

FLAQ- SARS- COV- 2

Advanced Molecular Detection
Southeast Region Bioinformatics

November 18, 2024

Bioinformatics Updates From ARLN

Candida auris

- MycoSNP v 1.6 (Coming Soon-End of Year):
 - Clade Assignment Functionality
 - Genome Coverage and Depth Metrics
 - Additional Validated Hotspot Regions
 - Downloadable Clade References
- Exploring tools for Long-Sequencing Analysis

PHoeNIx

- Phlyophoenix:
 - Seamlessly integrates with Phoenix Workflow
 - Output supports direct upload to Microreact
 - New TSV output includes Epidemiology-Related Metadata

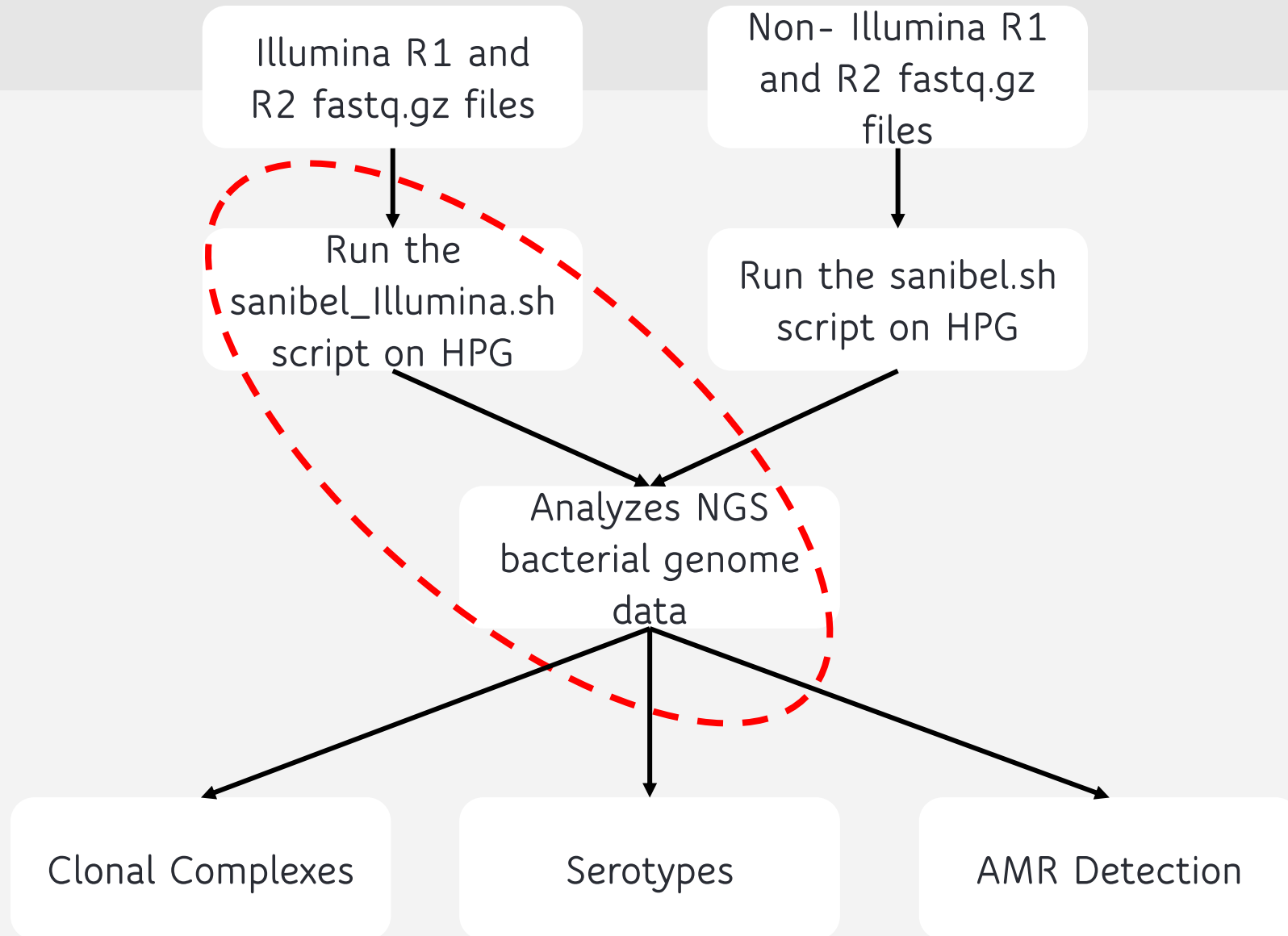
Office Hours

- November 25, 2024 – Daytona
- December 09, 2024 – FLAQ_SC2_Meta

Office Hours Updates



Recap of Sanibel



Sanibel Cont.

