The application of multi-objective genetic algorithms to protein-ligand docking

Sally Mardikian*, David R. Westhead and Richard M. Jackson

University of Leeds

Ligand docking is a process which computationally predicts the correct bound conformation of a given protein-ligand complex from atomic coordinates. A docking procedure employs search techniques which produce different conformations and orientations of a ligand to a target protein. A scoring function is then used to score the generated conformations. This is usually done by calculating the binding energy between ligand and protein. From the score values it is possible to infer at which confirmation the most optimal binding occurs.

The weakness of current docking procedures is that only one single objective (usually the scoring function) is optimized at a time. This neglects the individual effects of other objectives that could be important, such as interaction types (van der Waals, hydrogen bonding, etc.). MOGAs (Multi-Objective Genetic Algorithms) attempt to overcome this limitation by considering any number of objectives and generating multiple solutions. Each solution is a compromise of the different objectives, which gives the user the option to choose the most suitable solution for a given situation. MOGAs have already been applied in combinatorial library design (Gillet *et al.*, 2002), and are, in this project, being developed for a docking tool.

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References

Gillet, V.J., Khatib, W., Willet, P., Fleming, P.J. And Green V.S. (2002). Combinatorial library design using a multiobjective genetic algorithm. *Journal of Chemical Information and Computer Sciences*, **42**, 375-385.