



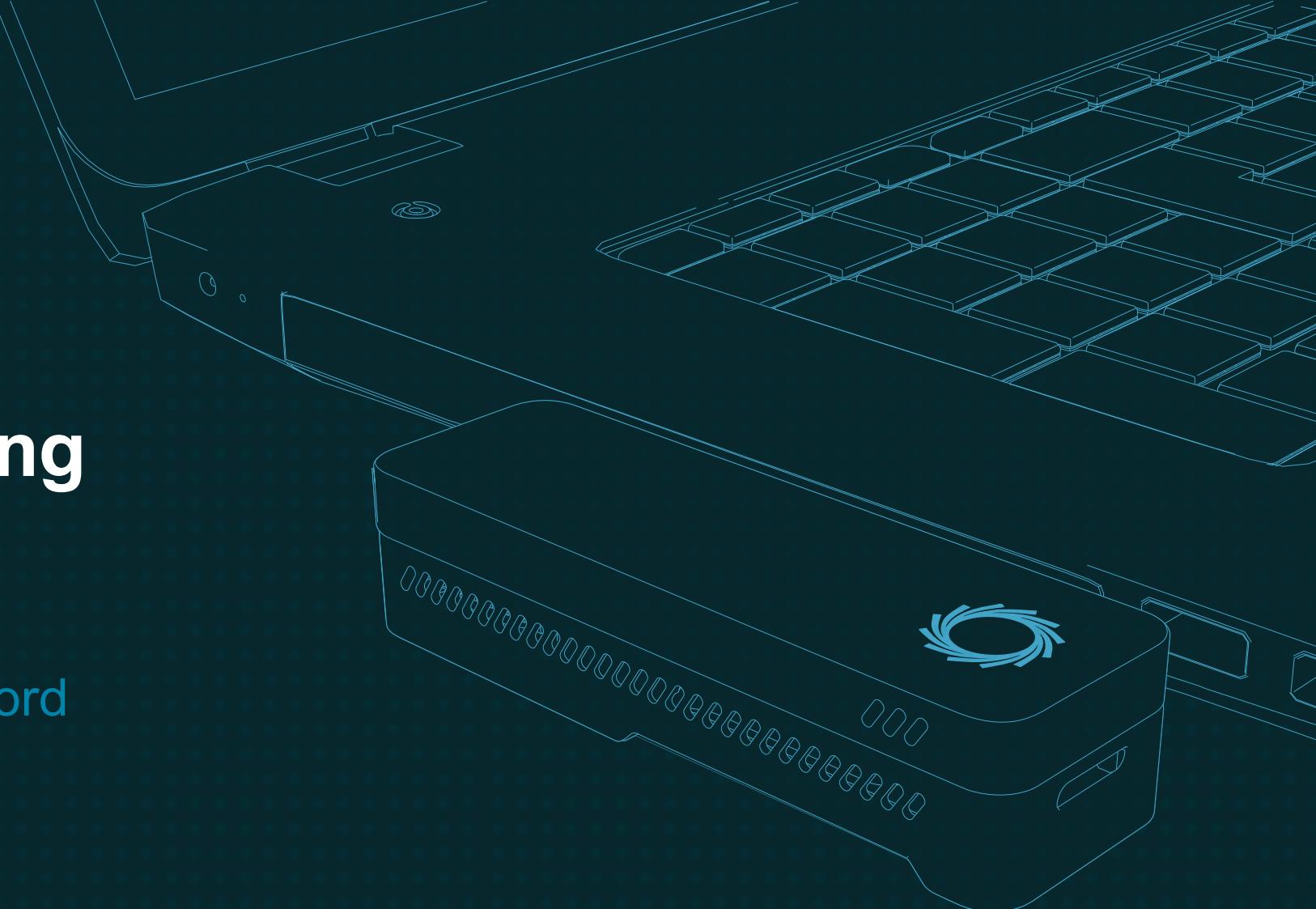
What you're missing matters

Delivering the future of
microbial genomics with Oxford
Nanopore

Mavis Tan

Clinical Sales Specialist, SEATK

Populations Genomics & Clinical Applications



Overview of nanopore sequencing for microbiology and infectious disease

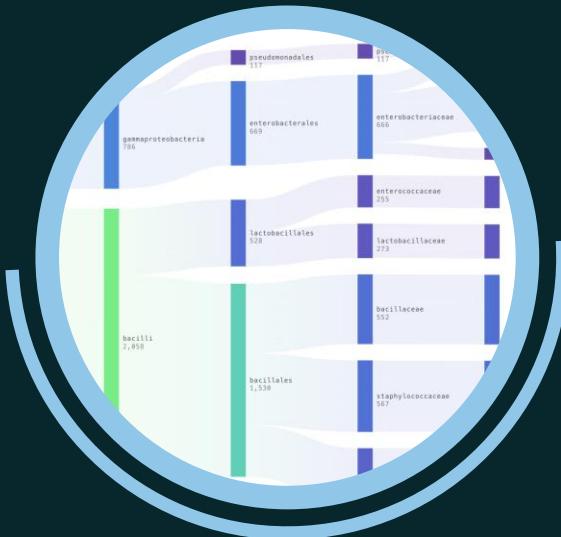
Microbiology and infectious disease applications with Oxford Nanopore

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

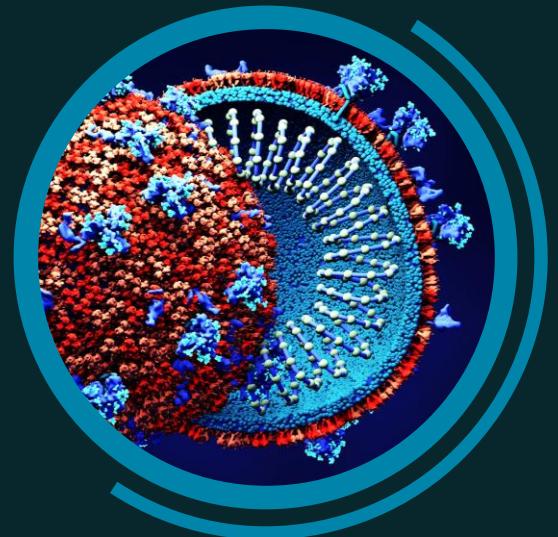
Microbial isolate WGS



Full-length 16S



Targeted viral WGS and AMR



Metagenomics



- Outbreak investigation
- Antimicrobial resistance
- Molecular epidemiology

- Microbial community profiling
- Polymicrobial detection
- High taxonomic resolution

- Classify known or novel variants
- Detect antimicrobial resistance (AMR)
- Guide public health

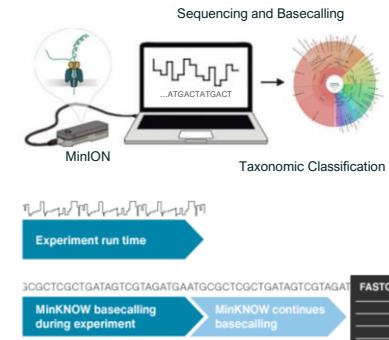
- Agnostic pathogen detection
- Rapid AMR profiling
- Metagenome-Assembled Genomes (MAGs)

Advantages of nanopore sequencing for microbiology and infectious disease

Accessible platforms and simple workflows empower labs to deploy genomic sequencing on-site

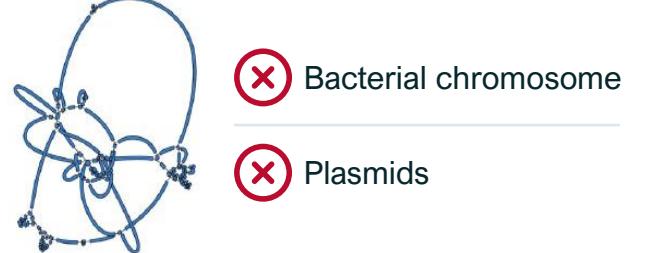


Real-time access to data enables **rapid turnaround** from sample to answer

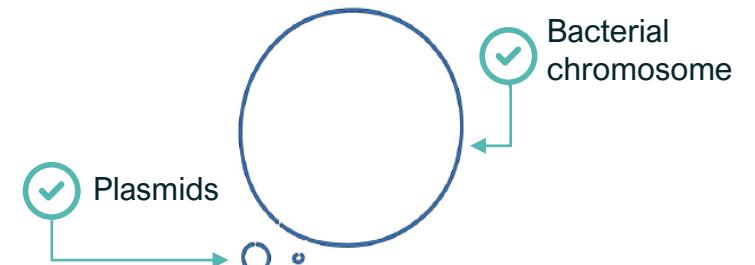


Long, accurate reads generate **complete** microbial genomes and resolve plasmids, mobile elements

Short-read genome assembly



Nanopore genome assembly



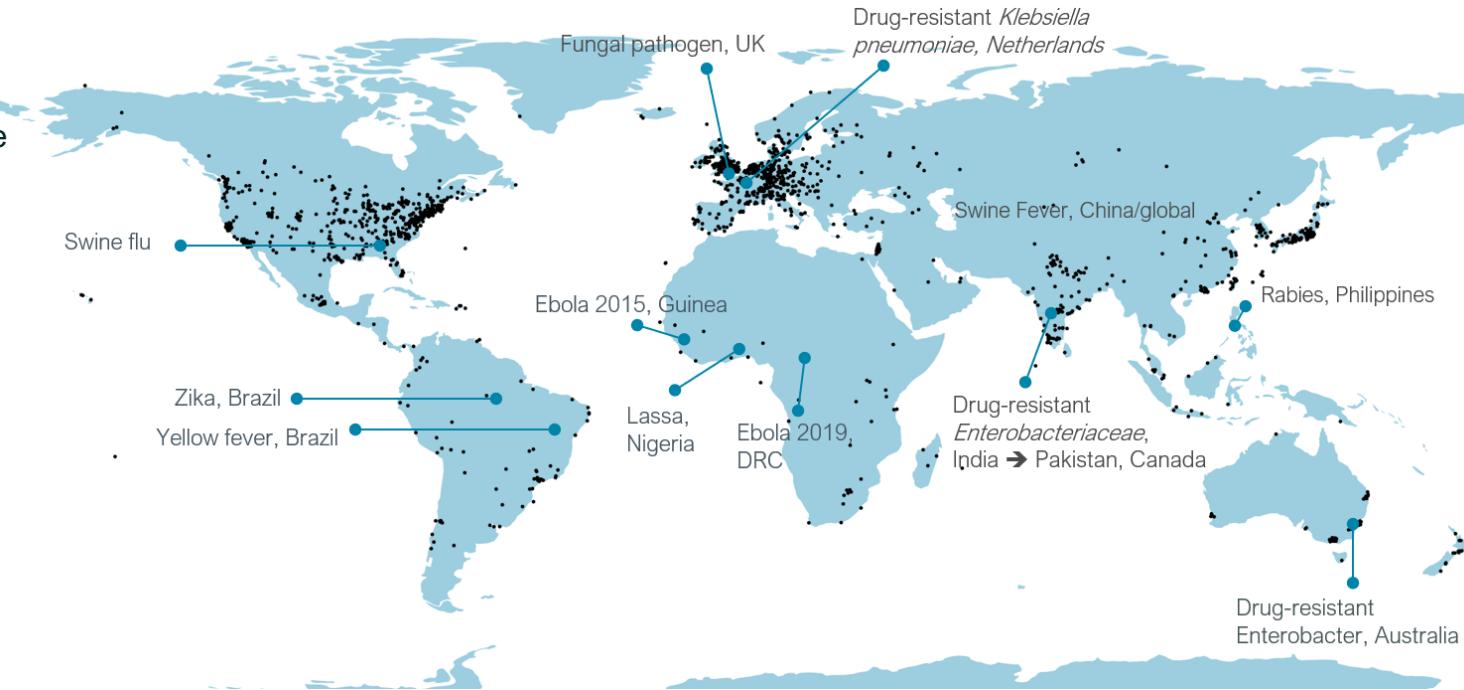
Nanopore sequencing serves as a critical tool in pathogen surveillance

Labs around the world have demonstrated advantages of nanopore sequencing for rapid epidemiological investigations

Real-time, portable genome sequencing for Ebola surveillance



Quick et al. *Nature* (2016)



Genomic and epidemiological monitoring of yellow fever virus



Faria et al. *Science* (2018)



"The fact that almost half of all SARS-CoV-2 sequencing in Africa was performed using the Oxford Nanopore technology (ONT), which is relatively low-cost compared to other sequencing technologies and better adapted to modest laboratory infrastructures, illustrates one component of how this rapid scale-up of local sequencing was achieved"

Tegally et al. "The evolving SARS-CoV-2 epidemic in Africa: Insights from rapidly expanding genomic surveillance" *Science* (2022)

Oxford Nanopore continues to support frontline rapid outbreak response

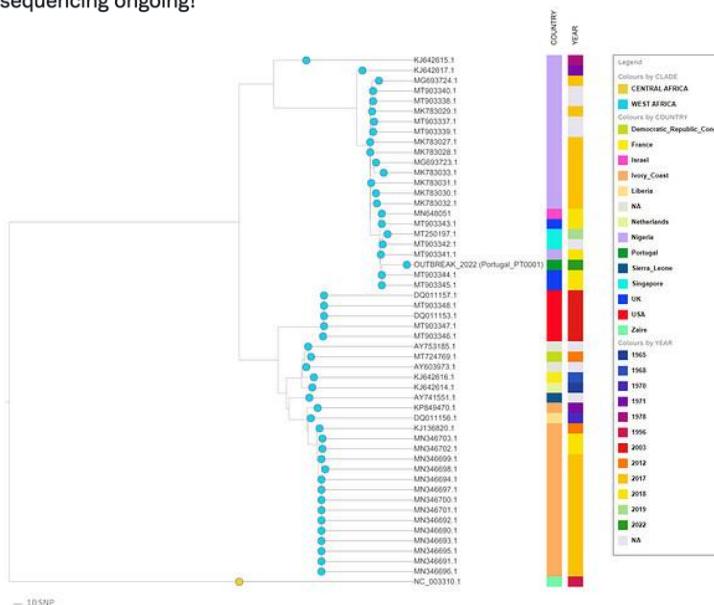
May 2022 - Portugal

First genome of Mpox from recent multi-country outbreak



Joana Isidro
@isidro_joana

Great team effort and real time data sharing. Overnight sequencing on MinION, raw sequence data available by 11am -> first #monkeypox draft genome and phylogenetics released by midnight. Further sequencing ongoing!



