

GridION Mk1 IT Requirements

Checklist

This checklist represents the minimal requirements for installing the GridION in your institution. For full explanation of requirements, please continue to the document.

Item/setup required	Reason	Provided?
1x 1 Gbp/s RJ45 port with DHCP service running	Connection to IT infrastructure and internet	
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	
USB mouse	Device control	
USB keyboard	Device control	
HDMI- or DisplayPort-compatible monitor	Device control	
Power supply capable of delivering 650 W	GridION power	
Storage: Sufficient infrastructure for required storage option*	Long-term data storage	

*Size of storage required will depend on use case. Please refer to the information below for storage guidelines.

GridION Mk1 device

Overview

The GridION is a benchtop device for nanopore sequencing designed to run and analyse up to five MinION or Flongle Flow Cells, or a combination thereof. It is ideal for labs with multiple projects that need the advantages of nanopore sequencing:

- Simple library preparation
- Real-time analysis
- Biological insights from long reads

In addition the GridION also enables users to offer nanopore sequencing as a service when [certified](#).

The GridION 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 GridION is carried out by pre-installed custom software created by

Oxford Nanopore Technologies. The default data analysis workflow when using the GridION Mk1 is as below:



Figure 1: Default data analysis workflow of the GridION device

Specifications

The GridION Mk1 is designed around a simple user interface on top of cutting-edge custom electronics providing real-time analysis solutions:

Component	Specification
Operating system	Ubuntu 20.04 running off Intel CPU Customers are advised to keep up to date with all software and security patches
Storage	4 TB internal SSD
GPU cards	1x Nvidia Quadro GV100
Memory	64 GB RAM
Size and weight	H220 x W365 x D370 mm Weight 14.4 kg
Environmental ranges	System functional range +5°C to +40°C Designed to sequence at +18°C to +25°C

Site requirements

Installing the GridION Mk1 in your institution is similar to installing any new computer. Requirements for the device are as follows:

Component	Requirements
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Component	Requirements
1x RJ45 port	<p>IP address via either DHCP service or statically assigned</p> <p>TCP running on port 443 HTTPS</p> <p>Requires perimeter firewall permissions:</p> <ul style="list-style-type: none"> - To access 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 for telemetry feedback - HTTPS/port 443 and TCP access to AWS eu-west-1 IP ranges: http://docs.aws.amazon.com/general/latest/gr/aws-ip-ranges.html for 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 for software updates <p>Connected to local storage infrastructure</p>
1x power supply	<p>1x country-specific C13 cable included with device</p> <ul style="list-style-type: none"> - Maximum power draw 650 W - Maximum current 6 A - Supply voltage 100–240 VAC (50/60 Hz)
1x monitor	Compatible with HDMI or DisplayPort connection (a DisplayPort to HDMI adapter is included in the GridION shipment)
1x keyboard	Compatible with USB connection
1x mouse	Compatible with USB connection

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. POD5 files are generated in batches every 10 minutes. The files can be split by barcode if barcoding is used, but splitting by barcode is off by default.
- .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. FASTQ files are generated in batches by time, with a default of one file generated every 10 minutes. However, you can configure this frequency to 10 minutes, one hour, or one file generated at the end of the run. You can also batch the reads based on the number of reads per file.
- BAM files are output if you perform alignment or modified base calling on the basecalled dataset. BAM file generation options are the same as for FASTQ files. BAM files are off by default and switched on automatically if alignment or modified base calling is used.
- `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.

Long-term storage

The GridION 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 in order to prevent successive runs from terminating due to lack of storage space. For this, a site must provide storage to transfer data off the device.

The GridION runs on Ubuntu and is able to mount multiple filesystem types. We recommend storage presented as NFS or CIFS. The form (and volume) of data to be stored 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 modified bases calling, 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

Can I use an uninterruptible power supply (UPS) with the GridION?

Yes you can use a UPS, however we are unable to recommend a specific product.

Do you have any recommendations for how to move data off the GridION in real time during a sequencing run?

Currently we recommend moving the data off the box using `rsync` run hourly through `crontab`. For further details, please email support@nanoporetech.com

Change log

Date	Version	Changes made
31st July 2024	V12	In "File types", updated information about data generation for POD5, FASTQ and BAM files.
28th September 2023	V11	<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	V10	<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.
10th March 2023	V9	Checklist and Site requirements have been updated to remove the requirement for HTTP port 80
22nd September 2022	V8	In "Site requirements", the URL for the AWS eu-west-1 IP ranges has been corrected.
19th August 2022	V7	<ul style="list-style-type: none"> - In "Specifications", the device weight has been updated to 14.4 kg and the system functional range has been updated to +5°C to +40°C. - The .fast5/FASTQ file size table has been updated.
21st April 2022	V6	Updated the portal link from mirror.oxfordnanoportal.com to cdn.oxfordnanoportal.com in the checklist and networking explanations section
12th November 2020	V5	Corrected DisplayPort and HDMI compatibility
14th September 2020	V4	Removed references to DisplayPort compatibility, as the GridION is now shipped with a DisplayPort to HDMI adapter
29th April 2020	V3	Amended output file sizes after the introduction of file compression
29th July 2019	V2	Updated information for GridION Mk1
9th July 2018	V1	Initial version