

Single Cell Toolkit System Requirements

- [Up to 100,000 cells per analysis](#)
- [More than 100,000 cells per analysis](#)

Because of the large size of single cell RNA-Seq data sets and the computationally-intensive tools used in single cell analysis, we have amended our system requirements and recommendations for installations of Partek® Flow® with the Single Cell toolkit.

Up to 100,000 cells per analysis

Required

- Linux: Ubuntu® 18.04, Redhat® 8, CentOS® 8, or newer
- CPU: 64-bit 2 GHz quad-core processor
- Memory: 64 GB of RAM
- Local scratch space¹: 1 TB with cached or native speeds of 2GB/s or higher
- Storage: > 2 TB available for data and > 100 GB on the root partition

Recommended

- Linux: Ubuntu® 18.04, Redhat® 8, CentOS® 8, or newer
- CPU: 64-bit 2 GHz quad-core processor
- Memory: 128 GB of RAM
- Local scratch space¹: 2 TB with cached or native speeds of 2GB/s or higher
- Storage: > 2 TB available for data and > 100 GB on the root partition

More than 100,000 cells per analysis

Required

- Linux: Ubuntu® 18.04, Redhat® 8, CentOS® 8, or newer
- CPU: 64-bit 2 GHz quad-core processor
- Memory: 256 GB of RAM
- Local scratch space¹: 2 TB with cached or native speeds of 2GB/s or higher
- Storage: > 4 TB available for data

Recommended

- Linux: Ubuntu® 18.04, Redhat® 8, CentOS® 8, or newer
- CPU: 64-bit 2 GHz quad-core processor
- Memory: 512 GB of RAM
- Local scratch space¹: 10 TB with cached or native speeds of 2GB/s or higher
- Storage: 10 TB available for data

For fastest performance:

- Newer generation CPU cores with avx2 or avx-512 are recommended.
- Performance scales proportionality to the number of CPU cores available.
- Hyper thread cores (threads) scales performance for most operations other than principal component analysis.

¹ Contact Partek support for recommended setup of local scratch storage

Additional Assistance

If you need additional assistance, please visit [our support page](#) to submit a help ticket or find phone numbers for regional support.



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