Dec. 2022 - United Kingdom

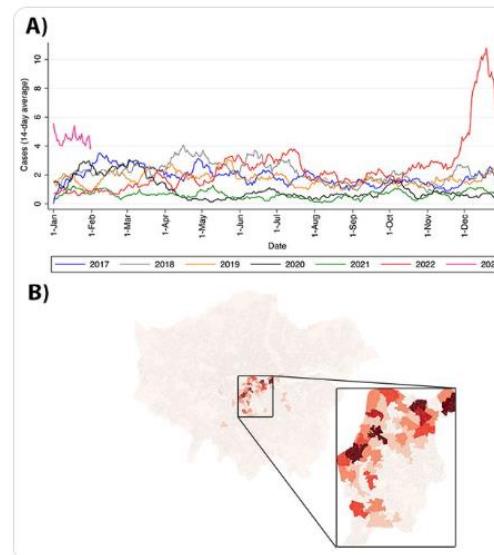
Prospective surveillance of Group A Strep outbreak



Luke Blagdon Snell
@lukebsnell

Today @CMIJournal: Analysis of the Group A Strep epidemic in London. Cases @ 4x usual & invasive disease assoc w/ superantigens A&J
doi.org/10.1016/j.cmi....

Seq & submitted in 4wks: rapid @nanopore genomics!
@madelaam @ThemisCharalam1 @stuartjneil @GaiaNebbia
@jonathanCIDR



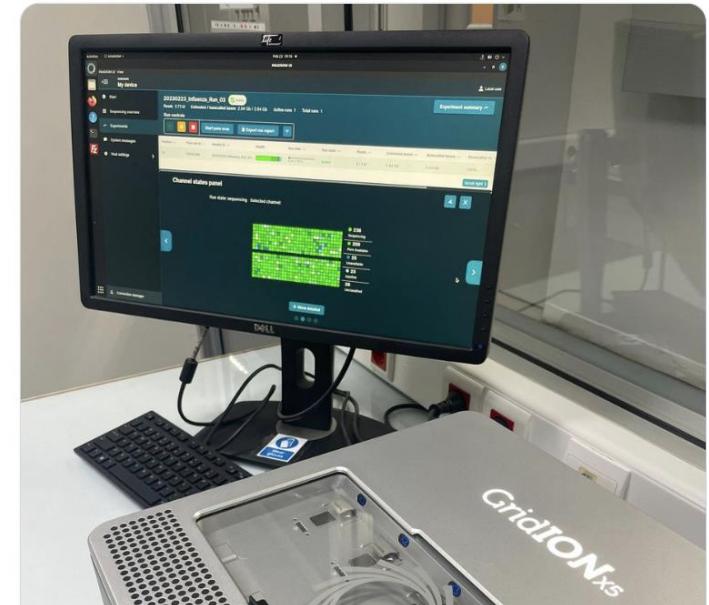
Feb, 2023 - Cambodia

Full genome from human infection with avian influenza (H5N1)



Erik Karlsson
@E_A_Karlsson

We were able to go from original sample to full genome sequence in <24 hours using iMS-PCR from @peter_thielen from @JHUAPL on @oxfordnanopore #ONT technology @nanopore #nanopore using capacity developed before and during the #COVID19 pandemic (2/)



Nanopore data delivers high accuracy for microbiology and infectious disease

Results from the community



Applied and Environmental
Microbiology

Biotechnology | Full-Length Text

The newest Oxford Nanopore R10.4.1 full-length 16S rRNA sequencing enables the accurate resolution of species-level microbial community profiling

Tianyuan Zhang,^{1,2,3} Hanzhou Li,³ Silin Ma,¹ Jian Cao,³ Hao Liao,¹ Qiaoyun Huang,^{1,4} Wenli Chen,^{1,2}

Benchmarking reveals superiority of deep learning variant callers on bacterial nanopore sequence data

Michael B. Hall^{1,✉}, Ryan R. Wick^{1,2}, Louise M. Judd^{1,2}, An N. T. Nguyen¹,
Eike J. Steinig¹, Ouli Xie^{3,4}, Mark R. Davies¹, Torsten Seemann^{1,2}, Timothy
P. Stinear^{1,2,†}, Lachlan J. M. Coin^{1,‡}

Oxford nanopore long-read sequencing enables the generation of complete bacterial and plasmid genomes without short-read sequencing

Wenxuan Zhao^{1,2}, Wei Zeng^{1,3}, Bo Pang¹, Ming Luo⁴, Yao Peng¹,
Jialiang Xu⁵, Biao Kan^{1,3*}, Zhenpeng Li^{1*} and Xin Lu^{1*}

Improved Resolution of Highly Pathogenic Avian Influenza Virus Haemagglutinin Cleavage Site Using Oxford Nanopore R10 Sequencing Chemistry

Jeremy D Ratcliff, Brian Merritt, Hannah Gooden, Jurre Y Siegers, Abhi Srikanth, Sokhoun Yann, Sonita Kol,
Sarah Sin, Songha Tok, Erik A Karlsson, Peter M Thielen

BRIEF REPORT

Open Access



Nanopore long-read-only metagenomics enables complete and high-quality genome reconstruction from mock and complex metagenomes

Lei Liu, Yu Yang, Yu Deng and Tong Zhang*



AMERICAN
SOCIETY FOR
MICROBIOLOGY

Journal of
Clinical Microbiology®

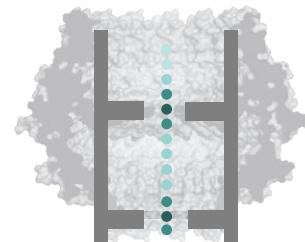
Kit V14,
R10.4.1

EPIDEMIOLOGY



Real-Time Nanopore Q20+ Sequencing Enables Extremely Fast and Accurate Core Genome MLST Typing and Democratizes Access to High-Resolution Bacterial Pathogen Surveillance

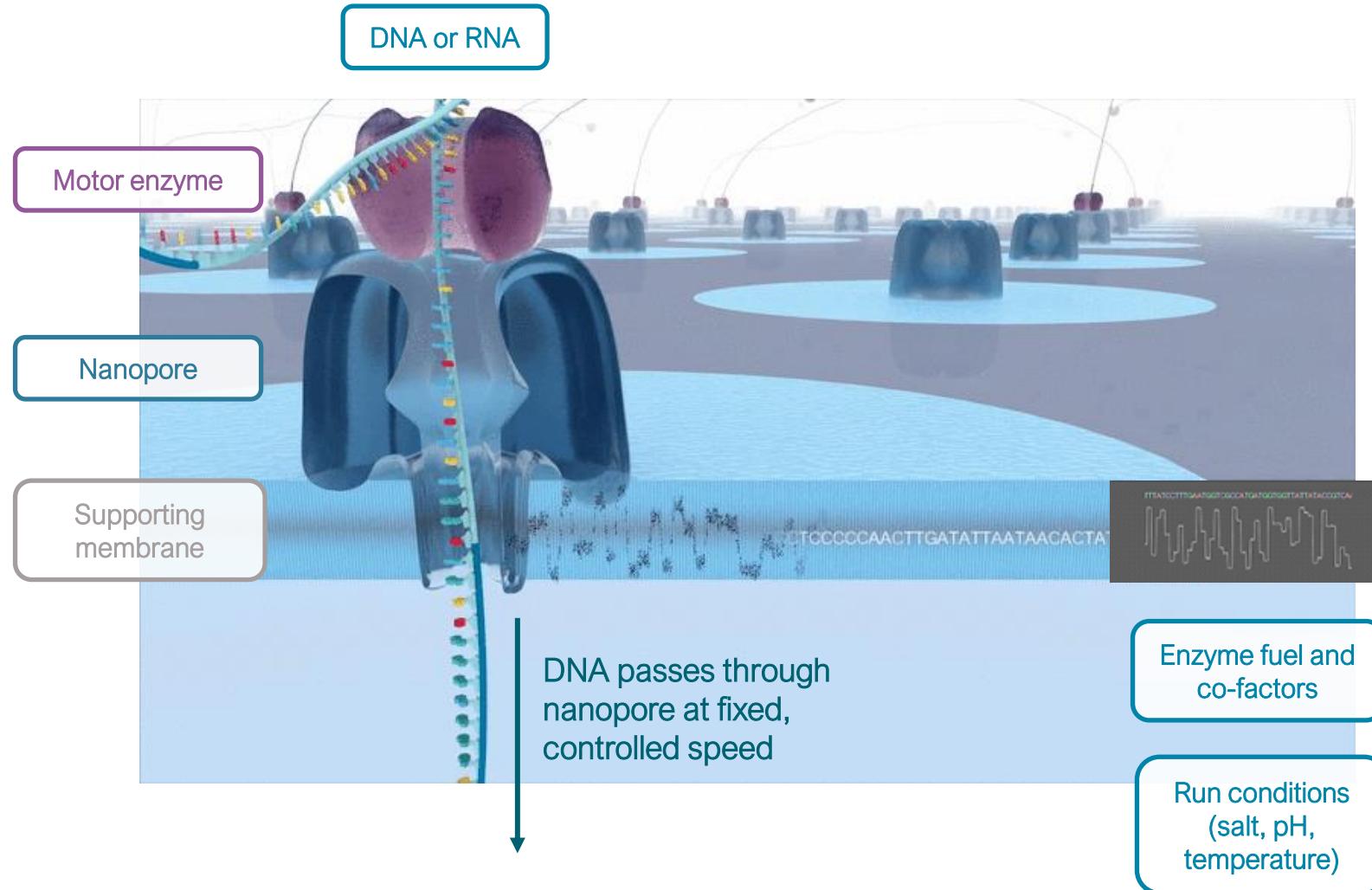
Gabriel E. Wagner,^a Johanna Dabernig-Heinz,^a Michaela Lipp,^a Adriana Cabal,^b Jonathan Simantzik,^c Matthias Kohl,^c
Martina Scheiber,^a Sabine Lichtenegger,^a Ralf Ehricht,^{d,e,f} Eva Leitner,^a Werner Ruppitsch,^b Ivo Steinmetz^a



Introduction to Oxford Nanopore Technologies

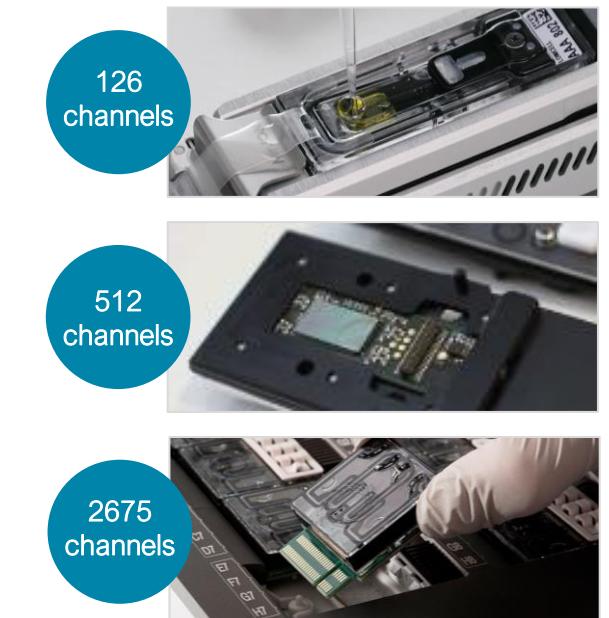
Nanopore DNA/RNA sequencing

DNA/RNA strand passes through pore → signal interpreted into sequence data



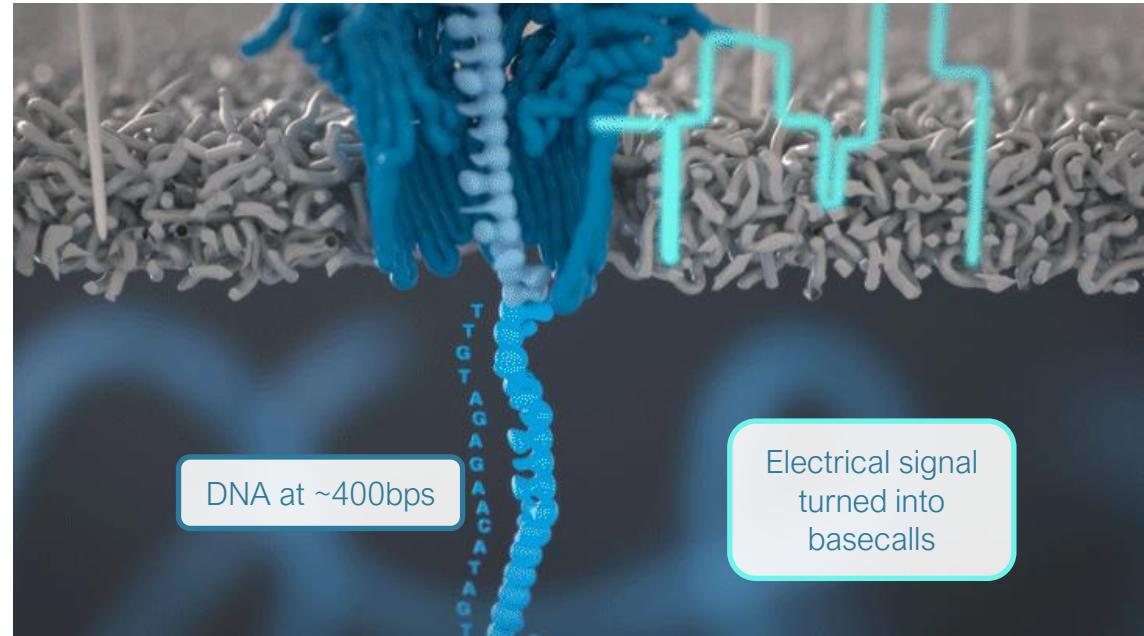
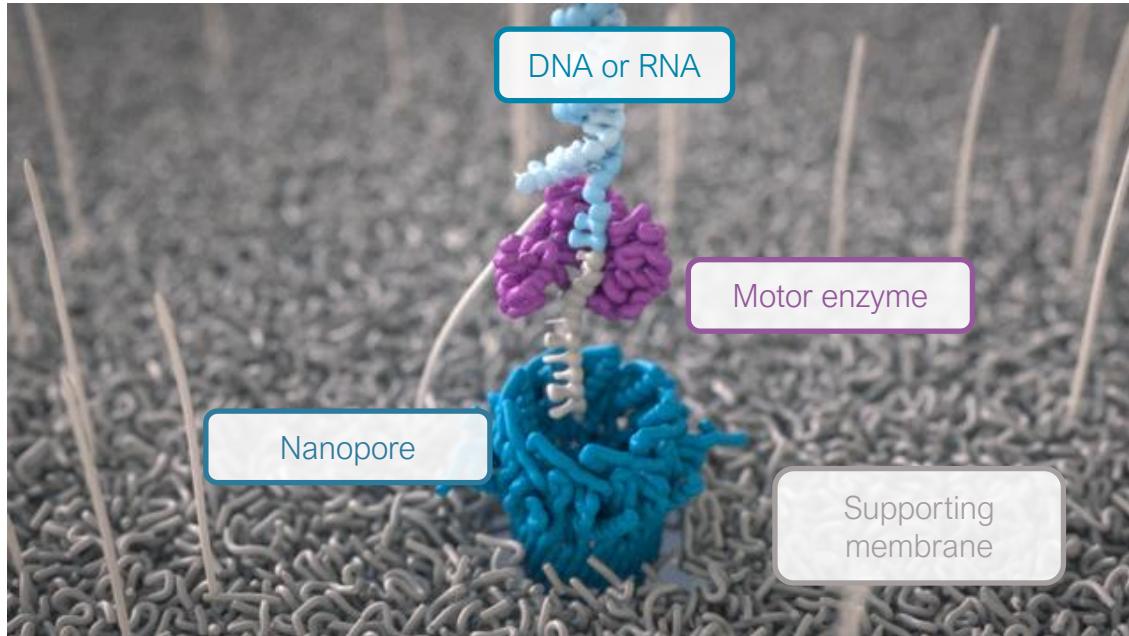
Passage of DNA and RNA bases (including modified bases) through the pore creates characteristic disruptions in the current

