Group reports

Most of these reports were provided as written material and more details from the individuals can be found there. We reviewed these quickly and so the comments here are simply those that I happened to catch in passing.

FB report (Becky)

In addition to existing GenBank/Swiss-Prot sequence curation and a paper-by-paper approach to literature curation, GO-annotations are being done on a gene-by-gene basis to fill in holes.

GO data from gene models that were split or merged in the Release 3 genome reannotation have been mostly re-partitioned. Chris Mungall has also given Becky a list of genes where the coding sequence has changed; GO data for these gene models has started to be assessed.

SGD report (Karen Christie)

Currently pushing to remove IEAs, all gone but those for about 60 Ty encoded ORFs.

Microbial Structure Ontology was described (for Fungal structures): Judy asks, are they interested, Karen says yes they are interested, some groups (*Neurospora, Aspergillus*) already participating. Mike, small community, not a lot of money to sustain, applying for grants now. Aspergillus already has a database set up (in Manchester I think) Cross-reference to SGD for annotation, *Candida, Aspergillus, Neurospora*. Chandra, Eurie, and Maria have initiated this and it is now a part of OBO.

In addition to Maria Costanzo and Jodi Hirschman, who are attending a GO meeting for the first time, SGD welcomes another curator, Rob Nash.

MGI (Harold)

RIKEN annotation increased total genes annotated by 37%, 3300 genes, this was done by inheriting GO annotation done on Riken clones. These came in mostly as ISS or TAS evidence codes.

They are developing (or collaborating on) three ontologies: GO, anatomy, and phenotype all with a common structure. This allows the use of common tools such as the DAG-editor and ontology browser.

The MGI GO browser now displays comment field (important for MGI annotators and users)

Changes to software so that users don't get links to obsolete GO nodes

Changes to software were implemented so that users don't get links to obsolete GO nodes. These include enhancements to the editorial interface, and automatic removal of obsolete terms being assigned via SP2GO and IP2GO translation tables.

Editorial interface enhancements were needed to aid reannotation of genes mapping to obsolete terms, because they go live within 24 hours of any changes. Much that is to assist with keeping the annotations up to date. MGI can now track original source of a GO annotation, to help track when a curator has manually changed an annotation that was originally obtained from dataloads. An additional enhancement they have added to the interface is the inclusion of a GO marker notes field to supplement the notes field associated with each individual annotation. The new notes field is meant for notes pertaining to the state of annotation rather than notes about the marker itself.

Other software development: A version of the GOTermFinder is being developed at MGI and is available at
http://www.spatial.maine.edu/~mdolan/MGI_Term_Finder.html

BDGP (Suzanna speaking for Chris Mungall)

Chris gave a talk on slots and cross products at Genome Informatics; there is concern, which we share here that this will make things overly complex. That is why we will prototype first and Chris has started work on this. He is also looking at third party tools. Chris proposes that the BDGP software folk meet with MGI (aka David and Joel, etc.) prior to next GO meeting for first implementation of properties (also for other ontologies). Since the words 'slots' and 'properties' are synonymous GO will go with the word properties (and properties have values)

DAG-Edit: next version (1.4) will support properties, which means we need a new flat file format (with tag-values). We will still have some backward compatibility with existing flat file format. Not using XML solely because it is not that easily readable by humans

GO-Slim – needs to know which slim files go with which annotation files

GO Database – monthly loads are now more regular and reliable with a new QC procedure, also daily loads of ontology terms with no QC, is now storing more data in GO database (not yet available in AmiGO). The 'with' column is now "fully normalized". He did note that not everyone is providing a gp2protein file – really need to have these from everyone who is providing an annotation file. This was added as an action item.

Karen Eilbeck joining Berkeley group to work on SO

TAIR (Suparna)

Annotation Update: The complete set of numbers is in the handout. The rate of annotations is about 150 genes a month or 2 genes a day per curator. To the GO ontology itself, they have added about 150 new terms since last meeting. They have updated their gp2protein file recently.

The main TAIR database is at NCGR in Santa Fe. The GO associations from Carnegie at Stanford are updated weekly

TAIR held a very successful literature curation meeting at TAIR in March 2003.

Updating MetaCyc2GO file: The mapping to MetaCyc has problems (going to function instead of process). Approximately 80 new pathways have been added (50 have existing GO terms, need about 30 more terms to complete mapping). TAIR (as personified by Suparna) are now updating the mappings from MetaCyc pathways to GO functions and once finished will this task will pass the mappings on to GO central (Amelia) to check errors.

