Convert bedGraph Files to bigWig Element

Convert bedGraph files to bigWig.

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.	
Genome	File with genome length.	human.hg18
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.	
Block size	Number of items to bundle in r-tree (-blockSize).	256
Items per slot	Number of data points bundled at lowest level (-itemsPerSlot).	1024
Uncompressed	If set, do not use compression.(-unc).	False

Parameters in Workflow File

Type: bgtbw-bam

Parameter	Parameter in the GUI	Type
out-mode	**Output directory**	*numeric*
custom-dir	**Custom directory**	*string*
genome	**Genome**	*string*
out-name	**Output name**	*string*
bs	**Block size**	*numeric*
its	**Items per slot**	*numeric*
unc	**Uncompressed**	*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*