

Map Reads with UGENE Genome Aligner Element

Unique UGENE algorithm for aligning short reads to reference genome.

Element type: genome-aligner

Parameters

Parameter	Description	Default value	Parameter in Workflow File	Type
Output file name	Base name of the output file. 'out.sam' by default.	out.sam	outname	<i>string</i>
Reference genome	Path to an indexed reference genome.		reference	<i>string</i>
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	if-absolute-mismatches-value	<i>boolean</i>
Absolute mismatches	Number of mismatches allowed while aligning reads.	0	absolute-mismatches	<i>numeric</i>
Align reverse complement reads	Set this option to align both direct and reverse complement reads.	False	reverse	<i>boolean</i>
Use "best"-mode	Report only the best alignment for each read (in terms of mismatches).	True	best	<i>boolean</i>
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	quality-threshold	<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>