A Mechanistic Model for Protein Evolution

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Amino acids in a protein are under selection based on factors such as their sizes and charge. At a given site, one amino acid may be optimal, while similar amino acids may also allow the protein to function, but less well. More frequently expressed proteins are likely under stronger selection. Thus, which amino acid is observed at a site depends on which amino acid is optimal, how different amino acids are from the optimal one, the efficacy of selection, and mutational distances between the amino acids in the underlying genetic code. We combine these factors to create a new mechanistic model for protein evolution that can be used for investigating how proteins change through time as well as inferring phylogenetic trees.

Bell Hall 130A
Friday, November 2, 2012, 10:30 AM