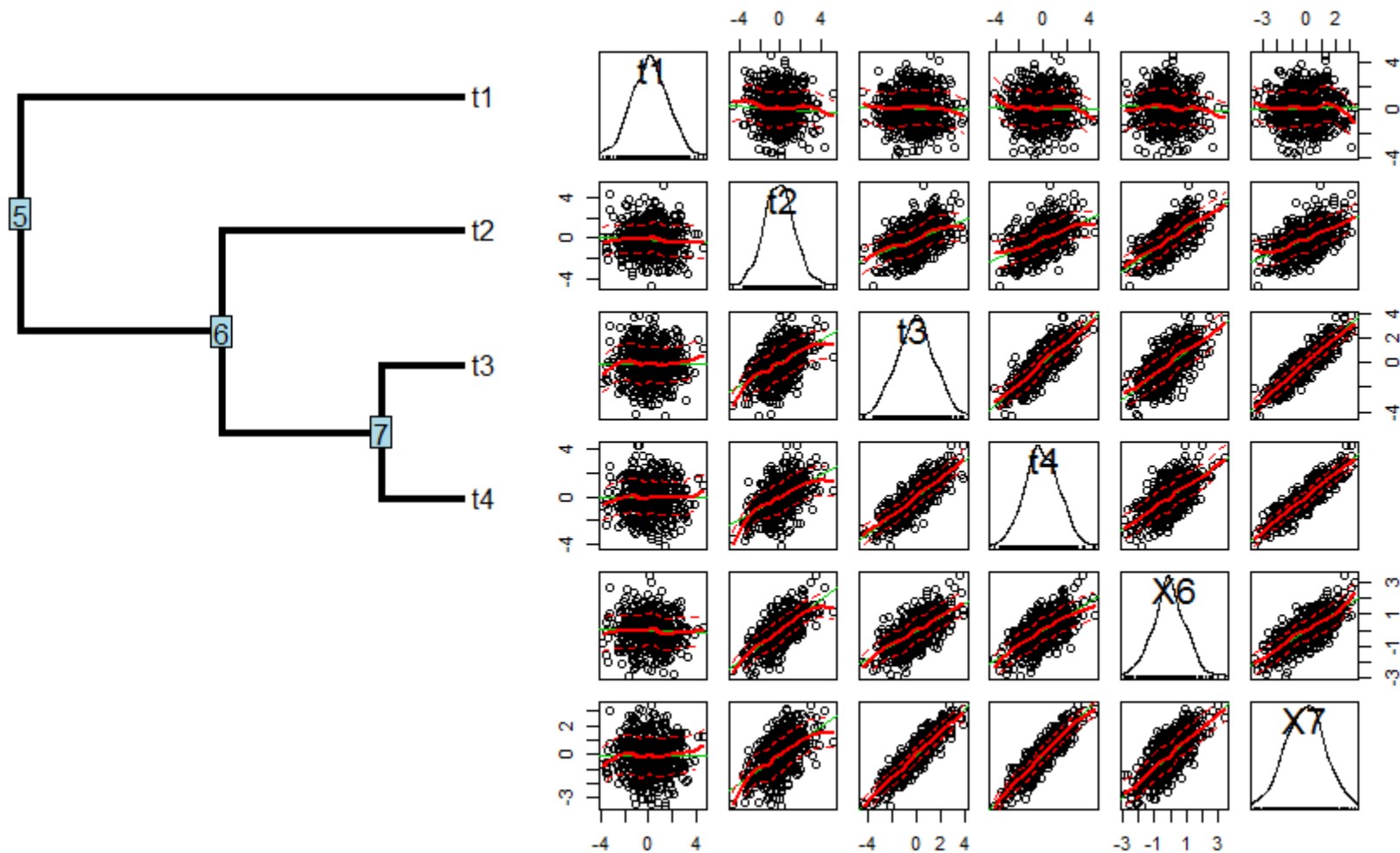
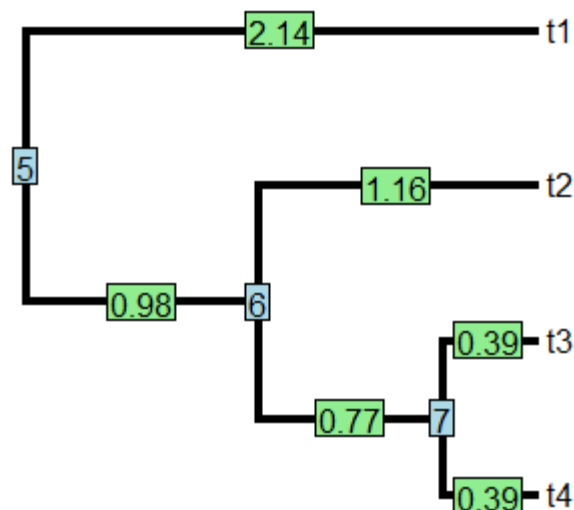


Brownian motion (on a phylogeny)



Brownian motion (on a phylogeny)



