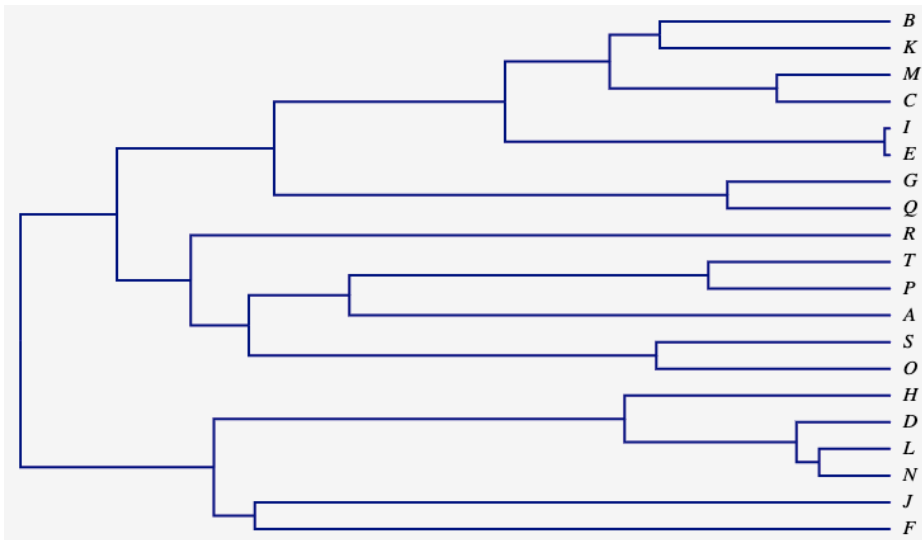


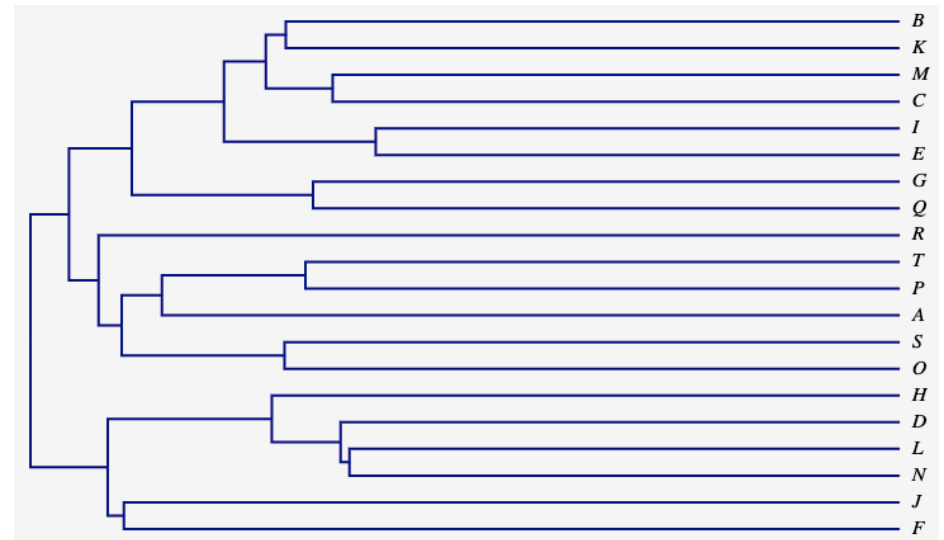
# Phylogenetic Signal in Continuous Traits

# True tree vs. assumed tree

What if you assumed this tree...



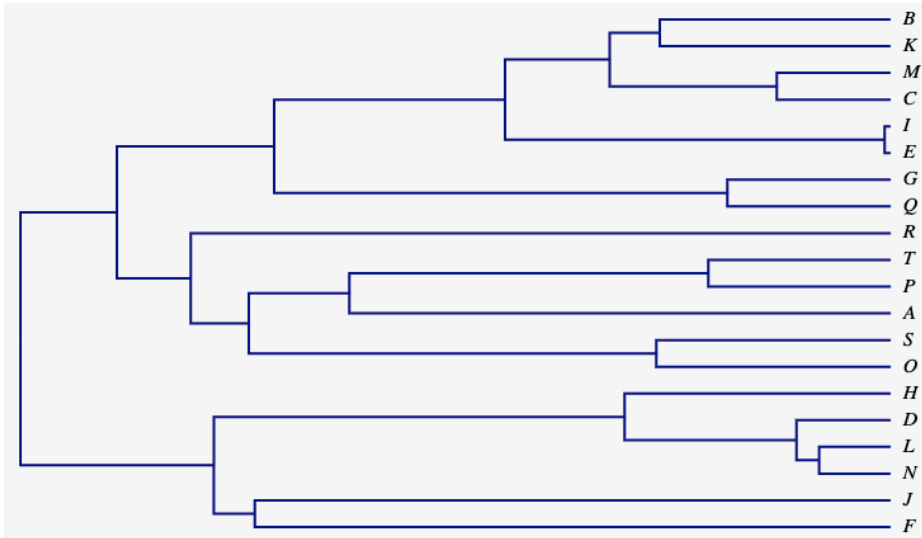
...but this was the true tree?



