

Controlling the OrthoFinder Analysis

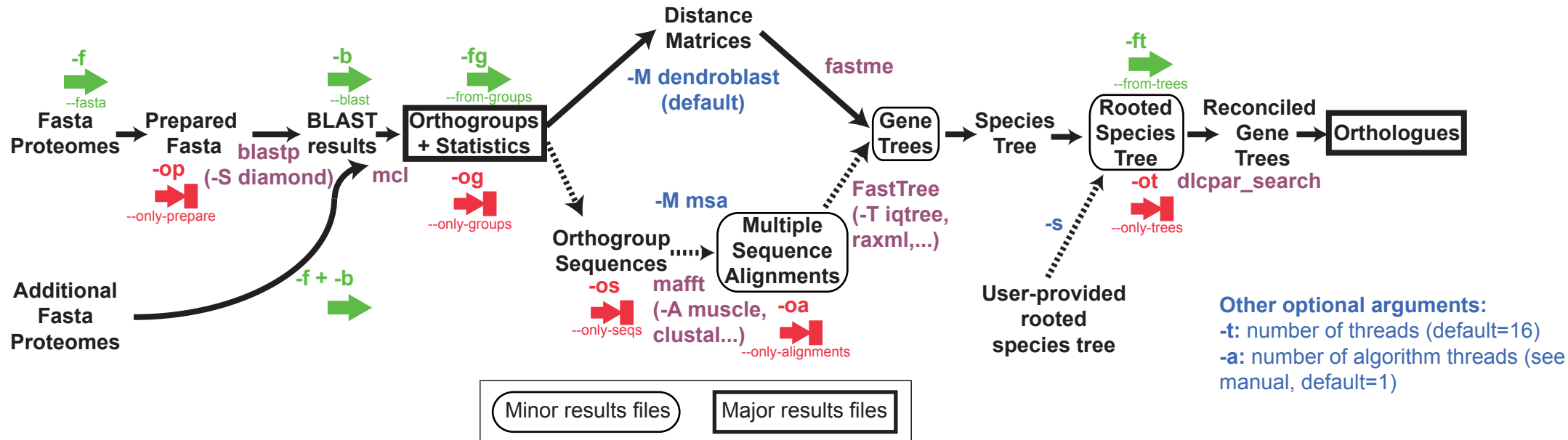
If you just want to run a full analysis automatically,
use: `'orthofinder -f fasta_dir'`

Control where OrthoFinder starts
Command-line switch takes directory containing files as argument.

Control where OrthoFinder stops (e.g. `-ot` = 'only up to & including trees')

Optional arguments

Programs required for each step (alternatives)



Other optional arguments:
`-t`: number of threads (default=16)
`-a`: number of algorithm threads (see manual, default=1)

Example commands:

`-f <fasta_dir>`

Perform a complete OrthoFinder analysis on the proteomes contained in `fasta_dir`, use the default dendroblast method to infer gene trees.

`-fg <orthogroups_dir> -ot`

Infer gene trees for the the orthogroups in `orthogroups_dir`, the rooted species tree and the all orthologues (use dendroblast for gene trees).

`-f <fasta_dir> -b <previous_blast_results_dir> -M msa -oa`

Reinfer orthogroups by adding the species from `fasta_dir` to species in `previous_blast_results_dir` and infer MSAs for each orthogroup.

`-f <fasta_dir> -t 64 -M msa`

Perform a complete OrthoFinder analysis on the proteomes contained in `fasta_dir`, use gene trees inferred from `multiple sequence alignments` and `64 threads`.