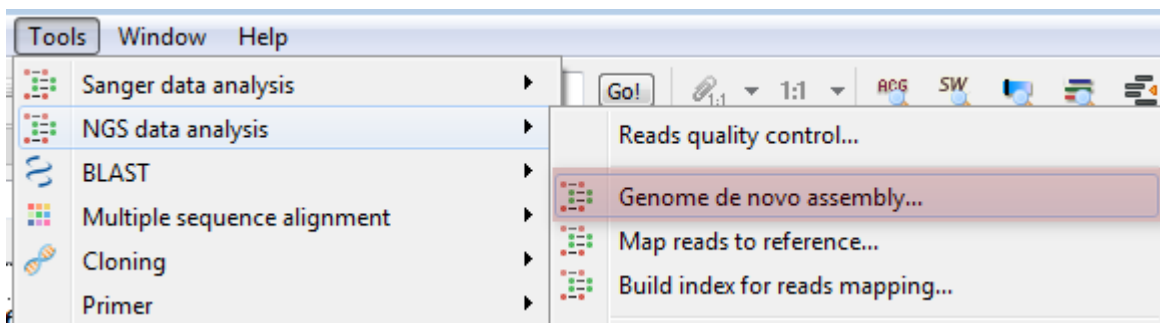


# SPAdes

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 has a title bar with a 'U' icon and standard window controls. 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'. There are two main sections for 'Left reads' and 'Right reads', each with a table for 'Properties' (columns: #, Type, Orientation) and 'Path'. Below these are 'Add' and 'Remove' buttons. The 'Base Options' section at the bottom contains: 'Dataset type' (Multi Cell), 'Running mode' (Error Correction and Assembly), 'k-mer sizes (-k)' (auto), 'Number of threads (-t)' (8), and 'Memory limit GB (-m)' (250). At the bottom right are 'Start', 'Cancel', and 'Help' buttons.

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.