

Phylogenetic terminology and applications

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(With thanks to Mark Holder, Paul Lewis, Joe Felsenstein, and David Hillis
for slides)

Phylogenies describe shared ancestry
and
inform our understanding of evolutionary processes

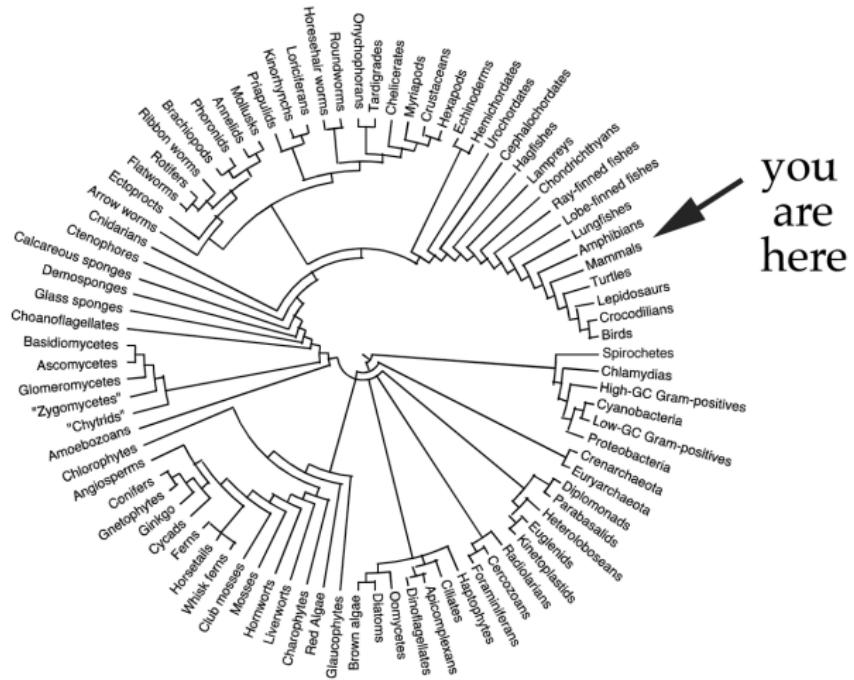


Image Ethan Hein

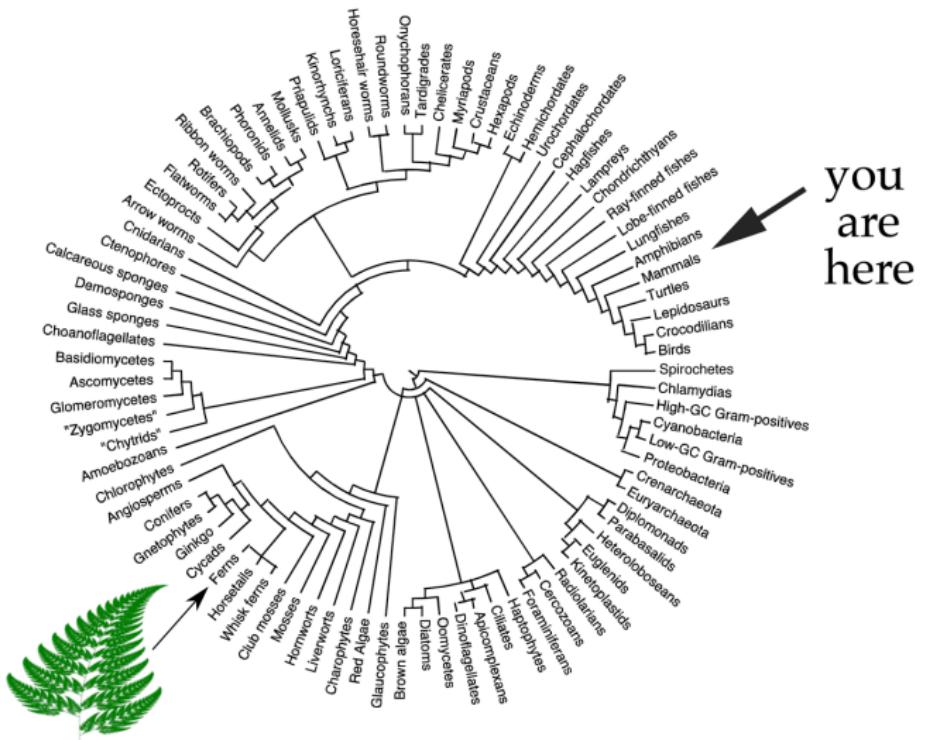
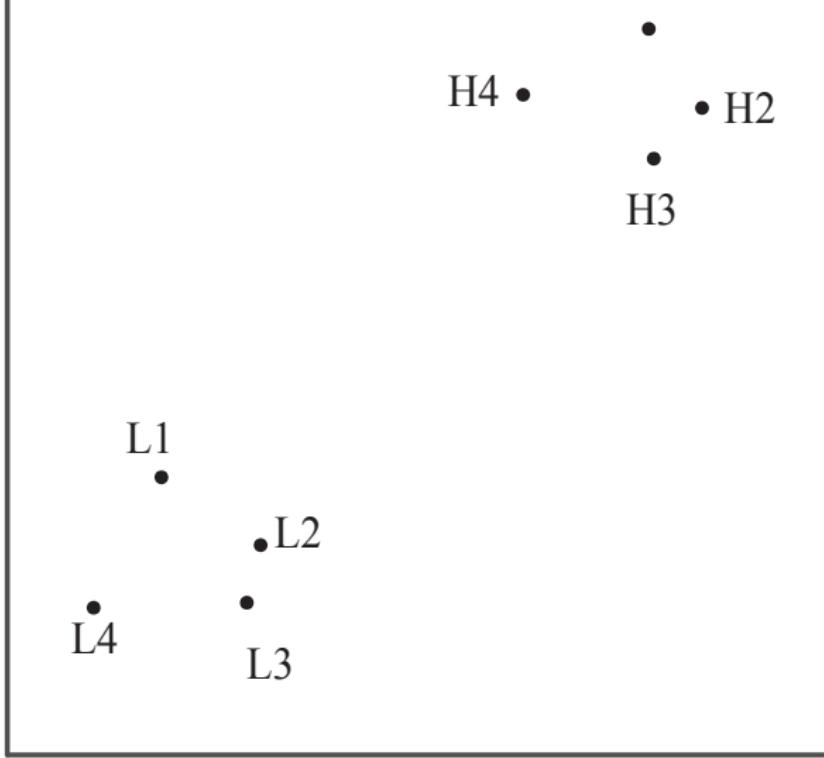


Image Ethan Hein

Simple test of Bergmann's rule: comparing latitude and mass (I made these data up)

lat. offset = degrees north of the 49th parallel.

species	lat. offset	mass
L1	3.1	5.9
L2	5.4	4.3
L3	5.1	3.1
L4	1.8	3.6
H1	13.5	15.2
H2	14.6	13.5
H3	13.6	12.4
H4	10.8	13.7

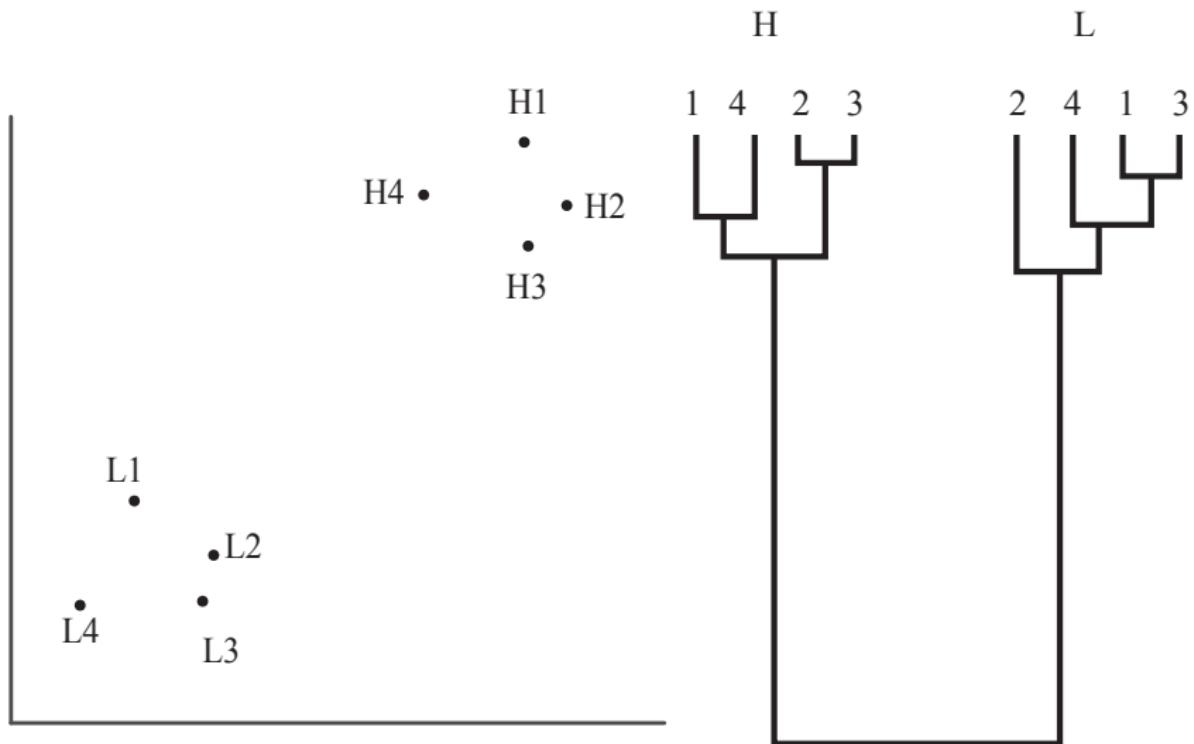


(cue cartoon videos)