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/Sanibel1031/			
Name	Size	Changed	Rights
..		10/31/2024 12:51:14 PM	rwxf--r--
configs		10/9/2024 11:19:55 AM	rwxf--r--
fastqs		10/30/2024 4:32:23 PM	rwxf--r--
modules		10/9/2024 11:19:56 AM	rwxf--r--
output-20241030193223		10/30/2024 4:32:23 PM	rwxf--r--
Runs		10/30/2024 10:57:57 AM	rwxf--r--
test files		10/29/2024 10:32:58 AM	rwxf--r--
flaq_amr_plus2.nf	2 KB	10/9/2024 11:19:56 AM	rw-r--r--
LICENSE	12 KB	10/9/2024 11:19:55 AM	rw-r--r--
nextflow.config	1 KB	10/9/2024 11:19:56 AM	rw-r--r--
params.yaml	1 KB	10/29/2024 11:25:41 AM	rw-r--r--
README.md	4 KB	10/9/2024 11:19:55 AM	rw-r--r--
sanibel.sh	2 KB	10/21/2024 1:08:05 PM	rw-r--r--
sanibel_docker.sh	2 KB	10/9/2024 11:19:56 AM	rw-r--r--
sanibel_illumina.sh	2 KB	10/30/2024 11:08:45 AM	rw-r--r--
sanibel_illumina_docker.sh	2 KB	10/9/2024 11:19:56 AM	rw-r--r--

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/Sanibel1031/fastqs/			
Name	Size	Changed	Rights
..		10/30/2024 4:32:26 PM	rwxf--r--
J4-FL-M08815-240126_S2_L001_R1...	281,807 KB	1/29/2024 5:26:14 AM	rw-r--r--
J4-FL-M08815-240126_S2_L001_R2...	309,616 KB	1/29/2024 5:26:19 AM	rw-r--r--
J7-FL-M08815-240126_S5_L001_R1...	183,359 KB	1/29/2024 5:26:08 AM	rw-r--r--
J7-FL-M08815-240126_S5_L001_R2...	201,412 KB	1/29/2024 5:26:09 AM	rw-r--r--
J8-FL-M08815-240126_S3_L001_R1...	239,909 KB	1/29/2024 5:26:13 AM	rw-r--r--
J8-FL-M08815-240126_S3_L001_R2...	248,004 KB	1/29/2024 5:26:11 AM	rw-r--r--
J9-FL-M08815-240126_S4_L001_R1...	219,984 KB	1/29/2024 5:26:14 AM	rw-r--r--
J9-FL-M08815-240126_S4_L001_R2...	254,486 KB	1/29/2024 5:26:12 AM	rw-r--r--
J17-FL-M08815-240126_S6_L001_R...	206,113 KB	1/29/2024 5:26:09 AM	rw-r--r--
J17-FL-M08815-240126_S6_L001_R...	225,527 KB	1/29/2024 5:26:11 AM	rw-r--r--
J36-FL-M08815-240126_S8_L001_R...	222,528 KB	1/29/2024 5:26:12 AM	rw-r--r--
J36-FL-M08815-240126_S8_L001_R...	241,234 KB	1/29/2024 5:26:15 AM	rw-r--r--
J40-FL-M08815-240126_S9_L001_R...	143,159 KB	1/29/2024 5:26:08 AM	rw-r--r--
J40-FL-M08815-240126_S9_L001_R...	154,693 KB	1/29/2024 5:26:10 AM	rw-r--r--
J52-FL-M08815-240126_S7_L001_R...	250,144 KB	1/29/2024 5:26:19 AM	rw-r--r--
J52-FL-M08815-240126_S7_L001_R...	293,104 KB	1/29/2024 5:26:14 AM	rw-r--r--
J100-FL-M08815-240126_S10_L00...	180,341 KB	1/29/2024 5:26:15 AM	rw-r--r--
J100-FL-M08815-240126_S10_L00...	203,012 KB	1/29/2024 5:26:14 AM	rw-r--r--
J102-FL-M08815-240126_S11_L00...	182,126 KB	1/29/2024 5:26:12 AM	rw-r--r--
J102-FL-M08815-240126_S11_L00...	208,703 KB	1/29/2024 5:26:10 AM	rw-r--r--
J120-FL-M08815-240126_S12_L00...	197,561 KB	1/29/2024 5:26:09 AM	rw-r--r--
J120-FL-M08815-240126_S12_L00...	217,662 KB	1/29/2024 5:26:12 AM	rw-r--r--
J217-FL-M08815-240126_S13_L00...	131,973 KB	1/29/2024 5:26:12 AM	rw-r--r--
J217-FL-M08815-240126_S13_L00...	148,638 KB	1/29/2024 5:26:08 AM	rw-r--r--
J414-FL-M08815-240126_S1_L001_...	250,511 KB	1/29/2024 5:26:13 AM	rw-r--r--
J414-FL-M08815-240126_S1_L001_...	277,255 KB	1/29/2024 5:26:14 AM	rw-r--r--
J756-FL-M08815-240126_S15_L00...	163,604 KB	1/29/2024 5:26:11 AM	rw-r--r--
J756-FL-M08815-240126_S15_L00...	196,408 KB	1/29/2024 5:26:10 AM	rw-r--r--
J762-FL-M08815-240126_S14_L00...	119,852 KB	1/29/2024 5:26:06 AM	rw-r--r--
J762-FL-M08815-240126_S14_L00...	121,244 KB	1/29/2024 5:26:07 AM	rw-r--r--
J780-FL-M08815-240126_S16_L00...	148,895 KB	1/29/2024 5:26:09 AM	rw-r--r--
J780-FL-M08815-240126_S16_L00...	147,986 KB	1/29/2024 5:26:07 AM	rw-r--r--

