

**BioPAX Group**  
**October 3, 2003 Meeting Minutes**

**Location:** Computational Biology Center, Memorial Sloan-Kettering Cancer Center, 307 East 63rd St, New York, NY.

**Participants:** Gary Bader, Michael Cary, Peter Karp, Joanne Luciano, Andrey Rzhetsky, Chris Sander, Imran Shah

**Note:** The majority of this meeting was dedicated to resolving open issues with the BioPAX ontology. **All of these issues, including those that were raised and resolved during the meeting, have been logged into the SourceForge bug-tracking system.** For details on the nature and status of these issues, please visit the SourceForge page:

[http://sourceforge.net/tracker/?group\\_id=85345&atid=575904](http://sourceforge.net/tracker/?group_id=85345&atid=575904)

**Overview:**

- I. Short overview of current ontology
  - a. WNT pathway → BioPAX format
  - b. Demo: Entering data via Protégé
  - c. PSI controlled vocabulary, DAG-Edit
- II. Ontology issue discussion (see SourceForge page)
  - a. Worked to resolve existing ontology issues
  - b. Several new issues were raised and discussed
- III. Next meeting
  - a. Video conference sometime in November
  - b. Face-to-face meeting: Denver, 12/8/03 (tent.)

**Summary:**

We began the meeting with a short overview by Gary of the ontology, as it stood at that time. Several important points were made during this overview; these were added to a list of ontology issues discussed later in the meeting.

Next, Mike demonstrated the Protégé ontology and walked the group through a demonstration of how Protégé could be used to create instances of the ontology. He translated a few steps of the WNT pathway (courtesy of the PATIKA group) into sparse BioPAX entries, and then showed the OWL output that Protégé created.

Gary then gave a short overview of how PSI is implementing controlled vocabularies (CVs). They are using a program called DAG-Edit, which Gary demonstrated, to build lists of terms that may occupy certain slots (e.g. “*interactionType*”). The tentative plan that Gary presented was for us to build on PSI’s CVs when appropriate, and use DAG-Edit to build our own CVs when needed. After Gary’s presentation we decided that we should discuss this plan further, so we added it to the list of open issues.

We then prioritized the list of all open ontology issues, intermixing issues of maximum importance to the overall design of BioPAX with those that we felt would be most easy to resolve. Proceeding through this list (see below, and SourceForge) throughout the remainder of the meeting allowed us to address both the major conceptual issues as well as the more trivial points that came to our attention over the past few months.

At the conclusion of the meeting we briefly discussed the venue for our next meeting. We decided that we would attempt a video-conference (1-2 hours) sometime in November. We tentatively set the date of our next face-to-face meeting for December 8, 2003 in Denver, Colorado.

#### Ontology issues discussed at 10/3/03 meeting

- 1) How should we represent common complex processes (transcription, translation, degradation, etc.)?
- 2) What value type should the delta-G, delta-H, and delta-S slots take? How should we specify units for these slots?
- 3) Should *molecular association* be a sub-class of *physical entity*?
- 4) How should we handle stoichiometry?
- 5) How do we represent activation and inhibition of enzyme catalysis?
- 6) Should we advocate naming conventions for reactions, pathways, complexes, etc.?
- 7) Is *cell component* too ambiguous?
- 8) How should we handle provenance in Level 1?
- 9) How should we handle spontaneity and reversibility of conversions?
- 10) How do we implement controlled vocabularies?
- 11) How do we represent compartments (e.g. during transport, or for processes that are compartment specific)?
- 12) Do we need the equivalence class in Level 1? If so, how should it be used?
- 13) Should we create sub-classes of the *pathway* class?