De novo Assembly with Spades

Use this workflow sample to assemble genomes from short reads with Spades.

How to Use This Sample

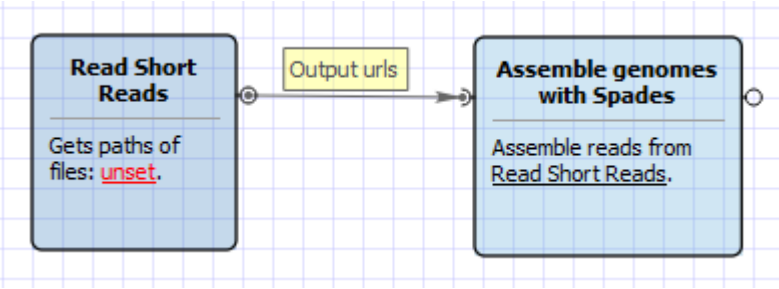
If you haven't used the workflow samples in UGENE before, look at the "How to Use Sample Workflows" section of the documentation.

Workflow Sample Location

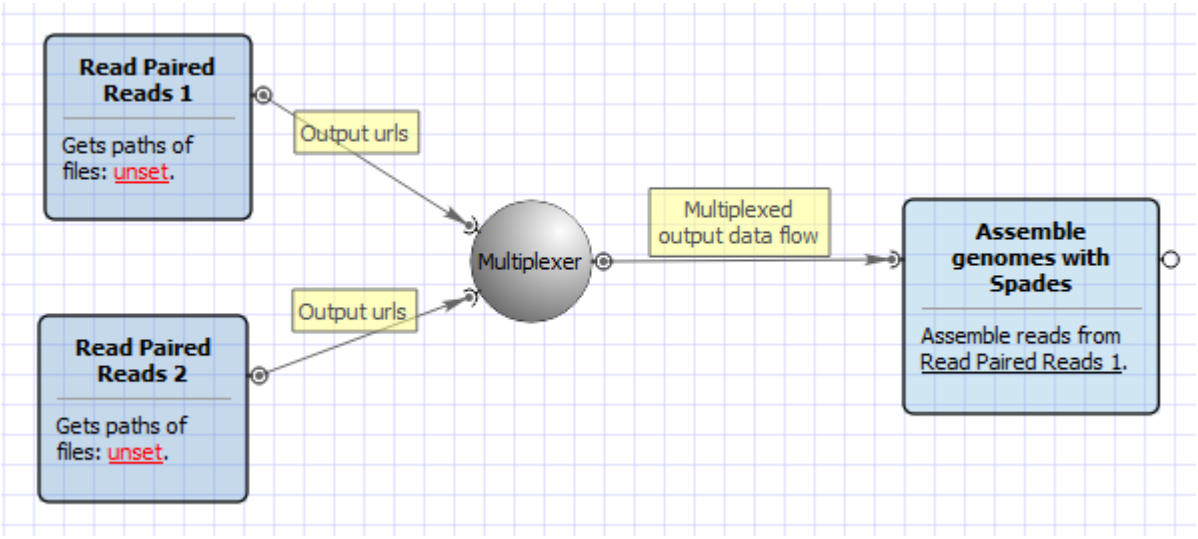
The workflow sample "Assembly with Spades" can be found in the "NGS" section of the Workflow Designer samples.

Workflow Image

There are two versions of the workflow available. The workflow for single tags looks as follows:



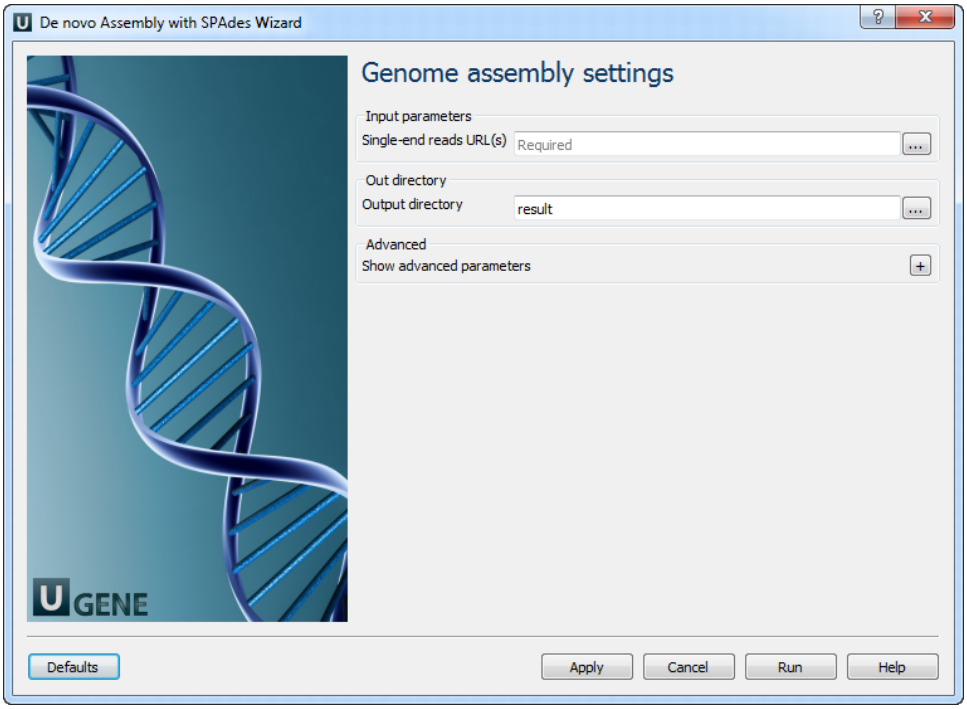
The workflow for paired tags appearance is the following:



Workflow Wizard

The wizard for single tags has 1 page.

1. Genome assembly settings: On this page you must input single reads and optionally modify advanced parameters.

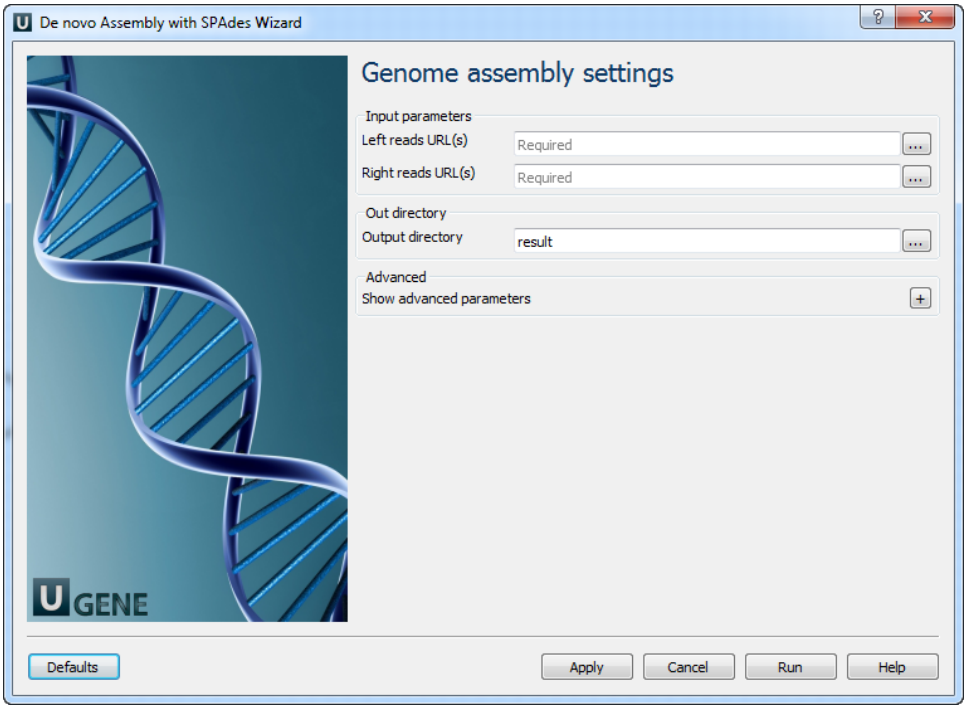


The following parameters are available:

Single-end reads URL(s)	Semicolon-separated list of pathes to the input files.
Output directory	Directory to save Spades output files.
Dataset type	Input dataset type.
Running mode	Running mode.
K-mers	k-mer sizes (-k).

The wizard for paired tags has 1 page.

1. Genome assembly settings: On this page you must input paired reads and optionally modify advanced parameters.



The following parameters are available:

Left reads URL(s)	Semicolon-separated list of pathes to the input files.
Right reads URL(s)	Semicolon-separated list of pathes to the input files.
Output directory	Directory to save Spades output files.
Dataset type	Input dataset type.
Running mode	Running mode.
K-mers	k-mer sizes (-k).