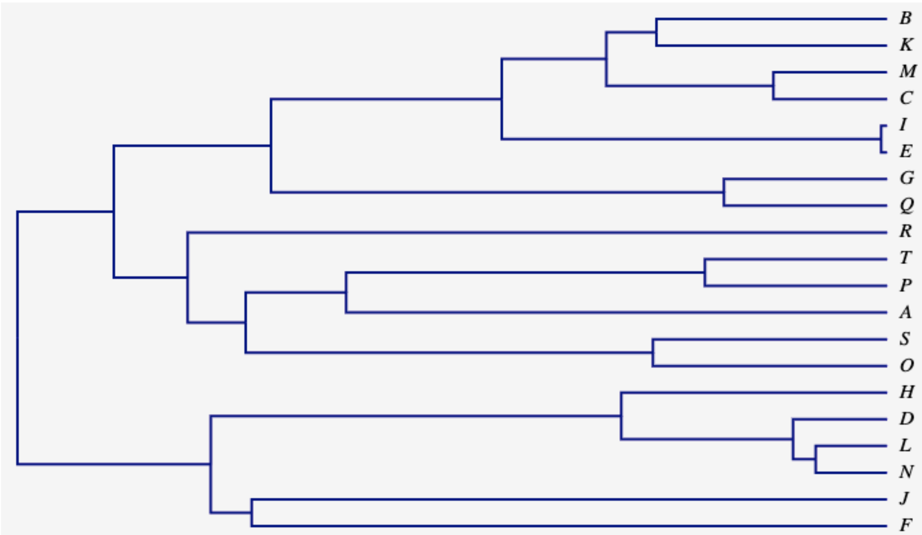
Phylogenetic Signal in Continuous Traits

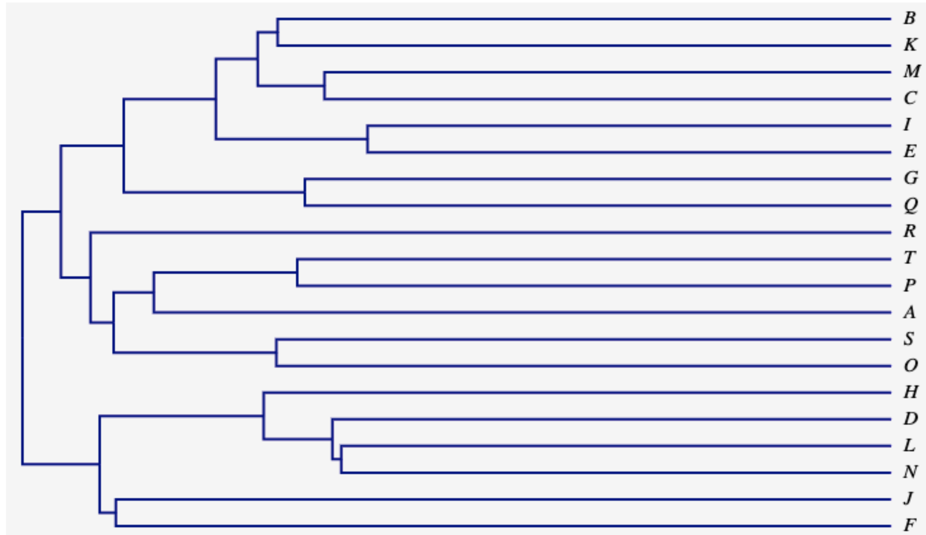
Paul O. Lewis ~ Phylogenetics, Spring 2026

True tree vs. assumed tree

What if you assumed this tree...



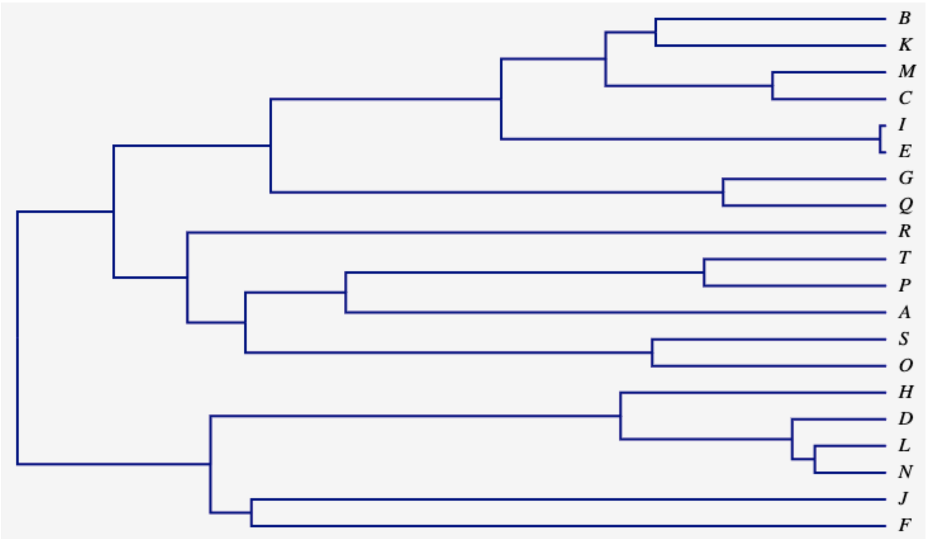
...but this was the true tree?



less phylogenetic structure
(internal edges shorter,
terminal edges longer)

True tree vs. assumed tree

What if you assumed this tree...