Data is instantly generated and analysable



Nanopore sequencing: how it works

Unique benefits



Features	Direct sequencing of DNA and RNA	PCR free, no amplification bias	Read length-agnostic	Real-time analysis	Chemistry on bespoke electronics
Benefits	Richer information including epigenetics	Simpler workflows, Richer information including epigenetics	One platform for any sample; see the true scope in your biology	Rapid results Intelligent analyses eg adaptive sampling	Scalable, from small to large formats Low-cost

Sequence with the device that's right for you

Utilise the flow cells that best serve your application

Output per device ↑

MinION flow cell Theoretical max output: 48Gb*



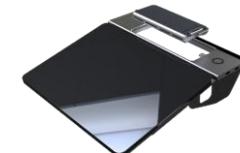
MinION™

MinION Mk1C

GridION™



MinION Mk1D



Increasing number of flow cells and / or pores

1
Flow cell

1
Flow cell

5
flow cells

2
flow cells

24
flow cells

48
flow cells

PromethION flow cell

Theoretical max output: 277 Gb*

PromethION™ 2
devices



PromethION 24



PromethION 48



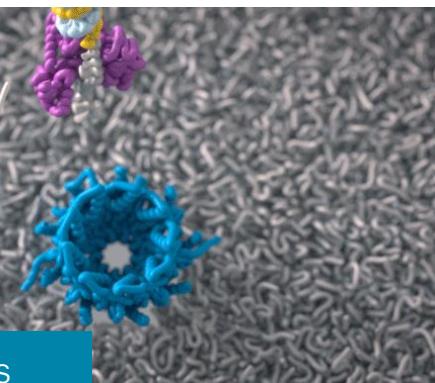
- 4,992 human WGS / year
- 96 human WGS / week

*Theoretical max output when system is run for 72 hours at 400 bases / second.

Adaptive sampling: enrich/deplete regions of interest

Targeted sequencing using software-based enrichment

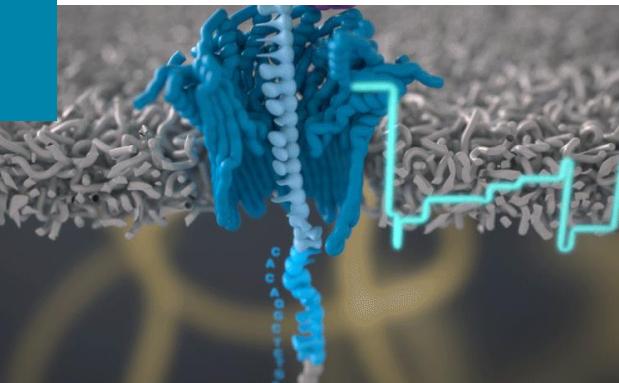
A	B	C	D
chr5	112697503	112856242	APC
chr11	108212484	108379150	ATM
chr17	65518565	65571652	AXIN2
chr2	214715644	214819682	BARD1
chr3	52391025	52420060	BAP1
chr10	86745786	86937969	BMPR1A
chr17	43034294	43135363	BRCA1
chr13	32305479	32409671	BRCA2
chr17	61669142	61874117	BRIP1
chr16	68727291	688455	
chr12	57737731	577623	
chr9	21957143	220053	
chr22	22077740	2207510	
chr14	48714763	487387	
chr2	36983352	370608	
chr15	47393067	476445	
chr17	8064465		
chr2	4777308		
chr1	4531924		
chr8	8992334		
chr17	3108493		
chr16	2029821	2057835	NTHL1
chr16	23593164	23651340	PALB2
chr7	5960927	6019104	PMS2
chr19	50374291	50428018	POLD1
chr12	132613758	132697521	POLE
chr10	87853697	87981920	PTEN
< > hereditary_cancer_panel_targets			



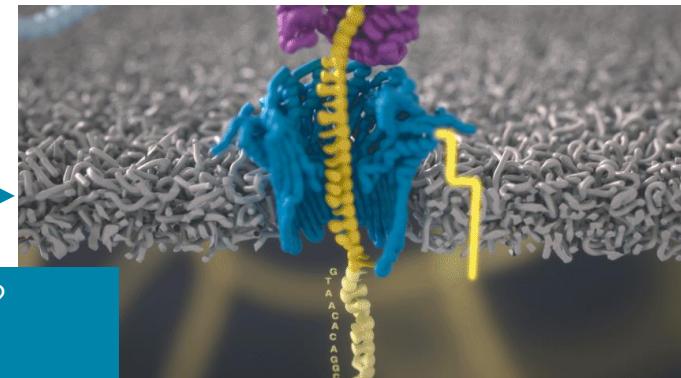
Upload .bed file to
MinKNOW

Strand approaches
nanopore and starts
sequencing

Not region of interest?
Strand rejected

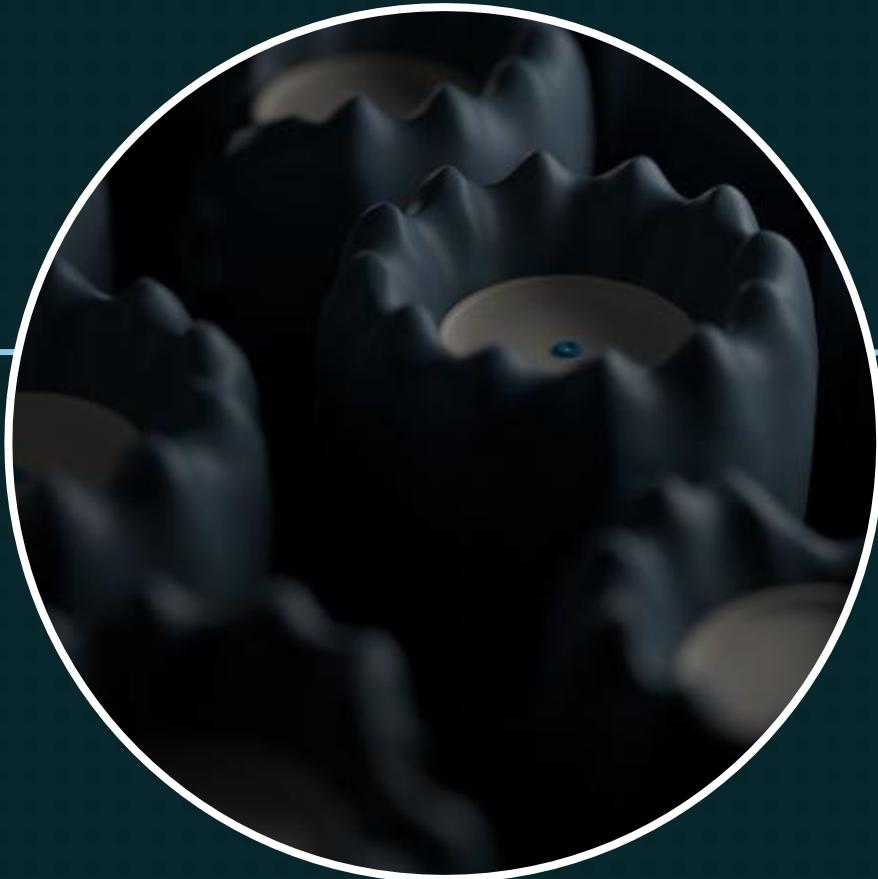


Real-time basecalling
and alignment



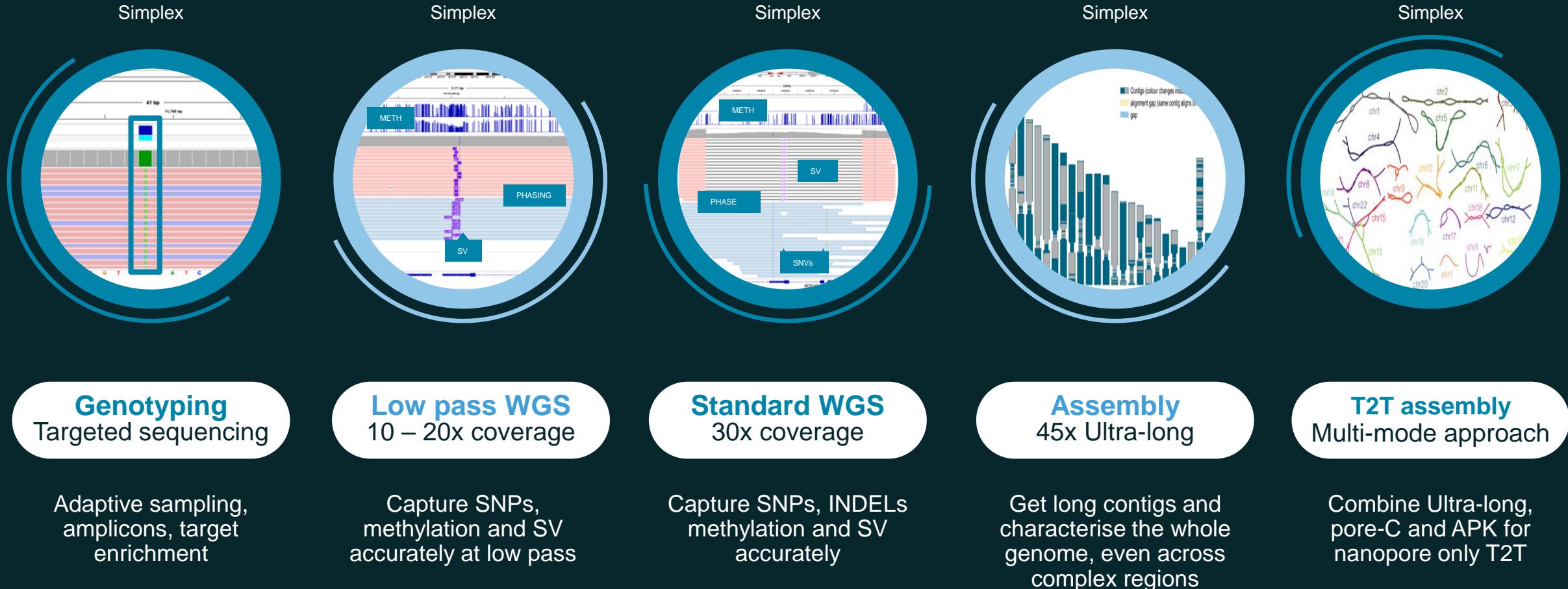
Region of interest?
Strand allowed to
continue sequencing

Performance updates



We have a highly versatile platform

From target sequencing to whole genomes assemblies



New basecaller model architecture for SUP achieves Q26 with simplex

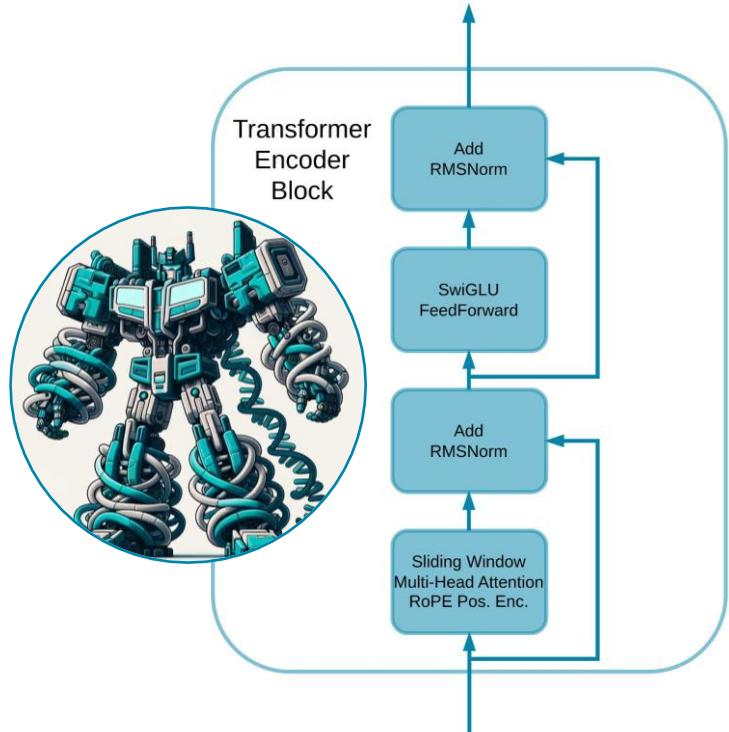


Released in Dorado

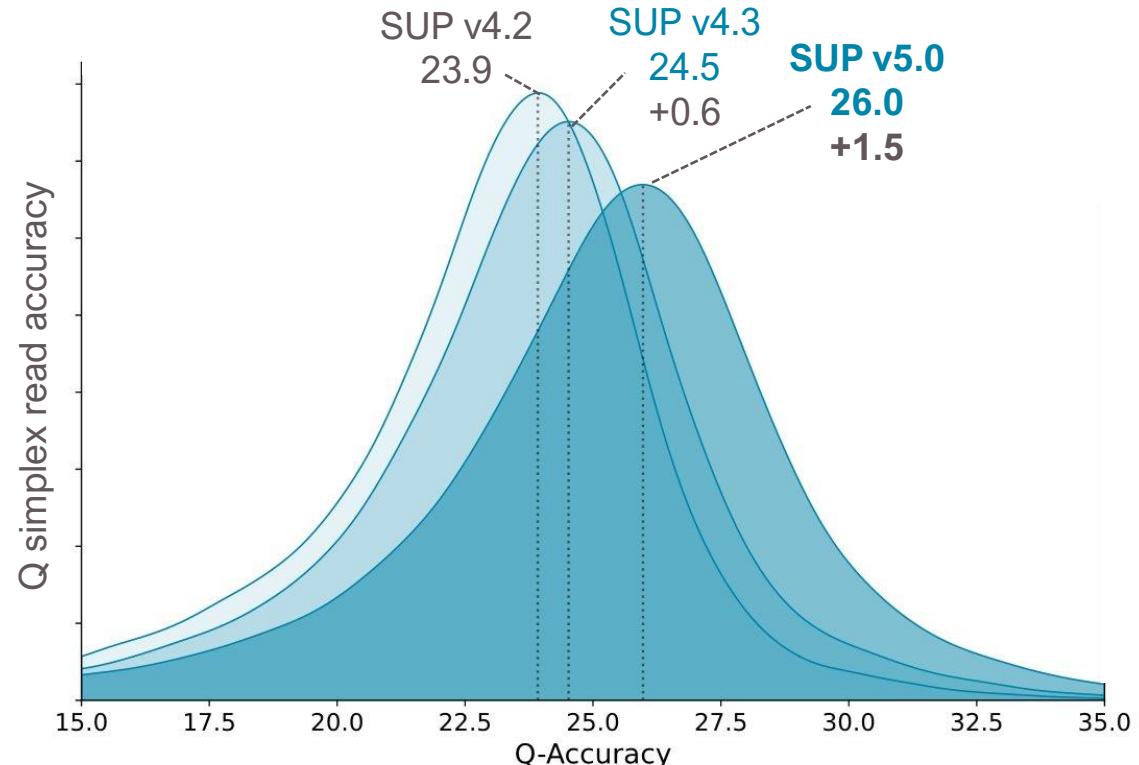
With transformer architecture, similar to the engine behind ChatGPT



