Assemble Genomes with SPAdes Element

Performes assembly of input short reads.

Parameters in GUI

Parameter	Description	Default value
Output directory	Directory to save Spades output files.	
Dataset type	Input dataset type.	Multi Cell
Running mode	Running mode.	Error correction and assembly
K-mers	k-mer sizes (-k).	auto
Number of threads	Number of threads (-t).	16
Memory limit (Gb)	Memory limit (-m).	250

Parameters in Workflow File

Type: spades-id

Parameter	Parameter in the GUI	Type
output-dir	**Output directory**	*string*
dataset-type	**Dataset type**	*string*
running-mode	**Running mode**	*string*
k-mer	**K-mers**	*numeric*
threads	**Number of threads**	*numeric*
memlimit	**Memory limit (Gb)**	*numeric*

Input/Output Ports

The element has 1 *input port*:

Name in GUI: Spades data

Name in Workflow File: in-data

Slots:

Slot In GUI	Slot in Workflow File	Type
URL of a file with right pair reads	url	*string*
URL of a file with reads	url	*string*

And 1 *output port*:

Name in GUI: SPAdes output data

Name in Workflow File: out-data

Slots:

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