# 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

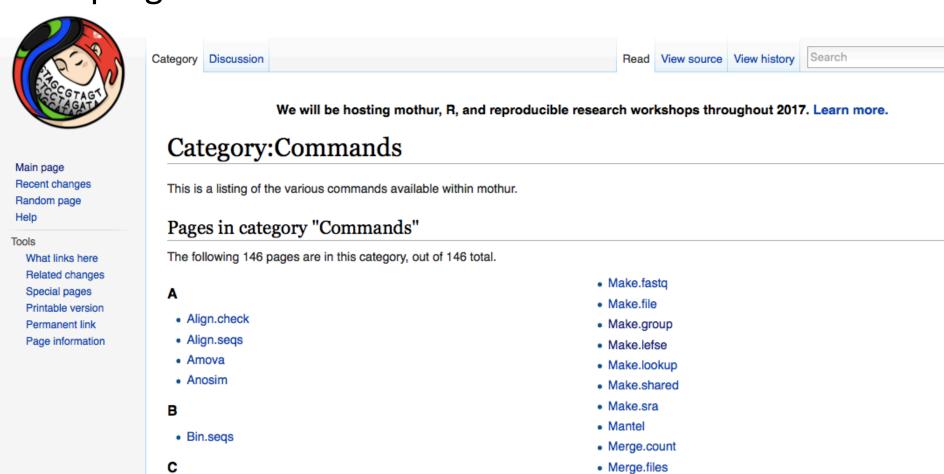
- Similar to usearch/vsearch (unlike qiime) in that it doesn't have numerous dependencies
  - Still incorporates algorithms from other developers – they're rewritten by the mothur team based on information from publications
- Installation straightforward, download from mothur.org

## Is mothur right for you?

- Got paired end data from small amplicons (<300bp)? YES</li>
- 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



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.lefse
- 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)

