

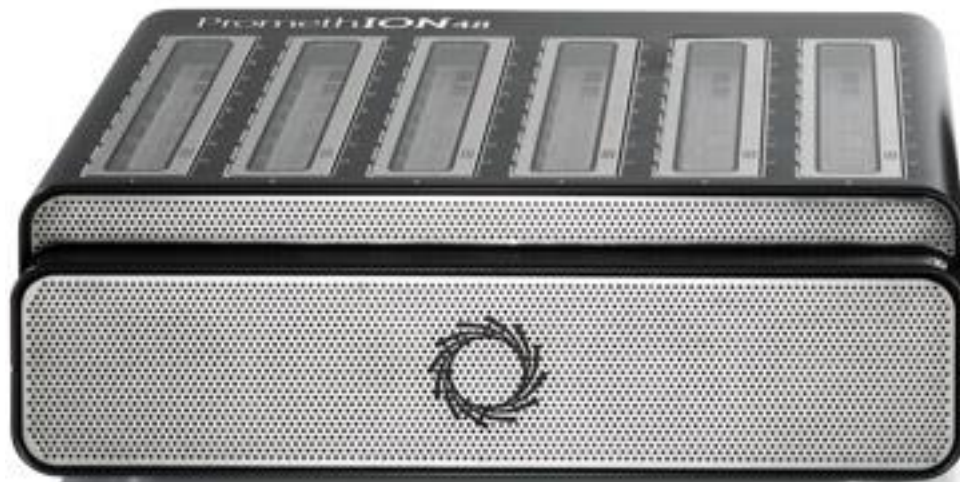
Third Generation Sequencing Platforms

	Second Generation sequencing	PacBio: Single Molecule Real-Time Sequencing SMRT	Oxford Nanopore Technology: MinION
Read Length (bp)	150	15,000	90,000
Read output	2.5-5,000,000	~500,000	1,000,000
Cost Per Run (\$)	3000	850	700
Hardware Cost (\$)	900,000	350,000	1000
Observed Error Rate	<1%	~12%	~12%