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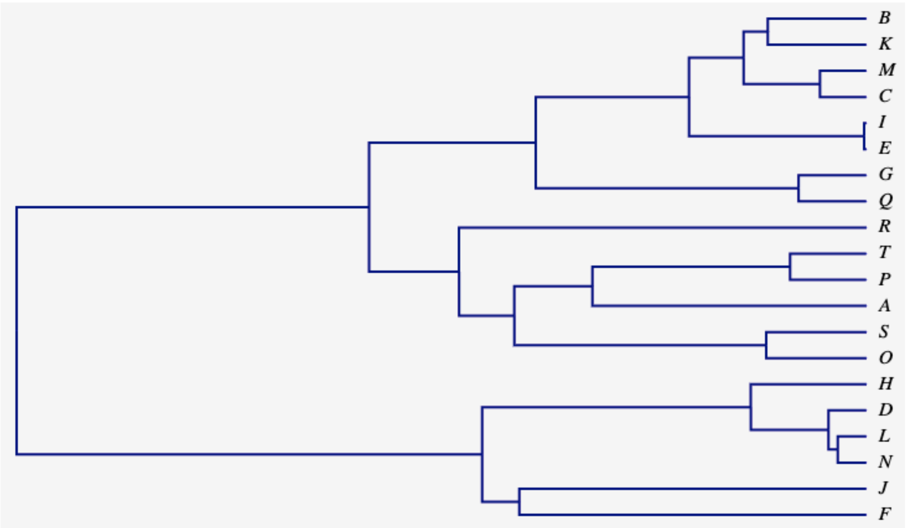
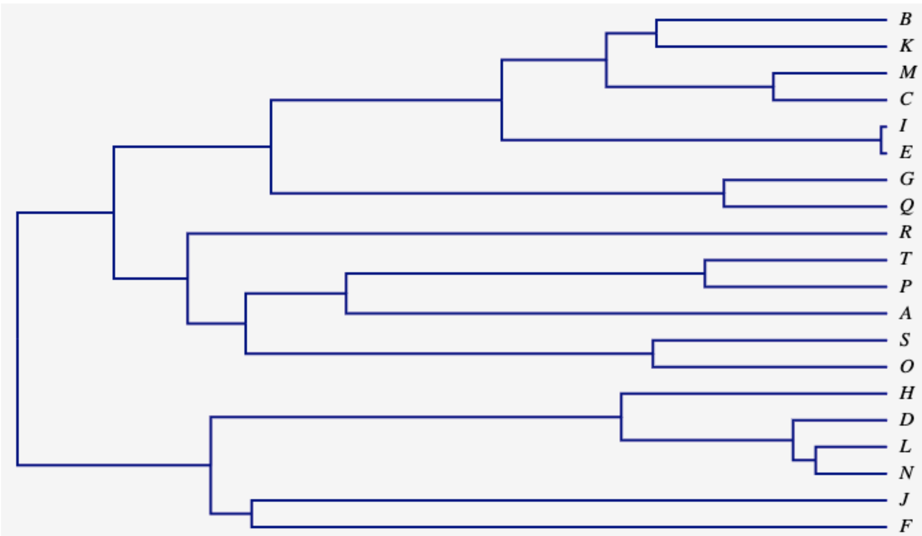


speciation rate increases toward the present

True tree vs. assumed tree

What if you assumed this tree...



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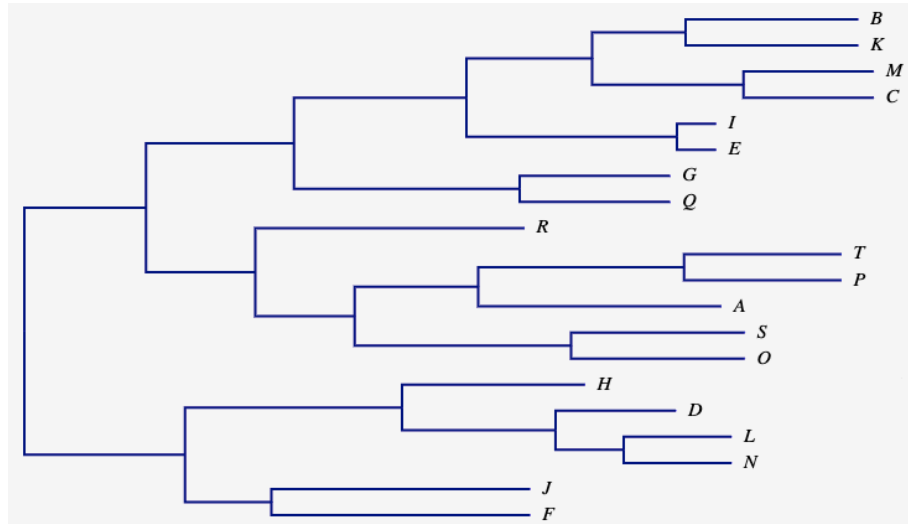
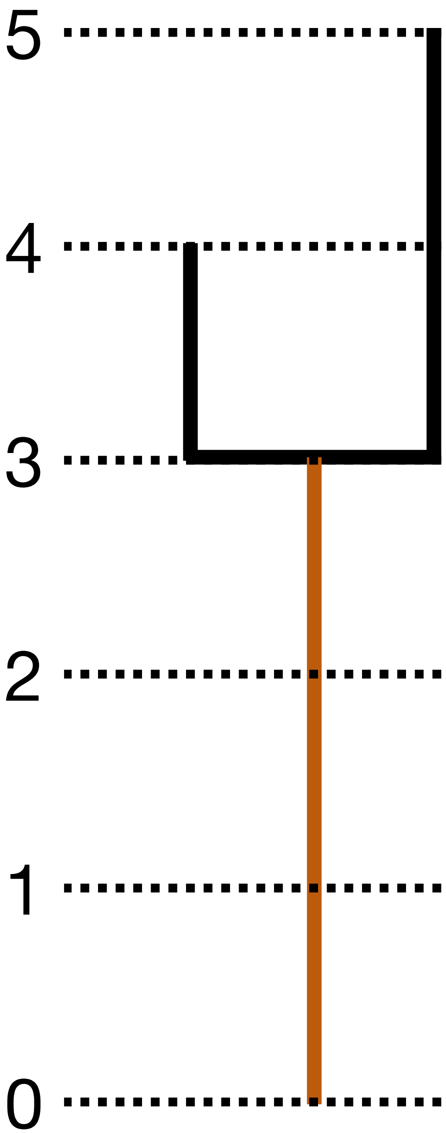