- Improved accuracy of SUP v5 models at lower speed than v4.3
- HAC models remain on previous architecture and speed



Q26 simplex with SUP



* Modal accuracy measured on 10x HG002:chr6_MATERNAL holdout dataset of R10.4.1-E8.2.1 data using Dorado 0.7 with the v4.2.0-sup, v4.3.0-sup, v5.0.0-sup basecall models

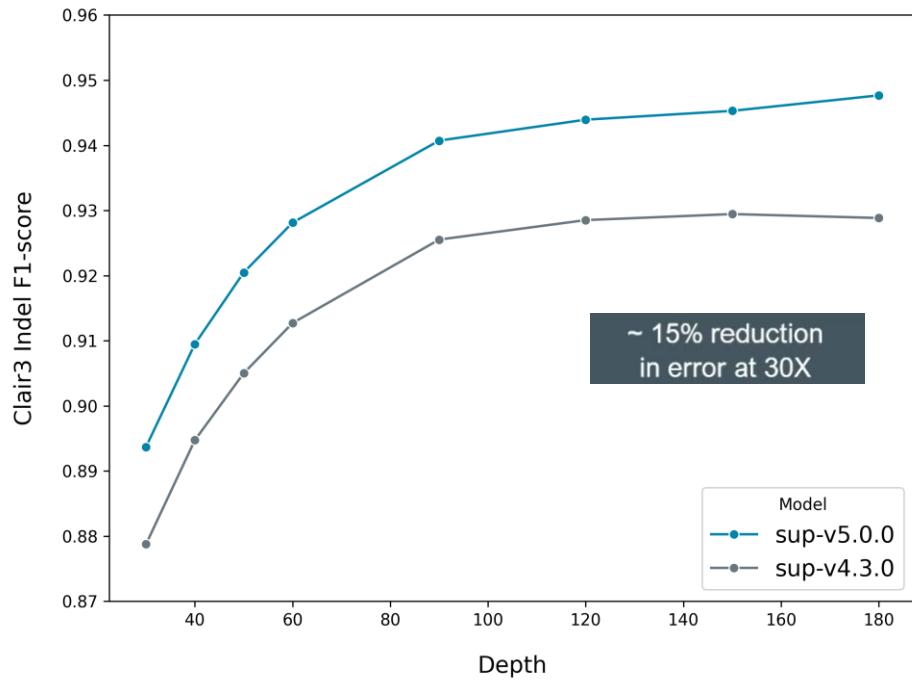
Significant improved variant calling for SUP v5.0

With newly trained variant caller models for Claire3 in Rerio



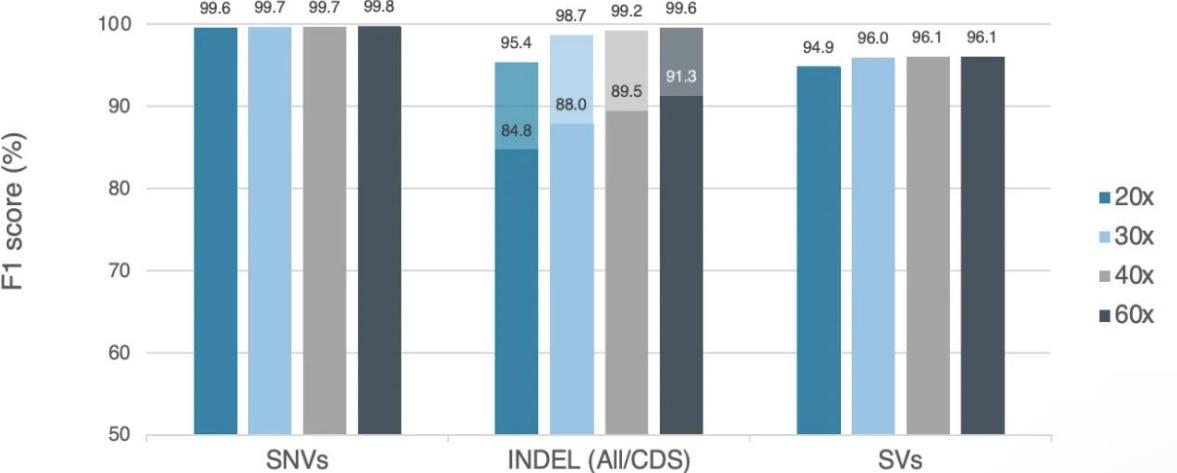
Dorado 0.7
Models v5.0

Indels F1 score improvements from 30x



Variant calling for SUP v5.0

SNP accuracy maintained at 99.9%



>Q50 nanopore-only bacterial assemblies



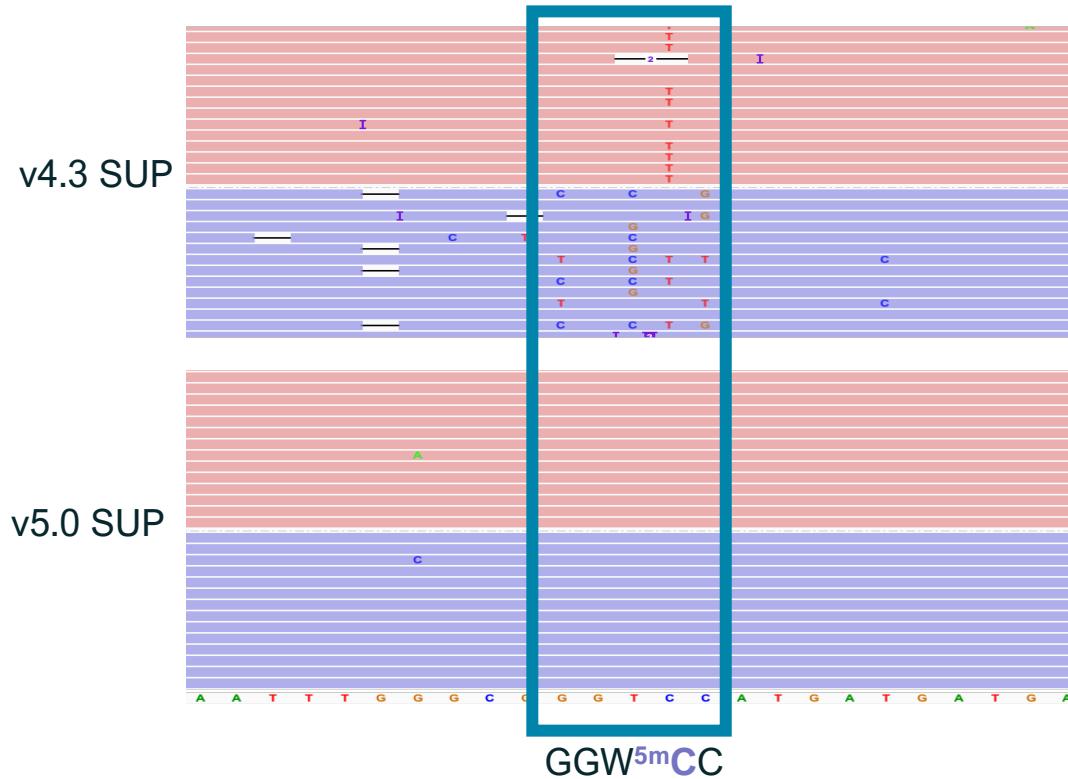
Released in Dorado

With Dorado 0.7, trained on native and synthetic data

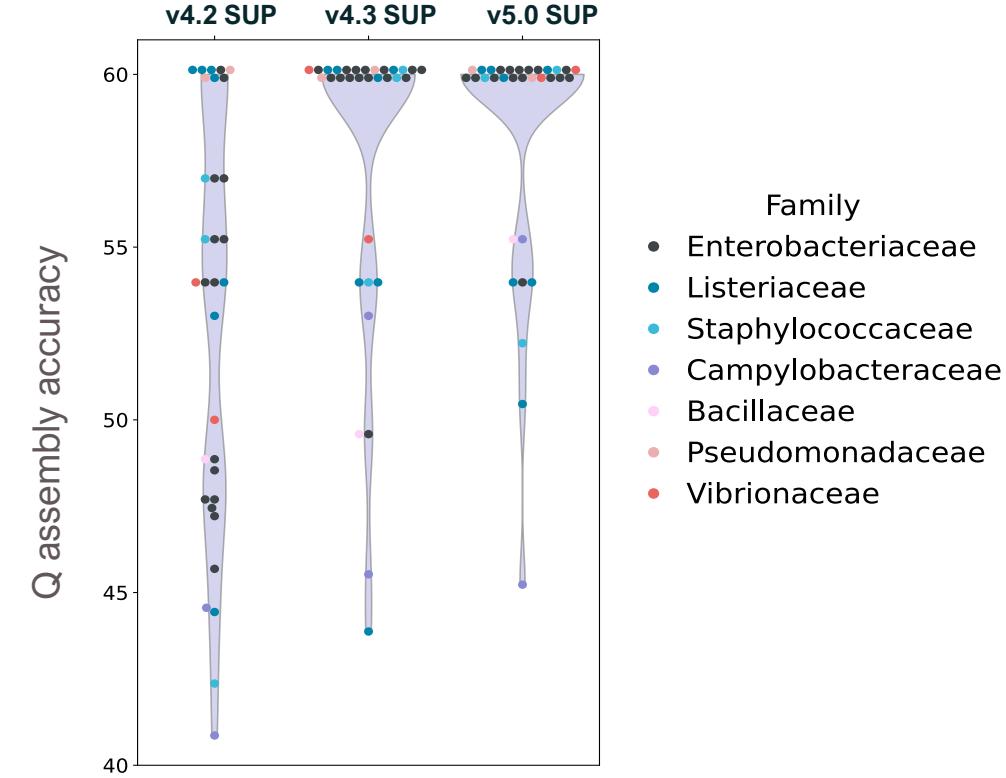


Higher consensus accuracy with new v5.0 models

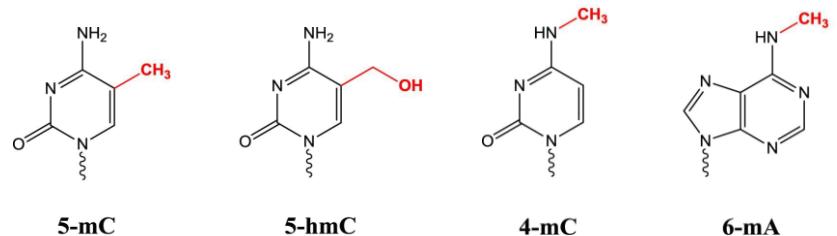
Overcoming the diversity of bacteria modifications in diverse contexts



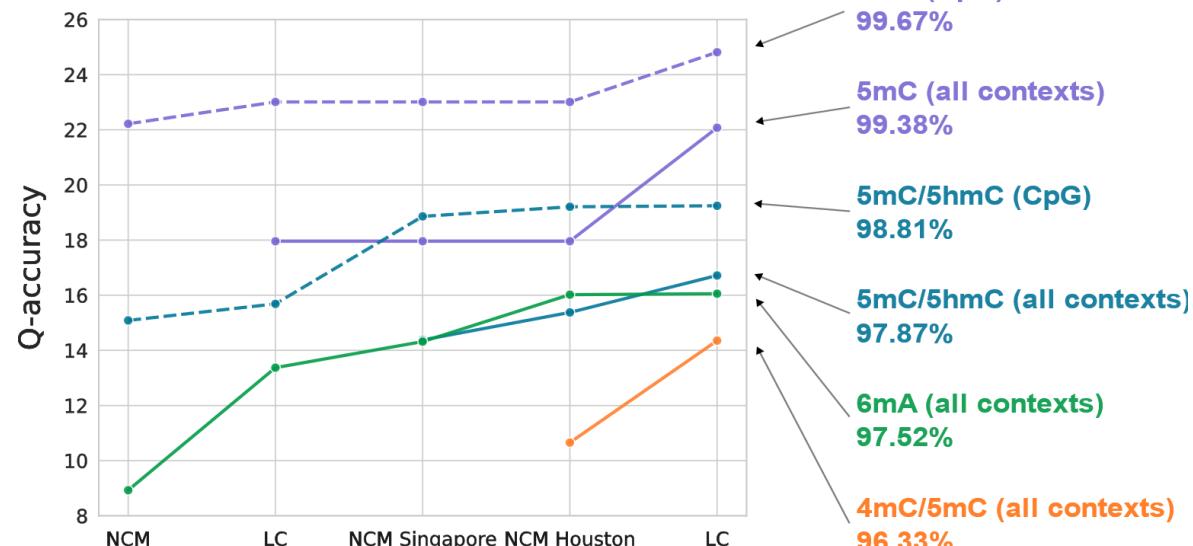
Nanopore-only assembly for diverse bacterial families



