To Boldly GO...

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A Brief History Of GO

Past:

- Began in 1998 as a collaboration between FlyBase, the *Saccharomyces* Genome Database (SGD) and the Mouse Genome Database (MGD)
- About 3800 terms by 1999
- Ontology text files edited by hand (!)

A Brief History Of GO

Present:

- GO Consortium includes 20+ genome databases
- Used by many groups in academia and industry
- Nearly 18000 terms
- Four full time GO curators
- Many tools and software
- GO paradigm much imitated



- Web-based repository for open biological ontologies
- Five criteria:
 - Open; no licensing or fees
 - Use common shared syntax
 - Orthogonal to existing OBO ontologies
 - Unique identifiers / namespace
 - Definitions for terms



http://obo.sf.net/

 Use GO in combination with other vocabularies to create more complex concepts

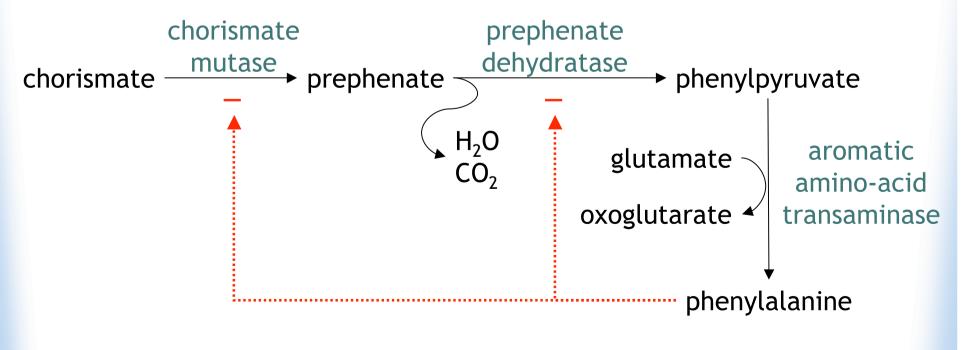
Extension and Integration of the Gene Ontology: Combining GO vocabularies with external vocabularies.

Hill DP, Blake JA, Richardson JE, Ringwald M. 2002. *Genome Res* **12:** 1982–1991

- GO has three ontologies
 - Biological process
 - Molecular function
 - Cellular component
- Extend by combining with terms from other vocabularies

 Narrative method: create terms manually as needed

phenylalanine biosynthesis



 Combinatorial approach: create all combinations of terms (preferably using a script!)

phenylalanine biosynthesis

- biological process ontology
 - metabolism, biosynthesis, catabolism, regulation
- biochemical ontology
 - chemicals involved in pathway

Demo

- Combinatorial method more thorough but may produce unwanted terms
- Can also lead to massive term proliferation
- Quality of terms (and definitions) depends on source ontologies
- May be better to create cross products as a separate ontology or during annotation

- Parsing of GO terms
- Work in progress; Chris Mungall, BDGP http://www.fruitfly.org/~cjm/obol-0.02/doc/obol-doc.html

Many GO term names have a regular structure:

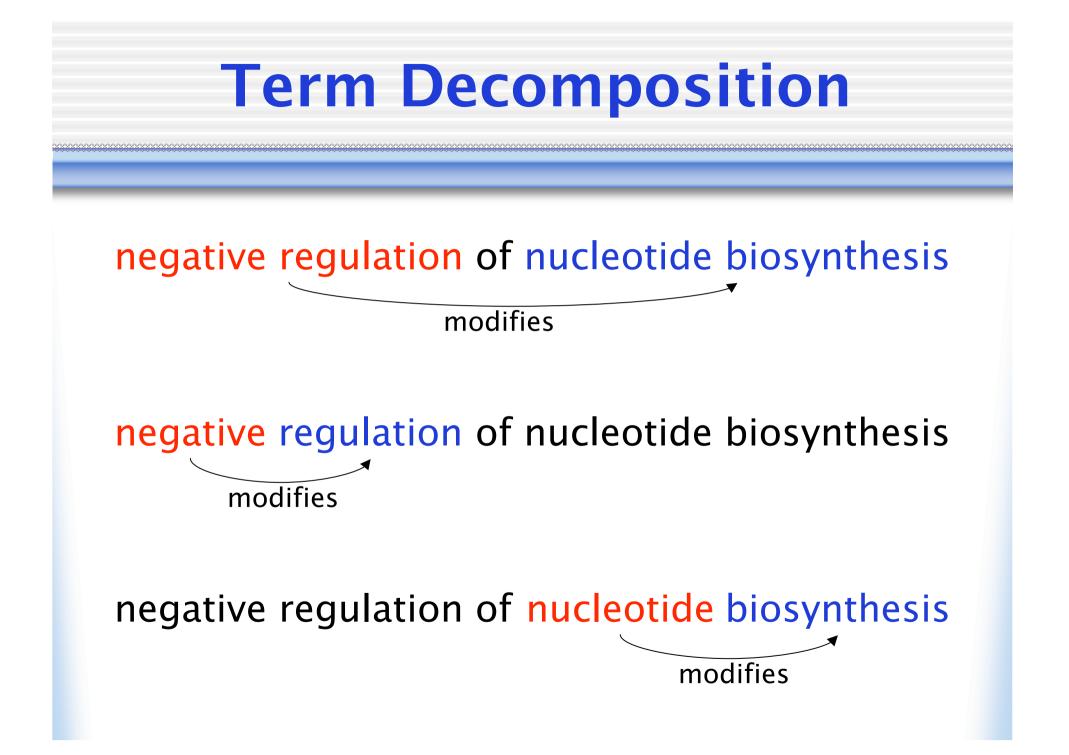
[compound] binding [anatomical part] morphogenesis regulation of [process]

