sine_finder [options] <fastafile_name>

OPTIONS:
  -h   (help:) display this message.
  -d   (description:) display a short description of the
        program.
  -v   (version:) print version number.

EVALUATION PARAMETERS:
-T (seqwise|chunkwise)
      (run type:) the way how infiles are processed (default:
      seqwise).

      'seqwise': each sequence is loaded and searched for patterns.
        For large sequences 'chunkwise' is the better choice.
      'chunkwise': only fragments (chunks) of the sequence are
        loaded and processed. The size is defined by option
        -C. To ensure that matches do not get lost by sequence
        splitting an overlap should be specified (option -O).
-t <integer>
      TSD mismatch tolerance (default:2).
-w <integer>
      word size TSD seed starts search with (default:5).
-p <integer>
      penalty for a nucleotide mismatch in TSD search (default:
      1).
-s <integer>
      TSD score cutoff (default:10).
-o (F|R|FR)
      direction of TSD search, allowed orientation (default:F).

(only chunkwise processing:)
-C <integer>
      (chunksize:) size of each fragment loaded and processed
      individually. Use only when -T is set to chunkwise (default:
      100000).
-O <integer>
      (overlap:) overlap of fragments treated by chunkwise processing.
      Use only when -T is set to chunkwise (default:8000).

OTHER OPTIONS:
-f (fasta|csv|both)
      (file type:) file type result is written to (default:fasta).

  -V   (verbose:) display program call.