They have updated web site, can now search for genes with GO terms as keywords; added an Evidence description to add more info about the experiment. They are also developing a new ontology browser. Along with this, they also are developing a GO awareness campaign for the Arabidopsis community.

Lukas Mueller will be going to Cornell and running Solanaceae database

TIGR (Linda) ()

- Arabidopsis: At TIGR this project is going through and renaming gene products correctly. Funding will end in fall and TIGR will then turn over all A. thaliana data to TAIR.
- T. brucei: This annotation effort is still active and progressing.

(Michelle)

- Bacillus anthracis and Coxiella burnetii: just released annotation files of the gene products to GO terms.
- Other prokaryotic genomes: These gene products been annotated with GO terms and are awaiting publication to be released.

TIGR uses 'Manatee' to assist curators in GO annotation. This adds new GO search capabilities that assist the curators in fully annotating prokaryotic and eukaryotic genomes. Manatee is available on SourceForge, but it depends on TIGR database schema. BDGP and TIGR may add an Apollo connection to manatee. Rex/Dictybase are interested in this as well.

Don't have gp2protein files for all prokaryotes, in some cases because the data was not available when the annotation file was released

Wormbase (?)

They provide biweekly updates for the public, including GO annotations.

They also raised one question regarding the cardinality of evidence codes to annotation. There followed a discussion about whether multiple evidence codes belong on one row or in individual rows (one row per evidence code).

Resolved: The decision was to do the latter and make the cardinality one to one.

Final question was whether conference abstracts are legitimate references.

Resolved: Yes! Conference abstracts can server as references.

Dictybase (Rex)

They are working for a late June official release of DictyBase (based on SGD's code and schema—special thanks to Mike and all). This release will include 1800 loci with 8949 GO annotations (all except 40 to IEA).

They now have two full-term curators (Petra and Pascale), and one new programmer (who will start in July). This developer can help John out since he is experienced with Java and is partially funded by GO. Suzi to ask John to contact Rex (done).

Gramene (Pankaj)

They will be making a new release in late June, with 4500 new non-IEA gene associations. Most of their recent focus has been on curating mutants and phenotypes. They are working with other databases with on mitochondrial and chloroplasts. Likewise, they are working with rice database on nomenclature issues. They are also now working with Maize people to try to get gene association file for maize incorporated.

GO-editorial (Mostly Jane, with a soupcon of comments from Midori)

Amelia has created a nice digest that is available monthly. This digest summarizes: new terms, obsoletes, new definitions, basic data on changes, and links to appropriate SourceForge entries. It is kept on the ftp site. Please send suggestions for improvements to Amelia. There will soon be a cron job that mails announcement of each new digests to go-friends (AI).

Component terms have increased quite a lot (with effort by BRENDA group to create complex terms for enzyme complexes). In addition, we now have definitions for 78% of terms (yeah!!). They have brought the GO synonyms file up-to-date. Molecular function terms now have the word 'activity' as part of term name. They have generated a list of obsolete terms with suggestions for remapping for review.

There are new web page drafts for review (presented later in meeting)

Interest groups – not linked to anything

GOA (Evelyn)

We can look on the GOA web site for latest statistics and news (http://www.ebi.ac.uk/GOA). They have produced three releases since February. They have now updated their associations file to include the source of the annotation, so credit/blame can be made appropriately. They have also now integrated the manual annotations from other sites (fly, MGI, and SGD). The HAMAP group at SIB, Geneva is working on a HAMAP2GO mapping and may be involved in manual GO annotation of Swiss-Prot microbial proteins. In total, the GOA project has released more than 3 million annotations to 600,000 proteins.

They have also written two papers about GOA (and GO) and two more are planned for this year.

Big news is that now LocusLink is now using the GOA annotations. SwissProt will henceforth be responsible for updating the former Proteome annotations to GOA annotations.

Evelyn is just back from ontology workshop in Japan. Edgar W from Transfac was one of the chairs. Evelyn spoke about GO and GOA and got a favorable response. She found that many Japanese were aware of GO but were generating other ontologies(cell types and anatomy) that are up and coming on the OBO site. Some groups had developed ontologies similar to GO, because they didn't seem to realize GO existence or didn't realize they could (and should) request new terms.. Because of this, she raised the question of how we will decide which ontology will go into OBO (this is a good question).Who decides which cell-type ontology will be the standard. Answer: Michael will probably just decide by fiat.

