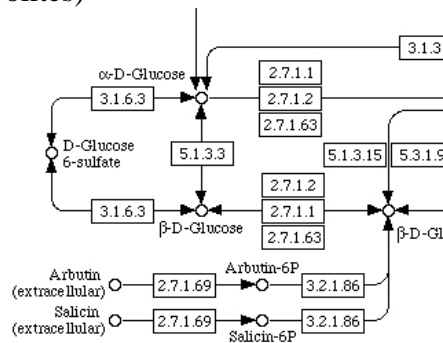


- Which proteins interact with each other
 - Nodes: proteins
 - Edges: interaction



- Metabolic networks: bipartite graphs
 - Which metabolites are converted into which metabolites, which enzymes catalyse the conversions
 - Nodes: set 1: metabolites, set 2: enzymes
 - Edges: conversion/connection (from metabolites to enzyme and from enzyme to metabolites)



- Alternative representation: hypergraph
- Ontologies
 - How are biological terms related to each other (controlled vocabulary)
 - Nodes: terms
 - Edges: relationships (is a, part of, etc.)

1.3. Attributes

- Different data can be mapped onto network elements (nodes, edges), for primary data clear mapping exists, but many ways to infer and map secondary data
- Time series, comparisons (e.g. different treatments, organisms)
- Data types
 - Nominal: sequence names, categories
 - Ordinal: ontologies, rankings, partly ordered information
 - Scalar: time series, comparisons, ratios
 - It is not always clear to which category the data belongs to
- Spatial data (see use case for sub-cellular location)

2. Problems - Use cases

- Just some typical use cases, not a complete collection
- Layout of hierarchical metabolic networks using given layouts for the single pathways (clusters) - Hierarchical clustering of pathways (3 levels)

- Find a good layout of the overview structure (arrangement of the pathways, backbone)
- Preserve as much of the given layout as necessary for mental map within one pathway
- Interaction methods for expanding and collapsing parts of the network
- Elements (nodes, edges) can occur several times in different pathways
- Given partial layout, find good complete layout
 - Example: KEGG pathways with coordinates only for a subset of nodes
- Overlapping networks
 - Layout of two networks (e.g. metabolism and protein interaction) which partly overlap
 - Layout of more overlapping networks (e.g. metabolism, protein interaction and gene regulation) and navigating between them (exploratory navigation)
- Using hierarchy to navigate through a network
 - Example: gene regulatory network and gene ontology as hierarchy over genes, use information of higher (abstract) ontology terms to infer network parts
 - Example: Metabolic pathways with hierarchy of clustering
- Layout of paths/fluxes in metabolic networks
 - Consider edge weights in the layout, such that “important” paths (paths with a high weight sum) are emphasised
- Emphasising given categories in network structure
 - Example: in protein interaction network investigation if given categories correlate with network structure (up/down regulated genes)
- Visualisation of additional information related to nodes or/and edges
 - Example: two time-series per node (two vectors for each node)
 - Example Projection of different data sets onto the same network
 - Comparison of the different data sets within the same networks
 - Example: Flow/Flux in the networks
 - Comparison of different fluxes in the same network
- Overlay of additional edges onto network
 - New edges with different meaning, e.g. correlation between the nodes (data attached to the nodes)
- Visualisation of membranes (borders of biological systems) and sub-cellular location
 - Good ways to include spatial relationship on an abstract level into the layout
- Exploration of high throughput data in the context of underlying networks
 - Navigation methods from abstract overview views (information which part of the network may contain relevant information) to the network parts