

Align Reads with UGENE Genime 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 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	<i>string</i>
reference	Reference genome	<i>string</i>
if-absolute-mismatches-value	Is absolute mismatches values?	<i>boolean</i>
absolute-mismatches	Absolute mismatches	<i>numeric</i>
reverse	Align reverse complement reads	<i>boolean</i>
best	Use "best"-mode	<i>boolean</i>
quality-threshold	Omit reads with qualities lower than	<i>numeric</i>

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	<i>string</i>
URL of a file with reads	readspairedurl	<i>string</i>

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	<i>string</i>