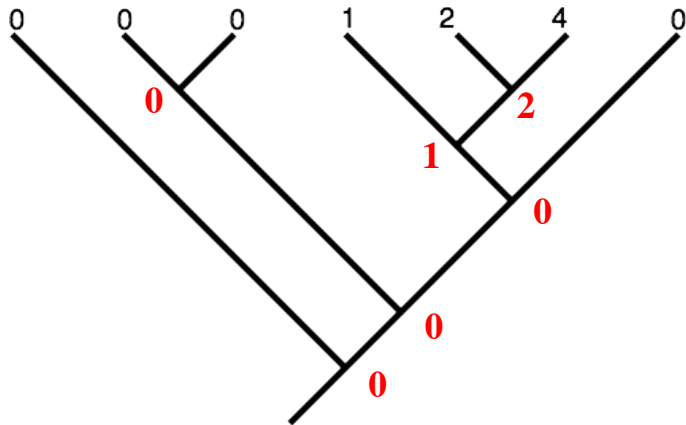
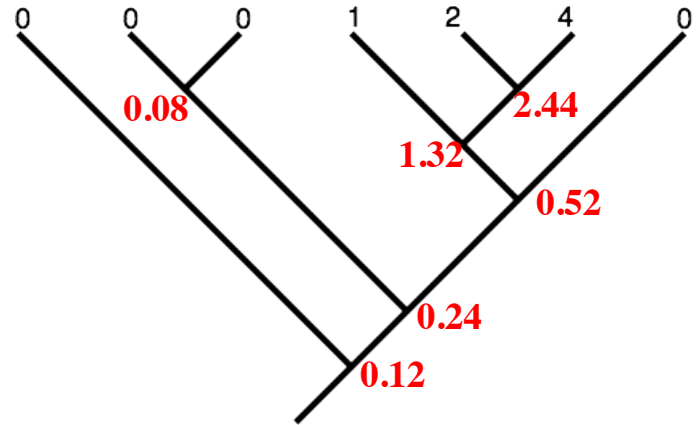


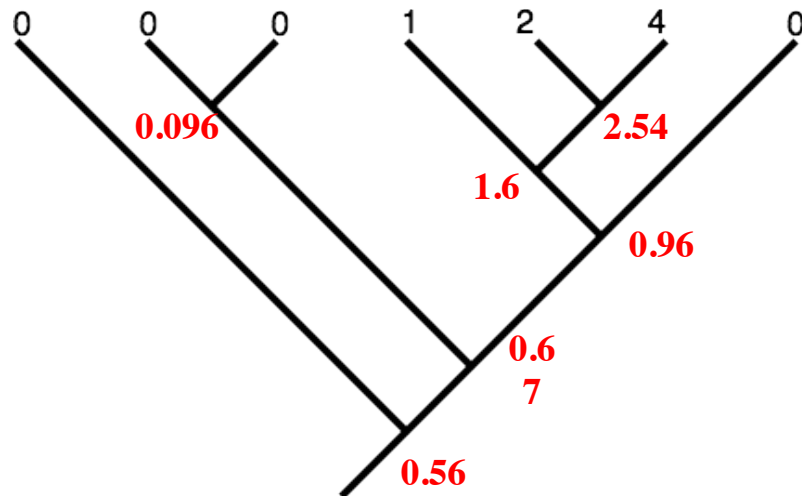
Linear parsimony



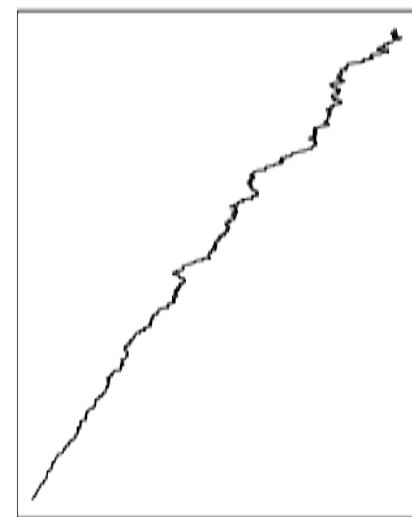
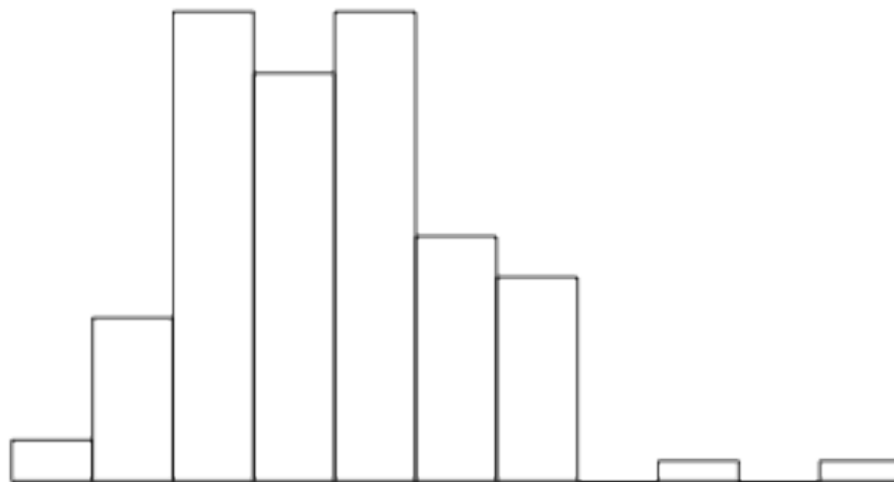
Squared change parsimony = ML with BL = I



