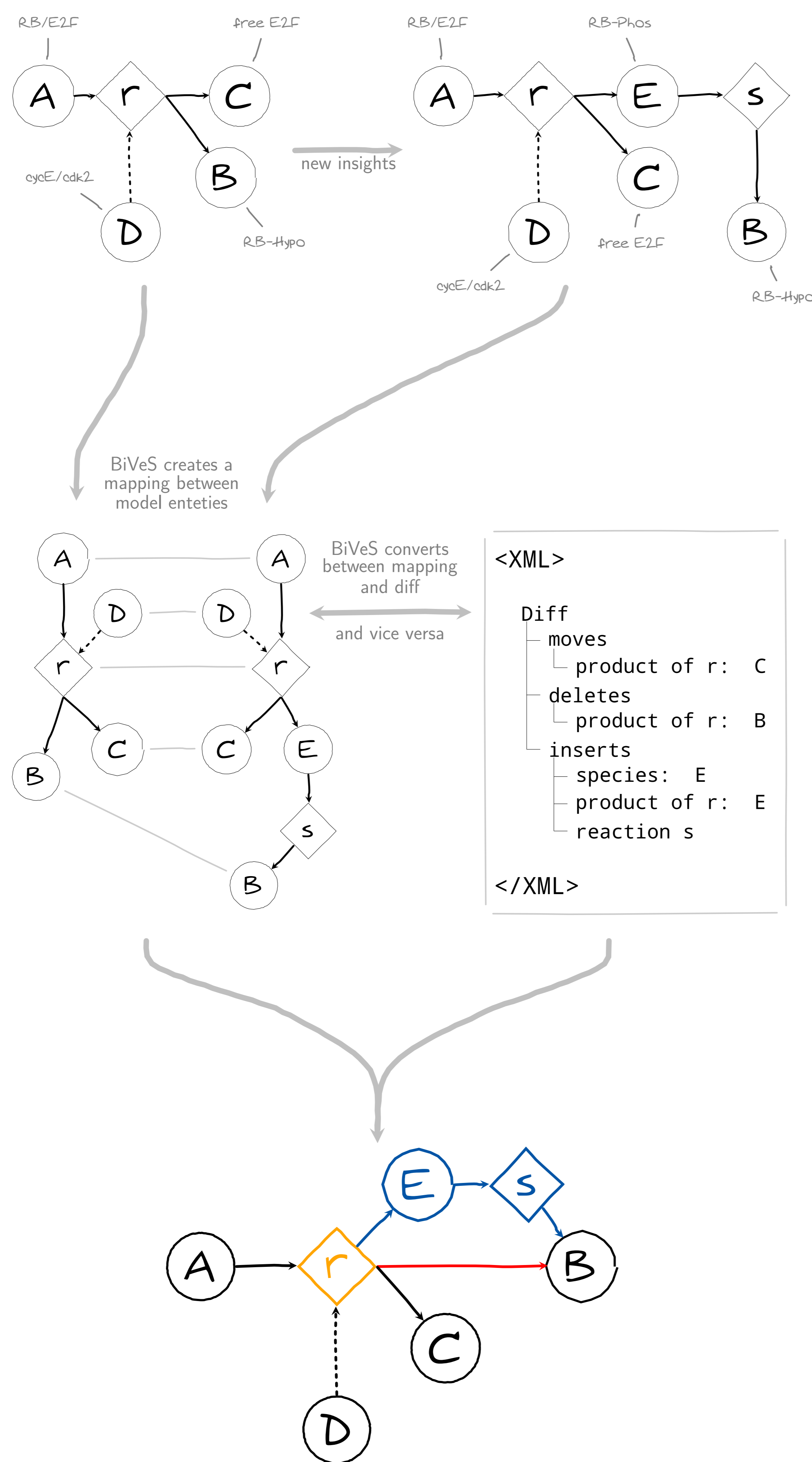
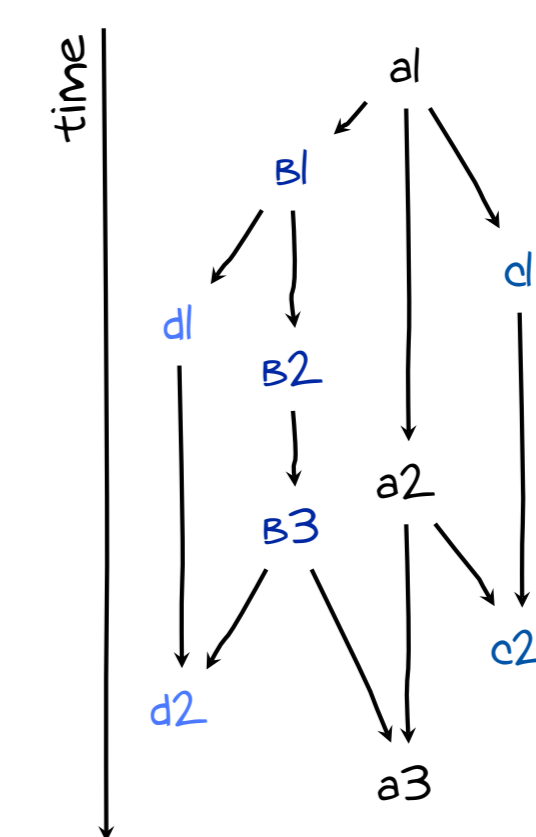


Disentangling the Evolution of Computational Models



Problem Statement

- Models evolve over time.
- New versions of a model, describing the same biological process, emerge before and after publication.
- Reconstructing the changes in a model and understanding what has been done to it pose two problems to modelers reusing existing code.