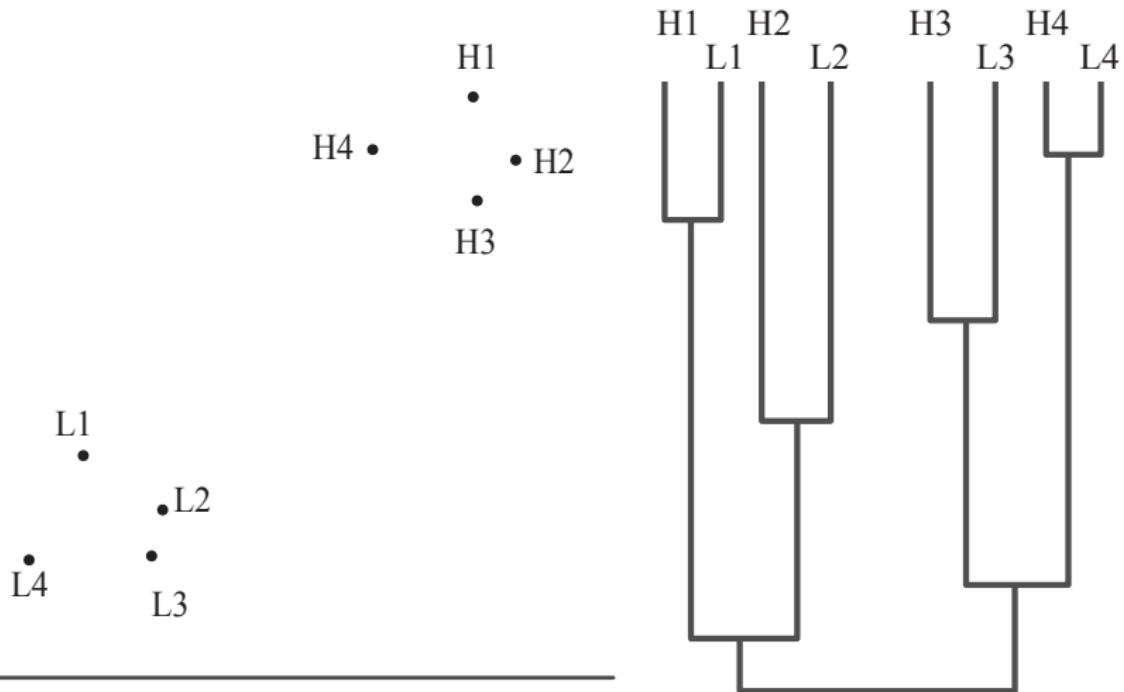
See <http://phylo.bio.ku.edu/slides/no-correl-anim.mov>

and <http://phylo.bio.ku.edu/slides/correl-anim2.mov>

No (or little) evidence for correlation



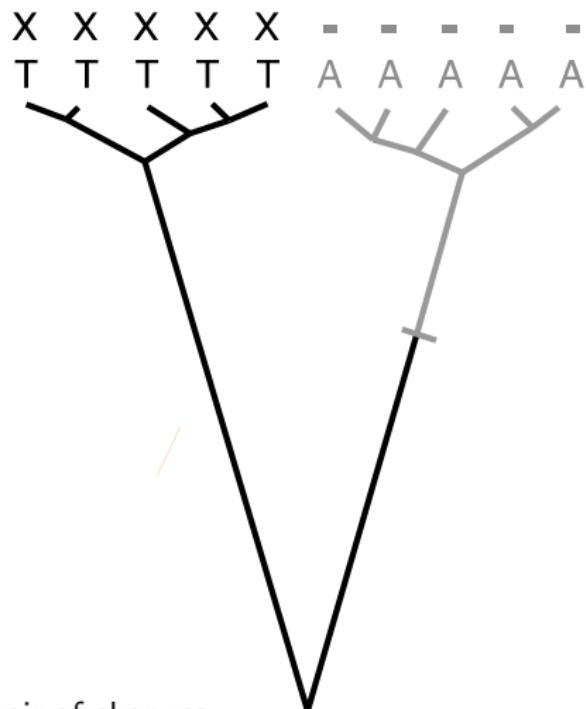
Evidence for correlation



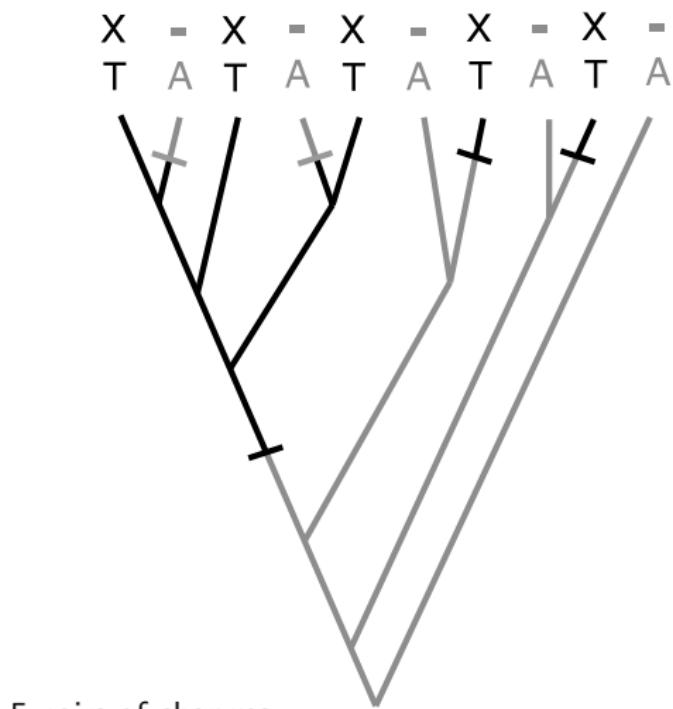
Do desert green algae use xanthophyll to protect against excessive light intensities?

Species	Habitat	Photoprotection
1	terrestrial	xanthophyll
2	terrestrial	xanthophyll
3	terrestrial	xanthophyll
4	terrestrial	xanthophyll
5	terrestrial	xanthophyll
6	aquatic	none
7	aquatic	none
8	aquatic	none
9	aquatic	none
10	aquatic	none

Phylogeny reveals the events that generate the pattern



1 pair of changes.
Coincidence?



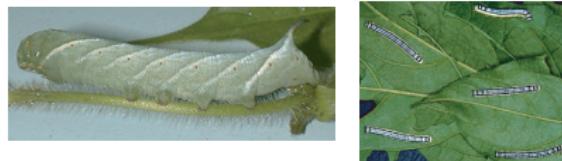
5 pairs of changes.
Much more convincing

Inferring Process from Pattern

Hypothesis:

Gregariousness should arise more frequently in unpalatable organisms than in tasty ones (**Sillén-Tullberg, 1988**)