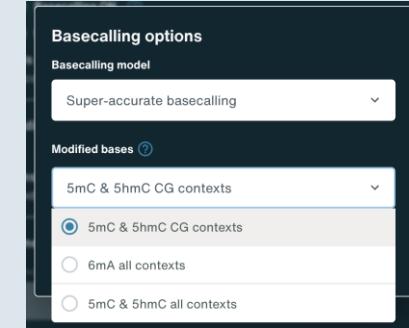
Broader DNA base modifications offering with improved accuracy



Evolution of raw read modification accuracy



Fully integrated in **MinKNOW**



Available live or post-run

- 5mC and 5hmC in CpGs
- 5mC and 5hmC in all contexts
- 6mA in all contexts

Offline offering – Dorado v0.7

DNA all contexts: **5mC, 5hmC, 6mA and 4mC**

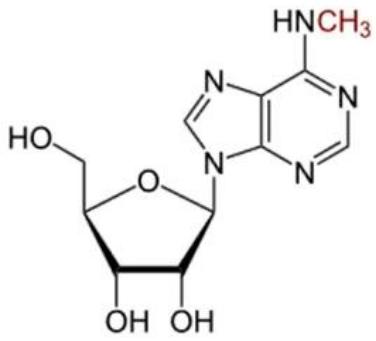
In development

- Genomic Uracil (dU, deoxy-Uracil)
- Oxidation G > 8oxoG
- Ribo-bases incorporation

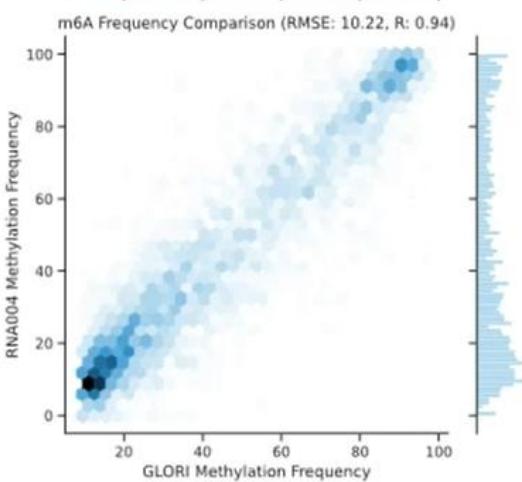
Direct RNA modified bases - SOTA

Available now

m⁶A



m⁶A detection correlation with GLORI

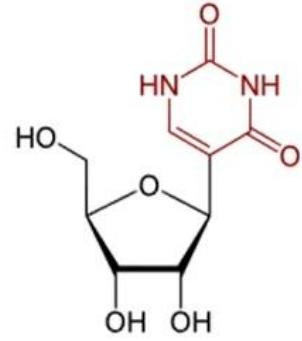


True labels	A	m ⁶ A
A	98.25	1.75
m ⁶ A	4.38	95.62

All-context per-read per-site accuracy

Single base comparison of the level of m⁶A methylation in DRACH context of WT HEK-293 cells between RNA004 data and a matched GLORI sequencing dataset obtained from Liu C et al. Nat Biotechnol. 2023;41(3):355-366.

PseudoU



Reads called with PseudoU model

PseudoU detection at known rRNA sites



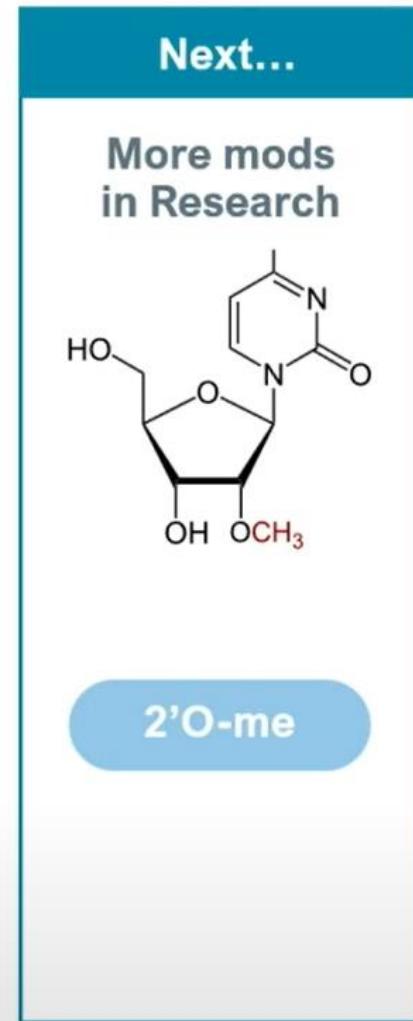
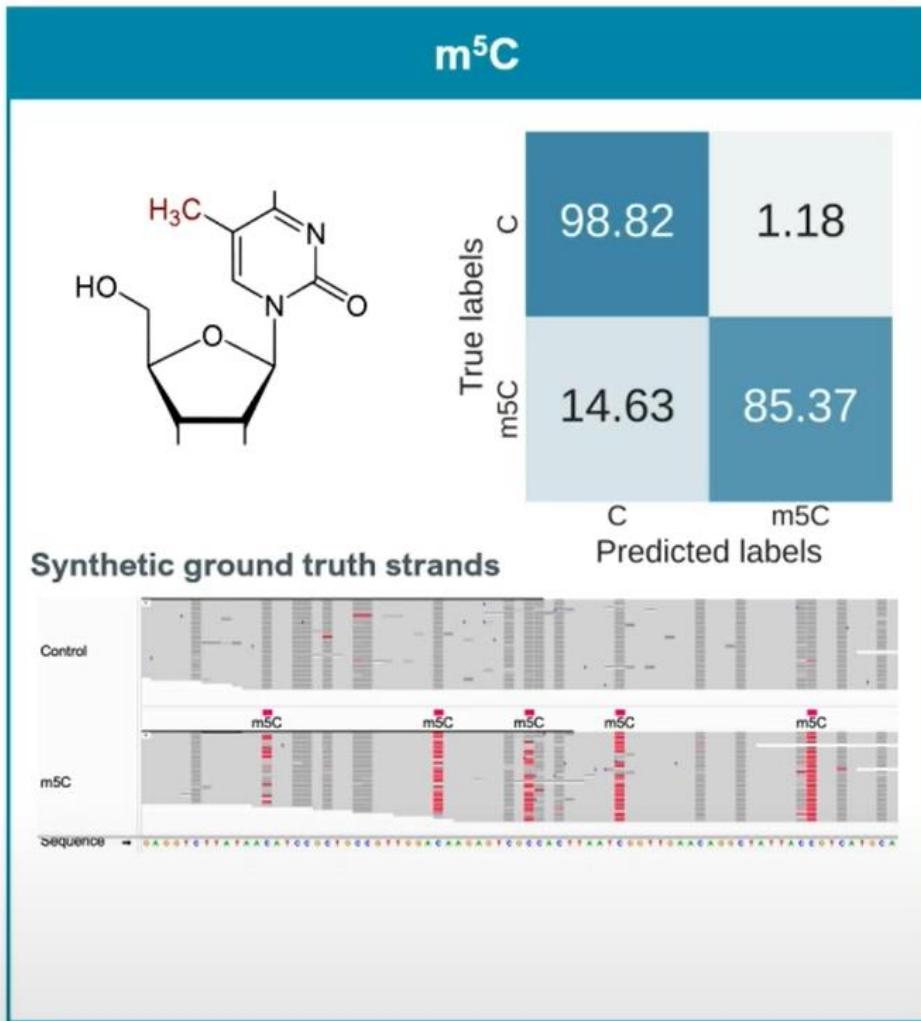
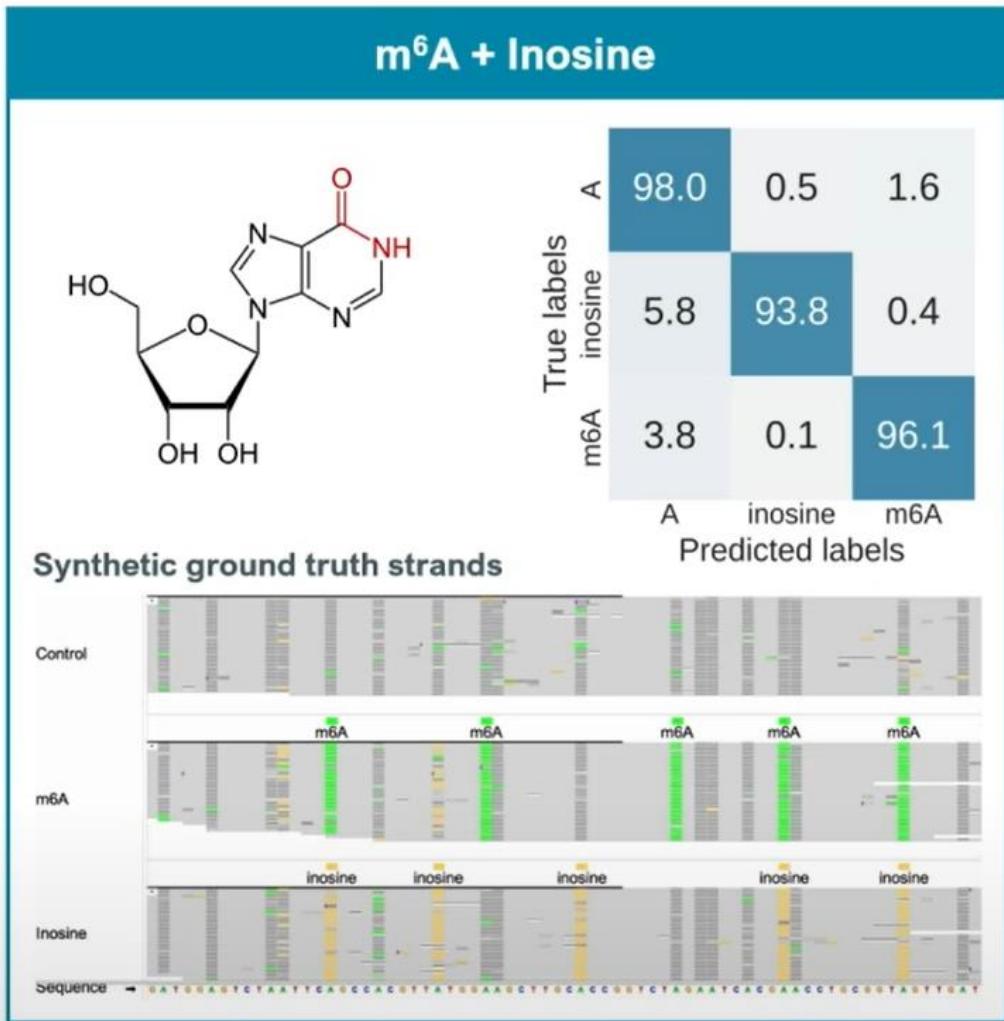
Known pseudoU Known other mod

True labels	U	pseU
U	98.86	1.14
pseU	3.99	96.01

All-context per-read per-site accuracy

IGV screenshot of rRNA 28S (4,369-4,445) from UHRR control RNA004 datasets produced with rRNA specific adapters. PseudoU calling performed with Dorado RNA004 v5 + PseU v1 models. Data courtesy of M. Jain. Genome Technology Laboratory, Northeastern University and M. Akeson. Deamer Laboratory, UCSC

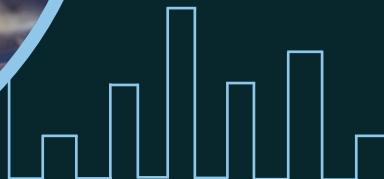
Direct RNA modified bases - SOTA



Microbial Isolate Whole Genome Sequencing

NO-MISS

Nanopore-Only Microbial Isolate Sequencing Solution



- ✓ Complete, high-quality genomes
- ✓ Resolve plasmids
- ✓ Locate AMR genes
- ✓ Flexible sample batching
- ✓ Rapid turnaround time

<https://nanoporetech.com/document/no-miss-isolate-sequencing-rapid-barcoding-v14>

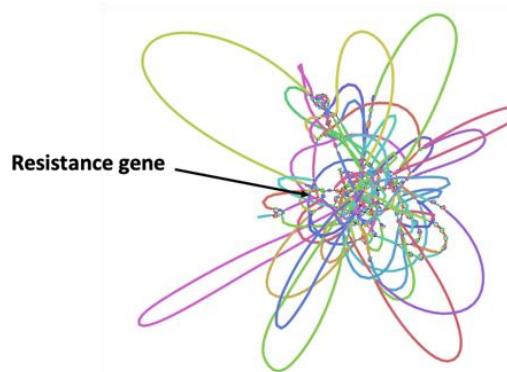
Generating closed, high-quality bacterial genome and plasmid assemblies

Most microbial genome assemblies produced with short-read sequencing technologies are fragmented and incomplete¹

Nanopore sequencing improves microbial genome quality, with the ability to:

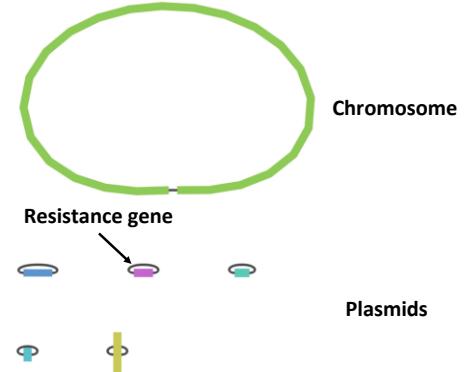
- Resolve repeat-rich sequences (characteristic of AMR genes) and structural variants
- Distinguish bacterial from plasmid transmission in healthcare settings to target interventions
- Understand mechanisms and drivers of antimicrobial resistance for outbreak investigation²

