

mothur



mothur

- Like qiime and usearch, mothur is a collection of scripts for manipulating, and analysing NGS sequencing data
- Open source, but primary development is by Pat Schloss
- New releases every couple of months
- Workshops and courses worldwide

mothur

- Similar to usearch/vsearch (unlike qiime) in that it doesn't have numerous dependencies
 - Still incorporates algorithms from other developers – they're rewritten by the mothur team based on information from publications
- Installation straightforward, download from mothur.org

Is mothur right for you?

- Got paired end data from small amplicons (<300bp)? YES
- Software sets itself aside from things like qiime/usearch/vsearch by taking a phylogenetic approach
 - Many analyses/steps in the workflow require a sequence alignment (good for 16S/18S and some LSU)

Mothur documentation

- Wiki for the program is online
- Tutorials give a good overview of how to use the program in different scenarios



[Main page](#)
[Recent changes](#)
[Random page](#)
[Help](#)

Tools

[What links here](#)
[Related changes](#)
[Special pages](#)
[Printable version](#)
[Permanent link](#)
[Page information](#)

Category

[Discussion](#)

Read

[View source](#)

[View history](#)

We will be hosting mothur, R, and reproducible research workshops throughout 2017. [Learn more.](#)

Category:Commands

This is a listing of the various commands available within mothur.

Pages in category "Commands"

The following 146 pages are in this category, out of 146 total.

A

- [Align.check](#)
- [Align.seqs](#)
- [Amova](#)
- [Anosim](#)

B

- [Bin.seqs](#)

C

- [Catchall](#)

- [Make.fastq](#)
- [Make.file](#)
- [Make.group](#)
- [Make.lefse](#)
- [Make.lookup](#)
- [Make.shared](#)
- [Make.sra](#)
- [Mantel](#)
- [Merge.count](#)
- [Merge.files](#)
- [Merge.groups](#)

Mothur Syntax

- All mothur commands follow the same format:

Script.name(option=value, option=value)

- name of the script you want to call
- usually intuitive eg. filter.seqs, make.lfse
- must always be in the first position

Mothur Syntax

- All mothur commands follow the same format:

Script.name(option=value, option=value)

- Comma separated list of options inside parentheses
- usually intuitive eg. filter.seqs, make.lefse
- order is not important
- Avoid space between value and ,

- value for the option
- separated from the option name by a space
- can be a filename, an algorithm name, a numeric value, or a TRUE/FALSE

Mothur Input Files

1. Sequences! (this is the only critical thing mothur needs, it can generate the rest of its information files)
2. Group File (only needed if you're bringing in sequences that have been processed in another program)

