WGS Assembly

1. fastp -i read1.fq.gz -o 01\_fastp/fastp1.fq -I read2.fq.gz -O 01\_fastp/fastp2.fq -5 -3 -q 20 -c -j 01\_fastp/fastp.json -h 01\_fastp/fastp.html -R 01\_fastp/out.prefix -l 30 1>01fastp.result 2>r1.fastp.sh.err
2. SOAPnuke filter -1 ./01\_fastp/fastp1.fq -2 ./01\_fastp/fastp2.fq -d -C soap1.fq -D soap2.fq -o ./02\_soap -Q 2 2>r1.soap.sh.err
3. spades.py -k 21,45,63 --phred-offset 33 -m 48 -t 4 --careful -1 ./02\_soap/soap1.fq -2 02\_soap/soap2.fq -o ./03\_spades 2>r3.spades.sh.err
4. quast -o ./06\_quast ../03\_spades/scaffolds.fasta 2>r6.quast.sh.err

Antibiotic Resistance Analysis

1. resfinder.py -I XX.fasta -o ../Resfinder\_640/FS199 -p ../software/resfinder/database/resfinder\_db -b ../ncbi-blast-2.6.0+/bin/blastn -t 0.8 -l 0.6
2. rgi main -t contig -I XX.fasta -o XX –clean
3. cardwork20190425.py
4. resfinderwork20190425.py

Phylogenic Tree Based on 16s Data

1. perl ../rnammer -S bac -m ssu --f XX\_rRNA.fasta XX.fasta
2. muscle -in ./data/16s\_611.fasta -out ./alg\_16s.fasta -maxiters 4
3. trimal/source/trimal -in ./alg\_16s.fasta -out ./trim\_16s -mega -gt 0.9 -cons 60
4. Mega7

Phylogenic Tree Based on WGS SNPs

1. nasp --config example-config.xml
2. Mega7