Task 4:
Resfinder:- Antibiotic Resistance Genes

Task 6: Summary

blast

Resfinder

ORFs

ORFs Resfinder Annotation
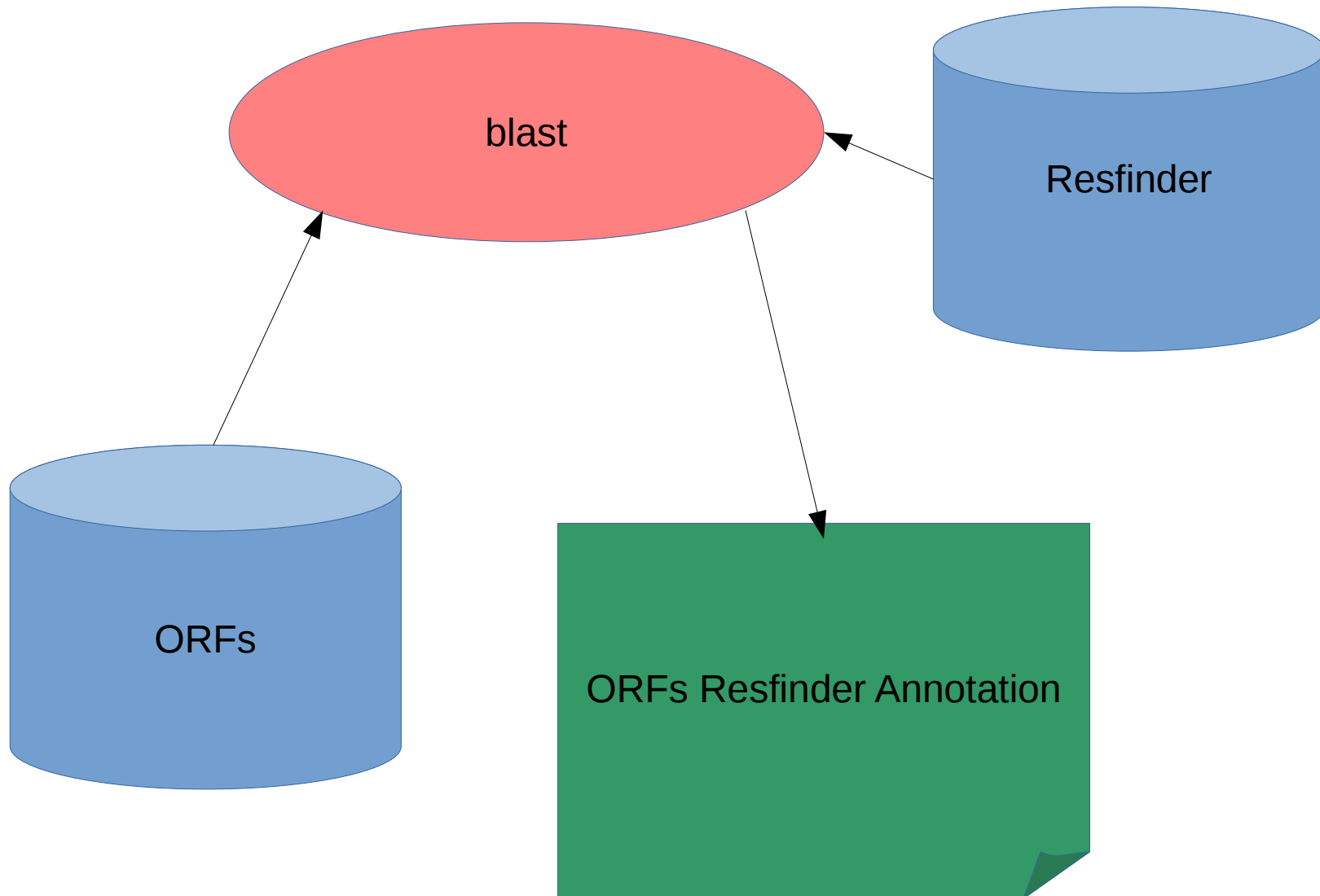
Task 4: Download Resfinder

to download the most updated version of resfinder

rm -rf ~/Databases/Resfinder

mkdir ~/Databases/Resfinder

cd ~/Databases/Resfinder

sudo yum install git

git clone https://bitbucket.org/genomicepidemiology/resfinder_db.git

cd resfinder_db

Task 4: Compile Fasta file

```
## make sure all files have a linux format

## todo that you need to install dos2unix

## sudo yum install dos2unix

ls *fsa | while read file; do dos2unix $file; done

## compile them all in one file.

ls *fsa |  ## show all fasta file

while read file; do  ## loop through them one by one.

cat $file |    ## print the whole file

awk -F"\t" '{print } END {print "\n"}';  ## add newline at the end of each file

done  > ../All.resfinder.fsa ## save all these files on the file ../All.resfinder.fsa
```

Task 4: compile gene.class file

to get map the Antibiotic resistance gene to a gene class

ls *fsa | while read file ; do ## loop through all fasta files

f=$(echo "$file" | cut -f1 -d.); ## get the class name from the file name.

extract gene names from the fasta file

grep ">" $file | # extract headers of the fasta files

sed 's/>//g' | awk -F"\t" -v class="$f" '{print $1"\t"class}'; done | ## pick the first to be gene name and map it to class name

awk -F"\t" 'BEGIN {print "Gene\tClass"} {print $1"\t"$2 }' > ../Resfinder.gene.class

to check if you have the right file format

two column

ARGGene   class

head ../Resfinder.gene.class

Task 4:
Compile blast

cd ..

mkdir blastNA

cd blastNA

~/Programs/ncbi-blast-2.6.0+/bin/makeblastdb -in ../All.resfinder.fsa -title RESFINDERNucl \

-out RESFINDERNucl -input_type fasta   -hash_index -dbtype nucl

How many sequences are there in Resfinder.

Task 4: Run Resfinder

cd ~/Data

mkdir Resfinder

cd Resfinder

nucleotide versus Resfinder nucleotide

blast orfs against the Resfinder nucleotide blastdb

time ~/Programs/ncbi-blast-2.6.0+/bin/blastn -query ../orfs.nucleotide.fa \

-db ~/Databases/Resfinder/blastNA/RESFINDERNucl -outfmt 6 \

-max_target_seqs 1 -evalue 1E-50 -word_size 6 -num_threads 1 -out
orf.resfinder.NA.versus.NA.tab

to see the result of the blast

cat orf.resfinder.NA.versus.NA.tab

Task 4: What antibiotic resistance genes maps to

##

join -t $'\t' -1 2 -2 1 <(sort -k2 orf.resfinder.NA.versus.NA.tab) \

<(sort ~/Databases/Resfinder/Resfinder.gene.class) >
orf.resfinder.NA.versus.NA.tab.geneClass

cat orf.resfinder.NA.versus.NA.tab.geneClass

how many gene classes are there?

how many betalactamases are there?