Nanopore technology

PromethION



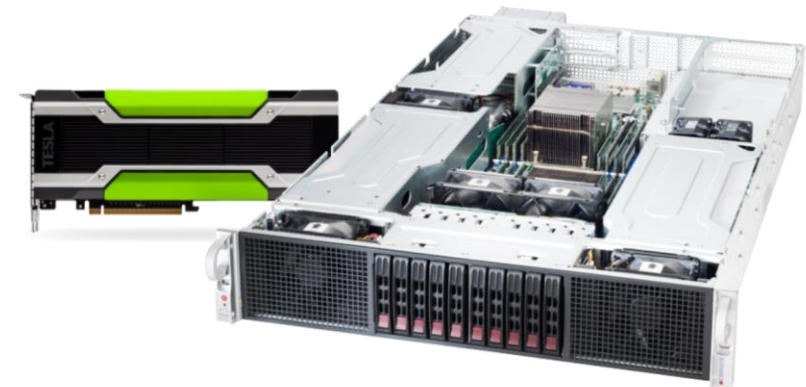
GridION



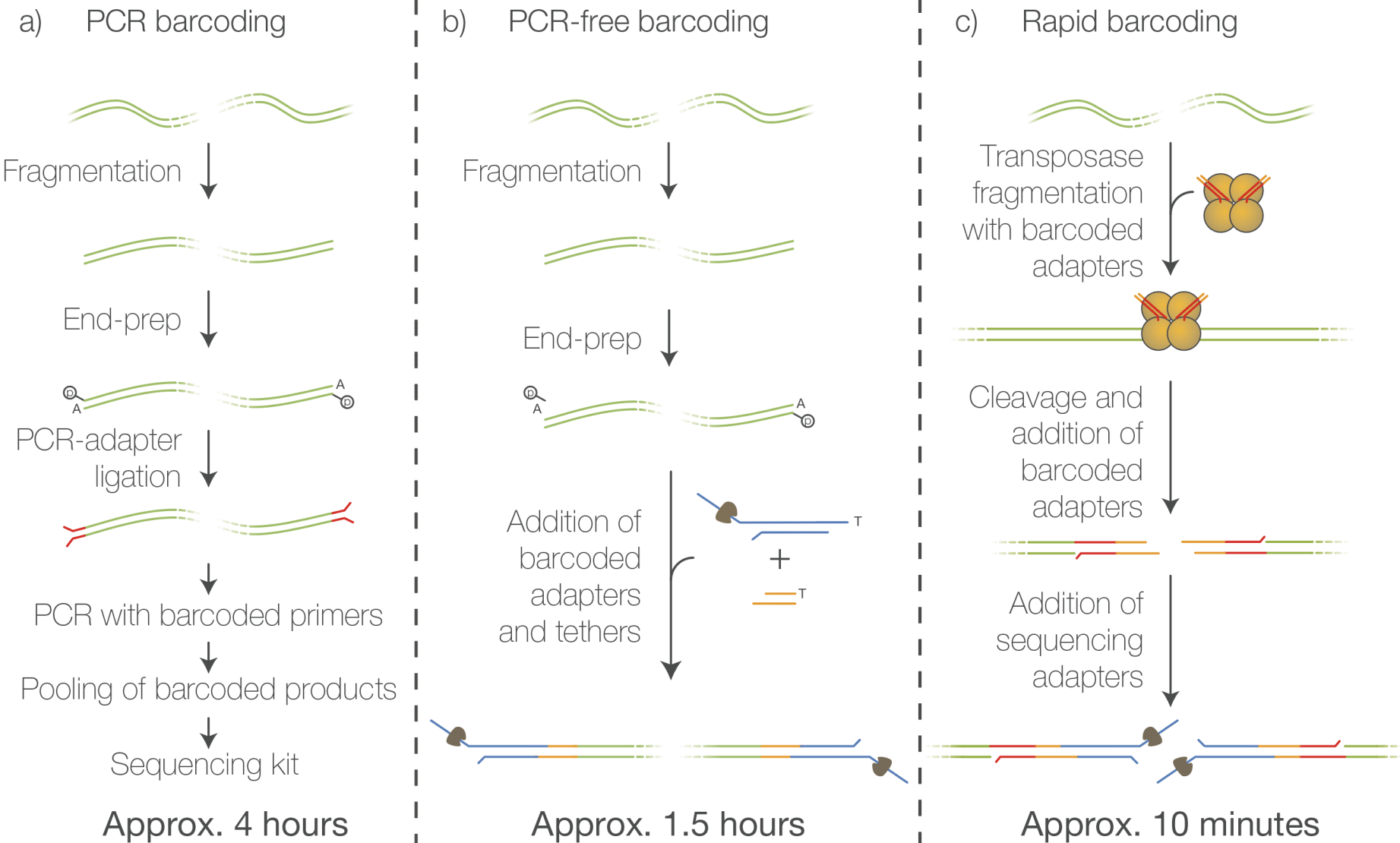
MinION

Flongle

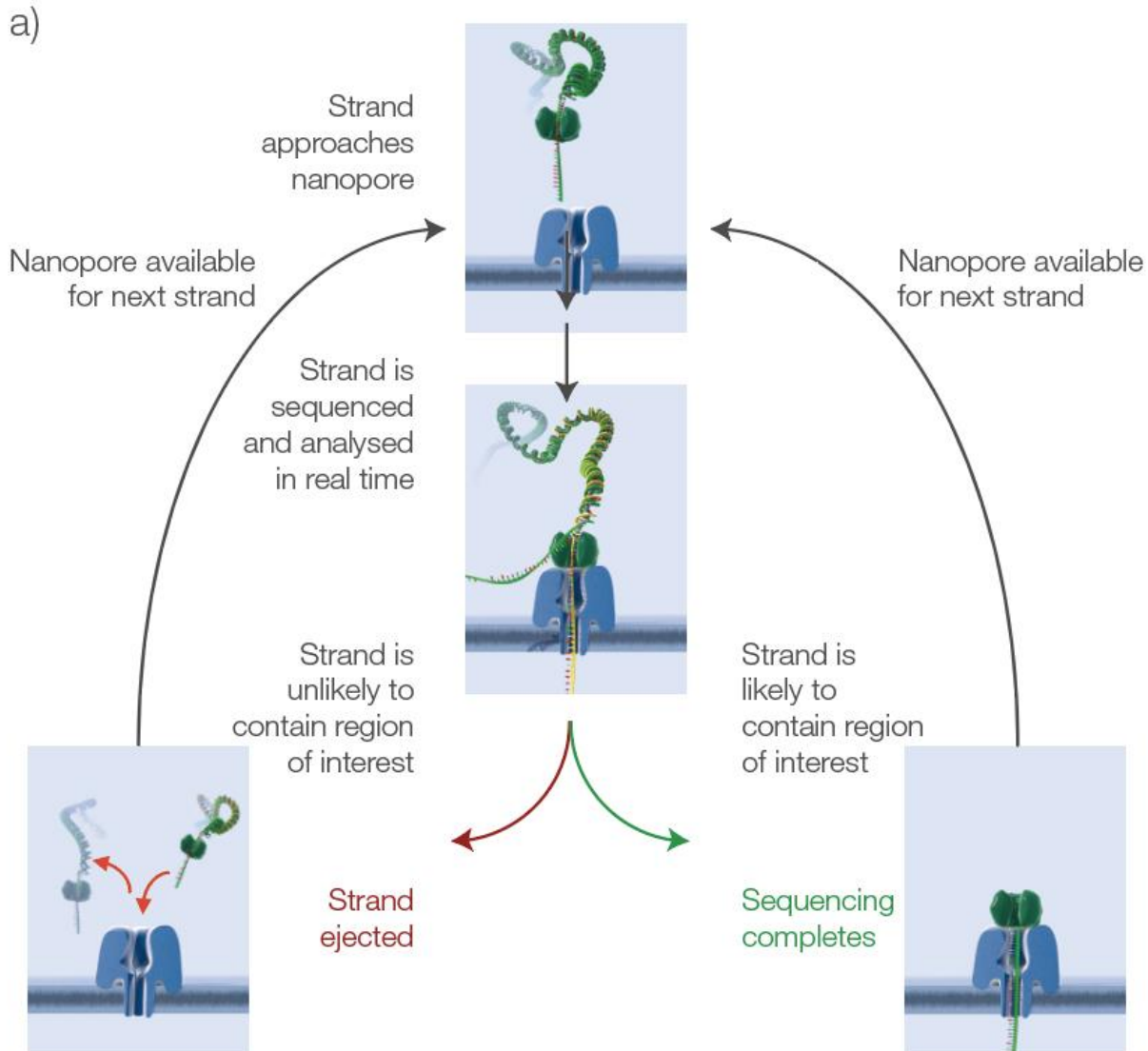
HPC + GPU



Library preparation and loading