ML with BL as shown

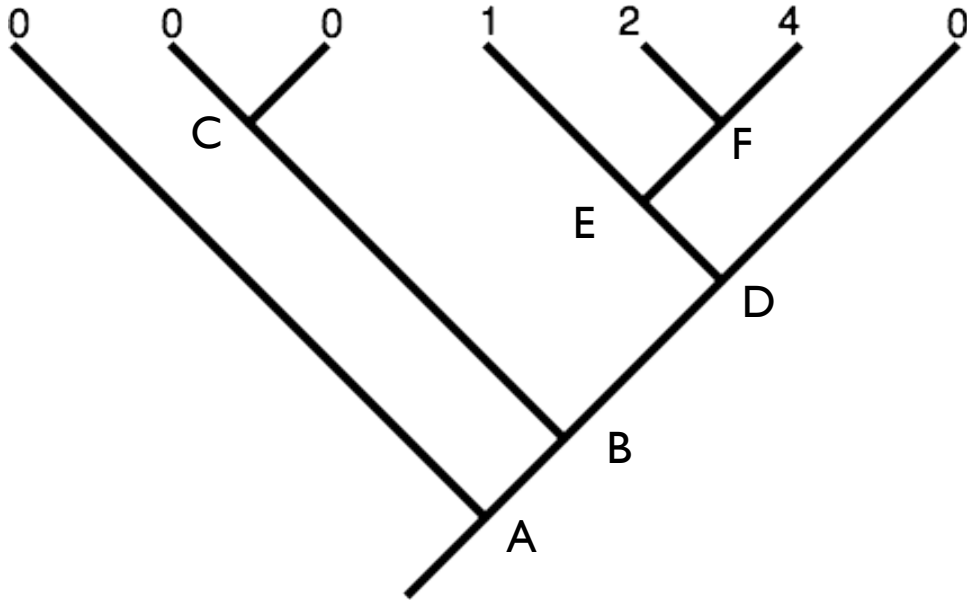


time



$\text{var}(x)$

# ML with BL as shown



Node	ML estimate	Lower 95% CI	Upper 95% CI
A	0.56	-0.77	1.89
B	0.67	-0.43	1.78
C	0.096	-0.61	0.81
D	0.96	0	1.95
E	1.6	0.76	2.45
F	2.54	1.86	3.2

