I-COMS: Interprotein-COrrelated Mutations Server

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Abstract Several computational methods have been developed to predict protion-protein interactions from multiple sequence alignments (MSAs) in recent years. These techniques are a useful approach to help detect interfaces between proteins in complexes. However, each method treats the problem in a different theoretical framework that leads to discrepancies in the results provided by them. In addition, there is no consensus on which methodology has the overall best performance. We develop I-COMS web server (interprotein COrrelated Mutations Server) to help address this problem this problem. I-COMS provides an interactive graphical output that allows comparing covariation estimates between residues of different proteins genererated by four different methodologies. Results are provided as a circos representation of intraprotein and/or interprotein covariating positions. Results comparison among methods is available as side by side circos representation of predicted contacts or a circos representation of the overlap between two or up to four methodologies. Complemetary data and graphical output are display additionally: a matrix visualization of the corresponding scores, a density plot distribution of calculated inter, intra and inter+intra scores and raw scores. The required data to start the analysis is a MSA of concatenated proteins. This MSA can be provided by user or automatically generated by I-COMS.

References

1. Iserte, J., Simonetti, F. L., Zea, D. J., Teppa, E., & Marino-Buslje, C. (2015). I-COMS: Interprotein-COrrelated Mutations Server. Nucleic acids research, 43(W1), W320-W325.