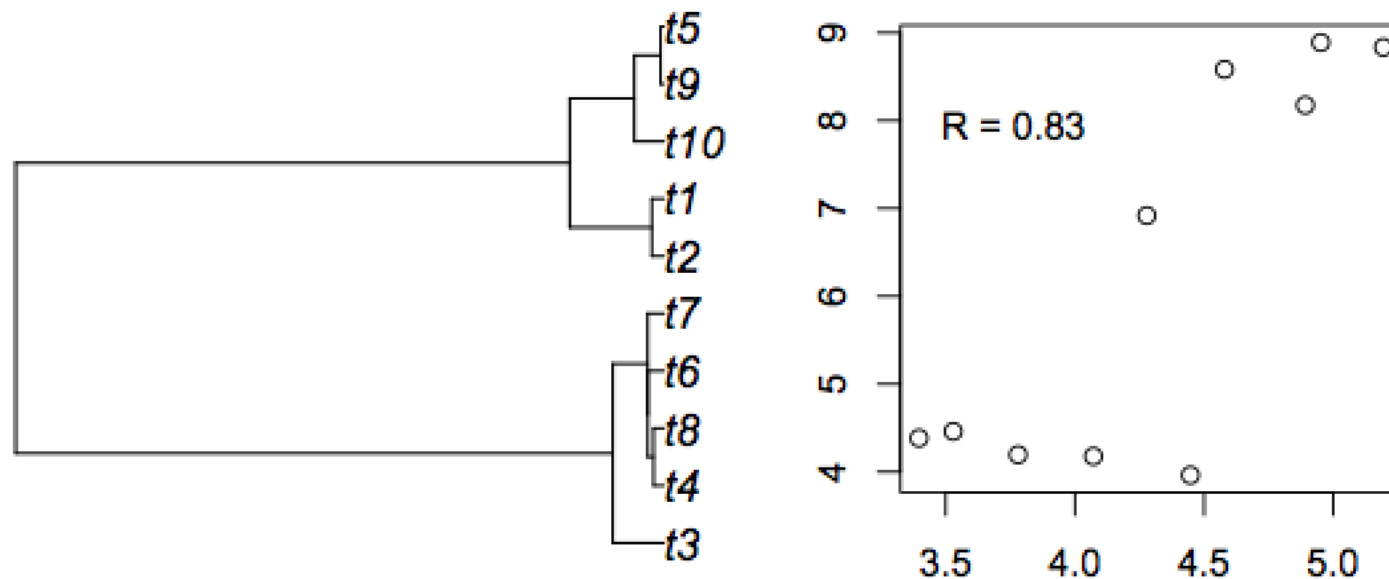
	t1	t2	t3	t4	6	7
t1	2.14	0.00	0.00	0.00	0.00	0.00
t2	0.00	2.14	0.98	0.98	0.98	0.98
t3	0.00	0.98	2.14	1.75	0.98	1.75
t4	0.00	0.98	1.75	2.14	0.98	1.75
6	0.00	0.98	0.98	0.98	0.98	0.98
7	0.00	0.98	1.75	1.75	0.98	1.75

The expected distribution of the tips & *nodes* of the tree under Brownian motion is multivariate normal with variance-covariance matrix in which each i,j th term is *proportional* to the height above the roots for the common ancestor of i and j .

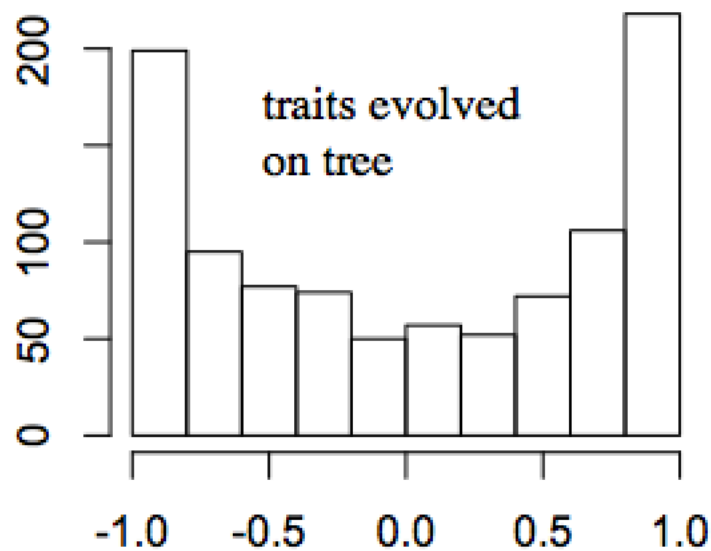
- Example:

1) Simulate the independent evolution of 2 traits on this tree:

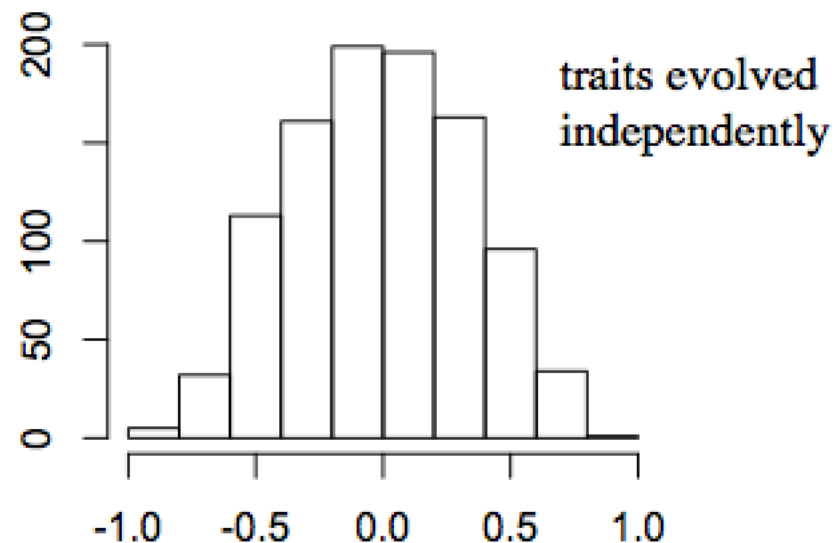
2) Calculate the pearson correlation coefficient between the two traits. Here is one example:



