Zebrafish Dataset Practical 3

These exercises can be done on any of the comparisons – it's up to you which you choose. Before you begin, copy the files you want from the Day 3 Practical folder on "penelopeprime" to your home directory.

Alternatively, you can download the files from:

https://funcgen2019.buschlab.org/downloads/practical3/inf_5dpf_hom_vs_sib.tsv
https://funcgen2019.buschlab.org/downloads/practical3/inf_5dpf_hom_vs_sib.sig.tsv

https://funcgen2019.buschlab.org/downloads/practical3/uninf_3dpf_hom_vs_sib.tsv
https://funcgen2019.buschlab.org/downloads/practical3/uninf_3dpf_hom_vs_sib.sig.tsv

https://funcgen2019.buschlab.org/downloads/practical3/uninf_5dpf_hom_vs_sib.tsv
https://funcgen2019.buschlab.org/downloads/practical3/uninf_5dpf_hom_vs_sib.sig.tsv

https://funcgen2019.buschlab.org/downloads/practical3/uninf_7dpf_hom_vs_sib.tsv
https://funcgen2019.buschlab.org/downloads/practical3/uninf_7dpf_hom_vs_sib.sig.tsv

For some of the tools you'll use, you'll need to reformat the data. For example, if you just need a list of all the Ensembl IDs in the experiment then you could do:

```
cut -f1 inf_5dpf_hom_vs_sib.tsv | grep ENSDARG > inf_5dpf_hom_vs_sib.ids.tsv
```

Or if you just need the significant Ensembl IDs then you could do:

```
cut -f1 inf_5dpf_hom_vs_sib.sig.tsv | grep ENSDARG > inf_5dpf_hom_vs_sib.sig.ids.tsv
```

You've been shown a number of tools today – PANTHER (and g:Profiler!), QuickGO, Reactome, Cytoscape, Ontologizer – and we'd like you to practise using them with our zebrafish dataset. For example, you've seen a demo of using PANTHER and g:Profiler with the 7 dpf uninfected comparison and now you should try using it with one of the other comparisons. Please try using all of the tools you've been introduced to today (although you'll probably have to carry on tomorrow to get through them all).