Using SGD GO Slim Mapper and Interaction Data to Predict Gene Function

The Gene Ontology (GO) is structured in a hierarchy, such that granular terms ("perinuclear space") are connected and further down the hierarchy than their related broader terms ("nucleus"). However, for many purposes, such as reporting the upregulated cellular functions of a transcriptomics experiment, is very useful to focus on the broad, high-level part of the GO. For example, if you were interested in which of your upregulated genes are involved in DNA replication, it would be useful to map genes that have been annotated to specific terms (e.g. "synthesis of RNA primer involved in nuclear cell cycle DNA replication") to more general terms (e.g. "DNA replication").
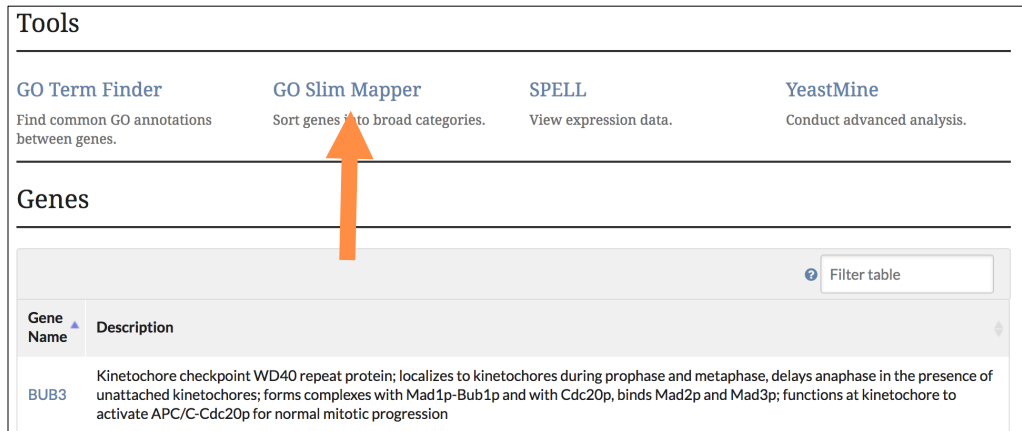
The **Gene Ontology (GO) Slim Mapper** at SGD maps granular GO annotations of a group of genes to more general terms and/or bins them into broad categories, i.e., "**GO Slim**" terms. Using GO Slim Mapper, predict what biological processes an uncharacterized gene may be involved in based on its genetic interactions.

- From the SGD home page (www.yeastgenome.org), go to the Locus Summary page for the uncharacterized gene **YLR287C.**

- Select **Genetic Interactions** tab. Here, we are interested in finding genes that have a genetic interaction with YLR287C, as the function of these genes may provide hints about the function of YLR287C.

- Search for "synthetic" in the **Genetic Interactions** table. This will filter the table for genes that, when knocked out in combination with YLR287C, elicit some sort of synthetic growth defect, haploinsufficiency, lethality, etc. These harsh phenotypes may suggest clues about related functions to YLR287C.
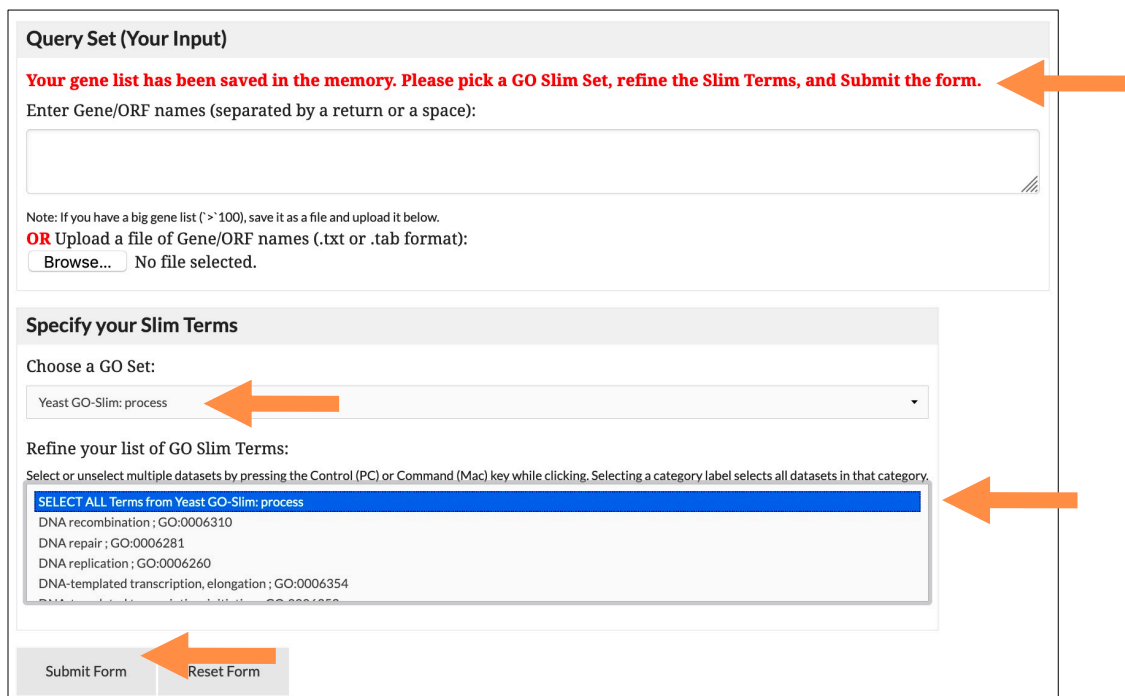