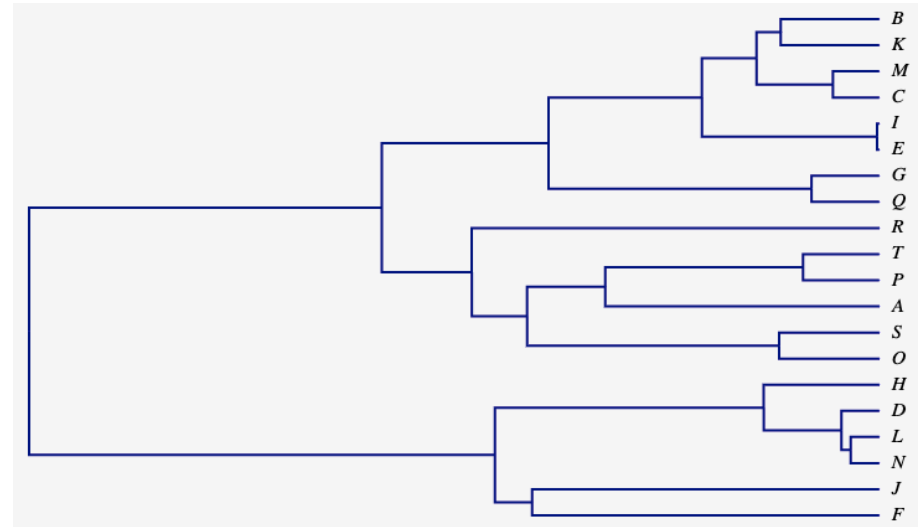
less phylogenetic structure  
(internal edges shorter,  
terminal edges longer)

# True tree vs. assumed tree

What if you assumed this tree...



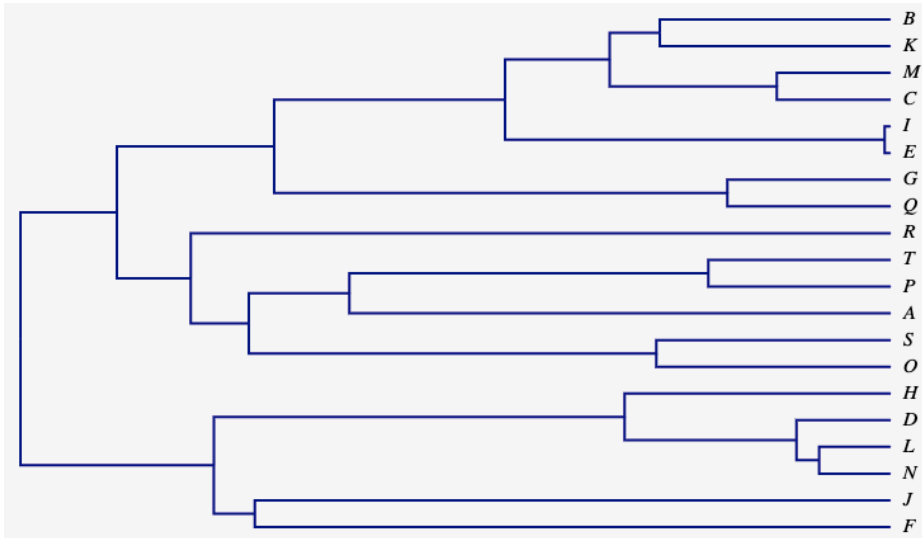
...but this was the true tree?



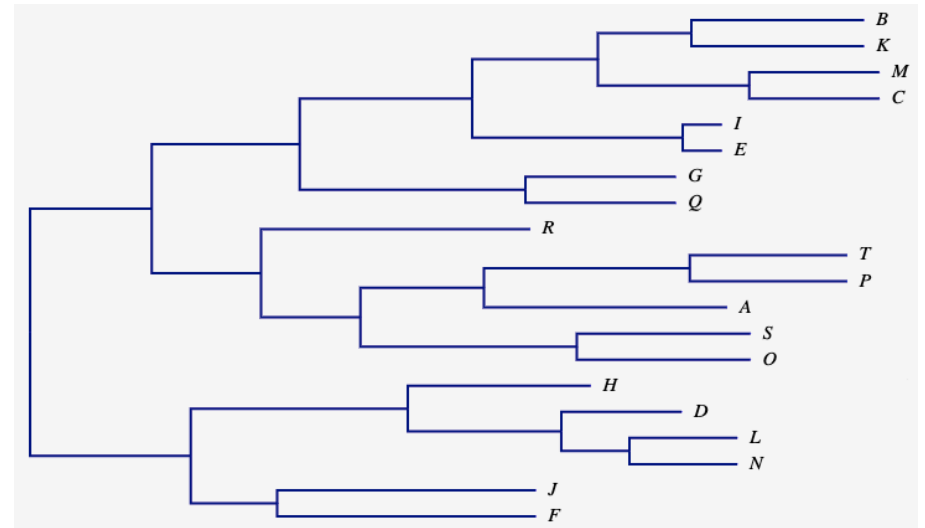
speciation rate increases toward  
the present

# True tree vs. assumed tree

What if you assumed this tree...



...but this was the true tree?