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/Sanibel1031/output-20241030193223/			
Name	Size	Changed	Rights
..		10/30/2024 4:32:26 PM	rwxf--r--
J4		10/30/2024 4:30:43 PM	rwxf--r--
J7		10/30/2024 3:03:12 PM	rwxf--r--
J8		10/30/2024 4:11:35 PM	rwxf--r--
J9		10/30/2024 4:11:02 PM	rwxf--r--
J17		10/30/2024 4:11:24 PM	rwxf--r--
J36		10/30/2024 2:58:13 PM	rwxf--r--
J40		10/30/2024 2:52:41 PM	rwxf--r--
J52		10/30/2024 4:08:44 PM	rwxf--r--
J100		10/30/2024 4:02:17 PM	rwxf--r--
J102		10/30/2024 3:24:13 PM	rwxf--r--
J120		10/30/2024 2:53:01 PM	rwxf--r--
J217		10/30/2024 3:03:34 PM	rwxf--r--
J414		10/30/2024 3:46:01 PM	rwxf--r--
J756		10/30/2024 3:08:57 PM	rwxf--r--
J762		10/30/2024 2:55:25 PM	rwxf--r--
J780		10/30/2024 3:25:37 PM	rwxf--r--
sanibel.48890209.err	2 KB	10/30/2024 1:06:12 PM	rw-r--r--
sanibel.48890209.out	496 KB	10/30/2024 4:32:21 PM	rw-r--r--
sum_report.txt	3 KB	10/30/2024 4:32:21 PM	rw-r--r--



Sanibel Cont.

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/Sanibel1031/output-20241030193223/

Name	Size	Changed	Rights
..		10/30/2024 4:32:26 PM	rwxt--t--
J4		10/30/2024 4:30:43 PM	rwxt--t--
J7		10/30/2024 3:03:12 PM	rwxt--t--
J8		10/30/2024 4:11:35 PM	rwxt--t--
J9		10/30/2024 4:11:02 PM	rwxt--t--
J17		10/30/2024 4:11:24 PM	rwxt--t--
J36		10/30/2024 2:58:13 PM	rwxt--t--
J40		10/30/2024 2:52:41 PM	rwxt--t--
J52		10/30/2024 4:08:44 PM	rwxt--t--
J100		10/30/2024 4:02:17 PM	rwxt--t--
J102		10/30/2024 3:24:13 PM	rwxt--t--
J120		10/30/2024 2:53:01 PM	rwxt--t--
J217		10/30/2024 3:03:34 PM	rwxt--t--
J414		10/30/2024 3:46:01 PM	rwxt--t--
J756		10/30/2024 3:08:57 PM	rwxt--t--
J762		10/30/2024 2:55:25 PM	rwxt--t--
J780		10/30/2024 3:25:37 PM	rwxt--t--
sanibel.48890209.err	2 KB	10/30/2024 1:06:12 PM	rw-r--r--
sanibel.48890209.out	496 KB	10/30/2024 4:32:21 PM	rw-r--r--
sum_report.txt	3 KB	10/30/2024 4:32:21 PM	rw-r--r--

