

Third Generation Sequencing: Zika Case Study

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Third Generation Sequencing Platforms

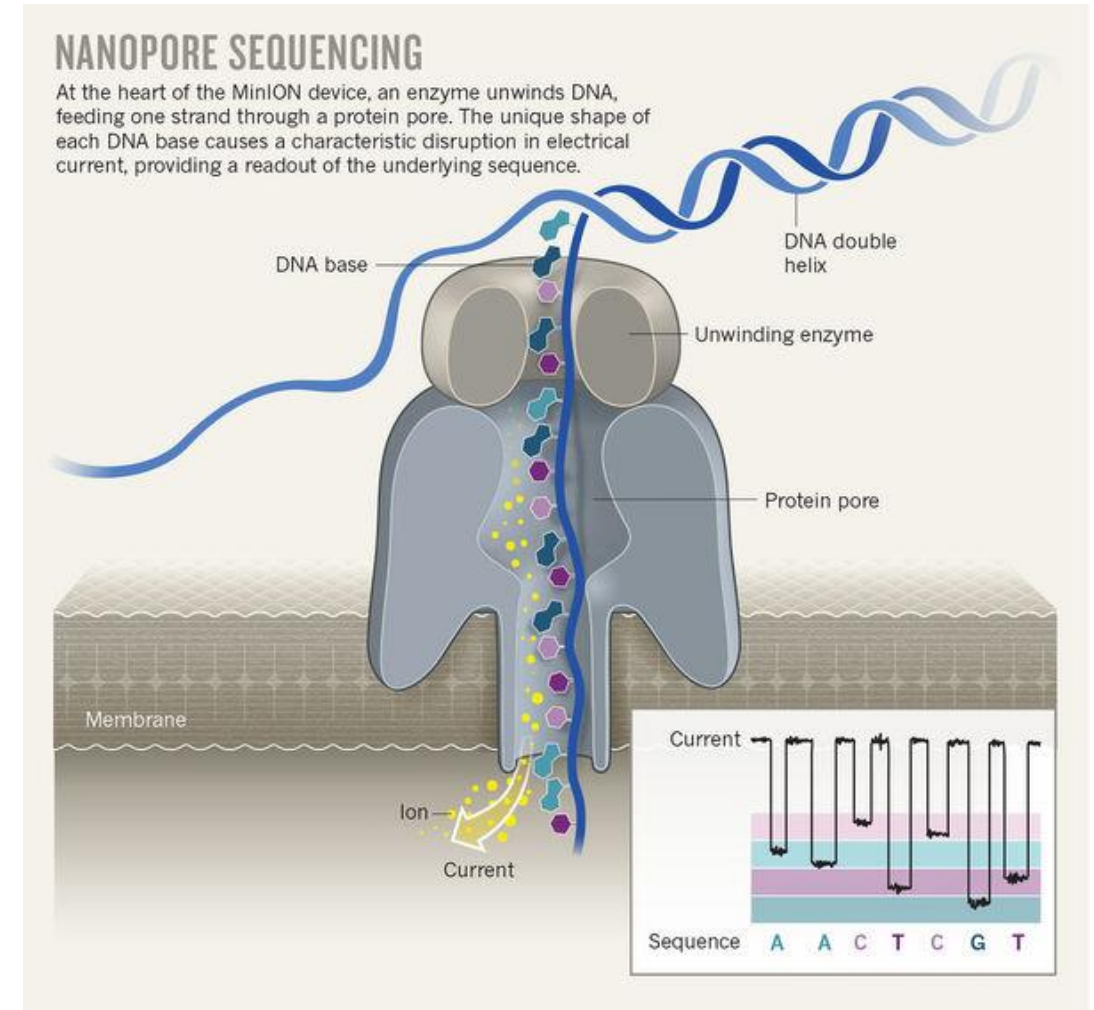
	PacBio: Single Molecule Real-Time Sequencing SMRT	Oxford Nanopore Technology: MinION
Ave. Read Length	>15,000 bp	>100,000 bp
Total Output	~500 Mb - 1 Gb	10–20 Gb
Cost Per Run	~£500	£1000
Hardware Cost	~£550,000	£1000
Observed Error Rate	~12%	~12%