edge lengths more  
homogeneous

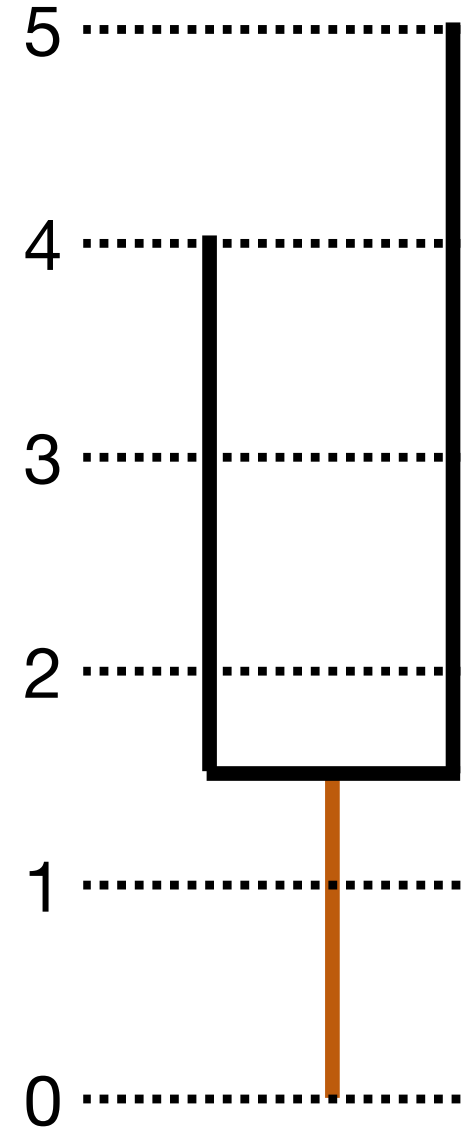
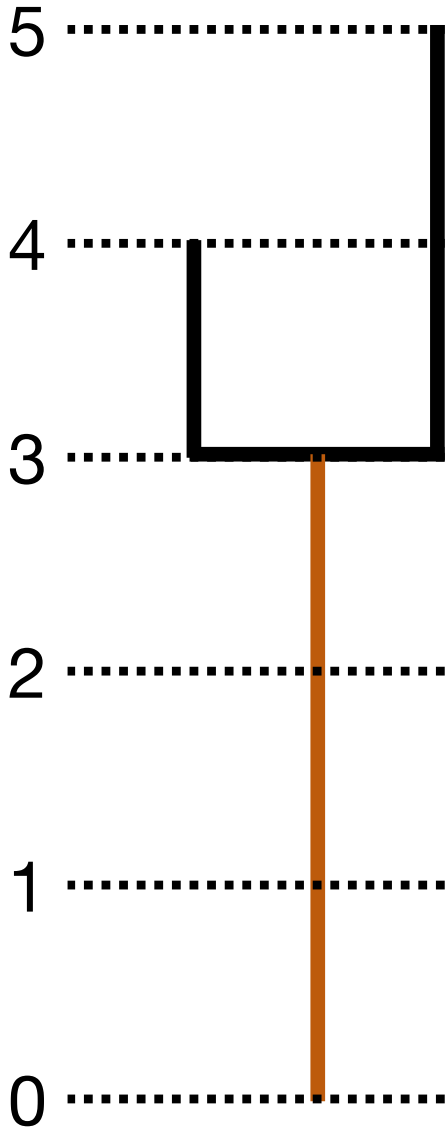
# Pagel's lambda

Multiply *internal* heights by lambda

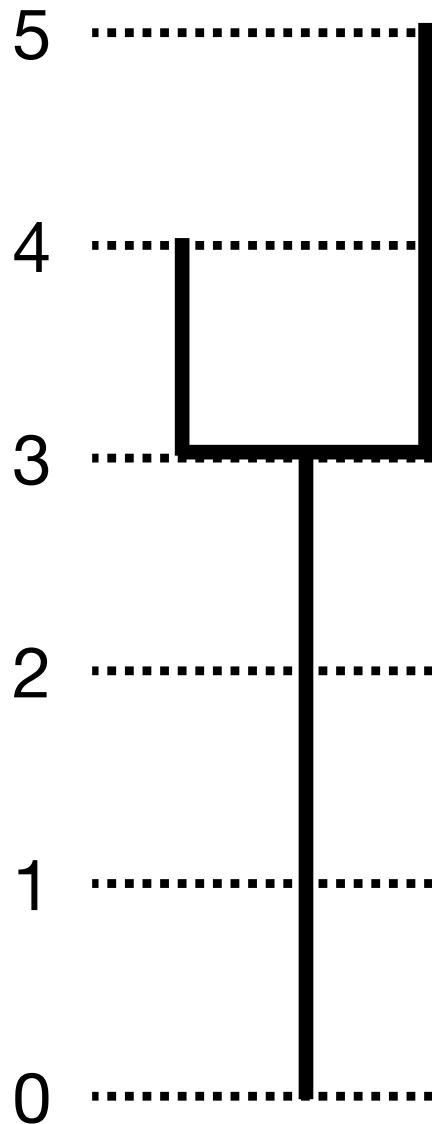
Keep tip heights the same

— lambda = 0.5 →

increases terminal edges at the expense of internal edges



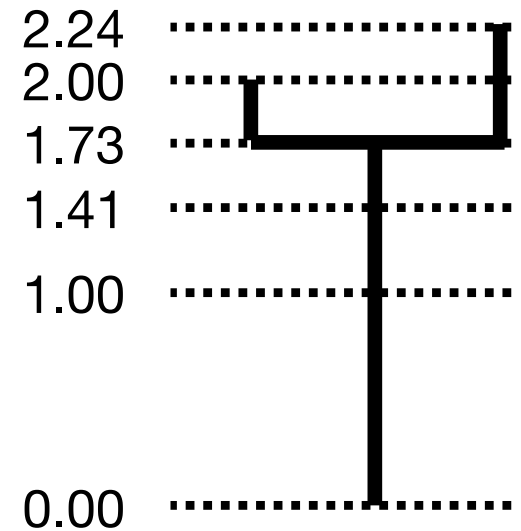
# Pagel's delta



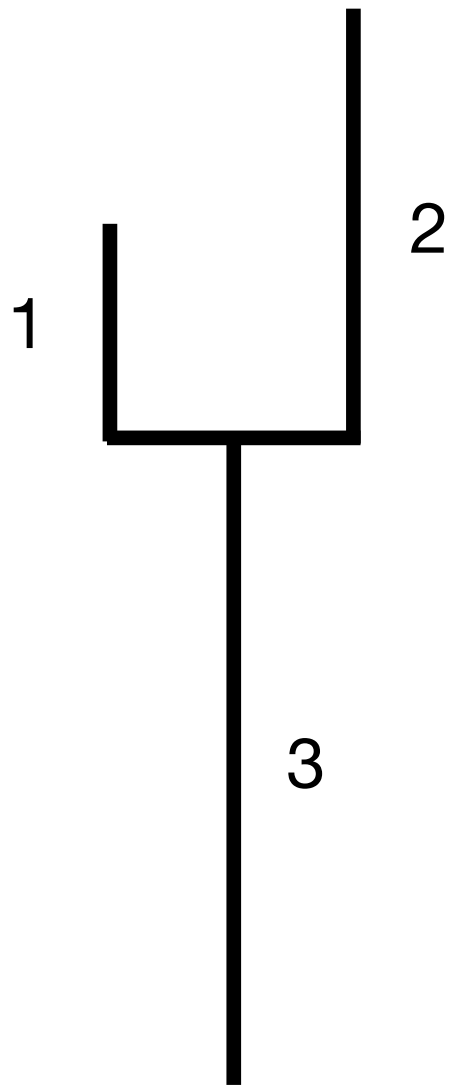
Raise all **node heights** to the power delta

