Remove Duplicates in BAM Files Element

Remove PCR duplicates of BAM files using SAMTools rmdup.

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
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.	
Remove for single-end reads	Remove duplicate for single-end reads. By default, the command works for paired-end reads only (-s).	False
Treat as single-end	Treat paired-end reads and single-end reads (-S).	False

Parameters in Workflow File

Type: rmdup-bam

Parameter	Parameter in the GUI	Type
out-mode	**Output directory**	*numeric*
out-name	**Output file name**	*string*
remove-single-end	**Remove for single-end reads**	*boolean*
treat_reads	**Treat as single-end**	*boolean*

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**	*string*

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**	*string*