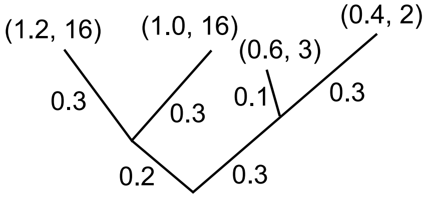
Exercise 1: The vector $\mathbf{X} = \begin{pmatrix} X_1 \\ X_2 \end{pmatrix}$ is normally distributed with $\mathbb{E}X_1 = 0.5$ and $\mathbb{E}X_2 = 1$. Further, the standard deviations of X_1 and X_2 are 0.2 and 0.4, respectively, and their correlation is -0.1. Calculate the expectation vector and the covariance matrix of the vector

$$\mathbf{Y} = \begin{pmatrix} 2 & 0.5 \\ 1 & -1 \end{pmatrix} \cdot \mathbf{X}$$

Exercise 2: The average values of two quantitative traits have been determined for four species of known phylogeny, as shown in the figure.



(a) Calculate the correlation of the traits (without taking the phylogeny into account).

(b) Calculate the independent contrasts for each of the two traits. Do this step by step without using special software.

(c) Calculate the correlation of the independent contrasts of the two traits.

(d) Is the correlation between the traits significant? Does the answer to this question depends on whether you take the phylogeny into account?

Exercise 3: The files QuantTraitsA.csv, QuantTraitsB.csv, and QuantTraitsC.csv contain datasets of quantitative traits for species whose phylogeny is given in the file QuantTraits_Tree.txt. Do you find evidence for selection and/or for correlated evolution of some of the traits?

Exercise 4: Write a python program or an R script that reads a tree in newick format and simulates the evolution of quantitative traits along the branches of the tree. The output should be the values of the traits at the tips of the tree.

Exercise 5: Explore with simulated data how robust posterior probabilities given by BEAST are against misspecification of priors, substitution models and relaxed-clock models.

Exercise 6: Based on the fossil record for lizards it is claimed that the most recent common ancestor (MRCA) of *Sphenodon punctatus* and *Cnemidophorus tigris* is at least 228.0 Mya old, the MRCA of *Cnemidophorus tigris* and *Rhineura floridana* is at least 113 Mya old, the MRCA of *Rhineura floridana* and *Gallotia galloti* at least 64.2 Mya, and the MRCA of *Timon lepidus* and *Dalmatolacerta oxycephala* at least 5.3 Mya.

(a) Use this information to estimate the phylogeny of lizards with time calibration.

(b) How does this result depend on the choice of model for the relaxed clock?

(c) How does the result change if you use only two or three of the given calibration points?

(d) How well are the given calibration points supported by fossils documented in the following references?

   Science (1990) 249:1020-1023,

   J Vertebr Paleontol (2006) 26:795-800,

   J Vertebr Paleontol (2002) 22:286-298,

   J Paleontol (1985) 59:1481-1485