Format Converting Sequences

Task Name: convert-seq

Converts a sequence from one format to another.

Parameters:

in — input sequence file. [String, Required]

out — name of the output file. [String, Required]

format — format of the output file. [String, Optional]

The following values are available:

- fasta
- fastq
- genbank
- raw

Example:

```
ugene convert-seq --in=human_T1.fa --out=human_T1.gbk --format=genbank
```