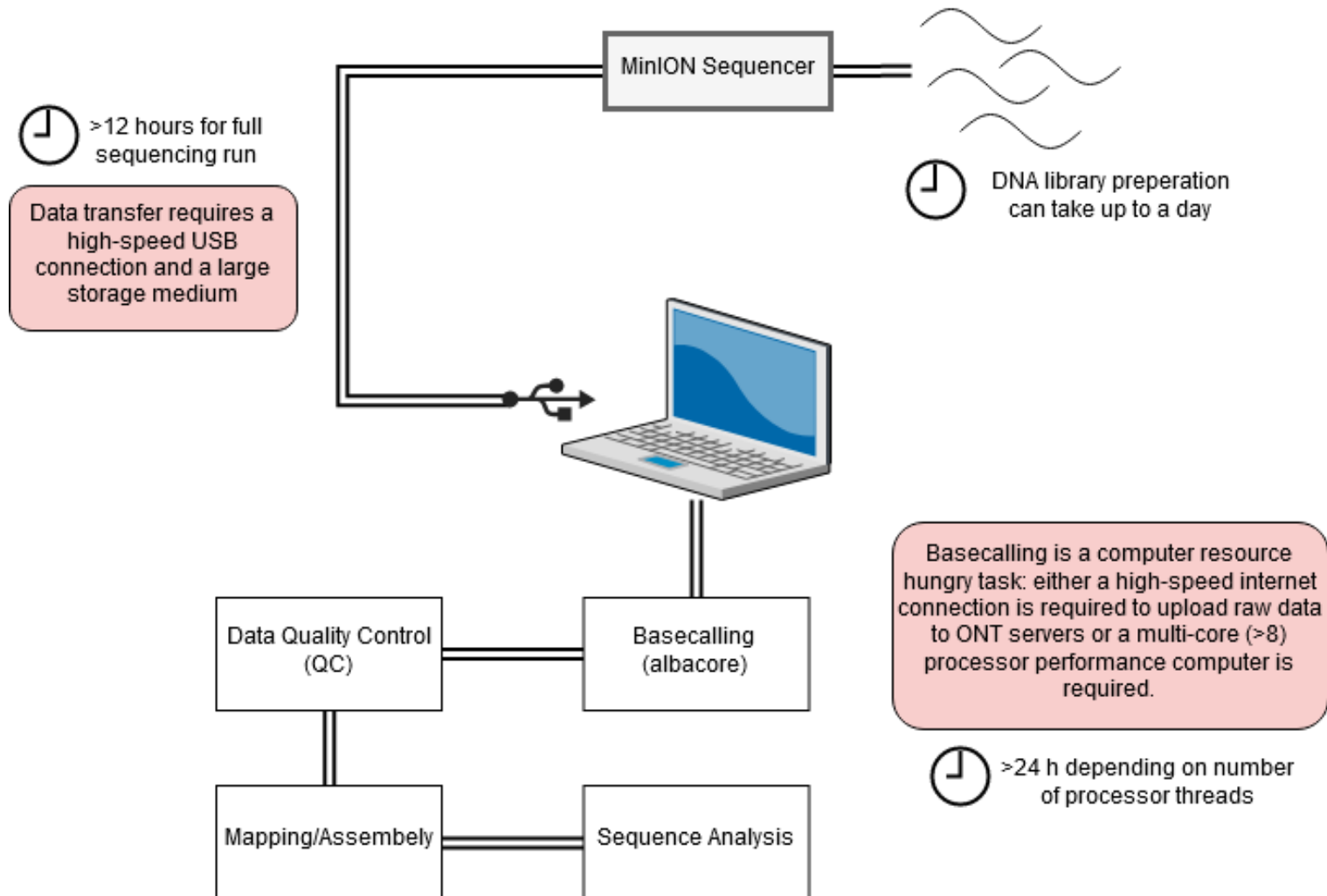


Adaptive sampling



Adaptive sampling allows the automatic selection of an unlimited number of regions of interest during a sequencing run, without the need for additional library-preparation steps

