

Run a SARS-CoV-2 workflow

C:\Users\StephanieKern-Allely\ncov

1. Download updated USAPI genomic surveillance data from GISAID
 - a. Use search terms
guam/,palau/pw/,micronesia/,marshall islands/,american samoa/,northern mariana
 - b. Filter to sequences that pass the following criteria:
 - i. Has a complete genome
 - ii. Has high coverage
 - iii. Has an exact collection date

The screenshot shows the GISAID Search interface. The 'Search' button is on the left, and 'Reset filters' is on the right. The search criteria are as follows:

- EPI_ISL ID: [] Virus name: []
- Location: [] Host: []
- Collection: [] to [] Submission: [] to []
- Clade: all Lineage: [] Substitutions: [] Variant: []

On the right side, the filter settings are:

- ☒ Complete 1
- ☒ High coverage 2
- ☐ Low coverage excluded
- ☐ With patient status
- ☒ Collection date complete 3
- ☐ Under investigation

- c. Download sequences and metadata files using Search in GISAID
 - i. Select Download in the bottom right of the search results.
 - ii. Select Input for the Augur pipeline as the download format.
 - d. Extract by opening the downloaded .tar file in your file explorer.
 - e. Save under Data folder: C:\Users\StephanieKern-Allely\ncov\data
 - i. Metadata: USAPI.metadata.tsv
 - ii. Sequences: USAPI.sequences.fasta
2. Open Docker
3. Open Anaconda Powershell
 - a. Check for Docker updates
nextstrain update docker
 - b. Check that Docker is working
nextstrain check-setup docker
 - c. Update Conda
nextstrain update conda
 - d. Check Ambient
nextstrain check-setup ambient
4. Activate conda environment
conda activate nextstrain
5. Change to correct directory
cd ncov
6. Run the workflow
nextstrain build . --configfile ncov-tutorial/genomic-surveillance-USAPI.yaml
7. View in Auspice
nextstrain view auspice/
8. To stop the server, press **Control-C** on your keyboard.
 - a. Or reset with:

- i. `conda activate base`
- ii. `conda env remove -n nextstrain`