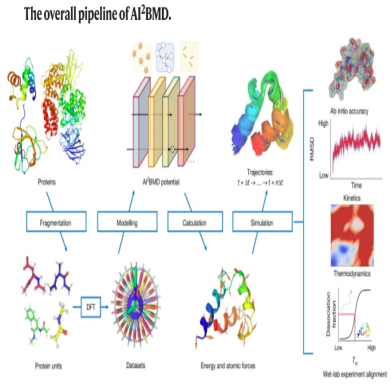
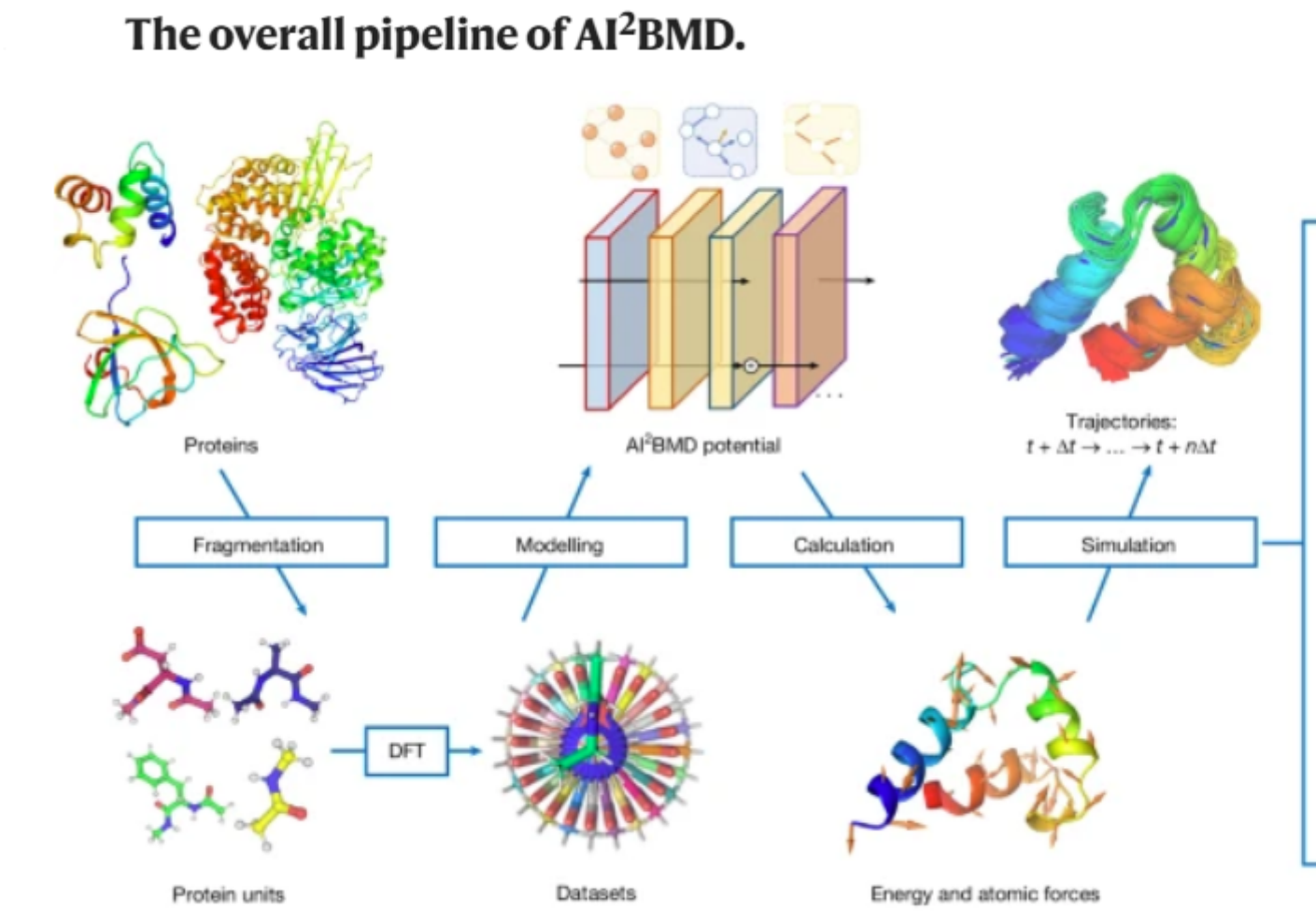


Ab initio characterization of protein molecular dynamics with AI2BMD

Description

Biomolecular dynamics simulation is a fundamental technology for life sciences research, and its usefulness depends on its accuracy and efficiency. Classical molecular dynamics simulation is fast but lacks chemical accuracy. Quantum chemistry methods such as density functional theory can reach chemical accuracy but cannot scale to support large biomolecules. The authors introduced an artificial intelligence-based ab initio biomolecular dynamics system (AI^{2}BMD) that can efficiently simulate full-atom large biomolecules with ab initio accuracy. AI^{2}BMD uses a protein fragmentation scheme and a machine learning force field to achieve generalizable ab initio accuracy for energy and force calculations for various proteins comprising more than 10,000 atoms. Compared to density functional theory, it reduces the computational time by several orders of magnitude.



Proteins are divided into protein units by a fragmentation process. The AI^{2}BMD potential is designed based on ViSNet, and the datasets are generated at the DFT level. It calculates the energy and atomic forces for the whole protein. The AI^{2}BMD simulation system is built on these components and provides a generalizable solution for simulating the MD of proteins. It achieves ab initio accuracy in energy and force calculations. Through comprehensive analysis from kinetics and thermodynamics perspectives, AI^{2}BMD exhibits good alignment with wet-lab experimental data and detects phenomena different from MM.

.With several hundred nanoseconds of dynamics simulations, AI^{2}BMD demonstrated its ability to efficiently explore the conformational space of peptides and proteins, deriving accurate 3*J* couplings that match nuclear magnetic resonance experiments and showing protein folding and unfolding processes. Furthermore, AI^{2}BMD enables precise free-energy calculations for protein folding, and the estimated thermodynamic properties are well aligned with experiments. AI^{2}BMD could potentially complement wet-lab experiments, detect the dynamic processes of bioactivities and enable biomedical research that is currently impossible to conduct.

Category

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