



Oxford
Nanopore
Technologies



Oxford Nanopore sequencing solutions

for microbiology
and infectious
disease research

What you're missing matters

Your all-in-one genomics platform to uncover the microbial world

Fast and accurate identification and characterisation of microbes is vital to guide public health, food safety, and clinical research to prevent the spread of pathogenic microbes. Assembling complete microbial genomes is not only valuable for outbreak investigations and antimicrobial resistance (AMR) surveillance, but also in microbial risk assessments, quality control (QC) monitoring, and novel food product development. Characterisation of microbial communities also provides invaluable insight for broad, real-time pathogen surveillance.

However, legacy sequencing technologies generate short reads that can miss critical genomic information, such as repetitive regions, limiting genome assemblies. Furthermore, legacy instruments are confined to centralised laboratories.

Oxford Nanopore sequencing overcomes these limitations to reveal rich microbial data with fast results.

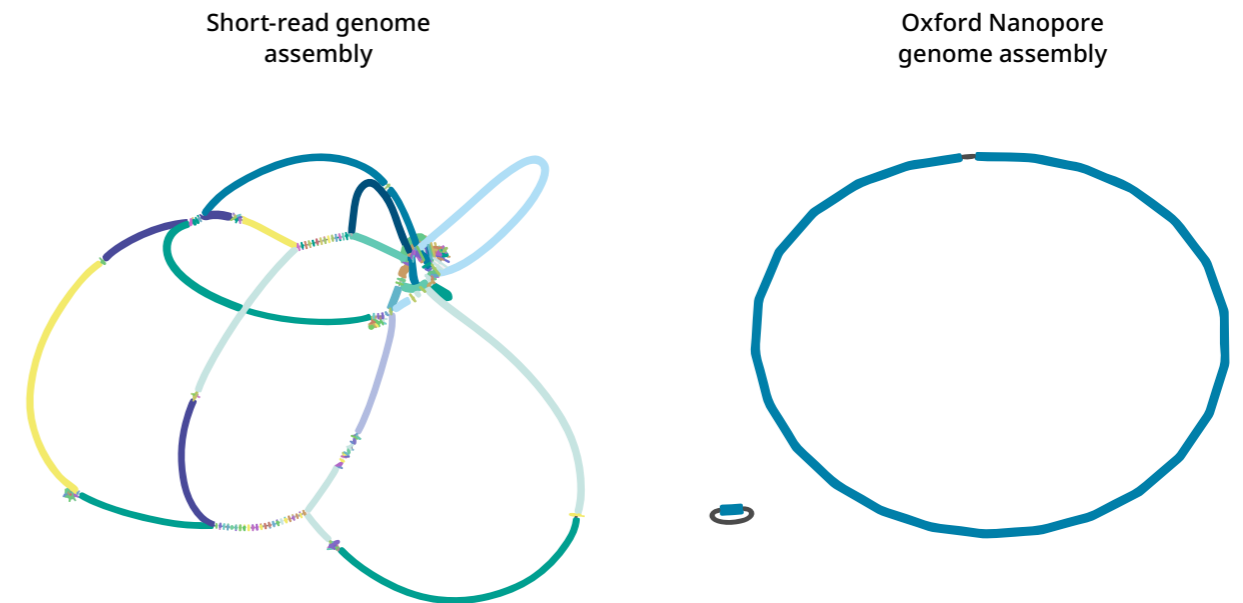
Oxford Nanopore sequencing delivers:

- Accurate, rich data — for comprehensive insights
- Any read length — generate complete microbial genomes
- PCR-free data — no amplification bias and built-in methylation detection
- Real-time analysis — immediate access to actionable insights
- Accessible sequencing technology — portable devices to sequence at source
- Scalable workflows — batch up to 96 samples on a single flow cell
- End-to-end analysis solutions — no bioinformatics experience required

Microbial isolate whole-genome sequencing (WGS)

