Powerful, real-time, long-read sequencing in the palm of your hand
Nanopore sequencing technology is advancing at an unprecedented pace, promising a future where portable sequencing will be routine in surveillance and many other fields.

Jana Batovska, La Trobe University

MinION is a powerful, portable sequencing device that delivers immediate access to gigabases of long-read data

The pocket-sized, USB-powered MinION allows you to sequence anything, anywhere — from the bench to the field — with real-time analysis providing immediate access to actionable results. The same long-read, direct RNA and DNA sequencing workflows are available across our products, providing truly scalable sequencing.

MinION™
Up to 30 Gb

GridION™ X5
Up to 150 Gb (all 5 flow cells sequencing)

PromethION™ 24 and 48
Up to 4,800 Gb (P24) or 9,600 Gb (P48) (all 24 or 48 flow cells sequencing respectively)

* Flongle is a flow cell adapter for MinION and GridION, designed for rapid and cost-effective analysis of smaller tests and samples. Best customer yield, 1.8 Gb.
† Based on current, internal flow cell performance (theoretical performance of up to 15 Tb).
‡ Devices may be run for longer. 48 hours used for comparison purposes only.

MinION ~5 kb amplicon run basecalling all done at 34.28 Gb, I’ll take that :)

Dr. John Tyson, University of British Columbia
All the benefits of long-read, real-time nanopore sequencing in a portable, low-cost device

Long reads
Discover and phase hidden variation — from repetitive regions and structural variants to novel, full-length transcript isoforms

High yields
As much as 30 Gb* data suitable for all applications — from whole genomes and transcriptomes to high-throughput targeted analyses

Real time
Immediate access to actionable results — from pathogen and antimicrobial resistance identification to fusion transcripts

Portable
Sequence samples at source — combine with VoTRAX™ and MinIT™ for portable sample prep and analysis

Accessible
Starter Packs from just $1,000 — with no capital investment or complex IT infrastructure required

Direct
Study native DNA and RNA, not a copy — eliminate amplification bias and detect base modifications

How will you use your MinION?

From the bench to the field, the MinION is being utilised throughout the world to deliver new insights and actionable, real-time results for a range of applications.
Choose your MinION Starter Pack

<table>
<thead>
<tr>
<th></th>
<th>Basic</th>
<th>Enhanced</th>
<th>Project</th>
</tr>
</thead>
<tbody>
<tr>
<td>MinION device</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Flow cells</td>
<td>2</td>
<td>8</td>
<td>14</td>
</tr>
<tr>
<td>Sequencing kits</td>
<td>1</td>
<td>2</td>
<td>3</td>
</tr>
<tr>
<td>Wash kits</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Community Support</td>
<td>Included</td>
<td>Included</td>
<td>Included</td>
</tr>
<tr>
<td>Training/Services included*</td>
<td>Optional</td>
<td>1-day workshop</td>
<td>Project support</td>
</tr>
</tbody>
</table>

$1,000† $4,500† $12,700†

* A wide range of training and support services are available, see page 14 or visit store.nanoporetech.com/services for more information.
† Delivery costs for device and consumables are not included.

Add individual MinIT (see page 12) for $1,850 when ordered together with MinION Starter Pack.

Buy now store.nanoporetech.com
A complete and streamlined workflow for rapid access to actionable results

Prepare
- Streamlined library prep — in as little as 10 minutes, with multiplexing options
- Scale according to your needs — same chemistry and kits used for Flongle, MiniION, GridION X5 and PromethION
- Automate library preparation using the portable, USB-powered VolTRAX

Sequence
- Sequence what you need, when and where you need it
- Read lengths determined by your sample and experimental needs
- MiniION sequences DNA and RNA directly — meaning no amplification bias and retained modification information
- Run smaller sequencing tests and experiments or cost-effectively check your sample quality using Flongle or MiniION