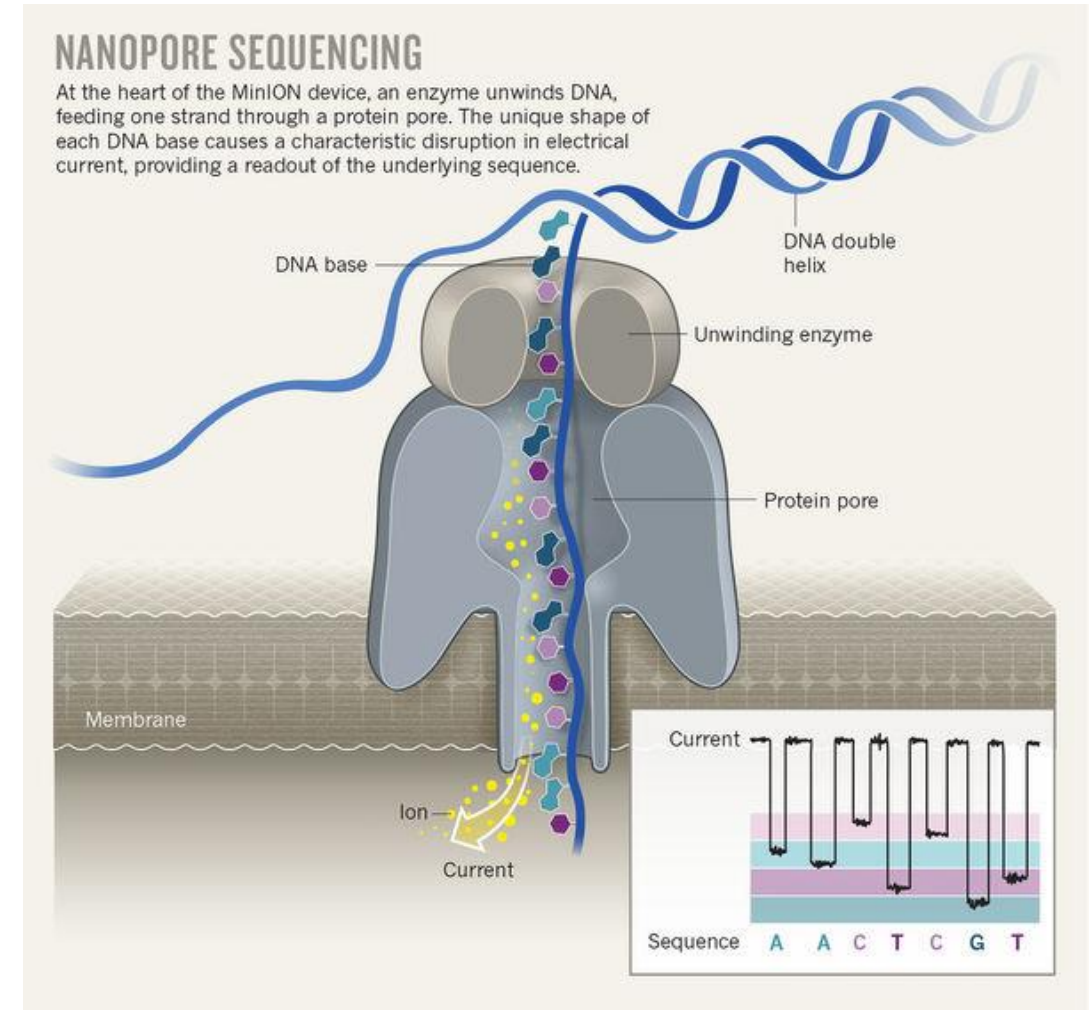
Sequencing Pipeline



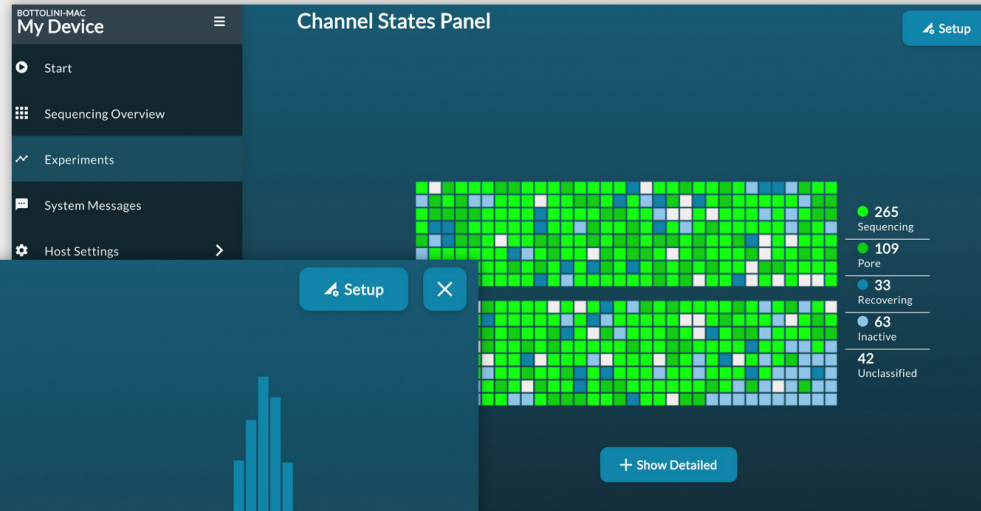
MinION – Nanopore Sequencing Technology

“Portable, real-time sequencing analyses”

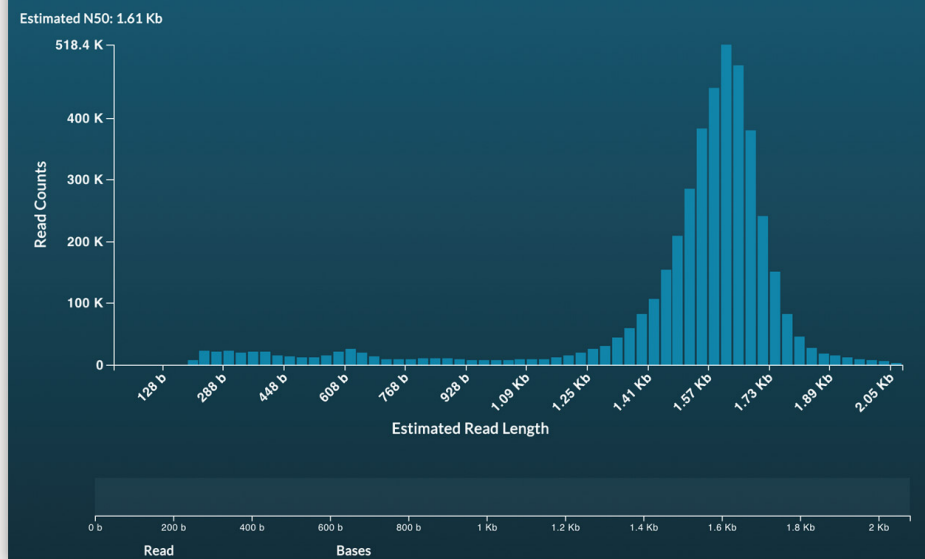
- Very portable – can take to the field*
- Produces long reads compared to NGS platforms
- Can produce very high depth and coverage – high data yield.
- Still requires sophisticated lab techniques for library preparation
- Has a very high error rate compared to Illumina
- Is still under development – high dependency on community contributions
- Data is very challenging to process and analyse



