Reference Data for NGS

To run some NGS data analysis (metagenomics classification or ChIP-Seq) it is required to provide reference data (e.g. RefSeq databases, NCBI taxonomy files, etc.).

> Both taxonomy classification and ChIP-Seq tools are available on macOS and Linux operating systems only. Also, make sure there is enough disk space on the target computer.

It is recommended to use the Online Installer to download these data, however, one can also download them directly (see links on the "Download UGENE and components" page). In the latter case it is required to additionally manually configure an installed UGENE package, see instructions below.