edge lengths more homogeneous

Pagel's lambda

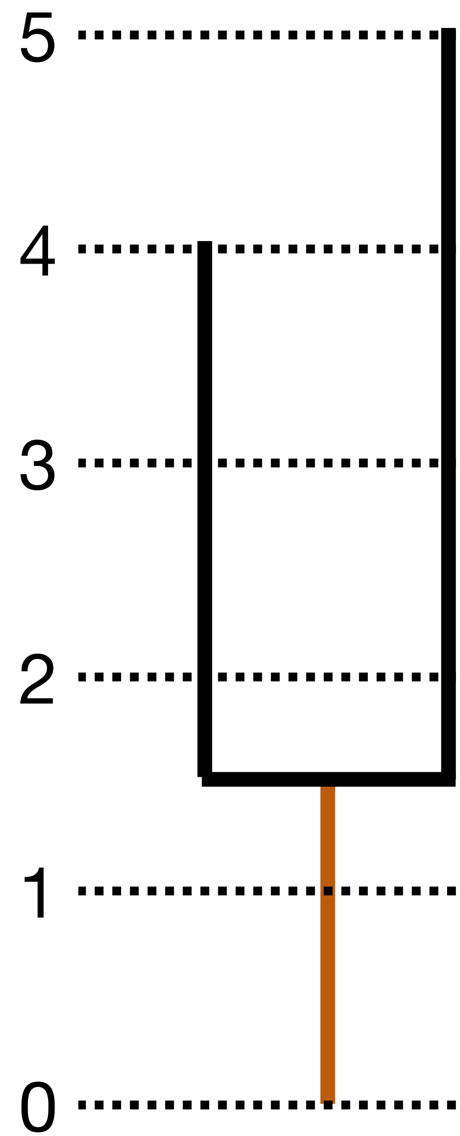


Multiply *internal* heights by lambda

Keep tip heights the same

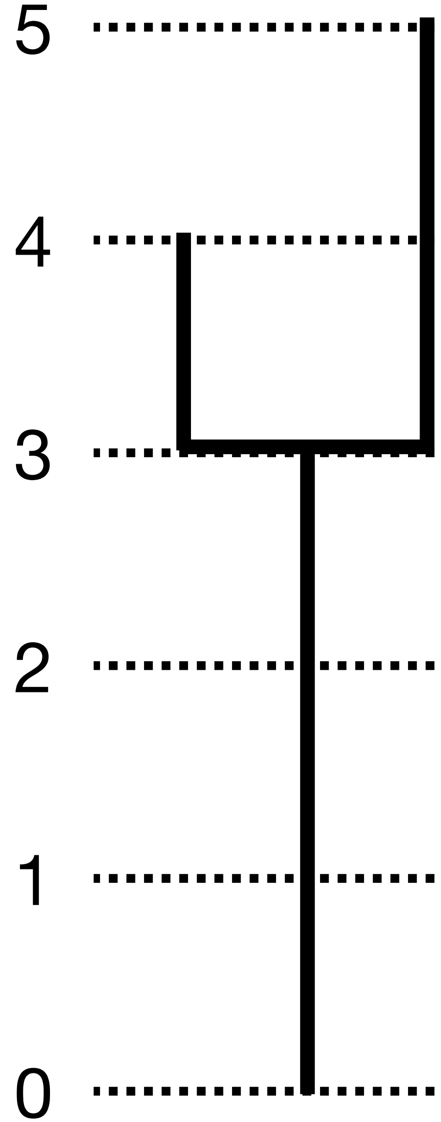
lambda = 0.5 →

increases terminal edges at the expense of internal edges



Pagel 1999

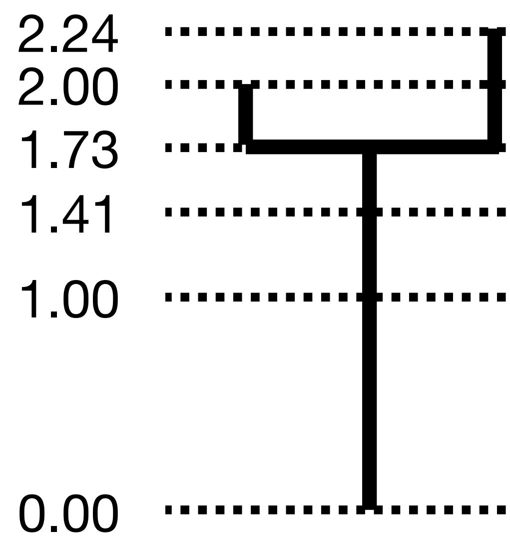
Pagel's delta



Raise all **node heights** to the power delta

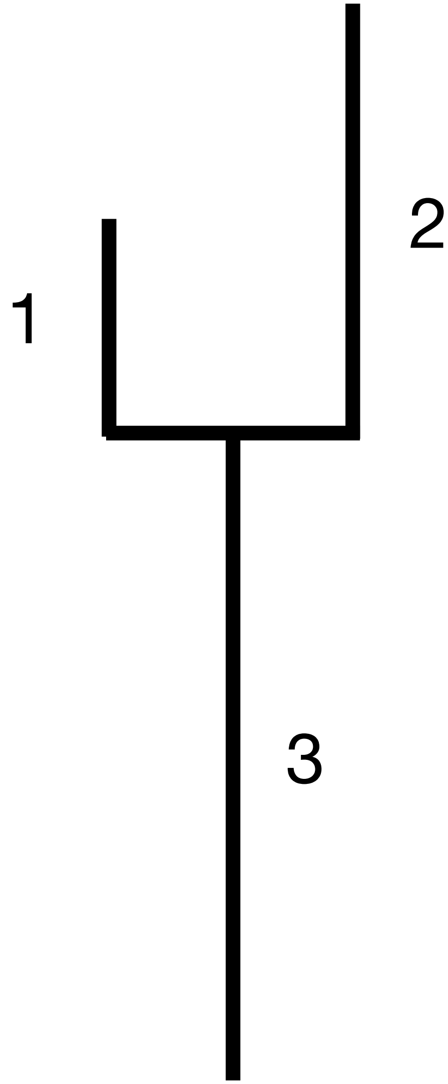
delta = 0.5 →

larger heights changed more than shorter heights



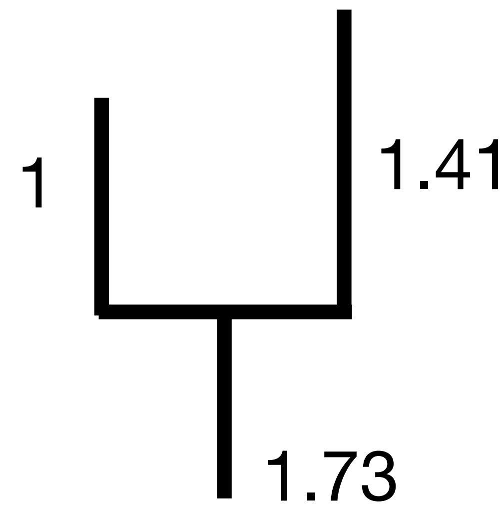
