

BiVeS & BudHat

Version Control for Computational Models

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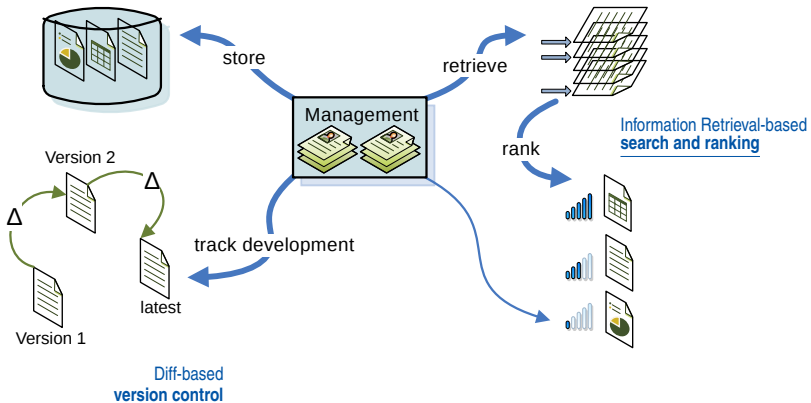
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Faculty of Computer Science & Electrical Engineering
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<http://sems.uni-rostock.de>

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Farmington, CT, USA



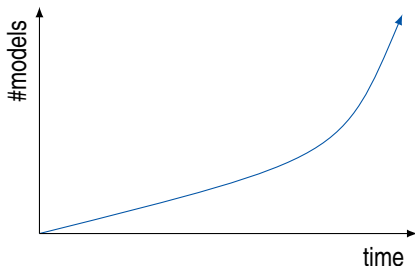
Format-independent,
graph-based storage



<http://sems.uni-rostock.de/>



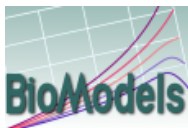
- many models
- multiple versions of each model
- several repositories



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- the FTP way
- the VCS way

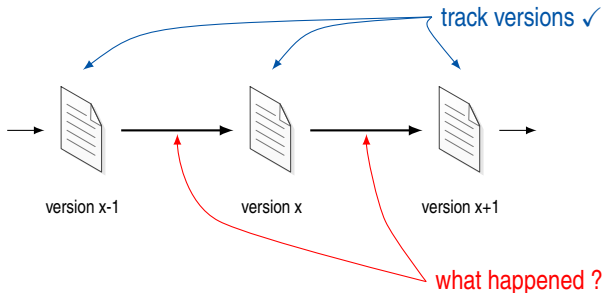
```
usr@srv % ftp ftp.ebi.ac.uk
Connected to ftp.gslb.ebi.ac.uk.
220-
[...]
230 Login successful.
Remote system type is UNIX.
Using binary mode to transfer files.
ftp> cd pub/databases/biomodels/releases/2012-08-11/
250 Directory successfully changed.
ftp> get BioModels_Database-r24_pub-sbml_files.tar.bz2
local: BioModels_Database-r24_pub-sbml_files.tar.bz2 remote:
    BioModels_Database-r24_pub-sbml_files.tar.bz2
200 PORT command successful. Consider using PASV.
150 Opening BINARY mode data connection for BioModels_Database-r24_pub-
    sbml_files.tar.bz2 (91772 bytes).
226 Transfer complete.
```

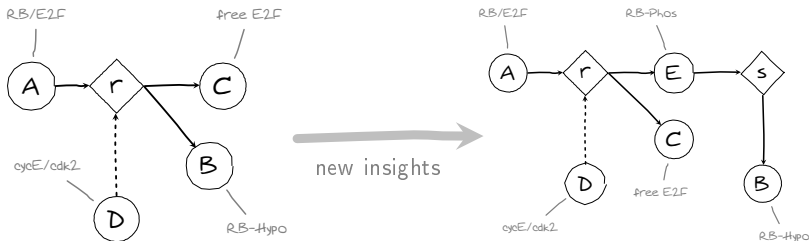


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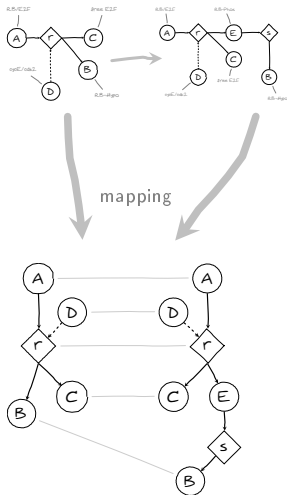
```
usr@srv % hg clone http://models.cellml.org/w/andre/nickerson-2008
destination directory: nickerson-2008
requesting all changes
adding changesets
adding manifests
adding file changes
added 2 changesets with 131 changes to 131 files
updating to branch default
131 files updated, 0 files merged, 0 files removed, 0 files unresolved
usr@srv % hg log path/to/model
[...]
```

