

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