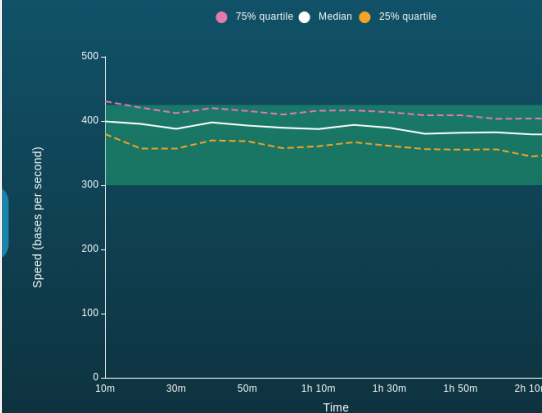
MinION run QC



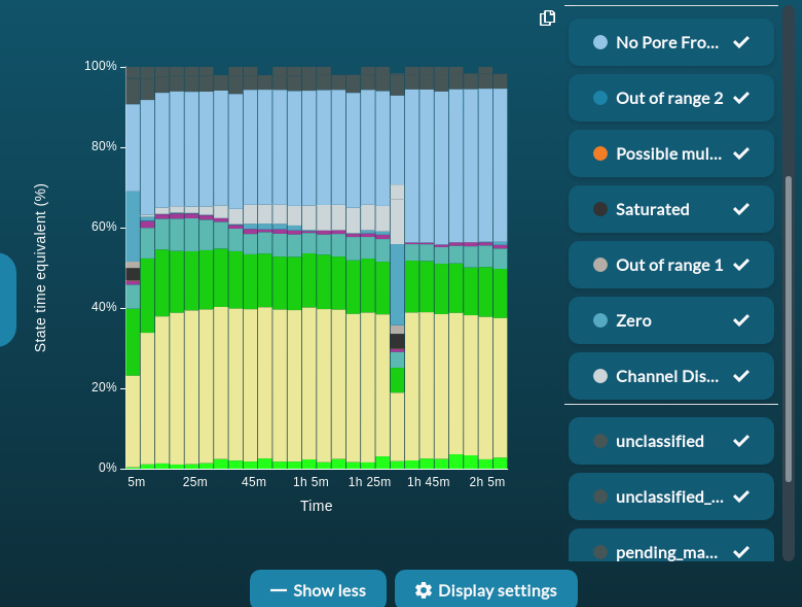
Read Length Histogram



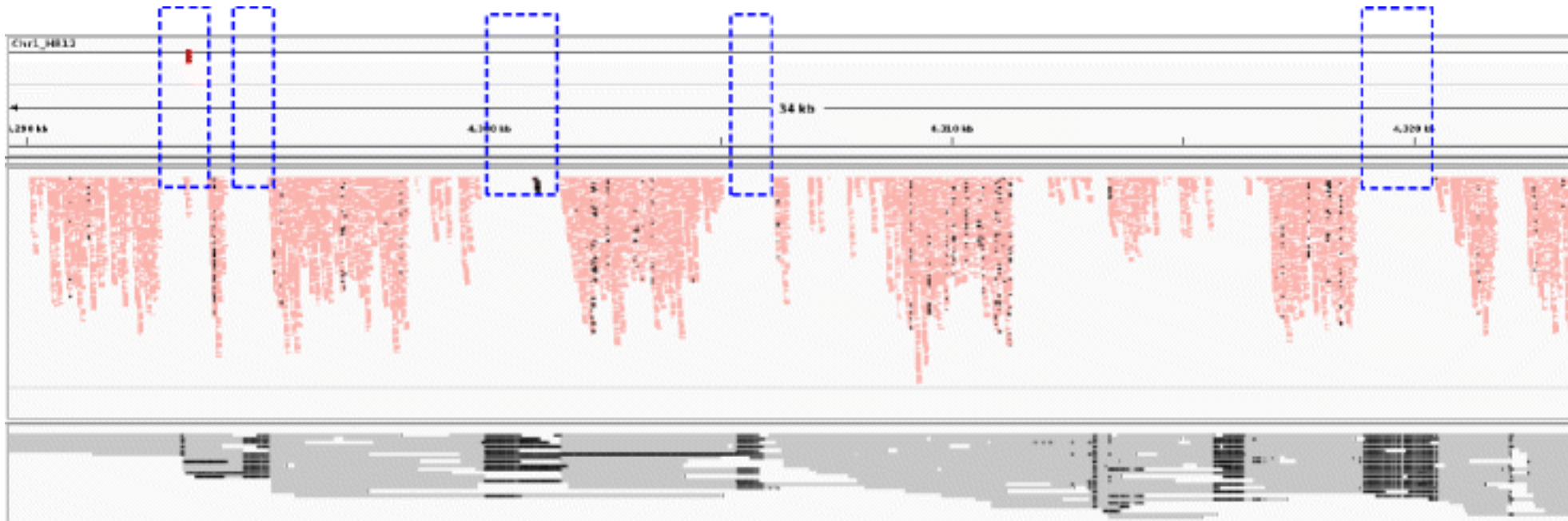
Translocation speed



Duty time



Hybrid assembly

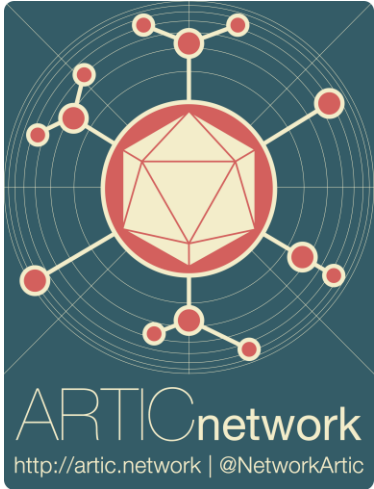


