Meeting Minutes 28 May 2004

Autumn A Cuellar

- Autumn's update: More on the script to sync developer and live servers. Andrew said that setting permissions might pose a small problem. It's up to Team CellML who should be given permission. Shane and David N. suggest that I get Andrew to set up a generic user and give the password to those who need to be updating the website. Another reminder - my last day with Team CellML is next Friday.

  Have received the CellML plugin for BioUML [http://www.biouml.org/] from Fedor Kopalkov. The collaboration with them should continue after I leave. Matt volunteers to keep up the communication. He suggests involving Edmund Crampin because he has much more knowledge of biochemical pathways than anyone in Team CellML.

- **Physiome Project Road Map** - completed and passed around earlier for our perusal. Peter explained that he started with Matt and Poul's draft CellML Road Map [../tool_development/projects.html] and Shane's FieldML Road Map, incorporating them into a bigger picture. Most of this has to do with tools and how they'll work together. Peter pulled the Repository and Model Use sections out of the section on CellML because they will have a wider function than CellML.

  DavidB: Who is the intended audience of this document? Peter: It will be posted on the physiome.org.nz website, so it's for people interested in contributing to the Physiome Project. This document won't be posted until it's been cleaned up. Will also wait for input from Nigel Lovell's and Socrates Dokos' group at the University of New South Wales.

  Peter: Was a bit confused about ModelML. Is it an extension of CellML? Poul: It's a new label meant to remove the ambiguity of CellML since it does have a wider application than biological models. It's meant to be a more accurate description. Peter: In that case, ModelML might be too general a name. There are plenty of models that the framework can't describe, and 'ModelML' might be equally misleading. [more discussion on a more appropriate name] Let's not get caught up in this discussion just yet...

  Shane: If all domain information is to be kept in the ontologies, is there even a need for a core ModelML? [lots of confusing discussion ensued. am again calling on my alter ego to paraphrase: (oh, and Matt and Poul seem to be in agreement on about 95% of things, so from here on I will just refer to them as one person - MP to make it easier for me)] From what I gather, MP and Peter have different ideas on what ModelML is and should be. MP is/are still referring to ModelML as CellML Core + ontologies (aka CellML 2.0 with a more generic label), although Poul admits he's leery of calling it ModelML anymore after the previous discussion. Peter refers to ModelML as an XML framework for everything needed to run a model including CellML, FieldML, and boundary and initial conditions. (This is why there is a separate section in the Physiome Project Road Map for ModelML from CellML.) Rather than having XML tags for all the other stuff, MP thinks that all the information that isn't described by CellML (core) and FieldML should be kept in ontologies.

  But going on with the ontologies, Shane pointed out that there's going to be plenty of ontologies that we're going to need that we haven't even thought of (for example, describing initial conditions). These need to be pointed to in the Road Map. Peter: They are.

  Returning to 'ModelML' as MP understands it, Peter wonders if a CellML section should be included in the Road Map at all. DavidB: Yes it should be because CellML will continue to be, it just might get superseded. MP: CellML will continue to describe the same type of models it has been.

  Discussion on the ordering of the sections in the Road Map. MP: 'ModelML' pulls in FieldML, MathML, and ontologies. Peter will try to make sure this is clear in the Road Map.

Note on Section 6.4 Simulation: Shane had suggested it needs to be made general, which Peter has done, but Shane also thinks the section should contain some specifics. We need to look at different *use cases* (officially a part of the CellML jargon now, thank you, Matt).

Note on Section 1.1 Open Source policy: Carey mentions it should be **L**GPL license. The L is important. Matt (and here he becomes an individual again) disagrees with using the LGPL license. He argues that modifications shouldn't necessarily have to be put back into the public domain, let's give people a reason to contribute to the project - BSD license, and here he used Zope development as an example. I think Shane's argument was that they don't have the make the source of the patches available under the LGPL license. Peter suggests Carey, Matt, and Shane get together to hash out which license would be best.

Matt: Should be note in there about the migration of CellML.

Carey: Will you add the group working on the kidney project to 1.4 Groups working on the Physiome project? Peter: Yes.

- Poul's update: Nigel Lovell will sponsor someone to come over for a week in July to start discussion on ModelML,FieldML/AFL,FRL. Follow-up discussions will take place at the EMBS meeting.

- Matt's update: Still no contact with Stephanie. Will try to get her contact details through Maria.

Has been communicating with Gary Bader from the BioPAX [http://www.biopax.org/] group about schema names. Has prompted a pondering of rules for naming models. What is a significant revision to justify renaming? There is a huge gray area. He's trying to come up with a proposal. One has to be able to describe all sorts of revisions - those based on published errata, errors you found when you tried to simulate the model, etc.

Matt's been given an updated version of the Java libraries that his project student has been working on. Matt will stick the library on SourceForge.

- Peter's update: The CMB CoRE [http://cmb1.auckland.ac.nz/], which helps fund the CellML project, is holding a half-day retreat in July. Each of the five groups that make up the CMB are being asked to make a presentation on what's come out of the funding.

HortResearch [http://www.hortresearch.co.nz/] has approximately one-half of the apple genome and two-thirds of the kiwi fruit genome deciphered. They are interested in working on a fruit physiome project, so to speak. A group from HortResearch will be visiting the Bioengineering Institute in July.