New Standard Resources for Systems Biology: BiGG Models Database and Visual Pathway Editing with Escher

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Background: Genome-scale metabolic network reconstructions enable the simulation and analysis of complex biological networks, thus providing insights into how thousands of genes together influence cell phenotypes. Accuracy in systems biology research requires standards in model construction, a variety of specific software tools, and access to high-quality metabolic networks.

Results: To meet these needs, we present BiGG Models database and a collection of software solutions for model building, curation, visualization, and simulation. BiGG Models currently contains more than 75 high-quality manually-curated genome-scale metabolic network reconstructions, which can be easily searched and browsed and include interactive pathway map visualizations.
These visualizations have been generated with the web-based Escher pathway builder. Escher allows users to draw pathways in a semi-automated way and can visualize data related to genes or proteins that are associated to pathways. An export function facilitates storing Escher maps in the community formats SBML and SBGN-ML. These features make Escher an ideal interactive model development tool.
In order to make all models in BiGG MIRIAM compliant, BiGG Models itself has become part of the MIRIAM registry and provides links a plethora of external databases for each model component. This rich annotation enables rapid comparison across models. New Systems Biology Ontology terms have been defined that are used to better highlight the role of model components. A comprehensive web API for programmatically accessing the database content enables interfacing with diverse modeling and analysis tools.

Conclusions: With these features and tools, BiGG Models provides a valuable database, structured for easy access and to help improve the quality, standardization, and accessibility of all genome-scale models. The development of this resource has boosted the development of community standards for constraint-based modeling.

Availability: http://bigg.ucsd.edu, https://escher.github.io