tea v1.0 - Manual

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1 Introduction

Tea is a simple multiple sequence aligner. It is a re-implementation of the T-Coffee program.

2 Options

The MSAA program distinguished between three kinds of options:

- **General options:** These options regulate the input and output behavior of MSAA - the input/output files and formats.

- **Pairwise alignment options:** These options regulate how the pairwise alignment library is generated.

- **Guide tree options:** These options change the computation of the guide tree.

2.1 General options

There are several general options available:

   i,in: The input sequence file in FASTA format.

   o,out: The output file for the computed alignment.

   f,format: The format which should be used to write the alignment. Currently supported: fasta, clustalw, msf, phylip_i (Phylip interleaved), phylip_s (Phylip sequential).

   n,n_threads: The number of threads to use to compute the alignment. Should be a number smaller or equal to the number of cores to use.

2.2 Pairwise alignment options

2.3 Guide tree options