BIOINFOMATIC ANALYSIS
NETWORK ANALYSIS

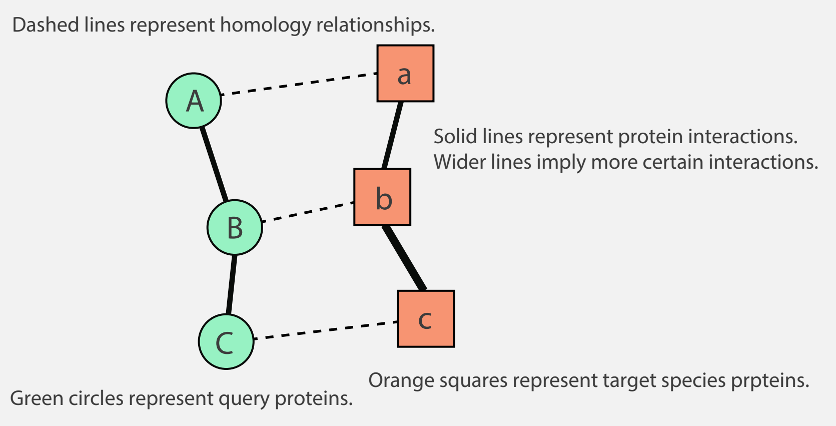
Protein–Protein Interactions Analysis

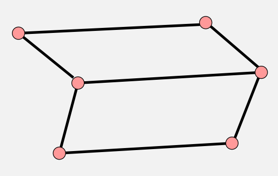
Proteins play a key role in molecular recognition and are at the core of all biological processes. They can interact with other components of the cell, such as small molecular metabolites, nucleic acids, membranes and other proteins to build supramolecular components and carefully design molecular machines that perform various functions, from chemical catalysis, mechanical work to signal transmission And adjustment. So far, large-scale protein-protein interactions have been identified, and all the generated data is collected in a special database, which can create large-scale protein interaction networks.

Like metabolism or genetic/epigenetic networks, the study of PPIs can help us understand the mechanisms of signal transduction, transmembrane transport, cell metabolism and other biological processes through stable or transient, covalent or non-covalent interactions.

Database of Interacting Proteins (DIP)

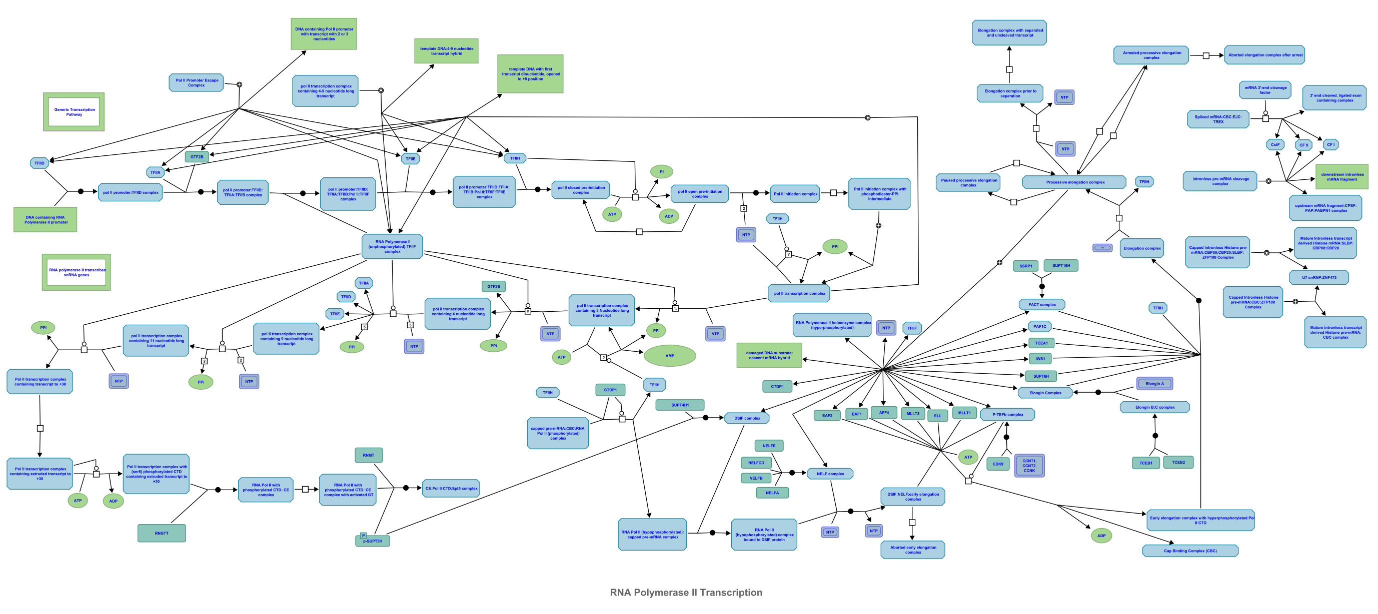
The Database of Interacting Proteins (DIP) is a biological database used to classify experimentally determined interactions between proteins. It combines information from various sources to create a single, consistent set of protein-protein interactions. The database can search the protein-protein interaction network of the target organism to extract all protein interaction pathways that align with the query pathway.