Inferring Process from Pattern



Solitary

Gregarious



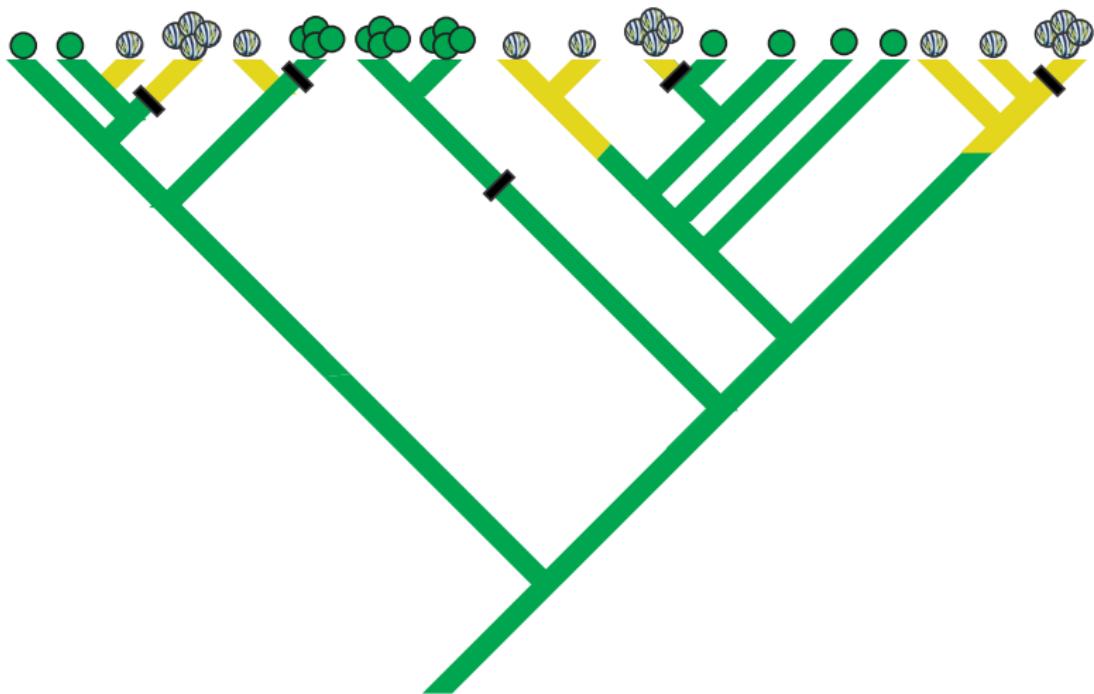
Cryptic



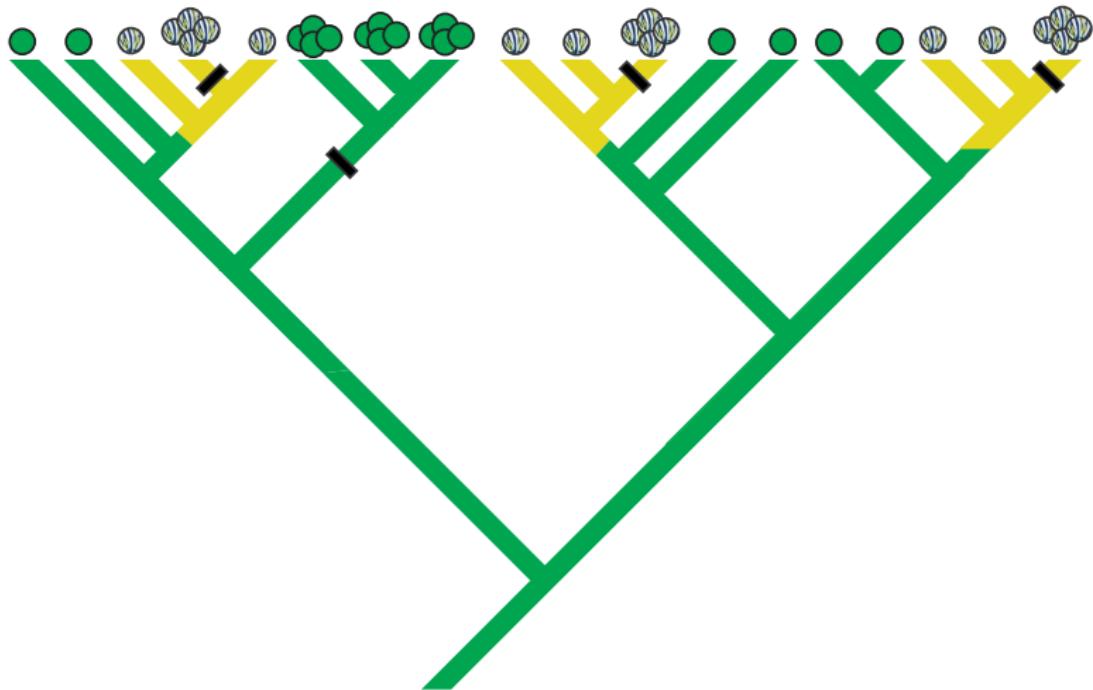
Aposematic



Sillén-Tullberg (1988), Dyer and Gentry (2002), Hill (2001)



One possible outcome:
No clear evidence of associations between traits



Cartoon of the real results ([Sillén-Tullberg, 1988](#))

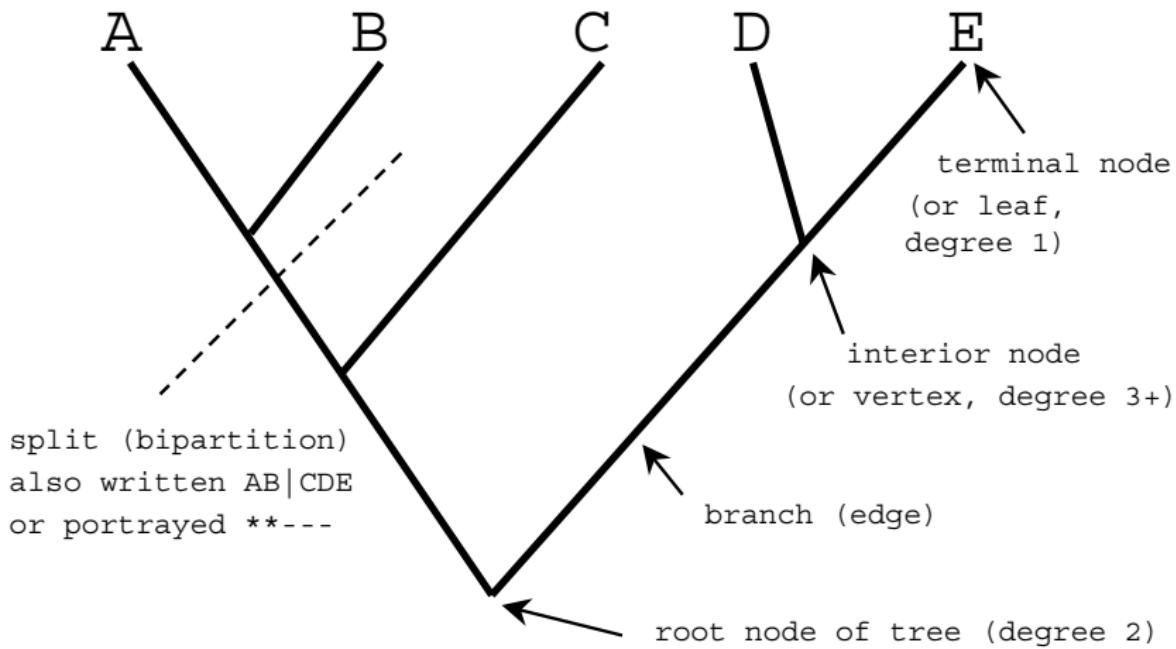
Aposematic species are more likely to evolve gregarious larvae

Importance of phylogeny

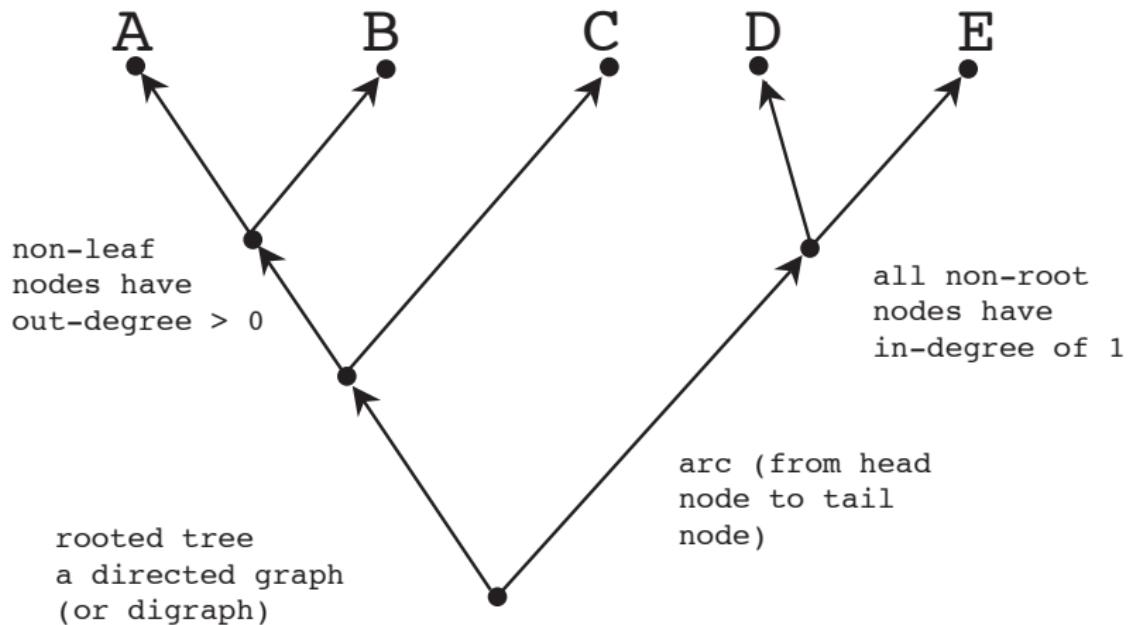
The previous slides had identical patterns of traits if the phylogeny is ignored.

Without knowledge of the tree, no conclusion would be reached.

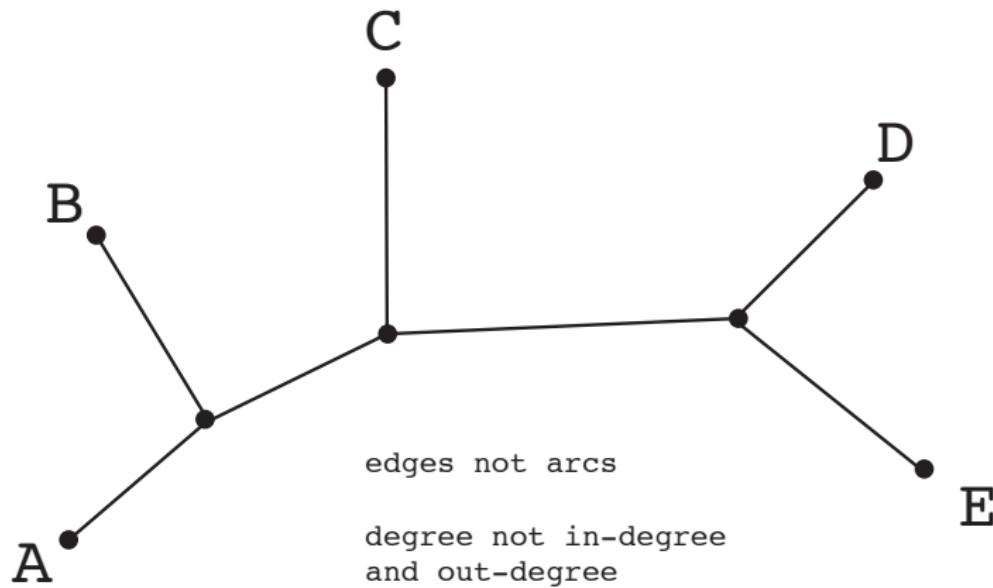
Tree terminology



Rooted tree terminology



Rooted tree terminology



Tree terms

A tree is a connected, acyclic graph.