Pagel 1999

Pagel's kappa



Raise all **edge lengths** to the power kappa

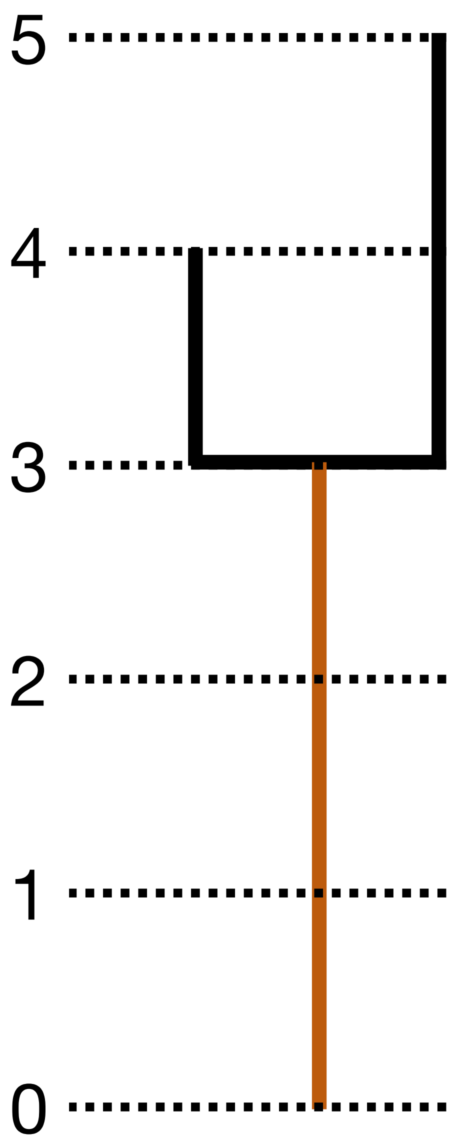
kappa = 0.5 →



shrinks/lengthens longer branches more than shorter ones

Pagel 1997

Pagel's lambda and information



C matrix

4	3
3	5

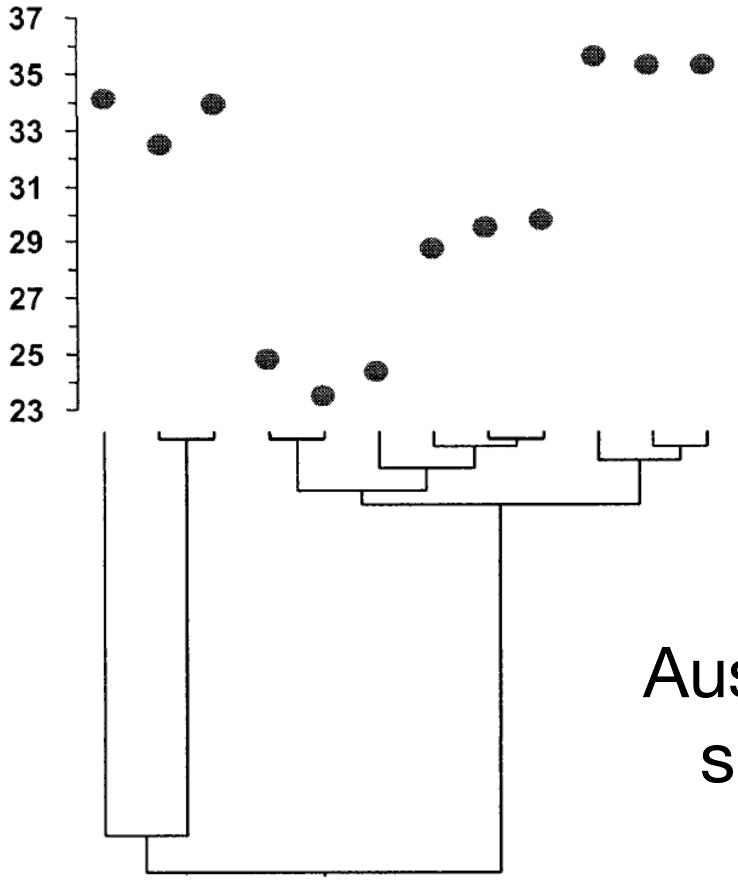
covariances proportional to heights of internal nodes

covariance = 0.0 is star tree: no phylogenetic structure

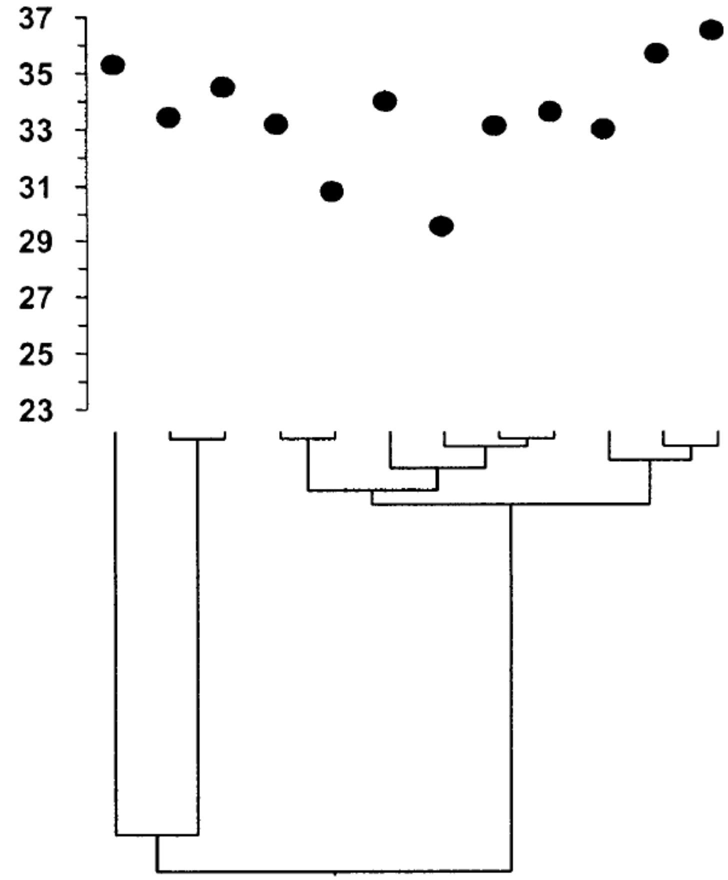
lambda < 1 thus implies less phylogenetic signal

