Proposal:
Towards Apoptosis Ontology?

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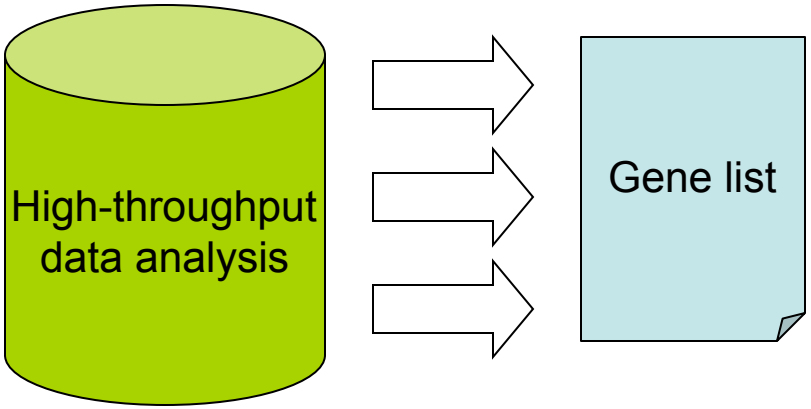
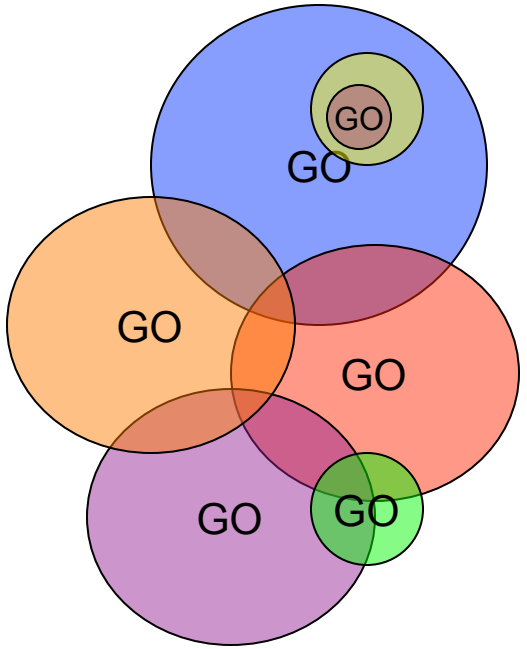
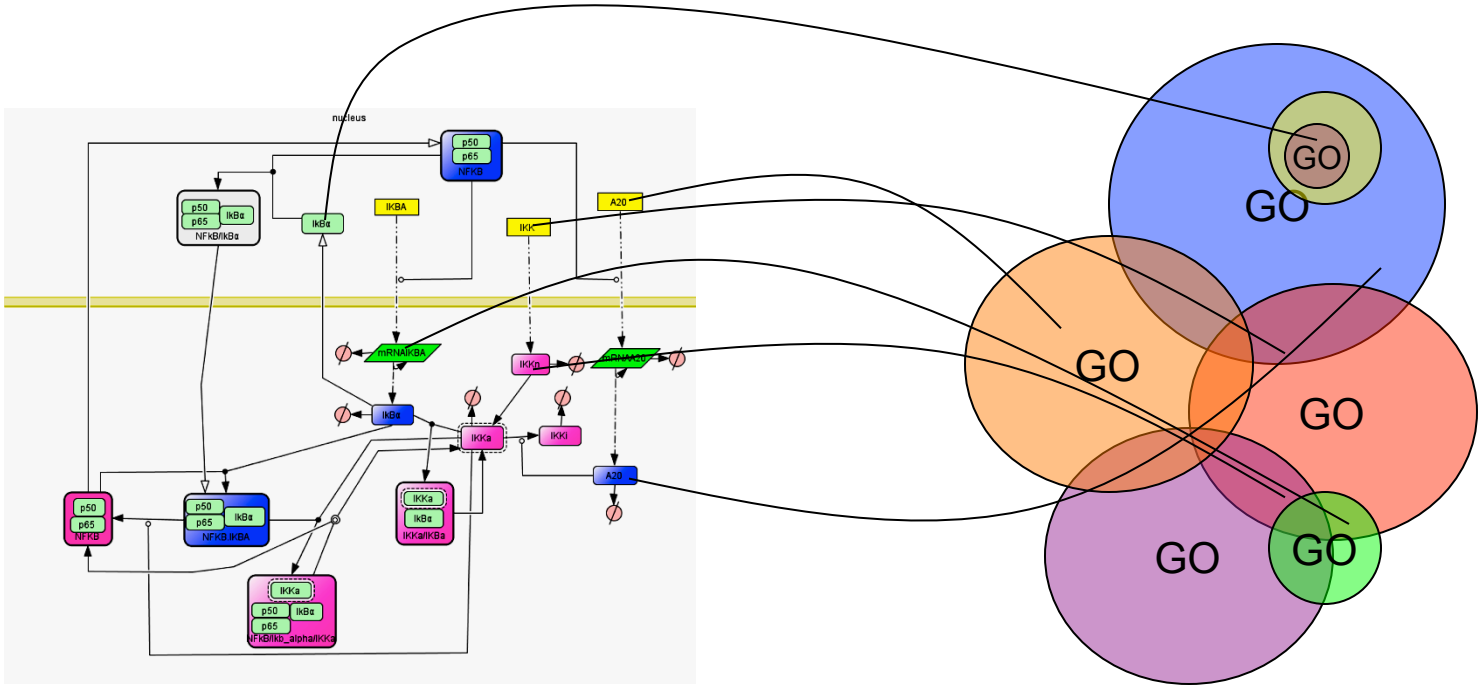
Functional annotation of high-throughput data