— delta = 0.5 →

larger heights  
changed more than  
shorter heights

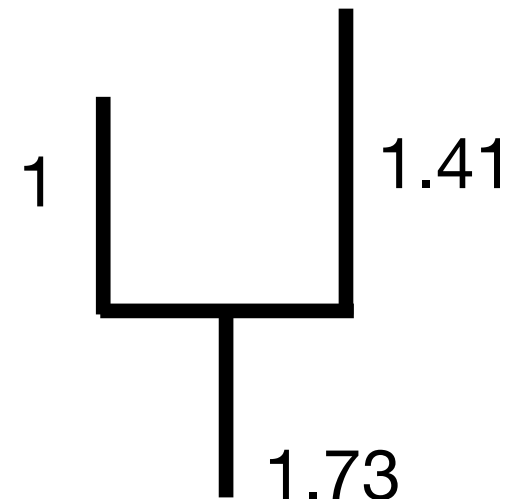


# Pagel's kappa



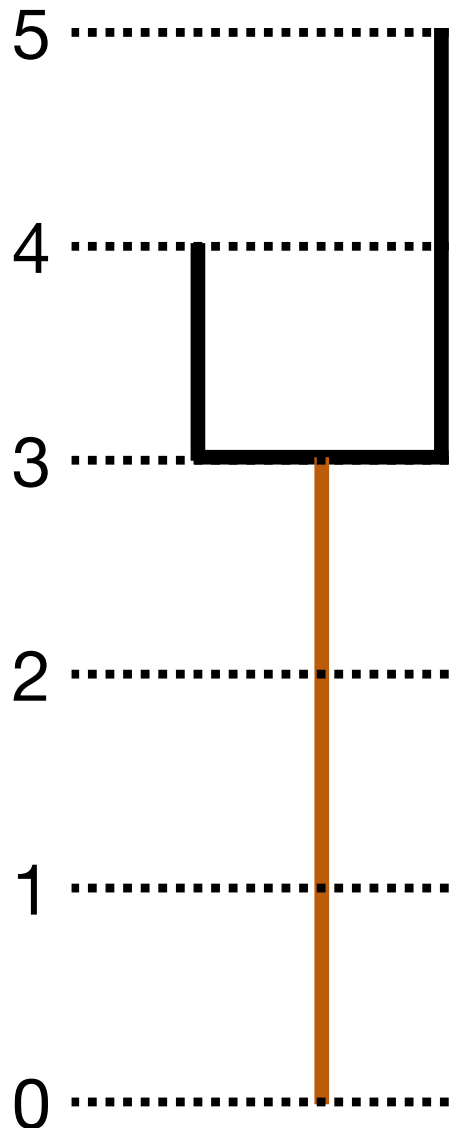
Raise all **edge lengths** to the power kappa

— kappa = 0.5 —>



shrinks/lengthens longer branches more than shorter ones

# Pagel's lambda and information



C matrix

4	3
3	5

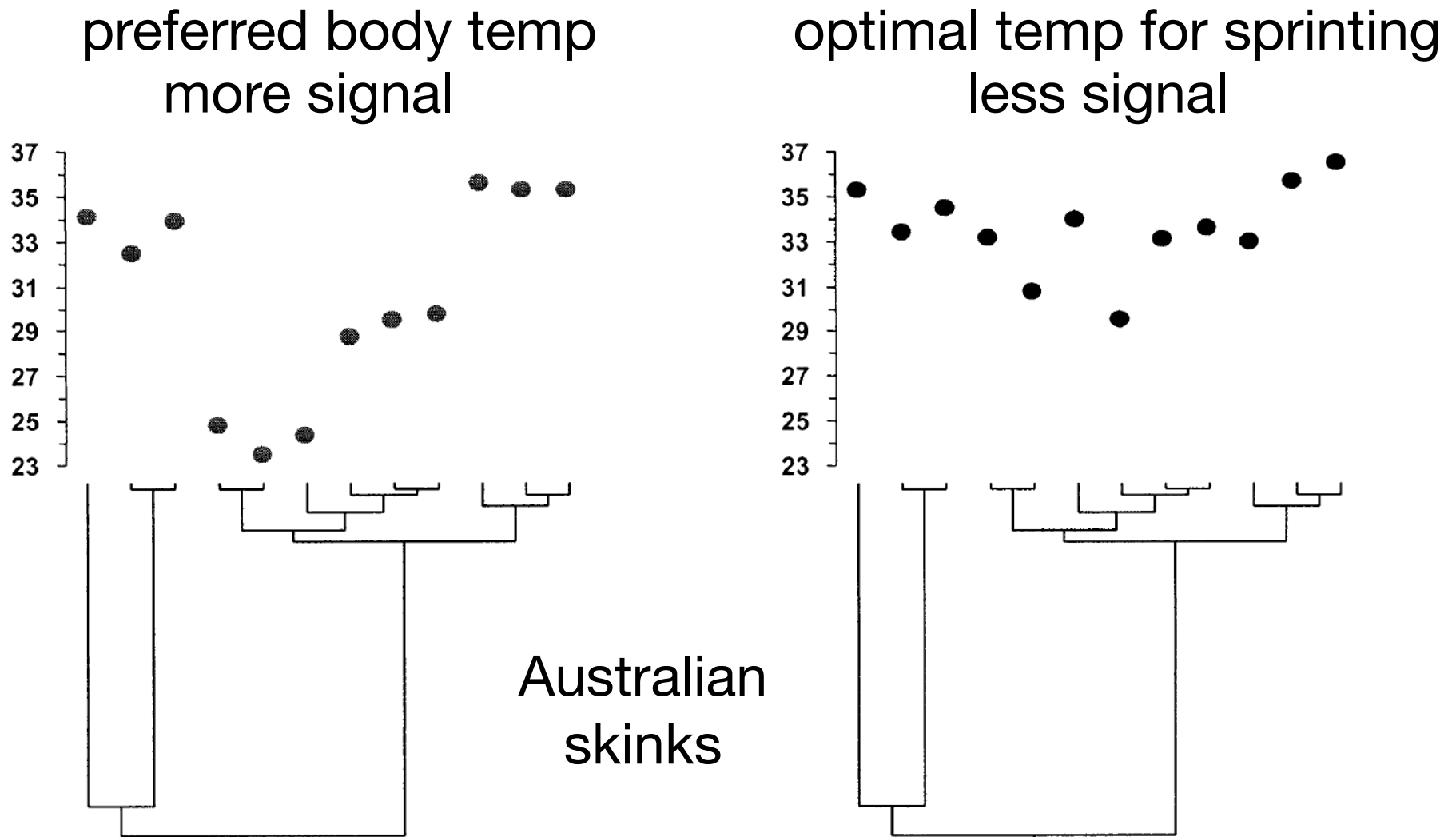
covariances proportional to heights of internal nodes