Blomberg's K

preferred body temp
more signal



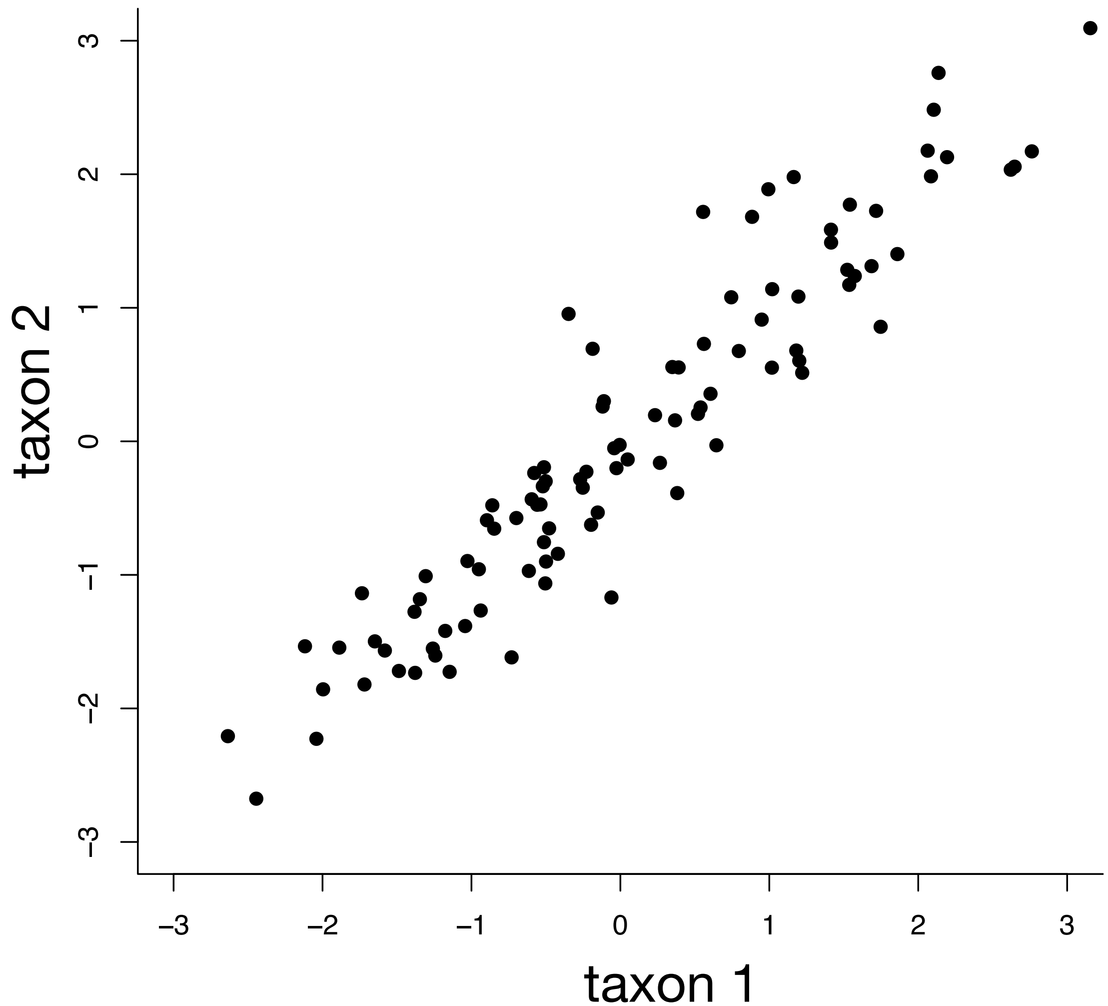
optimal temp for sprinting
less signal



Australian
skinks

From Fig. 4 in Blomberg et al. 2003

Some background



Bivariate normal:

