Interactive exploration of integrated biological datasets using context-sensitive workflows

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Abstract

Network inference utilizes experimental high-throughput data for the reconstruction of molecular interaction networks where new relationships between the network entities can be predicted. Despite the increasing amount of experimental data, the parameters of each modeling technique cannot be optimized based on the experimental data alone, but needs to be qualitatively assessed if the components of the resulting network describe the experimental setting. Candidate list prioritization and validation builds upon data integration and data visualization. The application of tools supporting this procedure is limited to the exploration of smaller information networks because the display and interpretation of large amounts of information is challenging regarding the computational effort and the users' experience. The Ondex software framework was extended with customizable context-sensitive menus which allow additional integration and data analysis options for a selected set of candidates during interactive data exploration. We provide new functionalities for on-the-fly data integration using InterProScan, PubMed Central literature search, and sequence-based homology search. We applied the Ondex system to the integration of publicly available data for Aspergillus nidulans and analyzed transcriptome data. We demonstrate the

advantages of our approach by proposing new hypotheses for the functional annotation of specific genes of differentially expressed fungal gene clusters. Our extension of the Ondex framework makes it possible to overcome the separation between data integration and interactive analysis. More specifically, computationally demanding calculations can be performed on selected sub-networks without losing any information from the whole network. Furthermore, our extensions allow for direct access to online biological databases which helps to keep the integrated information up-to-date.

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