Oxford Nanopore Technologies

Service Provider Programme

Transform your services

Deliver richer multiomic insights via scalable innovation

Attracting service projects in a competitive environment means navigating technology evolution alongside technical and operational risk to deliver differentiated, high-quality data. Service Providers tell us that strong technology partnerships are essential to becoming trusted experts for their users.

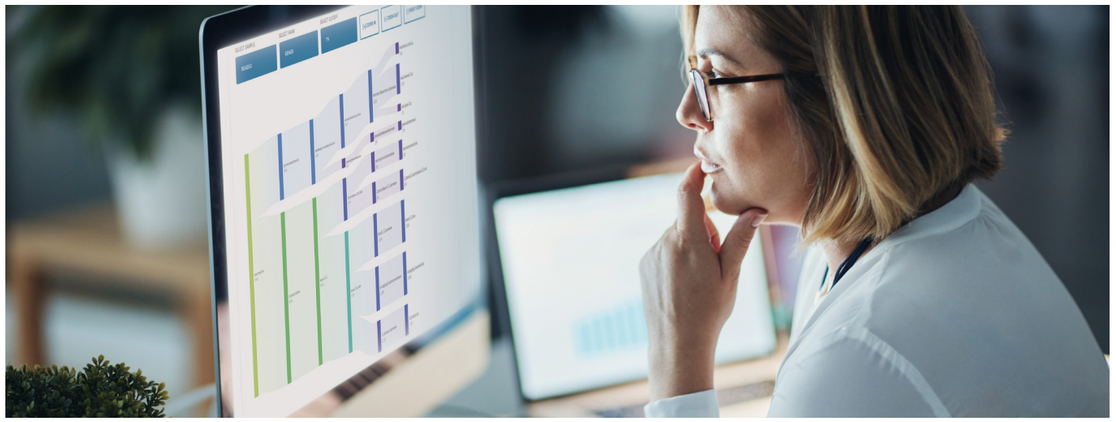
Our Service Provider Programme supports labs like yours — delivering technology innovation, scalable usability, and partnership to attract projects and deliver richer, multiomic insights to your users.

Data analysis for all levels of expertise

Enjoy free access to our powerful EPI2ME platform. Available through an intuitive interface or the command line, the pre-packaged, open-source EPI2ME workflows offer streamlined analysis of Oxford Nanopore sequencing data for you and your service users.

For data scientists comfortable with command-line interfaces, the latest basecallers, EPI2ME workflows, and cutting-edge tools can be found in the Oxford Nanopore GitHub repositories. You can also integrate your own code into our workflows.

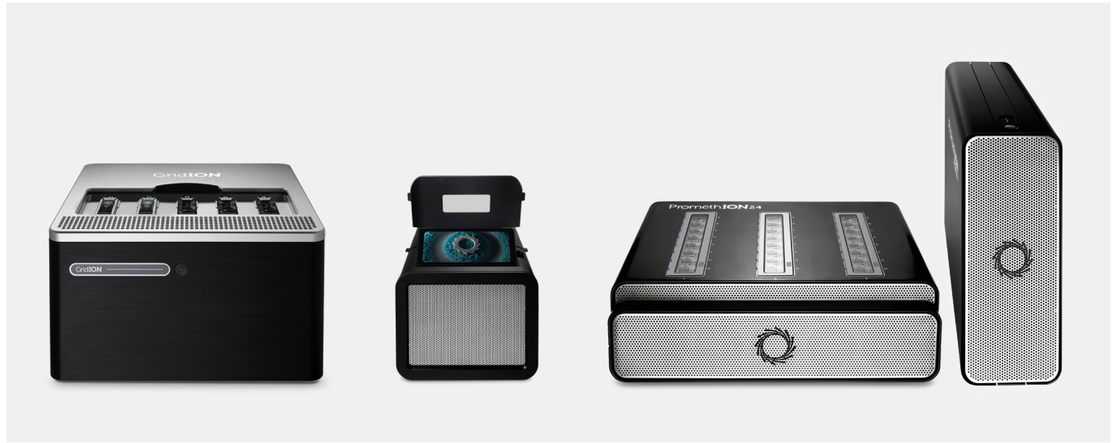
Full technical support ensures rapid, efficient delivery of maximum data insights.
Find out more at: nanoporetech.com/analyse.



Get started whatever your budget, and scale up easily

Choose from project-scale and production-scale GridION™ and PromethION™ sequencers with integrated compute, designed for plug-and-play installation without additional calibration. Independently controlled flow cell positions support flexible, on-demand sequencing — run multiple samples and multiple applications simultaneously on a single device. Maximise your device capacity and never waste time waiting for sample batching.

