



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 based on Ubuntu Linux 12.10.



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:

<https://bitbucket.org/biobakery/biobakery>

For help with a specific tool, please visit its individual web site; links to individual tool pages are available here:

<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 command prompt 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* at the command prompt; 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 command prompt at that location.



Sharing files with bioBakery

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 Vagrant folder.

[Click here to learn how to share additional folders/files from the host OS with bioBakery.](#)

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



PATH details

All programs installed by biobakery are located in:
`/usr/share/biobakery`

Executable programs located in this folder have been added to the PATH environment variable.

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



Adding/upgrading programs

<*.deb> installation files are available for Huttenhower Lab tools in this repository:

<http://huttenhower.sph.harvard.edu/biobakery-shop/deb-packages>

To add or upgrade a Huttenhower Lab tool run:

```
$ sudo apt-get install hutlab_tool
```

The same command can be used to install other linux utilities (these are not supported):

```
$ sudo apt-get install other_utility
```



For more help

Check out the bioBakery wiki for more information:

https://bitbucket.org/biobakery/biobakery/wiki/biobakery_wiki

You can also join and email the bioBakery user group:

biobakery-users@googlegroups.com