Looking Closely at Molecular Interactions

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Molecular interactions are an essential tool to support our understanding of biology; they can be determined at large scale by genome-wide technologies as well as at high resolution by small scale experiments, and they are amenable to computational analysis and visualisation through well established algorithms. However, though recent publications indicate major interactome differences for example between two human cell lines (Huttlin et al. 2021), the diversity of interaction data generating approaches and the ease of analysis by graph-based approaches often lead to aggregation of interaction data in a minimalistic form “a interacts with b”, losing essential fine grained details of the interaction context.

In the context of the International Molecular Exchange Consortium (IMEx), ten global organisations contribute to a fine-grained annotation of molecular interaction data, including experimental approaches, sequence variation, and binding regions (Porras et al. 2020), but tools exploiting this rich detail are still scarce. We demonstrate the richness of available interaction and complex datasets, recent tools for their visualisation in web and Cytoscape environments (Ragueneau et al. 2021), and their dynamic integration in the Reactome pathway database.

Huttlin, Edward L., Raphael J. Bruckner, Jose Navarrete-Perea, Joe R. Cannon, Kurt Baltier, Fana Gebreab, Melanie P. Gygi, et al. 2021. “Dual Proteome-Scale Networks Reveal Cell-Specific Remodeling of the Human Interactome.” Cell 184 (11): 3022–40.e28.

Porras, Pablo, Elisabet Barrera, Alan Bridge, Noemi Del-Toro, Gianni Cesareni, Margaret Duesbury, Henning Hermjakob, et al. 2020. “Towards a Unified Open Access Dataset of Molecular Interactions.” Nature Communications 11 (1): 6144.

Ragueneau, Eliot, Anjali Shrivastava, John H. Morris, Noemi Del-Toro, Henning Hermjakob, and Pablo Porras. 2021. “IntAct App: A Cytoscape Application for Molecular Interaction Network Visualisation and Analysis.” Bioinformatics , May. https://doi.org/10.1093/bioinformatics/btab319.