covariance = 0.0 is star tree:  
no phylogenetic structure

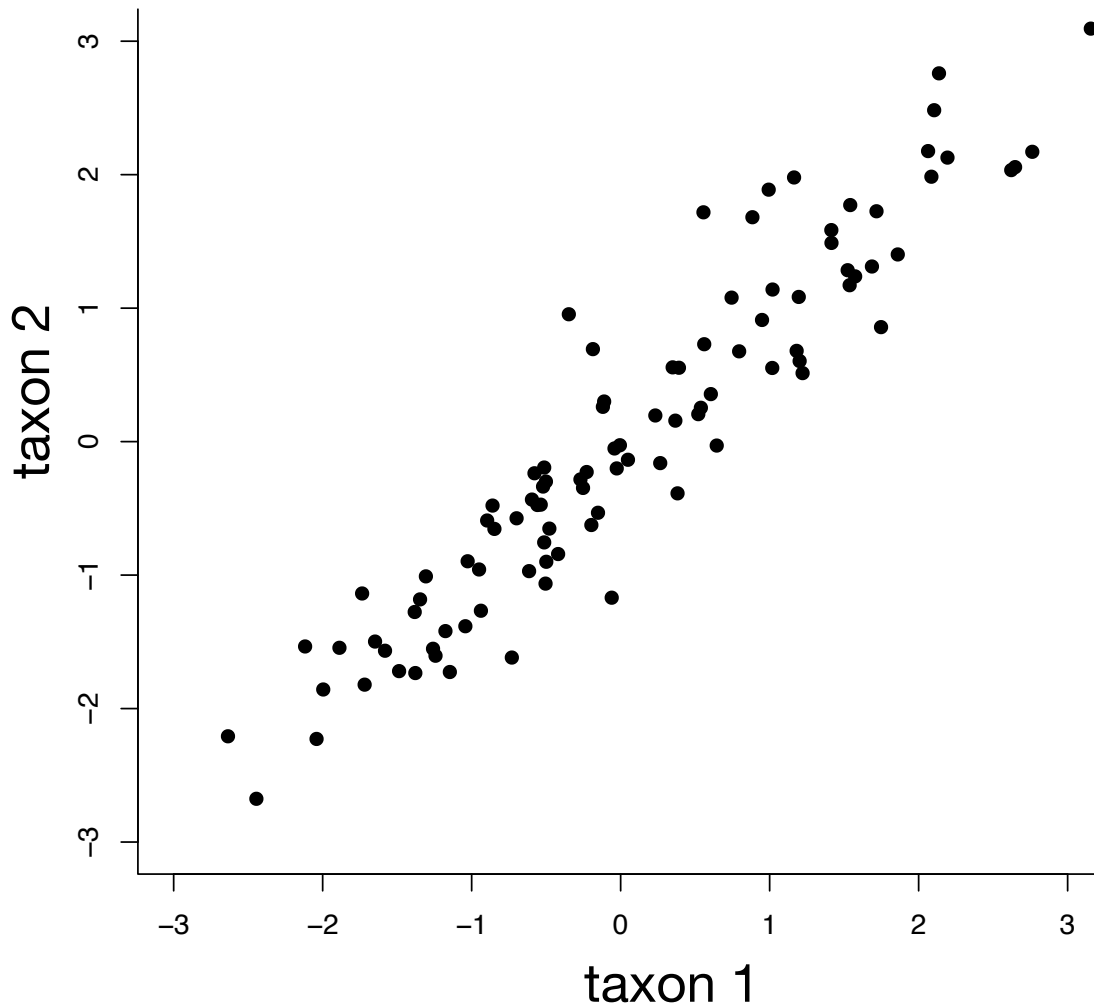
lambda < 1 thus implies less  
phylogenetic signal



# Blomberg's K



# Some background



Bivariate normal:

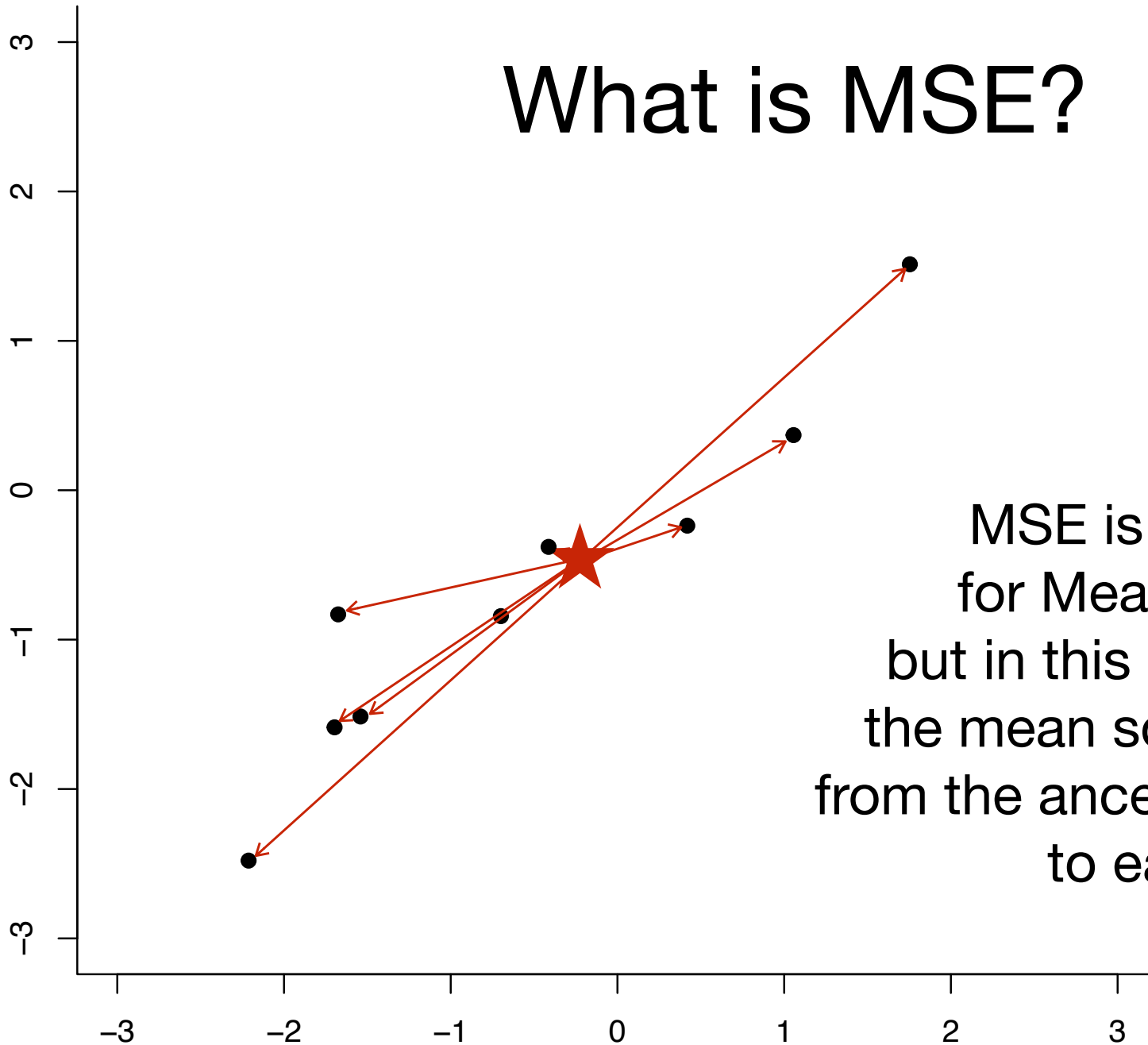
$$V = \begin{array}{|c|c|} \hline 2 & 1.9 \\ \hline 1.9 & 2 \\ \hline \end{array}$$

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.

$$MSE_0 = 3.7$$

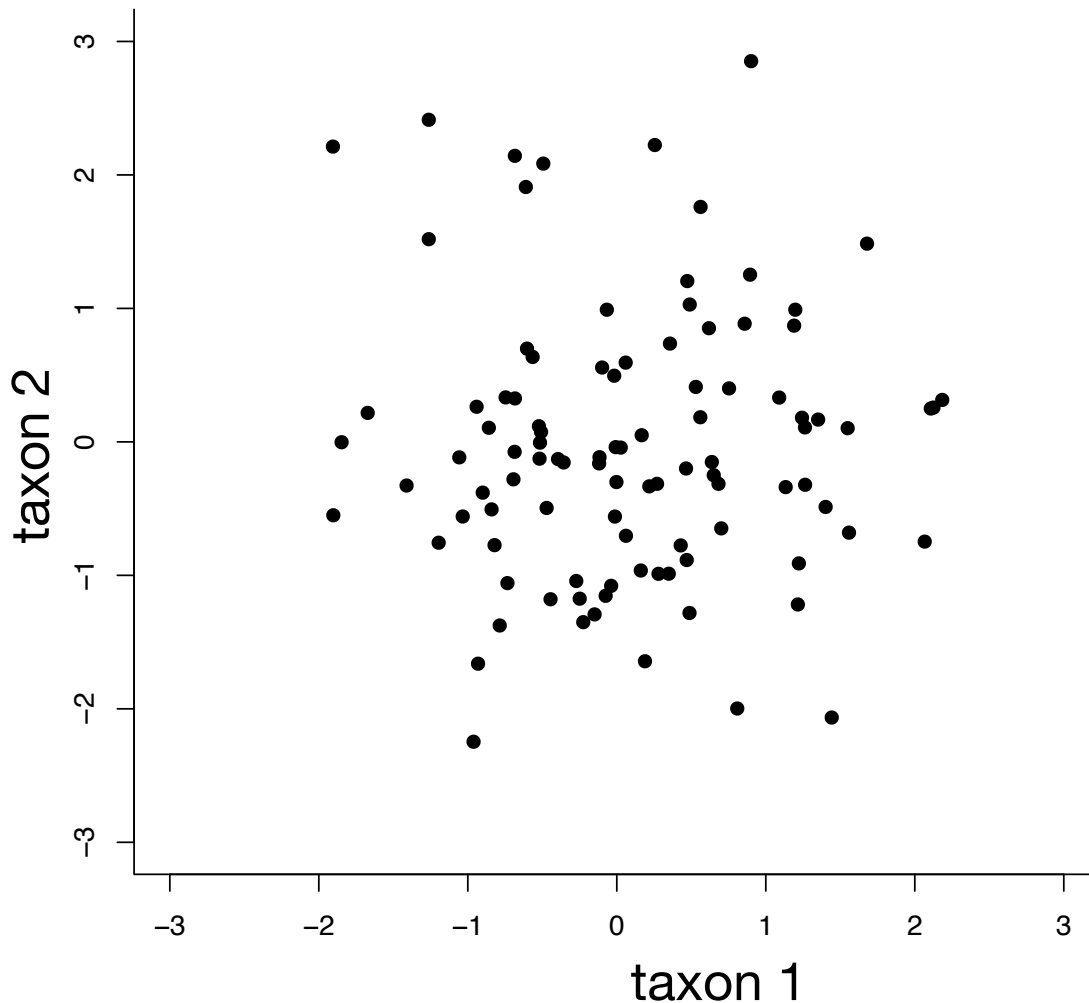
# What is MSE?



