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# Meeting Minutes 14 May 2004

Autumn A Cuellar

- No one took notes at last week's meeting, which I did not attend.
- **Tool Release.** There was discussion about tool development concepts as they apply to CellML tools. There is dissidence in the ranks regarding when CellML tools should be released. A few people believe that the source code of Stephanie's Content MathML editor and Hadley's reaction renderer (and limited java CellML libraries) should be released to the general public as they are with a statement about where the project is at and if it's still going. Other people believe that more work (or at least more testing) still needs to be done on the Content MathML editor before it's handed over, and Hadley's reaction renderer should not be released at all because it's of little use. In the end, there's really only one person who has any say in when and if the projects are ever released, and that person says "Not now." I was also a bit confused about the timeframe of release of the Content MathML Editor because the line between ready and not-ready seems like a hazy, well-smudged line. I've been assured, though, that The Person With Say will know when the time is right. But, yes, we did establish once again that any CellML tools that are released (if ever) by our group will be open-source.
- Autumn's update: I have four weeks left with Team CellML. My last day is June 11. The website administration part of the website is no longer password protected, but there is still no link to it from the main website. David N. expressed concern about this part being lost after I leave. I'll leave it up to the rest of Team CellML whether or not they want to add a link to it from the main site.

Andrew Cantell added a new phystools group that has permissions for a new /product/physiome/cvs/cellml\_tools/ directory in CVS. Members of the phystools group are currently Stephanie Jor, Matt's two 4th-year project students, me, Shane, Carey, David N., David B., Matt, and Poul.

I had a discussion with Andrew about setting up the website generation process on the developer server. Ideally we'd want to set up a script that any member of Team CellML can run to update the developer site so you can see the changes you make to any of the pages immediately. Andrew agrees that this will be possible, but warns me that it will take a bit of time because we have to make sure that the developer server has all the tools necessary. We'll start the process over the next week.

The pdfs are finally being generated correctly. There are still minor problems (like images looking fuzzy and url citations appearing in the text), but the website will have all the updated pdfs by the end of the day.

- Poul's update: We've determined that none of the e-mail going to cellml.org addresses are going through from outside the Institute intranet. Poul has e-mailed Andrew saying it's been a problem since 16 Dec. He also talked to Martyn Nash (who's been running the IT weekly meetings). Martyn says the issue has been brought up for weeks, and he'll bring it up again this week.
- Matt's update: Stephanie's (Content MathML editor) working with two project students (CellML editor) on merging the two editors. They've organized it so that the MathML editor will be embedded in the CellML editor (hopefully by Monday). The Content MathML editor will continue to be developed as a standalone application.

His other project student (visualization) has pulled out stuff from Hadley's java library and has modified it to handle CellML 1.1. His main goal was to find a useful way to visualize models, representing connected variables and components. This tool could potentially be a plug-in for a CellML editor.

Re: Anatomy ontology interface. Matt has come across a functional inference engine called 4Versa, which is part of 4Suite, an RDF library for python. This is just for future reference; for now he's still

planning on only allowing the simple view of a subclass and its parent classes.

Also looking at instance data for biochemical pathways (finding instances of pathways that have been represented in BioPAX [<http://www.biopax.org/>]) to compare the CellML and BioPAX representations. We might be able to use the instances as the ontological description of the relevant CellML model. Many of the MetaCyc [<http://metacyc.org/>] pathways will hopefully have BioPAX representations because the MetaCyc project lead Peter Karp is also heavily involved in the BioPAX project.

The python CellML library is about a week away from a state of release. It has changed much since he's been helping the project student with the import visualization. Eventually it will be stored on a publicly accessible CVS repository. Matt will start playing around with SourceForge. Short discussion about whether all projects should/can be hosted by the same CellML SourceForge [<http://cellml.sourceforge.net/>] site. David N, the current expert, says it's common to host many projects from one page.