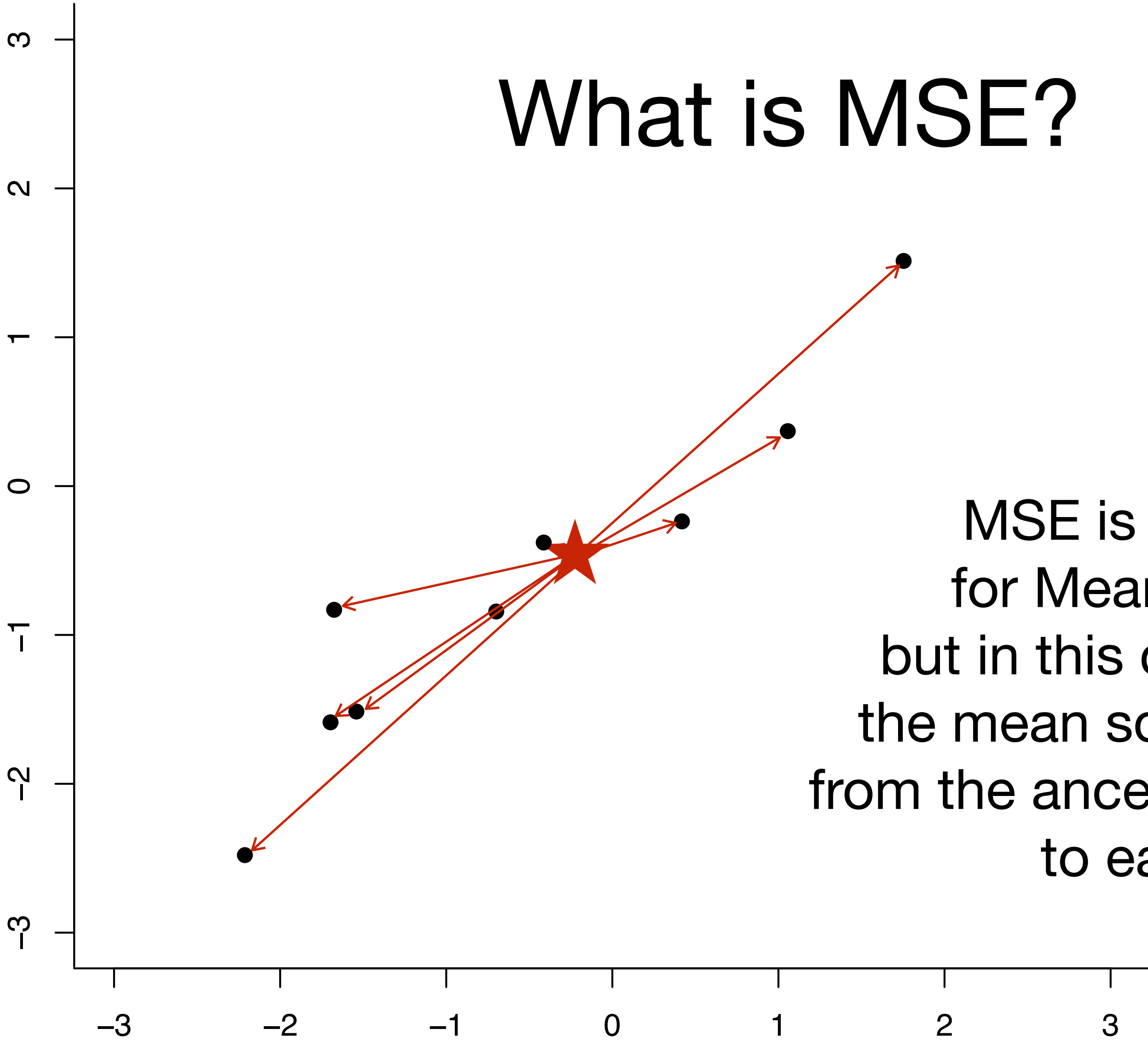
$$V = \begin{bmatrix} 2 & 1.9 \\ 1.9 & 2 \end{bmatrix}$$

variance-covariance matrix

If trait is far from 0 in taxon 1, then it will be far from 0 in taxon 2 also, leading to high MSE due to implicit double counting.

$MSE_0 = 3.7$

What is MSE?

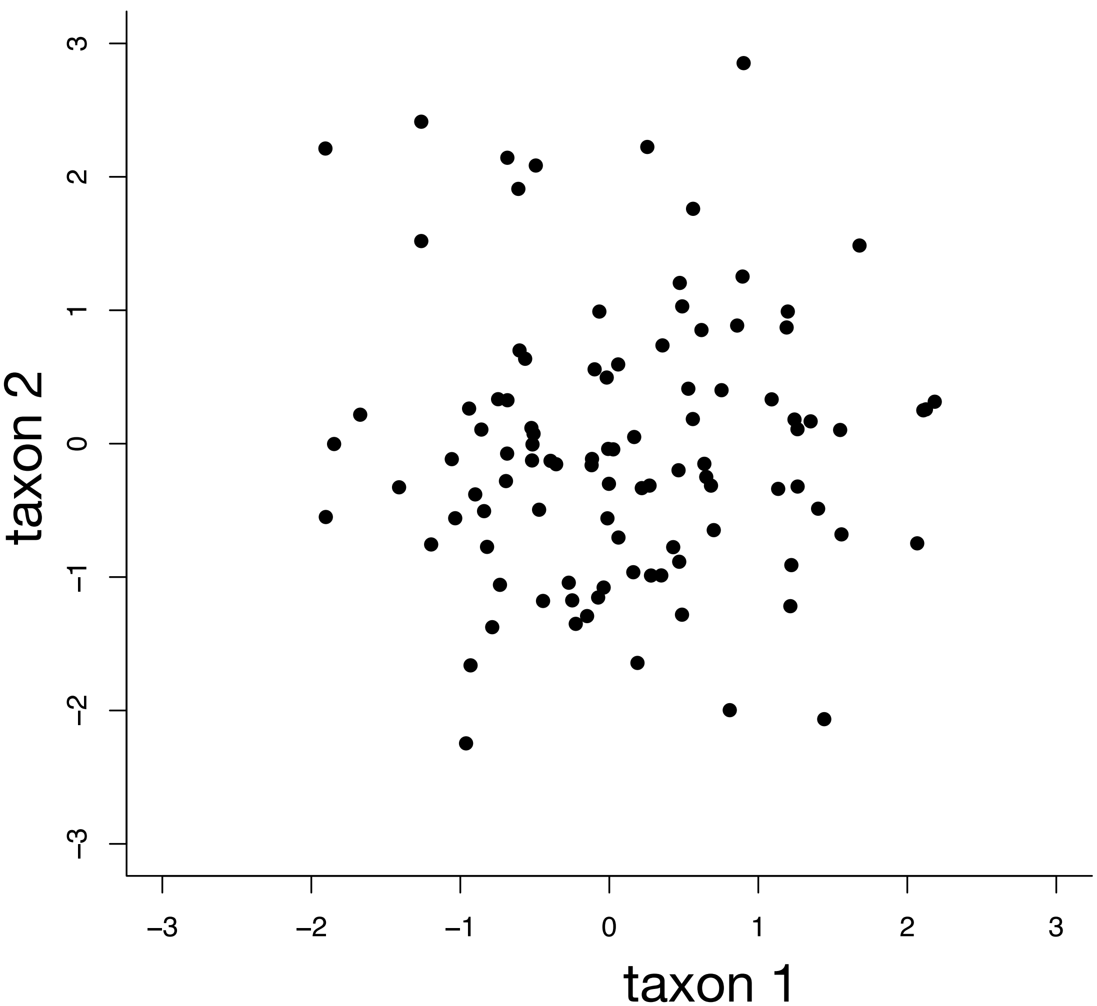


MSE is an abbreviation
for Mean Squared Error
but in this case it is simply
the mean squared distance
from the ancestral state (star)
to each descendant

Some background

$$\mathbf{V}^{-0.5}\left(\mathbf{Y}-\boldsymbol{\mu}\right)$$

Standardization of a sample from a *correlated* bivariate normal results in a sample from a *standard* bivariate normal.



