

Table of contents

- [General info](#)
- [Software](#)
- [How-to-use](#)
- [Troubleshooting](#)

General Info

This is the repository for the software required by for the Microbiome workshop. Please note that what is installed in /gpfs/group/dml129/default/microbiome_workshop2020 may differ from this repository as the actual setup version of this repository will contain conda environments.

To view this documentation in a different format then please see the doc directory of this repository.

Software

The repository contains the following software:

- RStudio
- Qiime2
- Megan
- MALT

How-to-use

- [RStudio](#)
- [Qiime2](#)
- [Megan](#)
- [MALT](#)

RStudio

Simply use the following commands to load the rstudio module:

```
$ module use /gpfs/group/dml129/default/microbiome_workshop2020/sw/modules  
$ module load rstudio
```

Now that you have the module loaded, here are the various ways that you can interact with it.

To launch rstudio:

```
$ rstudio
```

To use R:

```
$ R
```

To use Rscript:

```
$ Rscript
```

To use Rscript quietly:

```
$ chronic-Rscript
```

Qiime2

To setup access to Qiime2, you will first need to create a symlink to the environment in your home directory using the scripts module:

```
$ module use /gpfs/group/dml129/default/microbiome_workshop2020/sw/modules
$ module load scripts
$ link_qiime2
```

This will then create a symlink to the qiime2 environment in your home directory. You can use the following commands to activate the environment:

```
$ module load python/3.6.3-anaconda5.0.1
$ cd ~
$ source activate qiime2
```

To then verify that Qiime2 is working simply use the following command:

```
$ qiime --help
```

Megan

To setup access to Megan, you will first need to create a symlink to the environment in your home directory using the scripts module:

```
$ module use /gpfs/group/dml129/default/microbiome_workshop2020/sw/modules
$ module load scripts
$ link_megan
```

This will then create a symlink to the megan environment in your home directory. You can use the following commands to activate the environment:

```
$ module load python/3.6.3-anaconda5.0.1
$ cd ~
$ source activate megan
```

To then launch Megan's GUI (need to be in an Interactive Desktop session) use the following command:

```
$ MEGAN
```

MALT

To access MALT, all you need to do is activate the [Megan](#) environment:

```
$ module load python/3.6.3-anaconda5.0.1
$ cd ~
$ source activate megan
```

Then, to test that you have access to MALT simply use the following command:

```
malt-build -h
```

Troubleshooting

If you run into any issues regarding the use of this repository then please contact either Jason or Justin at iask@ics.psu.edu.