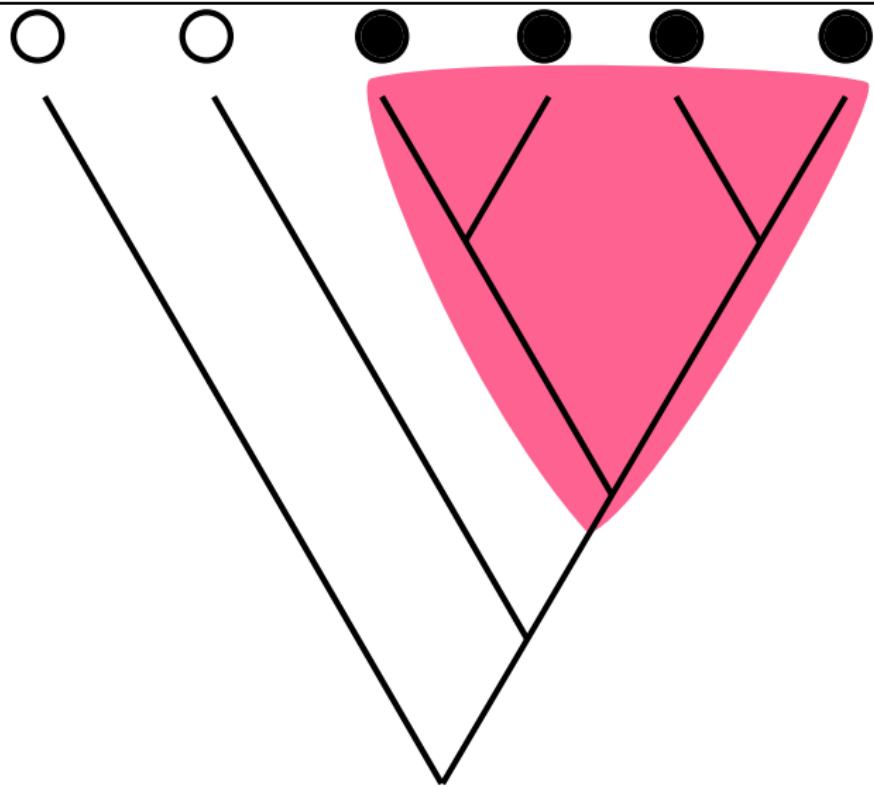
A rooted tree is a connected, acyclic directed graph.

A polytomy or multifurcation is a node with a degree > 3 (in an unrooted tree), or a node with an out-degree > 2 (in a rooted tree).

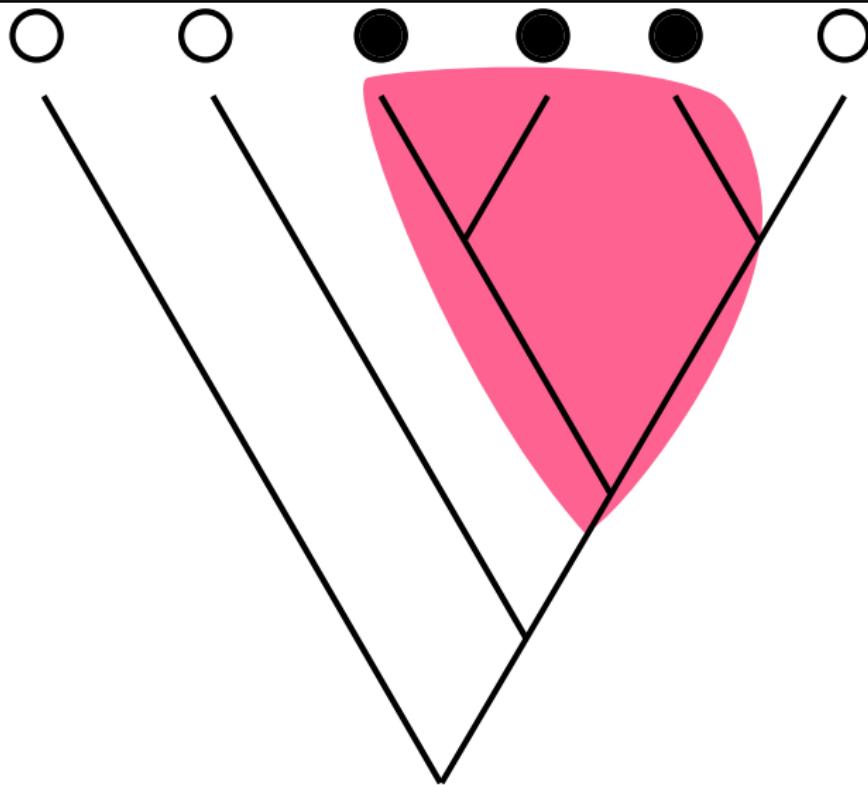
Collapsing an edge means to merge the nodes at the end of the branch (resulting in a polytomy in most cases).

Refining a polytomy means to “break” the node into two nodes that are connected by an edge.

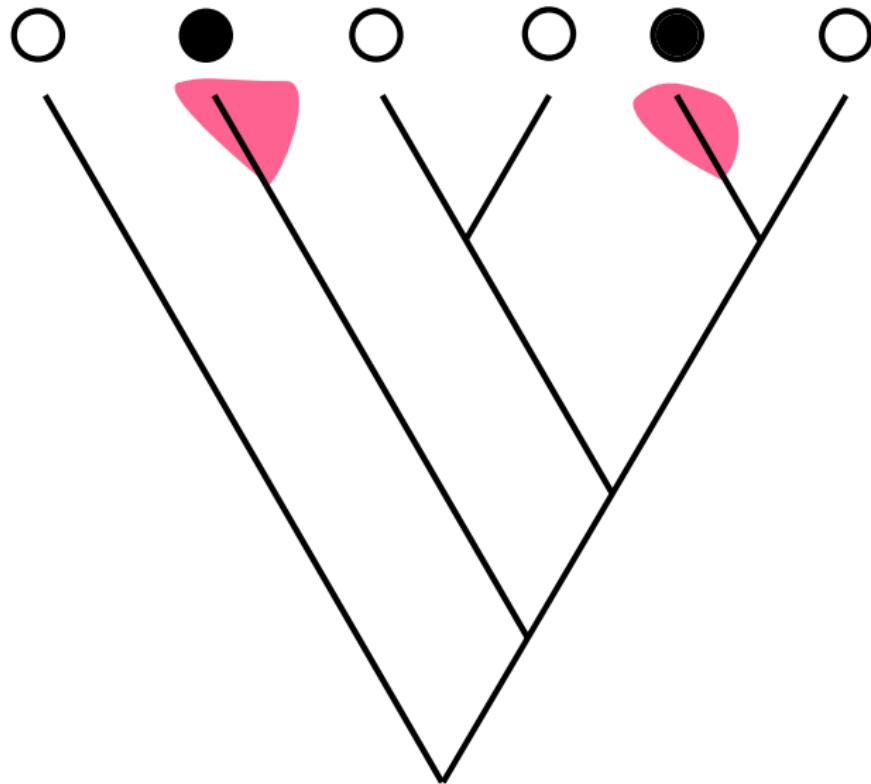
Monophyletic groups (“clades”): the basis of phylogenetic classification



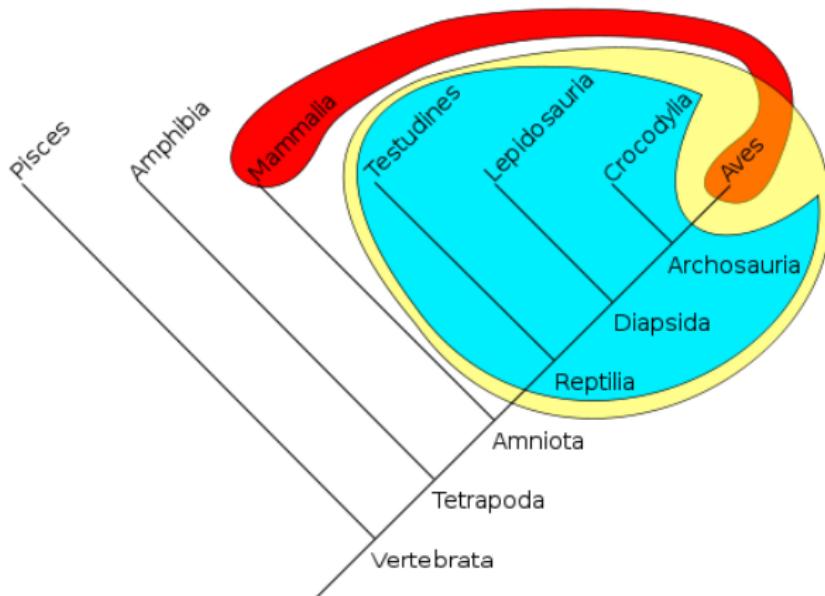
Paraphyletic groups: error of omitting some species



Polyphyletic groups: error of grouping “unrelated” species

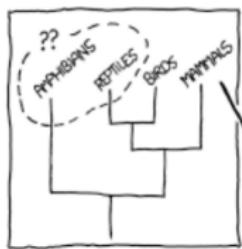


- Monophyly
- Paraphyly
- Polyphyly



from wikipedia

ORNITHOLOGY CONFERENCE:

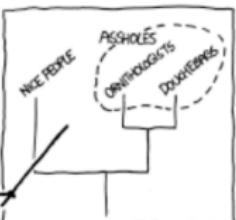


AS YOU CAN SEE, HERPETOLOGY IS A SILLY FIELD; REPTILES ARE ACTUALLY MORE CLOSELY RELATED TO BIRDS AND MAMMALS THAN TO AMPHIBIANS.