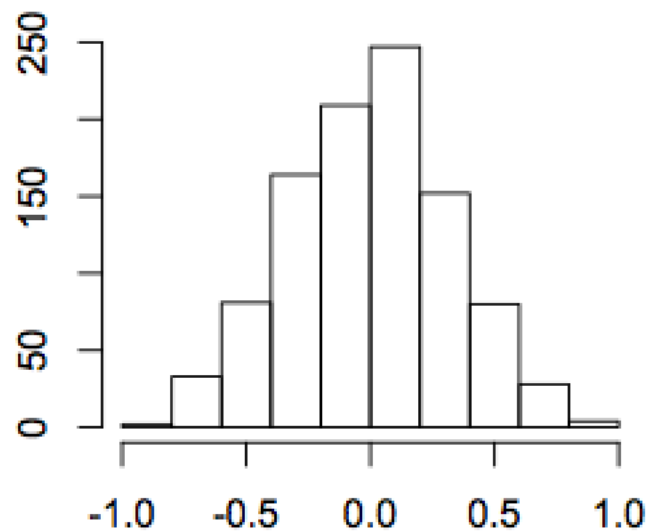
3) Repeat 1000 times and look at the distribution of correlation coefficients. In contrast, the expected distribution, for random data sets with $N = 10$ is shown on the right. For $N = 10$, the critical significance value at $p \leq 0.05$ is 0.63; the type I error rate is a whopping 60%!



pearR



pearR



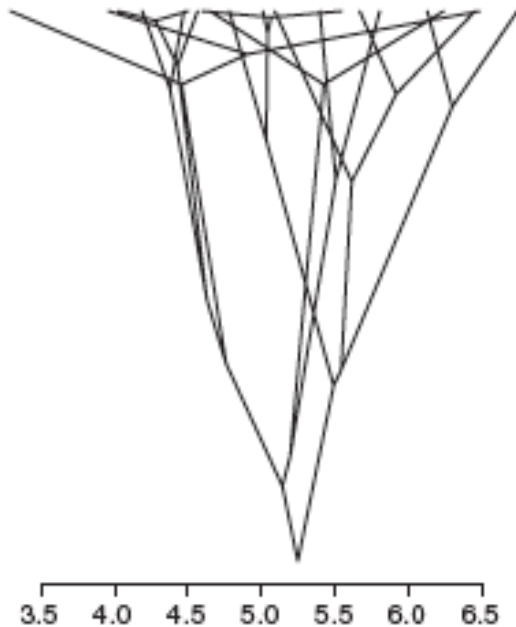
picR

Returning to our example above with the 10 taxon tree, here is the distribution of independent contrasts under the null hypothesis. Type I error for 1000 reps is 0.051% - perfect!

