**Genomic analysis lab notebook: Genomic analyses to defeat aging**

**Wednesday morning around 12.40 a.m., September 21st 2016**

**Searching for downloading all the GO terms:**

**I wrote the following keywords in Google: “downloading the names of all GO terms”. See** [**https://www.google.com/#q=downloading+the+names+of+all+GO+terms**](https://www.google.com/#q=downloading+the+names+of+all+GO+terms)**.**

**We need them to translate the GO terms from SGD into their names. Using all the GO terms allows us to analyze time series data from other species and compare results.**

**Need to find out where I downloaded the 294 yeast TF and safe URL**

**I went to:** [**http://geneontology.org/page/downloads**](http://geneontology.org/page/downloads)**.**

**How to read the files listed at the following URL?**

[**http://geneontology.org/page/download-ontology**](http://geneontology.org/page/download-ontology)

**The following URL tells how to get the GO term names for yeast:** [**http://geneontology.org/faq/how-do-i-get-term-names-my-list-go-ids**](http://geneontology.org/faq/how-do-i-get-term-names-my-list-go-ids)

**Source list:** [**http://yeastmine.yeastgenome.org/yeastmine/dataCategories.do**](http://yeastmine.yeastgenome.org/yeastmine/dataCategories.do)

**Query yeast mine with Perl:** [**http://yeastmine.yeastgenome.org/yeastmine/api.do**](http://yeastmine.yeastgenome.org/yeastmine/api.do)

**Downloading the GO database:** [**http://geneontology.org/page/go-database**](http://geneontology.org/page/go-database)

**GO databases:** [**http://geneontology.org/page/lead-database-schema-views**](http://geneontology.org/page/lead-database-schema-views)

**It seems that the files can be downloaded here:** [**http://geneontology.org/page/download-ontology**](http://geneontology.org/page/download-ontology)

**The GO slim terms are available at** [**http://geneontology.org/ontology/subsets/goslim\_yeast.obo**](http://geneontology.org/ontology/subsets/goslim_yeast.obo)

**All the GO terms are available here:** [**http://geneontology.org/ontology/go.obo**](http://geneontology.org/ontology/go.obo)

**GO files were downloaded from** [**http://geneontology.org/page/download-ontology**](http://geneontology.org/page/download-ontology)

**We can generate a list of those GO terms, which change with age.**

**Out of the file named GO\_complete.doc a GO term name lookup table can be generated because the rows of the same kind can be combined into columns but I don’t know exactly how to do this in R or Excel.**

**The genes, which belong to a particular GO term, can be determined by sorting the GO term column of the file Yeast\_GO\_terms.csv. R can do it but I need help to figure out how.**

**We can classify the pathways into those, in which all genes change together in the same direction, and those in which they don’t. Then we can look at other time series data, if there the pathways, BPs, MFs CCs and TF – target pairs behave similarly. Then we can also see how this was affected in our old dataset like Dr. Tang wants me to.**

**Are GO terms universal between all species so that we can compare time series data between species?**

**List of biological databases:** [**https://en.wikipedia.org/wiki/List\_of\_biological\_databases**](https://en.wikipedia.org/wiki/List_of_biological_databases)**. This list is important because we need to see, which kind of data is available to us to cue aging.**

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