**Bacteria Identification Exercise**

Instructions (download the FASTA files)

**Using KmerFinder:**

Navigate to the *Center for Genomic Epidemiology (CGE)* web tool using this link <https://cge.cbs.dtu.dk/services> , click on the ***“KmerFinder”*** tool under **Typing** and this takes you to the KmerFinder home page.

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

1. **Select the database -** Select the database you want to use in the search using the drop down menu and in this case it is **“Bacteria organisms”**
2. **Upload the file -** To input the sequences, upload a single FASTA file or two FASTQ files from your local disk. First click on **“Isolate file”** then choose your file and click **“Open”.**
3. **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 “uploads” 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, it takes you to a page and follow the instructions.

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 **KmerFinder** and **Pathogenwatch,**

1. Determine the species of the sequenced genomes
2. What is the query\_coverage for each of the genomes from the Kmerfinder result?
3. Which of these tools did you find most convenient to use and why?

*This assignment should be submitted to* ***“IFEOLUWA JANET AKINTAYO”*** *as a Direct Message on* ***“SLACK”***