)
IT SHOULD REALLY BE BROKEN UP, WITH LIZARDS FOLDED INTO ORNITHOLOGY.

HERPETOLOGY CONFERENCE:

AS YOU CAN SEE, ORNITHOLOGISTS ARE ACTUALLY ASSHOLES.



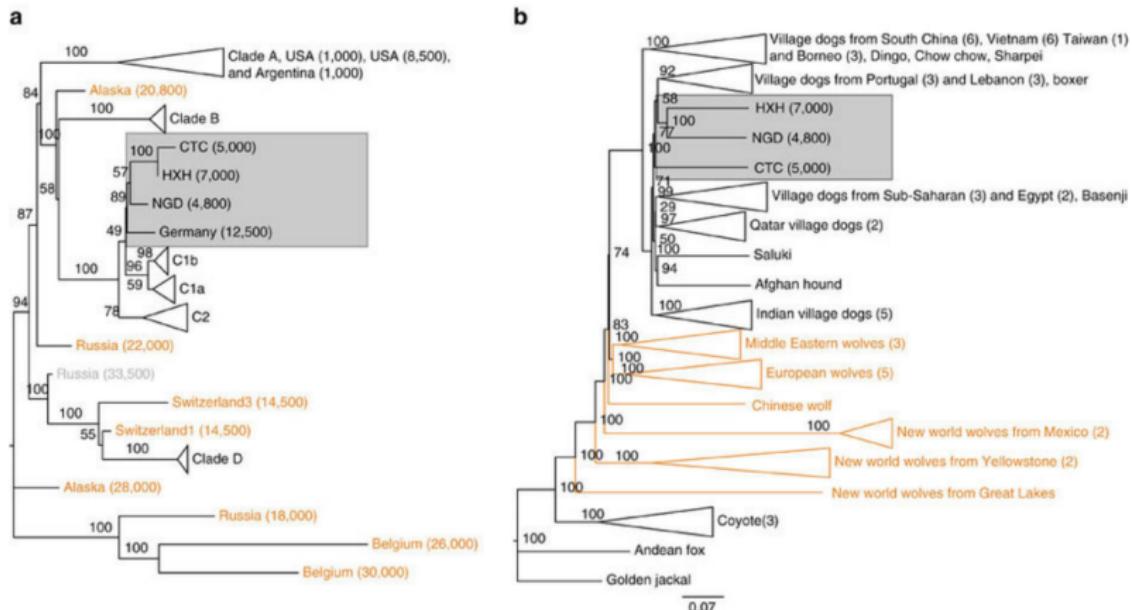
<https://xkcd.com/867/>

Are dogs a monophyletic group in this tree?

Are wolves?

Figure 1: Phylogeny of ancient and contemporary canids.

From: Ancient European dog genomes reveal continuity since the Early Neolithic

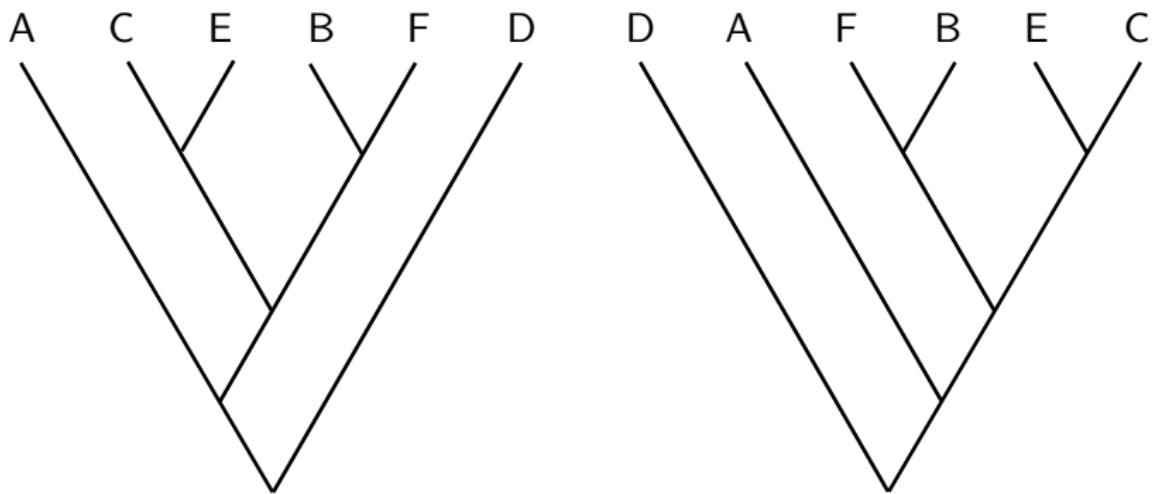


(a) Phylogeny based on mtDNA. Age of the samples is indicated in parentheses, wolf samples are shown in orange. (b) NJ tree based on pairwise sequence divergence from whole-genome data.

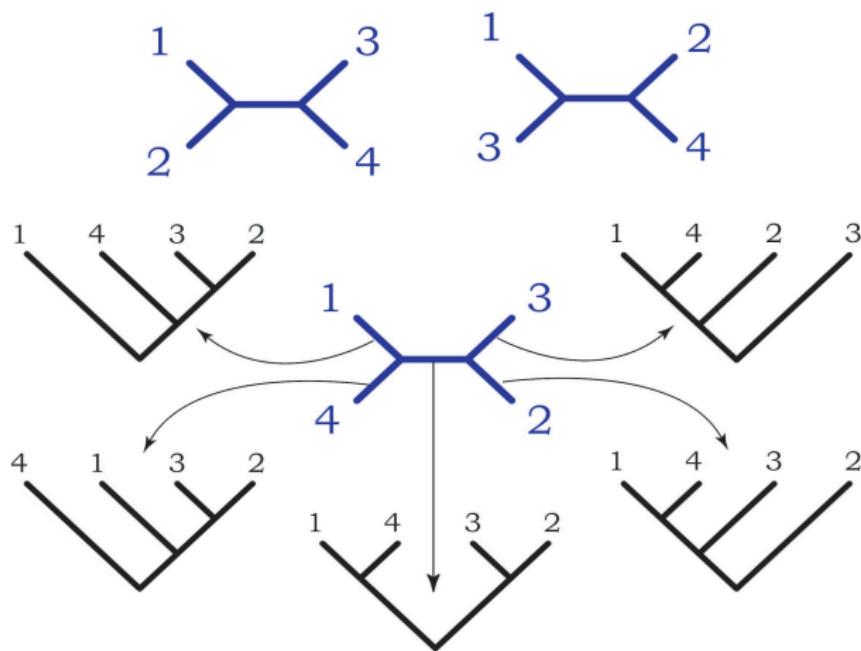
more terms:

- ▶ sister taxa: taxa or monophyletic groups which share a most recent common ancestor
- ▶ outgroup: taxon that is determined *a priori* to be sister to all other taxa in the analysis. Used for rooting tree

