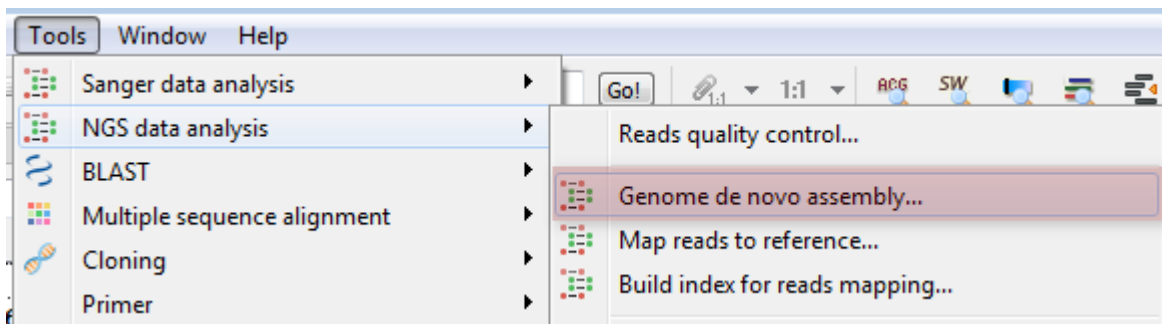


# SPAdes

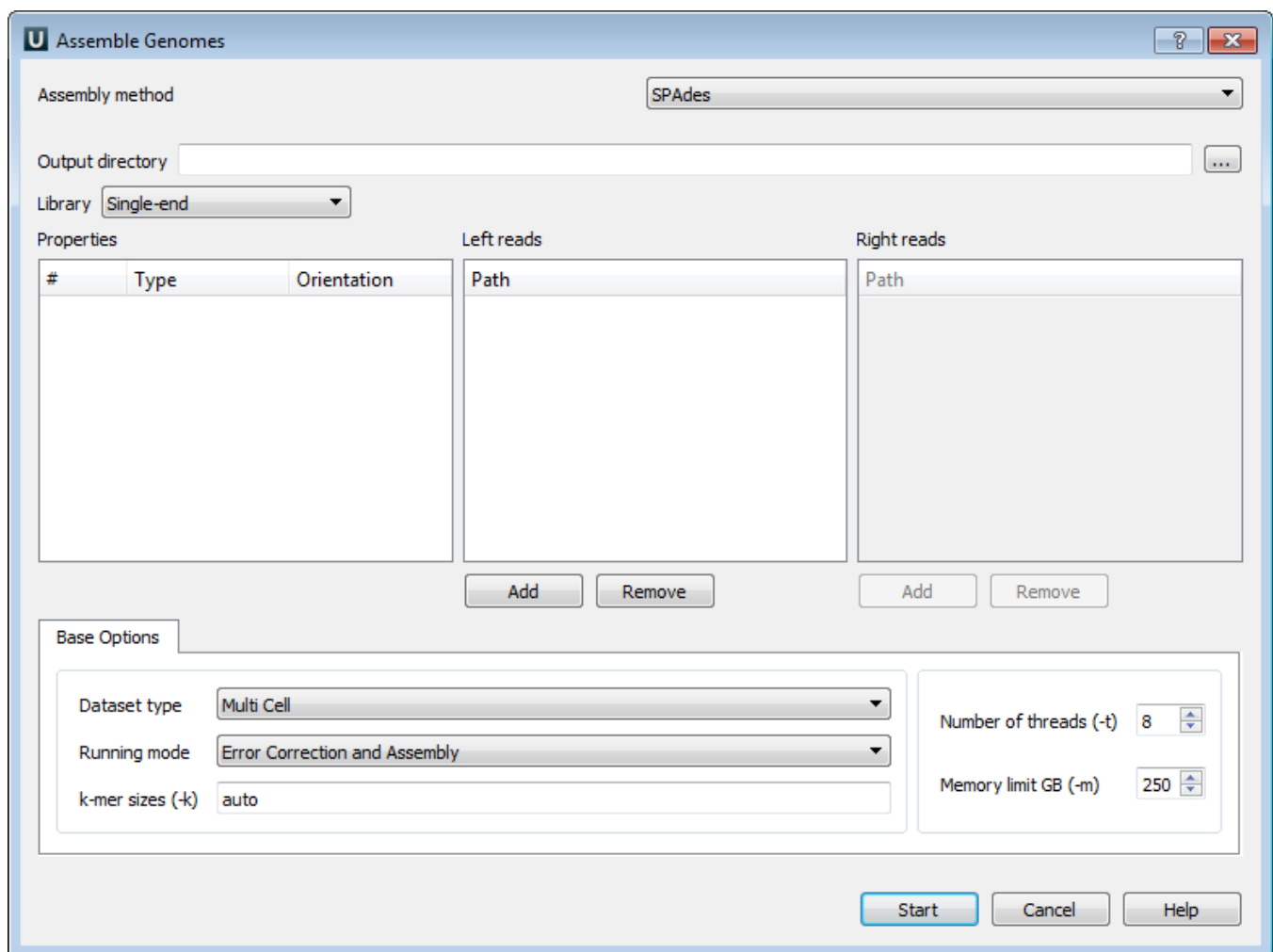
SPAdes – St. Petersburg genome assembler. Click [this link](#) to open SPAdes homepage. SPAdes is embedded as an [external tool](#) into UGENE.

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.