

Comparative Biology is a major contributor to biological understanding and can be applied to any biological objects that are homologous. The large application area presently is sequences, but other rising areas include structures, networks, organs and more. The strength of evolutionary comparison is the ability to detect features of functional importance and thus select properties that demand a functional explanation from a sea of noise. The only requirement for evolutionary comparison is that the objects to be compared are homologous. In this sense movements are perfectly homologous as the movements associated with an ancestral molecule would be inherited with modification, when the molecule evolved over evolutionary time. The recent rise in the capability of molecular dynamics, the number of known extant structures and the ability to predict structures, allows increasingly ambitious projects to be undertaken. This project combines all these components to a specific data set, attempting to solve a specific problem: A protein (Protein Z (PZ)) is found in humans in substantial concentration that appears to have cofactor function. It is homologous to several other proteins, all serine proteases. It appears to have either lost enzymatic activity or to have never properly evolved to have such function. Inferring the ancestral protein and exploring its properties computationally could solve this question. The project would also lead to the development of generally applicable techniques.