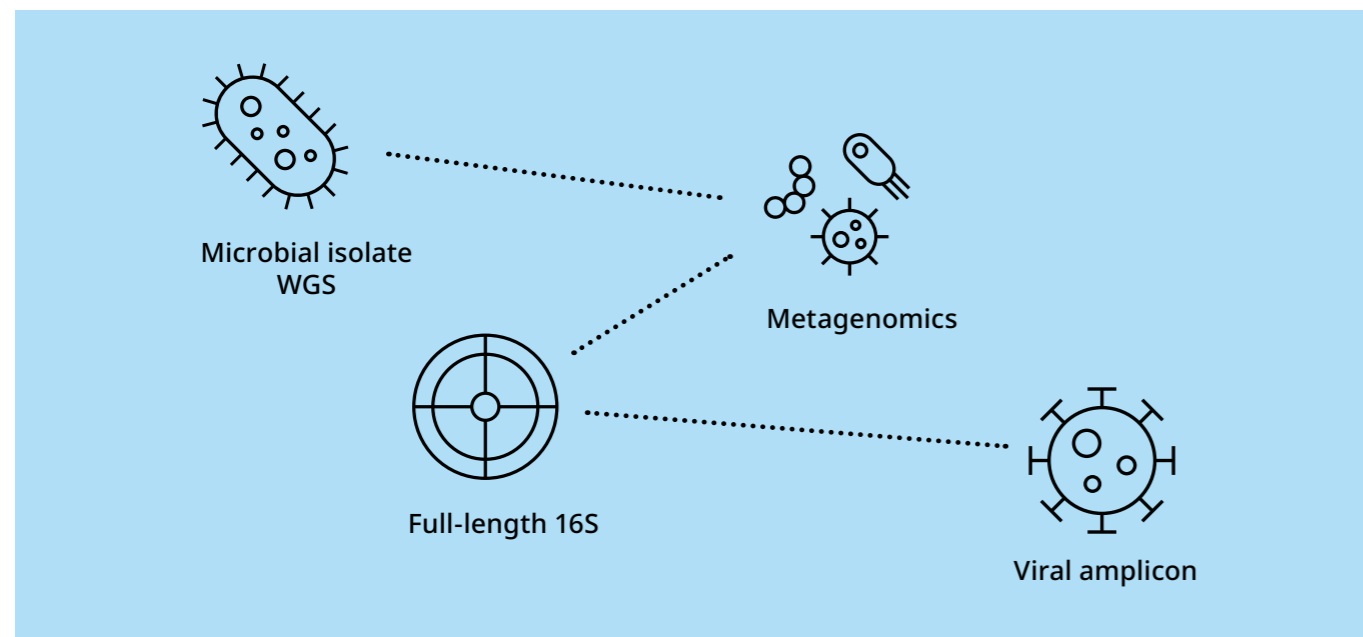
WGS enables complete analysis of microbial isolates for use cases including detection and characterisation of transmission clusters, AMR genes, virulence factors, serotypes, plasmids, and other mobile genetic elements. Reconstruction of complete microbial genomes by *de novo* assembly is unattainable through short-read sequencing as structural variants (SVs) and repetitive elements are larger than individual reads.

Oxford Nanopore has developed the nanopore-only microbial isolate sequencing solution (NO-MISS). This rapid, end-to-end workflow delivers complete, reference-quality microbial genomes. Microbial isolate whole-genome sequencing can also be performed on ElysION™, offering complete workflow automation — from sample extraction to sequencing and data analysis.



'Our results indicated that [Oxford Nanopore Technologies] sequences ... exhibited comparable accuracy to [a short-read sequencing technology], effectively discriminating among bacterial strains from outbreaks'

Hong, Y. *et al.*¹



Why Oxford Nanopore sequencing?

