This manual does not cover all the features of the latest version. See also tips and changelog. (Feb. 2011)

MAFFT

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NAME

mafft - Multiple alignment program for amino acid or nucleotide sequences

SYNOPSIS

mafft [options] input [> output]
linsi input [> output]
ginsi input [> output]
einsi input [> output]
fftnsi input [> output]
fftns input [> output]
mwns input [> output]
mwnsi input [> output]
mafft-profile group1 group2 [> output]

input, group1 and group2 must be in FASTA format.

DESCRIPTION

MAFFT is a multiple sequence alignment program for unix-like operating systems. It offers a range of multiple alignment methods.

Accuracy-oriented methods:

*L-INS-i (probably most accurate; recommended for <200 sequences; iterative refinement method incorporating local pairwise alignment information):

mafft --localpair --maxiterate 1000 input [> output]
linsi input [> output]

*G-INS-i (suitable for sequences of similar lengths; recommended for <200 sequences; iterative refinement method incorporating global pairwise alignment information):

mafft --globalpair --maxiterate 1000 input [> output]
ginsi input [> output]

*E-INS-i (suitable for sequences containing large unalignable regions; recommended for <200 sequences):

mafft --ep 0 --genafpair --maxiterate 1000 input [> output]
einsi input [> output]
For E-INS-i, the --ep 0 option is recommended to allow large gaps.

### Speed-oriented methods:

*FFT-NS-i (iterative refinement method; two cycles only):

```bash
mafft --retree 2 --maxiterate 2 input [> output]
fftinsi input [> output]
```

*FFT-NS-i (iterative refinement method; max. 1000 iterations):

```bash
mafft --retree 2 --maxiterate 1000 input [> output]
```

*FFT-NS-2 (fast; progressive method):

```bash
mafft --retree 2 --maxiterate 0 input [> output]
fftms input [> output]
```

*FFT-NS-1 (very fast; recommended for >2000 sequences; progressive method with a rough guide tree):

```bash
mafft --retree 1 --maxiterate 0 input [> output]
```

*NW-NS-i (iterative refinement method without FFT approximation; two cycles only):

```bash
mafft --retree 2 --maxiterate 2 --nofft input [> output]
nwinsi input [> output]
```

*NW-NS-2 (fast; progressive method without the FFT approximation):

```bash
mafft --retree 2 --maxiterate 0 --nofft input [> output]
nwnsi input [> output]
```

*NW-NS-PartTree-1 (recommended for ~10,000 to ~50,000 sequences; progressive method with the PartTree algorithm):

```bash
mafft --retree 1 --maxiterate 0 --nofft --parttree input [> output]
```

### Group-to-group alignments

```bash
mafft-profile group1 group2 [> output]
```

or:

```bash
mafft --maxiterate 1000 --seed group1 --seed group2 /dev/null [> output]
```

### OPTIONS

#### Algorithm

```bash
--auto
```

Automatically selects an appropriate strategy from L-INS-i, FFT-NS-i and FFT-NS-2, according to data size. Default: off (always FFT-NS-2)

```bash
--6merpair
```

Distance is calculated based on the number of shared 6mers. Default: on
--globalpair

All pairwise alignments are computed with the Needleman-Wunsch algorithm. More accurate but slower than --6merpair. Suitable for a set of globally alignable sequences. Applicable to up to ~200 sequences. A combination with --maxiterate 1000 is recommended (G-INS-i). Default: off (6mer distance is used)

--localpair

All pairwise alignments are computed with the Smith-Waterman algorithm. More accurate but slower than --6merpair. Suitable for a set of locally alignable sequences. Applicable to up to ~200 sequences. A combination with --maxiterate 1000 is recommended (L-INS-i). Default: off (6mer distance is used)

--genafpair

All pairwise alignments are computed with a local algorithm with the generalized affine gap cost (Altschul 1998). More accurate but slower than --6merpair. Suitable when large internal gaps are expected. Applicable to up to ~200 sequences. A combination with --maxiterate 1000 is recommended (E-INS-i). Default: off (6mer distance is used)

--fastapair

All pairwise alignments are computed with FASTA (Pearson and Lipman 1988). FASTA is required. Default: off (6mer distance is used)

--weighti number

Weighting factor for the consistency term calculated from pairwise alignments. Valid when either of --globalpair, --localpair, --genafpair, --fastapair or --blastpair is selected. Default: 2.7

--retree number

Guide tree is built number times in the progressive stage. Valid with 6mer distance. Default: 2

--maxiterate number

number cycles of iterative refinement are performed. Default: 0

--fft

Use FFT approximation in group-to-group alignment. Default: on

--nofft

Do not use FFT approximation in group-to-group alignment. Default: off

--noscore

Alignment score is not checked in the iterative refinement stage. Default: off (score is checked)

--memsave

Use the Myers-Miller (1988) algorithm. Default: automatically turned on when the alignment length exceeds 10,000 (aa/nt).

