GO Ontology
Extensions

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GO bridging ontologies

- History:
  - Cross Product files
  - Taxon Constraints

- Maintained as obo format “bridging ontologies” outside main ontology
  - oboedit does not handle imports well
2012 Q1 proposal

• Bridging axioms will be OWL
  • automated conversion to obo
    • may not be complete for some axioms
  • continue to live outside editors obo ontology
• Use owl:imports to see the ‘big picture’
• Do this in svn
Varieties of bridging axiom

- **Equivalence**
  - Between two classes (rare):
    - go:cell EquivalentTo cl:cell
  - Between class and class expression involving class from other ontology
    - ‘ornithine biosynthesis’ EquivalentTo ‘biosynthetic process’ and ‘has output’ some chebi:ornithine

- **SubClass**
  - dendrite SubClassOf ‘part of’ some neuron
  - ‘catalytic activity’ SubClassOf bfo:process
  - lactation SubClassOf ‘in taxon’ some Mammalia

- **Other**
  - odontogenesis DisjointWith ‘in taxon’ some Aves
## Extensions

<table>
<thead>
<tr>
<th>ontology</th>
<th>replaces</th>
<th>importer</th>
<th>imports</th>
<th>is source?</th>
</tr>
</thead>
<tbody>
<tr>
<td>x-cell</td>
<td>biological process xp cell</td>
<td>x-cell-importer</td>
<td>cl</td>
<td>yes</td>
</tr>
<tr>
<td>x-signaling</td>
<td>biological process xp signaling</td>
<td>x-signaling-importer</td>
<td></td>
<td>yes</td>
</tr>
<tr>
<td>x-chemical</td>
<td>biological process xp chebi molecular function xp chebi</td>
<td>x-chemical-importer</td>
<td>chebi*</td>
<td>no</td>
</tr>
<tr>
<td>x-disjoint</td>
<td>NEW</td>
<td>x-disjoint-importer</td>
<td></td>
<td>yes</td>
</tr>
<tr>
<td>x-fungal-anatomy</td>
<td>biological process xp fungal anatomy</td>
<td>x-fungal-anatomy-importer</td>
<td>fao</td>
<td>yes</td>
</tr>
<tr>
<td>x-metazoan-anatomy</td>
<td>biological process xp uberon</td>
<td>x-metazoan-anatomy-importer</td>
<td>uberon</td>
<td>yes</td>
</tr>
<tr>
<td>x-plant-anatomy</td>
<td>biological process xp plant</td>
<td>x-plant-anatomy-importer</td>
<td>po</td>
<td>yes</td>
</tr>
<tr>
<td>x-taxon</td>
<td>taxon_go_triggers</td>
<td>x-taxon-importer</td>
<td>ncbitaxon (subset)</td>
<td>yes</td>
</tr>
<tr>
<td>x-protein</td>
<td>biological process xp protein molecular function xp protein</td>
<td>x-protein-importer</td>
<td>pr</td>
<td>yes</td>
</tr>
<tr>
<td>x-bfo</td>
<td>NEW</td>
<td>x-bfo-importer</td>
<td>bfo</td>
<td>yes</td>
</tr>
</tbody>
</table>
Ontology Extensions: Editors Guide

• Requirements:
  • Protege 4.1 or higher
  • SVN client (optional)

• Info:
(Optional) check out GO repo

```
cd
svn co svn+ssh://ext.geneontology.org/share/go/svn/trunk go-trunk
cd go-trunk/ontology/extensions
```

Your directory structure will look like this:

```
ontlogy/
  external/
    cell-ontology/
      ncbitaxon-slim/
      ...
  editors/
    gene_ontology_write.obo
  extensions/
    x-FOO.owl
    x-FOO-importer.owl
    ...
    catalog-v001.xml
```

these are brought in automatically from other svn repos

Type this

Open this in Protege
Ensure your edits go into the right ontology
example current imports closure

<owl:Ontology rdf:about="http://purl.obolibrary.org/obo/go/extensions/x-cell-importer.owl">
  <owl:imports rdf:resource="http://purl.obolibrary.org/obo/cl-basic.owl"/> 
  <owl:imports rdf:resource="http://purl.obolibrary.org/obo/go.owl"/> 
  <owl:imports rdf:resource="http://purl.obolibrary.org/obo/ro.owl"/> 
</owl:Ontology>
future imports closure

- go.{owl,obo}
  - imports
    - cl, chebi, pr, ... 
- go-basic.{owl,obo}
  - no imports
  - no advanced axioms

```xml
<owl:Ontology rdf:about="http://purl.obolibrary.org/obo/go/owl">
  <owl:imports rdf:resource="http://purl.obolibrary.org/obo/cl-basic.owl"/>
  <owl:imports rdf:resource="http://purl.obolibrary.org/obo/ro.owl"/>
  ...
</owl:Ontology>
```

"astrocyte differentiation" EquivalentTo 'cell differentiation' and 'results in acquisition of features of' some astrocyte
Some challenges

- bfo/ro
- taxon constraints
- chebi
- Options
  - auto-generate union ontology
  - auto-generate general axioms
taxon constraints

- Slim subset
- Auto-add general axioms
  - ‘in taxon’ some Eukaryote DisjointWith ‘in taxon’ some Eubacteria ...
- never_in_taxon
  - expand to ‘in taxon only not’
  - or use disjoint classes
    - odontogenesis DisjointWith ‘in taxon’ some Aves
- constraint IDs as axiom annotations (demo?)
starts and ends of processes

a has_part b
a has_part c
a starts_with c
a has_part d
a ends_with d
chebi

- Option 1:
  - Create ontology with new IDs
  - E.g. 'citrate and conjugates' EquivalentTo 'citric acid' or 'citrate(-1)' or 'citrate(-2)' or 'citrate(-3)'
- Option 2:
  - Auto-generated general axioms
    - 'biological process' and 'has input' some 'citric acid'
      EquivalentTo 'biological process' and 'has input' some 'citrate(-1)'
      EquivalentTo ...
    - ...

...
Modeling genes and gene associations in OWL

- An OWL ‘ontology’ is any collection of statements
  - mixing genes, gene associations, and the main ontology is all possible
- Many ways to do this
- Want to avoid statements like
  - ‘human erk1 protein’ SubClassOf ‘participates in’ some ‘cell proliferation’
Proof of concept example

- Oort now accepts GAFs as input
- Translates gene associations to OWL
- Uses reasoner to
  - detect taxon constraint violations
  - automatically ‘deepen’ cl6 annotations