Nextstrain Tutorial
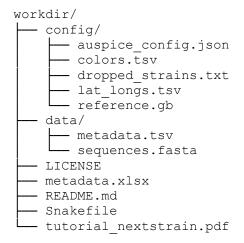
In this tutorial we are going to generate a nextstrain.org community build. To do so, we will run a bioinformatics pipeline (`augur`), which will perform sequence alignment, phylogenetic reconstruction, infer ancestral states (for location and mutations), and finally combine such results to be visualized using a tool named `auspice`.

(1) **Create** a folder in your directory of preference: it will be your working directory (`workdir`).

(2) **Access** the repository below and **download** its content as a `.zip` file:

  github.com/andersonbrito/nextstrain_course

(3) **Decompress** the downloaded `.zip` file and **copy** its content into your `workdir`.

(4) Now, your `workdir` should look as follows:

```
workdir/
├── config/
│   ├── auspice_config.json
│   ├── colors.tsv
│   ├── dropped_strains.txt
│   ├── lat_longs.tsv
│   └── reference.gb
├── data/
│   ├── metadata.tsv
│   └── sequences.fasta
├── LICENSE
├── metadata.xlsx
├── README.md
├── Snakefile
└── tutorial_nextstrain.pdf
```

(5) **Open** the file `metadata.xlsx`. This spreadsheet contains three tabs, named after some of the files in `workdir`, they are: `metadata`, `lat_longs`, and `colors`.

(6) **Copy** and **paste** the data from each tab in the corresponding files, replacing their existing data.

(7) The current `reference.gb` file is included in `config/` only as an example. **Inspect** the format of this file using a text editor, and **check** the fields 'CDS' and 'gene' in this annotation file. **Access** the link below, and **download** this new reference genome in `.gb` format (**click** on Send to > File > Format:Genbank > Create File).

  ncbi.nlm.nih.gov/nuccore/JX669468

(8) **Open** this `.gb` file on a text editor, and **edit** it as follows, so that it looks like the example file inspected at step (7):
   a. **Replace** 'mat_peptide' by 'CDS'
   b. **Replace** 'product' by 'gene'
   c. **Rename** long gene names in the 'gene' fields by standard gene acronyms (see literature)

(9) **Delete** the existing `reference.gb`; **move** the file created in the previous step to `workdir/config`, and; **rename** it as your new `reference.gb` file.

(10) **Open** the file `auspice_config.json` using a text editor and **edit** the lines showing the following content:
   a. 'Add your project title here'
   b. 'Add your name here'
   c. 'Add your github link repository here'

(11) **Open** the file `Snakefile` using a text editor, and **edit** the following lines as appropriate, keeping their suffixes ('_tree' and '_meta'):
   a. 'addHereYourProjectName_tree.json'
   b. 'addHereYourProjectName_meta.json'

(12) Having done all the edits above, **access** your `workdir` in the Terminal, and **run** `augur` using the command below:

```
snakemake export
```

(13) **Watch** for potential error messages: they may indicate issues with file formatting in previous steps.

(14) If no issues were flagged, now **run** `auspice` to visualize the results using the command below:

```
auspice view
```

(15) **Open** a web browser and **access** the results using the link generated by the command above, which may look like the url below:

```
http://localhost:4000
```