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

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

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



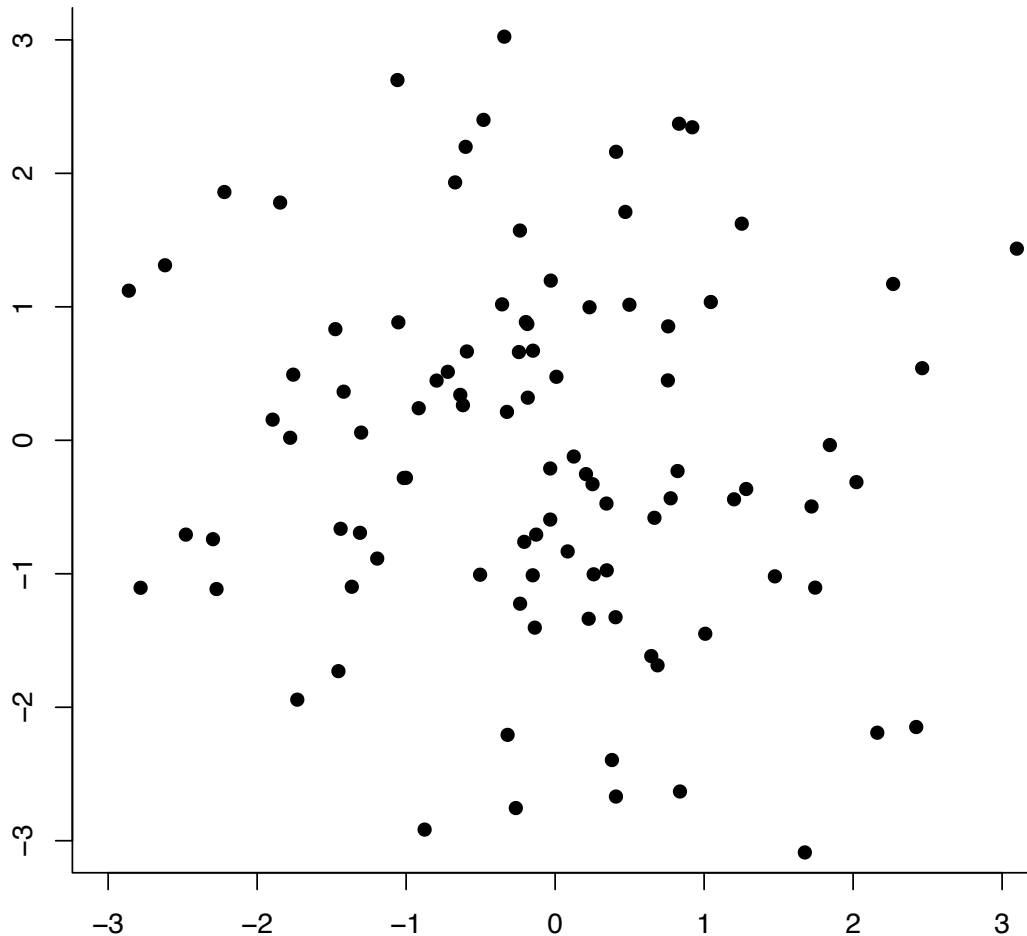
The sample is now uncorrelated and the MSE is **reduced** because value of trait in taxon 1 is now independent of the value in taxon 2

$$\text{MSE} = 1.9$$

$$\begin{aligned} \text{MSE}_0 / \text{MSE} \\ &= 3.7 / 1.9 \\ &= 1.9 \end{aligned}$$

# False standardization

sample from a standard  
bivariate normal distribution



$$V = \begin{array}{|c|c|} \hline 2 & 1.9 \\ \hline 1.9 & 2 \\ \hline \end{array}$$

