The bash script is needed to automate the 3'UTR Variant Prevalence.py, Common Genes.py, and Common Variants.py script for all the traits.

for file in \*.csv; do

[ -f "$file" ] || continue

The first part of the script allows the automation process of all .csv files to continue.

Following the first part, the next three parts automates each different python script.

for file1 in \*.csv; do

[ -f "$file1" ] || continue

python UTR3Comparison.py "$file" "$file1"

done

This allows the UTR3Comparison script to run all the traits.

Note: You need to change the name 3’UTR python script and python script name inside the bash script so that it matches.

for file1 in \*.csv; do

[ -f "$file1" ] || continue

python common\_variations.py "$file" "$file1"

done

This next part does the same thing as the previous part but with a different python script.

Note: You need to change the name common variants python script and python script name inside the bash script so that it matches.

for file1 in \*.txt; do

[ -f "$file1" ] || continue

python common\_genes.py "$file" "$file1"

Finally, the last part automates the python script for the common genes.

Note: You need to change the name common genes python script and python script name inside the bash script so that it matches.