SwissProt is going to be employing two fulltime GO annotators. Interviewing begins in July.

Daniel is thinking about doing a release of the GOA database (which is in Postgres) for the general public (from Suzi, he should get in touch with Chris in case we end up switching to Postgres here as well for GO).

Incyte

They are doing manual annotation (a la Proteome) using weekly updates from locus link and GenBank. The statistics for their annotations are in the handout. They have also restarted monthly term suggestions for GO terms

They are doing new product development – BioKnowledge Retriever. This will include two new ontologies (mammalian disease, mammalian expression) and they are interested in making these public and in working with other groups to develop these and make them public. This is something to consider for OBO.

Maize

MaizeDB will cease to exist in 3 months, now called maizeGDB. He is here to learn because they are just getting started with GO. The URL for the new maize database is http://www.maizegdb.org/

RGD

They have generated about 3000 annotations (distributed equally at ~1K GO ontology).

They are working on using the GO terms (building their own GO browser) for gene search strategies. Their browser will be utilizing GO terms as part of search strategies to identify genes, including genes annotated to terms descendents

They have a disease specific orientation and want to utilize other ontologies to organize this type of data in RGD

Pathogen at Sanger

Next time

Annotation Issues

IEA

TIGR is using an HMM scoring function for assignments and since this is more sophisticated than keyword matches they would like a means to add quality information to IEA. Someone pointed out that this is also true for multiple alignments. David says the appropriate thing to do is to use different references for different types of analysis. Suzi says that this argument can also be extended to all evidence types, as discussed before. David suggests extending filtering in AmiGO to also qualify the query to IEAs with certain references. (Brad, another issue is the bulk of IEAs. Too slow for web interface when IEAs are loaded.) TAIR solution is evidence description, but this is internal. MA if a db wants an internal one then they can. David we have reference. Midori- GO reference refers to GO pub. Added 3 action items below: BDGP needs to implement filter, group needs to establish a collection of references to methods, BDGP also needs to explore ways to deal with size explosion of associations other than omitting IEAs from AmiGO.

Suspect annotations

Rex, if inaccurate annotations are discovered at one site that came from another site they can't change/fix the annotation because it didn't arise from their own site. I second this because maintaining high quality in the associations is one of the main utilities of GO, people use it as the default golden reference set. Rex noticed an actin with motor activity, easy to notice. How are we to do this? Judy: what can the group as a whole do to help. Midori: they owner has to make the correction. How can notification that a correction is required occur? MA: every MOD has a mechanism in place to receive and make corrections. Question is, do we begin to build association quality assurance tools to detect these. Gp2protein could be used together with BLAST, using best-hit match and flagging discrepancies in associations. Suzi: GOST tool can be used for new

annotation. Karen E: how many levels up the tree is acceptable—any number. David: incompleteness of annotation is also an issue. MA: it would help even more if this tool were available and used during the process of annotation. Another means of improving quality is by adding the ability to file error reports directly from AmiGO pages. Three action items added below. late addendum from Evelyn: Concurrent Assignments tool from EBI, Manatee has something similar; AI for AmiGO to be able to do this type of thing, (Amazon-like: others who annotated to this also annotated…).

More 'rules' for annotation

Midori: The current rules are broad and do not contain specific guidelines for handling of every situation. Just make suggestions, best practices. How do you identify common proteins. Evelyn: amigo needs concurrent assignments. Midori: oral tradition is now written down. The rule is that we are annotating to potential. Long discussion of potential. Amelia: slide show. Solution is to use the word intrinsic to distinguish regulator activity versus extrinsic regulator activity. Harold: function is not necessarily an attribute of gene product, it can also be applied to complexes. Jane: Is transient activity okay? Yes. MA: complex should have a defined stoichiometry. Karen: Is there an issue with counting # of subunits? No. Midori: the point is not to have a component term for every ImmunoPrecipitation-able agglomeration; "defined stoichiometry" doesn't imply identical subunit composition between species

Resolved: use the word intrinsic to distinguish regulator activity (regulatory function that occurs when the gp is part of a complex) versus extrinsic regulator activity and to change the relationship type to is-a.

- CDK-cyclin example – start including the word 'intrinsic' for the regulator activity to clearly indicate that it is part of a complex, without which the kinase activity of CDK kinase subunit is not active either.