Short-read genome assembly



- ✗ Complete bacterial genome
- ✗ Resolve plasmids
- ✗ Locate AMR genes

Nanopore genome assembly



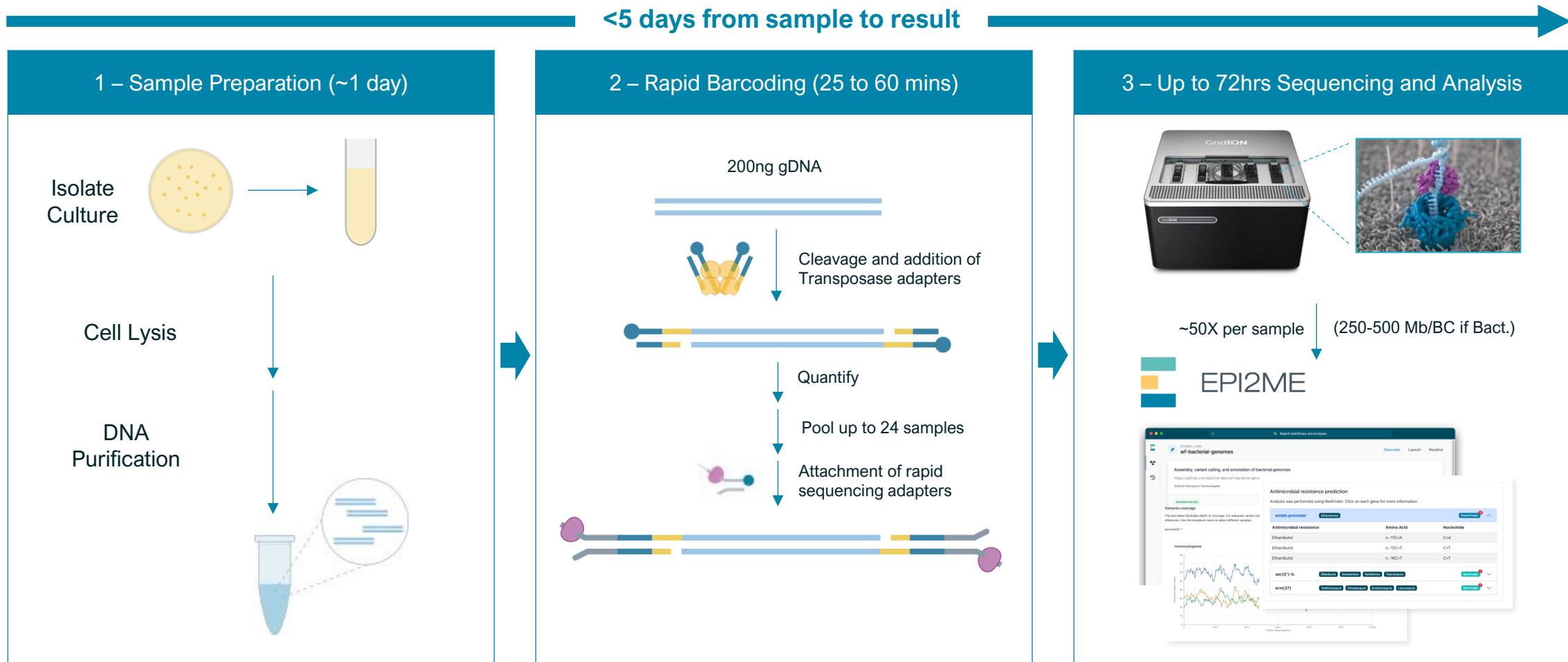
- ✓ Complete bacterial genome
- ✓ Resolve plasmids
- ✓ Locate AMR genes

1. Koren and Phillippy. "One chromosome, one contig: complete microbial genomes from long-read sequencing and assembly." Current opinion in microbiology 23 (2015): 110-120.

2. Figure from Dr. Kimberlee Musser, Wadsworth Center, NYSDOH, ['Improving bacterial disease public health testing with nanopore sequencing' presented at NCM 2023](#)

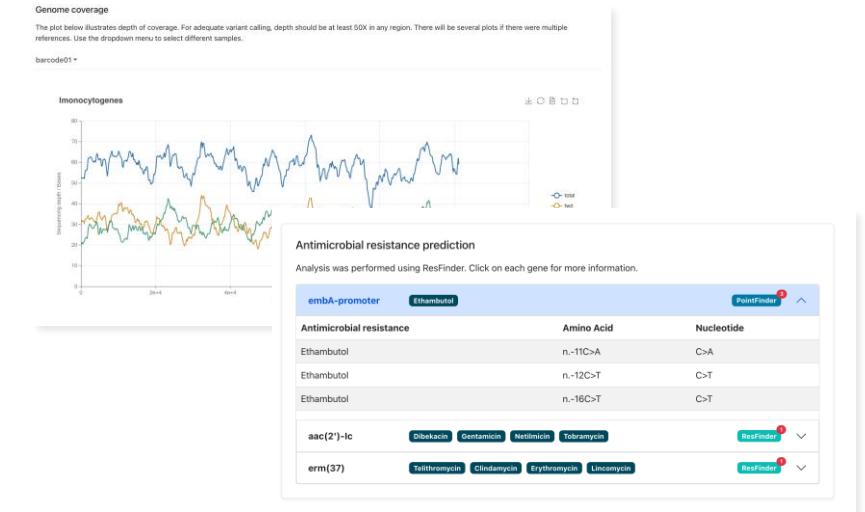
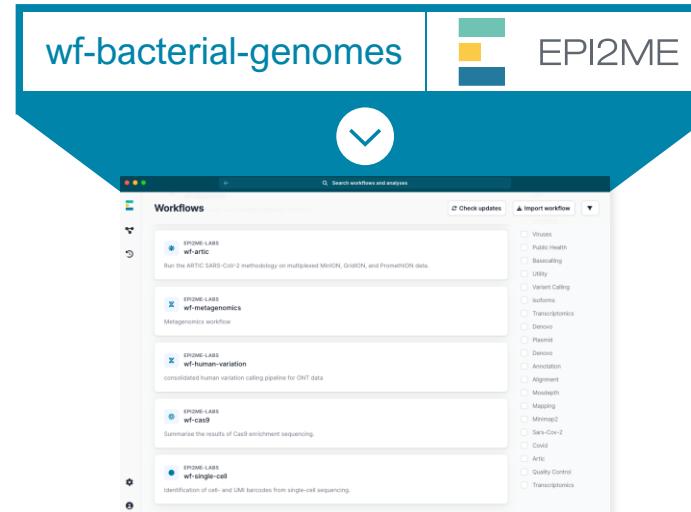
Overview of the End-to-End Microbial Isolate WGS protocol

NO-MISS (Nanopore-Only Microbial Isolate Sequencing Solution)



Intuitive bacterial genome analysis and report

Free software solution from Oxford Nanopore allows for bacterial assembly, annotation, MLST, AMR



Sample sequencing and
basecalling in MinKNOW

wf-bacterial-genomes

Alignment to reference
or assembly.
Consensus annotation,
resistance genes

Intuitive report, consensus
genome and annotation

MinKNOW

This workflow is accessible from both the intuitive graphical interface and the command line

Analysis with EPI2ME: wf-bacterial-genomes



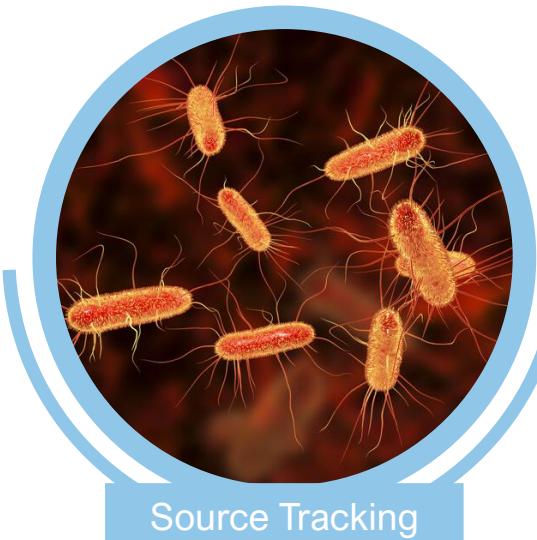
One easy-to-use analysis workflow to characterise your bacterial sample

Assembly



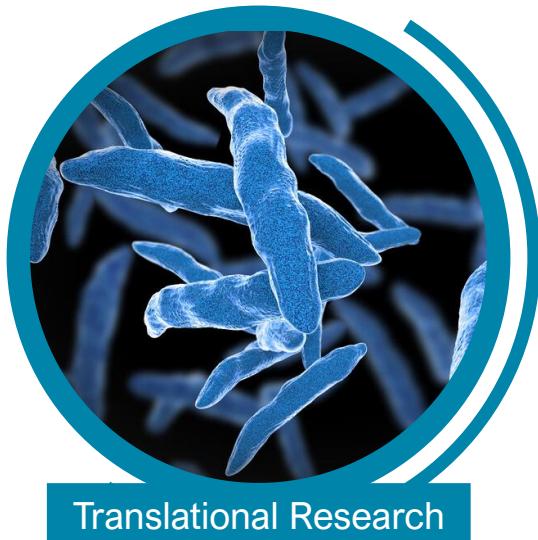
Complete Genomes

MLST Analysis



Source Tracking

Antimicrobial Resistance Profiling



Translational Research

Salmonella Serotyping



Food Safety

High quality genome assembly

Automatic species ID and profiling for species with a publicly available MLST profile

Identification of acquired genes and chromosomal mutations (select species) mediating antimicrobial resistance from a curated database

Salmonella serotyping prediction using FDA-approved SeqSero2

Provides information on Subspecies ID as well as O, H1 and H2 antigen predictions

Case study: WGS applied to bacterial outbreak in a clinical microbiology setting

Highly accurate, rapid nanopore sequencing for outbreak investigation and antimicrobial resistance prediction

Authors from the Providence Health Care lab in Canada performed WGS of multidrug resistant (MDR) *Shigella sonnei* utilizing nanopore sequencing

Through their analysis of 56 isolates, the team found strong evidence of a clonal strain causing infections:

- Near-identical strain typing by MLST, genotype, cgMLST and refMLST
- A highly conserved set of 10 plasmids across isolates
- Identical genotypic and phenotypic antimicrobial resistance profiles for four important antimicrobials

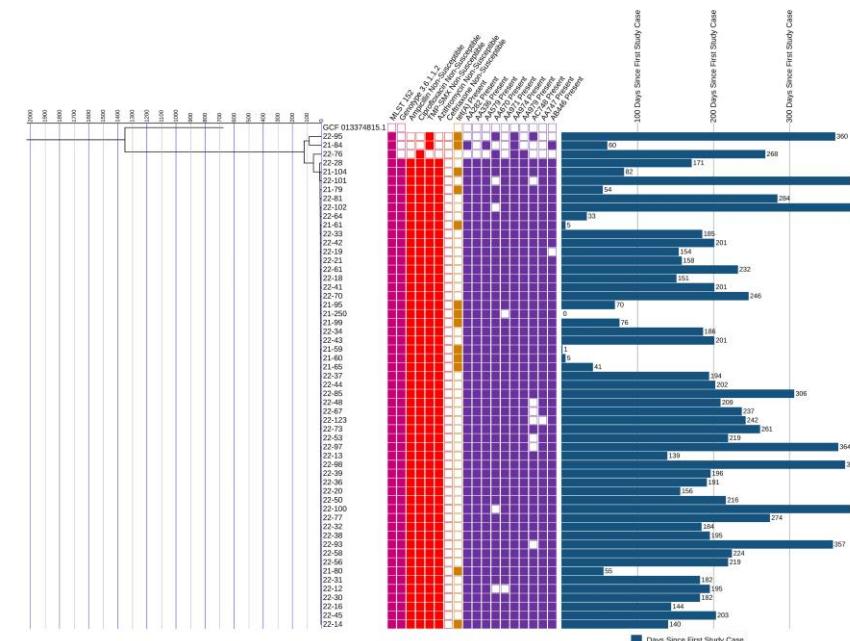


Figure 1 from Ritchie et al. Cluster isolates demonstrate highly similar strain types, plasmid profiles and antimicrobial resistance.

"Comparison of phenotypic antimicrobial susceptibility interpretation was concordant with the genotypic prediction using nanopore sequencing, including the detection of SNPs conferring quinolone resistance, which again demonstrates the base-level accuracy of our sequencing"

Ritchie et al. "WGS of a cluster of MDR *Shigella sonnei* utilizing Oxford Nanopore R10.4.1 long-read sequencing." Journal of Antimicrobial Chemotherapy 79.1 (2024): 55-60.

Community results: benchmarking nanopore-only bacterial genome accuracy

- Dr. Ryan Wick, Bioinformatician at the Doherty Institute, benchmarked bacterial genome accuracy using recently updated basecalling models
- Nanopore-only genome assemblies were compared to reference genomes
- Findings indicate that latest basecalling model yields large improvement over previous models in bacterial genome consensus accuracy



“Biggest improvement I've seen in a while! Most of these ONT-only bacterial genomes are now >Q60”

View the full blog post at: <https://rrwick.github.io/2023/12/18/ont-only-accuracy-update.html>



Ryan Wick
@rrwick

...

It hasn't been long since I last quantified @nanopore accuracy, but the release of Dorado v0.5.0 demanded another test:
rrwick.github.io/2023/12/18/ont...

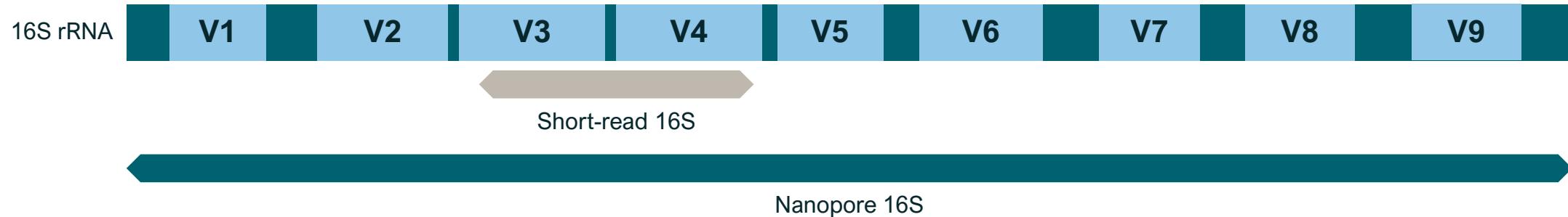
Biggest improvement I've seen in a while! Most of these ONT-only bacterial genomes are now >Q60 😲

Genome	Q score
<i>Campylobacter jejuni</i>	Q55.5
<i>Campylobacter lari</i>	Q49.2
<i>Escherichia coli</i>	Q67.2
<i>Listeria ivanovii</i>	Q57.7
<i>Listeria monocytogenes</i>	Q ∞
<i>Listeria welshimeri</i>	Q64.5
<i>Salmonella enterica</i>	Q62.0
<i>Vibrio cholerae</i>	Q63.2
<i>Vibrio parahaemolyticus</i>	Q64.1
Average	Q59.3

Full-length 16S microbial identification

Why implement nanopore sequencing for 16S analysis?