MinION – Nanopore Sequencing Technology

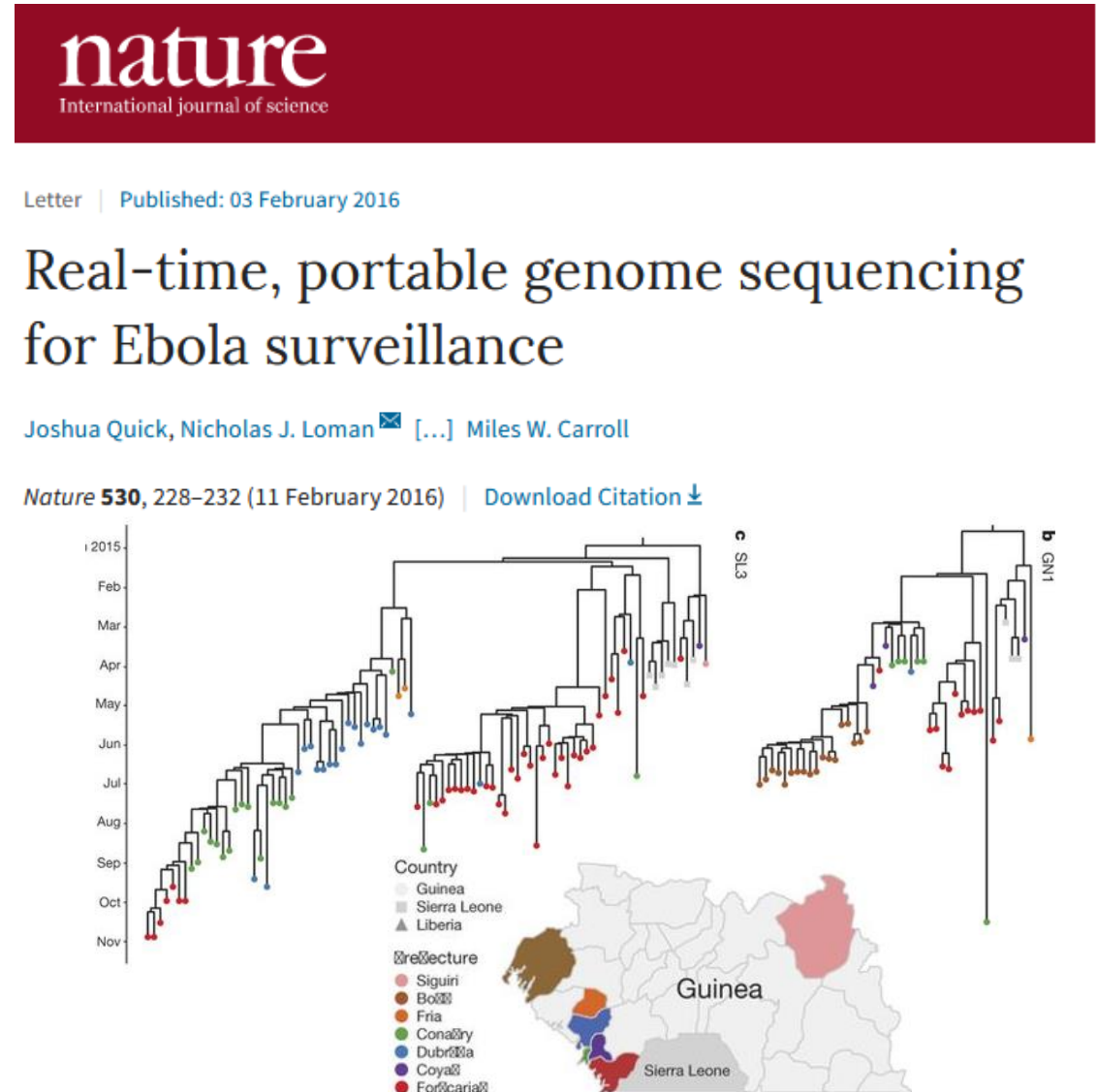
“Portable, real-time biological analyses”

