

Biochemical Space: A framework for formal description and annotation of complex biological processes

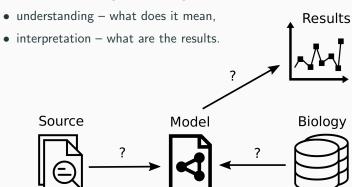
Matej Troják, David Šafránek, Jakub Šalagovič, Františka Romanovská, and Matej Hajnal

Systems Biology Laboratory @ Masaryk University

Motivation

Frequent issues with models:

• reconstruction - get it working,



Solution

Biochemical Space (BCS) is a semi-formal knowledge-base providing

- description,
- annotation,
- public sharing

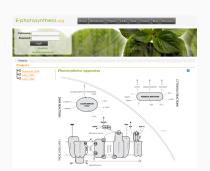
of domain-specific biological models.

Motto: formalization of biological description while annotating models.

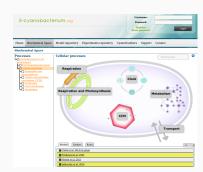
Comprehensive Modeling Platform

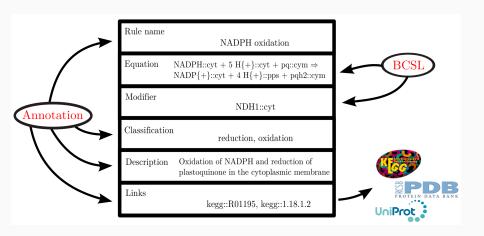
Web-based framework for integration of biological knowledge with computational models and wet-lab experiments.

• e-photosynthesis.org



• e-cyanobacterium.org

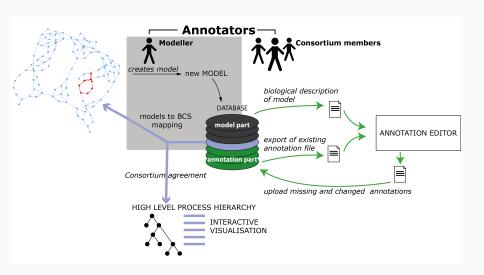




Why new language?

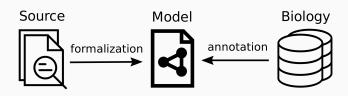
Biochemical Space Language (BCSL)

- internal representation easily editable and manageable,
- rule-based decrease size of the space,
- completely textual no graphical representation,
- human-readable direct interpretation to the user,
- not just a notation operational semantics suitable for analysis (translation to Kappa).

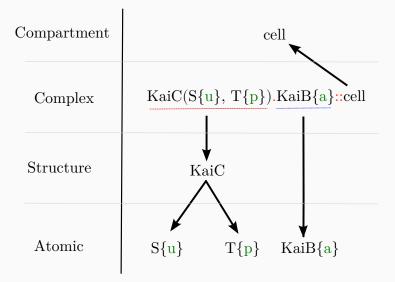


Advantages

- gives the model back its biological meaning
 - individual annotation for entities/reactions easily accessible
 - implemented model available online
- relating to BCS produces model described in BCSL
 - allows further analysis
 - provides qualitative formal description



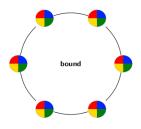
helps to reveal differences between models



Abstraction of the complex

Biology

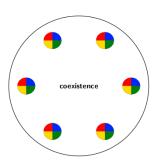
- graph "isomorphism"
- 700 different deviations



- Unphosphorylated protein
- Serine residue phosphorylated protein
- Threonine residue phosphorylated protein
 - Both residues phosphorylated protein

BCS abstraction

- mixture → order not important
- 84 different deviations



Rules

$$E + S \leftrightarrow ES$$

 $ES \rightarrow E + P$



$$E + S\{i\} \Rightarrow E.S\{u\}$$

 $E.S\{u\} \Rightarrow E.S\{a\}$
 $E.S \Rightarrow E + S$



$$R(active\{off\}, enzyme\{avail\}) \Rightarrow R(active\{on\}, enzyme\{avail\})$$

 $R(enzyme\{avail\}) \Leftrightarrow R(enzyme\{unavail\})$



BCS domain allows further abstractions

Entity ID	KaiC	
Entity name	KaiC protein	
Composition	S, T	
Type	structure	

Entity ID	KaiC6
Entity name	KaiC complex
Composition	KaiC.KaiC.KaiC.KaiC.KaiC
Type	complex

$$\label{eq:KaiC} \begin{tabular}{ll} & & \\ & &$$

 $S\{u\}::KaiC::KaiC6::cyt \Rightarrow S\{p\}::KaiC::KaiC6::cyt$

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Conclusions

Summary

- Biochemical Space framework for process modeling
- not strictly in the very same configuration
 - usage of alternative representation

Future work

- independent operational semantics / improved representation
- custom analysis tool for BCSL models
 - efficient static analysis
- BCS numbers extension
 - annotation of parameters