Version control helps to gain insights in the process of modelling and increases the confidence in computational models [3].

BiVeS

Biochemical Model Version Control System [2]

- Java library to map hierarchically structured content
- compares models encoded in standardized formats (currently: SBML [4] and CellML [5])
- matches unchanged or moved entities in model documents
- identifies inserts and deletes
- constructs a diff (in XML format)

The diff produced by BiVeS can be used to grasp the changes which occurred between two versions of a model.

BudHat

BudHat is a web interface to visualize the differences identified by BiVeS.

- calls BiVeS to construct the diff
- displays the result in various formats
 - the XML diff
 - a reaction network highlighting the changes using Cytoscape Web [6]
 - a human readable report
- is bound to a database backend holding the models

BudHat can be integrated in existing repositories.

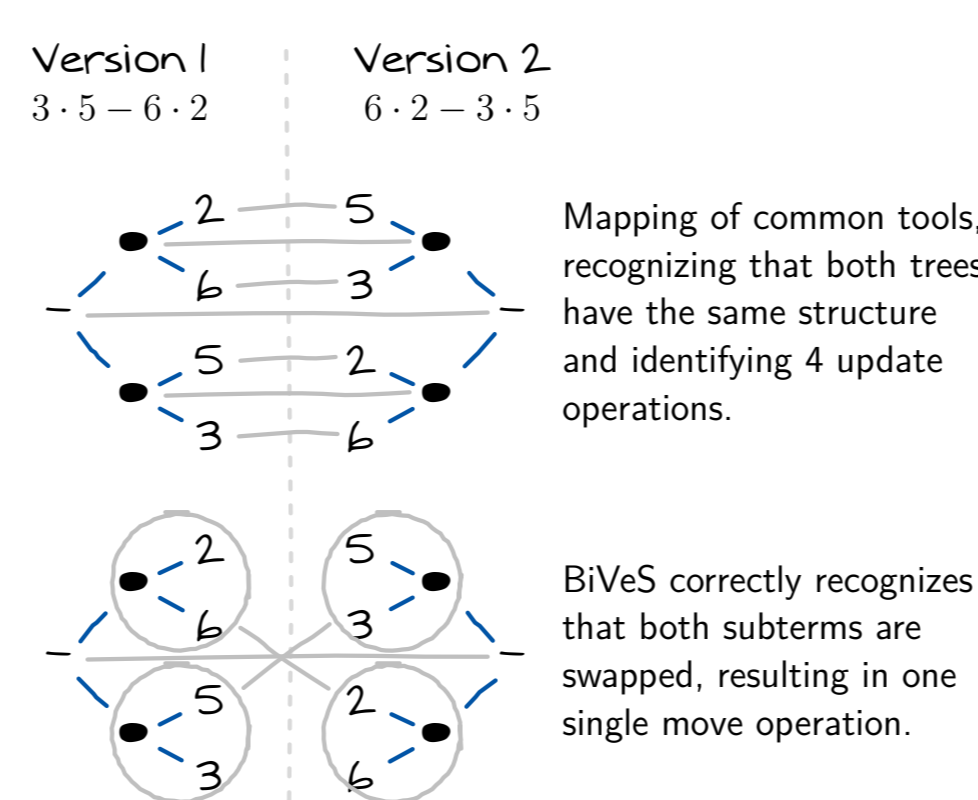
Why not simply use...

...your eyes? XML is not easy to read and even harder to compare. Moreover, models are far too complex to waste your precious time!

...unix' diff? The unix' diff tool is line-based and optimized to compare flat files. It is not able to handle hierarchical structures.

...SVN? SVN, like other common version control systems (VCSs), uses unix' diff tool to identify differences. Therefore, these VCSs are inappropriate for model version control.

...existing XML-diff detection tools? Their diffs are neither minimal nor very meaningful, see example on the right.



References

- [1] <http://sems.uni-rostock.de/budhat/>
- [2] <http://sems.uni-rostock.de/bives/>
- [3] Waltemath et al.: *Improving the reuse of computational models through version control* Bioinformatics, 2013
- [4] Hucka et al.: *The Systems Biology Markup Language (SBML): A medium for representation and exchange of biochemical network models* Bioinformatics, 2003
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- [6] Lopes et al.: *Cytoscape Web: an interactive web-based network browser* Bioinformatics, 2010



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