


June 9, 2025

PHoeNix

Advanced Molecular Detection
Southeast Region Bioinformatics



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Updates

- Reminder - don't forget to register for the BTL AMD virtual training
 - Open to all Southeast regional epis, laboratorians, and bioinformaticians
 - No limit to registrants!
 - Fridays for 15 weeks starting July 11

What is PHoeNix?

Overview

- CDC developed Nextflow pipeline for analyzing bacterial genomes with a focus on AMR.

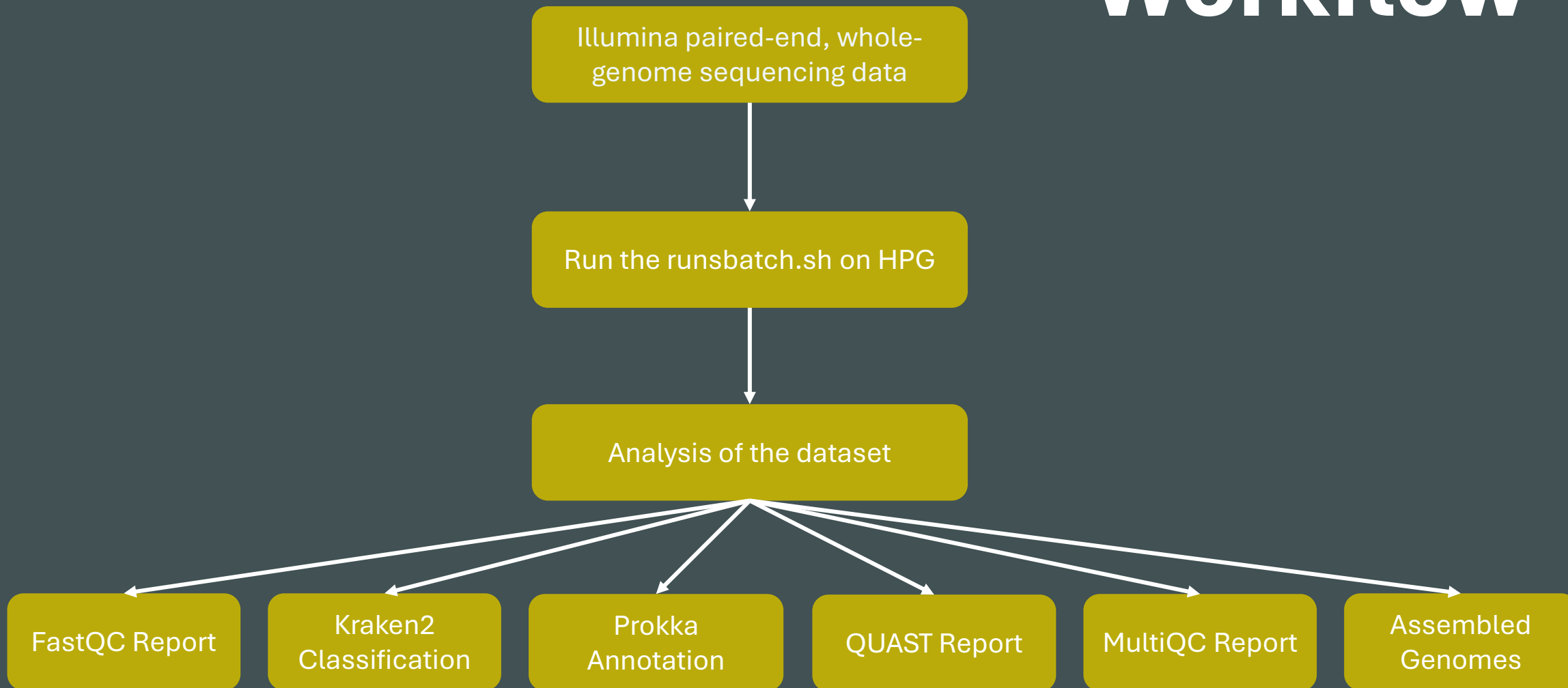
Usage

- Used by public health labs and researchers to analyze bacterial genomes, understand outbreaks, track pathogen evolution, and support studies on antimicrobial resistance and treatment response.

Dependencies

- FASTQC
- MultiQC
- Kraken2
- Nextflow
- Singularity

Workflow



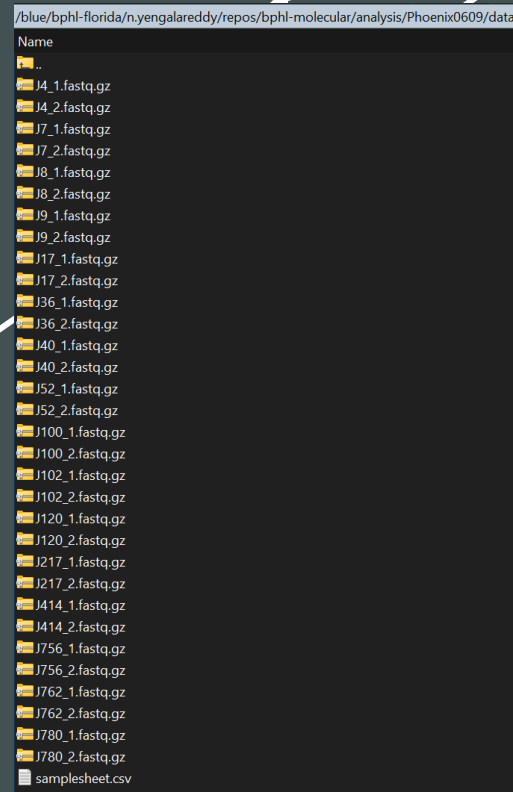
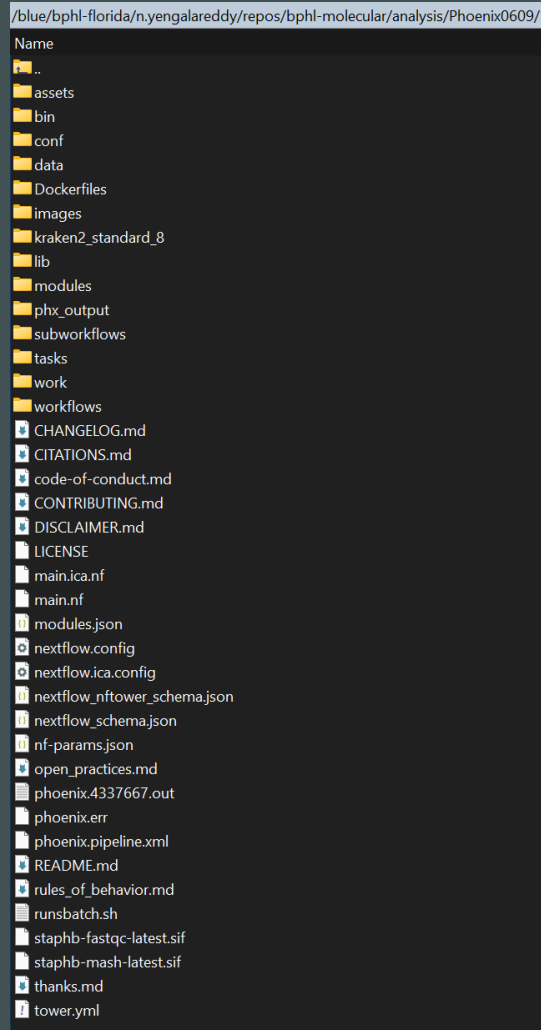
Application