Analyze
- Real-time results for time-critical applications such as pathogen identification
- User controlled run time — stop sequencing when sufficient data generated, wash and reuse flow cell
- Portable data analysis using a laptop or MiniT accessory — with pre-loaded EPI2ME workflows
- Output raw signal or basecalled .fastq files for use in custom analysis pipelines

Applications include:
- Rapid metagenomic species identification and antibiotic resistance profiling
- Accurate high-coverage microbial genome assemblies (DNA and RNA)
- Enhanced large genome analysis (e.g. cancer samples) through accurate mapping of structural variation, repetitive regions and phasing
- Quantify and characterise RNA splice variants, isoforms and fusion transcripts

Bioinformatic capability needed:
- Use cloud-based or local EPI2ME platform for real-time analysis workflows. epi2me.nanoporetech.com/workflow
- Get analysis recommendations and clear tutorials on the use of open-source tools. community.nanoporetech.com/knowledge
- Run open-source tools written and developed by the Nanopore Community. community.nanoporetech.com
- All the data, raw or basecalled, can be used in custom analysis pipelines written by the user for specific applications.

More information nanoporetech.com/products
Enhance your MinION sequencing workflow…

Prepare
Automated library preparation for nanopore sequencing.
• Small, USB-powered device
• Minimal hands-on time
• Reproducible results

Sequence
Adapting MinION for smaller, rapid tests and analyses. Delivering as much as 1.8 Gb data, Flongle is suitable for:
• Smaller samples (e.g. targeted regions and smaller genomes)
• Rapid sample ID or quality checking
• Low-cost regular testing

Analyse
Simple, preconfigured IT solution for MinION and Flongle sequencing.
• Performs instrument control, basecalling and EPI2ME real-time analysis workflows
• Eliminates need for dedicated laptop
• Bluetooth and Wi-Fi enabled — control using phone, tablet or laptop

…with data analysis in real time

EPI2ME
Real time data analysis workflows accessed through the cloud or locally using MinIT.

Example workflows:
What’s In My Pot (WIMP)
Species-level identification and quantification of microbes from metagenomic samples
ARMA
Builds on WIMP with full antibiotic resistance profiling
16S
Genus-level identification of bacteria and archaea in metagenomic samples
Custom Reference Alignment
Align genomes to any reference sequence

VolTRAX
Flongle
MinIT
Optimise your experiments with expert support

All nanopore users get open access to the Nanopore Community, a thriving online hub supporting scientists to maximise the benefits of long-read, real-time nanopore sequencing. A range of training courses are also available, providing everything you need to optimise your nanopore sequencing workflows.

Nanopore Community

• Access the online protocol builder and optimise your experimental workflow — from sample prep to analysis
• Post your questions to expert users and browse the extensive knowledge base
• Network and collaborate with your peers
• Get the latest protocols and software downloads
• Share feedback and help shape the next generation of nanopore sequencing products

Starter Pack support

Designed to get you up and running quickly, MinION Starter Packs include a range of support services, from Community-based support through to one-day workshops and consultancy.

Training options

We offer a range of training options to suit your specific needs, from regular one-day group workshops covering the essentials of nanopore sequencing and data analysis, to private one-day (Rapid Start Day) and two-day (Advanced Nanopore Training) courses which can be held at your lab, using your samples.

More information store.nanoporetech.com/services

The MinION Mk1C combines the real-time, rapid, portable sequencing of MinION and Flongle with powerful computing and a high-resolution screen — offering a complete, go-anywhere solution for long-read DNA and RNA sequencing and analysis.

Integrated, powerful, real-time compute with pre-installed basecalling and analysis software

High-resolution touch screen display allowing complete device control and easy visualisation of results

Integrated, portable sequencing and analysis

Bluetooth, Wi-Fi and cellular network enabled — upload and share your data, wherever you are

Get as much as 30 Gb data using MinION Flow Cells or, for smaller tests and analyses, use Flongle for as much as 1.8 Gb data

Data files are written to an onboard, high-capacity SSD; data can then be transferred to your own system

Pre-order* store.nanoporetech.com/minion-mk1c

* Available Q3 2019

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