- Perform outbreak surveillance at or near the sample source in healthcare settings or on farms to guide a rapid public health response
- Rapidly identify serotypes and locate AMR genes
- Resolve repeat-rich sequences and SVs
- Distinguish between chromosomal and plasmid AMR transmission in outbreak scenarios
- Conduct in-house QC monitoring and identify transient and resident strains at manufacturing plants
- Characterise engineered microorganisms in biomanufacturing

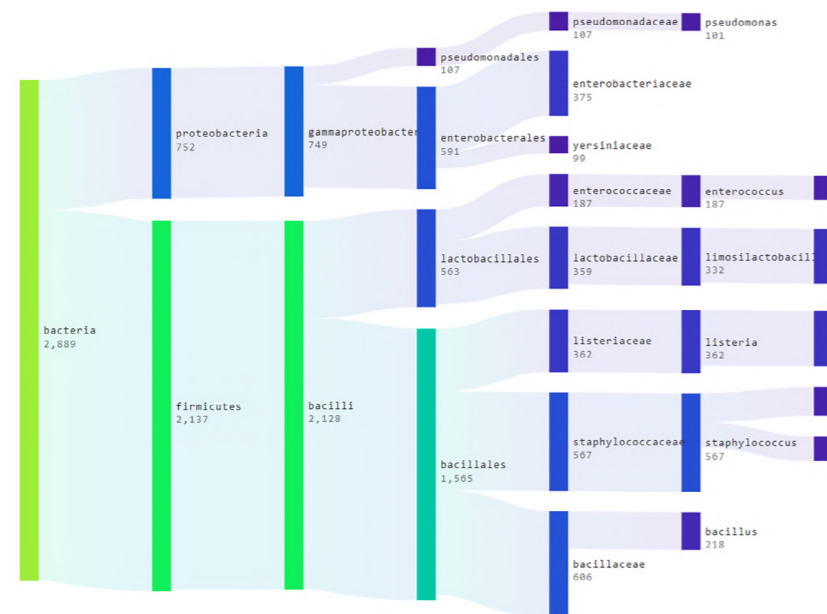


Metagenomic sequencing

Metagenomic sequencing enables the analysis of a community of microorganisms, including unculturable microbes, allowing the detection of known and unknown viruses, bacteria, and fungi. Legacy techniques rely on short-read data that cannot span complex regions, resulting in fragmented genome assemblies.

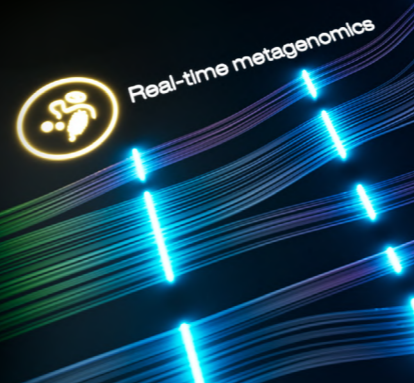
Conversely, Oxford Nanopore sequencing can generate unrestricted read lengths that can span complex regions to produce high-quality metagenome-assembled genomes (MAGs), enhancing the analysis of mixed microbial samples and revealing unprecedented insight into microbial communities.

Metagenomic Sankey plot of lineages



Why Oxford Nanopore sequencing?

- Detect known and unknown microorganisms in a 'hypothesis-free' manner
- Predict or detect novel variants of known pathogens and spoilage contaminants that escape routine detection methods
- Extract virulence and AMR gene information in a single assay
- Deliver rapid results in situations where an urgent public health or food safety response may be required
- Generate complete, high-quality MAGs and quantitative insights into microbiomes



'The integration of adaptive sampling with metagenomics presents a valuable strategy for more efficient and targeted analysis of microbial communities in foodborne outbreaks, contributing to improved food safety and public health'