Objective

Use an unknown dataset and analyze the dataset using PHoeNix pipeline

Application Cont.

```
cd /blue/bphl-<state>/<user>/repos/bphl-  
molecular/  
git clone https://github.com/CDCgov/phoenix  
mkdir analysis/  
cd analysis/  
cp /blue/bphl-<state>/<user>/repos/bphl-  
molecular/Phoenix/*  
Mkdir data/  
cp /path/to/data/*.fastq.gz data/
```



Application Cont.

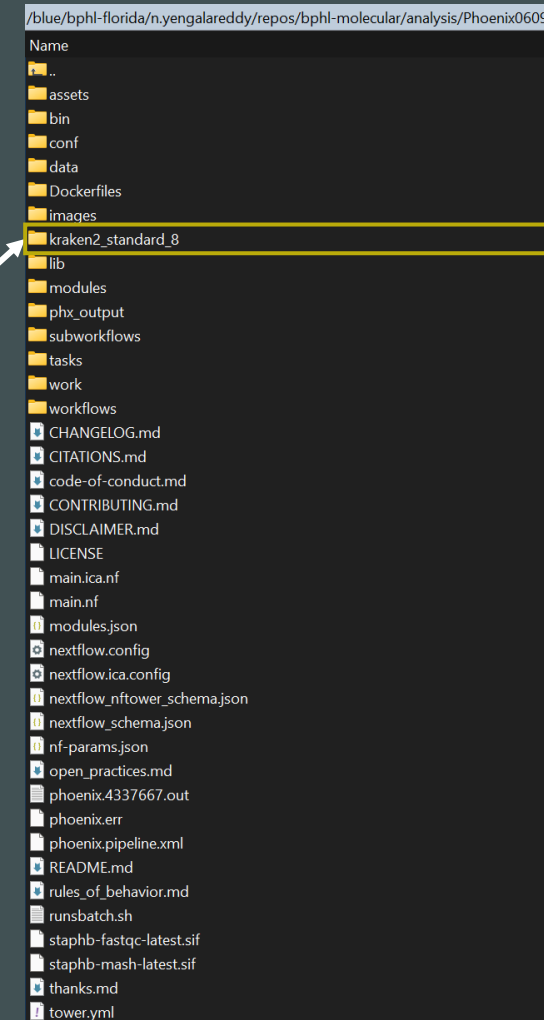
```
/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/Phoenix0609/data/  
Name  
..  
J4_1.fastq.gz  
J4_2.fastq.gz  
J7_1.fastq.gz  
J7_2.fastq.gz  
J8_1.fastq.gz  
J8_2.fastq.gz  
J9_1.fastq.gz  
J9_2.fastq.gz  
J17_1.fastq.gz  
J17_2.fastq.gz  
J36_1.fastq.gz  
J36_2.fastq.gz  
J40_1.fastq.gz  
J40_2.fastq.gz  
J52_1.fastq.gz  
J52_2.fastq.gz  
J100_1.fastq.gz  
J100_2.fastq.gz  
J102_1.fastq.gz  
J102_2.fastq.gz  
J120_1.fastq.gz  
J120_2.fastq.gz  
J217_1.fastq.gz  
J217_2.fastq.gz  
J414_1.fastq.gz  
J414_2.fastq.gz  
J756_1.fastq.gz  
J756_2.fastq.gz  
J762_1.fastq.gz  
J762_2.fastq.gz  
J780_1.fastq.gz  
J780_2.fastq.gz  
samplesheet.csv
```

sample,fastq_1,fastq_2

J4,/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/Phoenix0609/data/J4_1.fastq.gz,/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/Phoenix0609/data/J4_2.fastq.gz
J7,/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/Phoenix0609/data/J7_1.fastq.gz,/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/Phoenix0609/data/J7_2.fastq.gz
J8,/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/Phoenix0609/data/J8_1.fastq.gz,/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/Phoenix0609/data/J8_2.fastq.gz
J9,/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/Phoenix0609/data/J9_1.fastq.gz,/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/Phoenix0609/data/J9_2.fastq.gz
J17,/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/Phoenix0609/data/J17_1.fastq.gz,/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/Phoenix0609/data/J17_2.fastq.gz

Application Cont.

```
cd /blue/bphl-<state>/<user>/repos/bphl-  
molecular/Phoenix0609/*  
mkdir kraken2_standard_8/  
wget https://genome-  
idx.s3.amazonaws.com/kraken/k2_standard_  
08gb_20250402.tar.gz  
tar -xvzf k2_standard_08gb_20250402.tar.gz  
Delete k2_standard_08gb_20250402.tar.gz  
after  
Check for hash.k2d, opts.k2d, and taxo.k2d  
files
```

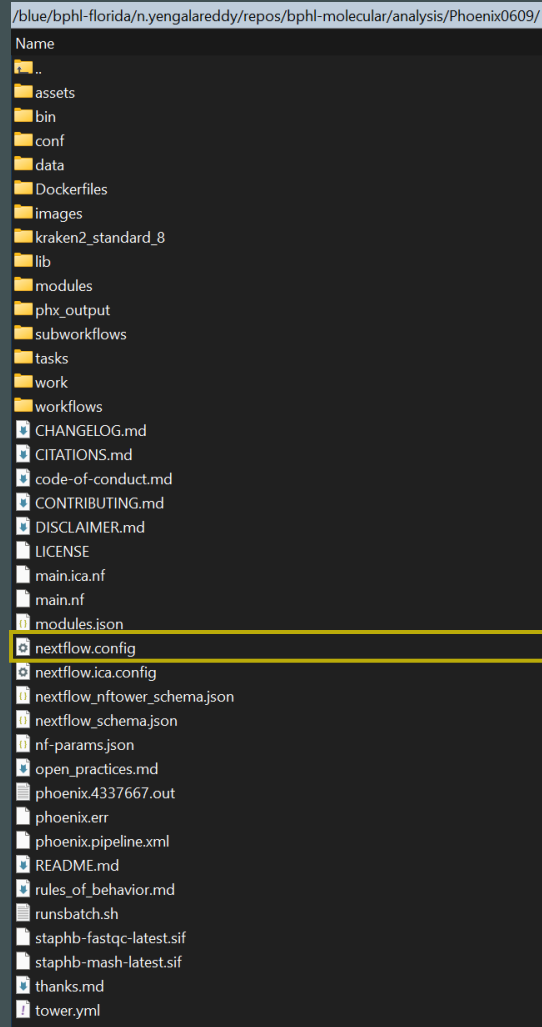


Application Cont.