- Very portable – can take to the field*
 - Produces long reads compared to NGS platforms
 - Can produce very high depth and coverage
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- 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

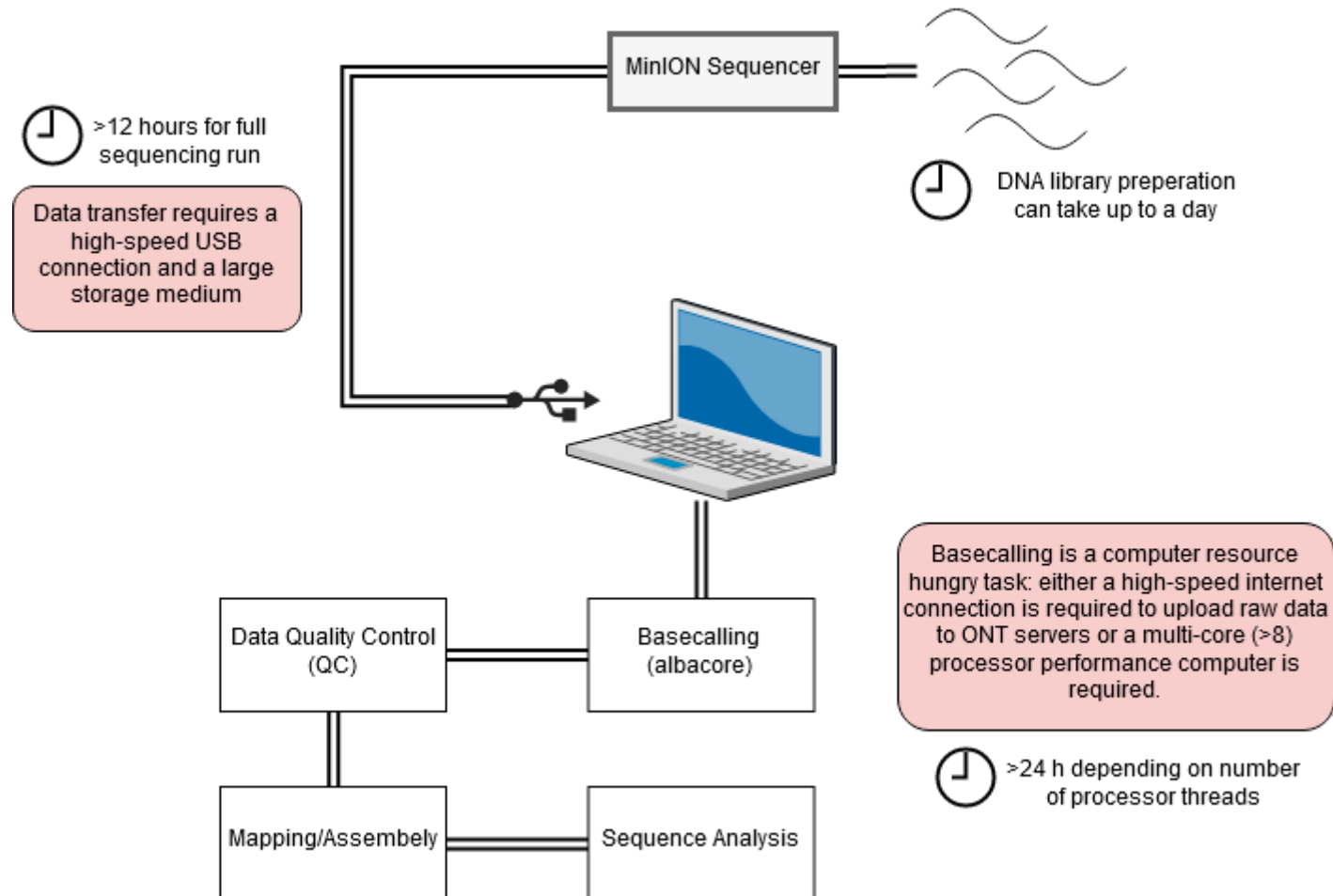


