

Assemble Genomes with SPAdes Element

Performs 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