Blomberg's K – measure of phylogenetic signal

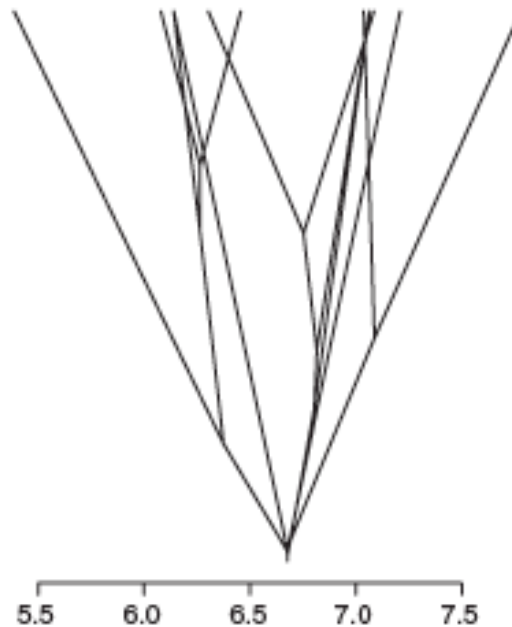
— phylogenetic signal →

low



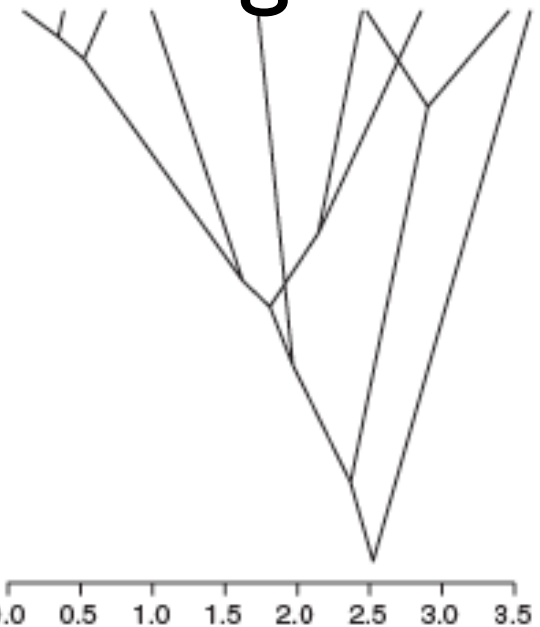
$K = 0.18$

brownian

