Annotating Sequence with UQL Schema

Task Name: query

Annotates a sequence in compliance with a UGENE Query Language (UQL) schema. This allows to analyze a sequence using different algorithms at the same time imposing constraints on the positional relationship of the results.

To learn more about the UQL schemas read the Query Designer Manual.

Parameters:

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

out — output Genbank file with the annotations. [String, Required]

schema — UQL schema. [String, Required]

merge — if true, merges regions of each result into a single annotation. [Boolean, Optional, Default: false]

offset — if *merge* is set to true, specified left and right offsets for merged annotations. [Number, Optional, Default: 0]

Example:

```
ugene query --in=input.fa --out=result.gb --schema=RepeatsWithORF.uql
```