

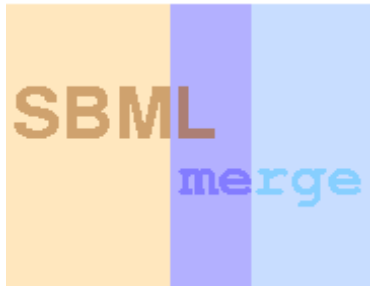
The SBMLmerge project

<http://sysbio.molgen.mpg.de/sbmlmerge/>

Problems in computer-assisted model combination

- Simple semantics problems (different names/IDs in models)
- Differences in the statements (e.g., component constant/variable)
- Partial overlap, unclear semantics (e.g., lumped reactions)
- Models stem from different biological/thermodynamic conditions

We try to tackle only the simple - structural - problems



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SBMLmerge will assist modellers in ...

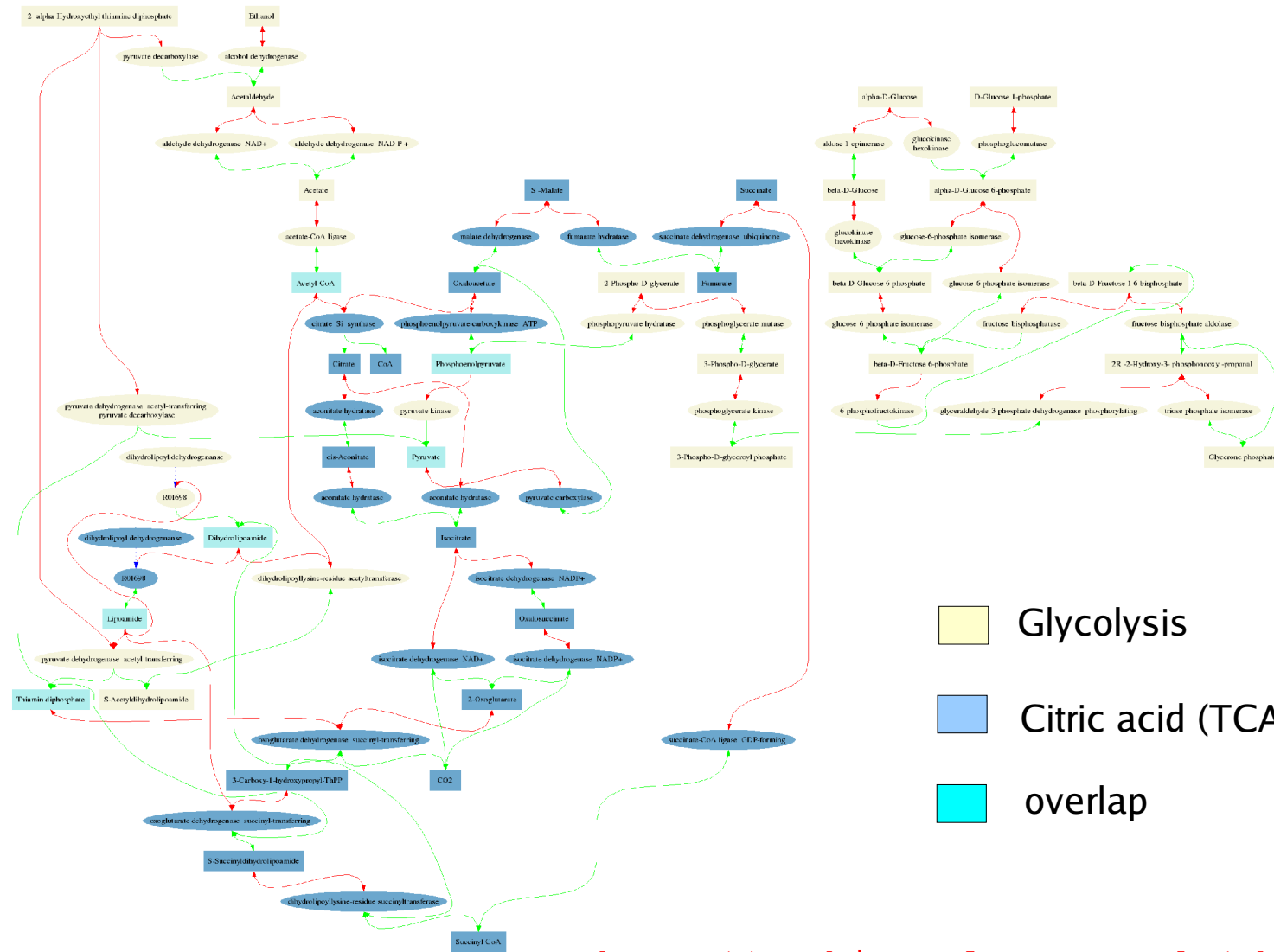
- adding annotations to SBML files (KEGG IDs for species, reactions, enzymes, and gene ontology IDs for compartments)
- combining annotated models in SBML format
- detecting potential conflicts and resolving them, while avoiding logical circles among rule tags

We have written a

- Python implementation based on libSBML
- Web-based version

... [that will soon be online and downloadable](#)

Example: Network combined from two KEGG tables



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We appreciate your comments
and lively discussions concerning

- Kinds and format of annotations necessary
- Semantic and biological problems in model combination
- Test cases or benchmarks for model combination

at

[SBML Discussions >> sbml-discuss >> Joining SBML Models](#)