

“Crosstalkr: an R package for the identification of related nodes in biological networks”

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Software

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Summary

Crosstalkr is designed to facilitate the identification of functional subnetworks in human or non-human interactomes. Given a set of user-provided set of seed proteins, crosstalkr will identify enriched subnetworks of proteins that have a high affinity for the provided seeds. It is a free, open-source R package designed to allow users to integrate functional analysis using the protein-protein interaction network into existing bioinformatic pipelines. This is accomplished using random walks with restarts, starting at the user-provided seed proteins. Random walks are implemented using sparse matrix multiplication to facilitate fast execution. Affinity scores from a given random walk with restarts are compared to a bootstrapped null distribution to assess statistical significance. The default behavior evaluates the human interactome to identify functionally important subnetworks given a set of user-defined seed proteins. However, users can also provide a different graph, allowing for flexible evaluation of graph or network-structured data. Further, users can evaluate more than 1000 non-human protein-protein interaction networks thanks to integration with StringDB. Crosstalkr is an extension of the crosstalkr webapp developed by Neoproteomics and Case Western Reserve University School of Medicine.

Statement of Need

Design and Data Sources

Functionality

Outlook

Acknowledgements

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References

Citations

For a quick reference, the following citation commands can be used: - `@author:2001` -> “Author et al. (2001)” - `[@author:2001]` -> “(Author et al., 2001)” - `[@author1:2001; @author2:2001]` -> “(Author1 et al., 2001; Author2 et al., 2002)”