Gene Ontology:
Set of terms and their relations +
Association of individual genes to terms

Annotation of mathematical models



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- Gene Ontology resource is an important and most used bridge between the world of biology and the world of bioinformatics/ mathematical modeling

- Question: how adequate cell death modalities are represented in GO (needed for all data analysis in APO-SYS)?

Gene Ontology resource for cell death

- GO:0008219 : cell death [2802 gene products]
  - GO:0019835 : cytolysis [46 gene products]
  - GO:0070265 : necrotic cell death [12 gene products]
    - GO:0070266 : necroptosis [0 gene products]
    - GO:0060547 : negative regulation of necrotic cell death [0 gene products]
    - GO:0070267 : oncosis [2 gene products]
    - GO:0010940 : positive regulation of necrotic cell death [5 gene products]
    - GO:0010939 : regulation of necrotic cell death [5 gene products]
  - GO:0060548 : negative regulation of cell death [944 gene products]
  - GO:0010942 : positive regulation of cell death [950 gene products]
  - GO:0012501 : programmed cell death [2592 gene products]
  - GO:0010941 : regulation of cell death [1982 gene products]

FADD, FASL, TNF,
RIPK1, TMEM123

necroptosis

Term information ⬇ Term lineage ⬇ External references ⬇ 0 gene product associations ➡

Term Information

Accession	GO:0070266
Ontology	**biological process**
Synonyms	**exact**: programmed necrotic cell death
Definition	A necrotic cell death process that results from the activation of endogenous cellular processes, such as signaling involving death domain receptors and Toll-like receptors. [source: GOC:mah, PMID:18846107]
Comment	None
Subset	None
Community	There have been 0 comments for this term. If you would like to view or participate in the community annotation, please continue to the GONUTS page.

