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!), 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.