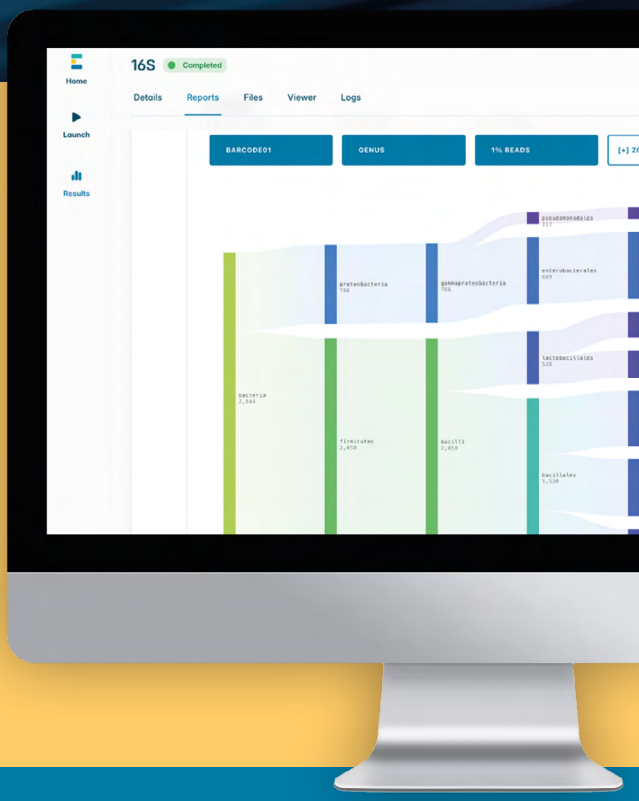
Oxford Nanopore Technologies

EPI2ME

Data analysis for all levels of expertise

Maximise the impact of your Oxford Nanopore sequencing data through flexible and powerful analysis using the intuitive EPI2ME™ desktop application and bioinformatics workflows.



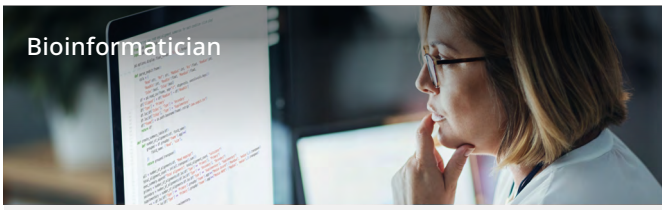
What is EPI2ME?

EPI2ME is a powerful yet easy to use bioinformatics platform that simplifies the analysis of Oxford Nanopore sequencing data using preconfigured, open-source, best-practice workflows.

- Intuitive interface
- Run locally or in the cloud
- Preconfigured, open-source workflows
- Detailed interactive reports
- Compatible with macOS, Windows, and Linux

How can EPI2ME streamline your analysis?

- Intuitive interface — no bioinformatics experience required
- Preconfigured workflows and interactive reports for rapid insights
- Run in the cloud or locally, on a laptop, desktop, server, or Oxford Nanopore sequencing device
- Real-time workflow options
- Full technical support from Oxford Nanopore



- Run open-source EPI2ME workflows from the command line
- Integrate your own code as Nextflow workflows — share with collaborators via the intuitive EPI2ME desktop application
- Access EPI2ME workflows on GitHub for integration into your custom pipelines (github.com/epi2me-labs)

'EPI2ME's strategic integration of Nextflow enables seamless cross-platform delivery of scalable and reproducible bioinformatics tools in a format accessible to users at all levels of proficiency'

Chao Chun Liu, Simon Fraser University, Canada

Preconfigured, best-practice analysis workflows

The EPI2ME platform utilises the latest, internally validated, open-source analysis pipelines to deliver a growing range of streamlined, best-practice analysis workflows.

Human genomics
All-in-one variant detection, including SNPs, SVs, CNVs, STRs, and methylation

Cancer genomics
Somatic variation detection from paired tumour/normal data

Single cell & transcriptomics
Comprehensive analysis of full-length transcripts

Microbiology & infectious disease
Real-time metagenomic species identification and pathogen analysis workflows

Genome assembly
Plasmid and bacterial genome assembly and annotation

Targeted sequencing
Variant calling in amplicon sequences

Explore EPI2ME and the full range of workflows at nanoporetech.com/products/analyse/epi2me

