Convert bedGraph Files to bigWig Element

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Element type: bgtbw-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**	*numeric*
Custom directory	Specify the output directory.		**custom-dir**	*string*
Genome	File with genome length.	human. hg18	**genome**	*string*
Output 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.		**out-name**	*string*
Block size	Number of items to bundle in r-tree (-blockSize).	256	**bs**	*numeric*
Items per slot	Number of data points bundled at lowest level (-itemsPerSlot).	1024	**its**	*numeric*
Uncompressed	If set, do not use compression.(-unc).	False	**unc**	*boolean*

Input/Output Ports

The element has 1 *input port*:

Name in GUI: BedGrapgh files

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: BigWig files

Name in Workflow File: out-file

Slots:

Slot In GUI	Slot in Workflow File	Type
Source URL	**url**	*string*