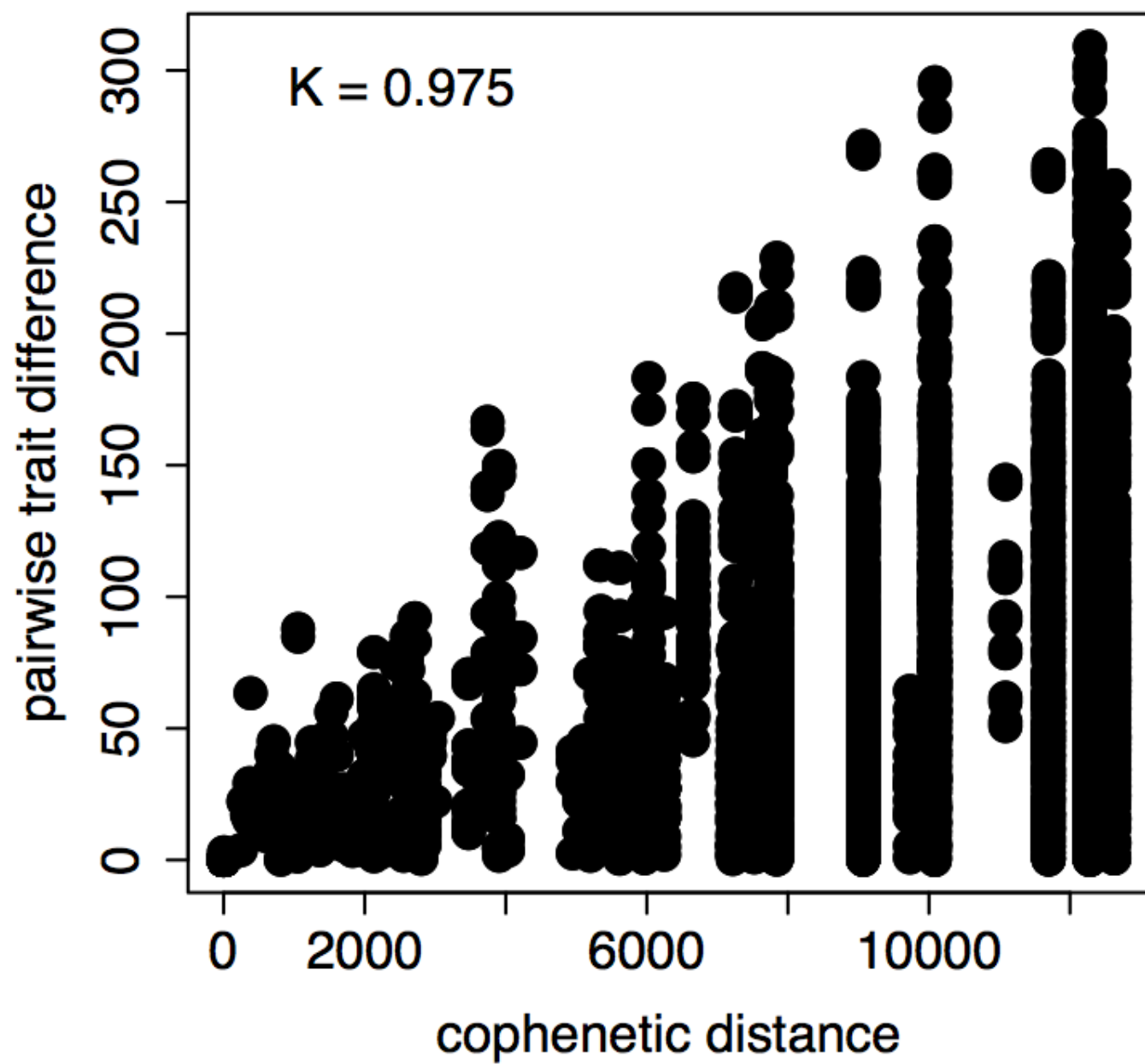


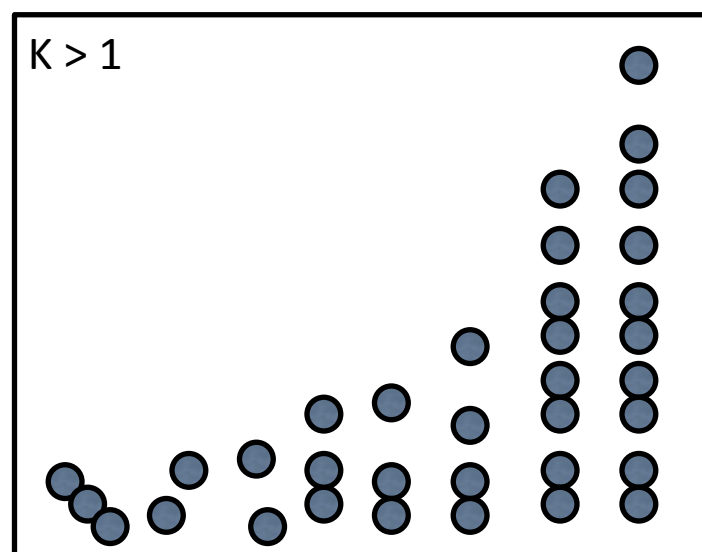
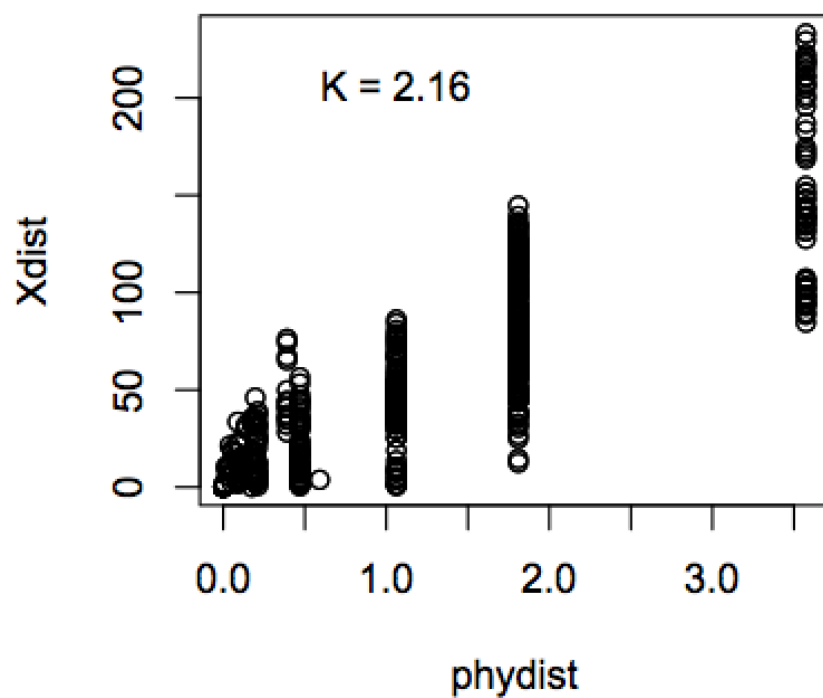
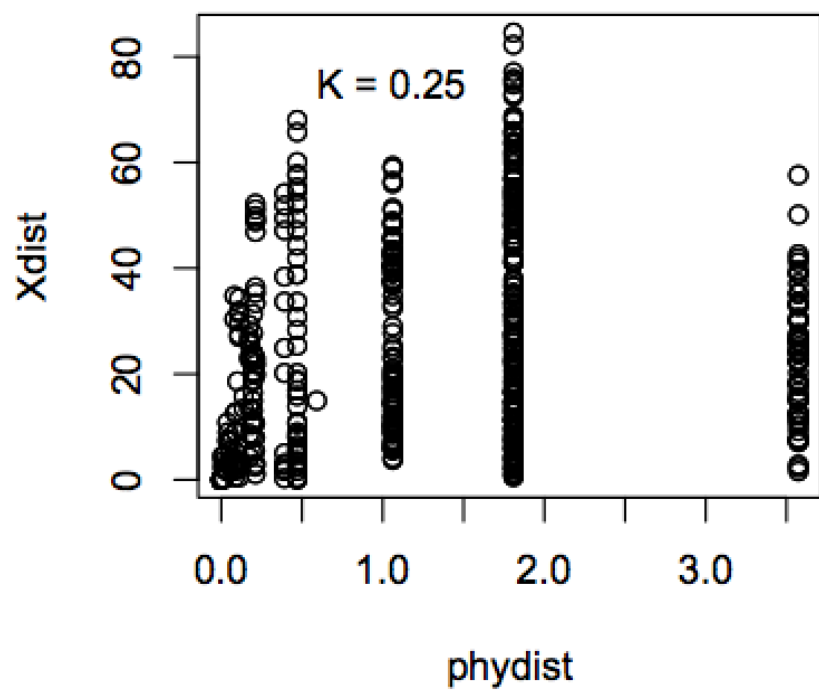
$K \sim 1$

