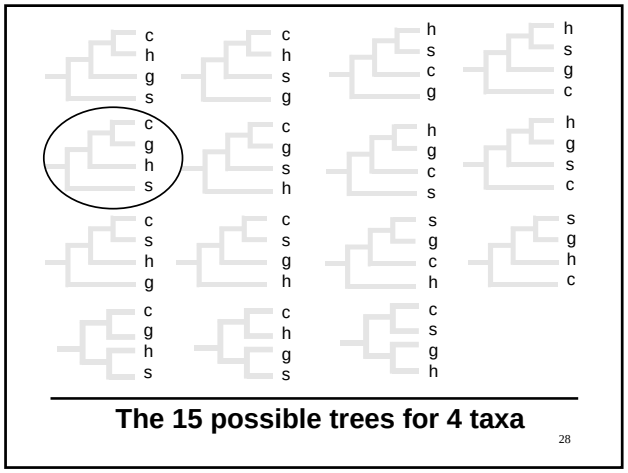
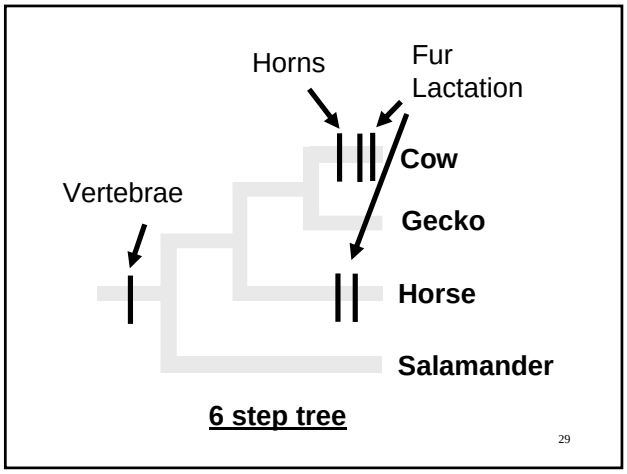


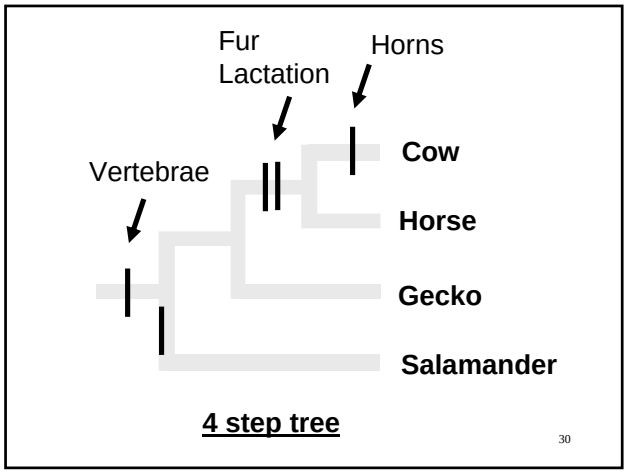
The 15 possible trees for 4 taxa

28



6 step tree

29



4 step tree

30

	1	2	3	4	5
	V	F	L	H	C
Cow	1	1	1	1	1
Horse	1	1	1	0	0
Gecko	1	0	0	0	1
Salamander	1	0	0	0	0

Data matrix

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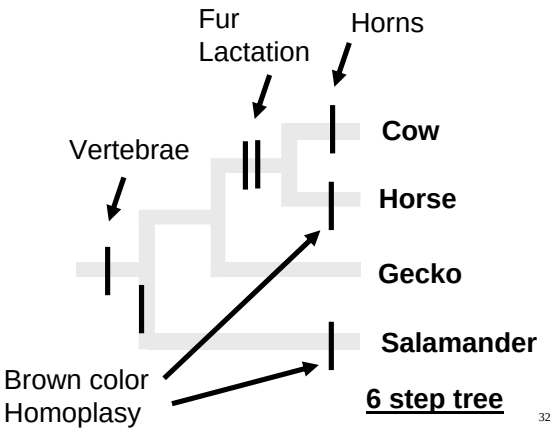

6 step tree

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The Outgroup

- Used to "root" the phylogenetic tree
- Differentiate shared, ancestral character states from shared, derived ones

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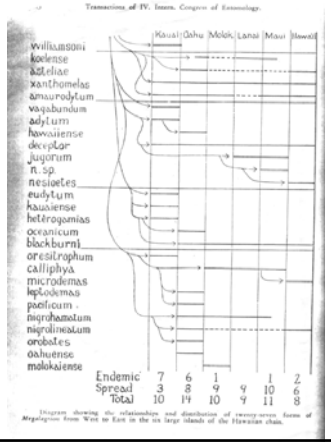

A brief history of Systematics

Phylogeny – a branching diagram representing the evolutionary relationships or history of genes, species or other taxa.

Kennedy (1929)

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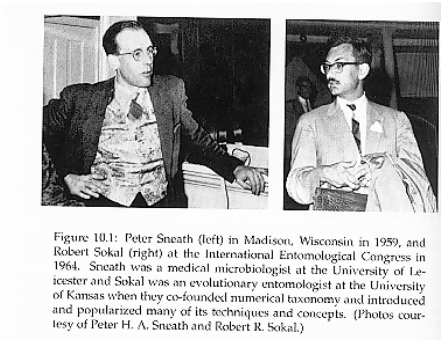

Figure 10.1: Peter Sneath (left) in Madison, Wisconsin in 1959, and Robert Sokal (right) at the International Entomological Congress in 1964. Sneath was a medical microbiologist at the University of Leicester and Sokal was an evolutionary entomologist at the University of Kansas when they co-founded numerical taxonomy and introduced and popularized many of its techniques and concepts. (Photos courtesy of Peter H. A. Sneath and Robert R. Sokal.)

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Willi Hennig

36

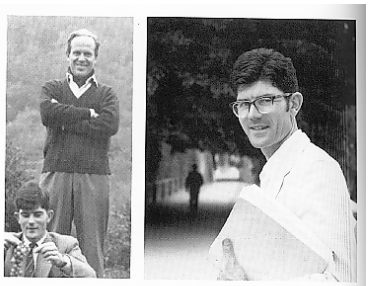

Figure 10.3: Luca Cavalli-Sforza (standing) with Anthony Edwards in Italy in 1963, and Anthony Edwards (right, in Cambridge, England, in 1970). Edwards and Cavalli-Sforza were both at the University of Pavia when they collaborated in founding numerical phylogenetics, seeing it as a problem in statistical inference and introducing the parsimony, likelihood, and distance matrix methods for inferring phylogenies. (Left photo by Motoo Kimura, courtesy of Mrs. Hiroko Kimura; right photo by the author.)

David Swofford

FSU

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Today's Goals

1. Construct a phylogeny of vertebrates using the "vertebrate example" data set
2. Construct a phylogeny for eight primate species using skulls in the lab.

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Using Mesquite

Analysis of phylogeny & character evolution

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