

Running CZI pipeline

1. CD into working directory (not home directory)

```
cd /mnt/ajung/ARTIC/
```

2. Download Kraken database

```
mkdir kraken2_db  
wget https://genome-idx.s3.amazonaws.com/kraken/k2\_viral\_20210517.tar.gz  
tar -xf k2_viral_20210517.tar.gz
```

<https://benlangmead.github.io/aws-indexes/k2>

Running CZI pipeline

3. Run command

```
nextflow run czbiohub/sc2-illumina-pipeline -profile artic,docker --reads  
'/mnt/atlantis1/ajung/tutorial/ARTIC_tutorial/WUSTL_data/*_R{1,2}.fastq.gz*' --primers 'SARS-CoV-  
2.dna_manifest.20200408.bed'  
--kraken2_db '/mnt/atlantis1/ajung/tutorial/ARTIC_tutorial/WUSTL_data/kraken2_db' --outdir  
'/mnt/atlantis1/ajung/tutorial/ARTIC_tutorial/WUSTL_data/outdir'
```

Post CZI analysis

- Full workflow

```
nextflow run anajung/CZI_addon --combinedfa 'combined.fa' --vcf 'sample-variants/*.vcf.gz' --outdir './out'
```

- Variant annotation

```
nextflow run anajung/variant_annotation --vcf 'sample-variants/*.vcf.gz' --outdir './out'
```




- Lineage and tree generation

```
nextflow run anajung/lineage --combinedfa 'combined.fa' --outdir './out'
```

https://github.com/anajung/CZI_addon

Tree generation

- <https://microreact.org/upload>

 SHOWCASE UPLOAD INSTRUCTIONS ABOUT SIGN IN  

Simply **drag and drop** files anywhere on this page,
[browse for files](#), or enter file URLs:

.csv file ☐

.nwk file ☐

.dot file ☐

One data file ([.csv](#) or [.tsv](#)) is required.

A tree file ([.nwk](#), [.newick](#), [.tre](#), [.nex](#), or [.nexus](#)) is optional.

A network file ([.dot](#)) is optional.

CONTINUE