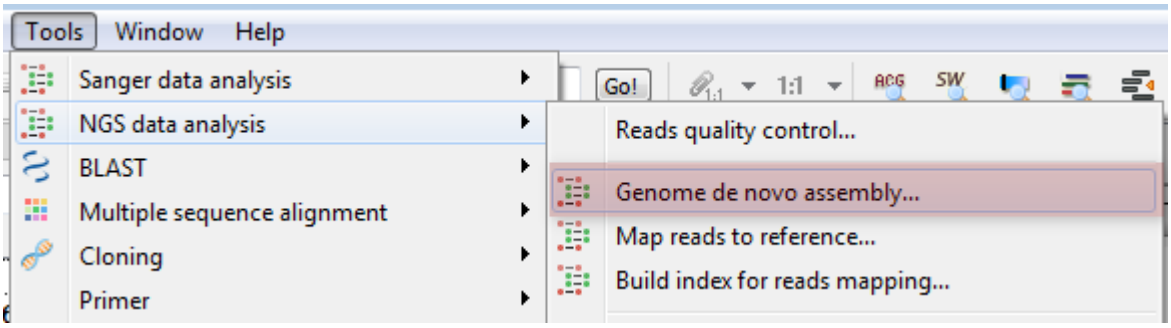
SPAdes

SPAdes – St. Petersburg genome assembler. Click this link to open SPAdes homepage. SPAdes is embedded as an *external tool* into UGENE.

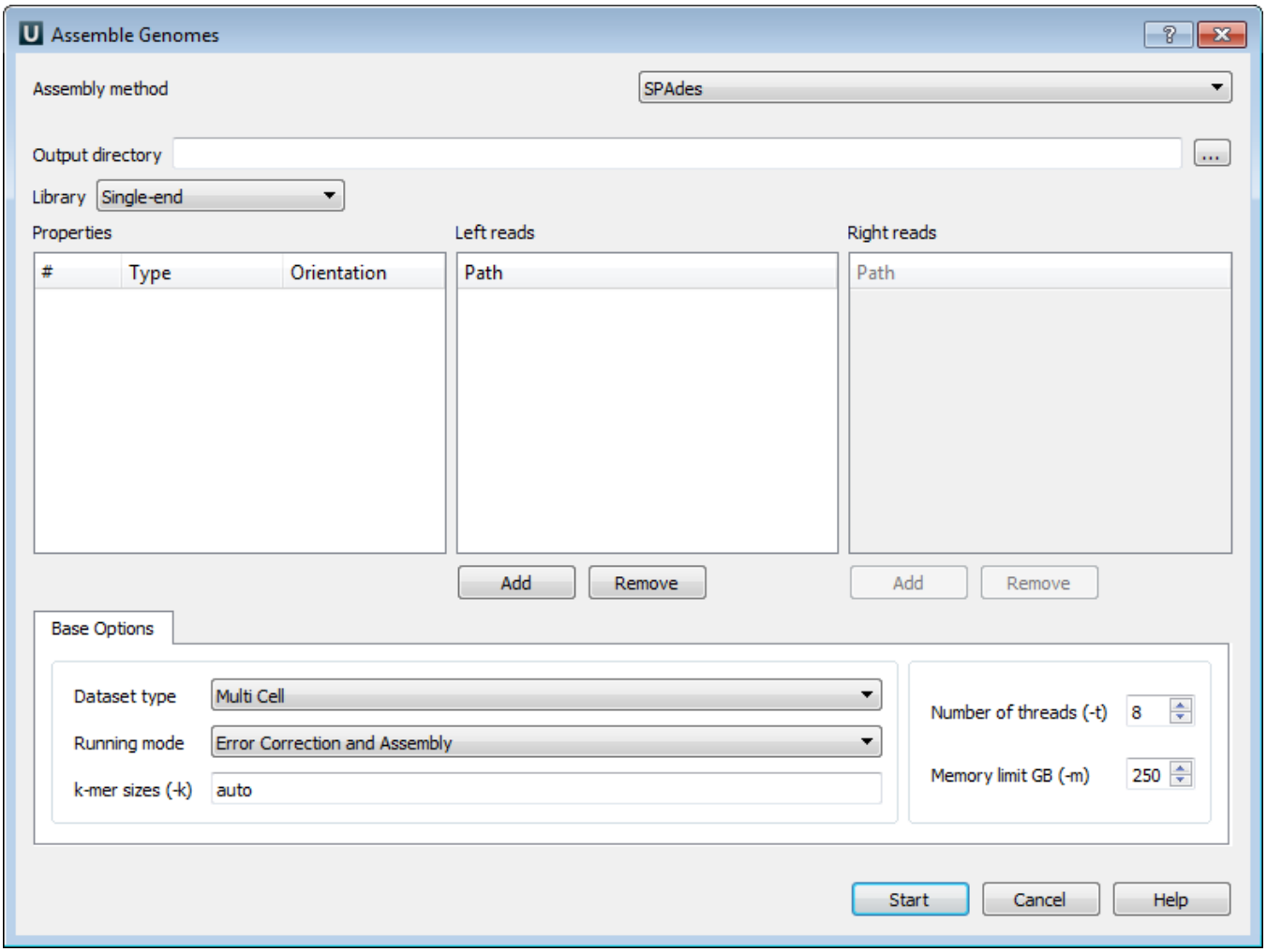
> SPAdes tool is available on macOS and Linux operating systems only.

Open *Tools NGS data analysis*.



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

The *Assemble Genomes* dialog will appear.



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.