Jane's item

Resolved: Binding stands alone (not binding activity)

Treemap demo (Eric Baehrecke)

He is interested in steroid activated programmed cell death signaling, both fly and human apoptosis. Ben Schneiderman is software person who is interested in information visualization (hyperlinks, Spotfire, Treemap) and has developed a strategy for analysis of genome data using GO and Treemap displays. The components of the tool include: a GO parser, parser for genome data, a view in Treemap. The visual variables that may be controlled are color hue, color intensity, and area of the rectangle representing the data. Eric B will look into what they need do in order to enable us to link to Treemap from the GO Tools list. See http://www.cs.umd.edu/hcil/treemap/ for more information.

Properties implementation

Group seemed to feel that the most important priority is completion of software for direct saves to the database. Believe that this will assist implementation of properties. Did allow that John's proposal for new flat file format looks good and useful and since most of this work is already done, it will be good to have around. We also agreed that the existing flat file format would **never** go away, although property information may be lost in a direct conversion.

Brad's report

Brad described STAG, which is an SQL templating system. It returns SQL query results as XML dumps. A generic piece of Perl software uses the template to generate the query.

Machete is a software package that sits on top of STAG. It is a lightweight Perl application that maps CGI parameters to the proper SQL, HTML, and XML templates. It uses a library of templates to replace the current Perl API. This will result in all SQL queries, HTML pages and XML transformations being maintained as a library of templates. This will allow future generations of AmiGO to be flexible, expandable, customizable and portable. As the GO schema becomes more integrated with Chado it will allow more types of queries across a wider collection of data in the future.

There was quite a bit of interest. Both Rex and Judy interested in having Chris and John talk to their counterparts of the technical staff at DictyBase and JAX.

Proteasome or part of relationships

Different forms of part of: David, if it always there then it is a child. Distinguish between those that never change and those that vary (where) where only the child will have that part. Midori: We all agree that there must be multiple is-a children for complexes of different composition, which is clear. The question we need to address is what to do when the composition is the same. David: If we don't know it is safer to create two subtypes). Judy: is-always-found-there and is-it-the-same are two separate questions.

Conclusion for the first question was to change the documentation to not require part-of to mean always. Different subunit composition implies different terms.

If the composition is identical, then this is a single term and multiple parents are allowed (nay encouraged). In other words, complexes that have the same composition in all locations may receive multiple parentage, however, complexes that have varying compositions need separate terms with the specific localizations

In the future, we may need to add more sub-types for things like myristoylated or phosphorylated forms of the compound.

Physiological processes

David: This area need revisions and continued discussions. We will create an interest group to handle the reorganization/structuring of the physiological process node of the biological process ontology. Those interested should contact Tanya (tberardi@acoma.stanford.edu) or David (dph@jax.informatics.org). The group will meet and discuss via email and present a report at the next meeting. Proposed top nodes right under 'physiological process' are 'organismal physiological process' and 'cellular physiological process'.

Behaviour

Peter Midford in Arizona, already is working on behaviour ontologies for loggerhead turtles, jumping spiders and we feel this level of detail seems to be beyond the scope of GO. However, there still needs to be some descriptive capabilities for behaviour within GO, both for Drosophila and maybe for mouse, to be able to annotate certain genes. The essential questions relates to what should be included in Process. It is clear in *Drosophila* that one can pin certain genes to behaviours like walking or circadian rhythms because these are hard-wired. Conversely, there is need for an auxiliary ontology developed specifically to deal with behaviors in mouse since much knowledge in this area is not tied directly to specific gene activity

Conclusion – we do want behaviour in GO, but there may be other ontologies, for groups like mouse, that will extend these. In these cases we'll recommend that these auxiliary ontologies be consistent with GO and include any necessary cross-references to GO terms. To support this the GO terms should be at a level that can be used for many organisms for behaviours that have a genetically defined component.

Localization of viruses

We had previously discussed (at earlier meetings) and considered expanding the definition of extracellular to include extraviral in order to be able to include viral host cells. There was an objection from virologists that it doesn't make sense to consider viral host cells as extracellular. Therefore, we have now decided to reverse this previous decision from meeting and will remove viral reference from the definition of extracellular. Added action item.

Purity vs. pragmatism aka obsoletism

Question: When do terms become obsolete? Two issues, when redefining the term and when removing gene product names. Word-smithing changes to the definitions that does not impact the meaning, only clarifies the original meaning do not require that the term be made obsolete (the criteria is that no annotations will ever be affected by the change to the definition). However, if the fundamental concept changes then the term needs a new ID and the older one must be made obsolete.

