mentha: the interactome browser

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Motivations

Protein interaction databases archive protein-protein interaction (PPI) information from published articles. However, no database alone has sufficient literature coverage to offer a complete resource to investigate "the interactome". We have developed mentha, a new resource that addresses this problem. mentha archives evidence about PPI in the human proteome – evidence collected from different PPI sources - and offers a series of tools to analyse these data. Users can search the database using a web search engine that returns interaction information for any protein of interest displaying it in the context of the "global interactome". A graphical application to represent this information helps scientists browse the collected data in order to ease and to inspire new experiments and outlooks.

Methods

All the remote protein-protein interaction (PPI) databases that are relevant to this project, namely Mint, IntAct, BioGRID, DIP and MatrixDB, are members of the IMEx consortium. IMEx databases adopt a common format and use controlled vocabularies that facilitates data integration. In addition they implement PSICQUIC, a project whose aim is to standardise the access to molecular interaction databases. PSICQUIC defines a list of common fields for each database, and specifies a standard web service with a well-defined list of methods. All the PPI databases are queried using the PSICQUIC protocol. mentha is assembled by a merging procedure that runs weekly and that creates non-redundant data. The information archived in the queried PPI databases is manually curated and annotated with controlled vocabularies. PPI evidence is represented with fixed sets of identifiers such as UniProt IDs and PMIDs. Most of the time proteins are represented with a UniProt identifiers. For any identifier different from UniProt, a sub-procedure gathers all the identifiers and tries to map them using a service offered by UniProt. The merging procedure behind mentha builds a non-redundant database that collects protein interactions from the aforementioned databases, together with their detailed annotation: interaction type, experimental methods and literature references.

Results

This approach has generated a consistent interactome (graph) that can be used in various analyses as demonstrated by its use in other projects carried out in our group. Most importantly, the procedure assigns to each interaction a reliability score - the MINT score - that takes into account all the supporting evidence. The user can decide to explore a high confidence interactome or a larger one, accepting more false positives. The application and the web site that have been developed are designed to make the data stored in mentha accessible to all users. All the information contained in the local database is accessible through a web server. The Graphical Application embodies a wide selection of functionalities that help the user navigate and interact with a network of interest. The graphical application, formally a Java web applet, can be embedded in a web page such as iGoogle or even a scientific paper just by feeding it with an SDA, a DOI, or with UniProt IDs.

Availability

http://mentha.uniroma2.it/