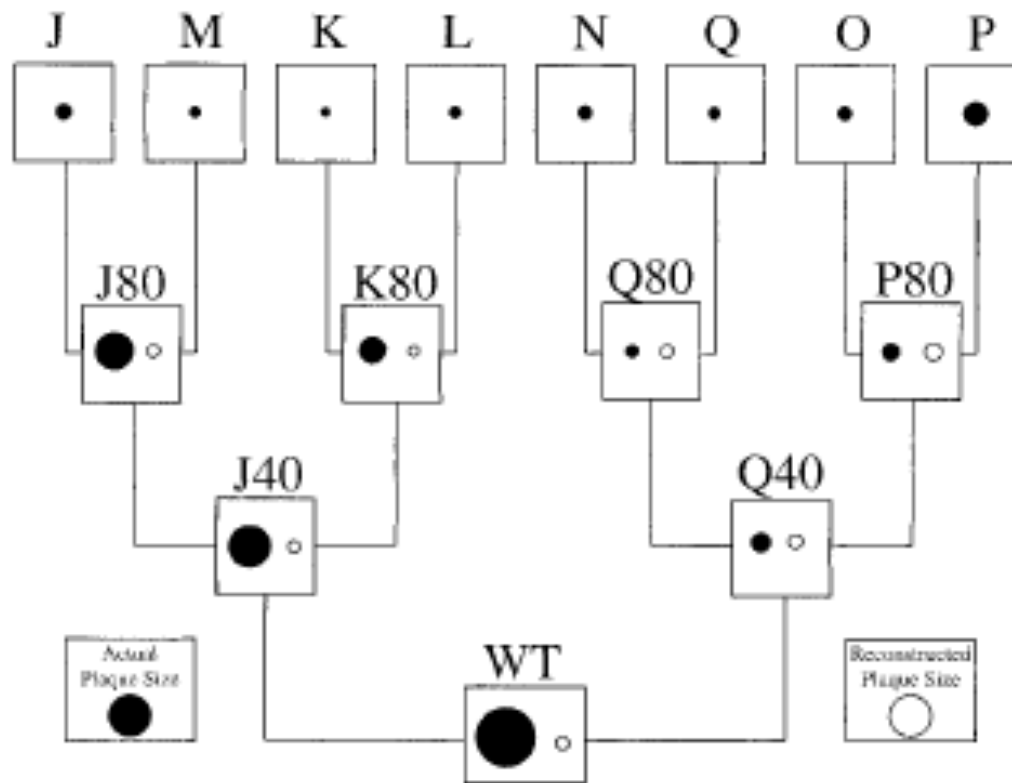
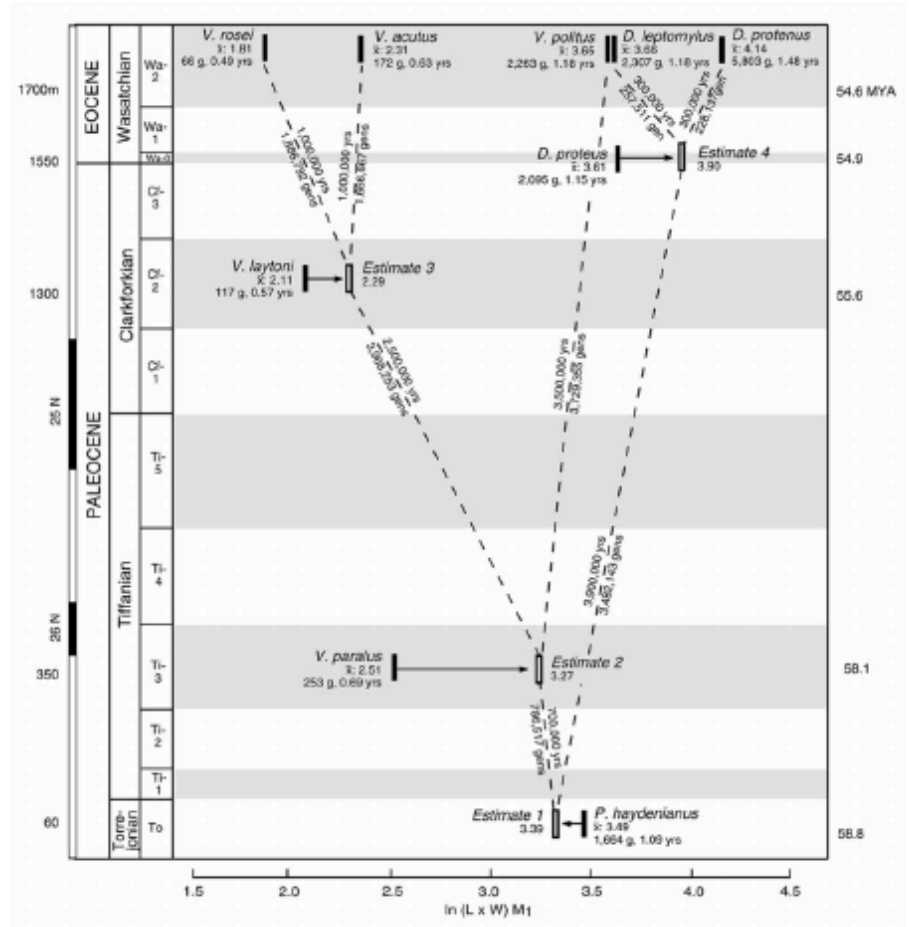
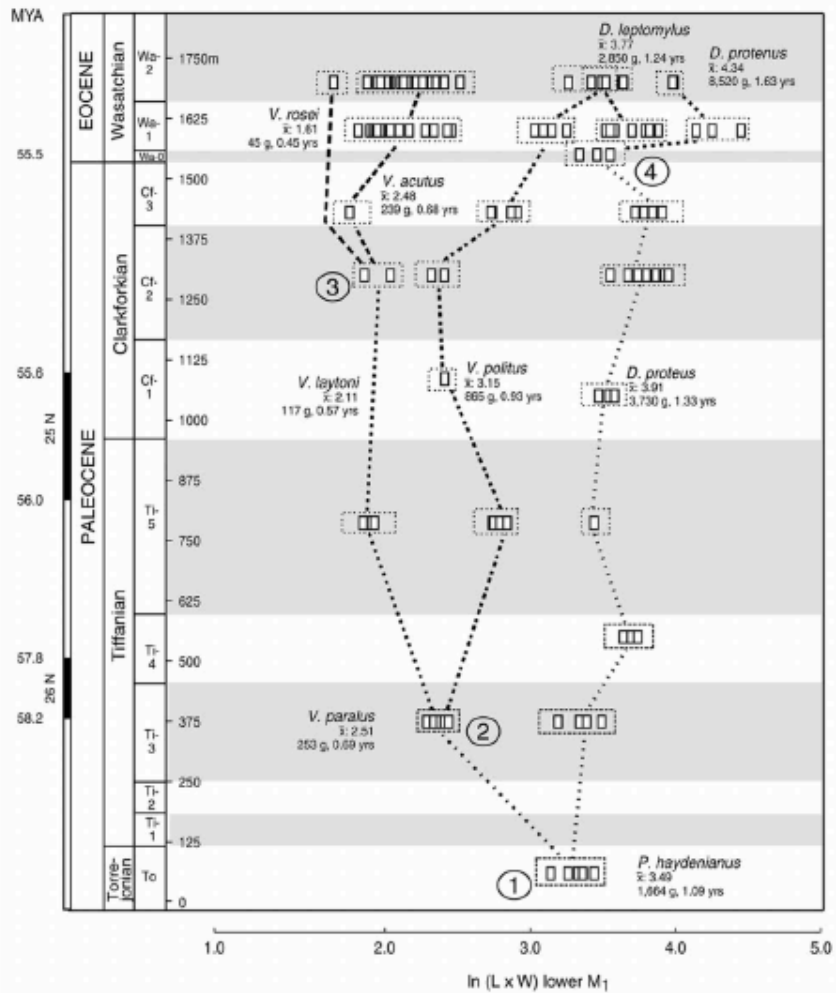
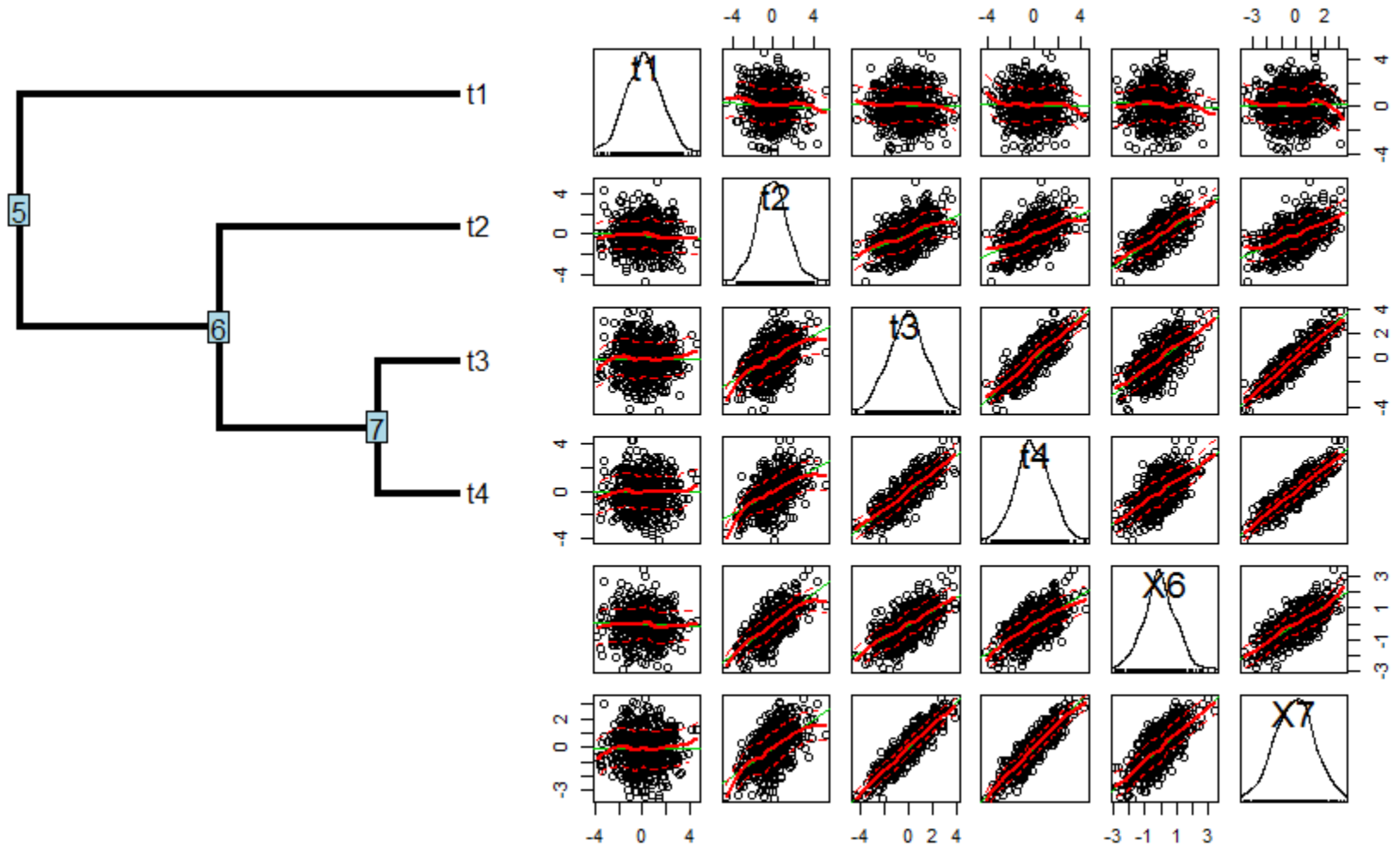