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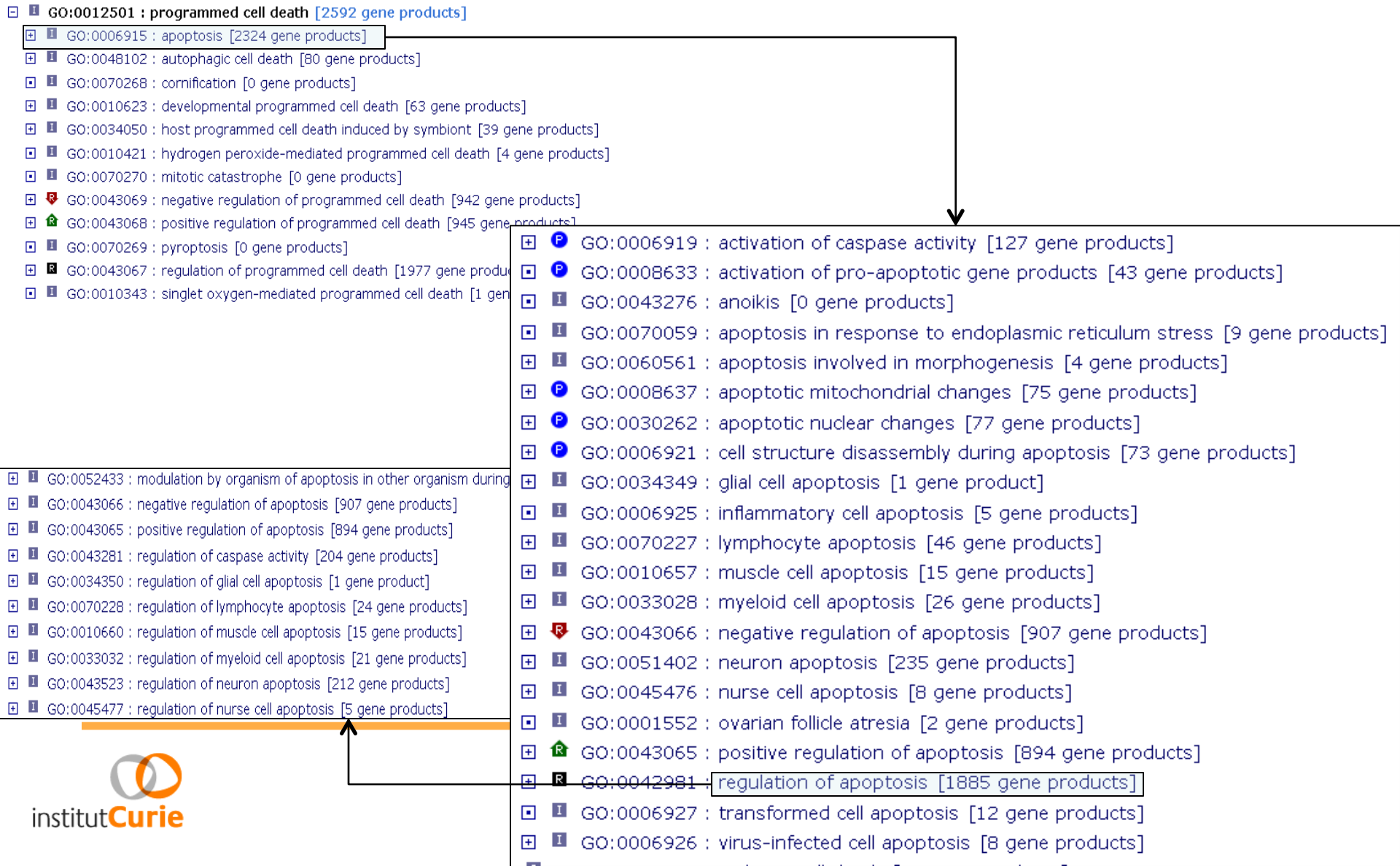
Gene Ontology resource for cell death



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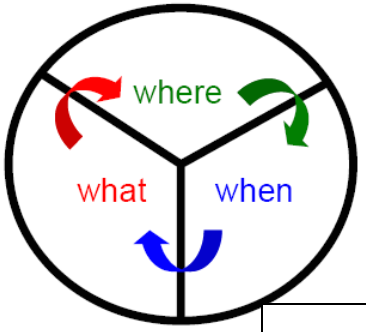
Gene Ontology resource

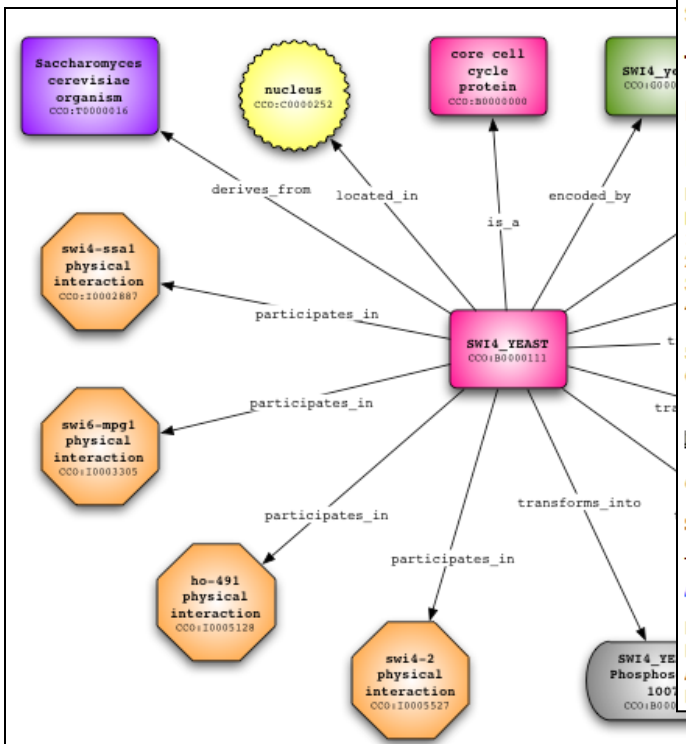
- Some limitations of GO:
  - Disease associated functions is out of the scope of GO
  - Molecular interactions are out of the scope of GO
  - Environment and expression are out of the scope of GO
  - GO only considers subsumption (is_a) and partonomic inclusion (part_of)