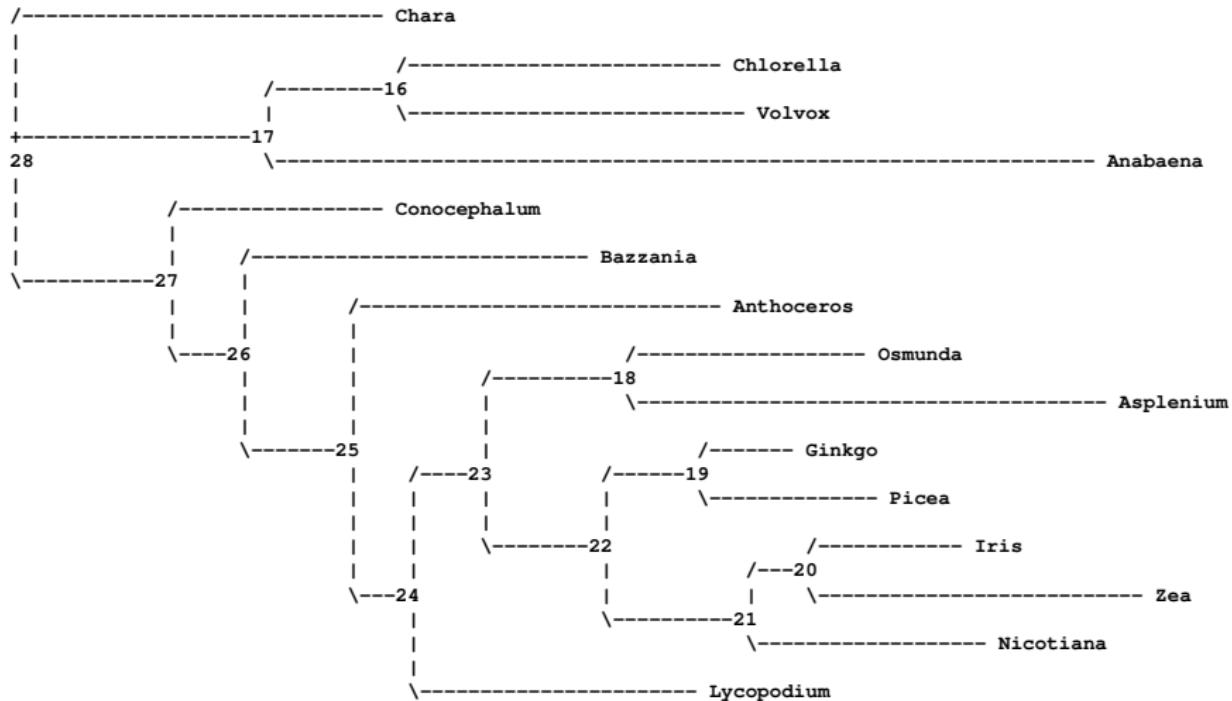
Branch rotation does not matter



Rooted vs unrooted trees

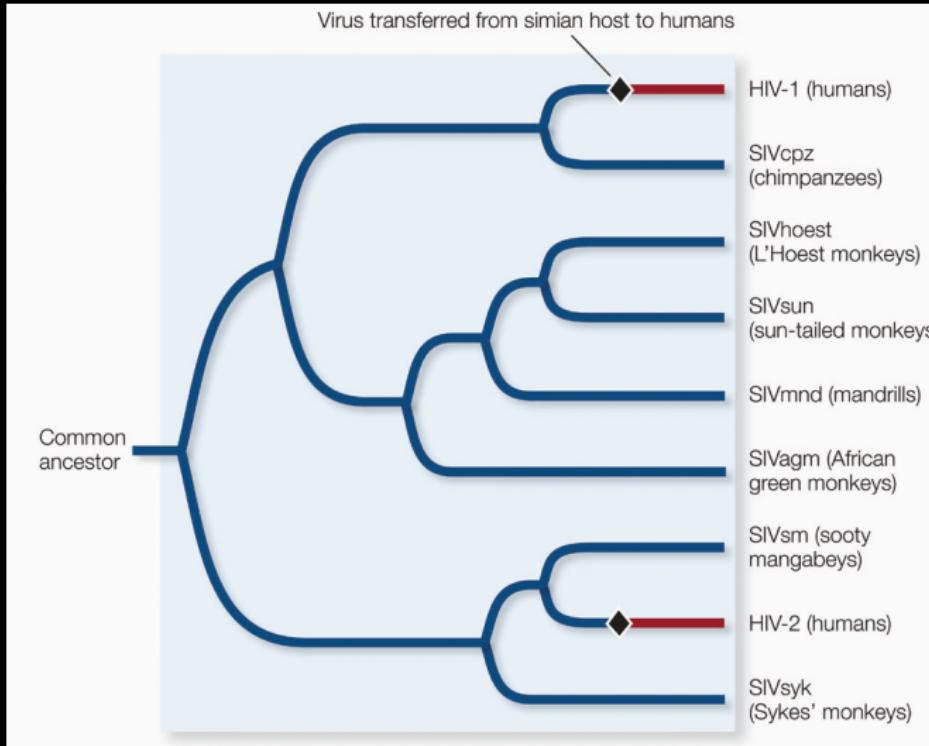


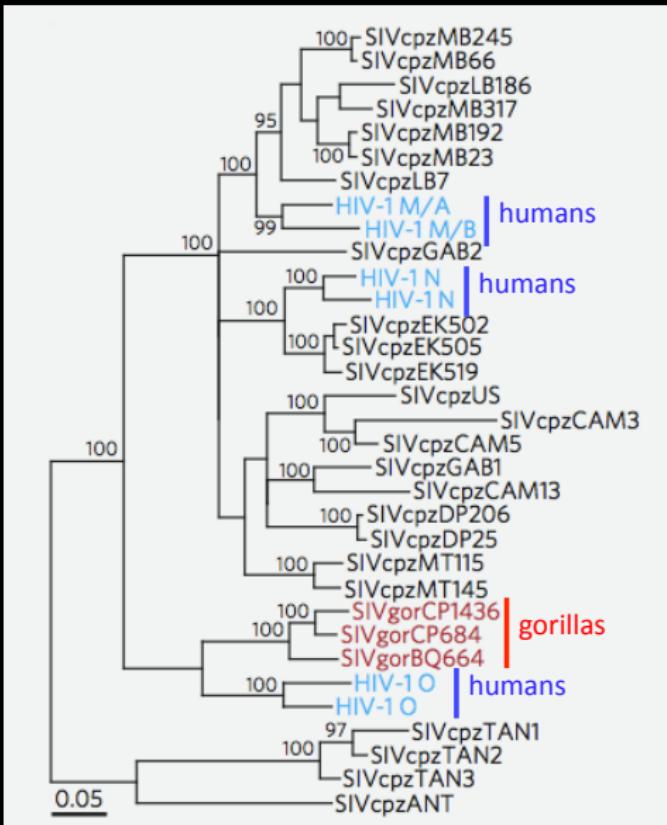
Warning: software often displays unrooted trees like this:



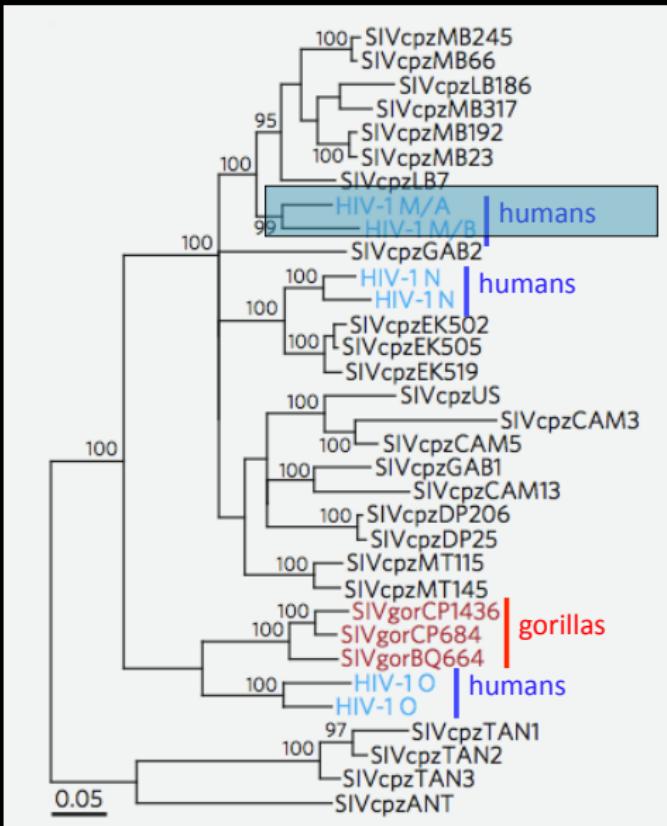
Origins of Emerging Diseases

- Where did HIV come from?
- How did it enter human populations?
- When did it enter human populations?
- How can we prevent similar diseases from entering human populations?

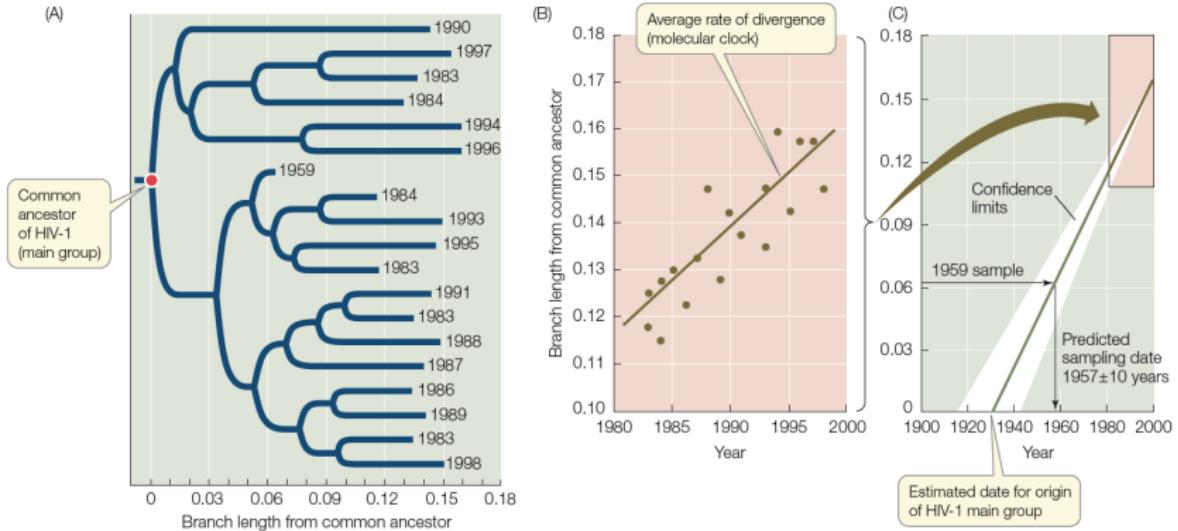




Van Heuverswyn et al., *Nature* 444: 164 (2006)



Van Heuverswyn et al., *Nature* 444: 164 (2006)



THE DAILY ADVERTISER

Louisiana

Acadiana's Daily Newspaper

Thursday, October 22, 1998

DNA debate

Jury hears AIDS DNA evidence against Schmidt

BILL DECKER
Staff Writer

LAFAYETTE — Testimony in the attempted murder trial of Dr. Richard Schmidt continued Wednesday to the prosecution's DNA evidence — and defense attorneys one by one were asked to provide affidavits.

A study College of Medicine researchers at the University of Texas at Austin found in 1995 that AIDS virus strains found in alleged victim Allen were identical to those found in Schmidt's patients. The study supports the prosecution's case that Schmidt injected Allen with the AIDS virus in 1985. Schmidt has denied injecting Allen with the AIDS virus, and he claims he was a patient Dunn McClelland on Aug. 4, 1985.

Dr. Michael Metker, who performed the study in 1995 and now works at the University of Baylor and David Hillis, a University of Texas expert who reviewed Schmidt's work, both testified Wednesday.



Defense attorney Michael Fawer, left, leaves court followed by Dr. Richard Schmidt, after Wednesday's proceedings. Testimony continues at 9 a.m. today.

Alleged source of AIDS-tainted blood testifies

BILL DECKER
Staff Writer

be drawn from McClelland and injected it into Allen that night. It is the first time he ended their 10-year affair.

