# MinION Mk1B IT requirements

Overview

The MinION™ is a small, self-contained device for nanopore sequencing. It plugs directly into a USB Type-A port or a USB Type-C port with a recommended adapter (5 Gbps).

The MinION device is controlled by the MinKNOW™ software.

MinKNOW carries out several core tasks. These include data acquisition, real-time analysis and feedback, basecalling, data streaming, device control including selecting the run parameters, sample identification and tracking. Furthermore, it ensures that the platform chemistry is performing correctly to run the samples.

Despite its small size, the MinION Mk1B can sequence many gigabases (Gbases) in a single sequencing experiment. As such, it is recommended that users purchase a powerful computer to ensure all the technology features are accessible.

The default data analysis workflow when starting to use the MinION is below:
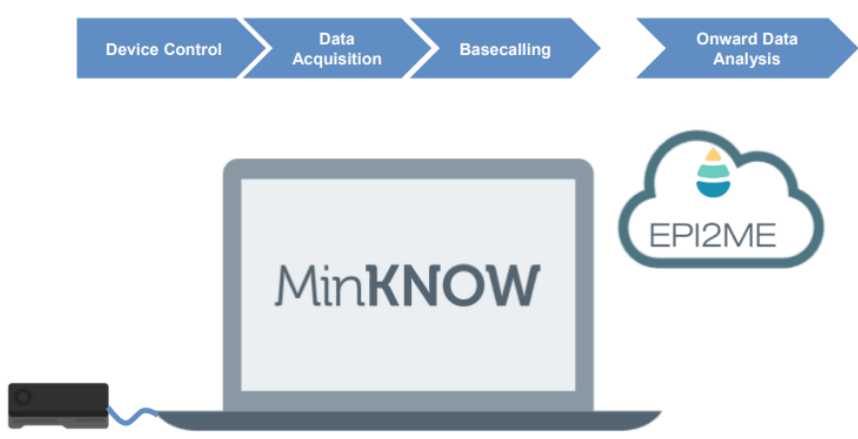
Host computer specification

From MinKNOW v23.07 onwards, our new basecaller Dorado is integrated into MinKNOW. This enables accelerated basecalling on both NVIDIA GPUs and Apple Silicon. We strongly recommend using an NVIDIA GPU or Apple Silicon Mac if you want basecalling to keep up with the rate of data generation.

Component	Required specification: GPU high-accuracy basecalling	Required specification: data acquisition/CPU basecalling (note: CPU basecalling performance is limited - a GPU is recommended)

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Operating system	Windows – 11 and 10 macOS – Sonoma (14), Ventura (13), Monterey (12) Linux – Ubuntu 22.04 and 20.04	Windows – 11 and 10 macOS – Sonoma (14), Ventura (13), Monterey (12) Linux – Ubuntu 22.04 and 20.04
Memory/RAM	16 GB RAM or higher	16 GB RAM or higher
CPU	Intel i7, i9, Xeon, or better, with at least 4 cores/8 threads Ryzen 5, 7, or better, with at least 4 cores/8 threads Apple silicon (M1, M2)	Intel i7, i9, Xeon, or better, with at least 4 cores/8 threads Ryzen 5, 7, or better, with at least 4 cores/8 threads Apple silicon (M1, M2)
GPU	NVIDIA GPU RTX 2060 SUPER or better, with at least 8 GB of GPU memory. Technical information can be found on various websites, for example https://www.techpowerup.com/gpu-specs/. Widely-available examples include the RTX 2060 SUPER, RTX 2070, RTX 3060, RTX 3070. Ampere-based GPUs (the 3000 series, A series etc.) are particularly recommended for optimal performance. Apple silicon (M1, M2) If you are working with a different type of GPU than the models listed above, please ensure that it has a CUDA Compute Capability >6.1 (for more information about CUDA-enabled GPUs, see the NVIDIA website).	-
Storage	1 TB internal SSD or higher	1 TB internal SSD or higher
Ports	USB3.0	USB3.0

We recommend internal solid-state storage for MinKNOW installation as well as data output/acquisition. Solid-state drives are much faster than traditional hard drives and are able to keep up with the flow of data generated during a sequencing run.

Computer recommendations

Below are some examples of models/workstations that meet or can be configured to meet the recommended specification for the MinION Mk1B. We have not extensively tested any of these computers, so purchasing is at your own risk. Ensure that you have configured the computer to meet the specification in the table above. Other manufacturers are available; check the availability for your region.

Performance band	Example laptop
Low: Fast basecalling model keep-up	M1 MacBook Air (2023)
Medium: High accuracy basecalling keep-up	M2 Max 16" MacBook Pro (2023) / MacStudio

Connecting the MinION Mk1B to a computer without a USB Type-A port
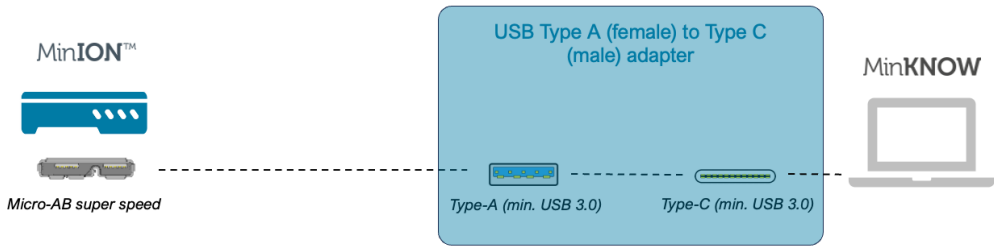
If your laptop does not have a USB Type-A port, we recommend using a USB Type-A to USB Type-C adapter (Female to Male 5 Gbps). Below is a non-exhaustive list of example adapters. We have not extensively tested all models below, so purchasing is at your own risk.