Cell Cycle Ontology (CCO)
(FP6 project DIAMONDS)
http://www.cellcycleontology.org

Sample: *"Cyclin B (what) is located in Cytoplasm (where) during Interphase (when)"*



- What is a X-type CDK?
- What is Y-type cyclin?
- In what events is CDK Z involved?
- In what events does Rb participate?
- Which CDKs are involved in the endoreduplication process?



Software

Highly accessed | Open Access

The Cell Cycle Ontology: an application ontology for the representation and integrated analysis of the cell cycle process

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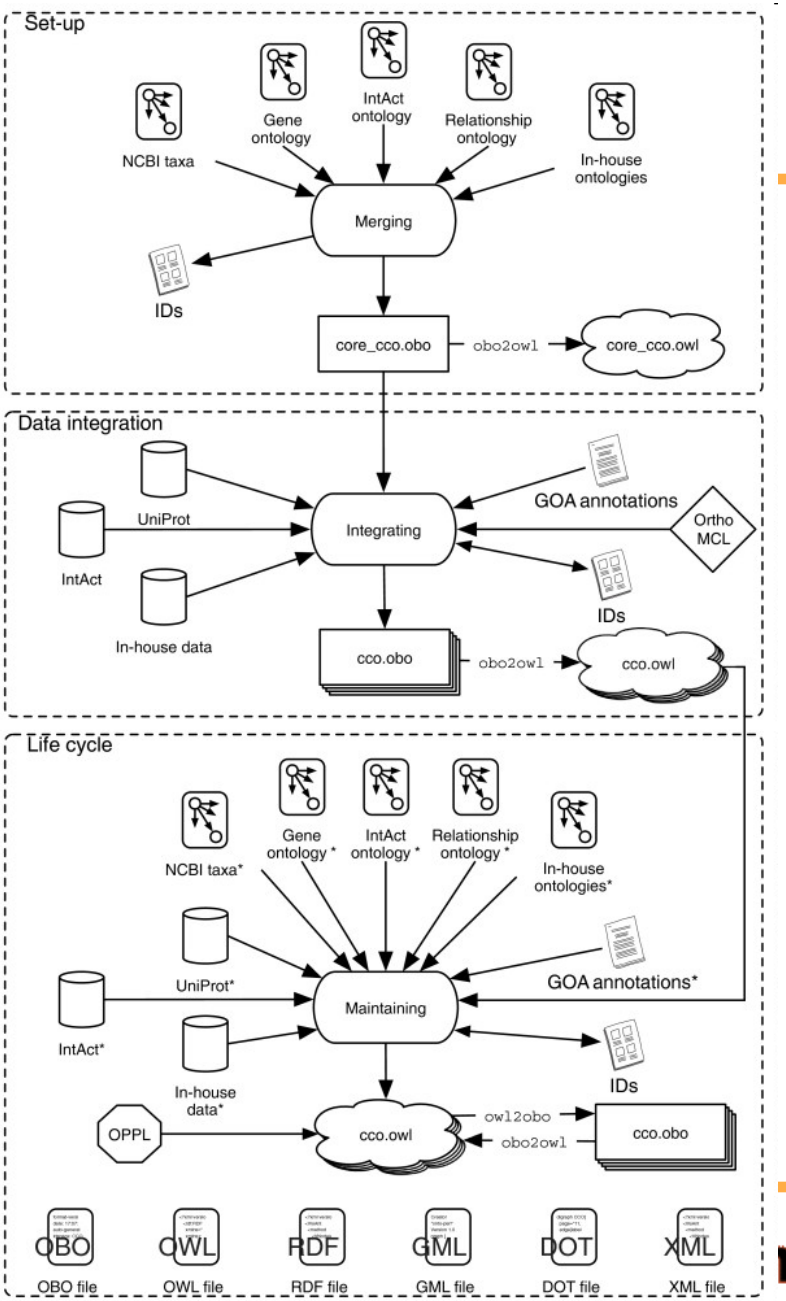

