**PIPELINE SCRIPT TO OBTAIN UNIQUE TARGET PRIMERS**

**STEP 1**

Download complete genomes from NCBI (fasta file)

**STEP 2**

Run pyANI script

Check phylogeny of genomes, discard ‘odd’ genomes

**STEP 3**

Run prokka script

Annotate gene content

Prokka

**STEP 5**

Run Roary script

Compare gene content

**STEP 6**

Analyze & produce list of interested genes

**STEP 8**

Blast genes to see if they target other species than those of interest

**STEP 7**

With list extract fasta files using the name of the genes

**STEP 13**

Extract Fasta files for each gene of interest and BLAST

**STEP 14**

Run faster2primer script to obtain desired primers