Full-length 16S rRNA sequencing improves taxonomic resolution of microbial communities



Key features	Sanger	Short-read	Oxford Nanopore
Read length	~500 bp	~150 – 300 bp	~1,500 bp
Resolves polymicrobial samples	✗	✓	✓
High taxonomic resolution ¹	✗	✗	✓
Rapid library preparation	✗	✗	✓
Real-time sequencing	✗	✗	✓

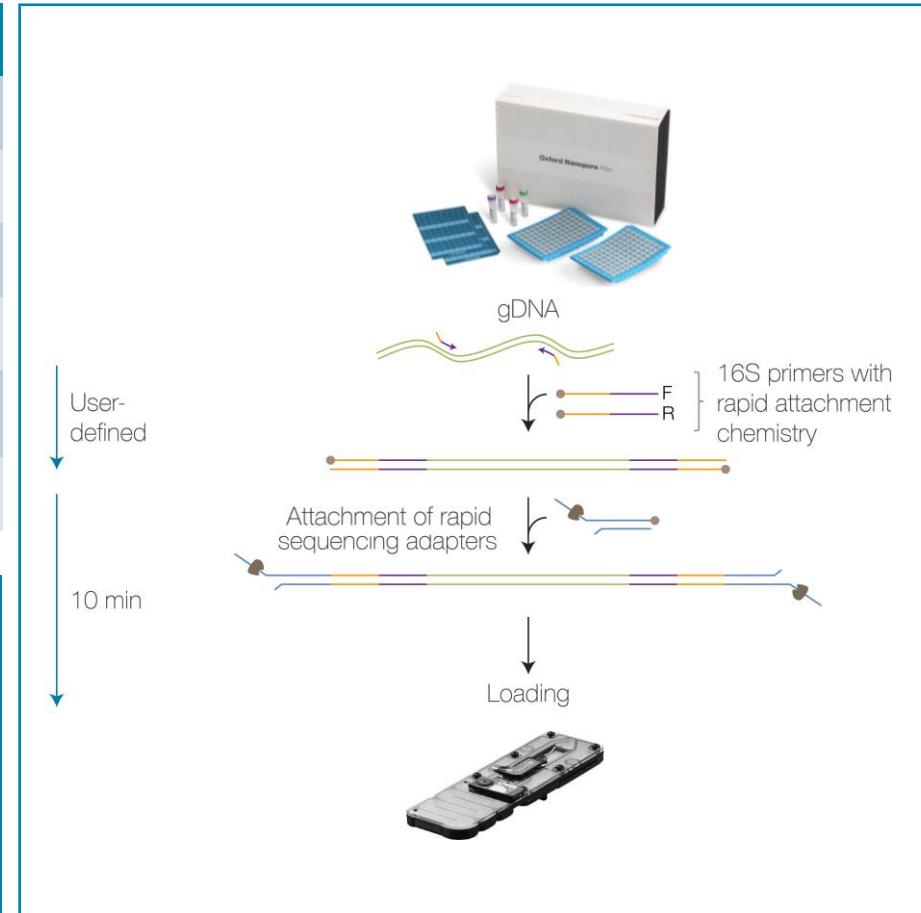
1. Zhang, et al. "The newest Oxford Nanopore R10.4.1 full-length 16S rRNA sequencing enables the accurate resolution of species-level microbial community profiling." Applied and Environ Microbiol 89.10 (2023): e00605-23.

Rapid library preparation with the 16S barcoding kit

Microbial identification with barcodes for up to 24 samples per run

Feature	Property
Preparation time	25 minutes + PCR
Input requirement	10 ng gDNA per sample
Read length	Full-length 16S gene (~1.5 kb)
Kit chemistry	Kit 14
Multiplexing options	<ul style="list-style-type: none">• 16S Barcoding Kit 24 V14• Flow Cell Wash Kit
Pack size	6 reactions

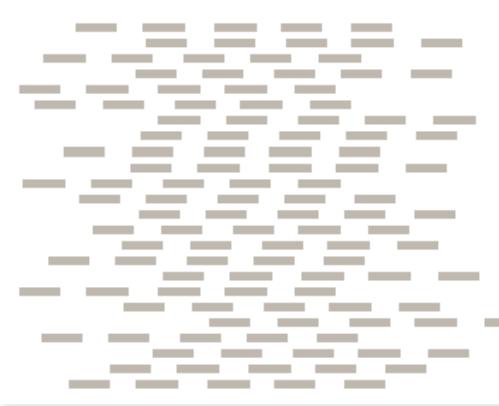
- The 16S Barcoding Kit 24 V14 enables rapid, cost-effective microbial identification
- The kit provides 24 unique barcodes, allowing you to pool up to 24 different samples in one sequencing experiment
- After sequencing, you can perform downstream analysis using the [EPI2ME Labs 16S workflow \(wf-16s\)](#)



View the full protocol at: [Rapid sequencing DNA - 16S Barcoding Kit 24 V14 \(SQK-16S114.24\)](#)

16S microbial identification analysis and report

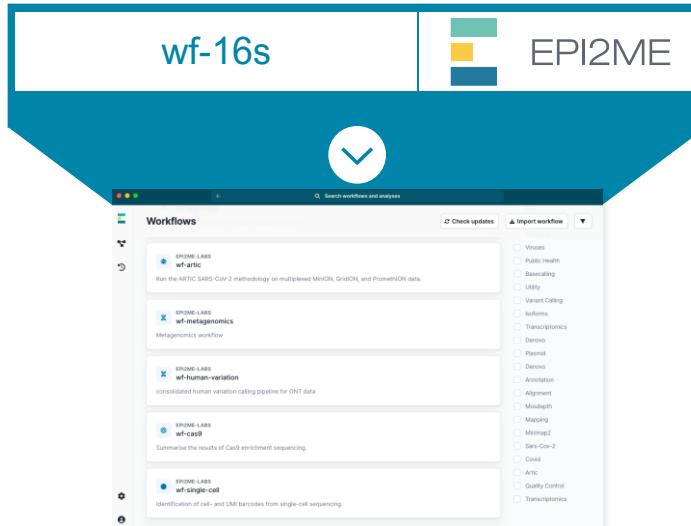
Free software solution from Oxford Nanopore allows visualisation of taxonomy, diversity, abundancies and more



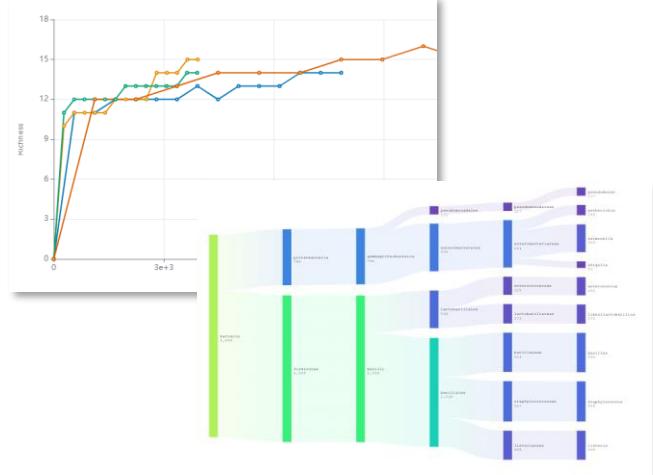
16S / 18S / ITS AMPLICONS



Sequence and basecall
amplicon-targeted 16S
/18S / ITS in MinKNOW



wf-16S



Quick, real-time reads
classification with kraken 2.
Fine classification with
minimap2 + database

Intuitive report, classified
and unclassified reads
and text files with
lineages details

MinKNOW

This workflow is accessible from both the intuitive graphical interface and the command line



Case study: Oxford Nanopore 16S sequencing with Q20+ chemistry

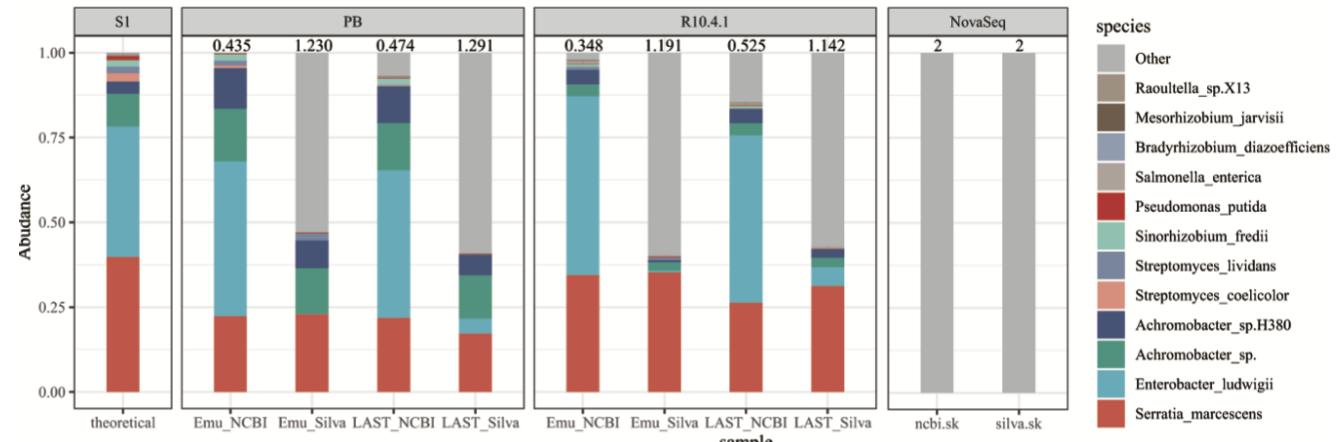
Accurate full-length 16S sequencing enables species-level profiling for environmental microbiota

- Authors assess the latest Q20+ chemistry for 16S experiments, generating raw read accuracy of ~99%
- Study highlighted that both Oxford Nanopore and an alternative long-read platform revealed similar microbial profiles, while short read sequencing had limited resolution for species-level identification



"Our findings show that the ONT R10.4.1 flowcell for full-length 16S enabled species-level taxonomic identification for environmental samples"

The newest Oxford Nanopore R10.4.1 full-length 16S rRNA sequencing enables the accurate resolution of species-level microbial community profiling



From Fig. 2: Classification results on species levels with PacBio ('PB', left), Oxford Nanopore ('R10.4.1', middle), and short-reads ('NovaSeq', right) compared to abundance of sample ('S1'). 'Other' includes unclassified.

Zhang et al. "The newest Oxford Nanopore R10.4.1 full-length 16S rRNA sequencing enables the accurate resolution of species-level microbial community profiling." Applied and Environ Microbiol 89.10 (2023): e00605-23.

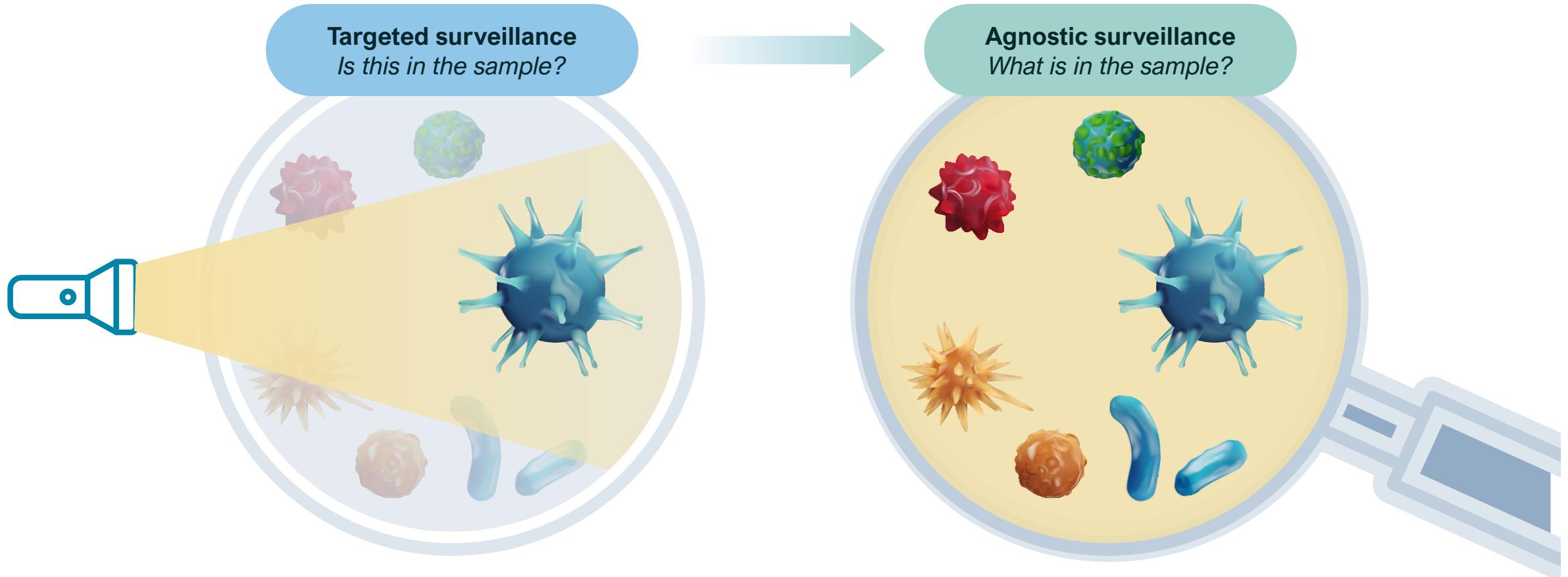
“Pathogen-agnostic” metagenomics

“Pathogen-agnostic” metagenomics

Nanopore sequencing is paving the way for rapid, unbiased pathogen surveillance methods

