#### FLAQ\_SC2\_Meta

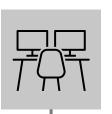
Advanced Molecular Detection Southeast Region Bioinformatics

December 09, 2024

#### <u>Updates</u>

#### **Office Hours**

2024

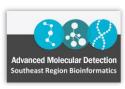


<u>December 23</u> Daytona Dengue

<u>January 6</u> Amelia



2025





#### **Purpose**

Analyze SARS-CoV-2 genetic data from environmental metagenomic samples (such as wastewater) and generates detailed reports

#### Usage

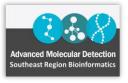
To support public health and researchers to provide insights into viral genetic diversity and prevalence within samples

#### Dependencies

Python3

Singularity

Freyja



#### WorkFlow

SC2 genetic (from wastewater) Fastq
Dataset

Run the sbatch\_all.sh on HPG

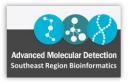
Analysis of the Dataset



Lineage Abundance Report

**QC** Reports

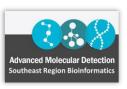
Consensus Sequences



## Application

#### Objective

Use SC2 genetic dataset (wastewater) and analyze the dataset using **FLAQ\_SC2\_Meta** pipeline.



```
cd /blue/bphl-<state>/<user>/repos/bphl-molecular/
git clone https://github.com/BPHL-Molecular/flaq_sc2_meta
mkdir analysis/
cd analysis/
cp /blue/bphl-<state>/<user>/repos/bphl-molecular/
flaq_sc2_meta /*
mkdir fastqs_ww/
cp /path/to/fastqs_ww/*.fastq.gz fastqs_ww/
```

lame ^	Size	Changed
<b>.</b>		12/2/2024 8:54:45 AM
2024-12-02-122021_flaq_ww_run		12/2/2024 9:36:29 AM
fastqs_ww		12/2/2024 9:15:25 AM
primers primers		12/2/2024 8:42:42 AM
reference		12/2/2024 8:42:44 AM
flaq_sc2_meta.51605080.err	21 KB	12/2/2024 9:37:04 AM
flaq_sc2_meta.51605080.out	0 KB	12/2/2024 9:20:10 AM
flaq_sc2_meta_all.py	15 KB	11/26/2024 9:32:41 AM
Guide_for_installation.txt	1 KB	11/26/2024 9:32:41 AM
LICENSE	2 KB	11/26/2024 9:32:41 AM
README.md	4 KB	11/26/2024 9:32:41 AM
sbatch_all.sh	1 KB	12/2/2024 9:18:04 AM

0 B of 40.9 KB in 0 of 11



```
nano sbatch_all.sh
 GNU nano 2.9.8
                                   sbatch all.sh
!/bin/bash
SBATCH --account=bphl-umbrella
#SBATCH --qos=bphl-umbrella
#SBATCH --job-name=flag sc2 meta
#SBATCH --mail-type=END,FAIL
SBATCH --ntasks=1
 SBATCH --mem=100ab
#SBATCH --time=24:00:00
SBATCH --output=flag sc2 meta.%j.out
nodule load apptainer
orimers="4.1"
```

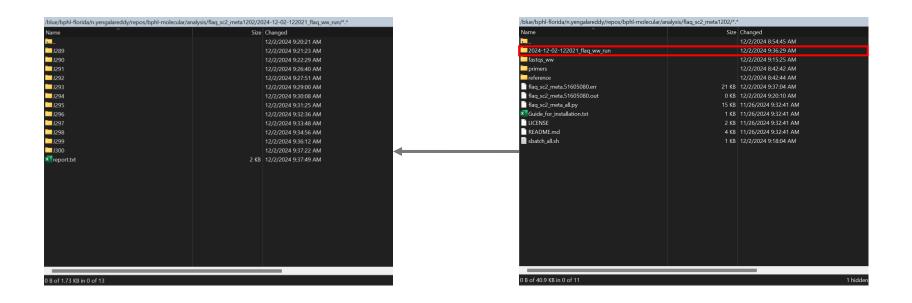


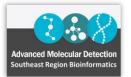
activate conda environment containing freyja

