

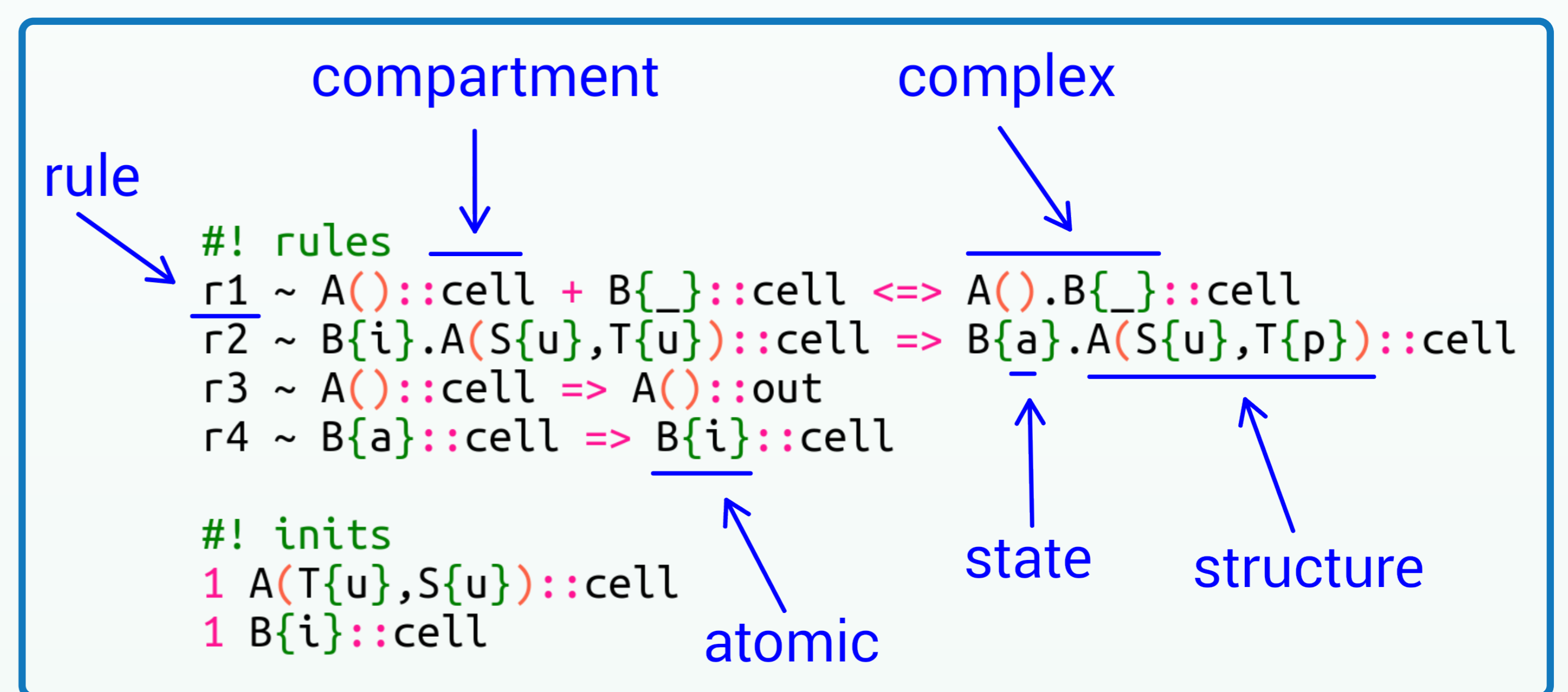
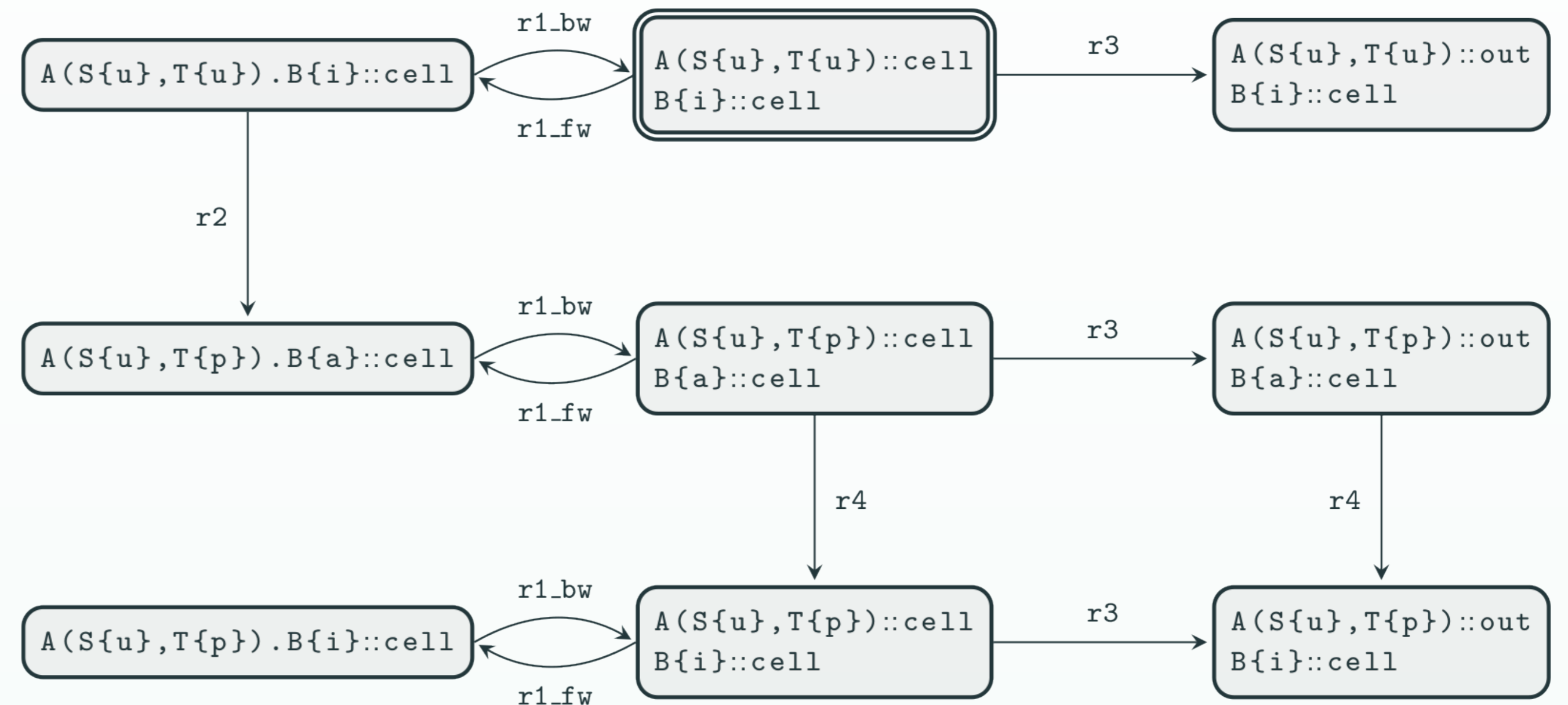
# Representing Biochemical Space Language in SBML-multi standard

