Long branch attraction – in maximum parsimony methods, if branches get too long the chance it thinks homoplasy is more likely gets higher

Lewis MKD model

Maximum likelihood uses solely data

Bayesian statistics uses “outside” information in prediction models

Bayes’ rule = probability of hypothesis given prior data = P(D/H)P(H)/sumP(D/Hi)P(Hi)

In evolutionary biology, what is the “prior” needs to be defined and appropriate

-Flat prior – will not have much impact

-Priors become less impactful with more data

Bootstrapping is a method of assessing confidence by resampling the same data used in making the tree

-numbers on nodes - # of bootstraps that confirm this relationship between branches

-completely separate from Bayesian

Maximum likelihood will give the same result even if the order is changed because it’s probability based?

Bayesian methods assess confidence based on MCMC methods (markov chain monte carlo [only based on previous result, random])

-Need time to allow for the chance to get the right tree, but can be very lengthy to run to get there (eventually the right tree will be reached but it goes through every possible iteration)

Throwing out taxons – if one does not have high chance of fitting somewhere on tree. Be mindful of those, find methods of detecting them

RAxML tips

Calculating homogeneity is for more complicated models – if your data is small enough a simpler model is much, much better (obtained alpha parameter above 10 and this warning message)

Plotting results using R:

Make sure you set directory to the folder with tree files generated by RAxML

\_\_\_variable name\_\_\_\_\_ <- read.tree(“\_\_\_filename\_\_\_”)

plot.phylo(variablename)