high

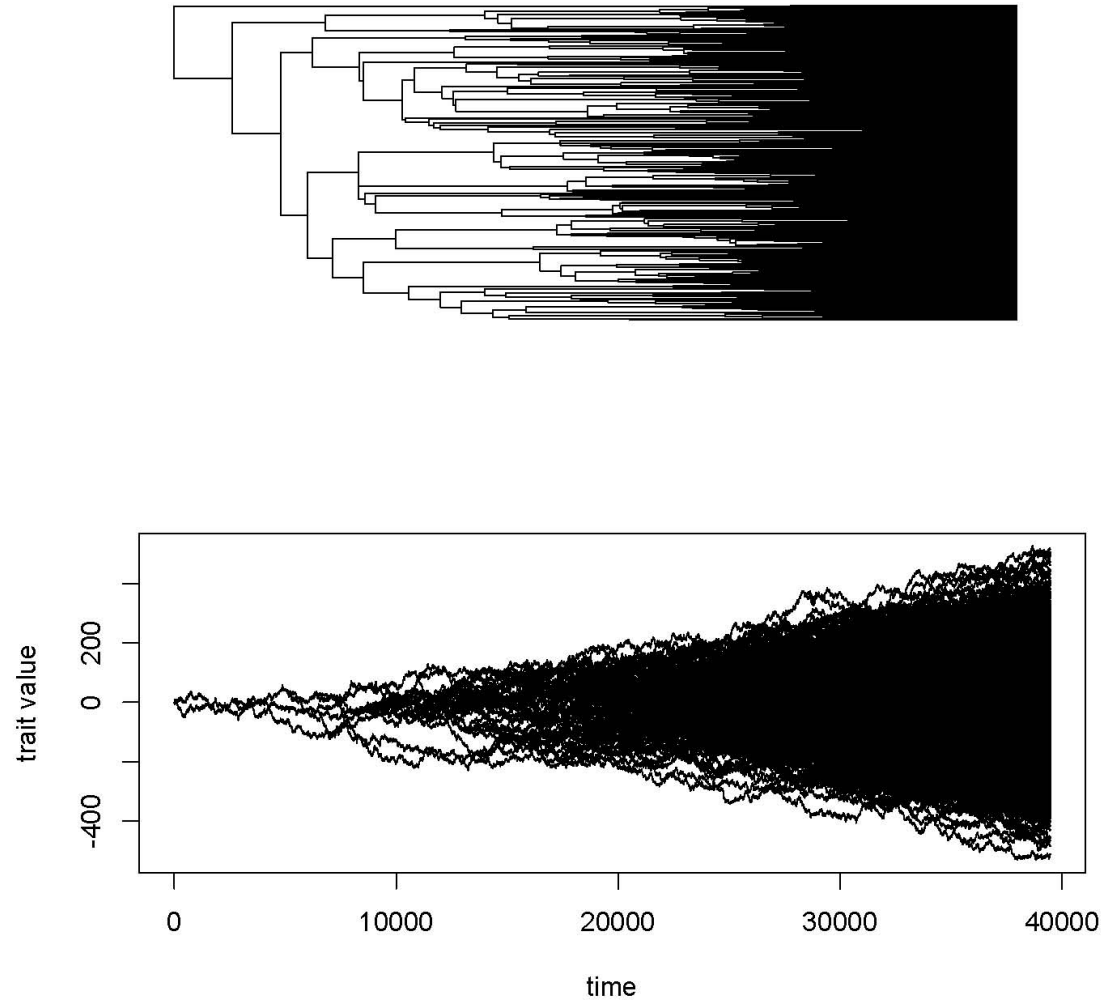


$K = 1.62$

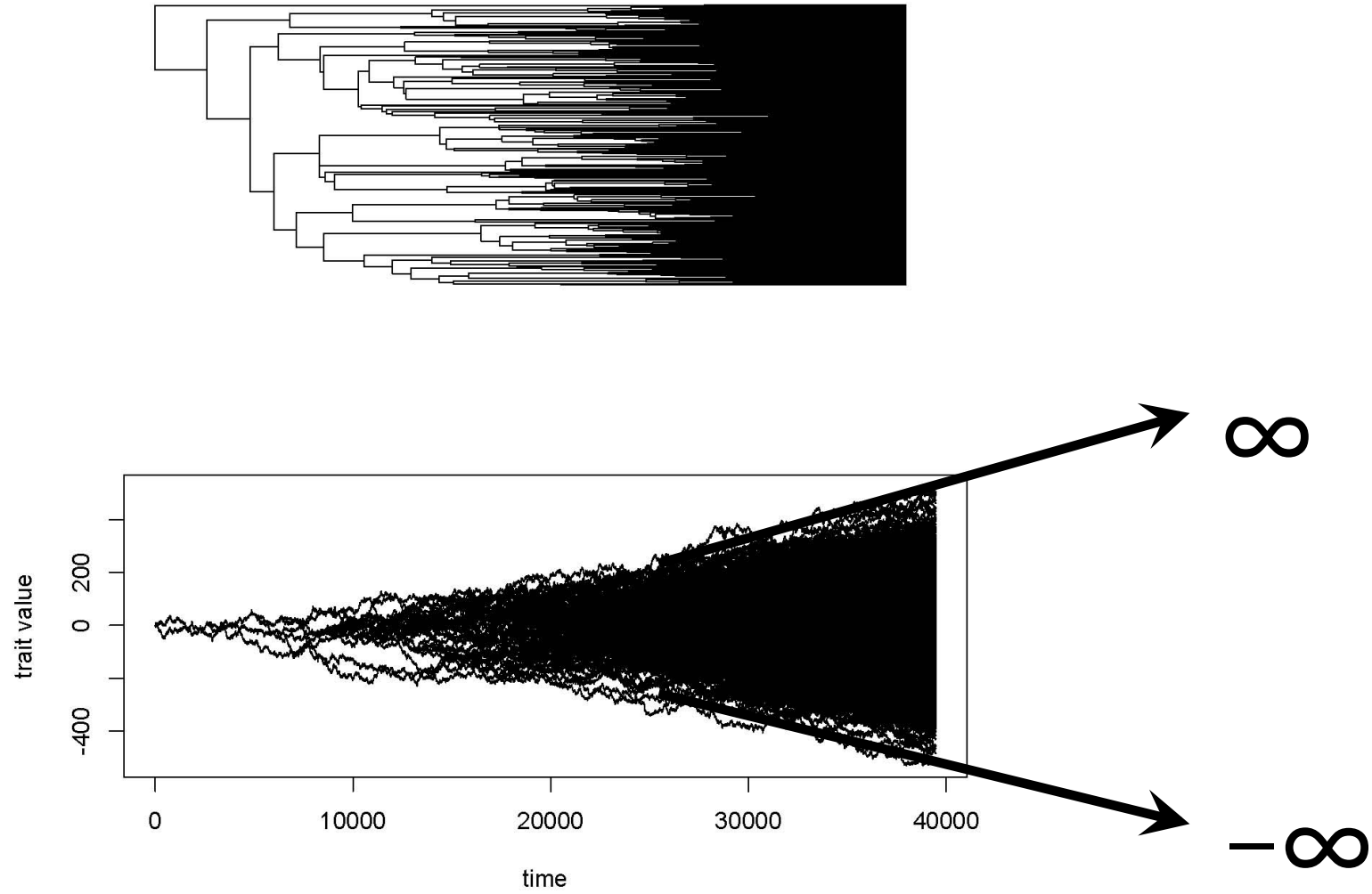




Brownian motion – assumptions and interpretations



Brownian motion – assumptions and interpretations



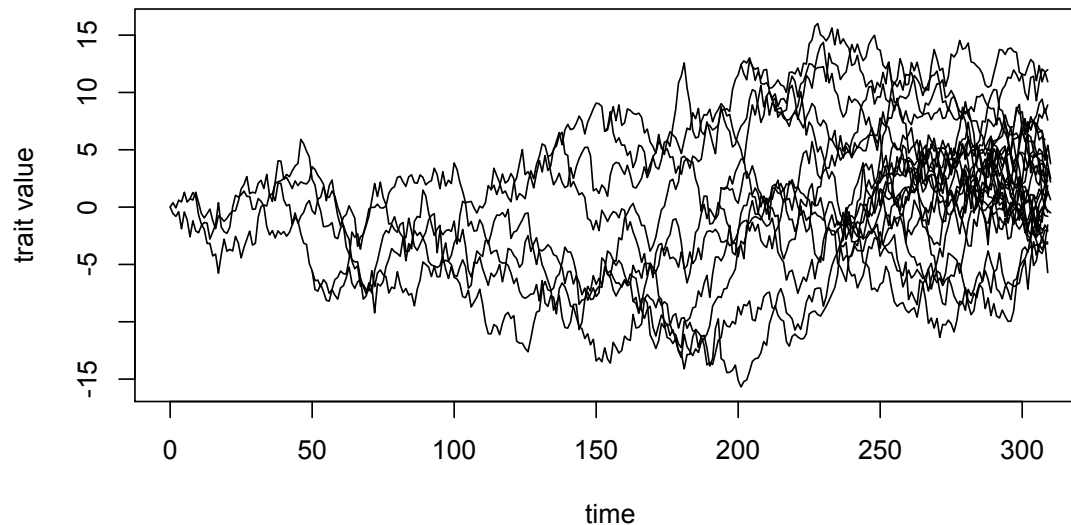
Ornstein-Uhlenbeck model (OU-1)

the math:

brownian motion + 'rubber band effect'

change is unbounded (in theory), but as rubber band gets stronger, bounds are established in practice

repeated movement back towards center erases phylogenetic signal, leading to $K \ll 1$



