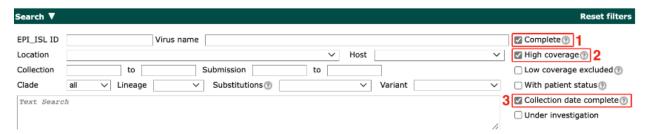
## Run a SARS-CoV-2 workflow

## 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



- 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
  - Update Conda nextstrain update conda
  - d. Check Ambient nextstrain check-setup ambient
- 4. Activate conda environment conda activate nextstrain
- Change to correct directory cd ncov
- 6. Run the workflow

nextstrain build . --configfile ncov-tutorial/genomic-surveillance-USAPI.yaml

- 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