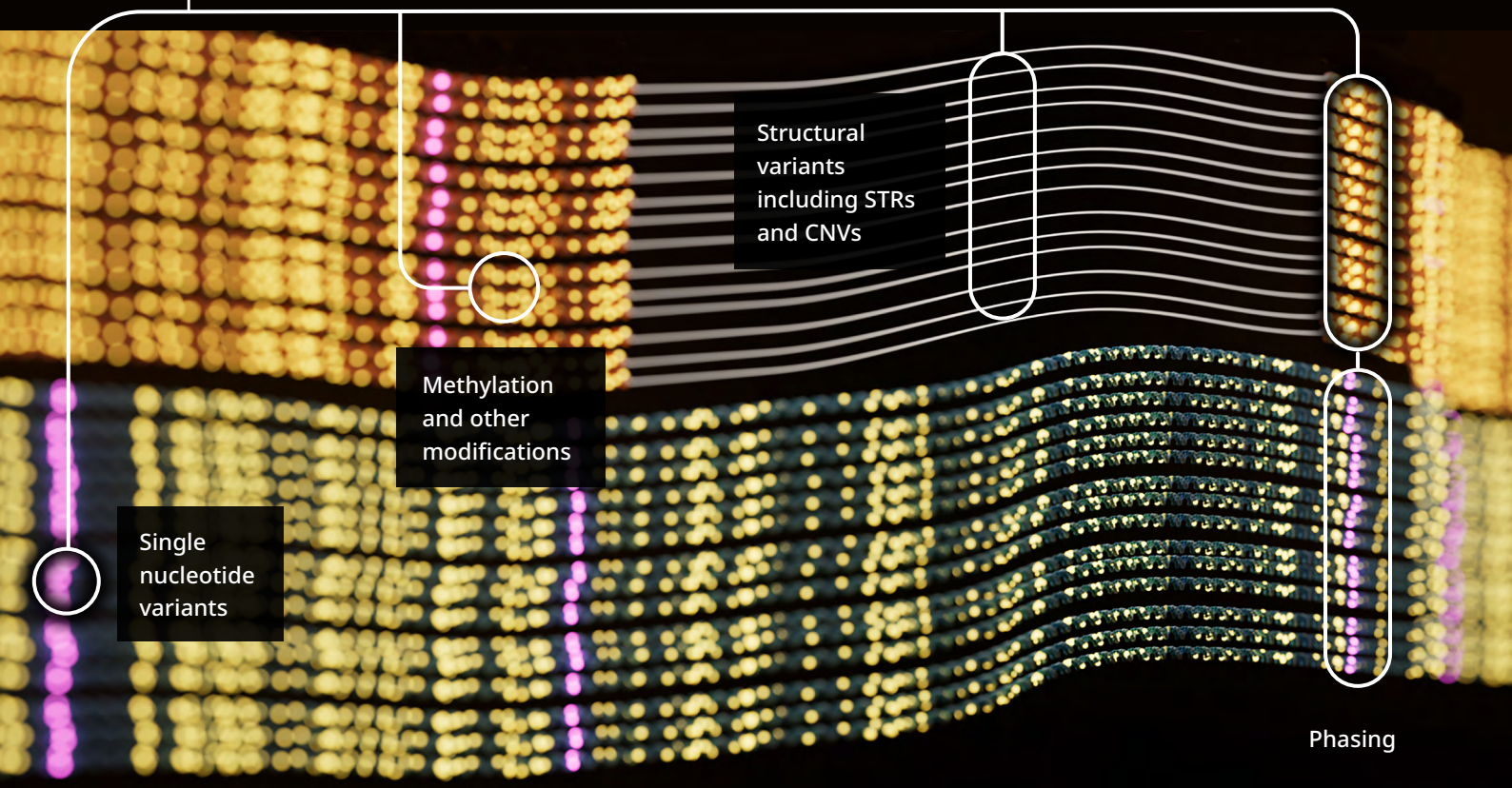
Prepare

Sequence

Analyse

From sample to answer — comprehensive end-to-end workflows

The EPI2ME platform is fully integrated into Oxford Nanopore's end-to-end sequencing workflows, which have been developed to deliver optimal results for a number of common research applications. Detailed protocols guide you, step-by-step, through the complete sequencing process — from sample extraction recommendations through to sequencing and data analysis.



EPI2ME

Interactive reports

Rich output files

Seamless integration

EPI2ME offers several integrations designed to enhance scientific collaboration and deliver greater insights into your sequencing data. For example, existing Nextflow-based pipelines can be incorporated into the platform, enabling them to be easily shared and utilised by colleagues and collaborators using the intuitive EPI2ME desktop application.

In addition, the EPI2ME platform provides industry-standard output files (e.g. VCF) as well as offering direct integration with selected tertiary analysis tools — enabling more comprehensive downstream data analysis, including the interpretation of human genomic variants.

Find out more about EPI2ME integrations at
nanoporetech.com/analyse

Download EPI2ME today

Simplify and accelerate your data analyses with the free EPI2ME desktop application. Download today and explore the full range of workflows and sample data:
epi2me.nanoporetech.com/downloads

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