Filter BAM/SAM Files Element

Filters BAM/SAM files using SAMTools view.

Parameters in GUI

Parameter	Description	Default value
Output directory	Select an output directory. Custom - specify the output directory in the 'Custom directory' parameter. Workflow - internal workflow directory. Input file - the directory of the input file.	
Custom directory	Custom output directory.	
Output name	A name of an output BAM/SAM file. If default of empty value is provided the output name is the name of the first BAM/SAM file with .filtered extention.	
Output format	Format of an output assembly file.	bam
Region	Regions to filter. For BAM output only. chr2 to output the whole chr2. chr2:1000 to output regions of chr 2 starting from 1000. chr2:1000-2000 to ouput regions of chr2 between 1000 and 2000 including the end point. To input multiple regions use the space seprator (e.g. chr1 chr2 chr3:1000-2000).	
MAPQ threshold	Minimum MAPQ quality score.	0
Skip flag	Skip alignment with the selected items. Select the items in the combobox to configure bit flag. Do not select the items to avoid filtration by this parameter.	

Parameters in Workflow File

Type: filter-bam

Parameter	Parameter in the GUI	Type
out-mode	**Output directory**	*numeric*
custom-dir	**Custom directory**	*string*
out-name	**Output name**	*string*
out-format	**Output format**	*string*
region	**Region**	*string*
mapq	**MAPQ threshold**	*numeric*
flag	**Skip flag**	*string*

Input/Output Ports

The element has 1 *input port*:

Name in GUI: BAM/SAM File

Name in Workflow File: in-file

Slots:

Slot In GUI	Slot in Workflow File	Type
Source URL	**input-url**	*string*

And 1 *output port*:

Name in GUI: Filtered BAM/SAM files

Name in Workflow File: out-file

Slots:

Slot In GUI	Slot in Workflow File	Type
Source URL	**output-url**	*string*