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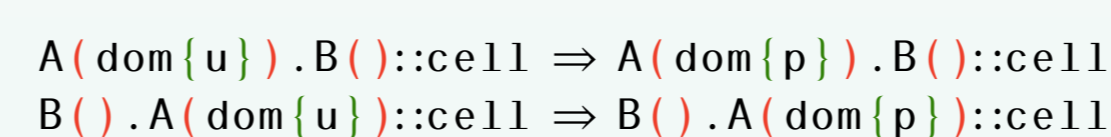
Biochemical Space Language (BCSL) is a rule-based formalism developed for biological modelling and precise mechanistic annotation of existing mathematical models. With the focus on the usability by the users beyond computer science, it is also necessary to provide tools that enable efficient analysis techniques that help reveal inconsistencies in models and allow to analyse the modelled system's dynamics. To this end, it is crucial to support export to standard notation, enabling the importing of the model to external tools and broadening the available analysis toolset. In the case of rule-based languages, this is provided by the SBML-multi package. We implemented (partial) support for the export in our software tool eBCSgen. In this poster, we discuss the process of relating BCSL to SBML-multi, focusing on the raised issues and open problems.

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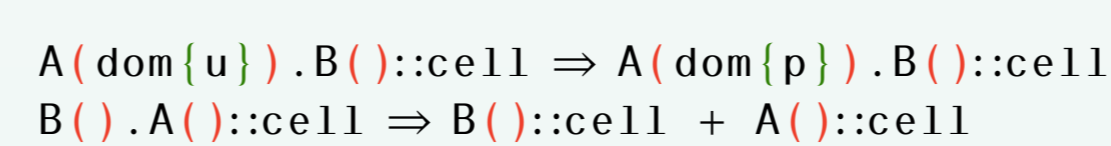


Abstraction employed in BCSL introduces non-trivial isomorphism which is not easy to capture on the level of SBML. We have identified three types of possible isomorphism occurring in a model:

- simple shuffling of identical agents



- shuffling of compatible agents



- multiple domains in a structure agent within incompatible complexes