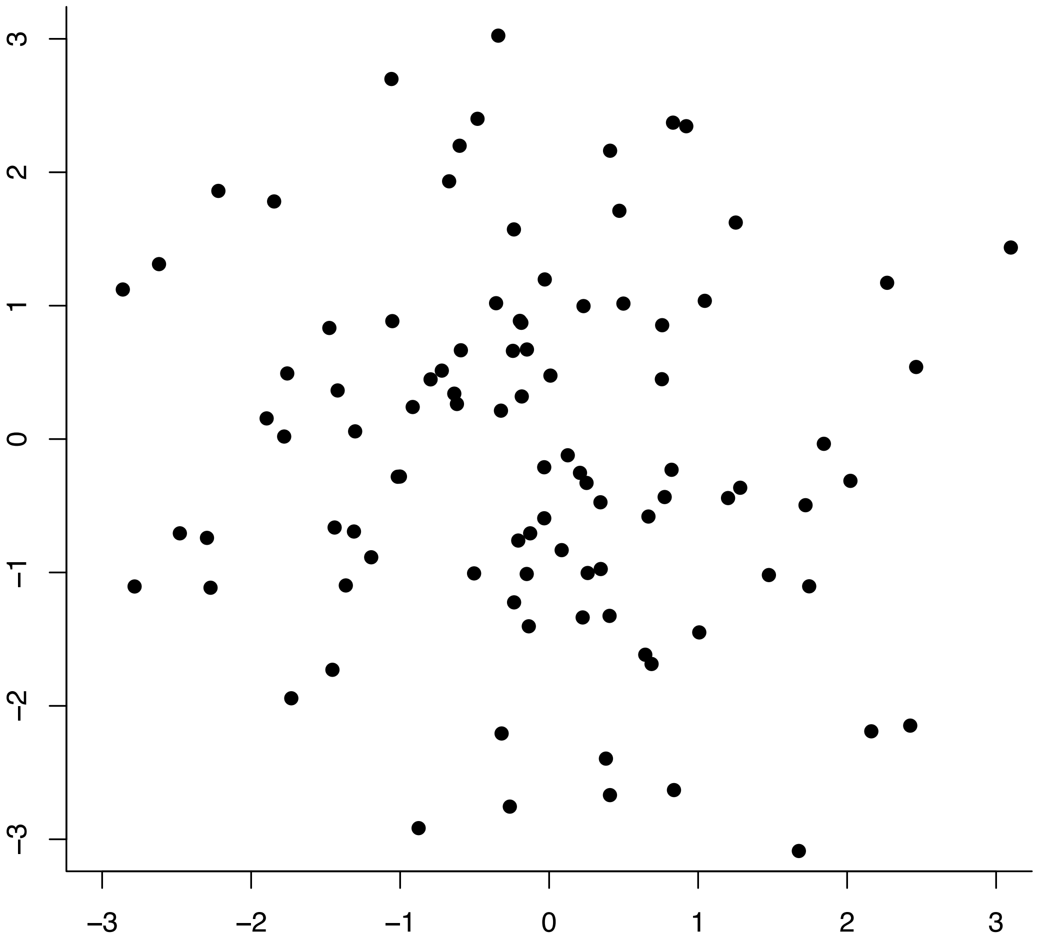
The sample is now uncorrelated and the MSE is **reduced** because value of trait in taxon 1 is now independent of the value in taxon 2

MSE = 1.9

MSE_0/MSE
= 3.7/1.9
= 1.9

False standardization

sample from a standard
bivariate normal distribution



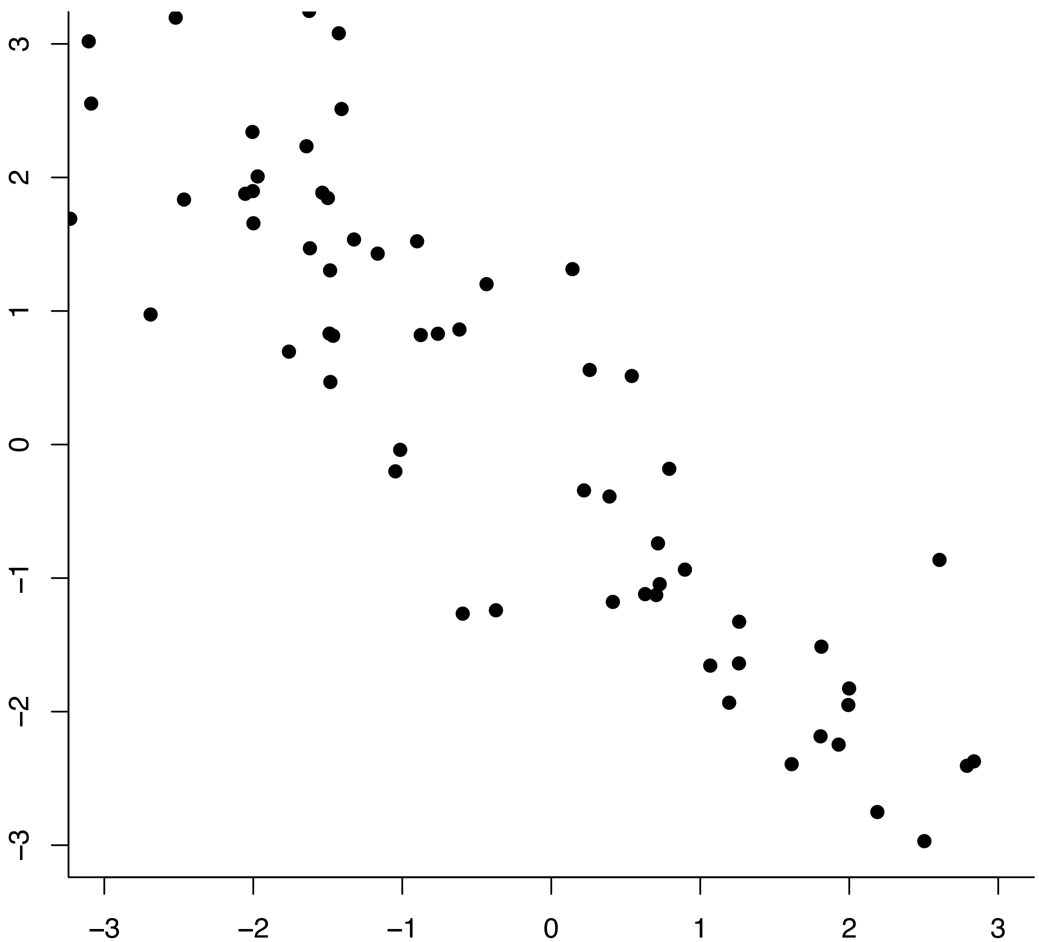
$$V = \begin{bmatrix} 2 & 1.9 \\ 1.9 & 2 \end{bmatrix}$$

