Remote NCBI BLAST and CDD Requests

Task Name: remote-request

Performs remote requests to the NCBI. Saves the results as annotations.

Parameters:

in — semicolon-separated list of input files. A file can be of any format containing sequences or alignments. [String, Required]

db — database to search in. [String, Optional, Default: “ncbi-blastn”]

The following databases are available:

- “ncbi-blastn” for nucleotide sequences
- “ncbi-cdd” for amino acid sequences
- “ncbi-blastp” for amino acid sequences

out — output Genbank file. [String, Required]

eval — specifies the statistical significance threshold for reporting matches against database sequences. [Number, Optional, Default: 10]

hits — maximum number of hits, that will be shown. [Number, Optional, Default: 10]

name — name of the result annotations. If not set, name will be specified with the “cdd” result or the “blast” result. [String, Optional, Default: “cdd” or “blast”]

short — optimizes search for short sequences. [Boolean, Optional, Default: false]

blast-output — path to the file with the NCBI-BLAST output (only for the “ncbi-blastp” and “ncbi-blastn” databases). [Boolean, Optional, Default: the file is not saved]

Example:

```
ugene remote-request --in=seq.fa --db=ncbi-blastp --out=res.gb
```