`singularity pull staphb-mash-latest.sif`
`docker://staphb/mash:latest`

```
/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/Phoenix0609/  
Name  
..  
assets  
bin  
conf  
data  
Dockerfiles  
images  
kraken2_standard_8  
lib  
modules  
phx_output  
subworkflows  
tasks  
work  
workflows  
CHANGELOG.md  
CITATIONS.md  
code-of-conduct.md  
CONTRIBUTING.md  
DISCLAIMER.md  
LICENSE  
main.ica.nf  
main.nf  
modules.json  
nextflow.config  
nextflow.ica.config  
nextflow_nftower_schema.json  
nextflow_schema.json  
nf-params.json  
open_practices.md  
phoenix.4337667.out  
phoenix.err  
phoenix.pipeline.xml  
README.md  
rules_of_behavior.md  
runsbatch.sh  
staphb-fastqc-latest.sif  
staphb-mash-latest.sif  
thanks.md  
tower.yml
```

Application Cont.



```
// Max resource options
// Defaults only, expecting to be overwritten
max_memory      = '128.GB'
max_cpus        = 16
max_time        = '240.h'

}

process {
  // Add this block to customize Kraken2 resource usage
  withName: KRAKEN2_TRIMD {
    cpus = 4
    memory = check_max(128.GB, 'memory')
    maxForks = 1

    ext {
      args = '--use-names'
    }

    publishDir = [
      path: { "${params.outdir}/${meta.id}/kraken2_trimd" },
      mode: 'copy',
      pattern: '**{classifiedreads.txt,summary.txt}'
    ]
  }

  withName: MASH_DIST {
    container = "${baseDir}/staphb-mash-latest.sif"
  }

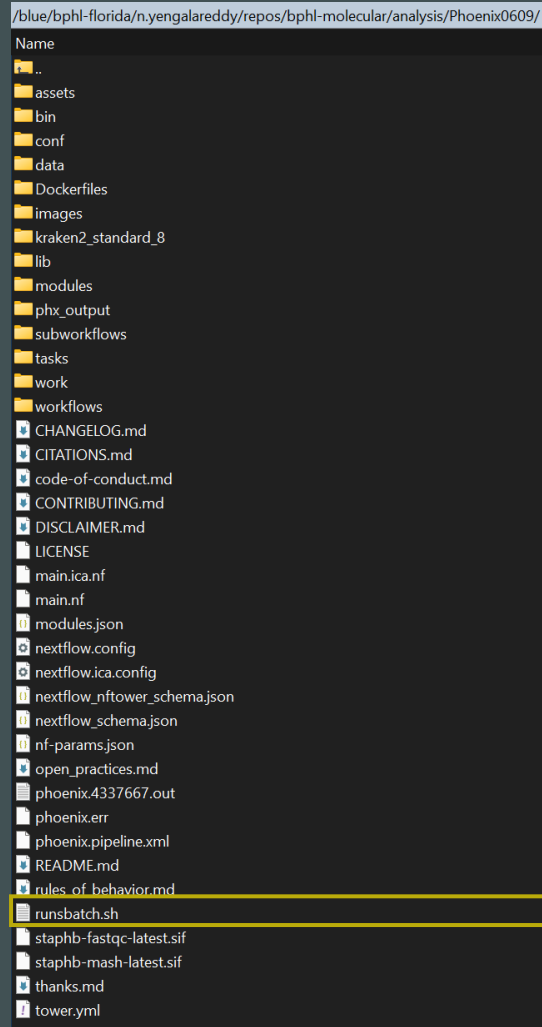
  withName: FASTQCTRIMD {
    container = "${baseDir}/staphb-fastqc-latest.sif"
  }

  shell = ['/bin/bash', '-euo', 'pipefail']
}

// Load base.config by default for all pipelines
includeConfig 'conf/base.config'
includeConfig 'conf/modules.config'

// Load nf-core custom profiles from different Institutions
try {
  includeConfig "${params.custom_config_base}/nfcore_custom.config"
} catch (Exception e) {
  System.err.println("WARNING: Could not load nf-core/config profiles: ${params.custom_config_base}/nfcore_custom.config")
}
```

