

# De novo Assembly with Spades

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



## How to Use This Sample

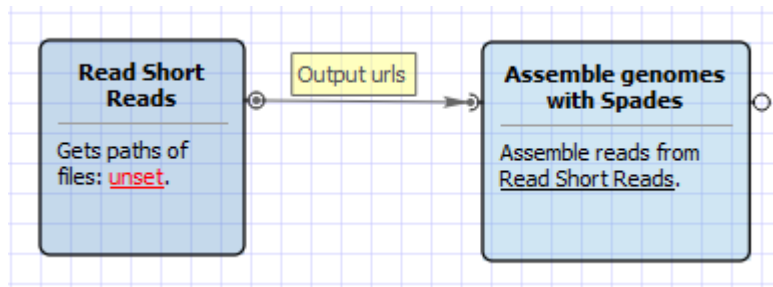
If you haven't used the workflow samples in UGENE before, look at the ["How to Use Sample Workflows"](#) section of the documentation.

## Workflow Sample Location

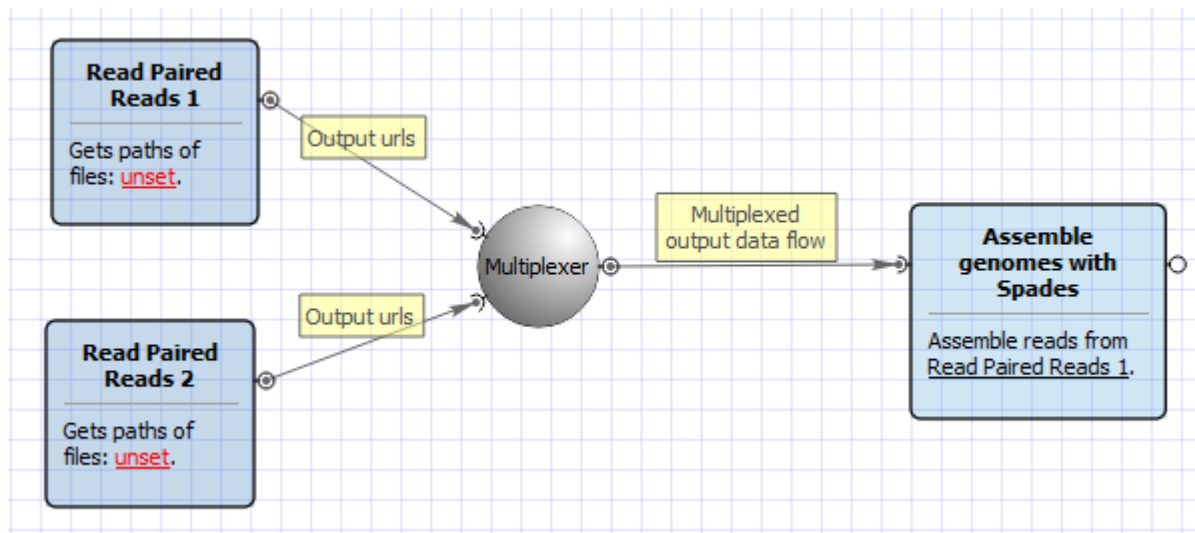
The workflow sample "Assembly with Spades" can be found in the "NGS" section of the Workflow Designer samples.

