XLPM Map: A protein-protein interaction 3D model viewer

Abstract

The main goal is to make the user able to see the interaction between two proteins based on the XLPM algorithm developed by the Bioinformatics department. The environment will include a desktop application based on OpenGL that shows 2 interacting 3D models of proteins and the ability to view these models in a Virtual Reality environment like the CAVE.

Details

X-Linked Peptide Mapping (XLPM) is an algorithm for the analyses of chemical cross-linking mass spectrometry (CXMS) data. XLPM identifies not only the peptide pair interacting with each other but also scores the pair of residues interacting with each other. XLPM map is a 3D model viewer of the XLPM results based on OpenGL showing the interaction between the two proteins in a 3D environment. XLPM map shows the protein-protein interactions between two proteins in three levels. The first level shows the highest ranked interactions between digested peptides. Selecting any of the interaction in the first level opens the second level of visualization. The second level of visualization shows all the precursor ions matching with the selected interaction. Selecting one of the spectra shows the third level. Third level shows the details scores for interaction between each pair of residues. The visualization within XLPM map makes understanding of the interactions between a protein pair efficient by providing easy access to all levels of information. This 3D visualization will be adapted to be viewed inside virtual reality environments like the CAVE.

References

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