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$ perl SFannotation.pl          Command line to list options of SFannotation

# SFannotation: Simple and Fast Functional Annotation System

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# Requirements
1. Linux system (64-bit)
2. Bash shell
3. Perl library

# How to run
perl SFannotation.pl --download --fasta <protein fasta file> --speedup

# Options
 --fasta                    [string]        Protein fasta file
 --t_evalue                 [float]         Threshold of e-value, default = 1e-5
 --n_cpu                    [integer]       The number of cpus, default = 1
 --sbh                                      Single best hit, default
 --bbh                                      Bidirectional best hit
 --speedup                                  Speed up annotaiton
 --download                                 Download four databases: Swiss-Prot, TIGRFAMs, Pfam, and NR, and programs: NCBI-BLAST+ and HMMER
 --swissprot                [string]        Path of Swiss-Prot fasta file (essential if not --download)
 --tigrfam                  [string]        Path of TIGRFAMs hmm profile (essential if not --download)
 --pfam                     [string]        Path of Pfam hmm profile (essential if not --download)
 --nr                       [string]        Path of NR fasta file (essential if not --download)
 --makeblastdb             [string]        Path of makeblastdb in NCBI-BLAST+ (essential if not --download)
 --blastp                   [string]        Path of blastp in NCBI_BLAST+ (essential if not --download)
 --hmmsearch                [string]        Path of hmmsearch in HMMER (essential if not --download)
 --help                                     Help
 --license                                  Academic Free License (AFL) 3.0

$ perl SFannotation.pl --download --fasta input.fasta --speedup > annotation.txt     Command line to execute SFannotation
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Supplementary Fig. 1. Snapshot for the various options and execution of SFannotation on Linux.