

FastaDecoy

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1. Overview

This application generates decoy sequences.

2. Usage

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usage: FastaDecoy <Fasta> [-a] [-d <arg>] [-e <arg>] [-f <arg>] [-h]
[-i <arg>] [-k <arg>] [-l <arg>] [-m <arg>] [-o <arg>] [-p <arg>] [-q] [-s
<arg>] [-t <arg>] [-v]

-a,--append                combine decoy and original in one result file
                           by default: true.
-d,--decoyFlag <arg>      decoy flag
                           by default: DECOY_.
-e,--enzymes <arg>        define enzyme that digest proteins separately
with:
                           enzyme name among 'Caspase-1, Caspase-10,
Glu-C_bicarbonate, Caspase-3,
                           Thermolysine, Lys-C, Pepsin_pH1.3, Caspase-8,
Glu-C_phosphate, Caspase-9,
                           Caspase-5, CNBr, ChymoTrypsin_lowspec, Trypsin,
ChymoTrypsin_FYL,
                           Proteinase-K, Caspase-7, Pepsin_pHgt2,
ChymoTrypsin_highspec,
                           BNPS-Skatole, Enterokinase, Caspase-6, Arg-C,
Asp-N, ChymoTrypsin_FYLR,
                           Caspase-4, Caspase-2'.
                           or custom motifs respecting the following
grammar:
                           <pre-cut> <cut-token>
                           <post-cut>
                           <cut-token> := '|'
                           <pre-cut> := (<AA> or <AA-class>)+
                           <post-cut> := (<AA> or <AA-class>)+
                           <AA> := [A-Z]
                           <AA-class> := '[' AA+ ']'
                           by default: Trypsin.
-f,--fastaFormat <arg>    Format of fasta header. Either simple ">P00001"
sp (SwissProt) ipi (IPI)
                           or user defined with the following syntax:
                           regexp@separator@index
                           regexp: regular expression to identify header
                           separator: char that separates header entries
                           index: index of protein name in list of header
entries
                           example (SwissProt header): "^sp\|.|.+ $"@|@1by
default: simple.
-h,--help                  print this message.
-i,--setting-file <arg>   give a property file with all input settings.
-k,--keepTerm <arg>       Keep terminus of shuffled peptides
                           (peptideShuffle method only). Either
```

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                                cterm (keep C-Terminus)
                                nterm (keep N-Terminus)
                                none (do not keep termini)
                                by default: cterm.
-1,--length <arg>              don't shuffle peptides shorter than : 5.
-m,--method <arg>              method for decoy sequence generation. Either
sequence leaving C-term)        peptideShuffle (random permutation of peptide
sequence)                       proteinShuffle (random permutation of protein
                                proteinReverse (reverse protein sequence)
                                by default: peptShuffle.
-o,--output <arg>              set the output filename
-p,--decoyFlagPos <arg>        where to insert decoy flag
                                beforeID: before protein id
                                startHead: beginning of header line (after '>'
sign)                             startHead&beforeID : both of the above
                                by default: beforeID.
-q,--quiet                      quiet mode (verbose off)
                                by default: false.
-s,--simThreshold <arg>        maximal similarity between shuffled und
                                original peptide spectrum : 0.0.
-t,--shuffleTrials <arg>       maximal number of peptide shuffling trials :
10.
-v,--version                     print the version info.
```

3. Releases

The latest version is v1.0 - [Download app.](#)