Application Cont.



```
#!/bin/bash

#SBATCH --account=bph1-umbrella
#SBATCH --qos=bph1-umbrella
#SBATCH --job-name=Phoenix
#SBATCH --ntasks=1
#SBATCH --cpus-per-task=10
#SBATCH --mem=256gb
#SBATCH --time=48:00:00
#SBATCH --output=phoenix.%j.out
#SBATCH --error=phoenix.err
#SBATCH --mail-user=nikhil.yengala@flhealth.gov
#SBATCH --mail-type=FAIL,END

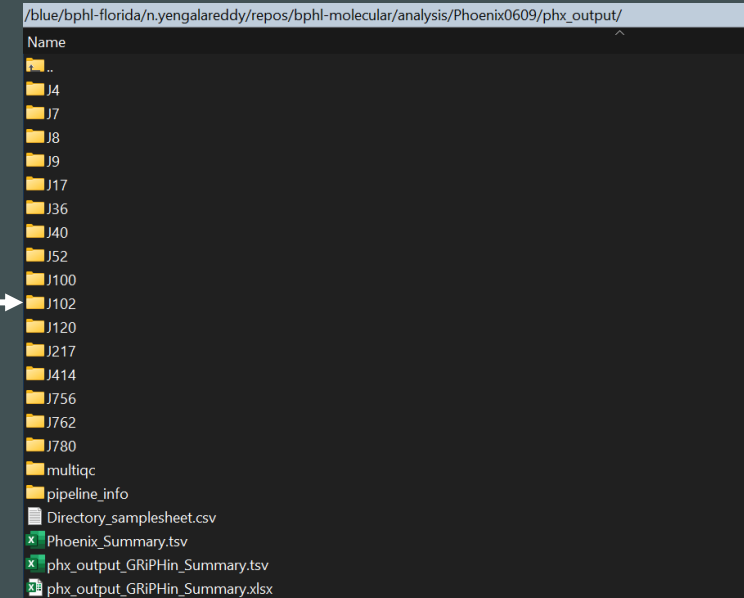
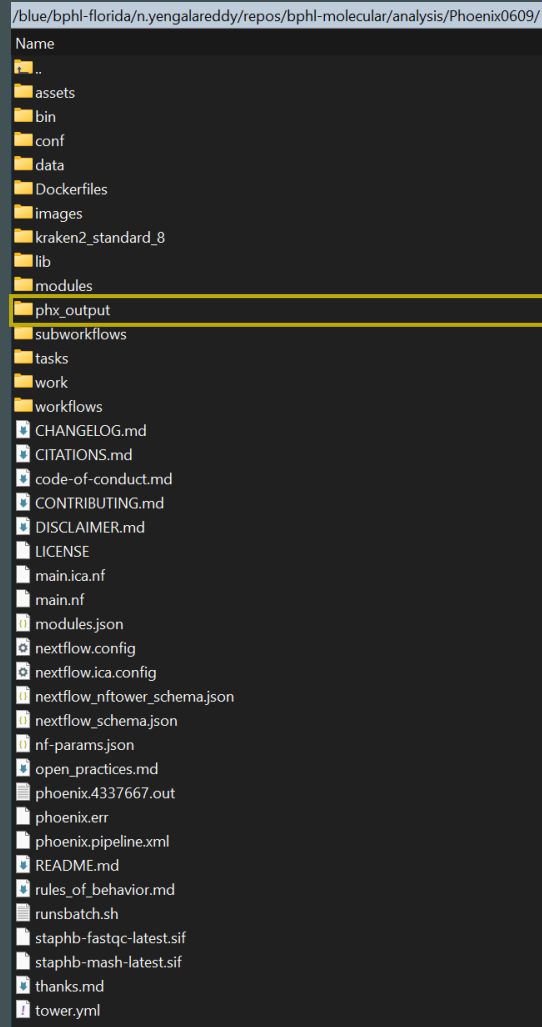
module load singularity

export SINGULARITY_BINDPATH="/blue/bph1-florida/n.yengalareddy/repos/bph1-molecular/analysis/Phoenix0609/work"
export NXF_SINGULARITY_CACHEDIR="/blue/bph1-florida/n.yengalareddy/repos/bph1-molecular/analysis/Phoenix0609/work/singularity"

#Paths
SAMPLESHEET="/blue/bph1-florida/n.yengalareddy/repos/bph1-molecular/analysis/Phoenix0609/data/samplesheet.csv"
KRAKEN_DB="/blue/bph1-florida/n.yengalareddy/repos/bph1-molecular/analysis/Phoenix0609/kraken2_standard_8/"

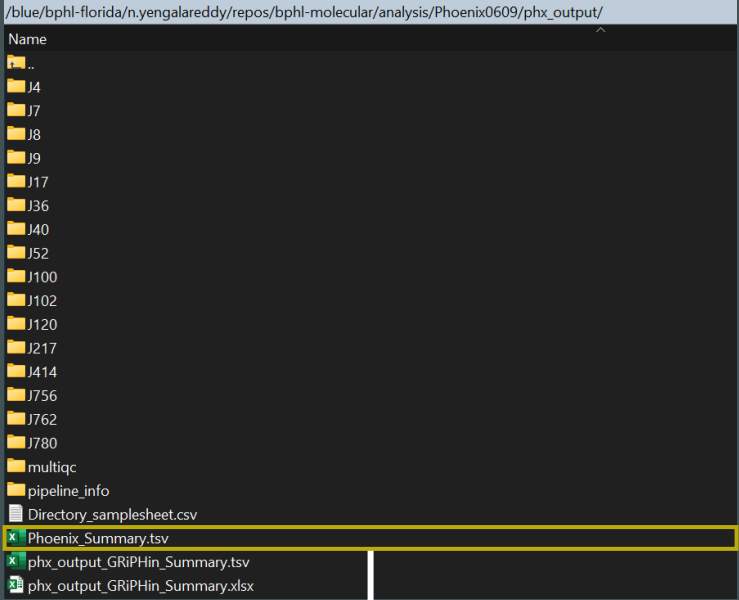
#Run
nextflow run main.nf -profile singularity \
  -entry PHOENIX \
  --input "$SAMPLESHEET" \
  --kraken2db "$KRAKEN_DB" \
```

Application Cont.



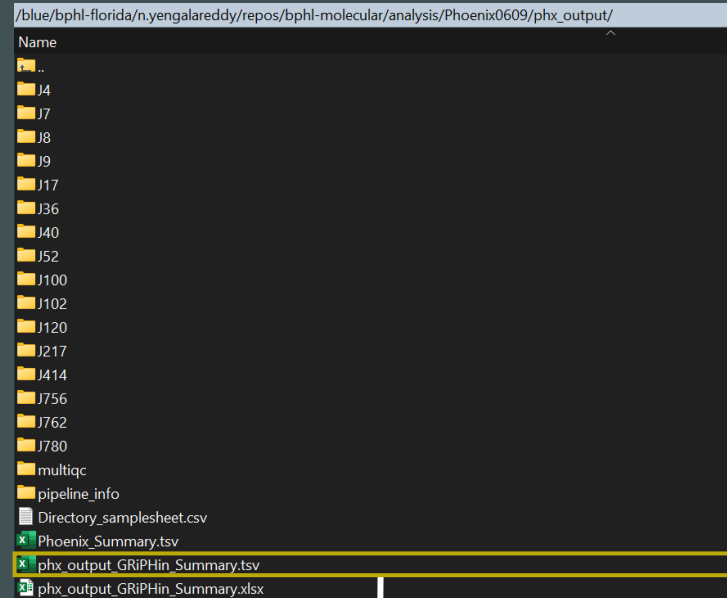


Application Cont.



