

Central to structure analysis is “How does a structure evolve?” We propose a model that basically describes what is known about structure evolution. It is coded for by a gene, that can mutate, and is translated into a protein, that functions satisfactorily dependent on its structure. This leads to a model: sequence evolution, folding structure, selection on structure. This is very general and at each step we have used a simple but reasonable model. Such evolutionary models can be used either just to explore the probability of observed structures and the frequency with which different structures evolve into each other. This of interest since the existence of such a process can shed light on problem on whether the distribution observed among existing protein structures are an evolutionary accident or a structural necessity.