From Antezana et al., 2009

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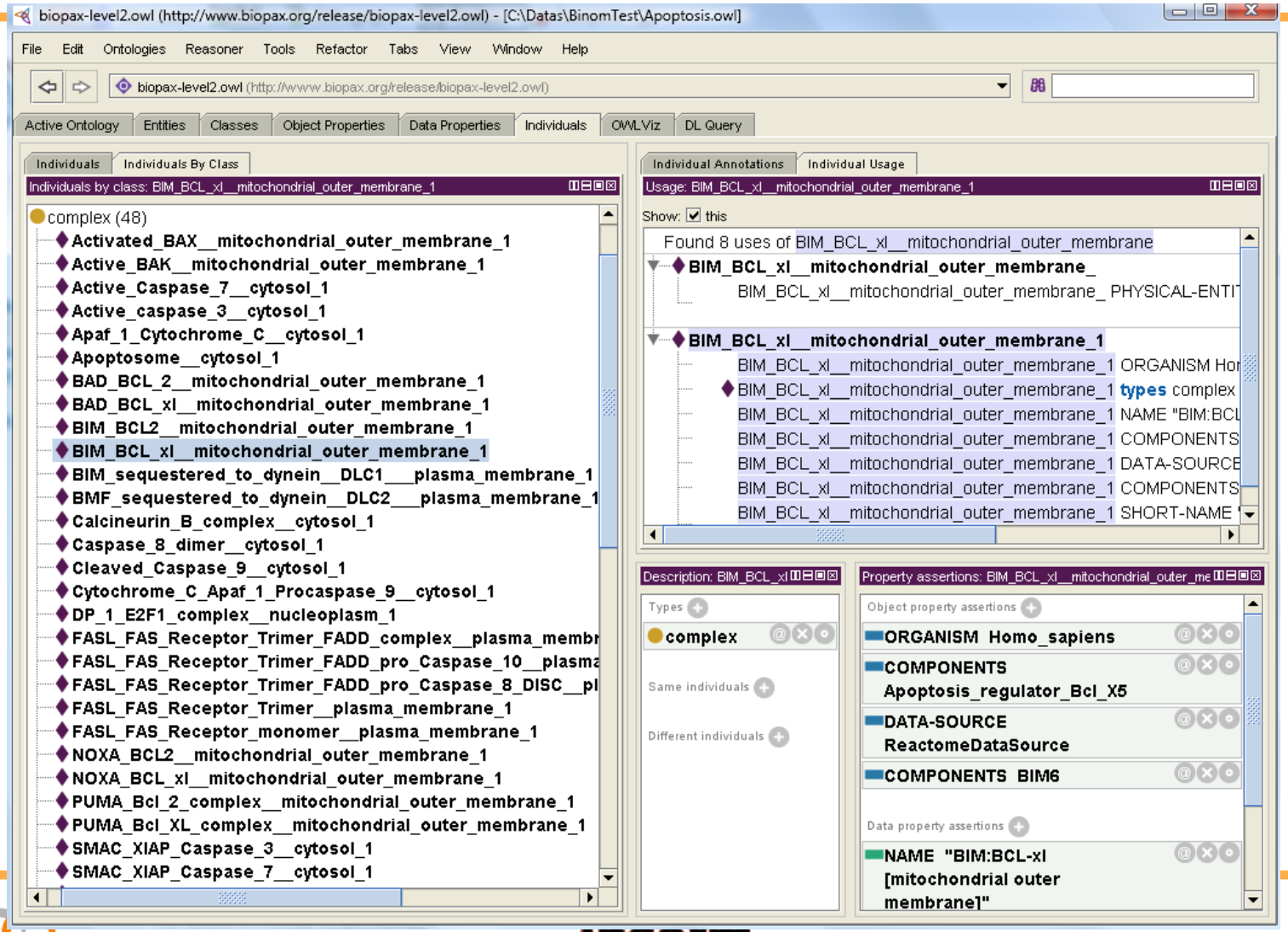
Protégé software



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Conclusion (questions)

- Improve Gene Ontology ‘cell death’ branch using expertise from APO-SYS project?
- Develop ‘APO-SYS approved’ Ontology for genes and processes easily exploitable?
- Cell Cycle Ontology project from FP6 as a template?
- Using APO-SYS Intranet site for flexible and rapid collaborative effort?