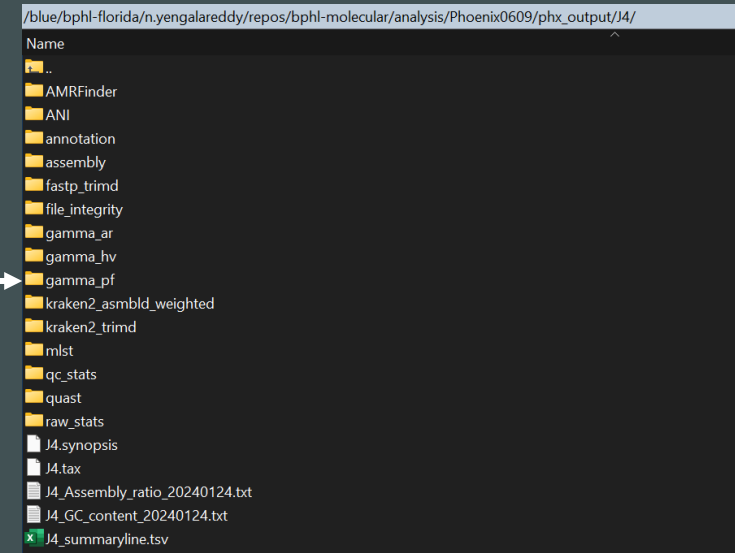
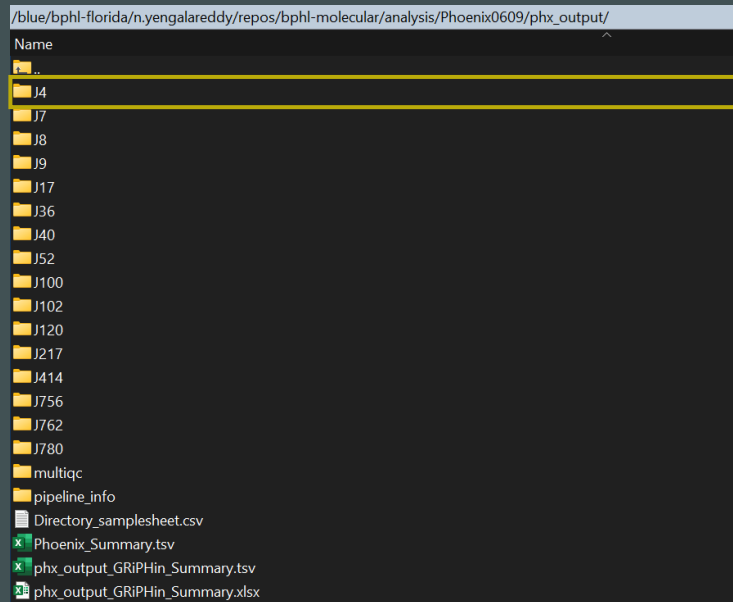
ID	Auto_QC_Outcome	Warning_Count	Estimated_Coverage	Genome_Length	Assembly_Ratio_(STDev)	#_of_Scaffolds_>500bp	GC_%	Species	Taxa_Confidence	Taxa_Coverage	Taxa_Source	Kraken2_Trimd	Kraken2_Weighted	MLST_Scheme_1	MLST_1	MLST_Scheme_2	MLST_2	GAMMA_Beta_Lactam_Resistance_Genes
J4	PASS	1	130.2	5263379	1.0308 (.4432)	179	50.8	Escherichia coli	99.89 ANI_match	96.96 ANI_REFSEQ	Escherichia(14.22%) coli(13.08%)	Unknown	ecoli(Achtman)	ST10	ecoli_2(Pasteur)	Novel_allele	AmpC1_Ecoli_FN649414, Penicillin_Binding_Protein_Ecoli_CP002291, ampH_Ecoli_AP012030, blaEC_U00096.3	
J7	PASS	2	80.52	5328404	1.0435 (.6263)	246	50.5	Escherichia coli	99.95 ANI_match	98.98 ANI_REFSEQ	Escherichia(16.87%) coli(13.30%)	Unknown	ecoli(Achtman)	ST21	ecoli_2(Pasteur)	ST481	AmpC1_Ecoli_FN649414, Penicillin_Binding_Protein_Ecoli_CP002291, ampH_Ecoli_AP012030, blaEC-18_NG_04	
J8	PASS	2	100.4	5505983	1.0783 (1.1266)	294	50.3	Escherichia coli	99.66 ANI_match	96.31 ANI_REFSEQ	Escherichia(17.96%) coli(12.65%)	Unknown	ecoli(Achtman)	ST29	ecoli_2(Pasteur)	ST481	AmpC1_Ecoli_FN649414, Penicillin_Binding_Protein_Ecoli_CP002291, ampH_Ecoli_AP012030, blaEC-18_NG_04	
J9	PASS	1	109.1	4684746	0.9175 (1.1868)	57	50.7	Escherichia coli	99.46 ANI_match	96.09 ANI_REFSEQ	Escherichia(7.71%) coli(6.54%)	Unknown	ecoli(Achtman)	ST1248	ecoli_2(Pasteur)	Novel_allele	AmpC1_Ecoli_FN649414, Penicillin_Binding_Protein_Ecoli_CP002291, ampH_Ecoli_AP012030, blaEC-18_NG_04	
J17	PASS	2	89.77	5350037	1.0478 (.6873)	267	50.5	Escherichia coli	99.86 ANI_match	99.16 ANI_REFSEQ	Escherichia(15.96%) coli(11.37%)	Unknown	ecoli(Achtman)	ST17	ecoli_2(Pasteur)	Novel_allele	AmpC1_Ecoli_FN649414, Penicillin_Binding_Protein_Ecoli_CP002291, ampH_Ecoli_AP012030, blaEC-18_NG_04	
J36	PASS	0	86.57	5427905	0.9678 (.6836)	51	57.5	Klebsiella pneumoniae	99.93 ANI_match	95.57 ANI_REFSEQ	Klebsiella(85.17%) pneumoniae(3.08%)	Unknown	kpneumoniae	ST11	-	-	ampH_CP003785, blaCTX-M-27_NG_048976.1, blaKPC-3_NG_049257.1, blaSHV-11_HM751098, blaTEM-1A_1_H	
J40	PASS	0	60.2	4872278	0.9778 (.4291)	70	55.1	Enterobacter hormaechei	99.83 ANI_match	96.17 ANI_REFSEQ	Enterobacter(84.33%) hormaechei(19.17%)	Unknown	eclocae	ST102	-	-	blaACT-47_NG_050710.1, blaKPC-3_NG_049257.1, blaSHV-7_NG_050104.1	
J52	PASS	2	119.7	5051000	0.9892 (.1550)	137	50.5	Escherichia coli	99.60 ANI_match	89.31 ANI_REFSEQ	Escherichia(10.20%) coli(8.59%)	Unknown	ecoli(Achtman)	ST10	ecoli_2(Pasteur)	ST367	AmpC1_Ecoli_FN649414, Penicillin_Binding_Protein_Ecoli_CP002291, ampH_Ecoli_AP012030, blaEC_U00096.3	
J100	PASS	1	87.21	4882908	0.9563 (.6285)	99	50.6	Escherichia coli	99.98 ANI_match	97.98 ANI_REFSEQ	Escherichia(11.17%) coli(9.41%)	Unknown	ecoli(Achtman)	ST410	ecoli_2(Pasteur)	Novel_allele	AmpC1_Ecoli_FN649414, Penicillin_Binding_Protein_Ecoli_CP002291, ampH_Ecoli_AP012030, blaCMY-2_NG_04	
J102	PASS	0	69.61	5752511	1.0257 (.5467)	67	56.8	Klebsiella pneumoniae	99.95 ANI_match	93.26 ANI_REFSEQ	Klebsiella(80.79%) pneumoniae(13.06%)	Unknown	kpneumoniae	ST307	-	-	ampH_CP003785, blaCTX-M-15_NG_048935.1, blaKPC-2_NG_049253.1, blaOXA-1_NG_049392.1, blaOXA-1-like	
J120	PASS	1	54.22	7316659	1.1005 (1.5743)	128	65.4	Pseudomonas aeruginosa	99.93 ANI_match	92.23 ANI_REFSEQ	Pseudomonas(93.43%) aeruginosa(21.96%)	Unknown	paeruginosa	ST244	-	-	blaOXA-675_NG_062270.1, blaOXA-1-like, blaOXA-847_NG_066520.1, blaOXA-50-like, blaPAO_1_AY083595, bla	
J217	PASS	0	93.49	3873477	0.9715 (.4391)	65	39	Acinetobacter baumannii	99.87 ANI_match	96.66 ANI_REFSEQ	Acinetobacter(95.11%) baumannii(4.81%)	Unknown	abaumannii(Oxford)	STNovel_profile-PARALOG, ST417	abaumannii(Pasteur)	ST2	Mbl_NC_010410, Zn-dependent_hydrolase_NC_010410, blaADC-143_NG_064698.1, blaOXA-202_NG_049500.1	
J414	PASS	1	108.2	5411032	1.0597 (.8591)	215	50.3	Escherichia coli	99.97 ANI_match	99.85 ANI_REFSEQ	Escherichia(33.70%) coli(29.16%)	Unknown	ecoli(Achtman)	ST11	ecoli_2(Pasteur)	ST628	AmpC1_Ecoli_FN649414, Penicillin_Binding_Protein_Ecoli_CP002291, ampH_Ecoli_AP012030, blaEC-15_NG_04	

