



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/](http://huttenhower.sph.harvard.edu/)

bioBakery is built on Ubuntu 16.04 LTS (Xenial Xerus).



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/BIODAKERY](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
`/home/vagrant/.linuxbrew/`

Executable programs are located the bin folder which has
been added to the PATH environment variable.

This means that you can type a command like
`$ metaphlan2.py --help`
from anywhere to see MetaPhlAn2'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).

Some additional dependencies (e.g. USEARCH) cannot be distributed with **bioBakery** because they require a license. However, they can be added manually if the user wishes.

[CLICK HERE TO LEARN HOW](#)



Adding/upgrading programs

To add or upgrade a bioBakery tool run:

```
$ brew install $TOOL
```

(replacing \$TOOL with the name of the bioBakery tool to install)

[CLICK HERE FOR A COMPLETE LIST OF BIOBAKERY HOMEBREW FORMULAS](#)

Homebrew can also be used to install other tools.

```
$ brew install $TOOL
```

[CLICK HERE FOR A COMPLETE LIST OF HOMEBREW FORMULAS](#)



For more help

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

[HTTPS://BITBUCKET.ORG/BIOBAKERY/BIOBAKERY/WIKI/BIOBAKERY_WIKI](https://bitbucket.org/bioBakery/bioBakery/wiki/bioBakery_wiki)

You can also join and email the **bioBakery** user group:

BIOBAKERY-USERS@GOOGLEGROUPS.COM