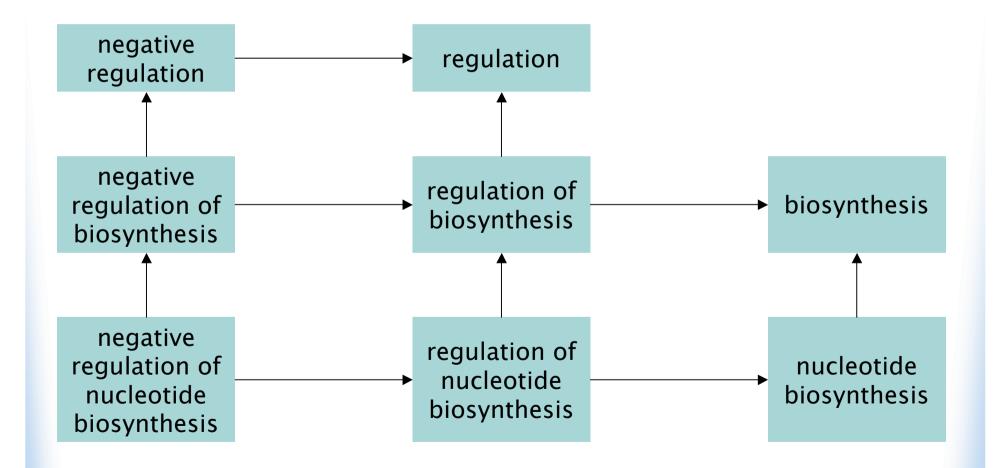
x biosynthesis from y

x biosynthesis, z pathway

 These GO term strings follow consistent implicit naming rules

- Formal grammar: a rule system for parsing (decomposing) and generating (composing) sequences of symbols
- Using an English language grammar, should be able to parse GO term strings into tokens and generate new GO term strings from these tokens
- Definite Clause Grammar used as it can be augmented with additional logical constraints; implemented in Prolog





- Over 40% of GO terms can be (at least partially) decomposed
- These can then be linked to terms from other OBO ontologies – anatomy, biochemistry, cell type, etc.
- Missing GO terms and relationships suggested
- Can also be used to suggest terms in other OBO ontologies

- Some standardization required
 cytosol vs *cytosolic*
- Terms with multiple parses require biological knowledge
 - smooth muscle contraction vs
 smooth muscle contraction
- Not all OBO ontologies complete
- No protein / protein complex ontology

Future GO

- Strip out specific instances to leave general concepts in GO
 - eg. metabolism, differentiation, development
- Develop a set of templates for creating composite terms from GO and other OBO ontologies for greater annotation accuracy and flexibility

Future GO

negative regulation of eye photoreceptor cell development

- negative regulation from universal modifier ontology
- eye from anatomy ontology
- photoreceptor cell from cell type ontology
- development from GO process ontology

For more information...

- GO
 - http://www.geneontology.org
- OBO
 - http://obo.sf.net
- Term decomposition / OBOL
 - <u>http://www.fruitfly.org/~cjm/obol-</u> 0.02/doc/obol-doc.html