

MinION Mk1C IT Requirements

Checklist

This checklist represents the minimal requirements for installing the MinION Mk1C in your institution. For full explanation of requirements, please read the rest of this document.

| Item/setup required | Reason |
|--|--|
| 1x 1 Gbp/s RJ45 port with DHCP service running (initial configuration only) or Wi-Fi hotspot with internet connectivity (captive portals unsupported. Initial configuration only) | Connection to IT infrastructure and internet |
| If using wired connection: 1x 1 Gbp/s Ethernet cable | Connection to IT infrastructure and internet |
| HTTPS/port 443 to 52.17.110.146, 52.31.111.95, 79.125.100.3 (outbound-only access) or DNS rule for ping.oxfordnanoportal.com | Telemetry feedback |
| Ethernet: HTTPS/port: 443 TCP access to AWS eu-west-1 IP ranges: http://docs.aws.amazon.com/general/latest/gr/aws-ip-ranges.html | EPI2ME analysis |
| HTTPS/port 443 to 178.79.175.200 and 96.126.99.215 (outbound-only access) or DNS rule for cdn.oxfordnanoportal.com | Software updates |
| Standard wall power socket | Device power |

MinION Mk1C device

Overview

The Oxford Nanopore Technologies® MinION™ Mk1C is a compact, portable device. It combines the hardware for running nanopore sequencing experiments with fully-integrated compute used for basecalling and onward analysis. The device is entirely self-contained and requires no other computing resource.

The MinION Mk1C can be used with MinION/GridION Flow Cells and the Flongle Adapter and Flow Cells. Users can operate the system in an offline or online mode, enabling full sequencing and analysis to be performed in the lab and field. A high-definition touch screen means users receive constant feedback regarding experiment progression and can easily interact with the device without additional hardware.

The MinION Mk1C benefits from the inclusion of on-board compute which permits data acquisition, analysis and feedback, basecalling, data streaming and device control, all without placing any additional burden on existing IT infrastructure.

All device control, basecalling, analysis and orchestration on the MinION Mk1C is carried out by pre-installed custom software created by Oxford Nanopore Technologies.

Specifications

The MinION Mk1C is designed around a simple user interface on top of cutting-edge custom electronics providing real-time analysis solutions:

| Component | Specification |
|--------------------------|---|
| Size and weight | H 32 mm x L 142 mm x W 118 mm; 440 g |
| Power | Supplied with a 6.3-19.6 VDC power supply Max rated current 10 A Max rated power 60 W |
| Compute spec | 1 TB SSD Storage, 8 GB RAM, GPU embedded analysis accelerator |
| Connectivity | WiFi, USB 2.0 with eSATA (the eSATA is currently non-functional), microSD, Ethernet |
| Pre-loaded software | Linux OS, MinKNOW |
| Security | Kensington Nano Security Slot |
| Environmental conditions | Designed to sequence in environmental temperatures of +10°C to +30°C. Tested to function between 0°C to +40°C. Do not cover vents on the top or sides of the device |

Telemetry

MinKNOW collects telemetry information during sequencing runs as per the Terms and Conditions to allow monitoring of device performance and enable remote troubleshooting. Some of this information comes from free-form text entry fields, therefore no personally-identifiable information should be included. We do not collect any sequence data.

The EPI2ME platform is hosted within AWS and provides cloud-based analysis solutions for multiple applications. Users upload sequence data in FASTQ format via the EPI2ME Agent, which processes the data through defined pipelines within the EPI2ME Portal. Downloads from EPI2ME are either in Data+Telemetry or Telemetry form. The EPI2ME portal uses telemetry information to populate reports.

Software updates

The IP address from which you receive software updates will depend on your geographical location. You can update through the software UI or through **apt** on the terminal, so you require outbound-only access. We notify users about software updates through the Nanopore Community and provide full instructions for updating in each release note.

