



Feb 02, 2024

Bacterial Genomics24

DOI

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

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DOI: <https://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: February 02, 2024



Last Modified: February 02, 2024

Protocol Integer ID: 94622

Keywords: bacterial genomics course, bacterial genomics24, genomic

Abstract

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

Troubleshooting

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
```