FIG. 2. Comparison of actual (mean) and reconstructed plaque diameters without an outgroup or fossil. Viral plaques from an experimentally generated phylogeny were measured and data for the terminal taxa were used to reconstruct ancestral states using squared-change parsimony (Maddison 1991). Actual values are proportional to black circles and reconstructed values are proportional to white circles.



Polly 2001 Am Nat

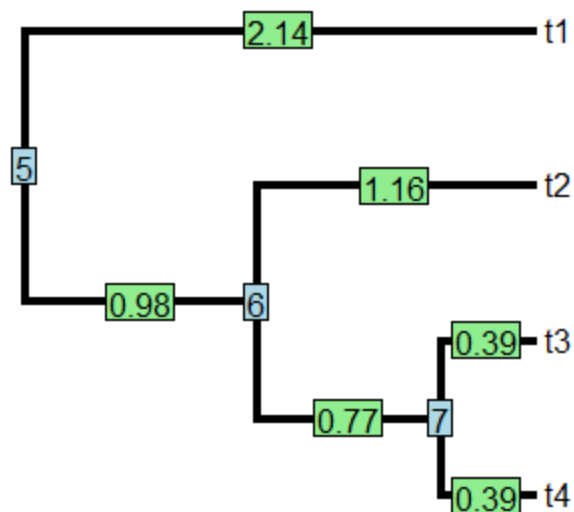
# Brownian motion (on a phylogeny)