Real-Time Sequencing = Real-Time Surveillance

- 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.

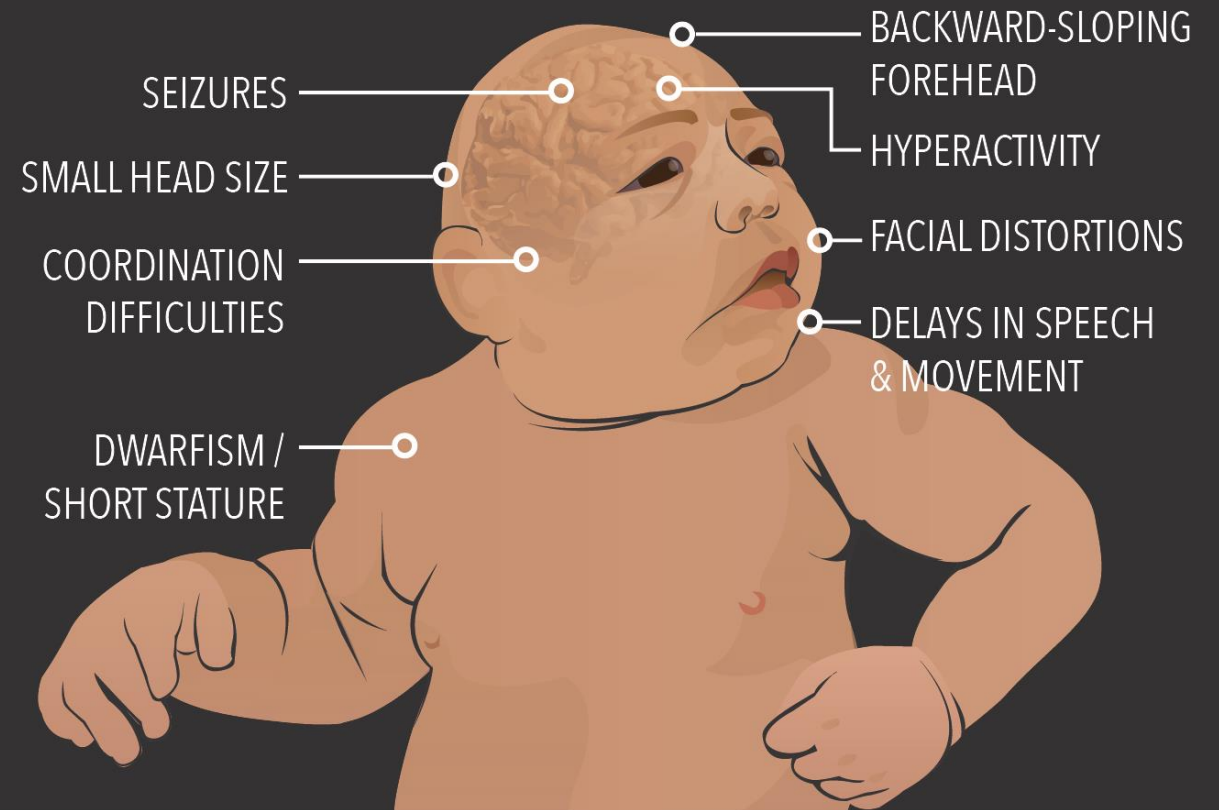


Sequencing Pipeline



- 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



Nanopore Sequencing Data Activity