McClelland, who has AIDS, died in 1996.

LAFAYETTE — Former teacher Dunn McClelland testi-

Phylogenetic analysis can be used to trace viral infections through a human population

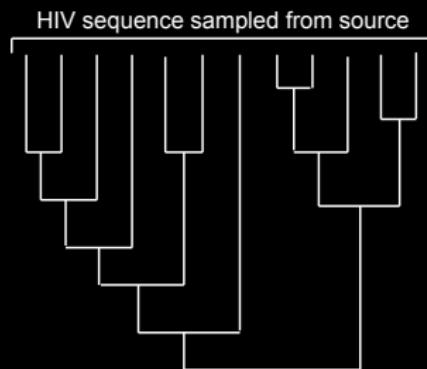
- **Origins of HIV, SARS and other viruses transmitted between animals and humans**
- **Global virus diversity for vaccine trials**
- **Epidemiological studies**
- **Identification of new diseases**
- **Forensic uses**

HIV transmission

Viral transmission events may be traced back through time among individuals in a population.

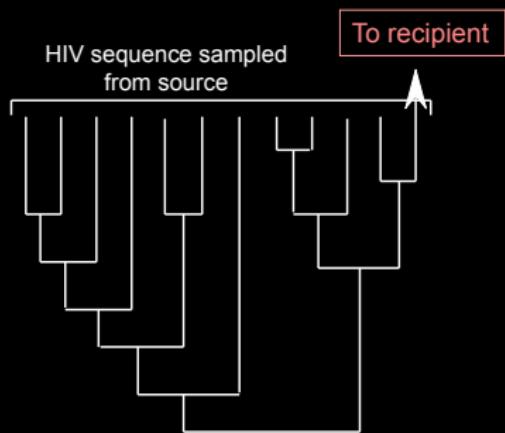
To imagine how this is possible, start by considering the diversity of HIV within one infected individual:

Time 1: Prior to Transmission event



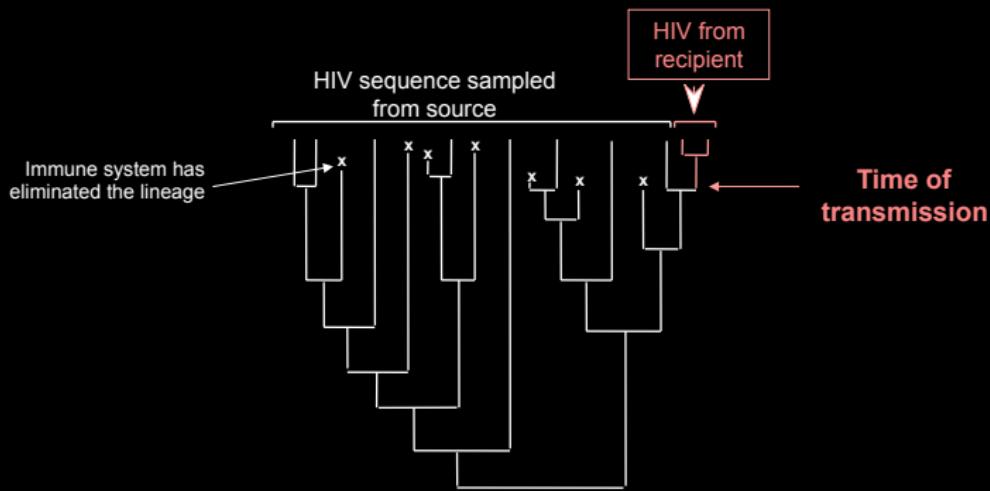
At the transmission event, the HIV in the recipient represents a small subset of the HIV present in the source:

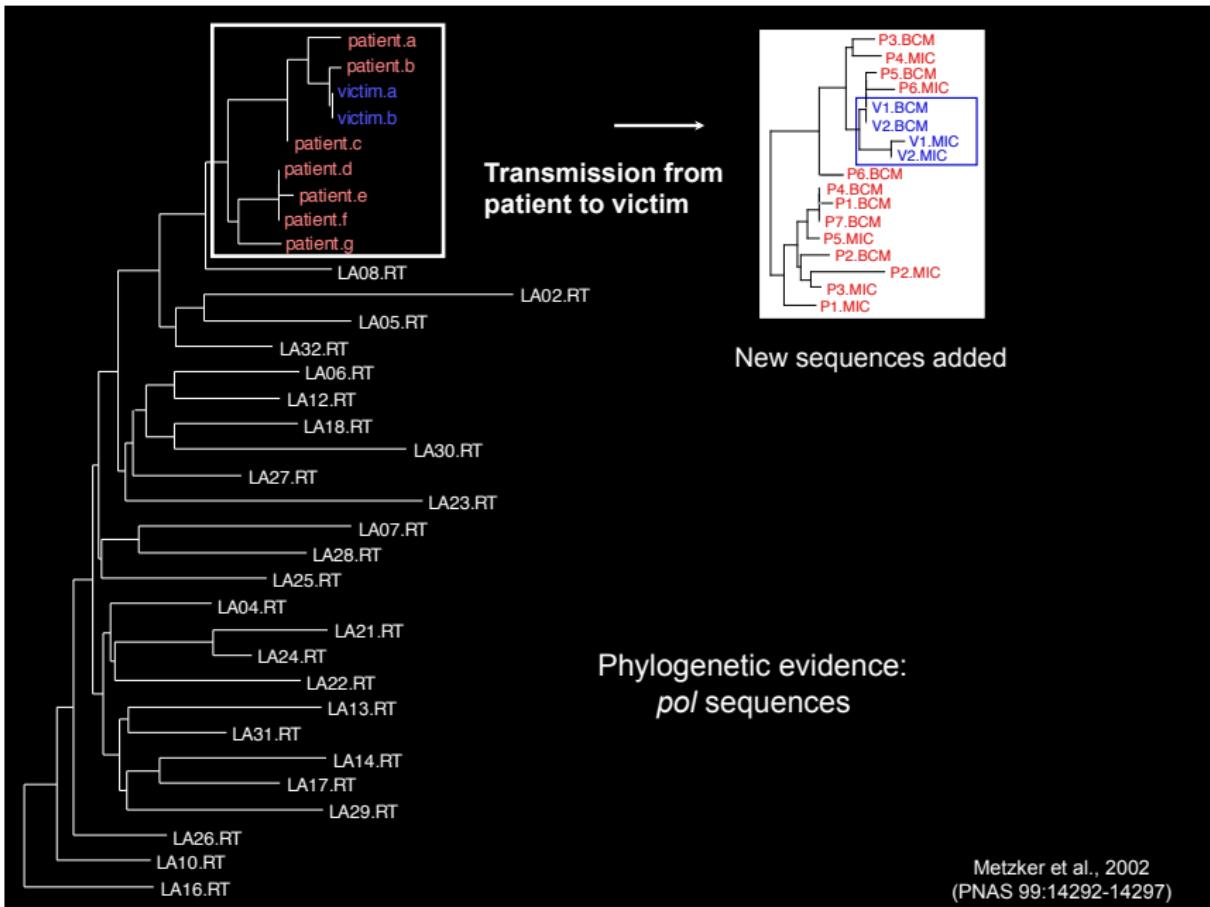
Time 2: The transmission event



As time passes, HIV lineages in the source and recipient diversify, and other lineages become extinct.

Time 3: Shortly after transmission event





THE DAILY ADVERTISER

Acadiana's Daily Newspaper

Louisiana

Saturday, October 24, 1998

Schmidt guilty

Doctor faces
50-year jail
sentence

By Bill Decker
Staff Writer

LAFAYETTE — A Lafayette Parish jury found Dr. Richard Schmidt guilty late Friday of attempted second-degree murder in a botched and premeditated shooting trial.

Schmidt, 54, was convicted of intentionally poisoning the AIDS virus into state Justice Thibaut Albin de Lapeyrière in 1988 after he was accused of killing off AIDS patients in New Orleans.

Waiting for the verdict, Schmidt, dressed in a suit after a 9½-hour trial, clutched the hand of his estranged wife, Barbara, 44, very tightly. When the clock read 8:45 p.m., Schmidt began sobbing loudly.

"I'm sorry," he said as the verdict was read, shaking his creation, but as the decision turned to him, Schmidt's face went pale. "I'm sorry." After being convicted of attempted pending sentencing, Schmidt sat up and put his head in his hands. Then he stood up and turned to embrace his wife, Barbara, who sobbed loudly.

Schmidt, 54, was born and was taken from the courtroom in a wheelchair.

He did not think this is what the jury should do, defense attorney Michael Finner said after the trial. "It's not clear to me why it's not clear that this case was brought with reasonably doubt."

The now-widowed Schmidt

had already been sentenced to mandatory life imprisonment without parole. The jury received the formal



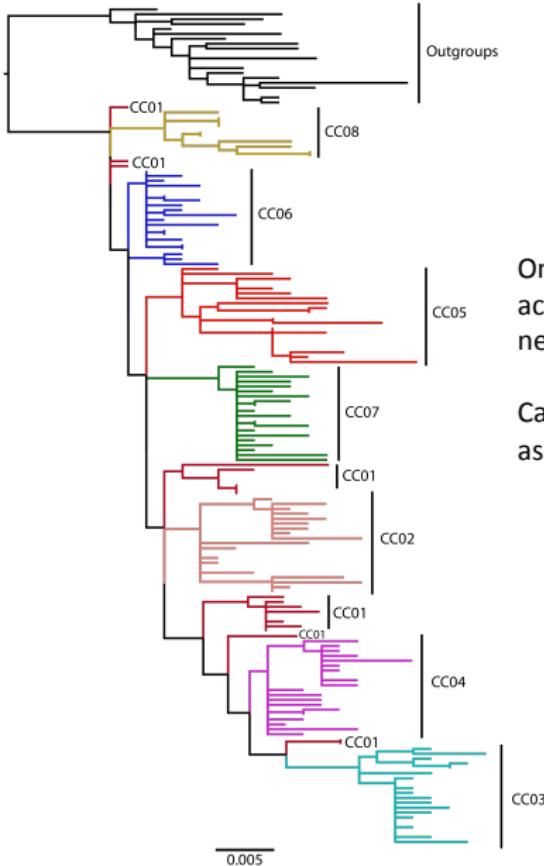
Dr. Richard Schmidt, center, leaves the Lafayette Parish Courthouse Friday night with his estranged wife, Barbara, after being convicted of attempted second-degree murder. Schmidt is accompanied by courthouse security and defense attorney Gerald Block, left.