'borrowed' from Liam Revell lecture notes



# Brownian motion (on a phylogeny)



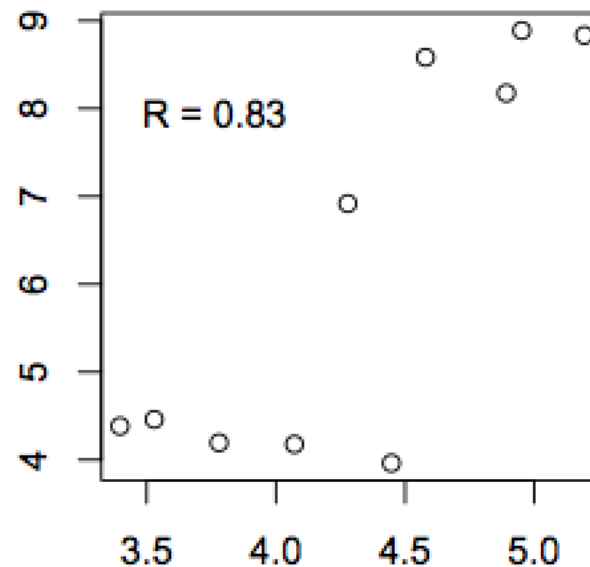
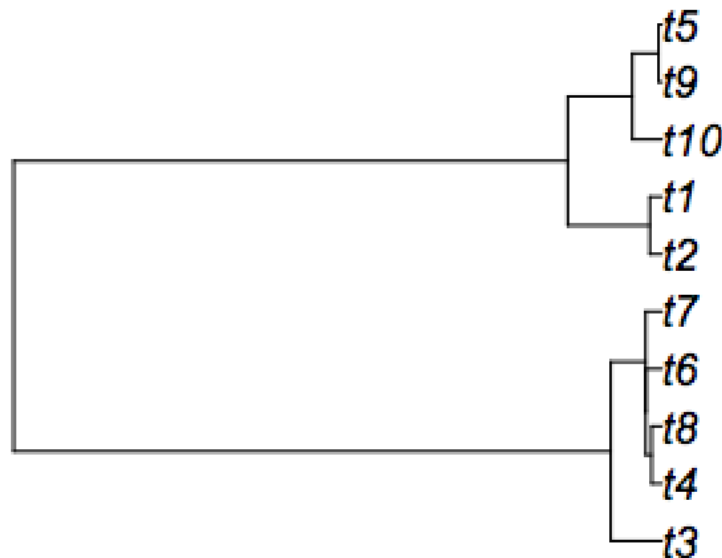
	t1	t2	t3	t4	6	7
t1	2.14	0.00	0.00	0.00	0.00	0.00
t2	0.00	2.14	0.98	0.98	0.98	0.98
t3	0.00	0.98	2.14	1.75	0.98	1.75
t4	0.00	0.98	1.75	2.14	0.98	1.75
6	0.00	0.98	0.98	0.98	0.98	0.98
7	0.00	0.98	1.75	1.75	0.98	1.75

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  $j$ .

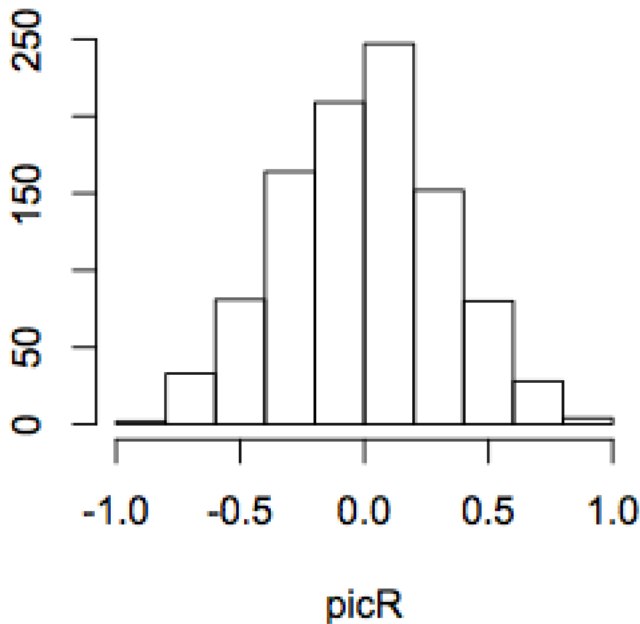
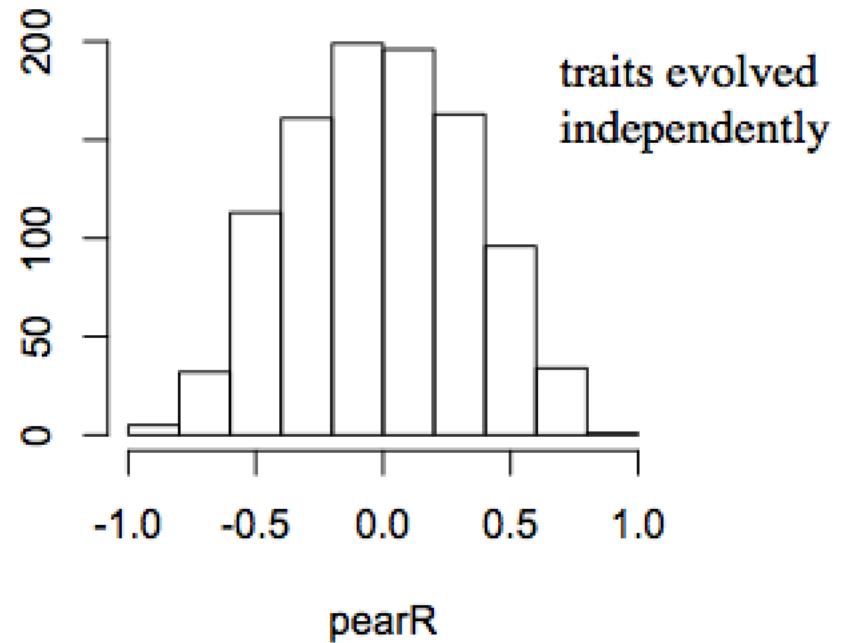
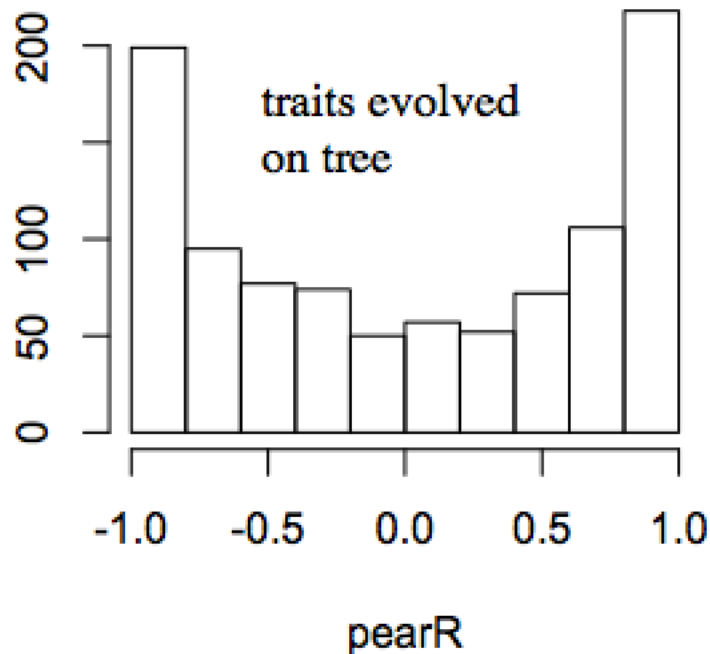
- Example:

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:

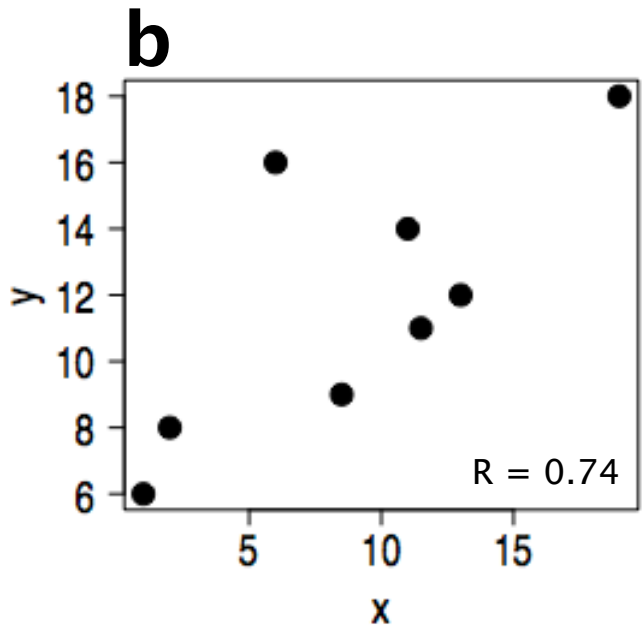
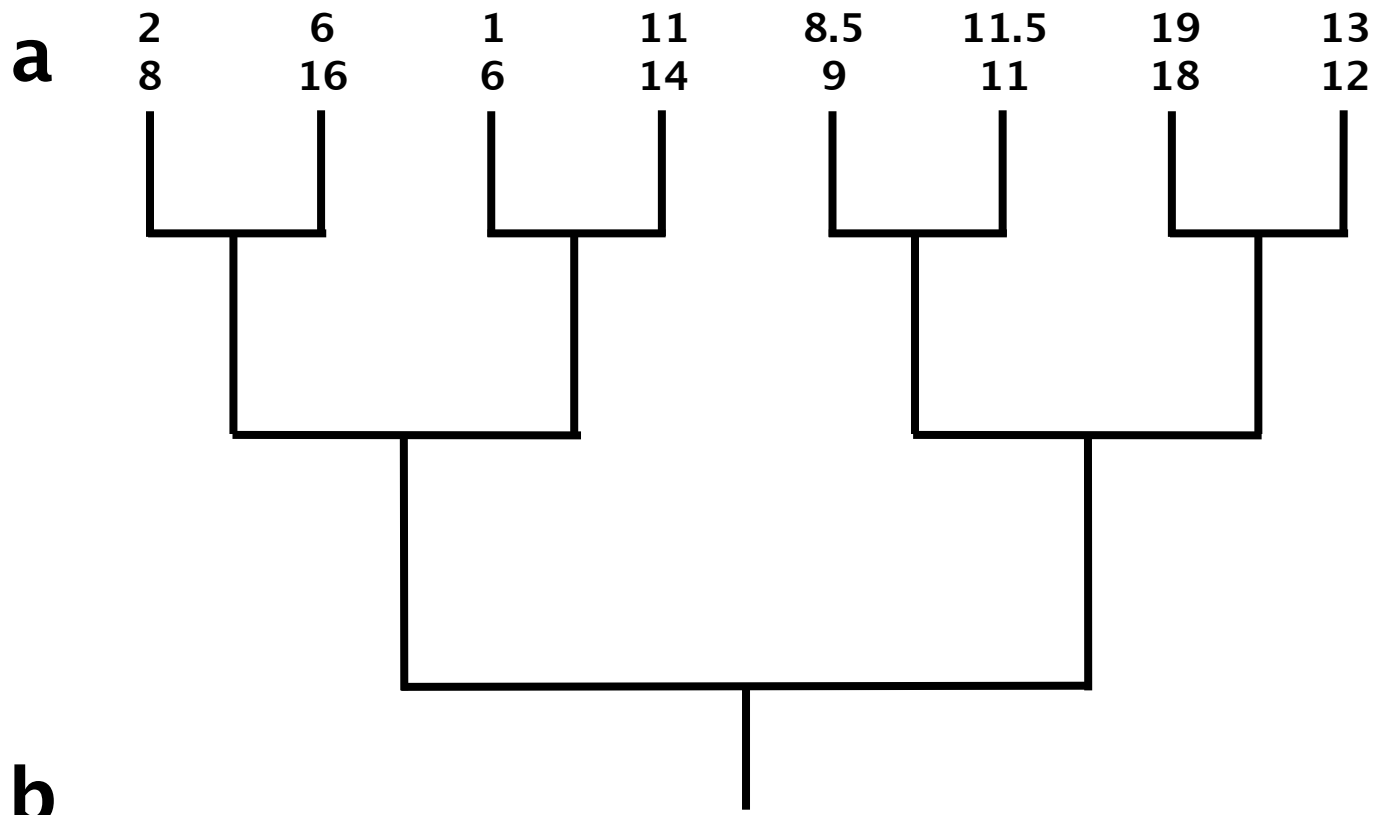