Interactor ▲	Allele	Assay	Annotation	Action	Phenotype	SGA score	P-value	Reference
BUB3		Synthetic Lethality	high-throughput	Hit	inviable Mutant Type: unspecified			Daniel JA, et al. (2006) PMID:16157669
ⓘ CCS1		Synthetic Growth Defect	high-throughput	Hit	vegetative growth: decreased Mutant Type: unspecified			Pan X, et al. (2006) PMID:16487579
ⓘ CSM3		Synthetic Growth Defect	high-throughput	Hit	vegetative growth: decreased Mutant Type: unspecified			Pan X, et al. (2006) PMID:16487579
ⓘ CTF4		Synthetic Growth Defect	high-throughput	Hit	vegetative growth: decreased Mutant Type: unspecified			Pan X, et al. (2006) PMID:16487579

- Find and click on the **Analyze** button at the bottom of the Annotation table. This will import the table you filtered to a page where you can send the genes to other SGD tools.

- On the next page that lists the YLR287C interactors, select **GO Slim Mapper**.

- The GO Slim Mapper has three steps (plus one optional step) in which you can specify your query. The Query Set (Your Input) box has been preloaded in memory with the list of genes you imported from the table.

- Choose a **GO Set** by selecting **Yeast GO-Slim: Process** from the pull-down.

- Highlight **SELECT ALL Terms from Yeast GO-Slim: Process.**

- Click the **Submit Form** button to use the default settings or go further down to customize your query.

- Results appear in a table with four columns:
  a. GO Slim terms picked by GO Slim Mapper
  b. Genes from your list that are annotated to that term, hyperlinked to their Locus Summary pages.
  c. GO Term Usage in Gene List (cluster frequency), the number and percentage of genes in your list annotated to each term.
  d. Genome frequency of use, the number and percentage of all genes in the genome annotated to each term.
- You can also download the results in a tab-delimited file.

Search Results

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GO Terms from the biological process Ontology			
GO Term (GO ID)	Genes Annotated to the GO Term	GO Term Usage in Gene List	Genome Frequency of Use
DNA replication (GO:0006260)	YMR048W, YNL273W, YOR080W, YPR135W	4 of 13 genes, 30.77%	140 of 6489 annotated genes, 2.16%
regulation of DNA metabolic process (GO:0051052)	YLR233C, YMR048W, YNL273W, YOR080W	4 of 13 genes, 30.77%	108 of 6489 annotated genes, 1.66%
mitotic cell cycle (GO:0000278)	YGL086W, YJL030W, YMR048W, YOR026W	4 of 13 genes, 30.77%	317 of 6489 annotated genes, 4.89%
protein modification by small protein conjugation or removal (GO:0070647)	YDR510W, YJL030W, YOR026W, YOR080W	4 of 13 genes, 30.77%	137 of 6489 annotated genes, 2.11%
regulation of cell cycle (GO:0051726)	YGL086W, YJL030W, YNL273W, YOR026W	4 of 13 genes, 30.77%	247 of 6489 annotated genes, 3.81%
chromosome segregation (GO:0007059)	YGL086W, YJL030W, YMR048W	3 of 13 genes, 23.08%	162 of 6489 annotated genes, 2.50%

- Based on the results, what biological processes might YLR287C be involved in?