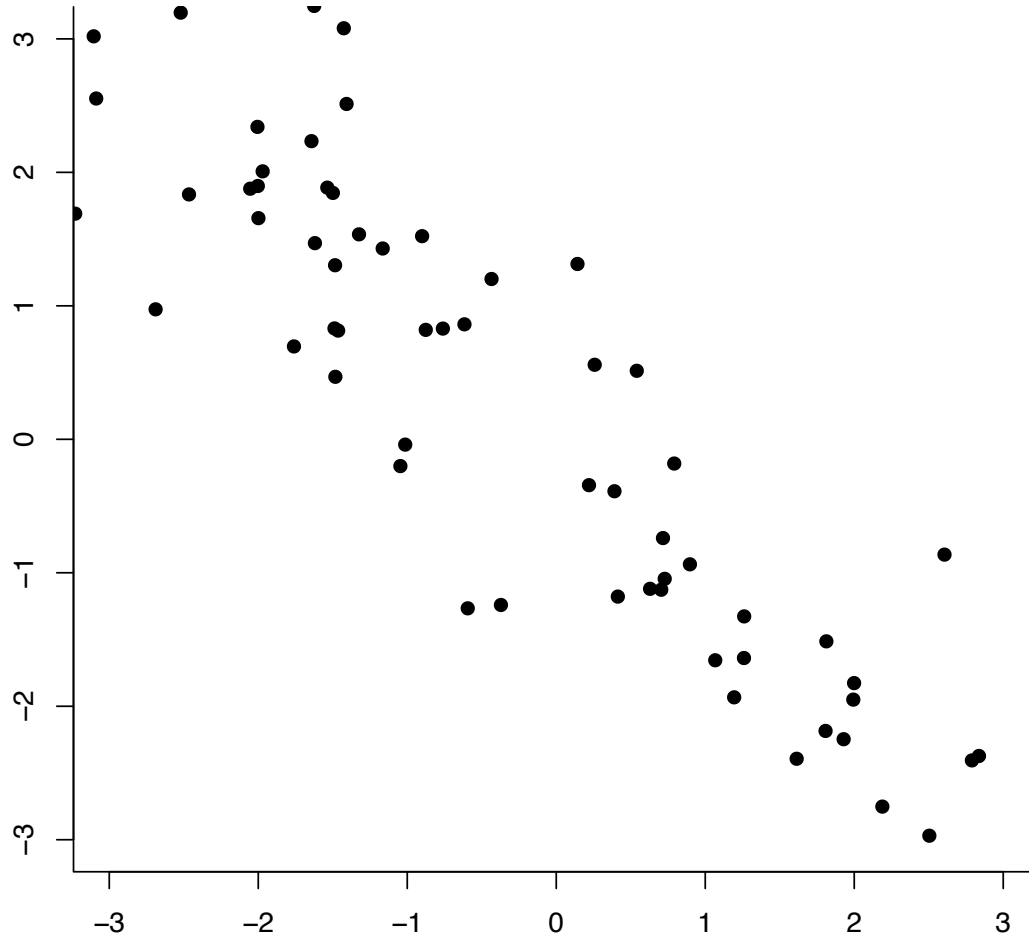
variance-covariance matrix

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

$$MSE_0 = 4.0$$

# False standardization

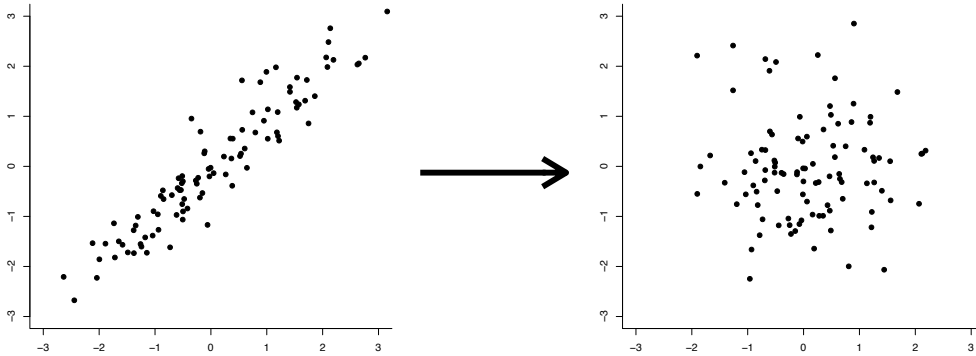
Instead of decreasing the MSE, we've increased it.



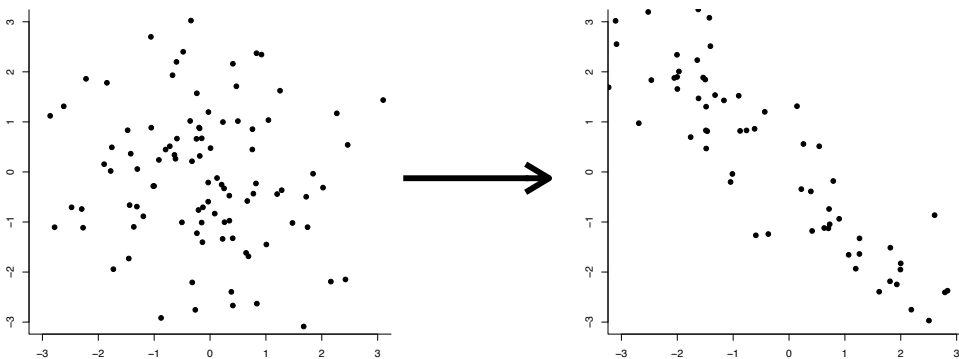
$$\text{MSE} = 23$$

$$\begin{aligned} \text{MSE}_0/\text{MSE} \\ &= 4/23 \\ &= 0.17 \end{aligned}$$

# Take-home message

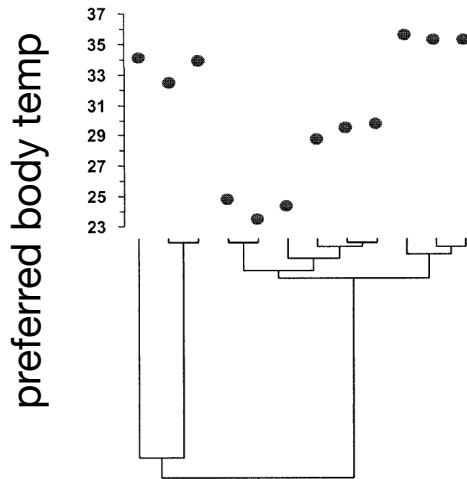


If data is **correlated** according to  $V$ , then MSE is **reduced** by standardization



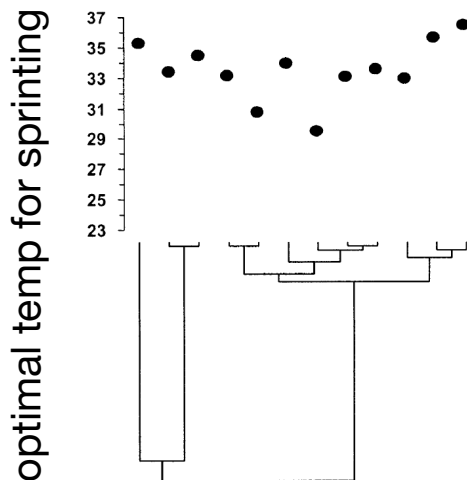
If data is **uncorrelated**, then MSE is **increased** by standardization

# Blomberg's K



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

$$K = \frac{\text{MSE}_0/\text{MSE}}{E[\text{MSE}_0/\text{MSE}]} = 0.453 \quad (\text{more signal})$$



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

$$K = \frac{\text{MSE}_0/\text{MSE}}{E[\text{MSE}_0/\text{MSE}]} = 0.101 \quad (\text{less signal})$$