

Assemble Reads with SPAdes Element

Performers assembly of input short reads.

Element type: spades-id

Parameters

Parameter	Description	Default value	Parameter in Workflow File	Type																
Input data	<p>Select the type of input for SPAdes. URL(s) to the input files of the selected type(s) should be provided to the corresponding port(s) of the workflow element.</p> <p>At least one library of the following types is required:</p> <ul style="list-style-type: none">• Illumina paired-end/high-quality mate-pairs/unpaired reads• IonTorrent paired-end/high-quality mate-pairs/unpaired reads• PacBio CCS reads (at least 5 reads coverage is recommended) <p>It is strongly suggested to provide multiple paired-end and mate-pair libraries according to their insert size (from smallest to longest).</p> <p>Additionally, one may input Oxford Nanopore reads, Sanger reads, contigs generated by other assembler(s), etc. Note that Illumina and IonTorrent libraries should not be assembled together. All other types of input data are compatible.</p> <p>It is also possible to set up reads orientation (forward-reverse (fr), reverse-forward (rf), forward-forward (ff)) and specify whether paired reads are separate or interlaced.</p> <p>Illumina, IonTorrent or PacBio CCS reads should be provided in FASTQ format. Illumina or PacBio read may also be provided in FASTA format. Error correction should be skipped in this case (see the "Running mode" parameter). Sanger, Oxford Nanopore, and PacBio CLR reads can be provided in both formats since SPAdes does not run error correction for these types of data.</p> <p>To configure input data use the following button:</p> <div><div><div>Parameters</div><table><thead><tr><th>Name</th><th>Value</th></tr></thead><tbody><tr><td>Input data</td><td><div>Configure input type</div><div>...</div></td></tr><tr><td>Dataset type</td><td>Standard isolate</td></tr><tr><td>Running mode</td><td>Error correction and assembly</td></tr><tr><td>K-mers</td><td>Auto</td></tr><tr><td>Number of threads</td><td>16</td></tr><tr><td>Memory limit</td><td>250 Gb</td></tr><tr><td>Output folder</td><td>Auto</td></tr></tbody></table></div></div> <p>The following dialog will appear:</p>	Name	Value	Input data	<div>Configure input type</div> <div>...</div>	Dataset type	Standard isolate	Running mode	Error correction and assembly	K-mers	Auto	Number of threads	16	Memory limit	250 Gb	Output folder	Auto		output-dir	string
Name	Value																			
Input data	<div>Configure input type</div> <div>...</div>																			
Dataset type	Standard isolate																			
Running mode	Error correction and assembly																			
K-mers	Auto																			
Number of threads	16																			
Memory limit	250 Gb																			
Output folder	Auto																			

Configure SPAdes Input Type

Required input (at least one)

Illumina/Ion Torrent reads

Sequencing platform Illumina

☒ Paired-end reads fr Separate reads

☐ High-quality mate-pairs fr Separate reads

☐ Unpaired reads

☐ PacBio CCS reads

Additional input

Illumina/Ion Torrent reads

☐ Mate-pairs fr Separate reads

☐ PacBio CLR reads

☐ Sanger reads

☐ Oxford Nanopore reads

☐ Trusted contigs

☐ Untrusted contigs

Help

✕ Cancel

✓ OK

Dataset type	Input dataset type.	Multi Cell	dataset-type	string
Running mode	Running mode.	Error correction and assembly	running-mode	string
K-mers	k-mersizes (-k).	auto	k-mer	numen
Number of threads	Number of threads (-t).	16	threads	numen
Memory limit (Gb)	Memory limit (-m).	250	memlimit	numen
Output folder	Folder to save Spades output files.	Auto		

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
Contig URL	url	string