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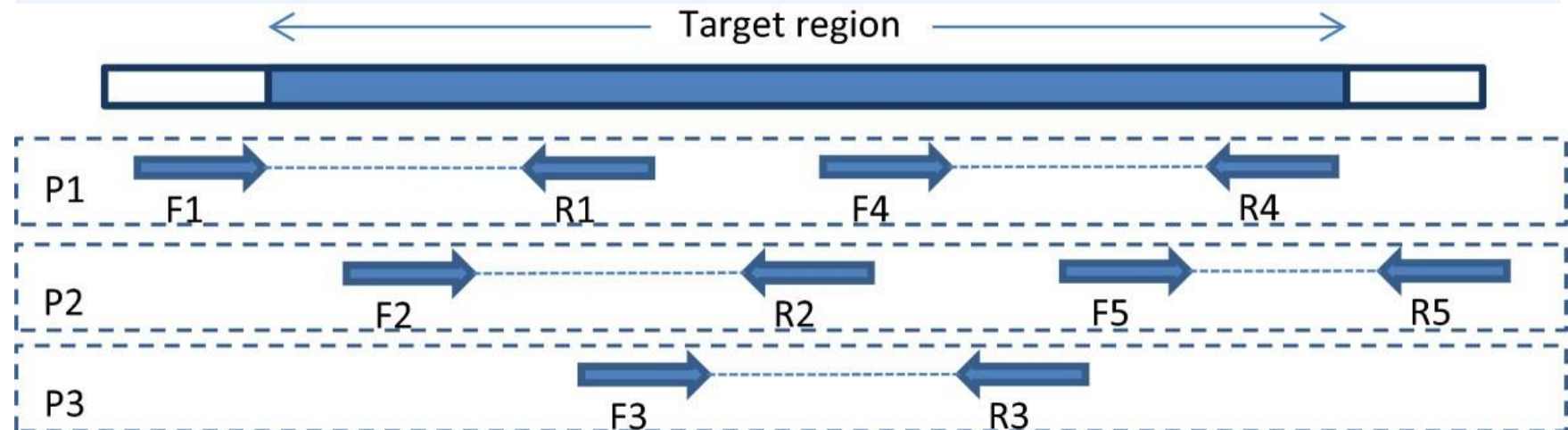
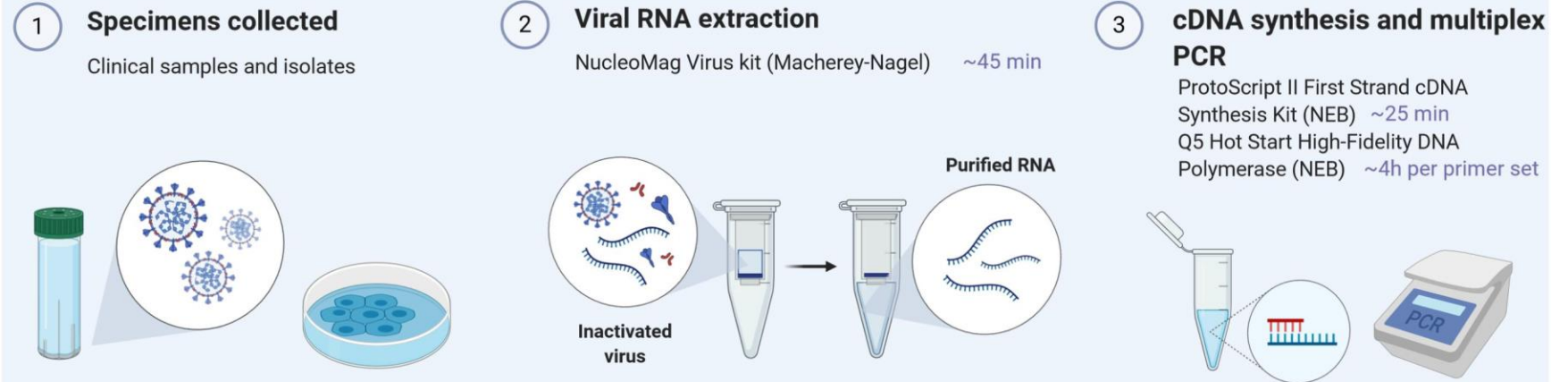
Hybrid assembly helps
resolve ambiguities with
higher coverage and
differing read lengths