## Workflow Image

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



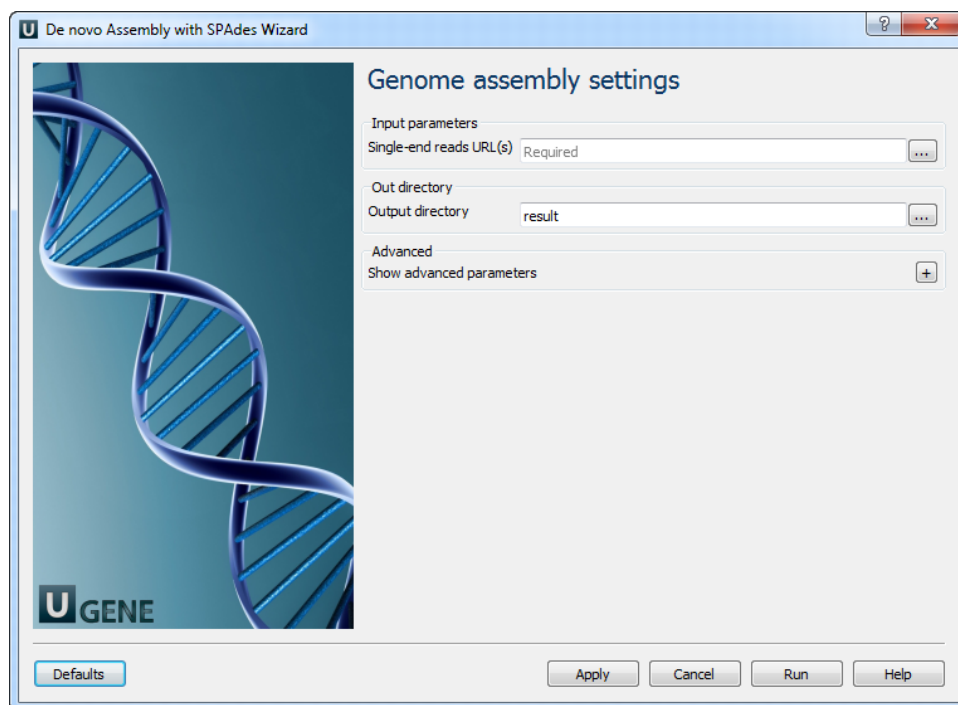
The workflow for paired tags appearance is the following:



## 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.

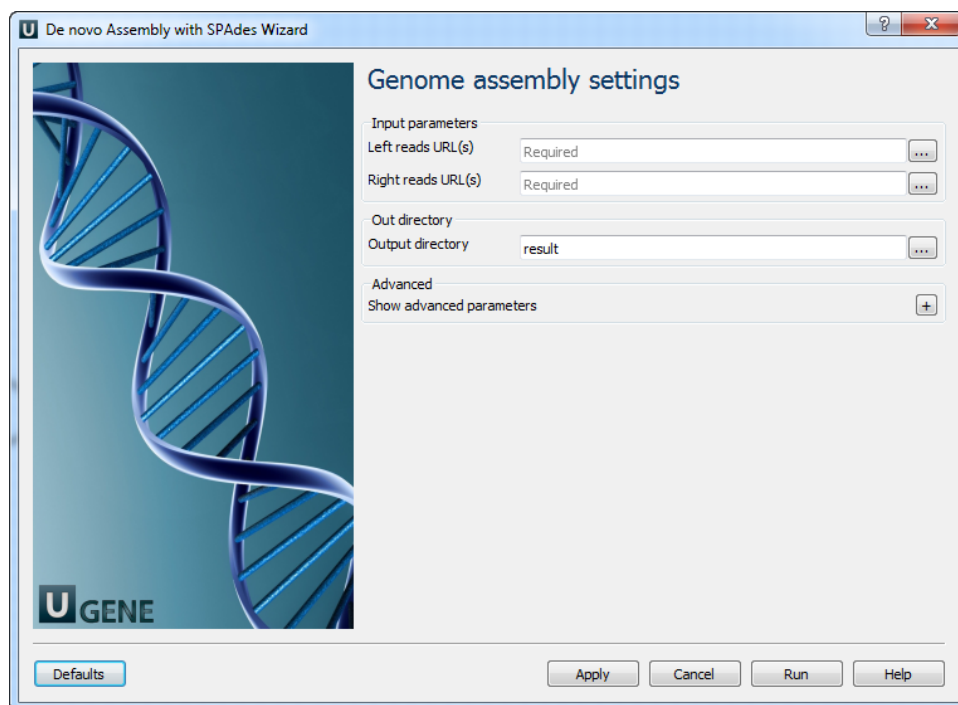


The following parameters are available:

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).