Explore our devices at: nanoporetech.com/sequence.



Show your scientific community what they've been missing

Empower your users to ask bolder questions and enhance their decision-making. Unlock multi-layered insights using a single multiomic platform that directly sequences native DNA and RNA — with simultaneous methylation detection. Detect more variation with high accuracy in complete genomes, transcriptomes, epigenomes, targeted regions, plasmids, and amplicons.

Don't let technology limit discovery and decision-making

19%
of the human genome is inaccessible to legacy short-read sequencing technology[1]

<3%
of all CpG sites are covered by standard genotyping approaches[2]

40%
of all structural variants are missed by legacy short-read sequencing technology[3]

Deliver greater insights on a single, streamlined platform

Richer insights

Highly accurate genomic data that captures more types of genetic variation

Faster results

Near-sample, real-time workflows that don't require batching

Accessible and affordable

Scalability that enables every application

- Any read length — short to ultra long
- Phasing and structural variants inaccessible to legacy technologies
- Full-length transcript isoforms at single-cell resolution
- Built-in, best-in-class methylation detection
- SNV accuracy comparable to short-read sequencing
- Complete genome assemblies, including dark regions

Explore platform performance at: nanoporetech.com/accuracy.

Our Service Provider Programme supports the growth of your service

Connect

Promote your Oxford Nanopore service and build your project pipeline.

- **Supercharge your online presence** with our marketing resources, and advertise on nanoporetech.com
- **Deliver engaging user events** with your Oxford Nanopore team and our seminar toolkits
- **Receive direct project referrals** from our website, events, and sales teams

Accelerate

Speed up your project workflow with specialised tools and support.

- **Quickly estimate project costs** using our online calculator
- **Streamline your lab work** with sample-to-answer protocols and simple EPI2ME™ data analysis
- **Access expert support when you need it**, for ordering, application setup, and complex projects

Expand

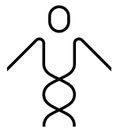
Enrich the value of your service menu for your user community.

- **Stay at the cutting edge** of application and platform developments via newsletters and events
- **Explore new applications**, user benefits, and lab requirements on our online Service Provider hub
- **Develop your differentiated service portfolio** with expert support and investment in optional Workflow-Trained application trainings

Expand your service portfolio with complete sample-to-answer workflows and training

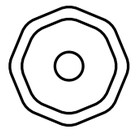
Expand your service offering by selecting from applications with optimised workflows that are recommended for service providers to simplify implementation.

Invest in optional Workflow-Trained training to streamline application integration and create marketable differentiation for your service. Sequencing workflow applications include:



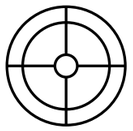
Human whole genome

Simultaneous variant and methylation detection



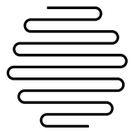
Single cell

Comprehensive isoform-level analysis



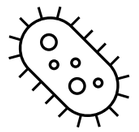
Amplicons

Targeted sequence and variant detection



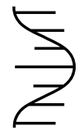
Whole plasmid

Fast, full-length characterisation



Bacterial isolates

Assembly and identification



Direct RNA

Simultaneous sequence and methylation detection

'... with few exceptions, there's only one real choice, and that's Oxford Nanopore'

Prof. Steven Salzberg,
Johns Hopkins University, USA[4]

Want to learn more?

For more information on how our Service Provider Programme can help your team and scientific community unlock richer genomic insights, visit: **nanoporetech.com/service-provider-programme**.

For any questions or to arrange a meeting with one of our sequencing experts, email: **support@nanoporetech.com**.

References:

1. Ahsan, M.U., Liu, Q., Fang, L., and Wang, K. NanoCaller for accurate detection of SNPs and indels in difficult-to-map regions from long-read sequencing by haplotype-aware deep neural networks. *Genome Biol.* 22, 261 (2021). DOI: https://doi.org/10.1186/s13059-021-02472-2
2. Flynn, R. et al. Evaluation of nanopore sequencing for epigenetic epidemiology: a comparison with DNA methylation microarrays. *Hum. Mol. Genet*. 31(18), 3181–3190 (2022). DOI: https://doi.org/10.1093/hmg/ddac112
3. Beyter, D. et al. Long-read sequencing of 3,622 Icelanders provides insight into the role of structural variants in human diseases and other traits. *Nat. Genet*. 53, 779–786 (2021). DOI: https://doi.org/10.1038/s41588-021-00865-4
4. Marx, V. Method of the year: long-read sequencing. *Nat. Methods* 20, 6–11 (2023). DOI: https://doi.org/10.1038/s41592-022-01730-w

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