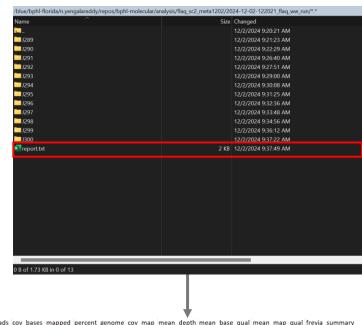
sbatch sbatch\_all.sh

ame ^	Size	Changed	
		12/2/2024 8:54:45 AM	
2024-12-02-122021_flaq_ww_run		12/2/2024 9:36:29 AM	
Tastqs_ww		12/2/2024 9:15:25 AM	
primers		12/2/2024 8:42:42 AM	
reference		12/2/2024 8:42:44 AM	
flaq_sc2_meta.51605080.err	21 KB	12/2/2024 9:37:04 AM	
flaq_sc2_meta.51605080.out	0 KB	12/2/2024 9:20:10 AM	
flaq_sc2_meta_all.py	15 KB	11/26/2024 9:32:41 AM	
Guide_for_installation.txt	1 KB	11/26/2024 9:32:41 AM	
LICENSE	2 KB	11/26/2024 9:32:41 AM	
README.md	4 KB	11/26/2024 9:32:41 AM	
sbatch_all.sh	1 KB	12/2/2024 9:18:04 AM	

