SeCon

nucleic acid sequence files batch converter

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Overview

SeCon is able to convert both single files and folders of diverse sequence formats.

Supported formats:

- FASTA
- GenBank
- EMBL

Requirements: Python 3.12.2

Examples

```
# single file

./secon.py ./input/gb/sequence.gb fasta -o my_output


# batch

./secon.py ./input/embl gb -o my_output


# batch exclude

./secon.py ./input/embl gb -o my_output_exclude -e *.1* -v
```

Warnings & Errors

```
# single file

./secon.py input/fasta/no_organism.fasta embl -v -o out_fasta_embl

./secon.py input/fasta/empty.fasta embl -v -o out_fasta_embl

./secon.py input/gb/sequence2.gb fasta


# whole folder

./secon.py input/fasta/ embl -v -o out_fasta_embl
```

Architecture