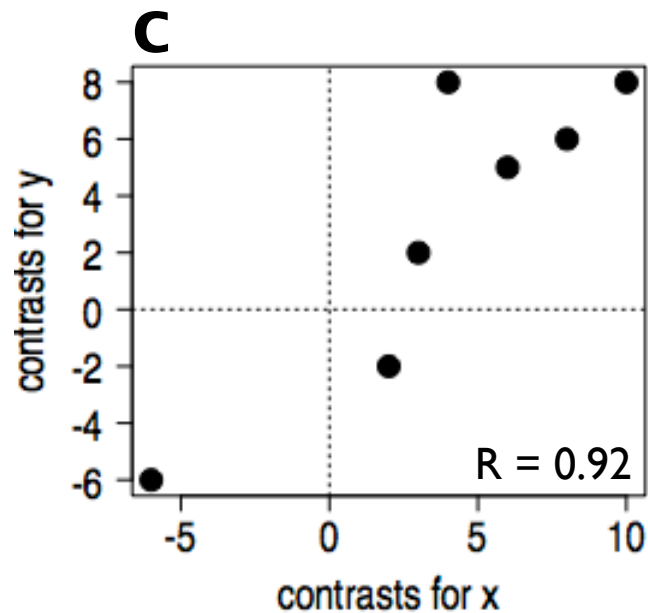
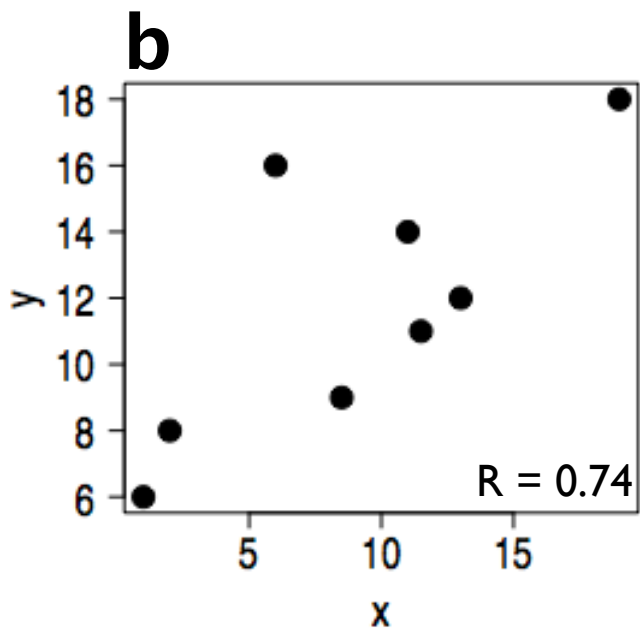
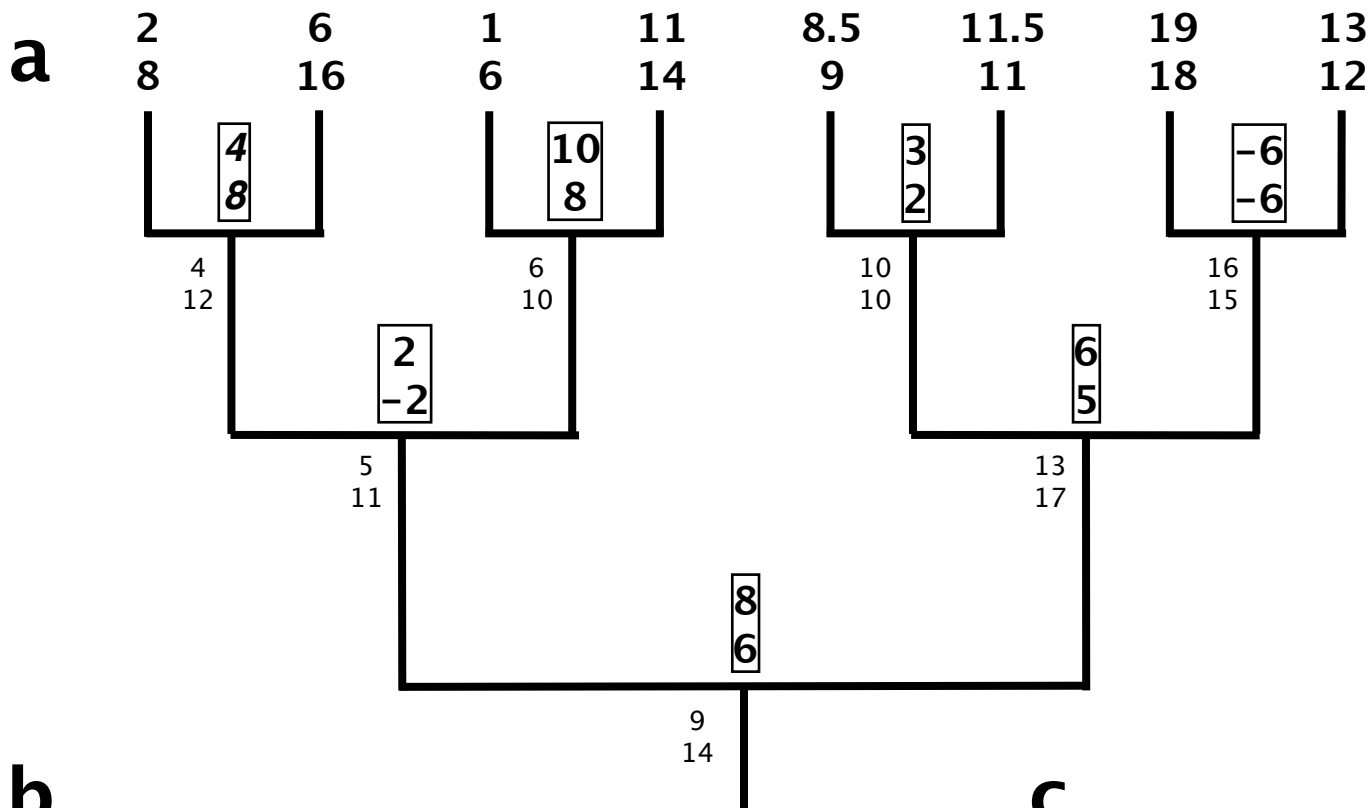
3) Repeat 1000 times and look at the distribution of correlation coefficients. In contrast, the expected distribution, for random data sets with  $N = 10$  is shown on the right. For  $N = 10$ , the critical significance value at  $p \leq 0.05$  is 0.63; the type I error rate is a whopping 60%!