SARS-CoV-2 Sequencing

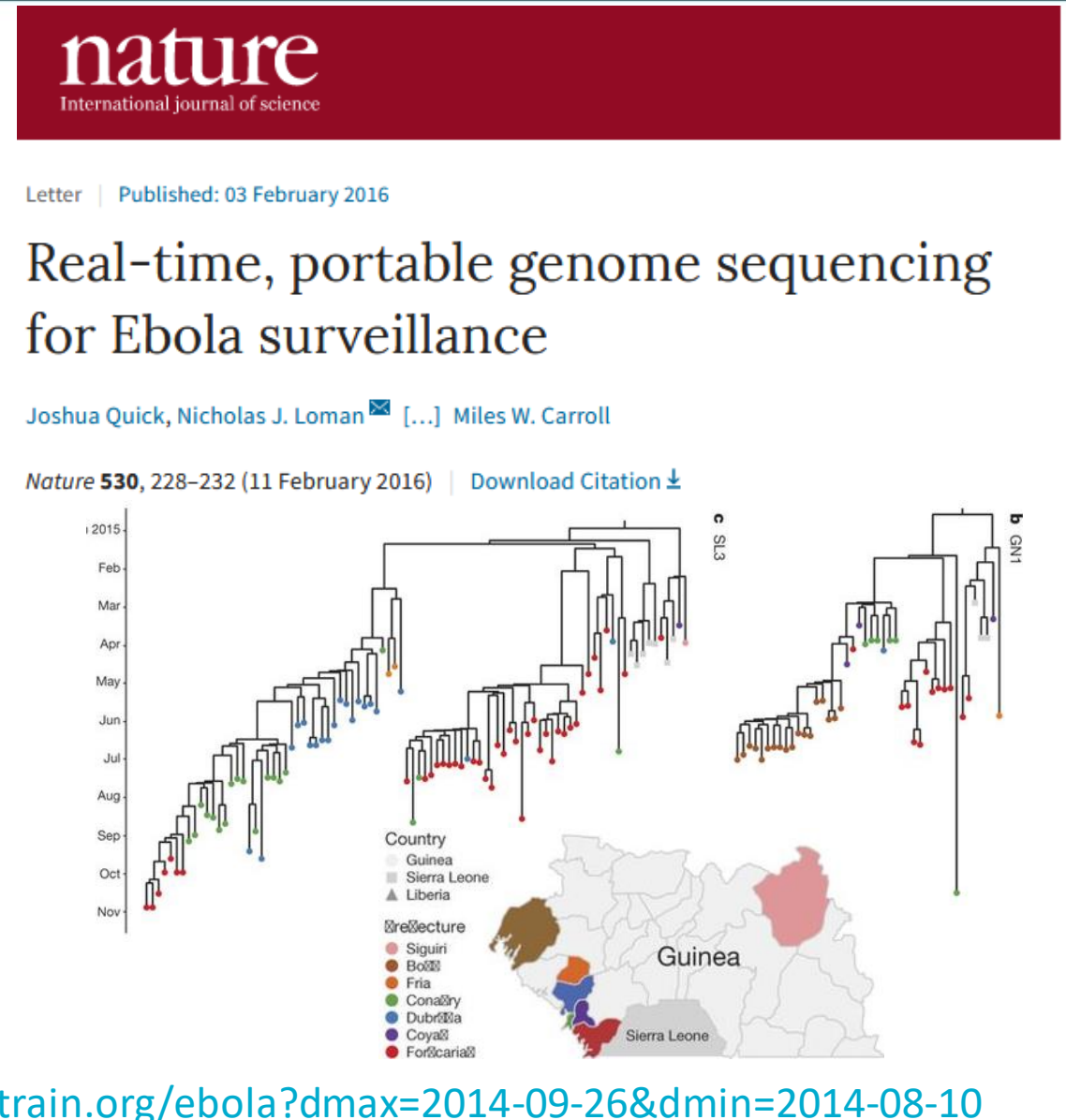


SARS-CoV-2 sequencing workflow



Real-Time Sequencing = Real-Time Surveillance

- Genome sequencing can provide a high-resolution view of pathogen evolution and is increasingly sought after for outbreak surveillance.
- Sequence data may be used to guide control measures, but only if the results are generated quickly enough to inform interventions.
- In April 2015 the MinION system was transported in standard airline luggage to Guinea and used for real-time genomic surveillance of the ongoing epidemic.
- They presented sequence data and analysis of 142 EBOV samples collected during the period March to October 2015.

