Lenni-Fischer method: time is basis for number of mutations – molecular clock model

Similar to neutral theory where genetic drift is the only factor that matters

Assuming neutral rate in the molecular clock doesn’t always work well in practice because:

-lots of selection pressures, including on keeping certain genes or structures

-some genes evolve more slowly than others

-external conditions/environment

-different generation times among organisms

-heritability

Sanderson paper:

Roughness penalty is used to bring rates closer to each other (these rates generally are different)

If roughness penalty is higher, there is more variance in the tree

Cross validation – vary sample size by taking away 1 data point at a time to see if still

Figure 5 shows how close divergences are when implementing the 3 different smoothing parameters

Drummond BEAST paper:

Tree priors needed – think about what factors to use as priors

Drummond paper:

Show that rate is not autocorrelated to many of the factors being tested

Beaulieu Paper:

Tries to go for caution. Model used may have problems in modeling angiosperm age, or there is lack of data

Autocorrelation was used here

Heath Paper:

Where do fossils go on a tree? Rates are very difficult to estimate with them

Tries to get rid of the need for priors that have to be estimated with fossils