Buytaers, F.E. *et al.*²

Targeted sequencing

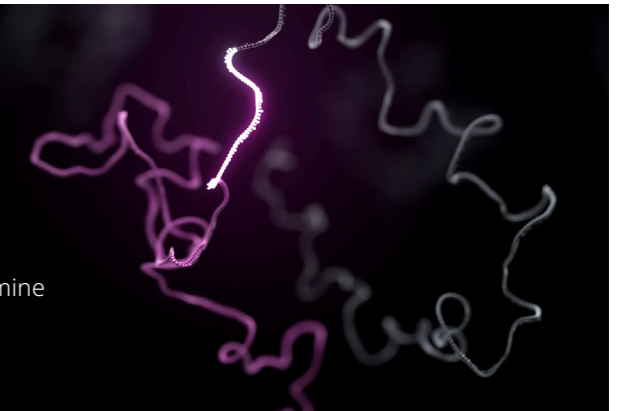
Full-length 16S sequencing

16S ribosomal RNA (rRNA) gene sequencing is the predominant method for microbial identification and has applications in microbiome characterisation, food safety, and clinical microbiology. Legacy techniques often use short-read data that cannot span the full length of the 16S rRNA gene, limiting resolution for species-level identification.

Oxford Nanopore offers an end-to-end workflow to sequence and analyse the full-length 16S rRNA gene to achieve greater taxonomic resolution for accurate profiling of polymicrobial communities, enabling rapid identification of new species and variants missed by basic screening methods.

Why Oxford Nanopore sequencing?

- Accurately resolve microbial communities
- Perform polymicrobial detection
- Sequence with high taxonomic resolution
- Rapidly identify pathogenic and spoilage microbes and determine product composition in probiotic products



Viral amplicon sequencing

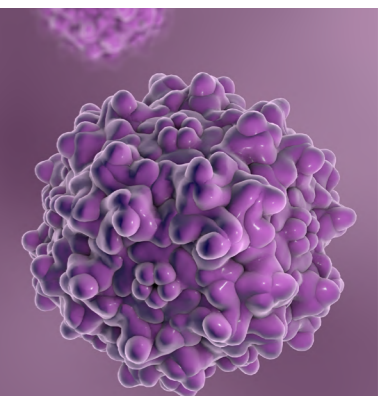
With the threat of infectious disease outbreaks from known and novel pathogens ever increasing, rapid access to pathogen data is of critical importance for fast and appropriate public health guidance. However, legacy techniques deliver data after sequencing, delaying turnaround times. In contrast, Oxford Nanopore sequencing provides rapid workflows:

- Fast library prep
- Real-time sequencing and analysis
- Flexible sample batch sizes
- Portable sequencing at the sample source

Oxford Nanopore provides end-to-end amplicon-based protocols for viral pathogen genome sequencing and analysis. This method provides fast results, achieving whole viral genome coverage to promptly deliver actionable insights into disease outbreaks and to inform vaccine programmes.

Why Oxford Nanopore sequencing?

- Rapidly classify known and novel or recombinant variants across viral pathogen genomes to inform vaccine programmes
- Deliver fast, actionable insights to guide public health measures
- Identify and characterise emerging pathogens to understand epidemiology and transmission patterns
- Perform accurate, cost-effective, and rapid pathogen surveillance



Why Oxford Nanopore for microbial sequencing?

- Accessible devices and simple workflows empower labs to deploy in-house genomic sequencing
- Real-time access to data for rapid turnaround times from sample to answer
- Long, accurate read generation to complete microbial genomes and resolve plasmids and mobile elements
- Generation of reference-quality microbial genomes from isolates
- Access to real-time genomic pathogen surveillance data
- Characterisation of complex microbial communities with long-read metagenomic sequencing




Find out more about microbial sequencing at nanoporetech.com/infectious-disease

References

1. Hong, Y. et al. *bioRxiv* 577746 (2024). DOI: <https://doi.org/10.1101/2024.01.29.577746>
2. Buytaers, F.E. et al. *Front. Microbiol.* 15:1330814 (2024). DOI: <https://doi.org/10.3389/fmicb.2024.1330814>

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