1. Because the traits at the tips are not independent (assumption of Fisher’s exact test) due to the shared ancestry. Neglecting phylogenetic background can lead to falsely detecting correlations between characteristics that are due to shared ancestry.
2. Independence and identical variance of data points are common assumption of many statistical models (e.g., linear regression). Fulfilling these assumptions by transforming the data we can apply these useful models correctly.
3. Independent variables: calculating the values of the contrasts (difference between trait values at two nodes) e.g.:

Diagram

Description automatically generated

Identical variances: the division of the independent contrast by the square root of the factor in which they differ from sigma^2. This is called normalisation.

A picture containing diagram

Description automatically generated

1. If both traits evolved in a uncorrelated way I would expect either:  
    - neither raw traits or normalized contrasts are correlated  
    - raw traits are correlated, but only due to shared ancestry; normalized contrasts are   
    not correlated  
   If both traits evolved in a correlated way I would expect:  
    - raw traits and normalized contrasts are correlated  
    (though raw traits may still be stronger correlated due to shared ancestry)  
   Any statistical method that reliably accounts for shared ancestry and would still detect a correlation between the traits could give evidence for correlated evolution.
2. We cannot really say how many character changes really happened on each branch, because we only observe data on the tips and have no ancestral data. Thus, we cannot precisely say from what ancestral character the tip characters might have changed. Additionally, discrete characters could have changed multiple times and still be (at the tip) the character that they started with (beginning of the branch). Also, we would have to consider how long each branch is and weigh the changes relative to branch length, because longer branches are likely to lead to more changes. Exact branch length can often be hard to estimate.