E-cyanobacterium.org

A Web-based Platform for Systems Biology of Cyanobacteria

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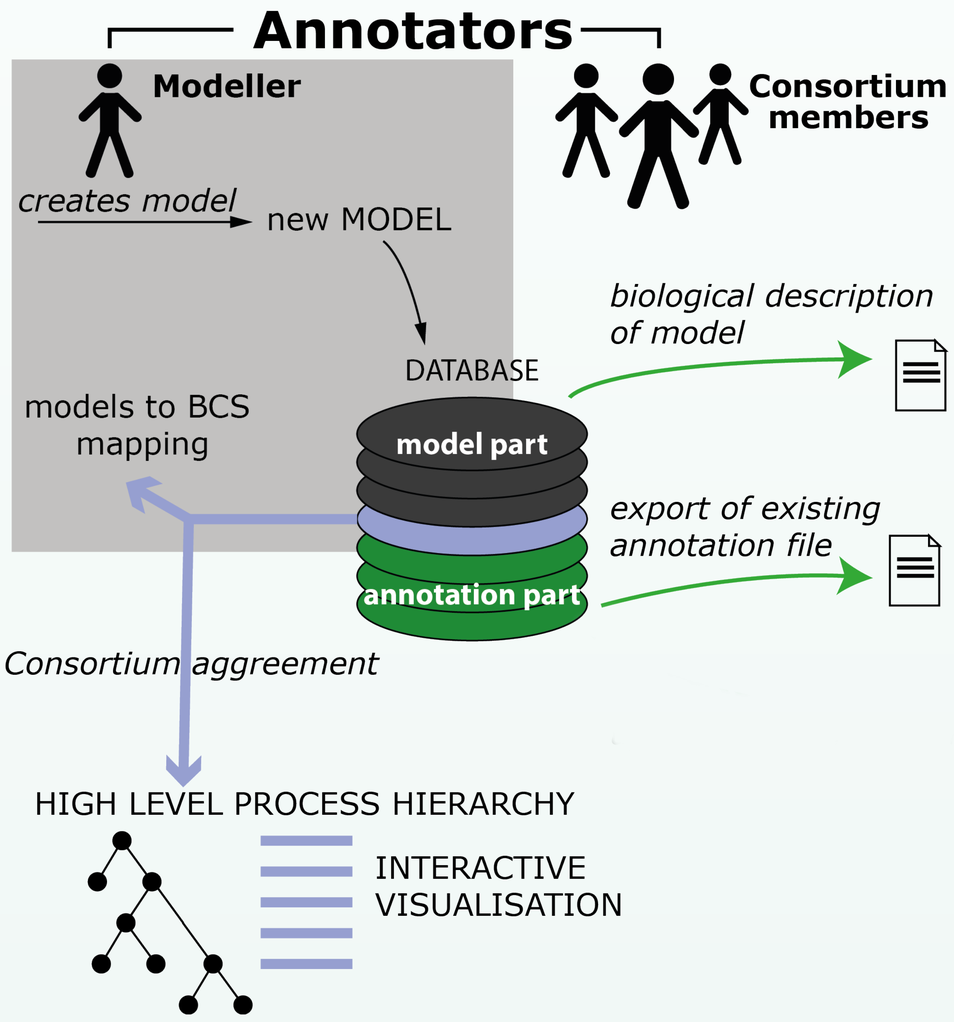
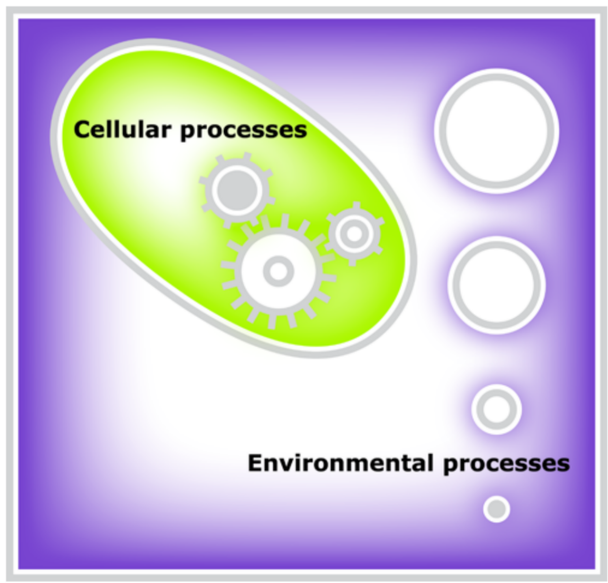
E-cyanobacterium.org is an online platform providing tools for public sharing, annotation, analysis, and visualization of dynamical models and wet-lab experiments related to cyanobacteria. The platform is unique in integrating abstract mathematical models with a precise consortium-agreed biochemical description provided in a rule-based formalism. The general aim is to stimulate collaboration between experimental and computational systems biologists to achieve better understanding of cyanobacteria.



