

classdir: /Network/Servers/bio8.bio.nd.edu/Volumes/class_data/bios60579

BLAST

path: *classdir*/bin/ncbi/bin/blastall

required arguments:

- p <program name> (blastn,blastp,blastx,tblastn,tblastx).
- d <path to target database>
- i <query file>

Everything else is optional. Simply run `blastall` to see all options.
To turn a fasta file into a database, use the program `formatdb` in the same dir.

CLUSTALW

path: *classdir*/bin/clustalw/clustalw

required arguments: none

optional arguments: <input sequence file>

HMMER Suite

path: *classdir*/bin/hmmer/bin/hmm*

required arguments:

Run each program to see specifics. The basics are:

`hmmbuild` <hmm output file> <alignment input file>

`hmmcalibrate` <hmm input file>

`hmmsearch` <hmm input file> <subject sequence file>

Phrap

path: *classdir*/bin/phrap/phrap

required arguments:

<input file>

Read the docs at <http://www.phrap.org> for more information if you want to use quality values in your assembly.