sampleID	speciesID_mash	nearest_neighb_mash	mash_distance	speciesID_kraken	kraken_percent	mlst_scheme	mlst_st	mlst_cc	pmga_species	serotype	num_clean_reads	avg_readlength	avg_read_qual	est_coverage	num_contigs	longest_contig	N50	L50	total_length	gc_content	annotated_cds
J100	Escherichia_coli	GCF_000692815.1	0.00492718	Escherichia coli	49.98	ecoli	410				1865832	226.99	37.09	87.27	101	327342	191011	10	4852648	50	4528
J102	Klebsiella_pneumoniae	NZ_CCGO	0.00308338	Klebsiella pneumoniae	81.39	kpneumoniae	307				1810976	219.9	36.79	69.51	74	464840	307140	8	5729338	56	5299
J120	Pseudomonas_aeruginosa	GCF_000629065.1	0.0037263	Pseudomonas aeruginosa	91.74	paeruginosa	244				1917736	211.78	36.36	55.77	130	661600	185918	11	7282290	65	6801
J17	Escherichia_coli	NZ_JHHE	0.00337267	Escherichia coli	57.04	ecoli	17				2119802	226.71	37.06	91.97	244	348576	125279	14	5225359	50	4989
J217	Acinetobacter_baumannii	NZ_AYGI	0.00393593	Acinetobacter baumannii	76.05	abaumannii_2	2				1590920	226.35	37.74	93.44	68	253267	148812	11	3853980	39	3598
J36	Klebsiella_pneumoniae	GCF_000445405.1	0.00508714	Klebsiella pneumoniae	83.9	kpneumoniae	11				2181456	218.57	36.64	88.16	69	747923	224752	8	5408374	57	5036
J40	Enterobacter_sp.	GCF_000958405.1	0.0111761	Enterobacter hormaechei	18.68	eclocae	102				1347996	219.73	36.63	61.04	75	339727	201259	9	4851991	55	4540
J414	Escherichia_coli	NZ_AVRE	0.00243596	Escherichia coli	67	ecoli	11				2575052	226.73	37.08	109.58	189	374706	163749	10	5327746	50	5062
J4	Escherichia_coli	NZ_JNRV	0.00936594	Escherichia coli	41.03	ecoli	10				3006450	227.56	37.18	131.65	184	267838	101673	16	5196939	50	4921
J52	Escherichia_coli	GCF_000461215.1	0.00680395	Escherichia coli	39.62	ecoli	10				2645448	225.13	37.12	118.98	128	290536	119249	15	5005322	50	4756
J756	Salmonella_enterica	GCF_000171495.1	0.00331442	Salmonella enterica	95.86	senterica	365				1530610	221.32	36.85	68.4	76	332968	162252	10	4952534	52	4629
J762	Salmonella_enterica	NZ_AJMO	0.00518381	Salmonella enterica	96.64	senterica	118				1144434	225.27	36.75	53.94	40	692679	416934	5	4779020	52	4473
J780	Salmonella_enterica	GCF_000493295.1	0.00737682	Salmonella enterica	93.56	senterica	964				1428284	221.39	36.72	63.81	93	561170	323319	7	4955382	52	4716
J7	Escherichia_coli	NZ_JHGK	0.00243596	Escherichia coli	57.49	ecoli	21				1893390	226.08	37.11	81.91	229	266530	125958	16	5225938	50	5019
J8	Escherichia_coli	NZ_AIBR	0.00638544	Escherichia coli	53.46	ecoli	29				2452914	227.54	37.06	103.7	281	211567	73415	23	5381948	50	5221
J9	Escherichia_coli	GCF_000458955.1	0.00375609	Escherichia coli	51.24	ecoli	1248				2227612	226.32	37.04	108	64	703240	213324	7	4667970	50	4352

