



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 15.10 (Wily Werewolf).



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`; a shortcut to this folder appears on the **bioBakery** Desktop.



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:

```
$ sudo 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.

```
$ sudo 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