Map Reads with UGENE Genome Aligner Element

Unique UGENE algorithm for aligning short reads to reference genome.

Parameters in GUI

| Parameter | Description | Default value |
|--------------------------------------|---|------------------|
| Output file name | Base name of the output file. 'out.sam' by default. | out.sam |
| Reference genome | Path to an indexed reference genome. | |
| Is absolute mismatches values? | true - absolute mismatches mode is used | True |
| | false - percentage mismatches mode is used | |
| | You can choose absolute or percentage mismatches values mode. | |
| Absolute mismatches | Number of mismatches allowed while aligning reads. | 0 |
| Align reverse complement reads | Set this option to align both direct and reverse complement reads. | False |
| Use "best"-mode | Report only the best alignment for each read (in terms of mismatches). | True |
| Omit reads with qualities lower than | Omit reads with qualities lower than the specified value. Reads that have no qualities are not omitted. | 0 |
| | Set "0" to switch off this option. | |

Parameters in Workflow File

Type: genome-aligner

| Parameter | Parameter in the GUI | Туре |
|------------------------------|--------------------------------------|---------|
| outname | Output file name | string |
| reference | Reference genome | string |
| if-absolute-mismatches-value | Is absolute mismatches values? | boolean |
| absolute-mismatches | Absolute mismatches | numeric |
| reverse | Align reverse complement reads | boolean |
| best | Use "best"-mode | boolean |
| quality-threshold | Omit reads with qualities lower than | numeric |

Input/Output Ports

The element has 1 input port.

Name in GUI: Genome aligner data

Name in Workflow File: in-data

Slots:

| Slot In GUI | Slot in Workflow File | Туре |
|-------------------------------|-----------------------|--------|
| URL of a file with mate reads | readsurl | string |
| URL of a file with reads | readspairedurl | string |

And 1 output port:

Name in GUI: Genome aligner output data

Name in Workflow File: out-data

Slots:

| Slot In GUI | Slot in Workflow File | Туре |
|--------------|-----------------------|--------|
| Assembly URL | assembly-out | string |