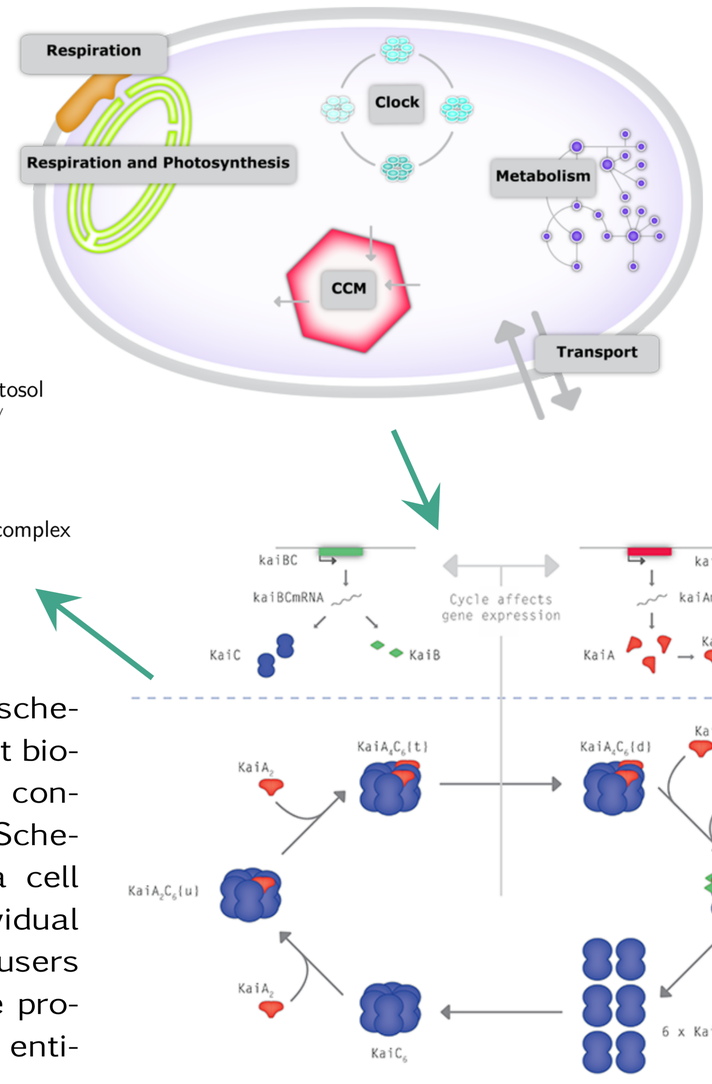
Experiments repository

Experiments repository is a tool for storage and presentation of time-series data from wet-lab experiments. Experiments are supplied with precise description (device, medium, organism, etc.) and appropriate annotations. Experiments are structured – several time series data can be attached to a single experiment. Every time series targets a specific list of measured substances together with time stamps of the individual measurements.



Biochemical Space

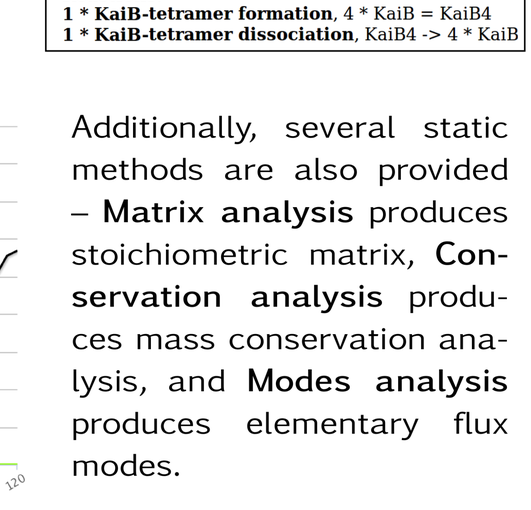
Biochemical Space (BCS) forms the backbone of the platform. It provides formal description of the biological problem and it is based on the hierarchy of selected biological processes. For each process, there are presented relevant models, chemical entities, and rules formally specified in **Biochemical Space Language**. Presentation of every process includes detailed information and links to relevant internal and external sources.

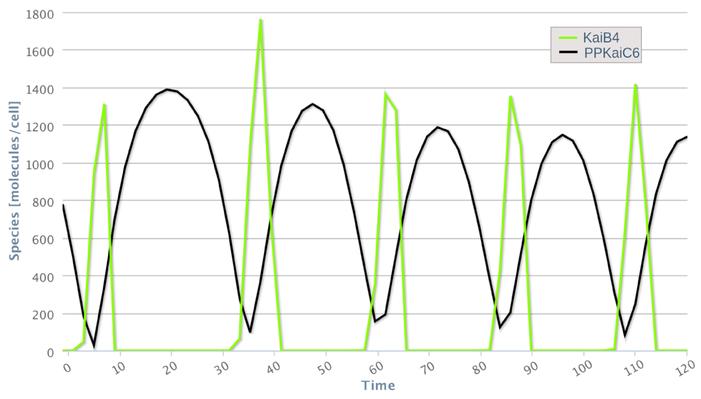


BCS is accompanied with schemes representing relevant biological processes in the context of cyanobacteria. Schemes are ranging from a cell in its enviroment to individual processes. Moreover, users can go deeper inside the processes to see particular entities interacting in rules.

Model repository

Model repository is a collection of implemented mathematical models describing particular parts of biological processes. Every model is represented as a set of ordinary differential equations generated from the model reaction network. Models are integrated within BCS. Moreover, a model is associated with some parameter value sets that enable **simulation** in a particular biologically-relevant scenarios.





Additionally, several static methods are also provided – **Matrix analysis** produces stoichiometric matrix, **Conservation analysis** produces mass conservation analysis, and **Modes analysis** produces elementary flux modes.

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