

UFBoot-MP version 1.0 (October 2015)

Ultrafast approximation for parsimony bootstrap

User Manual

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1 Introduction

UFBoot-MP is an efficient program for parsimony analysis. The program can reconstruct maximum parsimony trees for large DNA and protein sequence alignments. More importantly, it implements the method UFBoot-MP for approximating maximum parsimony bootstrap. The method was built on the ultrafast bootstrap approximation for maximum likelihood (UFBoot; Minh et al. 2013) and other local optimization techniques. UFBoot-MP is open-source and freely available from <http://www.cibiv.at/software/ufboot-mp>. It has been tested on Unix, Mac OS X.

2 Installation

- 1) Download the executable version of UFBoot-MP for your operating system if it is available (ufbootmp-XXX-OS.tar.gz or ufbootmp-XXX-OS.zip, where XXX is the current version number and OS the operating system) from <http://www.cibiv.at/software/ufboot-mp>
- 2) Extract the files (e.g., with `tar xvzf ufbootmp-XXX-OS.tar.gz` under Unix). This should create a directory ufbootmp-XXX-OS.
- 3) You will find the executable in ufbootmp-XXX-OS/. This executable you should rename to ufbootmp (or ufbootmp.exe on Windows systems) and copy it to your system search path such that it is found by your system.

3 Tutorial

3.1 Minimal command-line examples

(replace 'ufbootmp ...' with actual path to executable)

- 1) Reconstruct maximum parsimony tree from a sequence alignment (example.phy):

```
ufbootmp -s example.phy
```

- 2) Reconstruct MP tree and assess branch supports with the UFBoot-MP method (1000 replicates):

```
ufbootmp -s example.phy -bb 1000
```

3.2 All available options: run 'ufbootmp -h'

- mulhits Store multiple equally parsimonious trees per bootstrap replicate
- ratchet_iter <number> Number of non-ratchet iterations before each ratchet iteration (default: 1)
- ratchet_wgt <number> Weight to add to each site selected for perturbation during ratchet (default: 1)
- ratchet_percent <number> Percentage of informative sites selected for perturbation during ratchet (default: 50)
- ratchet_off Turn off ratchet, i.e. Only use tree perturbation
- spr_rad <number> Maximum radius of SPR (default: 3)
- cand_cutoff <#s> Use top #s percentile as cutoff for selecting bootstrap candidates (default: 10)
- opt_btree_off Turn off refinement step on the final bootstrap tree set
- nni_pars Hill-climb by NNI instead of SPR

3.3 Input/Output files description

- Input alignment file: example.phy
- UFBoot-MP report file: example.phy.ufbootmp
- Maximum-parsimony tree file: example.phy.treefile
- Split support values file: example.phy.splits.nex
- Consensus tree file: example.phy.contree
- Screen log file: example.phy.log

Credits and Acknowledgement

Some parts of the code were taken from the following packages/libraries: Phylogenetic likelihood library (Flouri et al., 2014), TREE-PUZZLE (Schmidt et al., 2002), BIONJ (Gascuel, 1997), Nexus Class Library (Lewis, 2003), Eigen library (Guennebaud et al., 2010), SPRNG library (Mascagni and Srinivasan, 2000), Zlib library (<http://www.zlib.net>).