Michelle found some terms that when going from primary ID to secondary ID (arise from merges only) were not strictly synonymous. This is a problem.

David: don't just remove gene products they need to be replaced.

There followed a very lengthy discussion regarding the issue of function grouping. Much of group wants to use synonyms (broader) to deal with these. For now put portmanteau terms into synonyms. Drive function to purely subsumption hierarchy. (Function grouping ontology).

Synonyms

Distinguishing between exact synonyms and inexact synonyms. Work is done, just need incremental improvements. John is on it so that DAG-Edit makes this easier.

Structure terms

We are keeping structure terms until we have properties. Values can come from anatomy or cellular component, or cell type. Wording is wrong, but we can live with it.

Disappearing GO ids

Michelle had this problem with DAG-Edit. Midori, special case of terms from Michael and shouldn't happen again. TAIR: Sporadically disappearing definitions. Michael: if term is not in ontology then definition is not saved. Need DAG-Edit to warn if there are definitions without terms. Another reason for going to database. Amelia: most problems apparently due to CVS rather than DAG-Edit.

Behaviour

Resolved: These are to remain as they are.

Viral component terms

Two action items were added to change extracellular definition and move terms.

Scope of Metabolism

What does 'part of' mean within the context of metabolism. The present definition is very broad and the question is should it include its own regulation. Currently it does. In general, this is an issue. Transport is not included as a 'part of' metabolism. Are regulation and transport equivalent (or analogous) concepts? On the other hand, is it more correctly called intermediate metabolism? Definition needs to be examined. Looking at a more sophisticated way to model, but in the meantime, regulation is an inherent part of process although strictly speaking the relationship is not the same PART OF as it is for the steps in a process. Because of this, we may need another relationship type for regulation. Midori will send some examples to Chris and BDGP for consideration. For now, transport will not be included in metabolism, but regulation will be.

Synonyms

Should gene products be included in synonyms? Yes, because people are going to be using these to look for them. Does this mean that gene products are permissible in term names then too? Yes, this is okay when the gene product is not the complete term, but indicates the substrate within the complete term. P53 is the common usage, but never is the name of a gene. Since the meaning is in the definition then the wording doesn't matter and it is okay to use the gene product as the string. However it is preferable to qualify this, that is, use something like 'p53-class' instead of just p53 in term names. However, if the gene product is used then it should be applicable across species and not restricted to a particular narrow group. Cyclin is another case, but it is more broadly used. We could possibly skirt the issue by using the string 'class' as a qualifier to gene product.

Transporters (aka ATP synthase terms)

Question was whether to create two separate terms for bi-directional reactions and then annotate to both terms.

Resolved: Policy is that we will create a single term (that describes both directions of a bidirectional reaction) unless you have reason to believe that there is a biological justification to separate the two directions of the reaction into separate functions.

Function Grouping Terms or Conglomerate functions

The examples used in this discussion were 'T cell receptor' and 'myosin'. There was a lot of discussion about whether or not it is appropriate to create function terms that describe the sum of the parts. That is, a term to represent the single unary function that is created through the contributions of all the different individual functions that make up a complex, *e.g.* The function of something like a T cell receptor or myosin may have. One of the advantages of representing the various activities of 'T cell receptor' with multiple parentage was elucidated by David that it is a way to help annotators, who

otherwise need to know that 'DNA helicase activity' includes ATPase activity, etc. Rex argued the other side, that this approach could lead to an unmanageable proliferation of terms to represent this sort of information.

Karen brought up the cautionary example of 'GTPase activator activity' which currently has two parentage lines one from 'enzyme regulator activity' which is fine, and a second line of descent from 'signal transducer activity', which is a problem because it makes 'receptor signaling protein activity' an ancestor of 'GTPase activator activity'. This is clearly wrong (there is a SourceForge entry already entered for this). 'GTPase activator activity' is an old term, so this may have come about because at the time the known GTPase(s) was/were all involved in receptor signaling.

The eventual thought seemed to settle on the idea that to create this sort of 'grouping term' in the function ontology opens up the potential for true path violations of the type illustrated by the 'GTPase activator activity' example.

It was suggested to have some sort of Function Of Gene product (FOG) Ontology to make the correlations between individual functions and a specific gene product or class of gene products. The Function ontology itself will become more like a hierarchy than a DAG. The relationships will not be 'ISA' but will be a flavor of 'PART OF" to indicate their contribution to the conglomerate function.