- StarTech 6"
- RS Pro 150 mm
- Belkin

The below requirements are to ensure correct operation of the MinION during a sequencing experiment:

Component	Minimum requirement
User account privilege level	Local Administrator privileges are needed for MinKNOW installation and updates. Local Administrator privileges are not required for running sequencing experiments.
Internet connection	An internet connection is required at all times for software updates and telemetry. Offline configurations can be made available for field use and expeditions. Please contact support@nanoporetech.com if you are planning to use your MinION offline.
Antivirus settings	Antivirus software scanning the entire hard drive uses significant amounts of resources and may cause performance issues. For this reason, it is recommended that the antivirus scans are switched to manual setting, rather than to automatic, so that they can be performed when the MinION is not in use.
OS update settings	OS system updates should be switched to manual mode, as downloading them during a sequencing experiment may impact performance. Updates that require restart will fatally halt a run.
Telemetry feedback	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

Component	Minimum requirement
EPI2ME analysis	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
Software updates	HTTPS/port 443 to 178.79.175.200 and 96.126.99.215 (outbound-only access) or DNS rule for cdn.oxfordnanoportal.com

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

Depending on your geographical region, only one of 178.79.175.200 or 96.126.99.215 will be used for provision of updates to device software. The Updates are triggered as pull requests, therefore outbound-only access is required.

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 contains 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 standard downstream analysis tools using the DNA/RNA sequence, but no further sequence data can be generated when improvements in basecalling become available.
- BAM files are output if you perform alignment or modified base calling 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 you choose to basecall your data, these reads are used by the MinKNOW software to generate sequence data which is then stored in FASTQ files and/or BAM files.

Change log

Date	Version	Changes made
24th April 2024	V18	- In "Host computer specification", updated operating system recommendations for Windows, macOS and Linux. - Updated CPU and GPU recommendations to include Apple silicon (M1 and M2)
20th February 2024	V17	- In "Computer recommendations", the high performance option has been removed; references to adaptive sampling have been removed.
28th September 2023	V16	- A file size table has been added to "File types" - Minor corrections and clarifications throughout the document
23rd August 2023	V15	- A new section has been added: "Computer recommendations" - A new section has been added: "Connecting the MinION Mk1B to a computer without a USB Type-A port" - A new introductory paragraph has been added to "Host computer specification" - The disclaimer "The MinION device is CE marked using USB3.0. If a user wished to use USB-C, they may, but this invalidates the CE marking and may cause issues when using an adapter" has been removed.
4th August 2022	V14	- 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.
28th June 2023	V13	- Ubuntu 20.04 support has been included - Host computer specifications have been updated from "recommended" to "required". The Intel CPU specification has been updated to requiring at least 4 cores/8 threads. Ampere-based GPUs have been added to GPU recommendations. - The requirement for solid-state storage has been reworded - The amount of storage space required for 1 Gbyte of sequence data has been revised. - In "Networking explanations", the AWS IP range has been updated to the global CloudFront IP range.
21st April 2022	V12	Updated the portal link from mirror.oxfordnanoportal.com to cdn.oxfordnanoportal.com in the host computer specifications section
10th September 2021	V11	Removed erroneous compatibility with Ubuntu 20.04
8th September 2021	V10	Added Windows 10 to the list of supported operating systems for GPU-enabled basecalling
22nd July 2021	V9	In the table of minimal requirements, two extra fields have been added: "Telemetry feedback, EPI2ME analysis", and "Software updates"

Date	Version	Changes made
30th June 2021	V8	- Checklist at the top of the document has been removed - Split IT requirements into Recommended (GPU) and Minimum (CPU) - Updated operating systems recommendations for Windows (10), Mac OS (Mojave, Catalina) and Linux (18.04 and 20.04) - Updated CPU recommendations to i7, i9, Xeon or better with 4+ cores - Updated description and use of .fast5 files in the MinKNOW section - Updated screenshot of the EPI2ME Agent - Added table of .fast5 and FASTQ file sizes with different flow cell outputs
23rd Dec 2020	V7	- Removed requirement for accessing IP address 106.187.40.102 - Updated the supported external NVIDIA GPUs to Tesla V100, Quadro GV100, Jetson TX2 and Jetson Xavier
23rd Oct 2020	V6	Updated OSX compatibility
3rd July 2020	V5	Updated Fig 1 to 4.0.8 UI
18th May 2020	V4	Removed Bluetooth compatibility for MinIT
Feb 2020	V3	More information about basecalling on GPUs using Guppy