Parse and Converting workshop

BLAST report

- Ecoli proteins
- S_enterica proteins
- Ecoli-vs-Senterica.BLASTP.tab.gz

Write script to read in the BLAST report. - Calculate for each alignment what the % aligned of the Ecoli query protein is? - Calculate the % of proteome that was aligned (out of the total number of Ecoli proteins)

 $\label{lem:parsing_blast_policy} Parsing BLAST\ https://github.com/biodataprog/GEN220_2019_examples/blob/master/Bioinformatics_2/parse_blast.py$

Orthofinder parsing

Here is a data file - OrthoFinder result

• Let's write a script which will summarize the data by Species.

The data look like ORTHOGROUP GENENAME_SP1, GENENAME2_SP1 GENENAME_SP2