

GETTING STARTED

Please note: these steps should be completed prior to the workshop.

1. Open your terminal and navigate to the conda_workshop directory

```
cd /mnt/c/Users/JRumore/Desktop/conda_workshop
```

2. Make a new directory called Reference_Databases

```
mkdir Reference_Databases
```

3. Open your internet browser and navigate to the MMID Bioinformatics Workshop Github 2023-03-30-Reference-Databases repository (<https://github.com/mmidiobioinformatics-workshop/2023-03-30-Reference-Databases>) and download the workshop datasets to the Reference_Databases directory.

```
https://drive.google.com/drive/folders/1vVc2KJnlAsy8u2l6VPgKWMEBtmL6zRwE?usp=share\_link
```

4. From the same repository, download the Kraken 2 database to the Reference_Databases directory.

```
https://drive.google.com/drive/folders/1Lzdp16XW4anl4lNtU5dN2Zuszb44FDJB?usp=share\_link
```

**This will take ~ 20 minutes to download*

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5. Move into the Reference_Databases directory and decompress the Kraken 2 database file (i.e., kraken2_STND-DB-8GB-001.tar.bz2).

```
cd Reference_Databases  
tar -xvf kraken2_STND-DB-8GB-001-tar.bz2
```