

Remove Duplicates in BAM Files Element

Remove PCR duplicates of BAM files using SAMTools rmdup.

Element type: rmdup-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.	Input file	out-mode	<i>numeric</i>
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 extension.		out-name	<i>string</i>
Remove for single-end reads	Remove duplicate for single-end reads. By default, the command works for paired-end reads only (-s).	False	remove-single-end	<i>boolean</i>
Treat as single-end	Treat paired-end reads and single-end reads (-S).	False	treat_reads	<i>boolean</i>

Input/Output Ports

The element has 1 *input port*.

Name in GUI: Input 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: Output File

Name in Workflow File: out-file

Slots:

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