

## Multi-Locus Sequence Typing Exercise

Instructions (download the FASTA files)

### Using CGE MLST tool:

Navigate to the *Center for Genomic Epidemiology (CGE)* MLST web tool using this link: <https://cge.cbs.dtu.dk/services/MLST/>.

To analyze a sequence with the MLST tool, you need to upload the files of raw or assembled reads which you want to analyze.

1. **Select MLST configuration** - Select the species most closely related to your organisms of interest
2. **Select type of data input** – if using raw sequences, choose “Raw sequencing reads” (fastq). “Assembled Genomes/Contigs” (fasta) should be selected if you have already assembled reads.
3. **Select isolate file:** To input the sequences, upload a single FASTA or FASTQ files from your local disk. First click on “**Isolate file**” then choose your file and click “**Open**”.
4. **Submit the job** - Click on the green “**Upload**” button and this displays the status of your job “*This job is been processed*”. At any time during the wait you may enter your e-mail address and simply leave the window and you will be notified by e-mail when the job is done or you wait for few minutes and the result shows up on the page.

### Using Pathogenwatch:

Navigate to pathogenwatch web page using this link <https://pathogen.watch/>, to input the sequences, click on “**UPLOAD**” tab on the top right corner of the page. This takes you to a page where you would have to sign in to pathogenwatch with your facebook account, google account, twitter account or with an email. After signing in, follow the instructions below:

1. **Select the file** – There are three options to select the file you wish to upload; *Single Genome FASTAs*, *Multi-genome FASTAs* or *FASTQs*. Click on “**Upload FASTA(s)**” under *Single Genome FASTAs*
2. **Upload the file** – Drag and drop the files on the page or select the “+” sign and choose the file(s) you wish to upload and click “**Open**”. This takes you to the processing screen. By the left corner of the page you can track the progress of the analyses and know when it is completed.

Once the tasks are complete, you can press the “**View Genomes**” to view the results of the analyses.

## Questions

Download the FASTA files.

Using **the CGE MLST tool** and **Pathogenwatch**,

1. Determine the sequence types of the sequenced genomes.
2. What sequence type is most prevalent?
3. What can you find out from the literature about the most prevalent sequence type?

*This assignment should be submitted to “**FAITH I. ONI**” as a Direct Message on “**SLACK**”*