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## **Biochemical Space**

**Biochemical Space Language** 

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Annotation – Biological meaning assignment



map

**Comprehensive Modelling Platform** is a general framework for public sharing, annotation, and visualisation of domain-specific dynamical models and wet-lab experiments. 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 the domain specific system.

#### E-cyanobacterium.org

is an instance of Comprehensive Modelling Platform related to cyanobacteria. The framework is instantiated as a web-based application which allows to capture several aspects of biological models represented as biochemical reaction networks or ordinary differential equations.

**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. The SBML with its packages is supported as the main format for representation and annotation of biological processes outside of the platform. The internal structure of the platform reflects the principles of SBML for both user and developer fidelity.

### Visualisation



# Analysis

Internal tools (BioDivine):

- Pithya
- Parasim
- BCSgen
- Esther

#### **External tools:**



- Parameter synthesis
- Conservation analysis
- Flux Modes Analysis
- Matrix analysis
- MATLAB
- Copasi



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