Application Cont.



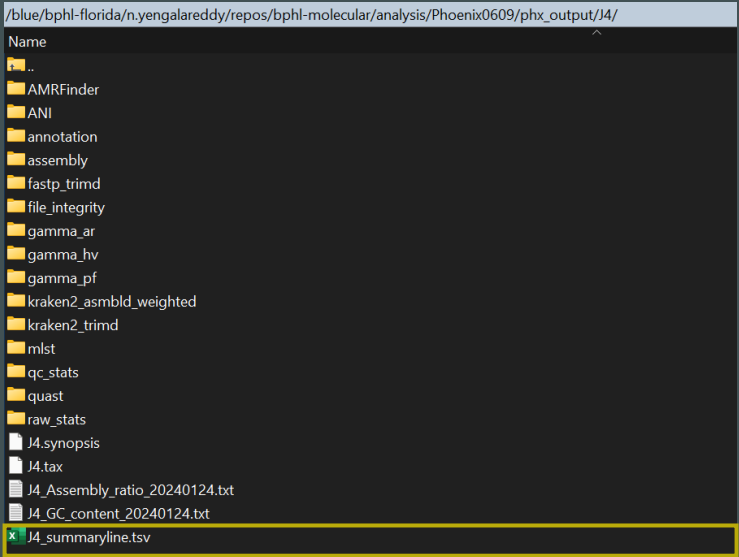
WGS_ID	Parent_Folder	Data_Location	Minimum_QC	Minimum_QC	Warnings	Alerts	Raw_Q30_R1	Raw_Q30_R2	Total_Raw	Reads_Paired	Trimmed_Total	Trimmed_Estimated	Trim_GC(%)	Scaffolds	Assembly_Len	Assembly_Ratio	Assembly_SiCh	Taxa_Source	Kraken_ID	Raw_Kraken_ID	WHA_FastANI	Organi_FastANI	NUID	FastANI	%Cov	Species	Suppc	Primary_MLST	Primary_MLST	Primary_MLST	Secondary_MLST	Secondary_MLST	Secondary_MLST	MLAR_Database	No
J4	/blue/bphl-flori	phx_output	PASS		<70% of reads : coverage >100		94.04	86.82	3399434	2946464	3122418	130.18	50.75	179	5263379	1.0308	0.4432	ANI_REFSEQ	Escherichia (14 Escherichia (97 Escherichia coli					99.89	96.96	Escherichia coli	ecoli_2(Pasteu assembly	Novel allele	ST10	adk(10).fumC(4)	ecoli_2(Pasteu assembly	Novel allele	dinB(8).icdA(2)	ResGANNCBI_2024	
J7	/blue/bphl-flori	phx_output	PASS		<70% of reads assigned to top		93.41	85.5	2176320	1852286	1976454	80.52	50.46	246	5328404	1.0435	0.6263	ANI_REFSEQ	Escherichia (16 Escherichia (96 Escherichia coli					99.95	96.98	Escherichia coli	ecoli_2(Pasteu assembly	Novel allele	ST10	adk(10).fumC(4)	ecoli_2(Pasteu assembly	Novel allele	dinB(8).icdA(3)	ResGANNCBI_2024	
J8	/blue/bphl-flori	phx_output	PASS		<70% of reads assigned to top		92.44	88.14	2738936	2400072	2528177	100.44	50.31	294	5505983	1.0783	1.1266	ANI_REFSEQ	Escherichia (17 Escherichia (96 Escherichia coli					99.66	96.31	Escherichia coli	ecoli_2(Pasteu assembly	Novel allele	ST129	adk(6).fumC(4)	ecoli_2(Pasteu assembly	Novel allele	dinB(8).icdA(4)	ResGANNCBI_2024	
J9	/blue/bphl-flori	phx_output	PASS		<70% of reads : coverage >100		93.95	82.47	2631834	2161400	2352199	109.14	50.71	57	4684746	0.9175	1.1868	ANI_REFSEQ	Escherichia (7 Escherichia (96 Escherichia coli					99.46	96.09	Escherichia coli	ecoli_2(Pasteu assembly	Novel allele	ST1248	adk(6).fumC(2)	ecoli_2(Pasteu assembly	Novel allele	dinB(8).icdA(4)	ResGANNCBI_2024	
J17	/blue/bphl-flori	phx_output	PASS		<70% of reads assigned to top		93.28	85.82	2418606	2071012	2205606	89.77	50.53	267	5350037	1.0478	0.6873	ANI_REFSEQ	Escherichia (15 Escherichia (96 Escherichia coli					99.86	99.16	Escherichia coli	ecoli_2(Pasteu assembly	Novel allele	ST117	adk(6).fumC(4)	ecoli_2(Pasteu assembly	Novel allele	dinB(8).icdA(4)	ResGANNCBI_2024	
J36	/blue/bphl-flori	phx_output	PASS				90.24	81.23	2526286	2138338	2286558	86.57	57.51	51	5427905	0.9878	0.6836	ANI_REFSEQ	Klebsiella (85.1 Klebsiella (96.3 Klebsiella pneumoniae					99.93	95.57	Klebsiella pneumoniae	kpn_pneumoniae assembly	ST111	gapA(3).infB(3)	-	-	-	-	-	ResGANNCBI_2024
J40	/blue/bphl-flori	phx_output	PASS				90.44	81.31	1588860	1309798	1415918	80.2	55.11	70	4872278	0.9778	0.4291	ANI_REFSEQ	Enterobacter (6 Enterobacter (8 Enterobacter hierdenii					99.83	96.17	Enterobacter hierdenii	ecoliaceae assembly	ST102	dnaA(59).fusA	-	-	-	-	-	ResGANNCBI_2024
J52	/blue/bphl-flori	phx_output	PASS		<70% of reads : coverage >100		94.54	83.86	3086434	2584824	2791309	119.7	50.45	137	5051000	0.9892	0.155	ANI_REFSEQ	Escherichia (10 Escherichia (96 Escherichia coli					99.6	89.31	Escherichia coli	ecoli_2(Pasteu assembly	Novel allele	ST10	adk(10).fumC(4)	ecoli_2(Pasteu assembly	Novel allele	dinB(8).icdA(1)	ResGANNCBI_2024	
J100	/blue/bphl-flori	phx_output	PASS		<70% of reads assigned to top		93.89	84.75	2153930	1818424	1950807	87.21	50.57	99	4882908	0.9563	0.6285	ANI_REFSEQ	Escherichia (11 Escherichia (96 Escherichia coli					99.98	97.98	Escherichia coli	ecoli_2(Pasteu assembly	Novel allele	ST1410	adk(6).fumC(4)	ecoli_2(Pasteu assembly	Novel allele	dinB(8).icdA(6)	ResGANNCBI_2024	
J102	/blue/bphl-flori	phx_output	PASS				92.05	79.29	2155298	1771506	1925033	69.61	56.81	67	5752511	1.0257	0.5467	ANI_REFSEQ	Klebsiella (80.7 Klebsiella (96.4 Klebsiella pneumoniae					99.95	93.26	Klebsiella pneumoniae	kpn_pneumoniae assembly	ST307	gapA(4).infB(1)	-	-	-	-	-	ResGANNCBI_2024
J120	/blue/bphl-flori	phx_output	PASS		Average Q30 of raw R1 reads <6		88.45	76.44	2245352	1895040	2031148	54.22	65.43	128	7310659	1.1005	1.5743	ANI_REFSEQ	Pseudomonas Pseudomonas Pseudomonas					99.93	92.23	Pseudomonas	paeruginosa assembly	ST244	acaA(17).aroE	-	-	-	-	-	ResGANNCBI_2024
J217	/blue/bphl-flori	phx_output	PASS				97.24	92.38	1750586	1571496	1638543	93.49	39.01	65	3873477	0.9715	0.4391	ANI_REFSEQ	Acinetobacter (Acinetobacter (Acinetobacter t					99.87	96.66	Acinetobacter	baumanniiPa assembly	ST417	gltA(1).gyrB(17)	abaumanniiPa assembly	ST2	cpn60(2).fusA	ResGANNCBI_2024		
J414	/blue/bphl-flori	phx_output	PASS		<70% of reads : coverage >100		93.48	85.19	2956942	2509628	2665208	108.15	50.28	215	5411032	1.0597	0.8591	ANI_REFSEQ	Escherichia (33 Escherichia (96 Escherichia coli					99.97	99.65	Escherichia coli	ecoli_2(Pasteu assembly	ST111	adk(12).fumC(4)	ecoli_2(Pasteu assembly	ST628	dinB(59).icdA(1)	ResGANNCBI_2024		
J756	/blue/bphl-flori	phx_output	PASS				93.2	76.25	1946216	1470394	1671624	70.98	52.03	73	4971473	1.0273	0.5331	ANI_REFSEQ	Salmonella (91 Salmonella (99 Salmonella enterica					99.98	99.07	Salmonella enterica	senterica assembly	ST365	aroC(130).dnaI	-	-	-	-	-	ResGANNCBI_2024
J765	/blue/bphl-flori	phx_output	FAIL		High scaffold count >500 (923).		90.07	85.93	1292508	1112648	1180250	46.55	51.88	923	5429563	1.122	2.3787	ANI_REFSEQ	Salmonella (89 Salmonella (88 Salmonella enterica					99.94	98.73	Salmonella enterica	senterica assembly	ST118	aroC(16).dnaN	-	-	-	-	-	ResGANNCBI_2024
J780	/blue/bphl-flori	phx_output	PASS		Average Q30 of raw R1 reads <6		89.62	86.62	1614562	1395998	1478162	58.78	51.74	268	5275810	1.0902	1.7593	ANI_REFSEQ	Salmonella (89 Salmonella (97 Salmonella enterica					99.64	94.34	Salmonella enterica	senterica assembly	ST964	aroC(13).dnaN	-	-	-	-	-	ResGANNCBI_2024