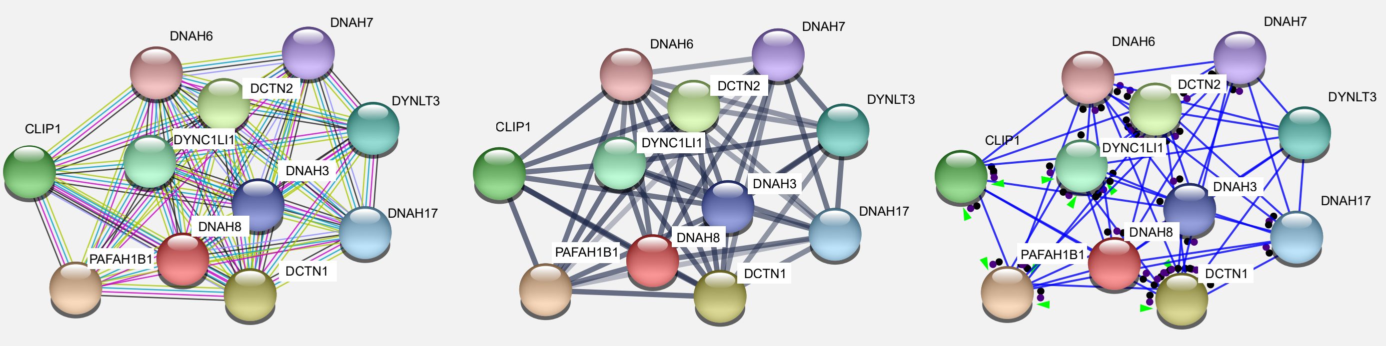
Reactome

The Reactome database is a database of man-made core biological pathways and reactions. The data information is provided by biological experts in related fields, edited and managed by Cold Spring Harbor Laboratory (CSHL) and European Institute of Bioinformatics (EBI), and then classified into related databases. It is then reviewed by other biological researchers to ensure consistency and accuracy, and finally the information is posted on the Internet. The basic unit of the reactome database is a biological reaction. The reactions are combined according to the chain of causality to form a biological pathway. The reactome data model can represent many different biological processes in the human system, including intermediate product metabolism pathways, regulatory pathways, signal transduction pathways, and advanced biological processes.



STRING

STRING is a database containing predicted and experimentally verified protein-protein interactions of multiple species, including direct physical interactions and indirect functional correlations. STRING combines the differential expression analysis results with the interaction pairs included in the database to construct a differentially expressed protein interaction network. During the analysis process, the differentially expressed proteins are mapped to the STRING database to obtain the information about the interaction relationship of the differential proteins. The STING database contains experimental data, the results of text mining from PubMed abstracts, and integrated other database data, as well as the results of predictions using bioinformatics methods. Therefore, protein interaction pairs can be screened out with a comprehensive score greater than 0.4 (Medium) from the search results, and used appropriate bioinformatics analysis software to visualize the interaction results.



Line color indicates the type of interaction evidence

Line thickness indicates the strength of data support

Line shape indicates the predicted mode of action

Circles (node) represent proteins. Different colors represent different proteins. Inside the circle is the three-dimensional structure of the protein.

BIND

The BIND database contains data on 200,000 interactions between 1,500 biomolecules. This includes the interaction between proteins and between proteins and DNA, RNA, small molecules, lipids and carbohydrates. In the BIND database, PPI is divided into three categories: binary interaction, molecular complex, and biological pathway, which show the interaction between molecules from different levels.

KEGG

The KEGG PATHWAY database in Kyoto Encyclopedia of Genes and Genomes (KEGG) is an important knowledge base for systematic analysis and interpretation of gene functions. The database covers the interactions and network relationships between molecules in important life processes ranging from basic cell processes to complex human diseases. It has become an important reference tool for studying cell biochemical processes such as metabolism, membrane transport, signal transmission and cell cycle, as well as the molecular mechanisms of human complex diseases.

Weighted Gene Co–Expression Network Analysis

Weighted Gene Co-Expression Network Analysis (WGCNA)

Weighted Gene Co-expression Network Analysis (WGCNA) is a tool suitable for multi-sample complex data analysis. WGCNA calculates the expression relationships between genes, identifies gene modules with similar expression patterns, analyzes the relationship between gene sets and sample phenotypes, maps the regulatory network between genes in the gene sets, and identifies key regulatory genes. It is suitable for complex multi-sample transcriptome data.

Compared with only focusing on differentially expressed genes, WGCNA uses the information of thousands or tens of thousands of genes with the greatest changes or all genes to identify the gene set of interest, and conducts significant association analysis with the phenotype.

Construct a gene co-expression network	Rationale: make use of interaction patterns among genes Tools: correlation as a measure of co-expression
Identifty modules	Rationale: module (pathway) based analysis Tools: hierarchical clustering, Dynamic Tree Cut
Relate modules to external information	Array Information: clinical data, SNPs, proteomics Gene Information: ontology, functional enrichement Rationale: find biologically interesting modules
Study module relationships	Rationale: biological data reduction, systems-level view Tools: Eigengene Networks
Find the key drivers in interesting modules	Rationale: experimental validation, biomarkers Tools: intramodular connectivity, causality testing

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