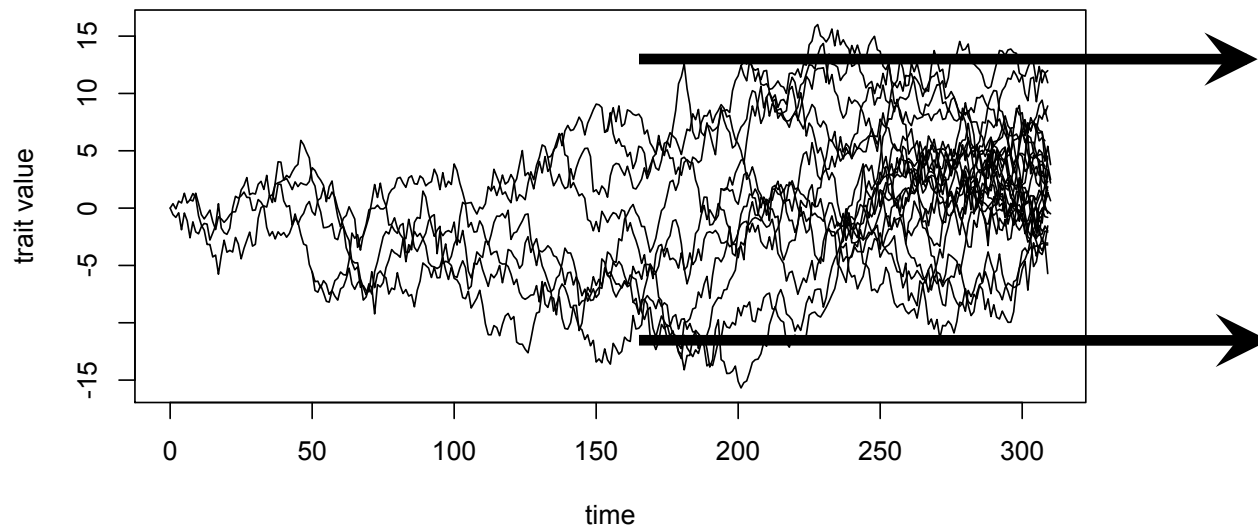
Ornstein-Uhlenbeck model (OU-1)

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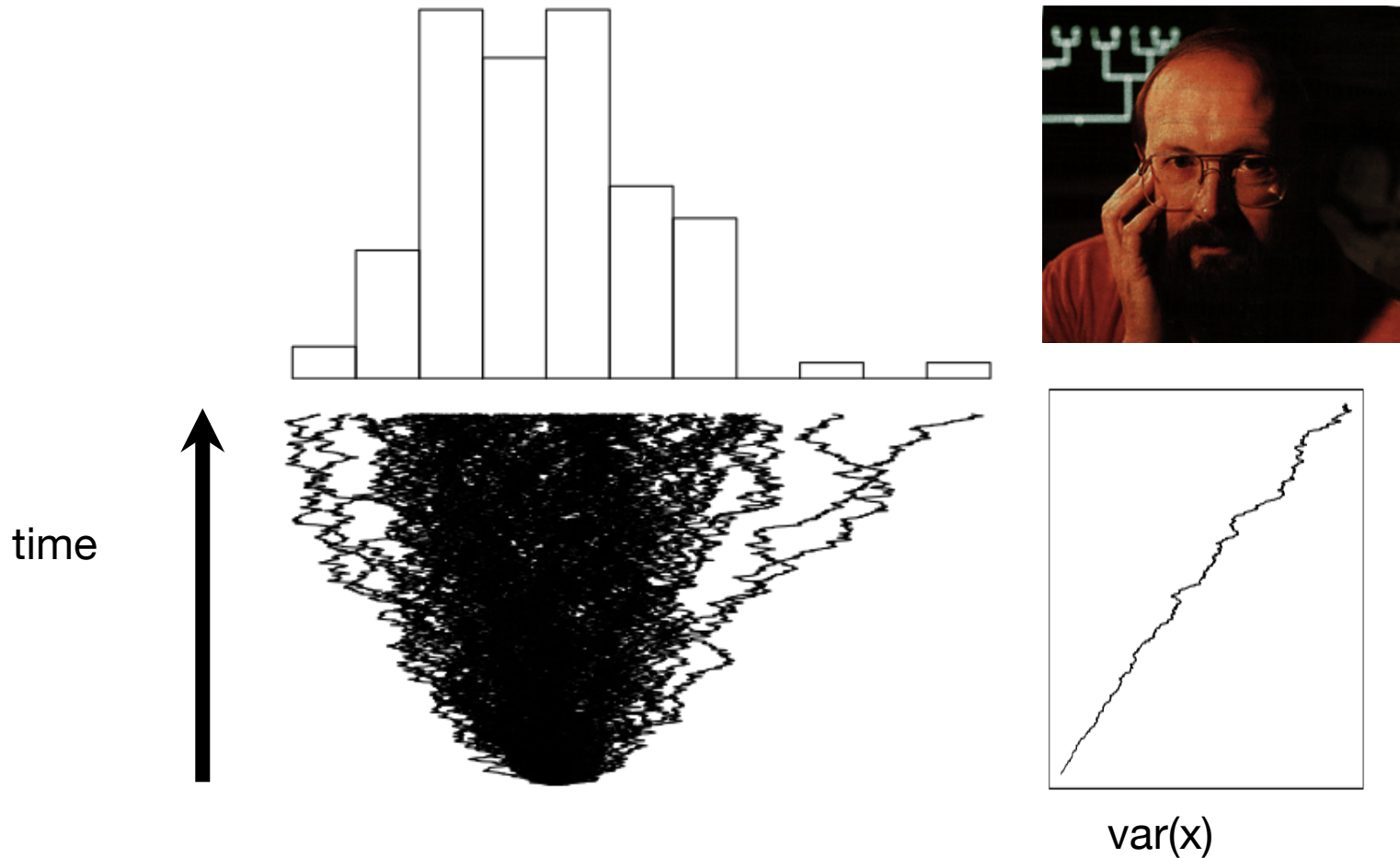
change is unbounded (in theory), but as rubber band gets stronger, bounds are established in practice

repeated movement back towards center erases phylogenetic signal, leading to $K \ll 1$



