

Phylogenetic thinking

Emily Jane McTavish

Life and Environmental Sciences
University of California, Merced

`ejmctavish@ucmerced.edu`, `twitter:snacktavish`

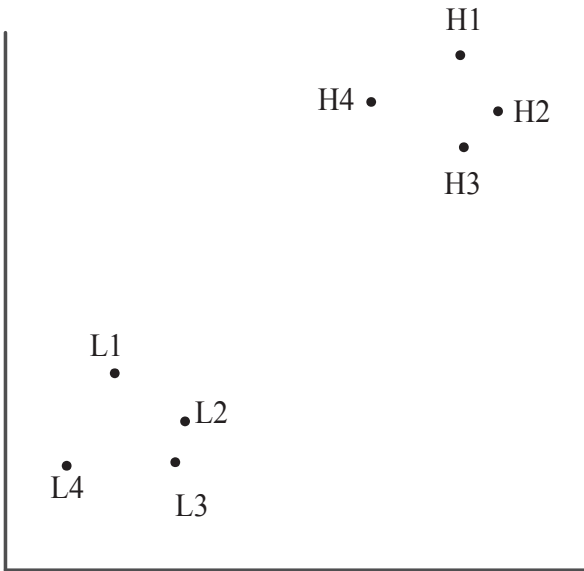
(With thanks to Mark Holder, Paul Lewis, Joe Felsenstein, and David Hillis for slides)

Phylogenies describe shared ancestry
and
inform our understanding of evolutionary processes

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

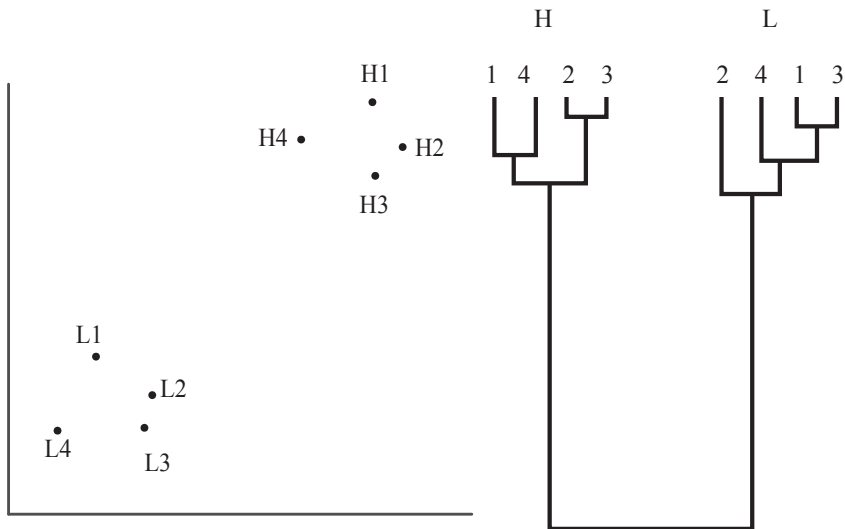


(cue cartoon videos)

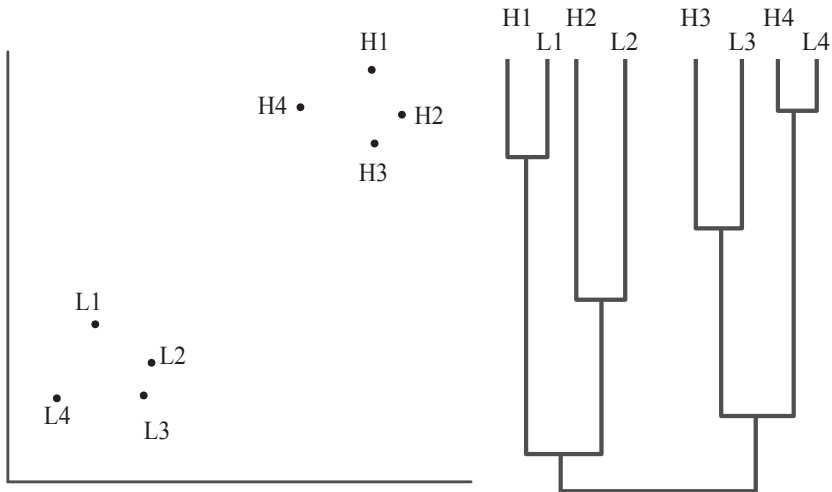
See <http://phylo.bio.ku.edu/slides/no-correl-anim.mov>