Purpose

- Analyzes SARS-COV-2 Genomic Data
- Generates Accurate Consensus Assemblies

Usage

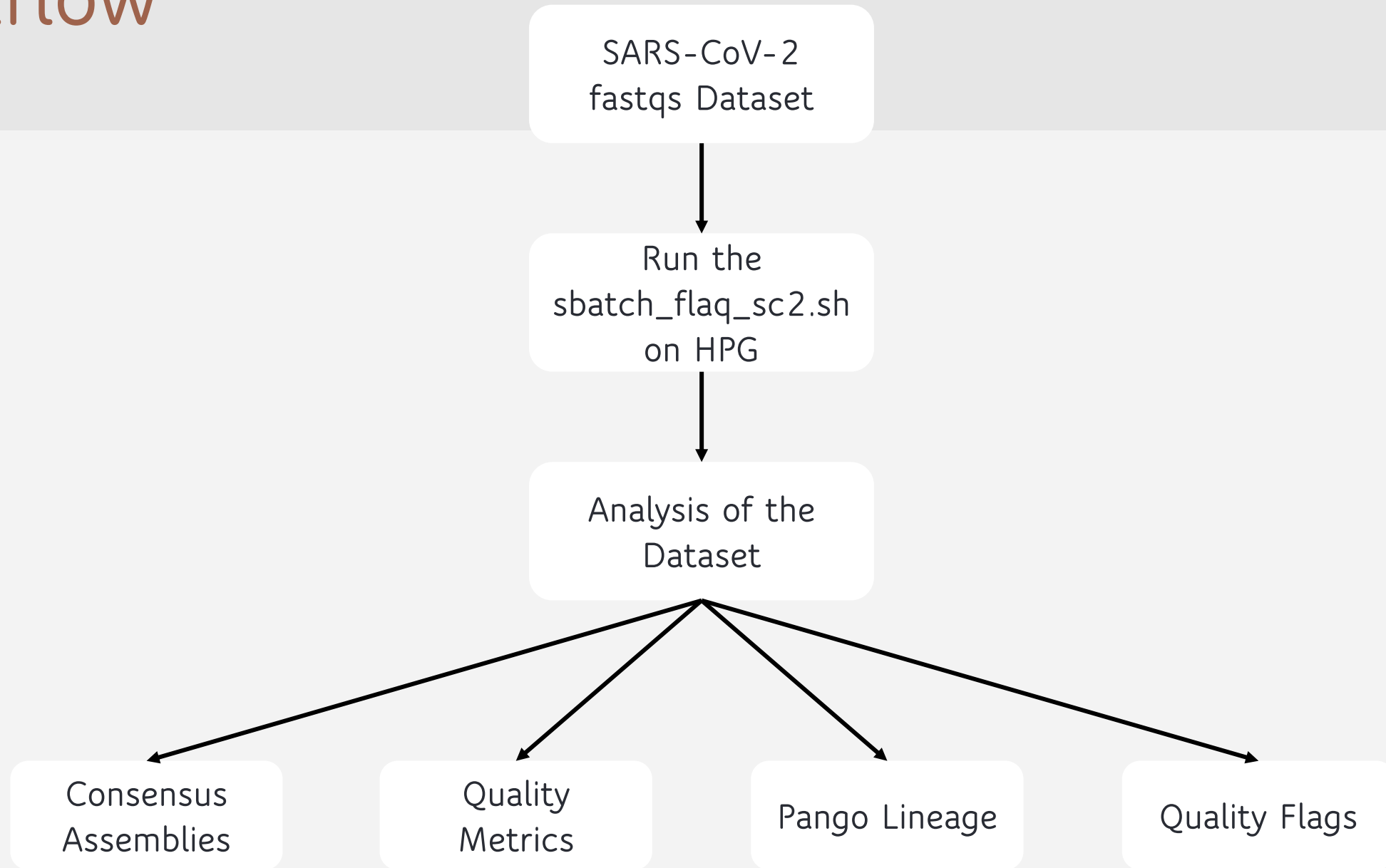
- To support public health and researchers to monitor the spread and evolution of COVID-19

Dependencies

- Python3
- Singularity/Apptainer
- iVar
- Git

FLAQ-SC2 Overview

Workflow



Application

Objective

- Use SC2-positive clinical datasets and analyze the dataset using FLAQ-SC2 pipeline.



```
cd /blue/bphl-<state>/<user>/repos/bphl-molecular/  
git clone https://github.com/BPHL-Molecular/flaq_sc2  
mkdir analysis/  
cd analysis/  
cp /blue/bphl-<state>/<user>/repos/bphl-molecular/flaq_sc2/*  
mkdir fastqs/  
cp /path/to/fastqs/*.fastq.gz fastqs/
```

Application Cont.

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/flaq_sc2/*.*

Name	Size	Changed
2024-10-30_flaq_run		10/31/2024 12:51:14 PM
assemblies		10/30/2024 1:23:46 PM
fastqs		10/30/2024 1:24:57 PM
primers		10/30/2024 10:36:27 AM
reference		8/21/2024 8:16:31 AM
vadr_error_reports		8/21/2024 8:16:31 AM
variants		10/30/2024 1:21:39 PM
assemblies.fasta	321 KB	10/30/2024 1:25:15 PM
flaq_sc2.48888753.err	63 KB	10/30/2024 1:25:13 PM
flaq_sc2.48888753.out	9 KB	10/30/2024 1:25:17 PM
flaq_sc2.py	19 KB	8/21/2024 8:16:31 AM
LICENSE	2 KB	8/21/2024 8:16:31 AM
nextclade_report.csv	5 KB	10/30/2024 1:25:17 PM
README.md	6 KB	8/21/2024 8:16:31 AM
sbatch_flaq_sc2.sh	1 KB	8/23/2024 9:10:21 AM



Application Cont.

nano sbatch_flgq_sc2.sh

```
#!/bin/bash
#SBATCH --account=bphl-umbrella
#SBATCH --qos=bphl-umbrella
#SBATCH --job-name=flaq_sc2
#SBATCH --mail-type=END,FAIL
#SBATCH --mail-user=nikhil.yengala@flhealth.gov
#SBATCH --ntasks=1
#SBATCH --cpus-per-task=15
#SBATCH --mem=100gb
#SBATCH --time=24:00:00
#SBATCH --output=flaq_sc2.%j.out
#SBATCH --error=flaq_sc2.%j.err

#Run script/command and use $SLURM_CPUS_ON_NODE
module load apptainer
module load conda
conda activate pyivar

primer_version="4.1"

python flaq_sc2.py fastqs/ --primer_bed primers/ARTIC-V${primer_version}.bed --lib_frag frag --threads $SLURM_CPUS_ON_NODE --r$
```



