Filter BAM/SAM Files Element

Filters BAM/SAM files using SAMTools view.

Element type: filter-bam

Parameters

Parameter	Description	Default value	Parameter in Workflow File	Type
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.		**out-mode**	*numeric*
Custom directory	Custom output directory.		**custom-dir**	*string*
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.		**out-name**	*string*
Output format	Format of an output assembly file.	bam	**out-format**	*string*
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).		**region**	*string*
MAPQ threshold	Minimum MAPQ quality score.	0	**mapq**	*numeric*
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.		**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*