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

No (or little) evidence for correlation



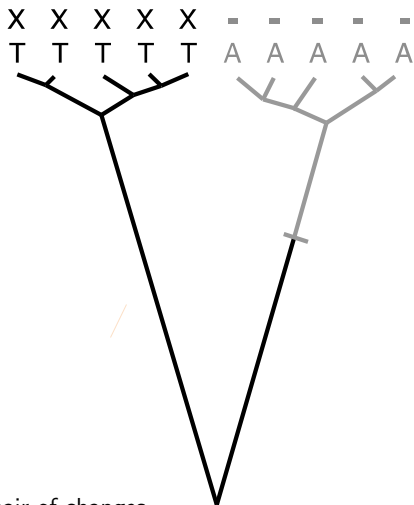
Evidence for correlation



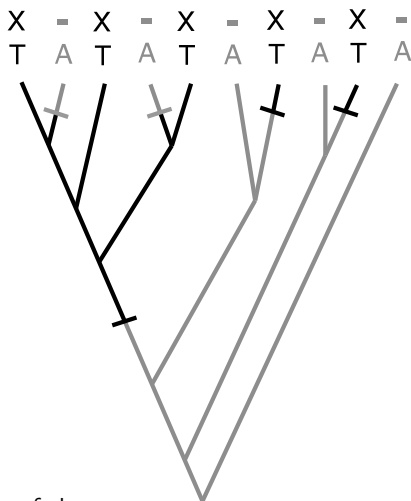
Do desert green algae use xanthophyll to protect against excessive light intensities?

