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**	*string*
Reference genome	Path to an indexed reference genome.		**reference**	*string*
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**	*boolean*
Absolute mismatches	Number of mismatches allowed while aligning reads.	0	**absolute-mismatches**	*numeric*
Align reverse complement reads	Set this option to align both direct and reverse complement reads.	False	**reverse**	*boolean*
Use "best"-mode	Report only the best alignment for each read (in terms of mismatches).	True	**best**	*boolean*
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**	*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*