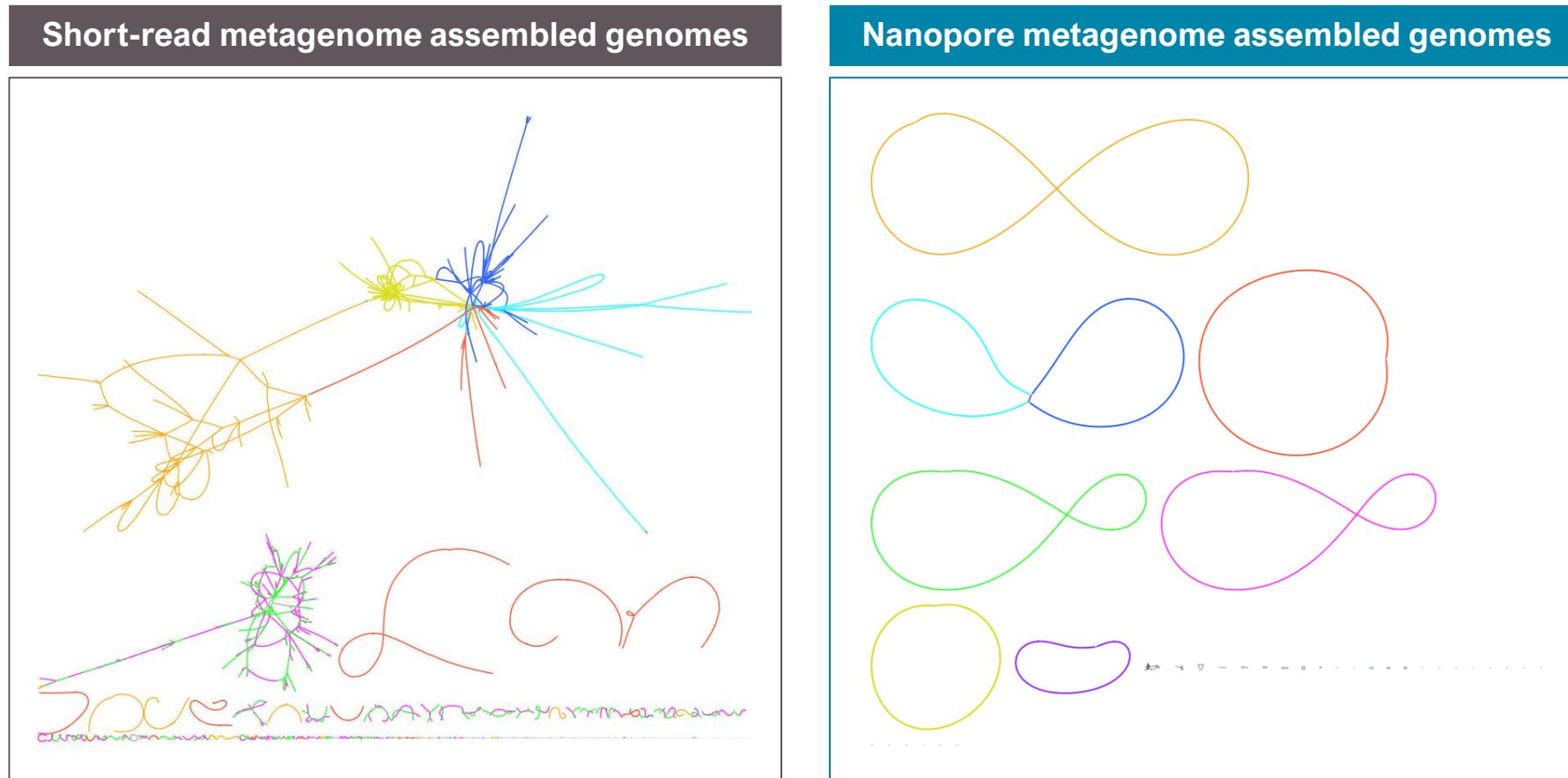
Today, pathogen surveillance strategies typically rely on retrospective investigations targeting known or suspected pathogens

Going forward, the field aims to move towards more agnostic sequencing methods for broad, real-time pathogen monitoring



Advantages of nanopore sequencing for metagenomics

Unrestricted read-lengths, complete metagenome-assembled genomes (MAGs), rapid access to results



Metagenomic approaches with short-reads typically produce highly fragmented and incomplete genome assemblies
Nanopore sequencing improves metagenomic assemblies and taxonomic profiling with rapid turnaround times

Nanopore technology enables rapid turnaround time for metagenomics

Sequencing of environmental or clinical research samples can be challenging, as they can contain a low abundance of pathogen DNA/RNA, while containing high background from host and commensals. Therefore, methods have been developed for microbial DNA/RNA enrichment:

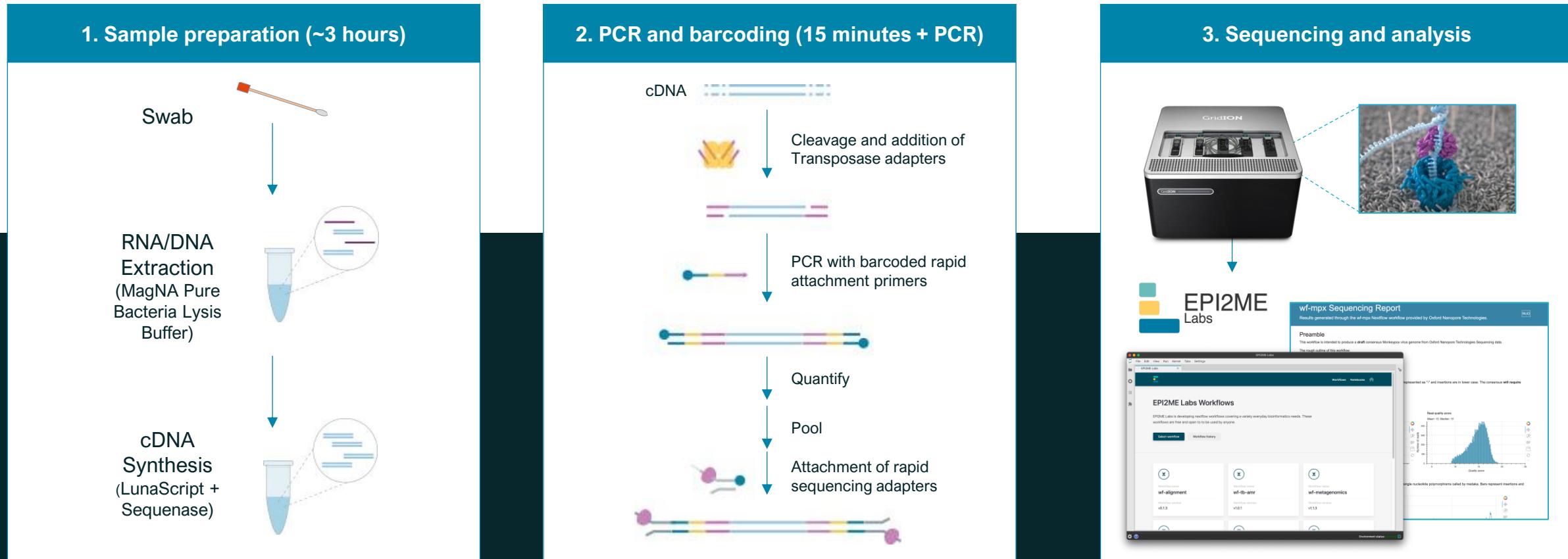
Metagenomics method	Pathogens detected in the study	Turnaround time (sample-to-result)	Reference
Respiratory metagenomics (RMg)	<ul style="list-style-type: none">Respiratory infections and antimicrobial resistance, including ICU-acquired <i>L. pneumophila</i>, <i>P. aeruginosa</i>, vancomycin-resistant <i>E. faecium</i>, Influenza, HSV-2	~7 hrs	Charalampous et al. 2023
Sequence-Independent Single Primer Amplification (SISPA)	<ul style="list-style-type: none">Chikungunya, Ebola, hepatitis C virus, novel paramyxoviruses, RSV, rhinovirus, Influenza	<6 hrs	Minor et al. 2023 Vanmechelen et al. 2022
SMART-9N	<ul style="list-style-type: none">Zika virus, yellow fever virus, SARS-CoV-2, Mpox virus	<6 hrs	Claro et al. 2023 , Claro et al. 2022
Nanopore Adaptive Sampling	<ul style="list-style-type: none">Bacterial pathogens, antimicrobial resistance	~5 hrs	Wren et al. 2023 Cheng et al. 2022

Metagenomic protocol for sequencing DNA and RNA from pathogens

Developed by Adela Alcolea-Medina, Prof. Jonathan Edgeworth and colleagues, with support from Oxford Nanopore

7h

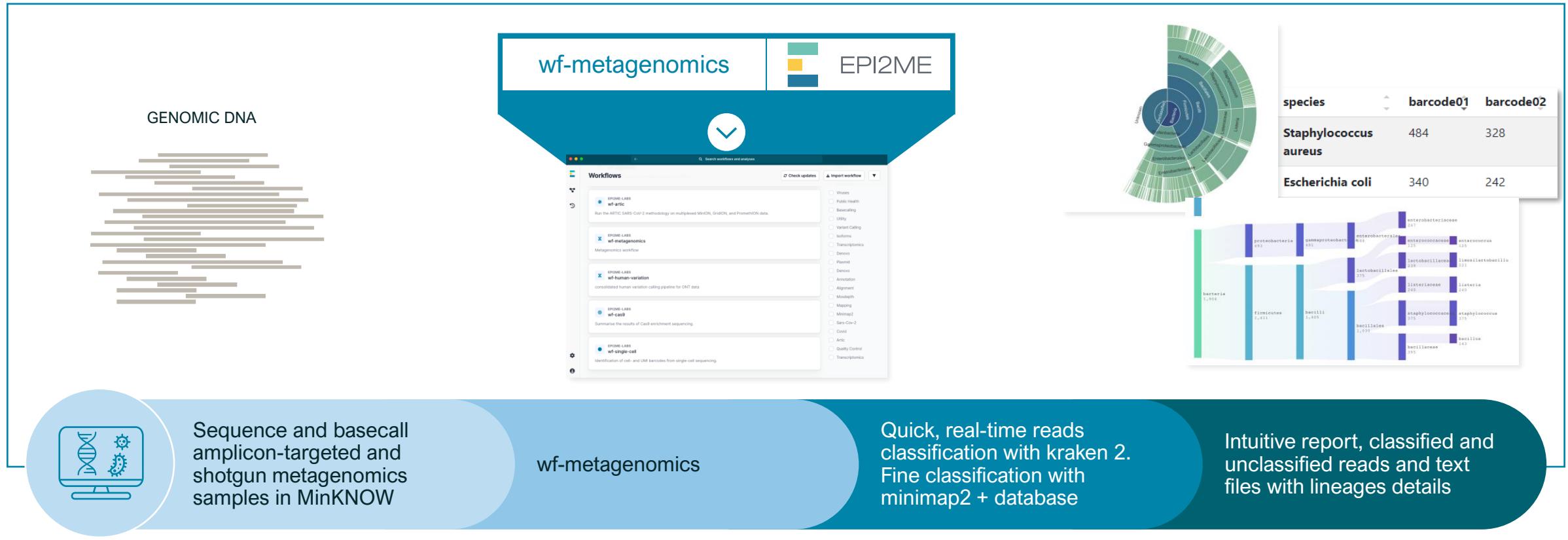
7h from sample to result



Alcolea-Medina, Adela, et al. "Novel, Rapid Metagenomic Method to Detect Emerging Viral Pathogens Applied to Human Monkeypox Infections." (2022).
See the full protocol at: https://community.nanoporetech.com/docs/prepare/library_prep_protocols/viral-metagenomics-RNA-DNA/v/vmrs_v9

EPI2ME workflow for metagenomics analysis

Intuitive visualisation of taxonomy, diversity, abundances and more



This workflow is accessible from both the intuitive graphical interface and the command line

"Each day costs about £2,500, depending on the complexity of the patient. For my sickest patients, it could be £10,000."

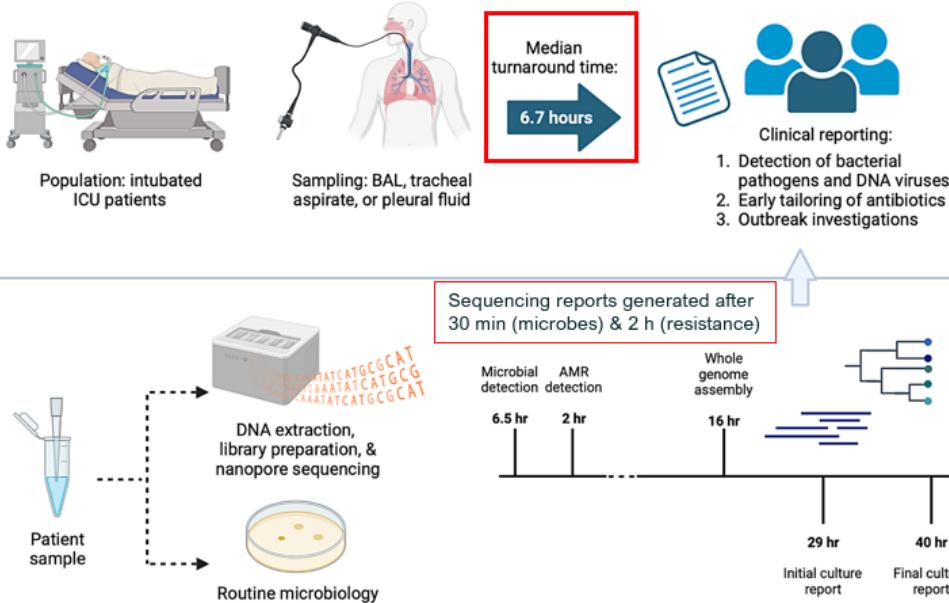
Professor Ian Abbs
CEO, Guys & St Thomas NHS Foundation Trust



CLINICAL

LABORATORY

Respiratory Metagenomics



Charalampous, T., Alcolea-Medina, A., Snell, L. B., Alder, C., Tan, M., Williams, T. G. S., Al-Yaakoubi, N., Humayun, G., Meadows, C. I. S., Wyncoll, D. L. A., Paul, R., Hemsley, C. J., Jeyaratnam, D., Newsholme, W., Goldenberg, S., Patel, A., Tucker, F., Nebbia, G., Wilks, M., Chand, M., ... Edgeworth, J. D. (2024). Routine Metagenomics Service for ICU Patients with Respiratory Infection. *American journal of respiratory and critical care medicine*, 209(2), 164–174. <https://doi.org/10.1164/rccm.202305-0901OC>

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Case Study: Potential of respiratory metagenomics (RMg) in a critical care setting

"This pilot study illustrates the potential of RMg testing to provide benefits for antimicrobial treatment, infection control, and public health when provided in a real-world critical care setting"

- » Evaluation performed on >500 samples with 250 samples as part of a pilot service at Guys & St Thomas NHS Foundation Trust over 3 winters
- » Average laboratory time to first sequence report: 6.7hrs
 - Sensitivity: 93%
 - Specificity: 95%
- » 45% informed antimicrobial prescribing changes
- » 20% escalation: mostly SAME day / 25% de-escalation: mostly NEXT day
- » 5% results informed infection control interventions or identified novel emerging hypervirulent organisms



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Thank you

