

Answers to Lab 6: PIC Assignment

1. All tests are two tailed, because you have no reason to expect a positive or a negative correlation. You do not even know what these characters are. (1 point)
2. Neither the data, nor the log transformed data fit the assumptions of multivariate normality, so I used a non-parametric test for correlation: Kendall's and/or Spearman's. (1 point)
- 3.***The first number is for cor.table and the second is for cor.test. They're different, because cor.table has an error that I will give you a correction for.

For Kendall's the 2-tailed ps are: (¾ point)

V2-V3	4.164559e-06	6.069e-10
V2-V4	6.320802e-15	2.2e-16
V3-V4	1.552561e-05	4.308e-09

Even better multiply by 3 again to correct for multiple tests: (+¼ point)

V2-V3	1.249367e-05	1.8207e-09
V2-V4	1.896240e-14	6.6e-16
V3-V4	4.657684e-05	1.2924e-08

For Spearman's, the same numbers are: (¾ point)

V2-V3	5.858564e-13	3.625e-13
V2-V4	2.094989e-29	2.2e-16
V3-V4	9.687686e-12	5.818e-12

+ Bonferroni: (+¼ point)

V2-V3	1.757570e-12	1.0875e-12
V2-V4	6.28497e-29	6.6e-16
V3-V4	2.906306e-11	1.7454e-11

4. All non phylogenetic correlations are significant. V2 vs V4 is positive. V2 v V3 and V2 v V4 are negative. (1point)
5. The untransformed data did not fit the assumptions of BM. In particular the contrasts vs Node value and contrasts vs node age were both significant. The log transformed data did fit the assumptions, so independent contrasts were derived from the log transformed data. (1point)
6. The PICs did not meet the expectations of multivariate normality either, so I used non-parametric tests: (1point)

7.***Only results from cor.table are valid, because they have correction for PICs. However, in reality all these numbers are bad, because cor.table has an error.

***You get p-values greater than one, because the Bonferroni correction only works for small values.

But it doesn't matter, because those results are insignificant anyways.

***Don't forget to use cor.type="c"

Kendall's results: (¾ point)

V2-V3 0.3248054

V2-V4 6.570840e-06

V3-V4 0.3967225

Bonferroni correction:(+¼ point)

V2-V3 0.9744162

V2-V4 1.971252e-05

V3-V4 1.1901675

Spearman's results: (¾ point)

V2-V3 0.1736300

V2-V4 1.517496e-09

V3-V4 0.3955777

Bonferroni correction:(+¼ point)

V2-V3 0.52089

V2-V4 4.552488e-09

V3-V4 1.186733

Sign test results: (½ point)

1-tailed

V2-V3 0.02973169

V2-V4 7.610913e-06

V3-V4 0.2354395

2-tailed:(+¼ point)

V2-V3 0.05946338

V2-V4 1.522183e-05

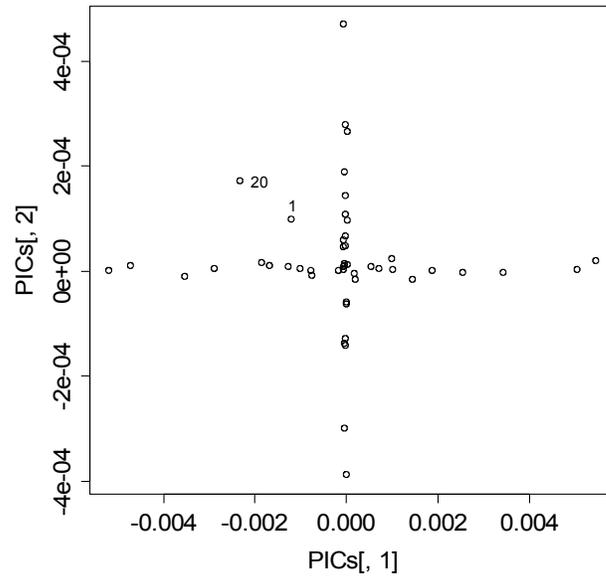
V3-V4 0.470879

Bonferroni correction:(+¼ point)

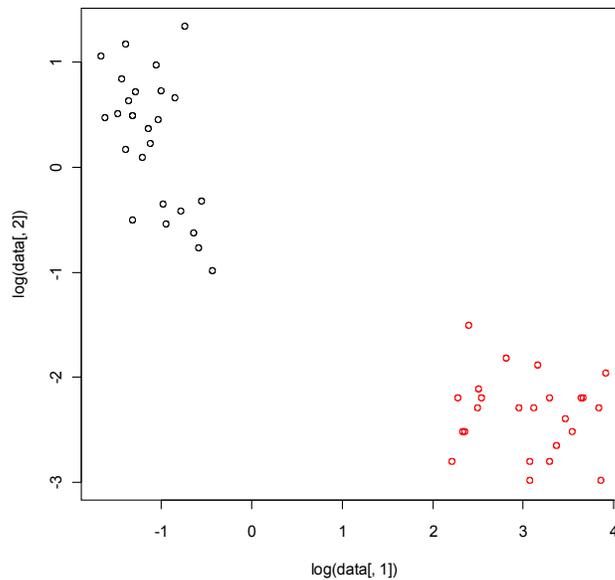
V2-V3 0.1783901

V2-V4 4.566548e-05

V3-V4 1.412637



You can also see this pattern by plotting the logs of the data at the tips against each other, and coloring the tips from our crazy clade red. As you can see, that clade has excessively high values for character 1 and low for character 2.



Thus, we can conclude that we see a large correlation in the untransformed data, because all three characters undergo a great deal of change along this one branch, which leads to correlation among the terminal taxa. However, this correlation is not found throughout the rest of the tree. This branch clearly underwent a great deal of evolution in all characters, and something interesting may have happened there.