Storage

File types

Nanopore sequencing data is stored in three file types: POD5, FASTQ and BAM. Basecalling summary information is stored in a sequencing_summary.txt file:

- POD5 is an Oxford Nanopore-developed file format which stores nanopore data in an accessible way and replaces the legacy .fast5 format. This output also reads and writes data faster, uses less compute and has smaller raw data file size than .fast5.
- .fast5 is a legacy file format based upon the .hdf5 file type, which is designed to contain all information needed for analysing nanopore sequencing data and tracking it back to its source. A .fast5 file contains data from multiple reads (4000 reads as default), and is several hundred Mb in size.
- FASTQ is a text-based sequence storage format, containing both the sequence of DNA/RNA and its quality scores. By default, nanopore sequencing experiments save up to 4000 DNA sequences in one FASTQ file. File size can vary from <1 Mb to tens of Mb depending on the number and length of sequences. Retaining only FASTQ files will allow use of downstream analysis tools, but no further sequence data can be generated when improvements in basecalling become available.
- BAM files are output if alignment or modified base calling has been performed on the basecalled dataset.
- sequencing_summary.txt contains metadata about all basecalled reads from an individual run. Information includes read ID, sequence length, per-read q-score, duration etc. The size of a sequence summary file will depend on the number of reads sequenced.

Example file sizes below are based on different throughputs from an individual flow cell, with a run saving POD5, FASTQ, and BAM files with a read N50 of 23 kb.

| Flow cell output (Gbases) | POD5 storage (Gbytes) | FASTQ.gz storage (Gbytes) | Unaligned BAM with modifications (Gbytes) |
|---------------------------|-----------------------|---------------------------|---|
| 10 | 70 | 6.5 | 6 |
| 15 | 105 | 9.75 | 9 |
| 30 | 210 | 19.5 | 18 |

As an experiment progresses, POD5 files are produced for all reads. If basecalling is chosen, these reads are used by the MinKNOW software to generate sequence data which is then stored in FASTQ files and/or BAM files.

Long-term storage

The MinION Mk1C has sufficient SSD disk space for multiple runs to be carried out, storing both POD5 and FASTQ data. However, it is imperative this data store is cleared regularly to prevent successive runs from terminating due to lack of storage space. For this, a user must provide storage to transfer data off the device.

The MinION Mk1C runs onboard admin software that is able to mount multiple filesystem types. If being installed within an institution, filesystem mounting can also be achieved through SSH and command line interactions. We recommend storage presented as NFS or CIFS.

The device can also directly mount and transfer data to USB and microSD storage peripherals. In addition, a password-protected samba share can be operated through a Wi-Fi hotspot for wireless data transmission.

The form and volume of data to be stored and transferred will depend on customer requirements:

- Storing POD5 files with raw read data in will permit re-basecalling of data when new algorithms are released by Oxford Nanopore. In such cases, new releases of basecallers have enabled significant improvements in basecalling accuracy of existing datasets through re-basecalling. Further, selected Oxford Nanopore and third-party tools use the raw signal information contained within the POD5 to extract additional information from the raw signal e.g. calling modified bases, reference-guided SNP calling or polishing of data.
- Retaining just FASTQ files will allow use of standard downstream analysis tools using the DNA/RNA sequence, but no further sequence data can be generated when improvements in basecalling become available.

Frequently asked questions

Does my device require an internet connection to function?

No, an internet connection is not a requirement for the device to start or to continue sequencing. An internet connection will however be required to provide telemetry and debug information in the case of troubleshooting support being required. Additionally, an internet connection will be required to make use of any cloud-based analysis through EPI2ME.

Does the device have a battery?

No, the MinION Mk1C does not contain an internal battery. It is however compatible with commercially-available power supplies for e.g. laptops.

Change log

| Date | Version | Changes made |
|-----------------|---------|---|
| 24th April 2024 | V8 | Corrected some values in "Specifications" |

| Date | Version | Changes made |
|---------------------|---------|---|
| 26th February 2024 | V7 | Minor corrections and clarifications |
| 28th September 2023 | V6 | <ul style="list-style-type: none"> - A file size table has been added to "File types" - Minor corrections and clarifications throughout the document |
| 28th June 2023 | V5 | <ul style="list-style-type: none"> - In "Checklist", the specs for telemetry feedback, EPI2ME analysis, and software updates have been changed. - "Networking explanations" has been removed. - In "File types", information has been added about POD5 files and BAM files. The file size comparison table has been temporarily removed. - The "Included software" section has been removed. - Minor corrections and clarifications throughout the document. |
| 19th August 2022 | V4 | The .fast5/FASTQ file size table has been updated. |
| 21st April 2022 | V3 | Updated the portal link from mirror.oxfordnanoportal.com to cdn.oxfordnanoportal.com in the checklist and network explanations |
| 28th April 2021 | V2 | - Added microSD under Connectivity and Kensington Nano Security slot under Security in "Technical specifications" |
| December 2020 | V1 | Initial version |