STEM® Biomedical

Hypothetica

A multi-component software for advanced molecular simulations.

BRIEF:

Molecular interactions are the fundamental basis upon which life exists. More specifically, interactions between specific atoms (as defined by their subatomic particles) make up the foundational framework of the biophysical properties of life. A vast array of molecules are involved in sustaining life, ranging from smaller molecules (such as H_2O, glucose, individual amino acids, lipids, etc.) to larger and more complex macromolecules (such as proteins, DNA, RNA, etc.). The known atomic composition of these molecules in combination with properties of molecular physics can be used to generate computational simulations reflecting their natural existence. Such simulations can integrate and account for varying physiological environments, mutagenically-induced variation in structural conformation, multi-component interactions, among numerous other variables. These simulations are designed to run alongside real-time physical screens for confirmation of accuracy. The incorporation of machine learning serves as an avenue for identifying drug targets and the development of novel therapeutic candidates at speeds exponentially greater than laborious manual research. Running advanced simulations without diminished accuracy requires remarkable and previously unavailable computational resources, a barrier which can now be overcome through advancements in the field of supercomputing.