Web page

1. for credits have people use the sourceforge style link to logo, so we can count some of the usage statistics.
2. home page is: about, what's new, downloads, credits.
3. Link to AmiGO and a search box all in the left panel.
4. Jennifer suggested that we use the Sanger style links: site links across the top and page links down the left (plus the standard search tools) and no one objected or offered a counter-proposal. She will implement that web site demonstrated within the next few weeks. AI is to prototype the Sanger style page. (Comment added later by Jennifer: This action item was for me, as stated in the bottom of the final list of action items in the minutes.)

Next meeting

September 13-19: Working group on first implementation of properties in Bar Harbor (Chris, John, David…).

September 24-25: phenotype meeting will immediately precede GO meeting in Bar Harbor.

September 26-27: next GO meeting in Bar Harbor

January 16-17 at Stanford.

Decision is still to be made regarding user's meeting in September

Action Items

1. ALL: update gp2protein on central CVS site.

2. Suparna & Amelia: update metacyc mappings (and check that no functions are mapped to)
3. Amelia: change monthly report file names so they'll sort by date. DONE!
4. Amelia: cron job that mails announcement of each new monthly digest to go-friends
5. BDGP, JAX: first prototype to be implemented for properties prior to JAX meeting
6. BDGP (SwissProt?): need to provide a tool for tentative assignment of GO terms.
7. one row, one term, one reference, one evidence code. DONE!
8. (IEA) Midori: to assemble method references for IEAs
9. (IEA) BDGP to explore means of including larger number of associations in DB and AmiGO.
10. (IEA) BDGP to add filtering that is a combination of evidence code and reference.
11. (suspect annotations) Midori *et al.*: Add some things to documentation to describe procedure for error reporting, whether in terms or in associations.
12. (suspect annotations) GO-central to add links on main web site to report errors in annotation.
13. (suspect annotations) Brad to add button to AmiGO to mail error reports.
14. SUZI: write a tool to look at and report on consistency of annotation.
15. ALL: review annotation documentation and send in comments to GO-central (Midori to oversee).
16. BRAD: to add term based page. This would show all gene products and the other terms that had been used on each of those terms. A "other customers who used this term, also used these terms".
17. JOHN: Need DAG-Edit to warn if there are definitions without terms when saving so that the definitions are not lost.
18. GO central: for all part-of children in the function ontology, change the relationship to is-a and change wording to 'intrinsic regulator' or 'intrinsic catalyst'.
19. Jane: remove 'activity' from 'binding' terms; DONE!
20. Midori & Jane to dredge up what problems were at end of database save testing; send to John. DONE!
21. JOHN: Need DAG-Edit and central repository to work more seamlessly…DB or transparent CVS must be implemented.
22. GO-central improve documentation on synonyms
23. David organizing physiological process interest group
24. Physiological interest group is to report on progress next time
25. GO-central delete references to viruses in the definition of extracellular.
26. GO-central move viral component terms back into intracellular.
27. Midori to send examples of regulation to BDGP and Chris *et al.* to examine how to correctly indicate and model regulation.

28. Eurie: can now proceed to use gene products in terms with the addition of the suffix class and other situations will be handled in the same way.
29. GO-central: Update the documentation to reflect the decision on transporters
30. Amelia: Check on the terms in question and make sure they are consistent with the decision regarding transporters (and other bi-directional functions).
31. Michelle: Originally this AI was to send examples of messed up merges to GO-central for resolution. This was done. There are a few "sensu Eukarya" terms with secondary ids that did not have "sensu Eukarya" in them (Amelia generated a list of about 10). However, it turns out that it is ok that they are that way because, due to the placement of the old terms in the graph (as children of mitochondrial things for example), it is logically implied that they are Eukaryotic and therefore it is fine to make them secondary ids of Eukaryotic specific new terms. The problem for TIGR arose when those terms with mitochondrial parents were used to annotate some bacterial proteins (even though we knew about the path violations for bacteria) because at that point bacterial counterparts did not exist for those terms and they still wanted to capture the information. Therefore, the new Action Item is for TIGR to fix these annotations now that the bacterial counterpart terms are in GO. Thanks to Midori and Amelia for clarification of this.
32. transcription factor is wrong (mis-defined and mis-annotated). Interest group is going to fix this and report the solution.
33. All interest groups to provide short (one page more or less) reports for next meeting.
34. Jennifer: to provide a mock-up of the GO home page using Sanger style links.

Minutes by Suzanna Lewis and Karen Christie. Thanks to everyone who could found the time to review, comment and fill in the holes.