Application Cont.



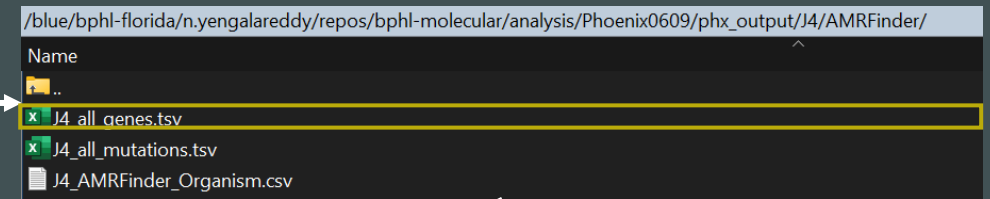
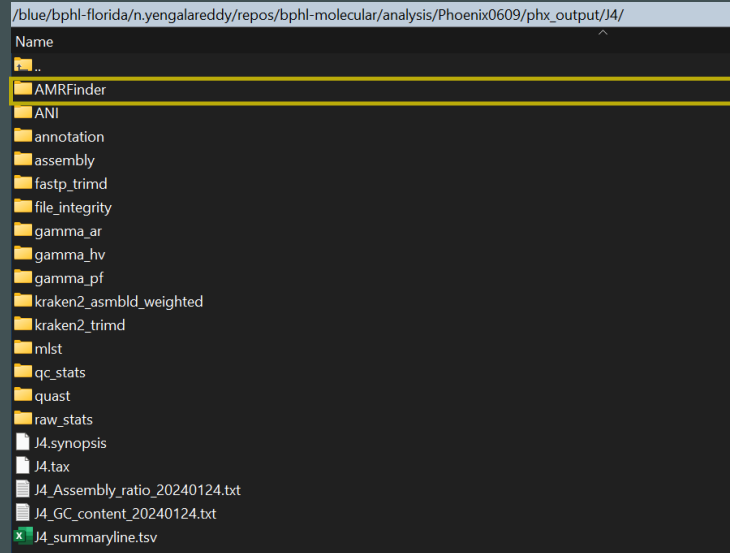


Application Cont.



