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Mindmapping literature information: extract, visualize and explore for modeling



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Short Abstract: When modeling genetic networks, we need tools to handle the wide variety of literature information. We designed a system to capture this information, and display it similar to how our brain works: a clickable 'mindmap', linking all proteins/events/.... Herewith a modeler can easily browse information gathered from many publications.

Long Abstract:

To model a new genetic network, the first step required is getting a detailed overview of what is currently known on the topic. When many publications already exist for an organism, one can read and take notes of all the interesting details. But the larger the amount of information grows, the more one eventually needs a structured method to write down and search back in the notes.

Current tools mostly only offer very specific terminology, quite often too narrow to capture much of the information interesting for modeling. For example, Gene Ontology only captures is-a relations, while another software package mainly focuses on activates-inhibits relations. But modeling information includes much richer content. In combination with the above, a modeler also wants to capture localization information, results from overexpression experiments, expression time-series, purely hypothetic statements, similarity hints coming from other species etc.

Therefore we designed a system to capture all types of biological information that we (as modelers) deem valuable, and we combined this with a really intuitive way of graphically browsing through all the gathered information. The first part, capturing information, happens within an extensive but very intuitive controlled vocabulary. It is based on the usual representation of genetic networks (like \rightarrow for an arrow), combined with elements from Kitano's graphical language and the widely used Kohn-diagrams. The second part, displaying and browsing through the information, happens via a clickable 'mindmap'. A mindmap is a representation that works like the human brain: each entity (protein/species/event/...) is linked to all other entities that relate to it. Only a subset of all information is displayed at any time, of course. But through clicking on related entities, the modeler can re-explore all the information s/he (or others) gathered during reading a stack of publications.

We notice that this system could be linked with datamining packages, to describe a wide variety of information or hypotheses on a specific topic. We also note that we here bypass the ultimate need for rigid ontologies, but as a first working step we give the modeler a way to capture and manage the wide variety of information in a very narrow field. For now, this approach is being used (and thus refined) by the author to model the genetic network of the

Arabidopsis cell cycle and leaf development.