

DiAlign-T: Parameters

usage: dialign-t [options] <conf-dir> <input-file> [output-file]

OPTIONS

input type

option: -D [DNA]
default: protein
usage: dialign-t -D <conf-dir> <input-file> [output-file]

Sets the input type and default values for the alignment to DNA (default protein values). This option is only needed, if the input type is DNA.

alignment on protein level for DNA sequences

option: -T [translation]
default: alignment computed on DNA level
usage: dialign-t -T <conf-dir> <input-file> [output-file]
WARNING: Do not use -D in this case although it is DNA input!

DNA sequences will be translated into aminoacids. The length of the sequences will be cut to $\text{mod } 3 = 0$. The aminoacids will be aligned and then retranslated into DNA sequences for output.

option: -O [with ORF finder]
default: alignment computed on DNA level
usage: dialign-t -O <conf-dir> <input-file> [output-file]
WARNING: Do not use -D in this case although it is DNA input!

DNA sequences will be translated into aminoacids. The reading frame for each sequence is calculated due to its Longest Open Reading Frame. The aminoacids will be aligned and then retranslated into DNA sequences for output.

option: -L [only ORF]
default: alignment computed on DNA level
usage: dialign-t -L <conf-dir> <input-file> [output-file]

WARNING: Do not use -D in this case although it is DNA input!

DNA sequences will be translated into aminoacids. Only the Longest Open Reading Frame of each sequence will be aligned. Retranslation into DNA Sequences for output.

output type

option: -P [protein output]
default: output type = input type
usage: dialign-t [-T, -O, -L] -P <conf-dir> <input-file> [output-file]

DNA sequences will not be retranslated after the alignment on protein level. One of the options -T, -O or -L is needed.

probability table

option: -C
default: no default
usage: dialign-t -C <conf-dir>

You can compute your own probability table from the score matrix. The computed file is saved in <conf-dir>/prob_table. There is no input-file needed to compute the table.

debugging

option: -d
default: 0
usage: dialign-t -d <number> <conf-dir> <input-file> [output-file]

You can debug the program by changing the default value to 1, 2 or 5

maximal number of input sequences

option: -s
default: 5000
usage: dialign-t -s <number> <conf-dir> <input-file> [output-file]

You can change the maximal number of input sequences if needed.

score matrix

option: -m
default: BLOSUM.scr [protein] / dna_matrix.scr [DNA]
usage: dialign-t -m <matrix-file-name> <conf-dir> <input-file> [output-file]

In case you want to try different scores.

change probability table

option: -p
default: BLOSUM.diag_prob_t10 [protein] / dna_diag_prob_100_exp_550000 [DNA]
usage: dialign-t -p <prob-table-file-name> <conf-dir> <input-file> [output-file]

If you want to use a different probability table.

help

option: -h, -H
usage: dialign-t [-h, -H]

To find all possible options have a look there.