# MS10. Structural bioinformatics (SBI)

Chairs: Guido Capitani, Oliviero Italo Carugo

## MS10-O1 Advances in PISA software for macromolecular assembly predictions from CCP4

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PISA (Protein Interfaces, Surfaces and Assemblies) software from CCP4 remains a popular computational tool for the prediction of biological assemblies from crystallography data [1]. The method is based on the estimation of the dissociation free energy of predicted complexes, and reaches 90-95% correct results for the current content of the PDB.

It was found that the likelihood of wrong predictions grows exponentially with the decrease in the dissociation free energy, reaching over 50% for complexes bound as weakly as few kcal/mol [2]. Among few reasons for this behaviour [2] is the fact that oligomeric state of weakly bound complexes is expected to vary in dependence of chemical environment, in particular, protein concentration. It has been noticed that most disagreements between predicted and measured oligomeric states belong to situations where the relation between experimental conditions and protein's working environment in the cell is unclear.

Further advance in PISA software is reported, which allows a researcher to model concentration dependence of predicted oligomeric states, and by this to improve the interpretation of experimental results in the biologically interesting case of weakly bound macromolecular associations. The new PISA is based on the concept of assembly stock, or an equilibrated set of all complexes compatible with crystal packing. Graphical representation of concentration (or newly introduced aggregation index) profiles of stock's components allows a user to quickly identify the most probable oligomeric state. This is vastly superior over the previous way of analysis, based on the interpretation of bare figures for dissociation free energies. Other developments include advanced graphical interface and multi-parametric interaction radar, which indicates the likelihood for interface to represent a biologically relevant interaction.

The new PISA is available from CCP4 Software Suite [3] as a standalone (command-prompt) application, graphical interface QtPISA and web-server jsPISA at http://www.ccp4.ac.uk/pisa.

References

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