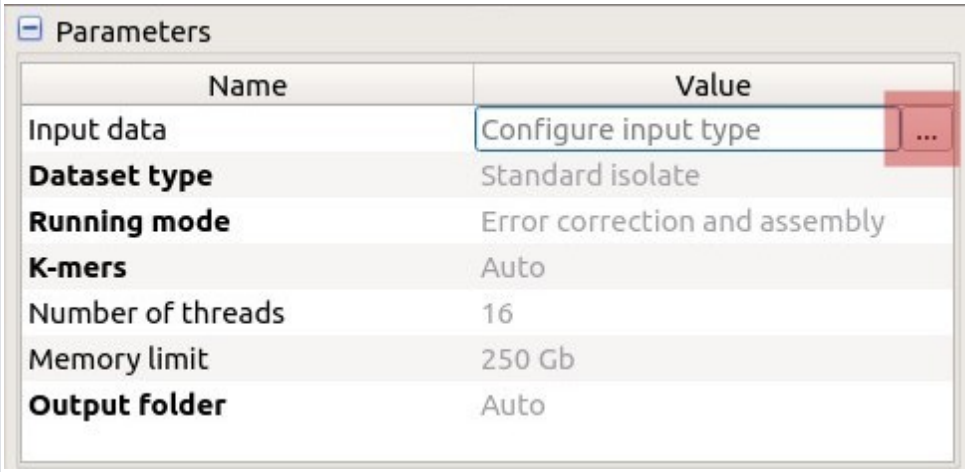
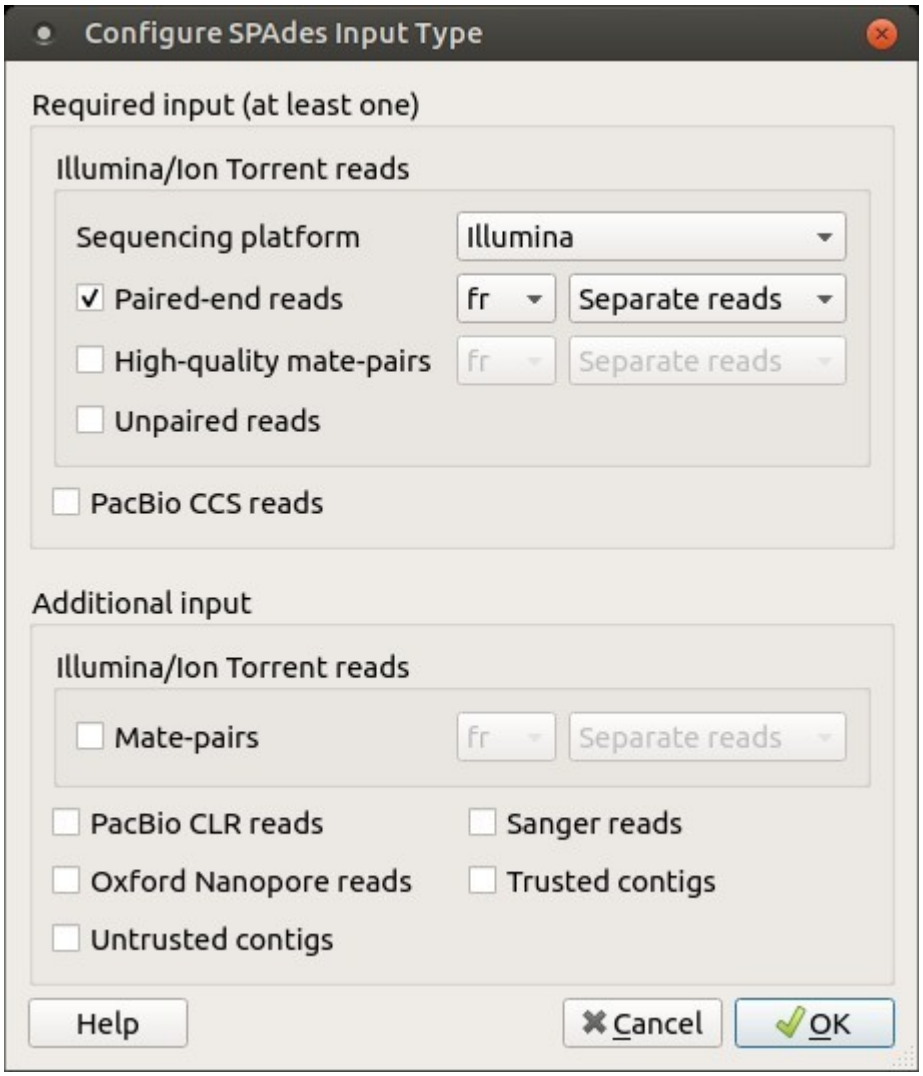
Assemble Reads with SPAdes Element

Performers assembly of input short reads.

Element type: spades-id

Parameters

Parameter	Description	Default value	Parameter in Workflow File	Type
Input data	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. At least one library of the following types is required: • 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) It is strongly suggested to provide multiple paired-end and mate-pair libraries according to their insert size (from smallest to longest). 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. 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. 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. To configure input data use the following button:  The following dialog will appear:		**output-dir**	*string*



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**	*numeri*
Number of threads	Number of threads (-t).	16	**threads**	*numeri*
Memory limit (Gb)	Memory limit (-m).	250	**memlimit**	*numeri*
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*