Biomolecular Dynamics
Stock Lab

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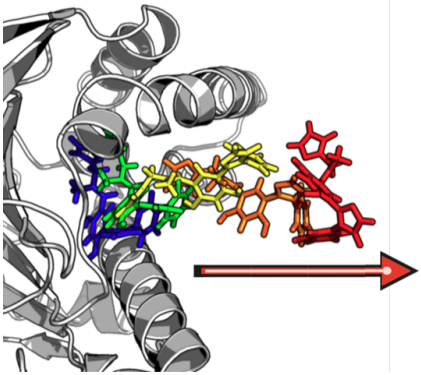
Bachelor/Master Project

Unbinding characteristics of kinase inhibitors

Binding and unbinding events between proteins and host molecules, e.g. drugs, are a crucial step in signalling between proteins. To understand the physics of these processes, our group has developed an approach called dissipation-corrected targeted molecular dynamics (dcTMD). This approach uses active pulling to force (un)binding and allows the parameterisation of free energy and friction profiles along the pulling distance.

In this project, you will apply dcTMD to a set of pulling simulations on a drug candidate bound to a kinase, which is a pharmacologically highly relevant target for anti-cancer drugs. Your aim is to analyze the pathways that the drug candidates take when binding and unbinding from the kinase, determine the associated path free energy profiles, and (if time permits) estimate (un)binding rates using Langevin equation simulations.



Useful information

Wolf, S., & Stock, G. (2018). Targeted Molecular Dynamics Calculations of Free Energy Profiles Using a Nonequilibrium Friction Correction. J. Chem.Theory Comput. 14, 6175–6182.

Talk to:

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