

MulRF Software Manual

Input

MulRF takes as input a single file (specified using `-i` option) containing one or more gene trees. All input trees must be expressed using the Newick format terminated by a semicolon.

Example, `((speciesA, speciesB),speciesC);`

If a initial species tree is provided it should be the first tree in the input file. Input gene trees are allowed to be non-binary, not only binary, but initial species tree should always be a binary tree. Input trees can be rooted or unrooted. However, MulRF treats all trees as unrooted. An unrooted gene tree must still be written as a rooted tree in Newick format, but must have the tag `[&U]` included at the beginning of that gene tree.

Example, `[&U]((speciesA, speciesB),speciesC);`

Output

MulRF's output contains a single file consisting the resulting species tree in Newick format, with its MulRF cost. Depending on the selected options input gene tree and the initial species tree can also be included.

Available Command Line Options

<code>-i, --input</code>	input file
<code>-o, --output</code>	output file
<code>--stree</code>	first input tree is a starting species tree
<code>--initialtree</code>	output the initial species tree
<code>--inputtrees</code>	output the input trees
<code>--alltrees</code>	synonym for <code>--initialtree</code> and <code>--inputtrees</code>
<code>--seed</code>	random generator seed
<code>-h, --help</code>	produce help message

Running MulRF

Download the executable, and sample input files from the web page and put both in one working directory. For Windows, Mac, or Linux, type the corresponding command (with appropriate options):

- Windows: `MulRF-Win.exe -i <input-file.newick> -o <output-file.newick>`
- Mac: `./MulRF-Mac -i <input-file.newick> -o <output-file.newick>`
- Linux: `./MulRF-Lin -i <input-file.newick> -o <output-file.newick>`

† Note: Make the program executable for Linux and Mac in advance.