ParaDockS - An Open Source Framework for Molecular Docking

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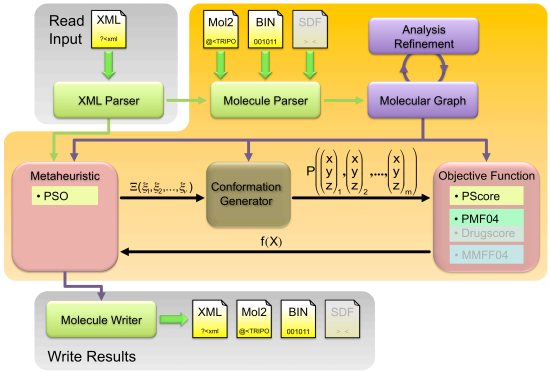
The prediction of possible binding geometries as well as ranking of putative protein-ligand complexes according their binding affinities is the intention of so called molecular docking approaches. Recently, the docking program ParaDockS (Parallel Docking Suite)[1] was developed in our working group. The goal of this work pursues the line of thought that ParaDockS is open source. We want to initiate a molecular docking community so that both users and developers contribute with their experience and knowledge to this very interesting field of science.

The framework of ParaDockS was modified to clearly separate optimizer, conformation generator and scoring function parts. Therefore the development of scoring functions can be implemented without touching parts of conformation generation or optimization. The following picture shows the overall framework of ParaDockS:



To better process molecular data, algorithms for ring perception and aromaticity detection were included. The complete implementation of the Merck Molecular Force Field 94[2] is in progress.

Due to the sucess of target specific scoring functions we implemented a workflow to derive PMF[3] atom-pair potentials. This involves the preparation of pdb structures to get a clean structural database. The defintion of atom types and the derivation of the potentitial can completely be accomplished by ParaDockS. The resulting atom pair-potentials can be directly used as scoring function. The whole workflow was applied and validated for kinases.

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[2] Thomas A. Halgren, *J. Comput. Chem.*, **1996**, *17*, 490-519
[3] Ingo Muegge, Yvonne C. Martin, *J. Med. Chem.*, **1999**, *42*, 791-804