

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

Input/Output Ports

The element has 1 *input port*.

Name in GUI: BedGraph files

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: BigWig files

Name in Workflow File: out-file

Slots:

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