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## 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](#rstudio)
* [Qiime2](#qiime2)
* [Megan](#megan)
* [MALT](#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](#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.