



VisInt-X: Visualizing Interactions in Cross-linked proteins

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Conclusion

- ⇒ VizInt-X is the first attempt at visualization of chemical cross-linking mass spectrometry (CXMS) data.
- ⇒ The three level visualization describes details of all the matched spectra and entire protein.
- ⇒ Heat map in the first level gives a profile of interaction between a pair of proteins on a single page.
- ⇒ The second level gives in depth details of all spectra representing the interaction between a pair of peptides and the third level heat map for the residues interaction.
- ⇒ Mapping of results onto protein tertiary structure gives a physical view of the interaction and better analytical capability.
- ⇒ An offline package and virtual reality solution will add to usability of VizInt-X in future.

References

- ⇒ Mihir Jaiswal *et. al.* (2014) BMC Bioinfo 15(suppl 11):S16.
- ⇒ Michael Bostock *et. al.* (2011) IEEE Trans. Visualization & Comp. Graphics (Proc. InfoVis)

Figure 1: VisInt-X screen. Top panel shows protein 3-D structures. Bottom panel shows results of a cross-linking experiments. Left: Heat map showing first level of visualization, Middle: heat map showing third level of visualization, Right: Tree map showing second level of visualization. First level describes protein wide interactions from a cross-linking experiment. Second level shows all peptide pairs identified for a selected interaction. Third level shows residue level interaction for a peptide pair selected in level 2. Blue colored residues in protein structures show all interacting residues, while brown colored residues show selection in the third level visualization.