pyDockDNA: A pyDock upgrade for protein-DNA docking

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L.A. Rodríguez-Lumbreras[I], B. Jiménez-García[I], J. Fernández-Recio[I]

[I]Barcelona Supercomputing Center, Department of Life Sciences - Protein Interactions and Docking group, Carrer de Jordi Girona, 29-31, 08034, Barcelona, Spain

Structural prediction of protein-DNA interactions can contribute to the understanding of essential cell processes at molecular level, such as those related to gene transcription and regulation. Very often, protein-DNA are structurally modelled by protein-protein docking tools, but the association between proteins and DNA has specific characteristics regarding the energetics and conformational flexibility of the nucleic acids that are not fully captured with standard protein docking methods. A few computational methods for protein-DNA docking have been reported such ParaDock [1], but the field is still in development.

Here we have explored the use of different energy-based functions for the scoring of rigid-body protein-DNA docking poses generated by FTDock. We have implemented the different terms of the scoring function used in pyDock [2], that is, van der Waals, desolvation and electrostatics terms. Charges for the DNA molecule have been defined from Amber 94 force-field. Different parameters and combinations of these functions have been tested on an available DNA-protein docking benchmark [3]. For the scoring of the initial rigid-body protein-DNA docking decoys, best results are obtained with a combination of electrostatics and van der Waals terms. The protocol is implemented in a new module called pyDockDNA. Success rates and limitations according to protein and DNA flexibility, DNA type, etc. will be discussed.

Referencies:

[1] Banitt, I. and H.J. Wolfson, *ParaDock: a flexible non-specific DNA--rigid protein docking algorithm.* Nucleic Acids Res, 2011. 39(20): p. e135.

[2] Cheng, T.M.-K., T.L. Blundell, and J. Fernandez-Recio, *pyDock: electrostatics and desolvation for effective scoring of rigid-body protein-protein docking.* Proteins, 2007. 68(2): p. 503-515

[3] van Dijk, M. and A.M.J.J. Bonvin, *A protein-DNA docking benchmark.* Nucleic Acids Research, 2008. 36(14): p. e88-e88.