Optimization

Using these models, I wrote various log likelihood scripts that calculate the probability that a certain data set would have occurred if the natural system behaved as the model/parameters would predict. I used fminsearch to optimize the fitness values of the amino acids as to find the highest probability of the results occurring as they did

Model 3

In this model, we account for the possibility of an amino acid mutating but not fixating and thus having no effect upon the population. This way the probability an individual with a certain amino acid remaining with the same amino acid is not underestimated

Model 1

In this model, the distinguishing feature is that the R generating matrix is exponentiated to find the probabilities associated with mutation/fixation

Model 2

Uses R Generating matrix to find the rate that is used in an exponential distribution to find the probability of an amino acid mutating by a certain time AND fixating

Models

The R generating matrix serves as the crux for many of the models we implemented

R Generating Matrix

Determines the rate of an amino acid mutating to any of the other 19 amino acids AND fixating in the population which uses the Q Generator Matrix

(Q) Generator Matrix

determines the rate at which j individuals in a population with a mutation that affects the fitness of the observed trait transitions to j-1 individuals, stays at j, or increase to j+1 individuals