

# 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 |