variance-covariance matrix

What would happen if we used the wrong matrix V to standardize our sample?

$$MSE_0 = 4.0$$

False standardization

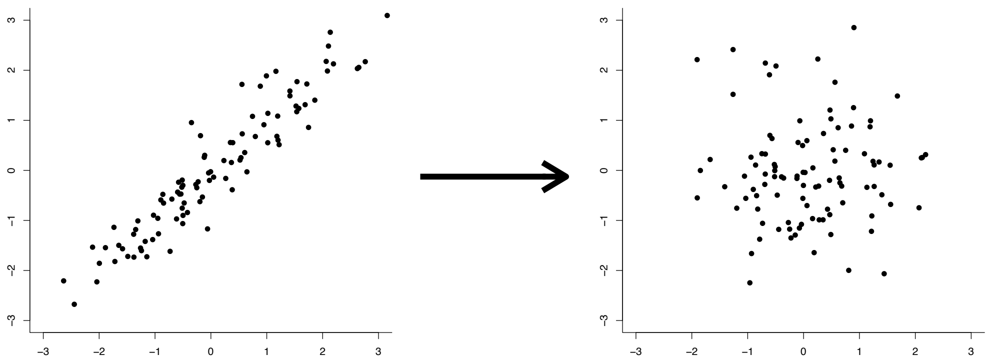


Instead of decreasing the MSE, we've increased it.

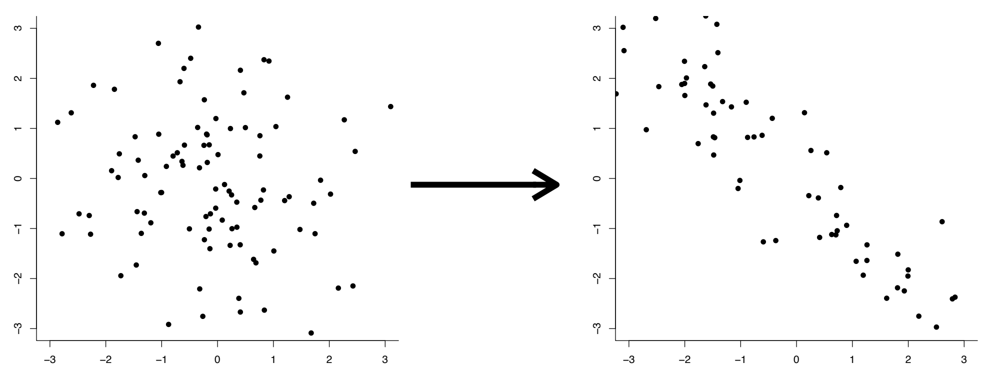
MSE = 23

MSE_0/MSE
$= 4/23$
$= 0.17$

Take-home message

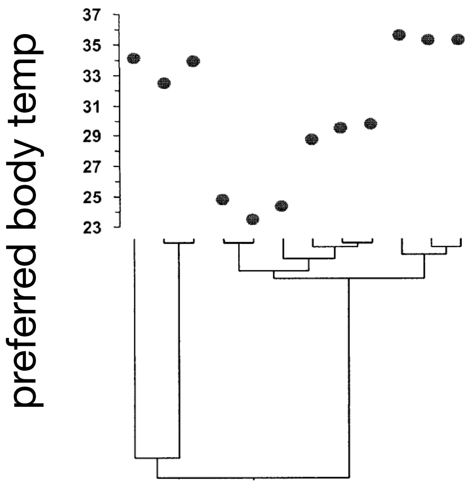


If data is **correlated** according to V, then MSE is **reduced** by standardization



If data is **uncorrelated**, then MSE is **increased** by standardization

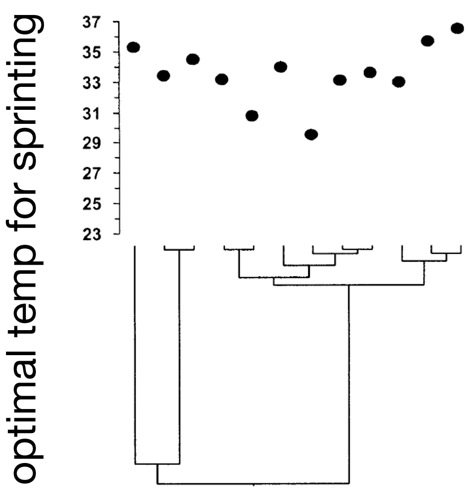
Blomberg's K



If data is **correlated** because it evolved on the phylogeny, then MSE is **reduced** by standardization

$$K = \frac{MSE_0/MSE}{E[MSE_0/MSE]} = 0.453$$

(more signal)



If data is **uncorrelated** with the phylogeny then MSE is **increased** by standardization

$$K = \frac{MSE_0/MSE}{E[MSE_0/MSE]} = 0.101$$

(less signal)