activate conda environment
containing iVar
&
sbatch sbatch_flgq_sc2.sh

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/flaq_sc2/

Name	Size	Changed
..		10/31/2024 12:51:14 PM
2024-10-30_flgq_run		10/30/2024 1:23:46 PM
assemblies		10/30/2024 1:24:57 PM
fastqs		10/30/2024 10:36:27 AM
primers		8/21/2024 8:16:31 AM
reference		8/21/2024 8:16:31 AM
vadr_error_reports		10/30/2024 1:21:39 PM
variants		10/30/2024 1:24:57 PM
assemblies.fasta	321 KB	10/30/2024 1:25:15 PM
flaq_sc2.48888753.err	63 KB	10/30/2024 1:25:13 PM
flaq_sc2.48888753.out	9 KB	10/30/2024 1:25:17 PM
flaq_sc2.py	19 KB	8/21/2024 8:16:31 AM
LICENSE	2 KB	8/21/2024 8:16:31 AM
nextclade_report.csv	5 KB	10/30/2024 1:25:17 PM
README.md	6 KB	8/21/2024 8:16:31 AM
sbatch_flgq_sc2.sh	1 KB	8/23/2024 9:10:21 AM

Application
Cont.



Application Cont.

ls variants

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/flaq_sc2/variants/			
Name	Size	Changed	Rights
		10/30/2024 1:25:17 PM	rwxr-sr-x
J84.variants.tsv	1 KB	10/30/2024 1:10:27 PM	rw-r--r--
J682.variants.tsv	2 KB	10/30/2024 1:06:39 PM	rw-r--r--
J711.variants.tsv	1 KB	10/30/2024 1:08:06 PM	rw-r--r--
J886.variants.tsv	1 KB	10/30/2024 1:11:49 PM	rw-r--r--
M109.variants.tsv	1 KB	10/30/2024 1:14:46 PM	rw-r--r--
M300.variants.tsv	2 KB	10/30/2024 1:16:08 PM	rw-r--r--
M301.variants.tsv	2 KB	10/30/2024 1:17:31 PM	rw-r--r--
M330.variants.tsv	1 KB	10/30/2024 1:19:11 PM	rw-r--r--
M653.variants.tsv	2 KB	10/30/2024 1:21:33 PM	rw-r--r--
M908.variants.tsv	1 KB	10/30/2024 1:23:28 PM	rw-r--r--
T45.variants.tsv	1 KB	10/30/2024 1:24:57 PM	rw-r--r--

REGION	POS	REF	ALT	REF_DP	REF_RV	REF_QUAL	ALT_DP	ALT_RV	ALT_QUAL	ALT_FREQ	TOTAL_DP	PVAL	PASS	GFF_FEATURE	REF_CODON	REF_AA	ALT_CODON	ALT_AA	POS_AA
MN908947.3	241	C	T	0	0	0	400	86	48	1	400	1.93E-272	TRUE	NA	NA	NA	NA	NA	NA
MN908947.3	514	T	#NAME?	954	306	48	1180	0	20	0.907692	1300	5.94E-296	TRUE	NA	NA	NA	NA	NA	NA
MN908947.3	3037	C	T	0	0	0	1144	433	50	1	1144	0	TRUE	ORF1ab:cds-YP_009724389.1	TTC	F	TTT	F	924
MN908947.3	3037	C	T	0	0	0	1144	433	50	1	1144	0	TRUE	ORF1ab:cds-YP_009725295.1	TTC	F	TTT	F	924
MN908947.3	14408	C	T	1	1	76	5611	3615	47	0.999822	5612	0	TRUE	ORF1ab:cds-YP_009724389.1	CCT	P	CTT	L	314
MN908947.3	18877	C	T	2	1	37	2918	2036	47	0.999315	2920	0	TRUE	ORF1ab:cds-YP_009724389.1	CTA	L	TTA	L	1804
MN908947.3	23403	A	G	3	2	36	5722	3527	44	0.999476	5725	0	TRUE	S:cds-YP_009724390.1	GAT	D	GGT	G	614
MN908947.3	25563	G	T	0	0	0	1774	882	44	0.999437	1775	0	TRUE	ORF3a:cds-YP_009724391.1	CAG	Q	CAT	H	57

ls vadr_error_reports

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/flaq_sc2/vadr_error_reports/			
Name	Size	Changed	Rights
..		10/30/2024 1:25:17 PM	rwxr-sr-x
M300.vadr.alt.list	4 KB	10/30/2024 1:16:16 PM	rw-r--r--
M301.vadr.alt.list	4 KB	10/30/2024 1:17:37 PM	rw-r--r--
M653.vadr.alt.list	1 KB	10/30/2024 1:21:39 PM	rw-r--r--