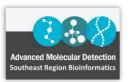


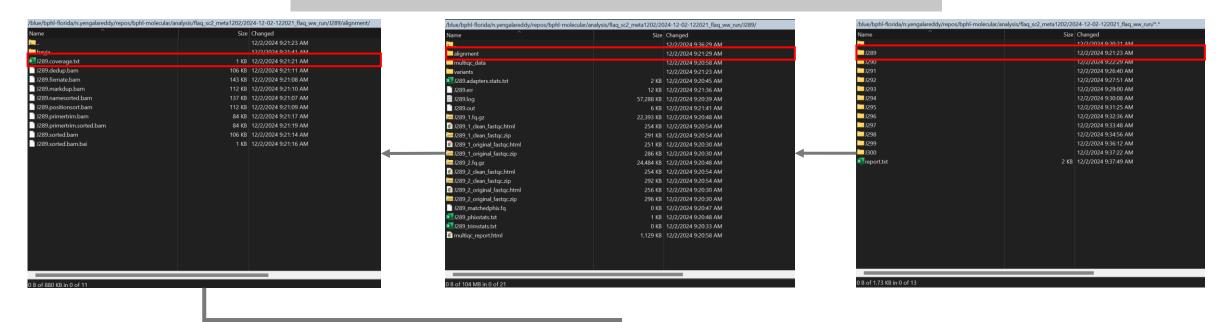




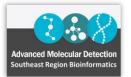


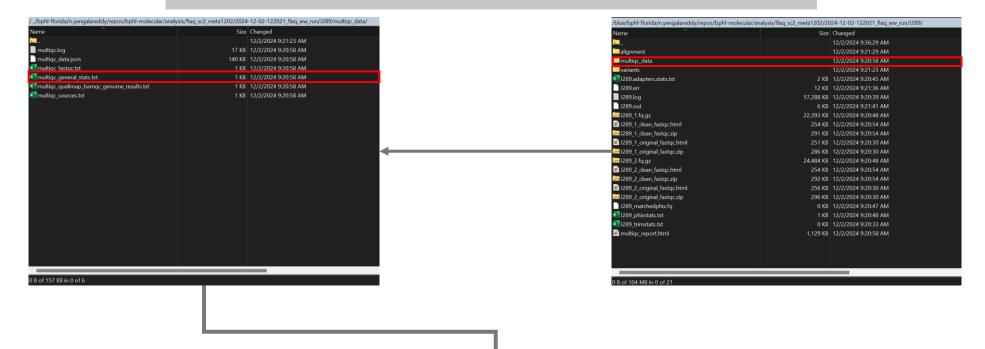
ampleID	reference	start end	num_raw_reads num	_clean_reads n	um_mapped_reads cov_bas	es_mapped	percent_genome_cov_map	mean_depth	mean_base_qual mean_map_	qual	freyja_summary	freyja_lineage	freya_lineage_abund
189	MN908947.3	1 29903	732162	605762	1531	9698	32.4315	9.87536	37.8	60	[('Omicron', 0.99999999993279)]	BA.2.86	1
90	MN908947.3	1 29903	481512	380672	1339	12007	40.1532	8.92462	37.8	60	[('Other', 0.959999999960572), ('XBB* (XBB.X)', 0.03999999999651294)]	Misc(3) FW.3	0.96000000 0.04000000
91	MN908947.3	1 29903	7034546	5373614	9138	21954	73.4174	61.7148	37.8	60	[('Omicron', 0.99999999997757)]	BA.2.86	1
92	MN908947.3	1 29903	456732	339100	1345	12773	42.7148	9.4336	37.8	60	[('Omicron', 0.9999999998744)]	BA.2.86	1
93	MN908947.3	1 29903	505188	388982	10097	22406	74.9289	71.8924	37.8	60	[('Omicron', 0.99999999996849)]	BA.2.86	1
94	MN908947.3	1 29903	509984	401620	2089	10540	35.2473	14.0039	37.8	59.7	[('Omicron', 0.99999999996887)]	BA.2.86	1
95	MN908947.3	1 29903	645836	519726	3831	16461	55.048	25.7244	37.8	60	[('Omicron', 0.999999999960009)]	BA.2.86	1
96	MN908947.3	1 29903	602970	482166	1348	13439	44.942	8.77601	37.8	60	[('Omicron', 0.999999999999883)]	BA.2.86	1
97	MN908947.3	1 29903	578962	454888	5675	20750	69.391	40.7982	37.8	60	[('Omicron', 0.99999999997226)]	BA.2.86	1
98	MN908947.3	1 29903	527304	412700	11703	23424	78.3333	86.9987	37.8	60	[('Omicron', 0.99999999992387)]	BA.2.86	1
99	MN908947.3	1 29903	524950	394188	1216	11047	36.9428	8.62733	37.8	60	[('Omicron', 0.999999999999623)]	BA.2.86	1
800	MN908947.3	1 29903	530160	406042	14546	26132	87.3892	107.853	37.8	60	[('Omicron', 0.999999999999696)]	BA.2.86	



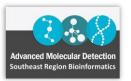


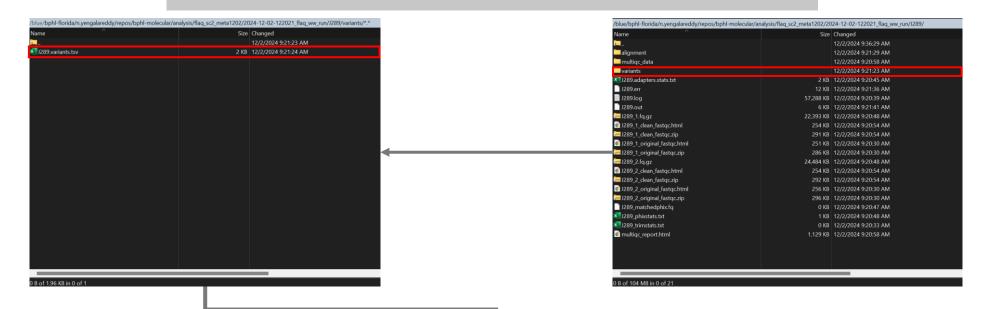
#rname	startpos	endpos	numreads	covbases	coverage	meandepth	meanbaseq	meanmapq
MN908947.3	1	29903	1531	9698	32.4315	9.87536	37.8	60



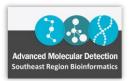


Sample FastQC\_mqc-generalstats-fastqc-percent\_gc FastQC\_mqc-generalstats-fastqc-percent\_duplicates FastQC\_mqc-generalstats-fastqc-percent\_fails FastQC\_mqc-generalstats-fastqc-avg\_sequence\_length FastQC\_mqc-gene





