Welcome to bioBakery

bioBakery is a virtual machine (VM) environment designed to help you execute metagenomics analyses.

bioBakery and the tools therein were developed by the Huttenhower lab at the Harvard School of Public Health:
HTTP://HUTTENHOWER.SPH.HARVARD.EDU/

bioBakery is built on Ubuntu 18.04 LTS (Bionic Beaver).

Using bioBakery tools

This document introduces some important details of the **bioBakery** environment.

For an overview of the types of software and analyses available in **bioBakery**, please visit the **bioBakery** website. It also includes links to the individual websites for each tool installed in **bioBakery**.

HTTP://HUTTENHOWER.SPH.HARVARD.EDU/BIOBAKERY

Differences from standard linux (1)

We have customized **bioBakery** to be a bit more forgiving than the typical linux environment.

In linux, typing `rm` *`file`* in the terminal will permanently delete the file; in **bioBakery**, this command moves the file to the trash. (Use `hardrm` *`file`* to delete permanently.)

bioBakery will also prompt you before overwriting a file. (E.g. if you attempt to move or copy a file to a location with an identically named file.)

Differences from standard linux (2)

You can open a file in **bioBakery** by typing **open** *file* in the terminal; this will open the file in its associated default program.

Right clicking on the Desktop, a folder icon, or inside of a folder will give you the option to open a terminal at that location. (Select "open terminal here")

Sharing files with bioBakery (1)

Using Vagrant and VirtualBox, your computer's operating system (the "host OS") runs **bioBakery** within a window as a separate operating system (the "guest OS").

By default, the guest OS can only see files on the host OS if they are located within the host's `vagrant` folder.

The vagrant folder appears in **bioBakery** as `/vagrant`.

Sharing files with bioBakery (2)

We strongly recommend saving important files to the host OS so they are available outside of **bioBakery**.

You may also be interested to share additional data folders from your host OS with **bioBakery**.

CLICK HERE TO LEARN HOW

PATH details

All programs installed by **bioBakery** are located in
`/usr/local/`

Executable programs are located the bin folder.

This means that you can type a command like
`$ metaphlan --help`
from anywhere to see MetaPhlAn's help output.

Additional software

In addition to packaging Huttenhower lab tools, **bioBakery** contains all of the freely-distributable dependencies of those tools (e.g. bowtie2, blast+, diamond).

Adding/upgrading programs

To upgrade a bioBakery tool run:

```
$ pip3 install $TOOL --upgrade
(replacing $TOOL with the name of the bioBakery tool to install)
```

Pip can also be used to install other tools.

```
$ pip3 install $TOOL
```

For more help

Check out the **bioBakery** wiki for more information:

HTTPS://GITHUB.COM/BIOBAKERY/BIOBAKERY/WIKI/BIOBAKERY_WIKI

You can also join and post to the **bioBakery** user forum:

HTTPS://FORUM.BIOBAKERY.ORG/