E-cyanobacterium.org: A Web-based Platform for Systems Biology of Cyanobacteria

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Abstract. E-cyanobacterium framework is a web-based platform for modelling and analysis of biological processes occurring in cyanobacteria. It provides an easy and intuitive navigation through the structure of cyanobacteria and aims on being intelligible for experts in the field. The platform facilitates simulation of complex mathematical models represented by ODE systems, storage and presentation of wet-lab experiments, and unified representation of related biological networks.

1 Background

The tool focuses on providing a general online platform for systems biology of cyanobacteria unifying the state-of-the-art knowledge-base, related kinetic models and wet-lab experiments. In contrast to existing tools such as Biomodels.net [2] or CellML [1] which provide general repositories for biological models, e-cyanobacteria.org is directly focused on cyanobacteria organisms.

Another issue is a specific aspect of cyanobacteria processes such as photosynthesis or circadian clock that need to be represented by means of combinatorial states. Current online modelling repositories do not provide sufficient support to handle this issue. Moreover, existing annotation databases have insufficient coverage of terms related to cyanobacteria components and processes.

To this end, our platform provides a unique solution based on integrating the well-acknowledged systems biology standards with advanced computer scientific techniques targeting the mentioned issues. The platform has been introduced in detail in [3].

2 Platform Description

Current version is available at `http://www.e-cyanobacterium.org/` and includes the following functions (schematically summarised in Figure 1):

- Biochemical Space [4] – formal representation of elemental reactions facilitated by cyanobacteria biochemical entities, the representation is systematically organised by reflecting the hierarchy of biochemical processes ranging from the environment to the cell compartments;
- Computational Models – repository of stoichiometric and kinetic (ODE) models providing basic analysis tools (simulation, static analysis);
- SBML Compatibility [7] – computational models projected onto the biochemical space can be exported into well-annotated SBML files respecting the annotation standards (MIRIAM [8]);
- Wet-lab Experiments – import and storage of time-series experiments, relation to models and model vs. experiments data comparison;
- Annotation – detailed annotation of all system components reflecting annotation standards (OBO, OWL);
- Content Visualization (graphical presentation of models, biochemical space and modelling/experimental data).

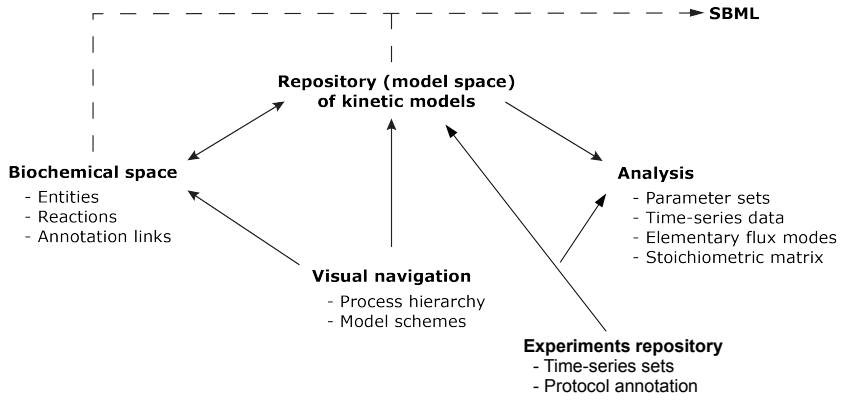

Fig. 1. Scheme of the platform.

In the current version (August 2014), the following processes of cyanobacteria are covered: environmental processes, respiration and photosynthesis, and metabolism. Environmental processes focus on precise positioning of cyanobacteria into the context of its environment. Since the website primarily targets *in vitro* cultivation conditions in a bioreactor, we have compiled relevant elemental reactions. Processes of respiration and photosynthesis cover the energetic components of cyanobacteria. Above these cellular processes, the metabolic part of the biochemical space forms a backbone that connects the bioenergetic components with metabolome and connects all key cellular processes with the general processes occurring in the environment.

3 Conclusions

Currently available tools mostly do not provide sufficient means of supporting entire systems biology workflow. Especially, this applies to existing domain-specific tools devoted to cyanobacteria [5, 6]. Therefore we believe that our web service makes a significant contribution. In future work we plan to further refine and equip the platform with new tools, some of which are currently in late stages of their development.

References

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