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2D-SIFt – A Matrix Describing Detailed Interactions Between Ligand and Receptor

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Structural Interaction Fingerprints (SIFts), as defined in [1], is a well-established method of formalized description of molecular contacts between a ligand and the residues of the protein, in form of a bit string depicting presence (1) or absence (0) of interaction of given type. The main disadvantage of SIFt formalism is ignoring the chemical features of the ligand and focusing on the interactions solely from a protein point of view.
Here we present a step further in the development of interaction fingerprints – encapsulating interactions between the features of ligand and receptor in form of 6x9xN matrix (6 standard pharmacophore features, 9 types of interactions with amino acid [2], N – number of residues in described receptor). Matrix fields can take values greater than 1, there can be more than one separate pharmacophore feature of one type within a ligand interacting with one residue (for instance three phenyl groups surrounding a phenylalanine). Such approach provides more detailed, yet easy to handle and use, view of contacts with the binding site.
Analogously to the previously demonstrated methodology, such matrices can be averaged to create profiles showing the most important interactions, thus being a hybrid between structure-based pharmacophore model and a classical interaction fingerprint.

Acknowledgements

The study was partially supported by the Polish-Norwegian Research Programme operated by the National Centre for Research and Development under the Norwegian Financial Mechanism 2009-2014 in the frame of the Project PLATFORMex (Pol-Nor/198887/73/2013).

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