ID	Auto_QC_(Warning_C	Estimated_Genome_L	Assembly_#_of_Scaff	GC_%	Species	Taxa_Conf	Taxa_Cove	Taxa_Sour	Kraken2_T	Kraken2_V	MLST_Sch	MLST_1	MLST_Sch	MLST_2	GAMMA_B	GAMMA_O	AMRFinder	Hypervirul	Plasmid_Ir	Auto_QC_Failure_Reason
J4	PASS	1	130.2	5263379	1.0308 (.4	179	50.75	Escherichi	99.89 ANI	96.96 ANI	REFSE	Escherichi	Unknown	ecoli(Acht ST10	ecoli_2(Pa Novel	alle AmpC1	EcSMR	efflu	gyrA	S83L iucA 45

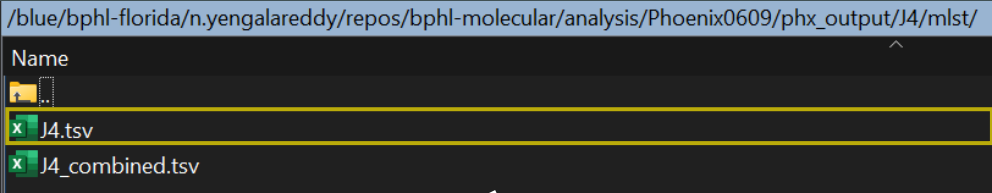
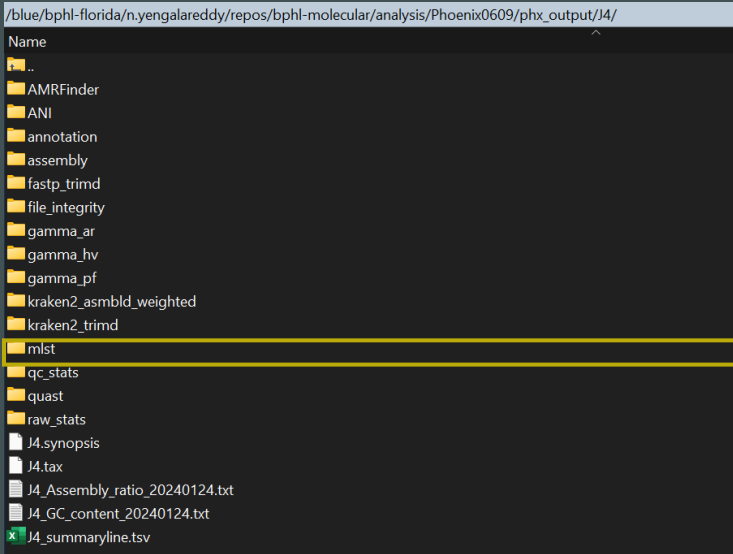
Application Cont.



Protein_id	Contig_id	Start	Stop	Strand	Gene_sym	Sequence	Scope	Element_t	Element_s	Class	Subclass	Method	Target_len	Reference	%_Covera	%_Identity	Alignment	Accession	Name_of	HMM_id	HMM_description				
AJLJLOCN_J4_107_ler		123	2213	+	iha	bifunction:	plus	VIRULENC	VIRULENC	NA	NA	EXACTP	696	696	100	100	696	AAG55323	bifunction:	NA	NA				
AJLJLOCN_J4_17_leng		5910	7712	-	ybtQ	yersiniaba	plus	VIRULENC	VIRULENC	NA	NA	BLASTP	600	600	100	99.83	600	AAC69584	yersiniaba	NA	NA				
AJLJLOCN_J4_17_leng		7699	9501	-	ybtP	yersiniaba	plus	VIRULENC	VIRULENC	NA	NA	BLASTP	600	600	100	99.83	600	CAA21388	yersiniaba	NA	NA				
AJLJLOCN_J4_1_lengt		138497	141124	-	gyrA_S83L	Escherichi	core	AMR	POINT	QUINOLOI	QUINOLOI	POINTP	875	878	99.66	99.09	875	WP_00128	DNA gyra	NA	NA				
AJLJLOCN_J4_26_leng		63039	63854	+	sul2	sulfonamic	core	AMR	AMR	SULFONAI	SULFONAI	EXACTP	271	271	100	100	271	WP_00104	sulfonami	NF000295	sulfonamide-resistant dihydropteroate synthase Sul2				
AJLJLOCN_J4_26_leng		66467	67303	-	aph(6)-Ib	aminoglyc:	core	AMR	AMR	AMINOGL	STREPTON	EXACTP	278	278	100	100	278	WP_00048	aminoglyc:	NF012171	APH(6)-I family aminoglycoside O-phosphotransferase				
AJLJLOCN_J4_26_leng		67303	68106	-	aph(3'')-Ib	aminoglyc:	core	AMR	AMR	AMINOGL	STREPTON	BLASTP	267	267	100	99.63	267	WP_00108	aminoglyc:	NF032895	aminoglycoside O-phosphotransferase APH(3'')-Ib				
AJLJLOCN_J4_2_lengt		25969	27201	-	mdtM	multidrug	plus	AMR	AMR	EFFLUX	EFFLUX	BLASTP	410	410	100	97.8	410	AAC77293	multidrug	NA	NA				



Application Cont.



source_file	Database	ST	locus_1	locus_2	locus_3	locus_4	locus_5	locus_6	locus_7	locus_8	locus_9	locus_10	
J4.filtered.ecoli_2	ecoli_2	-	dinB(8)	icdA(2)	pabB(~7)	polB(3)	putP(7)	trpA(~1)	trpB(4)	uidA(2)			
J4.filtered.ecoli	ecoli	10	adk(10)	fumC(11)	gyrB(4)	icd(8)	mdh(8)	purA(8)	recA(2)				



Application Cont.

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/Phoenix0609/phx_output/J4/

Name

- ..
- AMRFinder
- ANI
- annotation
- assembly
- fastp_trimd
- file_integrity
- gamma_ar
- gamma_hv
- gamma_pf
- kraken2_asmbld_weighted
- kraken2_trimd
- mlst
- qc_stats
- quast**
- raw_stats
- J4.synopsis
- J4.tax
- J4_Assembly_ratio_20240124.txt
- J4_GC_content_20240124.txt
- J4_summaryline.tsv

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/Phoenix0609/phx_output/J4/quast/

Name

- ..
- J4_summary.tsv**

Assembly	J4.filtered.scaffolds
contigs (179
contigs (141
contigs (82
contigs (66
contigs (49
contigs (37
Total lengt	5263379
Total lengt	5238529
Total lengt	5092565
Total lengt	4967774
Total lengt	4663900
Total lengt	4240153
# contigs	179
Largest co	268884
Total lengt	5263379
GC (%)	50.75
N50	103768
N75	58075
L50	16
L75	32
# N's per 1	9.69

Conclusion



Fundamentals of
PHoeNlx



Installation and setup
of PHoeNlx in HPG



Successfully executed
job query for PHoeNlx



Generated output files



Advanced Molecular Detection

Southeast Region Bioinformatics

Questions?

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