#sequence	model	feature-type	feature-name	error	seq-coords	mdl-coords	error-description
M300	NC_045512	CDS	ORF1ab polyprotein	CDS_HAS_STOP_CODON	16990..16992:+	17120..17122:+	in-frame stop codon exists 5' of stop position predicted by homology to reference [TAG, shifted S:4433,M:4433]
M300	NC_045512	CDS	ORF1ab polyprotein	POSSIBLE_FRAMESHIFT	16944..21425:+	17070..21555:+	possible frameshift at 3' end of CDS [length:4482; inserts:none; deletes:S:16943,M:17070..17073(4); shifted_frame:3; dominant_frame:1,]
M300	NC_045512	CDS	ORF1ab polyprotein	INDEFINITE_ANNOTATION_END	16948..21425:+	21555..21555:+	protein-based alignment does not extend close enough to nucleotide-based alignment 3' endpoint [4478>8]
M300	NC_045512	CDS	ORF1ab polyprotein	UNEXPECTED_LENGTH	140..13342+;13342..21425:+	266..13468+;13468..21555:+	length of complete coding (CDS or mat_peptide) feature is not a multiple of 3 [21287]
M300	NC_045512	mat_peptide	leader protein	PEPTIDE_TRANSLATION_PROBLEM	-	-	mat_peptide may not be translated because its parent CDS has a problem [-]
M300	NC_045512	mat_peptide	nsp2	PEPTIDE_TRANSLATION_PROBLEM	-	-	mat_peptide may not be translated because its parent CDS has a problem [-]
M300	NC_045512	mat_peptide	nsp3	PEPTIDE_TRANSLATION_PROBLEM	-	-	mat_peptide may not be translated because its parent CDS has a problem [-]
M300	NC_045512	mat_peptide	nsp4	PEPTIDE_TRANSLATION_PROBLEM	-	-	mat_peptide may not be translated because its parent CDS has a problem [-]
M300	NC_045512	mat_peptide	3C-like proteinase	PEPTIDE_TRANSLATION_PROBLEM	-	-	mat_peptide may not be translated because its parent CDS has a problem [-]
M300	NC_045512	mat_peptide	nsp6	PEPTIDE_TRANSLATION_PROBLEM	-	-	mat_peptide may not be translated because its parent CDS has a problem [-]
M300	NC_045512	mat_peptide	nsp7	PEPTIDE_TRANSLATION_PROBLEM	-	-	mat_peptide may not be translated because its parent CDS has a problem [-]
M300	NC_045512	mat_peptide	nsp8	PEPTIDE_TRANSLATION_PROBLEM	-	-	mat_peptide may not be translated because its parent CDS has a problem [-]
M300	NC_045512	mat_peptide	nsp9	PEPTIDE_TRANSLATION_PROBLEM	-	-	mat_peptide may not be translated because its parent CDS has a problem [-]
M300	NC_045512	mat_peptide	nsp10	PEPTIDE_TRANSLATION_PROBLEM	-	-	mat_peptide may not be translated because its parent CDS has a problem [-]
M300	NC_045512	mat_peptide	RNA-dependent RNA polymerase	PEPTIDE_TRANSLATION_PROBLEM	-	-	mat_peptide may not be translated because its parent CDS has a problem [-]
M300	NC_045512	mat_peptide	helicase	PEPTIDE_TRANSLATION_PROBLEM	-	-	mat_peptide may not be translated because its parent CDS has a problem [-]
M300	NC_045512	mat_peptide	helicase	UNEXPECTED_LENGTH	16111..17909:+	16237..18039:+	length of complete coding (CDS or mat_peptide) feature is not a multiple of 3 [1799]
M300	NC_045512	mat_peptide	3'-to-5' exonuclease	PEPTIDE_TRANSLATION_PROBLEM	-	-	mat_peptide may not be translated because its parent CDS has a problem [-]
M300	NC_045512	mat_peptide	endoRNase	PEPTIDE_TRANSLATION_PROBLEM	-	-	mat_peptide may not be translated because its parent CDS has a problem [-]
M300	NC_045512	mat_peptide	2'-O-ribose methyltransferase	PEPTIDE_TRANSLATION_PROBLEM	-	-	mat_peptide may not be translated because its parent CDS has a problem [-]

Application
Cont.