REGION	POS REI	FALT	REF_DP REI	_RV RE	EF_QUAL ALT_	P ALT_	RV ALT_	QUAL	ALT_FREQ	TOTAL_DP	PVAL PASS	GFF_FEATURE	REF_CODON	REF_AA	ALT_CODON	ALT_AA	POS_A
MN908947.3	241 C	Т	0	0	0	7	4	70	1	. 7	0.000582751 TRUE	NA	NA	NA	NA	NA	NA
MN908947.3	9424 A	G	0	0	0	1	0	76	1	. 1	1 FALSE	NA	NA	NA	NA	NA	NA
MN908947.3	10029 C	T	0	0	0	5	2	76	1	. 5	0.00793651 TRUE	NA	NA	NA	NA	NA	NA
MN908947.3	10198 C	T	0	0	0	2	1	54	1	. 2	0.333333 FALSE	NA	NA	NA	NA	NA	NA
MN908947.3	10752 T	#NAME?	2	1	38	2	0	20	1	. 2	0.6 FALSE	NA	NA	NA	NA	NA	NA
MN908947.3	12101 T	Α	0	0	0	1	1	75	1	. 1	1 FALSE	NA	NA	NA	NA	NA	NA
MN908947.3	15714 C	T	0	0	0	2	0	57	1	. 2	0.333333 FALSE	NA	NA	NA	NA	NA	NA
MN908947.3	15756 T	Α	0	0	0	2	0	57	1	. 2	0.333333 FALSE	NA	NA	NA	NA	NA	NA
MN908947.3	17223 A	G	3	0	74	2	1	76	0.4	5	0.277778 FALSE	NA	NA	NA	NA	NA	NA
MN908947.3	17230 A	T	3	1	74	1	0	76	0.25	4	0.571429 FALSE	NA	NA	NA	NA	NA	NA
MN908947.3	17410 C	T	0	0	0	5	3	60	1	. 5	0.00793651 TRUE	NA	NA	NA	NA	NA	NA
MN908947.3	17803 T	С	64	41	58	1	1	76	0.0153846	65	0.503876 FALSE	NA	NA	NA	NA	NA	NA
MN908947.3	17809 A	#NAME?	64	42	58	1	0	20	0.015625	64	0.507813 FALSE	NA	NA	NA	NA	NA	NA
MN908947.3	18492 A	G	0	0	0	38	10	50	1	. 38	2.90E-22 TRUE	NA	NA	NA	NA	NA	NA
MN908947.3	18582 C	T	125	46	60	2	1	24	0.015748	127	0.502976 FALSE	NA	NA	NA	NA	NA	NA
MN908947.3	18692 C	Α	132	69	72	1	1	74	0.0075188	133	0.501887 FALSE	NA	NA	NA	NA	NA	NA
MN908947.3	18701 C	T	137	73	72	1	0	48	0.00724638	138	0.501818 FALSE	NA	NA	NA	NA	NA	NA
MN908947.3	18716 G	T	138	73	72	1	0	76	0.00719424	139	0.501805 FALSE	NA	NA	NA	NA	NA	NA
MN908947.3	18719 G	Α	138	73	71	1	1	76	0.00719424	139	0.501805 FALSE	NA	NA	NA	NA	NA	NA
MN908947.3	18735 A	#NAME?	139	81	67	1	0	20	0.00719424	139	0.754487 FALSE	NA	NA	NA	NA	NA	NA
MANIOCOCA 7 2	10756 6	HALANAES	120	0.1	C2	4		20	0.00775407	120	0.754024 54165	NIA	NIA	NIA	NIA	NIA	NIA



# Conclusion



Fundamentals of FLAO\_SC2\_Meta



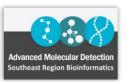
Installation and setup of FLAO\_SC2\_Meta in HPG



Successfully executed Job query for FLAO\_SC2\_Meta



**Generated Output Files** 





# Advanced Molecular Detection Southeast Region Bioinformatics

**Questions?** 

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