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



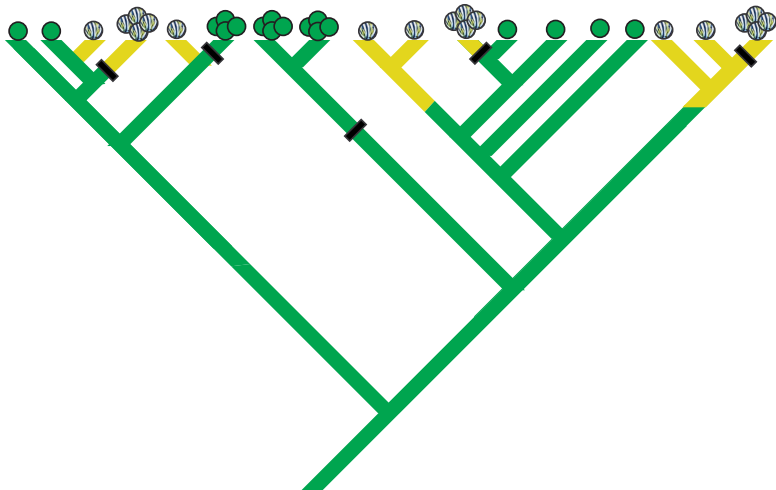
Cryptic



Aposematic

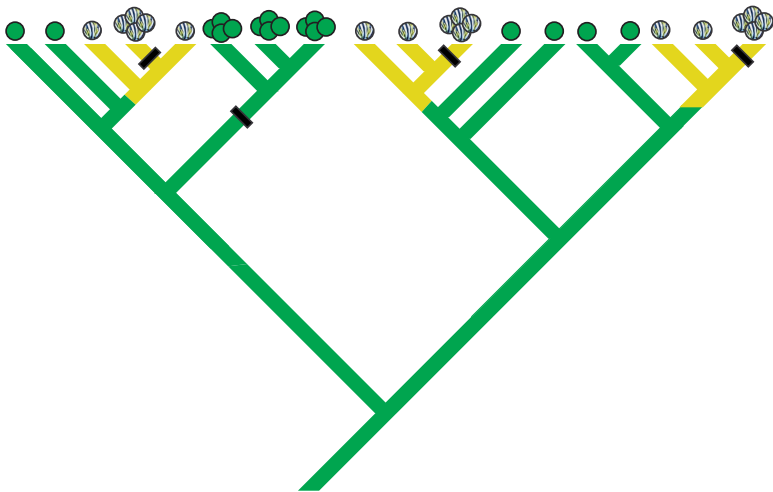


Sillén-Tullberg (1988), Dyer and Gentry (2002), Hill (2001)



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.

Phylogenies can reveal suprising patterns



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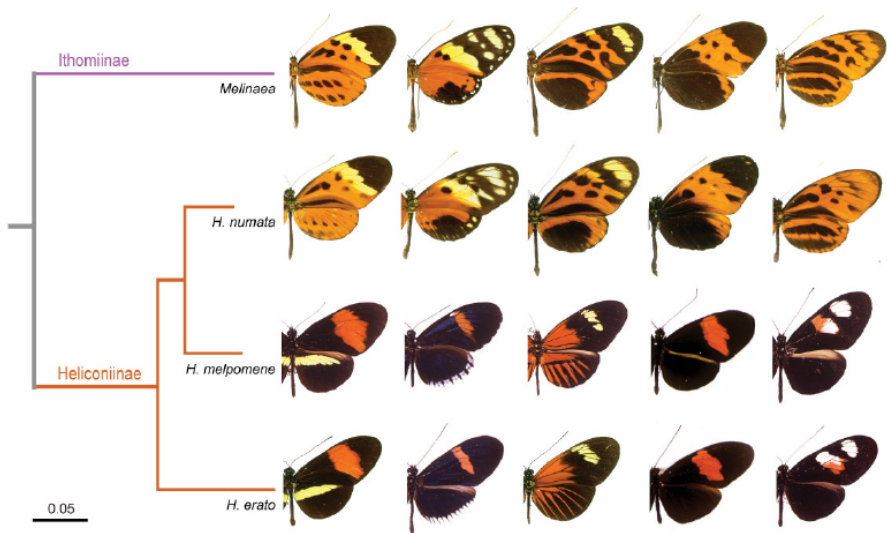


Figure by Mathieu Joron: <http://xyala.cap.ed.ac.uk/joron/>

What evolutionary processes can drive these patterns?

- ▶ Convergence
- ▶ Horizontal gene transfer
- ▶ Incomplete lineage sorting
- ▶ ?

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

The challenge of phylogenetics:

The tree is real. There is some true past history that happened!

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How do we find out what that history was?

Estimating a tree from character data

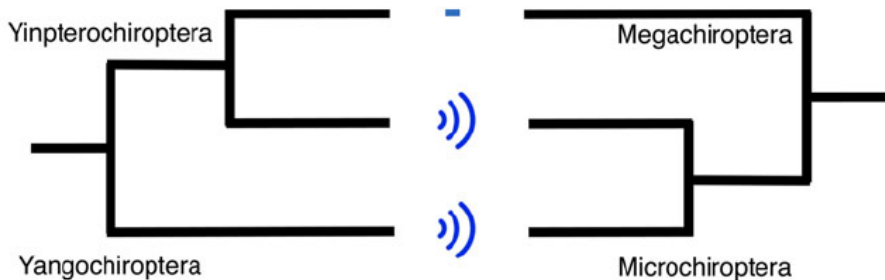
Tree construction:

- ▶ 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).

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)

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 French Constant, R. H. (2011). Chromosomal rearrangements maintain a polymorphic supergene controlling butterfly mimicry. *Nature*, 477(7363):203–206.