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!







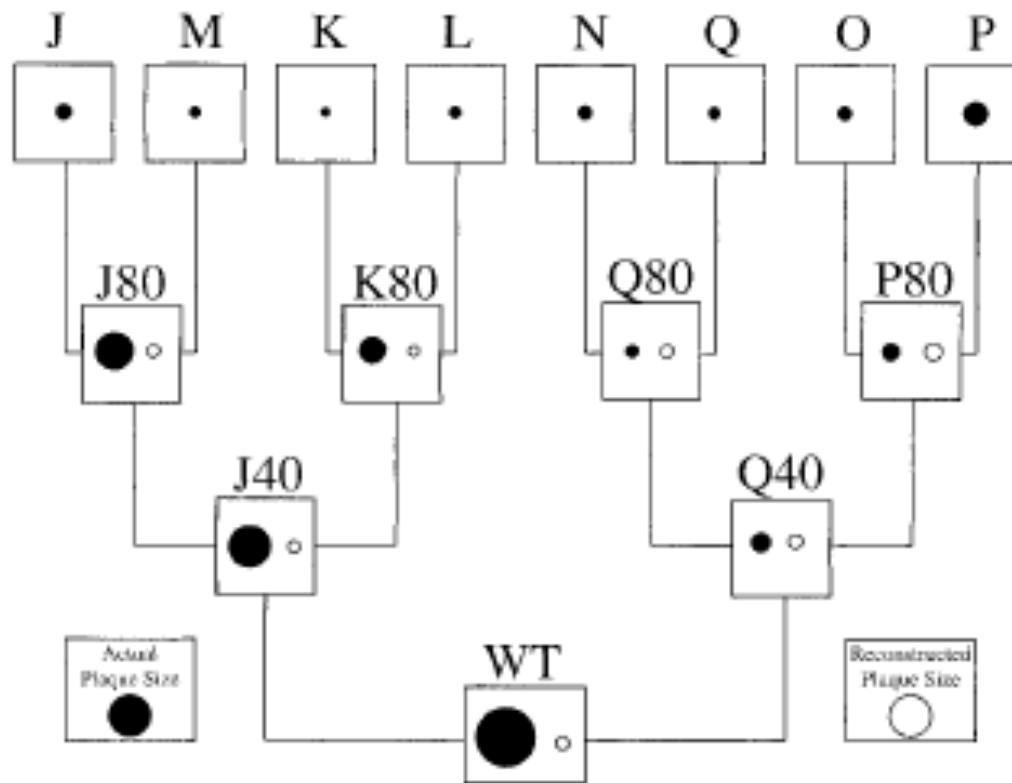


FIG. 2. Comparison of actual (mean) and reconstructed plaque diameters without an outgroup or fossil. Viral plaques from an experimentally generated phylogeny were measured and data for the terminal taxa were used to reconstruct ancestral states using squared-change parsimony (Maddison 1991). Actual values are proportional to black circles and reconstructed values are proportional to white circles.

TABLE 4. Comparison of correlational methods. Values are absolute value of "R" and associated *P*-values are in parentheses. Percentages are percent error of R assuming change along branches (using actual ancestors; CAB) is the actual correlation. IC-AA, independent contrasts calculated with actual ancestors; IC, independent contrasts; NP, nonphylogenetic regression.

Characters compared	Actual correlation		Correlative method	
	CAB	IC-AA	IC	NP
Diameter vs. liquid	0.931 (< 0.0001)	0.866 (0.0055)	0.834 (0.0100) -10.4%	0.762 (0.0280) -18.2%
Diameter vs. shape	0.954 (< 0.0001)	0.956 (0.0002)	0.959 (0.0002) 0.5%	0.971 (< 0.0001) 1.8%
Liquid vs. lysis	0.673 (0.0059)	0.749 (0.0324)	0.546 (0.1618) -18.9%	0.108 (0.7990) -84.0%
Diameter vs. lysis	0.517 (0.0485)	0.801 (0.0169)	0.685 (0.0607) 32.5%	0.363 (0.3772) -29.8%
Shape vs. lysis	0.633 (0.0112)	0.681 (0.0630)	0.552 (0.1557) -12.8%	0.214 (0.6113) -66.2%
Shape vs. liquid	0.980 (< 0.0001)	0.849 (0.0076)	0.834 (0.0100) -14.9%	0.783 (0.0216) -20.1%
Mean error			-4.0%	-36.1%
Mean absolute error			15.0%	-36.7%



