

PROBALIGN Beta Version 1.1 (Nov 2006)

Written by Satish Chikkagoudar and Usman Roshan using PROBCONS 1.1 code (written by Chuong Do) and based upon probA (written by Ulrike Muckstein).

PROBALIGN has been made freely available as PUBLIC DOMAIN software and hence is not subject to copyright in the United States. This system and/or any portion of the source code may be used, modified, or redistributed without restrictions.

PROBALIGN is distributed WITHOUT WARRANTY, express or implied. The authors accept NO LEGAL LIABILITY OR RESPONSIBILITY for loss due to reliance on the program.

PROBALIGN aligns inputted sequences and displays the output to the screen.

USAGE:-

./probalign [file containing sequences in MFA format]

[-T temperature]

[-v|--verbose]

[-a|--alignment-order]

[-clustalw]

[-prot|-nuc]

[-go|--gap-open gap_open]

[-ge|--gap-extension gap_ext]

[-score_matrix scoring_matrix]

MFA (Multiple Fasta) Format:

MFA format consists of multiple sequences in fasta format.

Each sequence begins with a single-line description, followed by lines of sequence data. The description line is distinguished from the sequence data by a greater-than (>) symbol in the first column.

OPTION DETAILS:

-T This option is used to specify the thermodynamic temperature.

(Default: 5 because -prot is default, and 5 is default for -prot

when -prot option is used: 5

when -nuc option is used : 1).

-score_matrix This option can be used to specify the scoring matrix. The values that can be entered under this option are:

gonnet_160 = Gonnet 160 [DEFAULT]

nuc_simple = Identity nucleotide scoring matrix [DEFAULT for RNA/DNA]

-clustalw

use CLUSTALW output format instead of MFA

-v, --verbose

report progress while aligning (default: off)

-a, --alignment-order

print sequences in alignment order rather than input order (default: off)

-go, --gap-open

specify the gap open parameter. Default for Gonnet 160 (protein) is 22 and nucleotide (simple matrix) is 4.

-ge, --gap-extension

This option can be used to specify the gap extend parameter. Default for Gonnet 160 (protein) is 1 and nucleotide (simple matrix) is 0.25.

-nuc

Specify this option to indicate that input sequences are nucleotide sequences.

-prot

Specify this option to indicate that input sequences are protein sequences [DEFAULT MODE]

-showPP Outputs the posterior probabilities of alignment columns as a new sequence named Posterior Probabilities (The probability values are scaled to be between integers between 0 and 9).