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 **false** - percentage mismatches mode is used You can choose absolute or percentage mismatches values mode.	True
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. Set "0" to switch off this option.	0

Parameters in Workflow File

Type: genome-aligner

Parameter	Parameter in the GUI	Type
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	Type
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	Type
Assembly URL	**assembly-out**	*string*