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- the VCS way







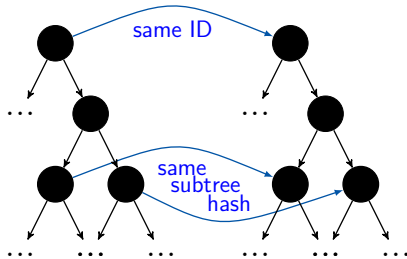
Waltemath *et al.*: Improving the reuse of computational models through version control. *Bioinformatics* (2013) 29(6): 742-728;



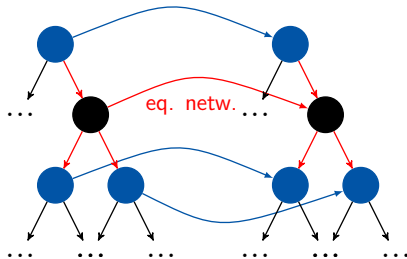
Biochemical Model Version Control System

- compares models encoded in standardized formats (currently:  and )
- maps hierarchically structured content

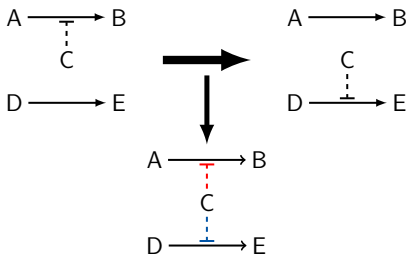
- input: 2 XML documents
- map unambiguous nodes/subtrees
- propagate mapping up/down
- exploit further knowledge of biol. systems

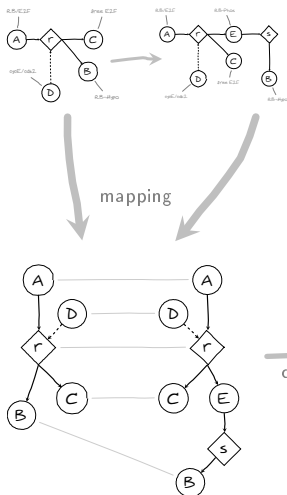


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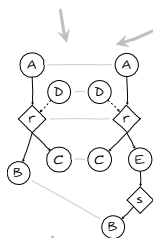


Biochemical Model **Version Control System**

- compares models encoded in standardized formats (currently:  and )
- maps hierarchically structured content
- constructs a diff (in XML format)


```

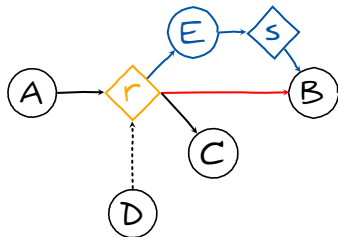
<XML>
  Diff
  |
  |-- moves
  |   |-- product of r: C
  |
  |-- deletes
  |   |-- product of r: B
  |
  |-- inserts
  |   |-- species: E
  |   |-- product of r: E
  |   |-- reaction s
  </XML>
  
```



```

<XML>
Diff
├── moves
│   └── product of r: C
├── deletes
│   └── product of r: B
├── inserts
│   ├── species: E
│   ├── product of r: E
│   └── reaction s
</XML>
    
```

- calls BiVeS to construct the diff
- displays the result in various formats
 - the XML diff
 - a reaction network highlighting the changes using 
 - a human readable report





lets take a look at our tools in action!

<http://budhat.sems.uni-rostock.de>



BiVeS & BudHat can be integrated in existing repositories!

Requirements:

- Models must be encoded in standardized formats (e.g. CellML or SBML)
- Each version of a model must be accessible for BudHat (either physically or through an API)
- Java based web server (e.g. tomcat), may run on a separate node

If you are interested in using our tools feel free to contact us.



- BiVeS = Difference detection for hierarchical structures
- BudHat = Visualization of changes
- Both tools are open source
- We do not want to establish yet another platform
- Our goal is to extend existing models repositories with a valuable version control mechanism

That's it! Stay tuned ;-)



@SemsProject

<http://sems.uni-rostock.de>

<http://budhat.sems.uni-rostock.de>

Questions? Suggestions? Recommendations? Drop me an email:

[<martin.scharm@uni-rostock.de>](mailto:martin.scharm@uni-rostock.de)