Claps, sobs, fainting
spell greet verdict

By Ester Avi
Staff Writer

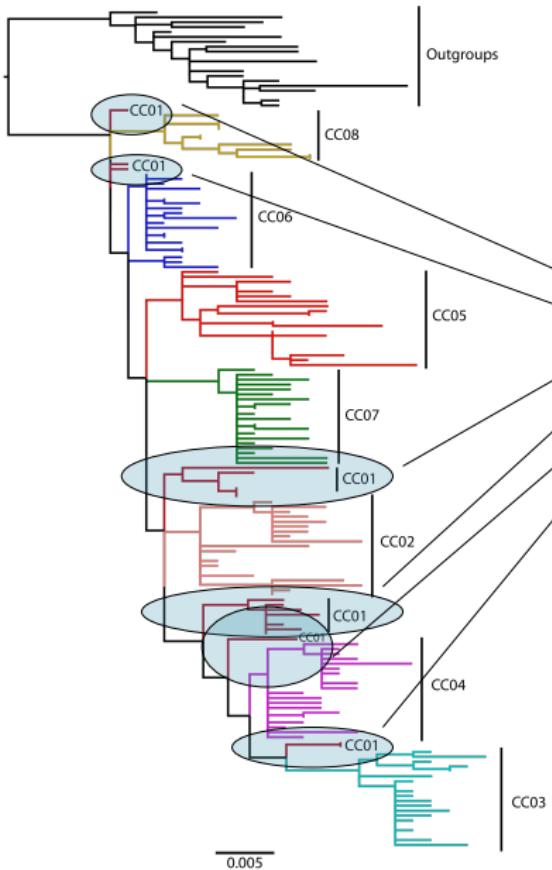


- Schmidt was convicted of attempted murder; currently serving term of 50 years of hard labor
- First use of phylogenetic analysis in U.S. criminal case
- Phylogenetics can be used to trace infections of human pathogens among individuals



One of these individuals is accused of knowingly and negligently infecting the others.

Can one person be identified as the source of the infections?



One individual (CC01) is paraphyletic to all the rest. At the trial, CC01 was revealed to be the defendant, who was accused of six counts of motivated assault. He was found guilty by the jury in May 2009.

Changing the rooting of this phylogeny would change inferences!

Phylogenies can reveal surprising patterns



Phylogenies can reveal surprising patterns

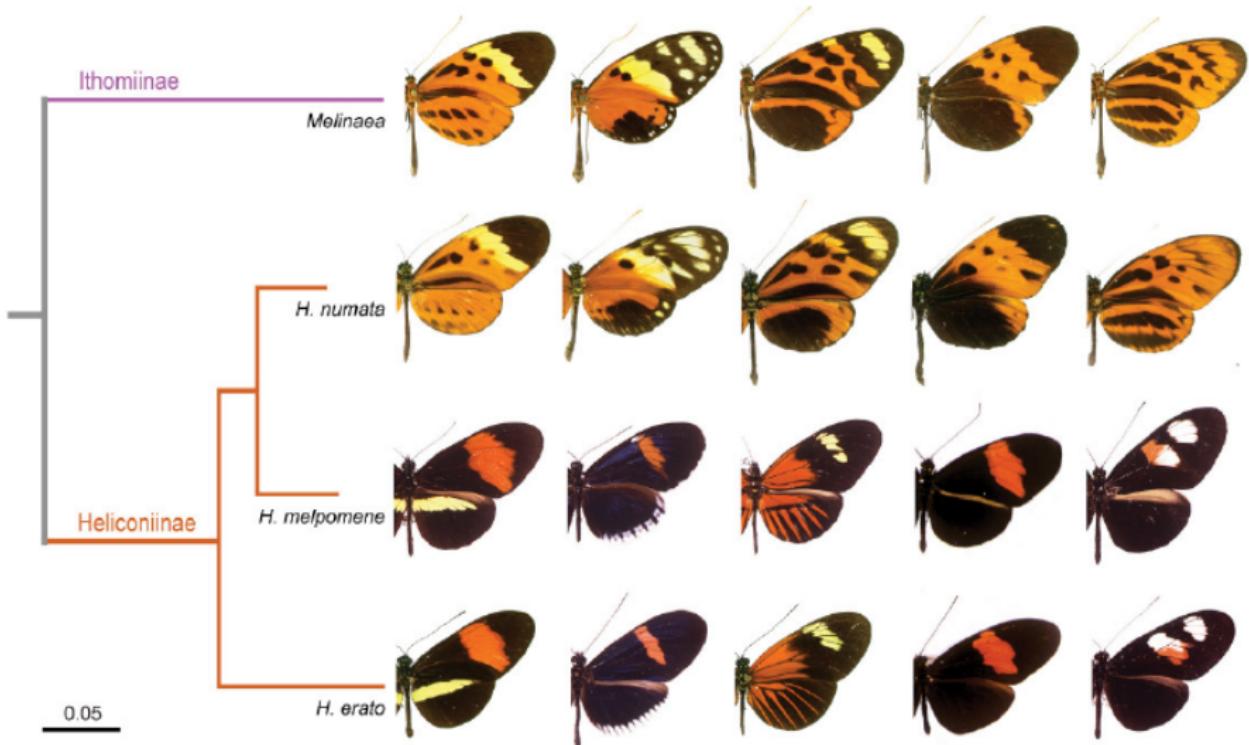


Figure by Mathieu Joron: <http://xyala.cap.ed.ac.uk/joron/>

What evolutionary processes can drive these patterns?

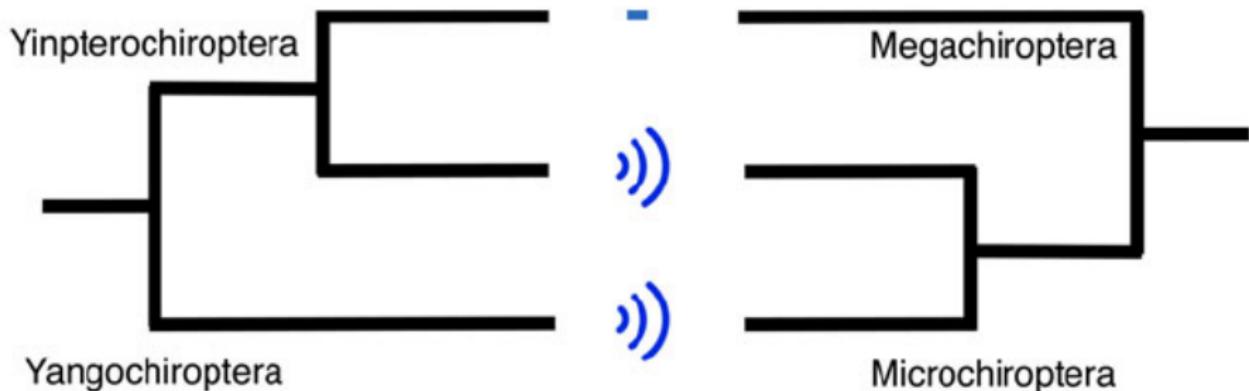
- ▶ Convergence
- ▶ Horizontal gene transfer
- ▶ Within species variation (Incomplete lineage sorting)
- ▶ ?

What evolutionary processes can drive these patterns?

- ▶ Convergence
- ▶ Horizontal gene transfer
- ▶ Within species variation (Incomplete lineage sorting)
- ▶ ?

We will discuss how to recognize and (try to) differentiate these processes.

Different data can drive different conclusions



Species relationships between echolocating and nonecholocating bats (after Teeling 2009). Left: inferences from DNA sequence data.
Right: traditional species relationships inferred from morphological characters (and limited sequence data). (Hahn and Nakhleh, 2016)

Estimating a tree from character data

Tree construction:

- ▶ strictly algorithmic approaches - use a “recipe” to construct a tree
- ▶ optimality based approaches - choose a way to “score” a trees and then search for the tree that has the best score.

Expressing support for aspects of the tree:

- ▶ bootstrapping,
- ▶ testing competing trees against each other,
- ▶ posterior probabilities (in Bayesian approaches).

- Hahn, M. W. and Nakhleh, L. (2016). Irrational exuberance for resolved species trees. *Evolution*, 70(1):7–17.
- Joron, M., Frezal, L., Jones, R. T., Chamberlain, N. L., Lee, S. F., Haag, C. R., Whibley, A., Becuwe, M., Baxter, S. W., Ferguson, L., Wilkinson, P. A., Salazar, C., Davidson, C., Clark, R., Quail, M. A., Beasley, H., Glithero, R., Lloyd, C., Sims, S., Jones, M. C., Rogers, J., Jiggins, C. D., and ffrench Constant, R. H. (2011). Chromosomal rearrangements maintain a polymorphic supergene controlling butterfly mimicry. *Nature*, 477(7363):203–206.