Aligning with T-Coffee

Task Name: align-tcoffee

Create alignment with T-Coffee. T-Coffee is a collection of tools for computing, evaluating and manipulating multiple alignments of DNA, RNA, Protein Sequences.

T-Coffee is used as an *external tool* and must be installed on your system.

Parameters:

gap-ext-penalty - Gap Extension Penalty. Positive values give rewards to gaps and prevent the alignment of unrelated segments (using '0' by default) [Number]

gap-open-penalty - Gap Open Penalty. Must be negative, best matches get a score of 1000 (using '-50' by default) [Number]

iter-max - Number of iteration on the progressive alignment: 0 - no iteration (default), -1 - Nseq iterations (using '0' by default) [Number]

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

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

in - Input alignment [Url datasets]

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

out - Output alignment [String]

Example:

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