Rates of phenotypic diversification under Brownian motion

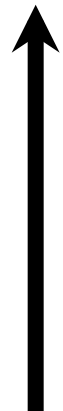
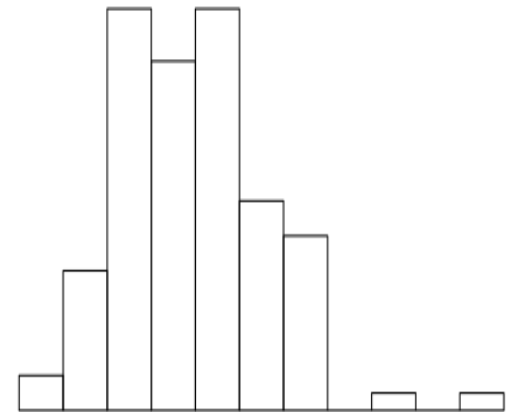
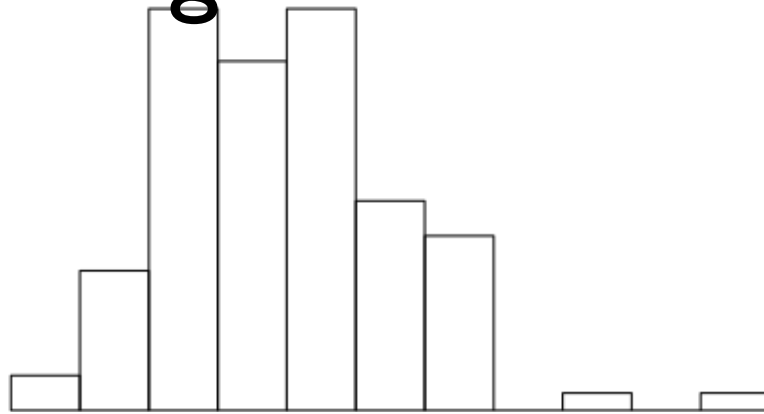
$$1 \text{ felsen} = \frac{1 \text{ Var}(\log_e(\text{trait}))}{\text{million yrs}}$$



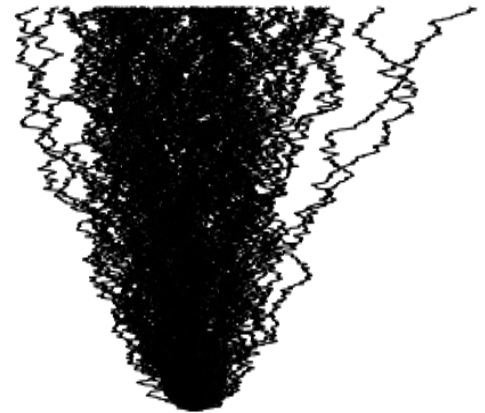
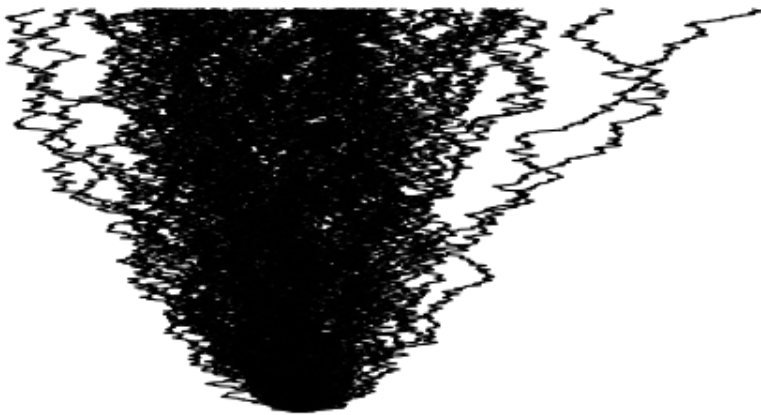
Rates of phenotypic diversification under Brownian motion

higher rate

lower rate



time

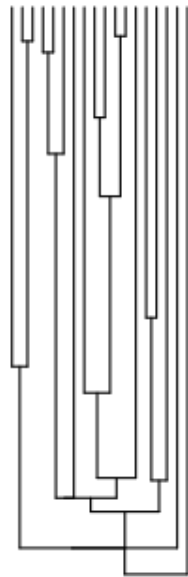
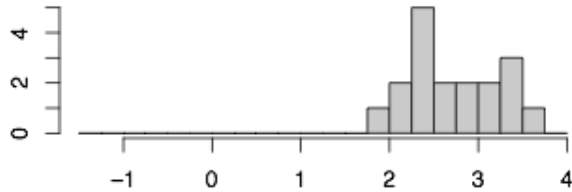


$\text{var}(x)$

Diversification of height in maples, *Ceanothus* and silverswords

rate = 0.015 felsens

Max height (m,ln)

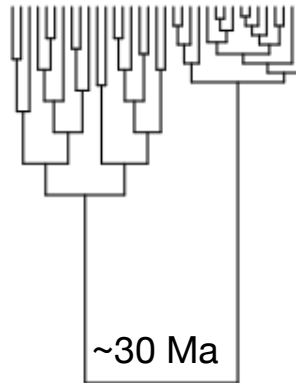
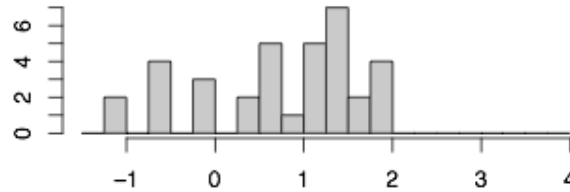


~45 Ma



0.10 felsens

Max height (m,ln)

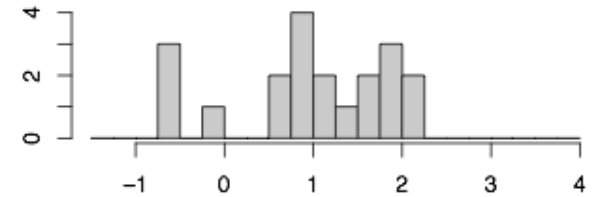


~30 Ma



0.83 felsens

Max height (m,ln)



~5.2 Ma



Rates of phenotypic diversification (estimated for Brownian motion model)

