Developing a standalone toolbox for processing FASTA files

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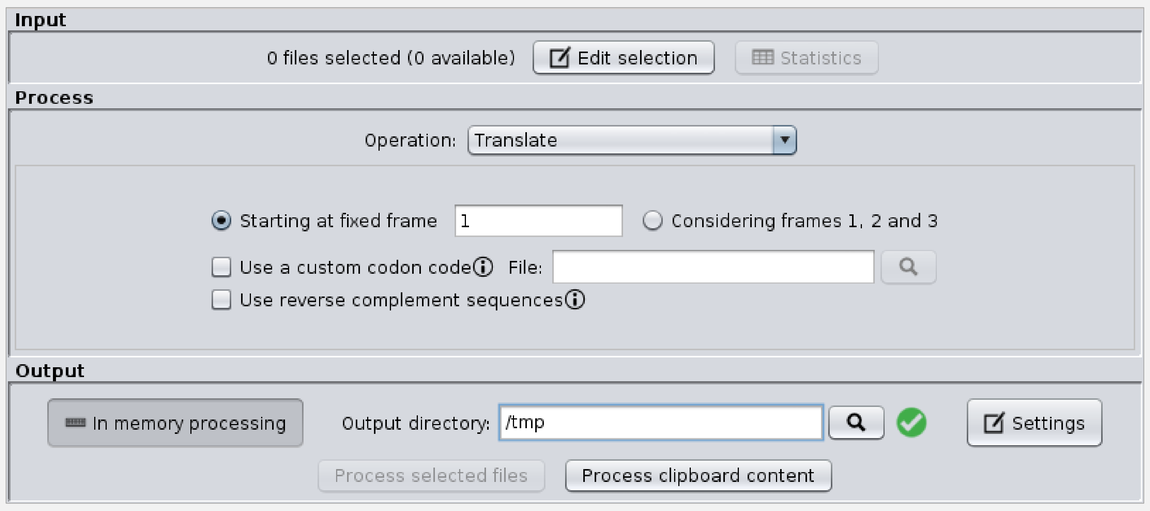
Motivation

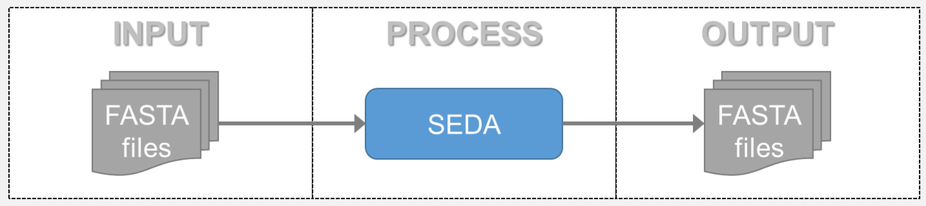
One of the most important types of data used in biological research is DNA or protein sequence data. They are usually stored in FASTA files, which can store one or more sequences. Public databases such as GenBank, NCBI or Ensembl provide huge collections of genomes, genome annotations, and so on, in FASTA format. Nevertheless, downloaded files usually must be preprocessed before subsequent analysis depending on each researcher needs. Despite the simplicity of these preprocessing operations (e.g. remove sequences without a minimum number of bases), processing of large batches of FASTA files is a complex task that usually requires advanced bioinformatics skills and the combination of different tools (including the bash command line) to achieve the desired result. In order to allow researchers to easily perform these operations we are developing the SEDA software application.

Results: SEDA

www.sing-group.org/seda



What is SEDA? *SEDA* is a desktop multiplatform application for ease the processing of FASTA files containing DNA and protein sequences.



SEDA Functions

- Sequence filtering.
- Sequence filtering based on text patterns.
- Remove redundant sequences.
- Sort sequences.
- Split FASTA files.
- Reallocate reference sequences.
- Rename sequence headers.
- Reformat FASTA files.
- Grow sequences.
- Rename NCBI accession numbers.
- Merge FASTA files.
- Concatenate sequences.
- Undo alignment.
- Sequence translation.
- Disambiguate sequence names.
- Consensus sequence creation.
- BLAST analysis.

SEDA for Programmers

Additionally:

- Programmers can take advantage of the *SEDA* core to develop new operations to process FASTA files.
- *SEDA* has a plugin-based architecture, new functions can be easily added to the *SEDA* GUI through the creation of new plugins.

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