

Sort BAM Files Element

Sort BAM Files using SAMTools Sort.

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.	Input file
Custom directory	Specify the output directory.	
Output BAM name	A name of an output file. If default of empty value is provided the output name is the name of the first file with additional extention.	
Build index	Build index for the sorted file with SAMTools index.	human. hg18

Parameters in Workflow File

Type: Sort-bam

Parameter	Parameter in the GUI	Type
out-mode	Output directory	<i>numeric</i>
custom-dir	Output BAM name	<i>string</i>
out-name	Output file name	<i>string</i>
index	Build index	<i>boolean</i>

Input/Output Ports

The element has 1 *input port*:

Name in GUI: BAM File

Name in Workflow File: in-file

Slots:

Slot In GUI	Slot in Workflow File	Type
Source URL	url	<i>string</i>

And 1 *output port*:

Name in GUI: Sorted BAM File

Name in Workflow File: out-file

Slots:

Slot In GUI	Slot in Workflow File	Type
Source URL	url	<i>string</i>