Application Cont.

ls assemblies

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/flaq_sc2/assemblies/*.*			
Name	Size	Changed	Rights
..		10/30/2024 1:25:17 PM	rwxr-sr-x
J84.consensus.fa	30 KB	10/30/2024 1:10:27 PM	rw-r--r--
J682.consensus.fa	30 KB	10/30/2024 1:06:39 PM	rw-r--r--
J711.consensus.fa	30 KB	10/30/2024 1:08:06 PM	rw-r--r--
J886.consensus.fa	30 KB	10/30/2024 1:11:49 PM	rw-r--r--
M109.consensus.fa	30 KB	10/30/2024 1:14:46 PM	rw-r--r--
M300.consensus.fa	30 KB	10/30/2024 1:16:08 PM	rw-r--r--
M301.consensus.fa	30 KB	10/30/2024 1:17:31 PM	rw-r--r--
M330.consensus.fa	30 KB	10/30/2024 1:19:11 PM	rw-r--r--
M653.consensus.fa	30 KB	10/30/2024 1:21:33 PM	rw-r--r--
M908.consensus.fa	30 KB	10/30/2024 1:23:28 PM	rw-r--r--
T45.consensus.fa	30 KB	10/30/2024 1:24:57 PM	rw-r--r--








ls 2024-10-30_flgq_run

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/flaq_sc2/2024-10-30_flgq_run/*.*			
Name	Size	Changed	Rights
..		10/30/2024 1:25:17 PM	rwXr-sr-X
J84		10/30/2024 1:10:19 PM	rwXr-sr-X
J682		10/30/2024 1:06:38 PM	rwXr-sr-X
J711		10/30/2024 1:08:04 PM	rwXr-sr-X
J886		10/30/2024 1:11:48 PM	rwXr-sr-X
M109		10/30/2024 1:14:37 PM	rwXr-sr-X
M300		10/30/2024 1:16:06 PM	rwXr-sr-X
M301		10/30/2024 1:17:30 PM	rwXr-sr-X
M330		10/30/2024 1:19:08 PM	rwXr-sr-X
M653		10/30/2024 1:21:28 PM	rwXr-sr-X
M908		10/30/2024 1:23:24 PM	rwXr-sr-X
T45		10/30/2024 1:24:55 PM	rwXr-sr-X
report.txt	2 KB	10/30/2024 1:25:15 PM	rw-r--r--

Application
Cont.

sampleID	reference	start	end	num_raw_reads	num_clean_reads	num_mapped_reads	percent_mapped_clean_reads	cov_bases_mapped	percent_genome_cov_map	mean_depth	mean_base_qual	mean_map_qual	assembly_length	numN	percent_ref_genome	cov	VADR_flag	QC_flag	pangolin_version	lineage	SOTC
J682	MN908947.3	1	29903	176476	125270	71227		56.8588	29497	98.6423	503.937	37.8	60	29777	1310	95.1978	PASS	PASS	v4.3.1_pdata-v1.29	B.1	
J711	MN908947.3	1	29903	442888	279008	167235		59.9391	29818	99.7157	776.595	35.6	60	29829	650	97.5788	PASS	PASS	v4.3.1_pdata-v1.29	B.1	
J84	MN908947.3	1	29903	733132	606216	458864		75.6932	29868	99.883	3602.92	37.7	60	29862	50	99.6957	PASS	PASS	v4.3.1_pdata-v1.29	B.1	
J886	MN908947.3	1	29903	467264	295070	143787		48.7298	29634	99.1004	673.339	35.6	60	29777	1125	95.8165	PASS	PASS	v4.3.1_pdata-v1.29	B.1	
M109	MN908947.3	1	29903	1062220	898804	550019		61.1945	29858	99.8495	4225.17	37.7	60	29858	115	99.4649	PASS	PASS	v4.3.1_pdata-v1.29	B.1	
M300	MN908947.3	1	29903	289620	252704	121936		48.2525	29718	99.3813	878.313	37.8	60	29773	1439	94.753	REVIEW	PASS	v4.3.1_pdata-v1.29	B.1	
M301	MN908947.3	1	29903	447296	349038	67383		19.3053	29585	98.9366	494.466	37.8	60	29754	3041	89.3322	REVIEW	PASS	v4.3.1_pdata-v1.29	B.1	
M330	MN908947.3	1	29903	407520	363380	169527		46.6528	29756	99.5084	1226.17	37.8	60	29774	726	97.1408	PASS	PASS	v4.3.1_pdata-v1.29	B.1	
M653	MN908947.3	1	29903	872474	758820	333828		43.993	29825	99.7392	2292.56	37.8	60	29813	664	97.4785	REVIEW	PASS	v4.3.1_pdata-v1.29	B.1	
M908	MN908947.3	1	29903	530524	467348	253716		54.2885	29807	99.679	1836.15	37.8	60	29807	90	99.378	PASS	PASS	v4.3.1_pdata-v1.29	B.1	
T45	MN908947.3	1	29903	442412	340932	130766		38.3554	29777	99.5786	757.439	37.7	60	29777	1370	94.9972	PASS	PASS	v4.3.1_pdata-v1.29	B.1	

Conclusion

-  Recap of Sanibel
-  Fundamentals of FLAQ-SC2
-  Installation and setup of FLAQ-SC2 in HPG
-  Successfully executed job query for FLAQ-SC2
-  Generated Output Files





Advanced Molecular Detection Southeast Region Bioinformatics

Questions?

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