FEB 02, 2024

Bacterial Genomics24

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ABSTRACT

This is the protocol for going through the bacterial genomics course.

OPEN ACCESS

DOI:
dx.doi.org/10.17504/protocols.io.x54v9pxpzg3e/v1

Protocol Citation: George Odette 2024. Bacterial Genomics24. **protocols.io** https://dx.doi.org/10.17504/protocols.io.x54v9pxpzg3e/v1

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Protocol status: In development
We are still developing and optimizing this protocol

Created: Feb 02, 2024

Last Modified: Feb 02, 2024

PROTOCOL integer ID: 94622

Installing software for the Bacterial Genomics24

1 We will install many of the software we will use using conda.

Conda

To install conda, run the following script

```
wget https://repo.anaconda.com/archive/Anaconda3-2023.09-0-Linux-x86_64.sh
```

Once the download is complete, run this script:

```
bash Anaconda3-2023.09-0-Linux-x86_64.sh
```

The first time you call conda you might get the error below:

conda: command not found

If that happens, run this script to add conda to path:

```
export PATH=~/anaconda3/bin:$PATH
```

But again, if you refresh the shell, you will bump into *conda: command not found* again. So, add the script to the bashrc file.

Open bashrc using

```
nano ~/.bashrc
```

The add the export PATH=~/anaconda3/bin:$PATH at the bottom of the file. Click **ctrl + o,** to save, press enter, the ctrl + x to exit.

Configuring bioconda

Run the following scripts to configure Bioconda

```
conda config --add channels defaults
conda config --add channels biocondac
onda config --add channels conda-forge
```