
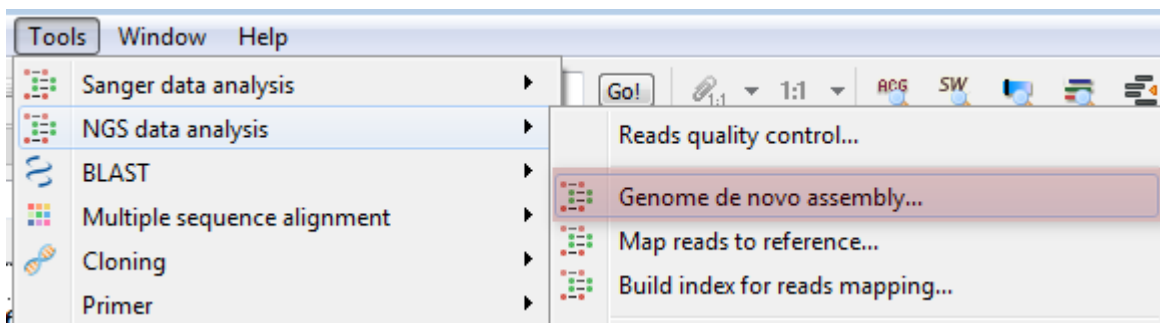


SPAdes

SPAdes – St. Petersburg genome assembler. Click [this link](#) to open SPAdes homepage. SPAdes is embedded as an [external tool](#) into UGENE.

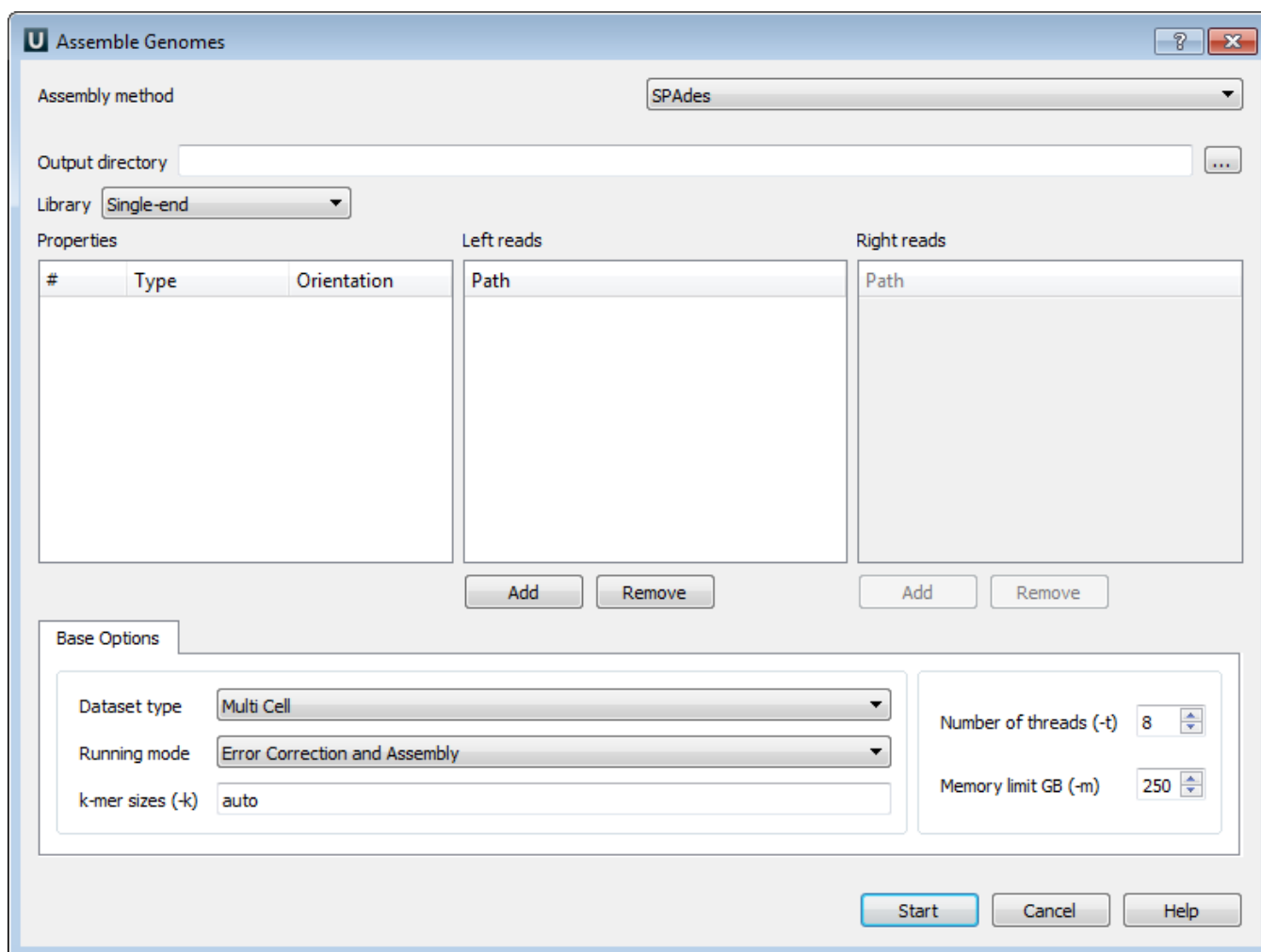
 SPAdes tool is available on macOS and Linux operating systems only.

Open *Tools* *NGS data analysis*.



Select the *Genome de novo assembly* item to use the *SPAdes*.

The *Assemble Genomes* dialog will appear.

A screenshot of the 'Assemble Genomes' dialog box in UGENE. The dialog is titled 'U Assemble Genomes'. It features a 'Tools' menu icon, a question mark, and a close button. The 'Assembly method' is set to 'SPAdes'. The 'Output directory' is an empty text field with a browse button. The 'Library' is set to 'Single-end'. Below this is a 'Properties' section with a table for 'Left reads' and 'Right reads'. The table has columns for '#', 'Type', 'Orientation', and 'Path'. Below the table are 'Add' and 'Remove' buttons. The 'Base Options' section is expanded, showing 'Dataset type' set to 'Multi Cell', 'Running mode' set to 'Error Correction and Assembly', and 'k-mer sizes (-k)' set to 'auto'. On the right, 'Number of threads (-t)' is set to 8 and 'Memory limit GB (-m)' is set to 250. At the bottom are 'Start', 'Cancel', and 'Help' buttons.

#	Type	Orientation	Path
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The following parameters are available:

Output directory - SPAdes stores all output files in output directory, which is set by the user.

Library - to run SPAdes choose one of the following libraries:

- Single-end
- Paired-end
- Paired-end (Interplaced)
- Paired-end (Unpaired files)
- Sanger
- PacBio

Left reads - file(s) with left reads.

Right reads - file(s) with right reads.

For each dataset in the paired-end libraries you can change type and orientation.

Datasest type - dataset type.

Running mode - running mode.

k-mer sizes (-k) - k-mer sizes.

Number of threads (-t) - number of threads.

Memory limit GB (-m) - memory limit.