--parttree

Use a fast tree-building method (PartTree, Katoh and Toh 2007) with the 6mer distance. Recommended for a large number (> ~10,000) of sequences are input. Default: off

--dpparttree
The PartTree algorithm is used with distances based on DP. Slightly more accurate and slower than --parttree. Recommended for a large number (> ~10,000) of sequences are input. Default: off

--fastaparttree

The PartTree algorithm is used with distances based on FASTA. Slightly more accurate and slower than --parttree. Recommended for a large number (> ~10,000) of sequences are input. FASTA is required. Default: off

--partsize number

The number of partitions in the PartTree algorithm. Default: 50

--groupsize number

Do not make alignment larger than number sequences. Valid only with the -*parttree options. Default: the number of input sequences

Parameter

--op number

Gap opening penalty at group-to-group alignment. Default: 1.53

--ep number

Offset value, which works like gap extension penalty, for group-to-group alignment. Default: 0.123

--lop number

Gap opening penalty at local pairwise alignment. Valid when the --localpair or --genafpair option is selected. Default: -2.00

--lep number

Offset value at local pairwise alignment. Valid when the --localpair or --genafpair option is selected. Default: 0.1

--lexp number

Gap extension penalty at local pairwise alignment. Valid when the --localpair or --genafpair option is selected. Default: -0.1

--LOP number

Gap opening penalty to skip the alignment. Valid when the --genafpair option is selected. Default: -6.00

--LEXP number

Gap extension penalty to skip the alignment. Valid when the --genafpair option is selected. Default: 0.00

--bl number

BLOSUM number matrix (Henikoff and Henikoff 1992) is used. number=30, 45, 62 or 80. Default: 62

--jtt number

JTT PAM number (Jones et al. 1992) matrix is used. number>0. Default: BLOSUM62

--tm number

Transmembrane PAM number (Jones et al. 1994) matrix is used. number>0.
Default: BLOSUM62

--aamatrix matrixfile

Use a user-defined AA scoring matrix. The format of matrixfile is the
same to that of BLAST. Ignored when nucleotide sequences are input.
Default: BLOSUM62

--fmodel

Incorporate the AA/nuc composition information into the scoring matrix.
Default: off

Output

--clustalout

Output format: clustal format. Default: off (fasta format)

--inputorder

Output order: same as input. Default: on

--reorder

Output order: aligned. Default: off (inputorder)

--treeout

Guide tree is output to the input.tree file. Default: off

--quiet

Do not report progress. Default: off

Input

--nuc

Assume the sequences are nucleotide. Default: auto

--amino

Assume the sequences are amino acid. Default: auto

--seed alignment1 [--seed alignment2 --seed alignment3 ...]

Seed alignments given in alignment_n (fasta format) are aligned with
sequences in input. The alignment within every seed is preserved.

FILES

Mafft stores the input sequences and other files in a temporary directory,
which by default is located in /tmp.

ENVIRONMENT

MAFFT_BINARIES

Indicates the location of the binary files used by mafft. By default,
they are searched in /usr/local/lib/mafft, but on Debian systems, they are searched in /usr/lib/mafft.

FASTA_4_MAFFT

This variable can be set to indicate to mafft the location to the fasta34 program if it is not in the PATH.

SEE ALSO

mafft-homologs(1)

REFERENCES

In English

*Katoh and Toh (Bioinformatics 23:372-374, 2007) PartTree: an algorithm to build an approximate tree from a large number of unaligned sequences (describes the PartTree algorithm).


*Katoh, Misawa, Kuma and Miyata (Nucleic Acids Res. 30:3059-3066, 2002) MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform (describes the FFT-NS-1, FFT-NS-2 and FFT-NS-i strategies)

In Japanese

*Katoh and Misawa (Seibutsubutsuri 46:312-317, 2006) Multiple Sequence Alignments: the Next Generation


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Wrote this manpage in DocBook XML for the Debian distribution, using Mafft's homepage as a template.

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