

Extracting Sequence

Task Name: extract-sequence

Extracts annotated regions from an input sequence.

Parameters:

in — semicolon-separated list of input files. [String, Required]

out — output file. [String, Required]

annotation-names — list of annotations names which will be accepted or filtered. [String, Required]

accept-or-filter — if set to *true*, accepts only the specified annotations, if set to *false*, accepts all annotations except the specified ones. [Boolean, Optional]

complement — complements the annotated regions if the corresponding annotation is located on the complement strand. [Boolean, Optional]

extend-left — extends the resulting regions to the left for the specified number of base symbols. [Number, Optional]

extend-right — extends the resulting regions to the right for the specified number of base symbols. [Number, Optional]

gap-length — inserts a gap of the specified length between the merged annotations.

transl - translates the annotated regions. [Boolean, Optional]

Example:

```
ugene extract-sequence --in=sars.gb --out=res.fa --annotation-names=gene
```