Bash: A Command Language Interpreter, Part 2

Write a bash script that splits the `saccharomyces_cerevisiae.gff` file from the previous example into two files.

- One containing records for genes with verified open reading frames (ORFs).

- And another containing the rest of the genes.

All the information to do this is contained in `saccharomyces_cerevisiae.gff`, you only need to determine how to extract it.

Remember that the url for the file is https://downloads.yeastgenome.org/curation/chromosomal_feature/saccharomyces_cerevisiae.gff.

Recall that a GFF file contains both a table of features and FASTA formatted genome sequences. The description of the format is described at https://github.com/The-Sequence-Ontology/Specifications/blob/master/gff3.md.

Submitting

Feel free to discuss your answers with each other and ask for help. Google is also very helpful to understand what commands do.

When you are finished upload your annotated script to canvas. Remember to include the information/references of any resources you used to complete the assignment (apart from manual pages and help messages). This includes fellow students.