

武汉物数所理论交叉学术交流系列报告

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Fragment Based Drug Design and Virtual Screening



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Abstract: The success of Fragment based drug design (FBDD) and structure-based drug design in general depends crucially on the accuracy of the algorithms used in the underlying docking and evaluation methods. Available software packages almost exclusively use molecular mechanics approximations based on Newtonian mechanics to describe target and ligand molecules. While reliable force fields are available for proteins and DNA molecules, a force field representation, and often even the 3D coordinates, of a given small organic molecules that is accurate and consistent with the protein force field used is in most cases still a hit-and-miss. In particular hydrogen bond interactions between ligands and protein and interactions involving metal ions are often misrepresented.

We have implemented a computational FBDD approach ("MFMD") based on molecular dynamics simulations combined with quantum mechanical optimization, in order to avoid artifacts from empirical force fields and to take more accurately into account electron-electron interactions between fragments and protein side chains. Examples for FBDD using MFMD for the inhibitor design for kinases and malaria aminopeptidases will be presented. More importantly, the feasibility of advanced quantum mechanical based virtual screening of chemical library for the first time is demonstrated.

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