

MisawaTajima: A program for weighting methods for phylogenetic tree reconstruction among multiple loci

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Users can set parameters of MisawaTajima by using command-line options.

To conduct a phylogenetic tree by using sequences of multiple loci:

```
java -jar MisawaTajima.jar -m PO -u 0.5 -alpha 1.0 -l 100 -n 10 -t 10000 -r 10 -T A -d PO -o exact -w TATA
```

To reconstruct a phylogenetic tree by using sequences of multiple loci:

```
java -jar MisawaTajima.jar -f o list.txt -f c atp6.txt -f c atp8.txt -f c col.txt -w TATA -t 10000
```

Options:

-m mutation_pattern

PO Poisson for Protein

K2 Kimura's (1980) 2-parameter model for DNA

-u mutation_rate

-alpha gamma_shape_parameter

-l gene_length

-n number_of_loci

-t number_of_trials

number_of_bootstrap_resampling, when a phylogenetic tree is reconstructed

-T model_tree

A an asymmetric tree

B a symmetric tree

-d distance

PO Poisson distance for protein sequence

PG Poisson gamma distance for protein sequence

K2 Kimura's 2 parameter distance for DNA sequence

GP Goldstein and Pollock (1994) distance for DNA sequence

TT Tajima and Takezaki (1994) distance for DNA sequence

-w weighting_method

K or length: no weight

L or LS: the least square method

M or TATA: the new method

-i input

list filename list of OTUs

fasta filename sequence file in fasta format

clustal filename sequence file in clustal format

-o output

exact count the number of exact match when simulation is conducted

topology calculate the mean of topological distance when simulation is conducted

sequence outputs concatenated sequences