Aligning with ClustalO

Task Name: align-clustalo

Create alignment with ClustalO. ClustalO is a general purpose multiple sequence alignment program for proteins.

ClustalO is used as an *external tool* and must be installed on your system.

Parameters:

in - Input alignment [Url datasets]

format - Document format of output alignment (using 'clustal' by default) [String]

out - Output alignment [String]

max-guidetree-iterations - Maximum number guidetree iterations (using '0' by default) [Number]

max-hmm-iterations - Maximum number of HMM iterations (using '0' by default) [Number]

iter - Number of (combined guide-tree/HMM) iterations (using '1' by default) [Number]

toolpath - ClustalO location (using the path specified in UGENE by default) [String]

auto - Set options automatically (might overwrite some of your options) (using 'False' by default) [Boolean]

tmpdir - Directory to store temporary files (using UGENE temporary directory by default) [String]

Example:

```
ugene align-clustalw  --in=test.aln --out=test_out.aln --format=clustal
```