

## Advanced usage

### Manually installing dependencies

To run OrthoFinder3 on default setting, you will need **diamond**, **famsa**, **fasttree**, **MCL**

If you install OrthoFinder using a recommended method, you shouldn't need to install any of the dependencies manually, but in case you do;

#### *Diamond*

<https://github.com/bbuchfink/diamond>

#### *FAMSA*

<https://github.com/refresh-bio/FAMSA>

#### *FastTree*

<http://www.microbesonline.org/fasttree/#Install>

#### *MCL*

<https://github.com/micans/mcl>

### Running BLAST searches separately

The '-op' option will prepare the files in the format required by

OrthoFinder and print the set of BLAST commands to run.

```
orthofinder -f fasta_files_directory -op
```

This is useful if you want to manage the BLAST searches yourself. For example, you may want to distribute them across multiple machines. Once the BLAST searches have been completed the orthogroups can be calculated using the '-b' command (see below)

### Use pre-computed BLAST

It is possible to run OrthoFinder with pre-computed BLAST results provided they are in the correct format. They can be prepared in the correct format using the '-op' command and, equally, the files from a previous OrthoFinder run are also in the correct format to rerun using the '-b' option. The command is simply:

```
orthofinder -b directory_with_processed_fasta_and_blast_results
```

If you are running the BLAST searches yourself it is strongly recommended that you use the '-op' option to prepare the files first (see Section "Running BLAST Searches Separately")