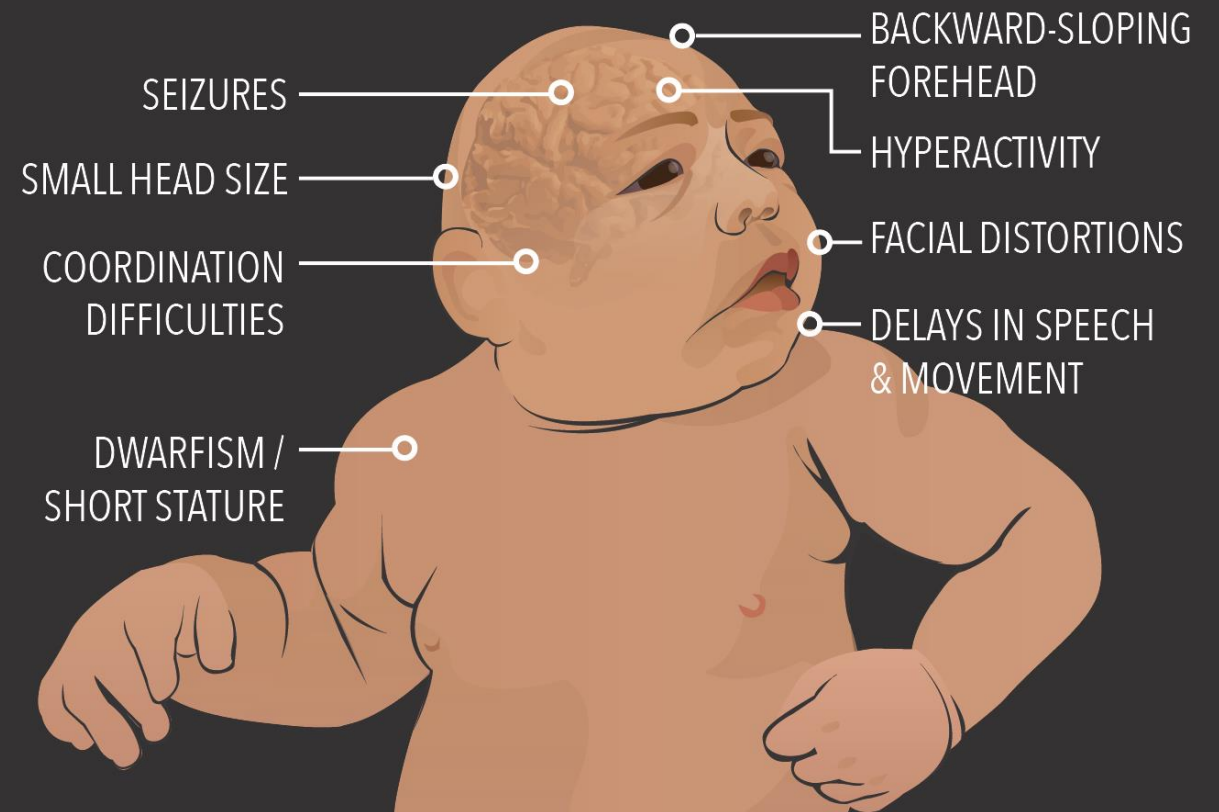


<https://nextstrain.org/ebola?dmax=2014-09-26&dmin=2014-08-10>

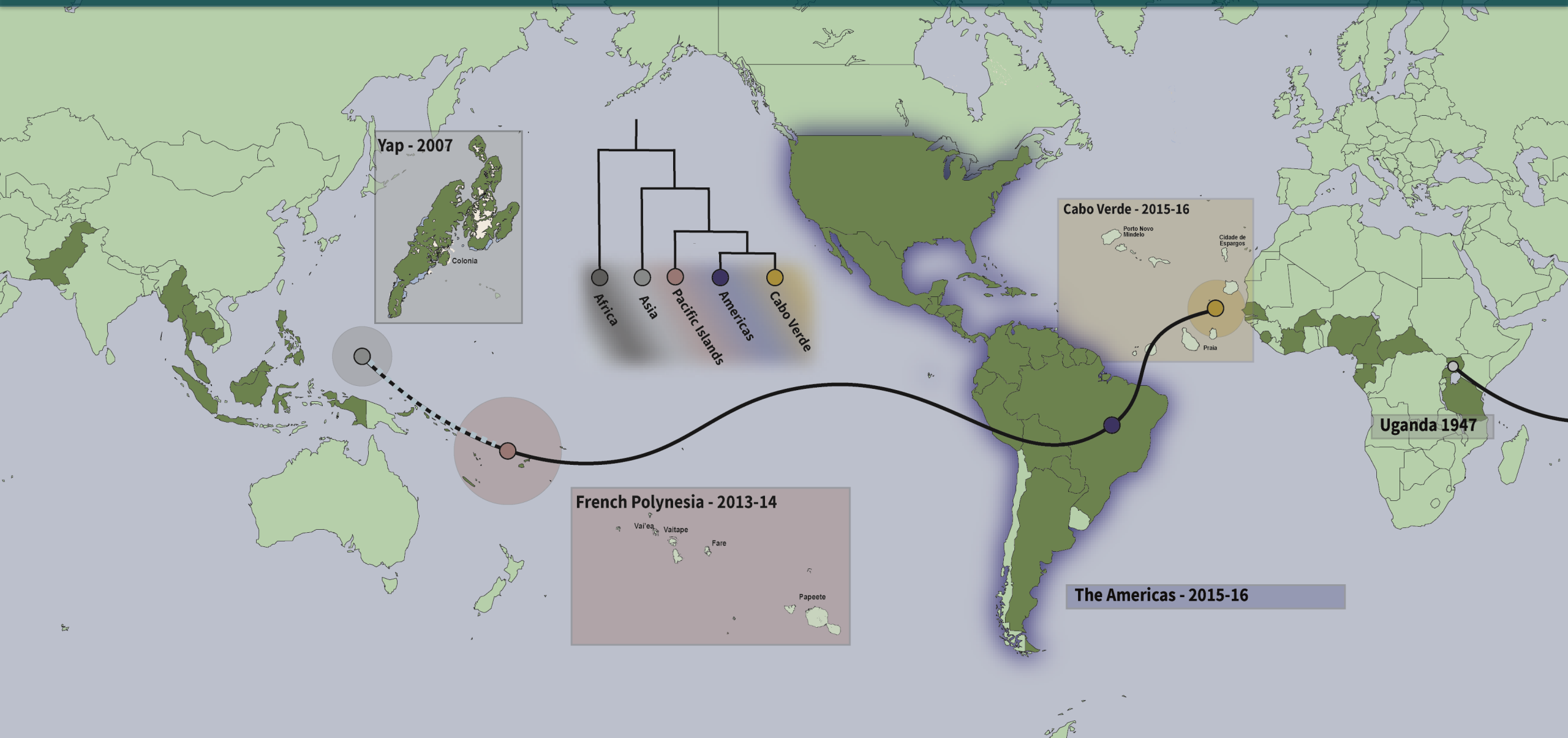
Zika Virus Morbidity

- Zika virus disease is caused by an RNA virus, a member of the *Flavivirus* genus.
- Other flavivirus include Dengue, yellow fever and West Nile Virus.
- The 2015-16 Zika outbreak in South America triggered the most recent WHO PHEIC, following association with microcephaly.
- The primary vector (transmitting agent) is the *Aedes Aegypti* mosquito.

SYMPTOMS OF MICROCEPHALY



Global Zika Burden



Nanopore Sequencing Data Activity

