



# Towards Error Mitigation Applications for Oxford Nanopore Technologies

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# 3GS Tech Overview

Platform	PacBio RS	ONT MinION
Cost (\$ K)	695	MAP ( 1 + .270/run )
Size (in <sup>3</sup> / lbs)	176,000 / 1,895	12 / <2
Throughput (Gb)	0.5	0.05
Run time (hrs)	3-4	48-72
Read length (bp)	10K	8K
Observed error	~11% (single-pass)	>20%
Quality score	Q40	<Q10

**ONT MinION**

(++) portability

(+) cost

(+) direct interrogation

(--) high error rates/

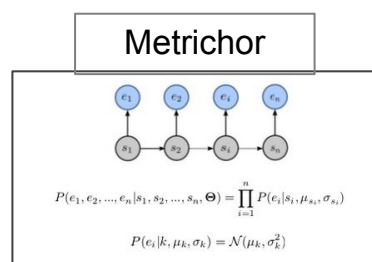
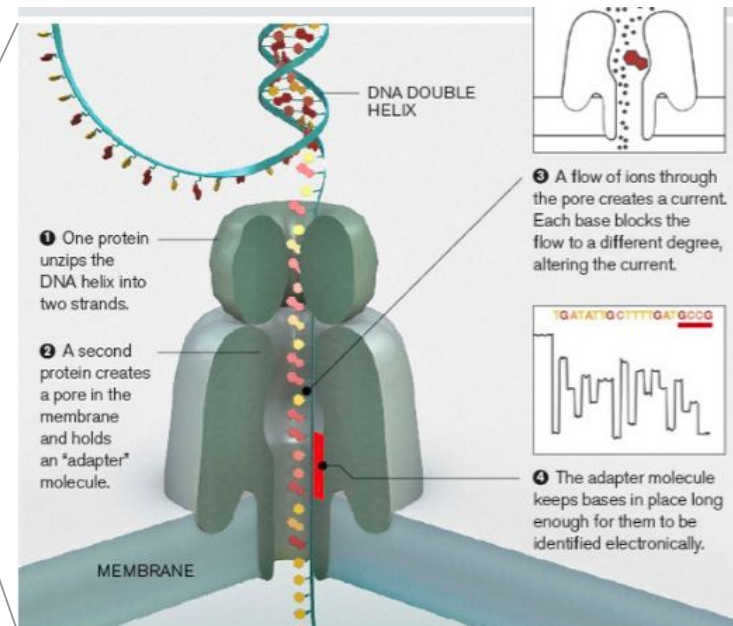
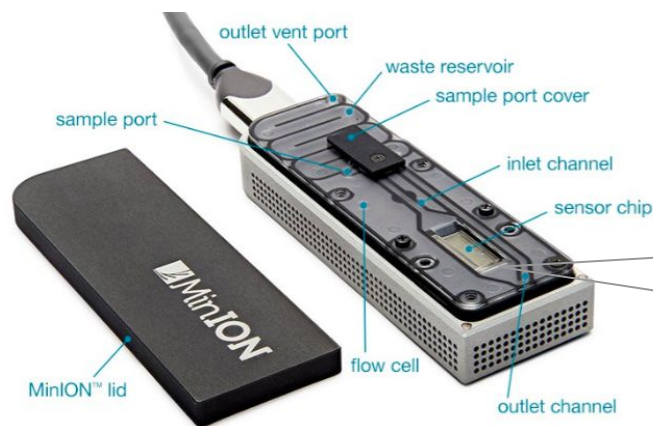
(--) size

**ONT-specific Applications**

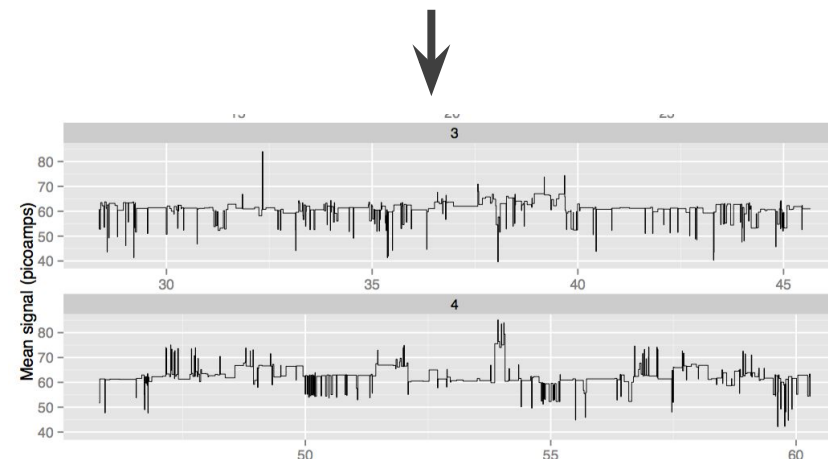
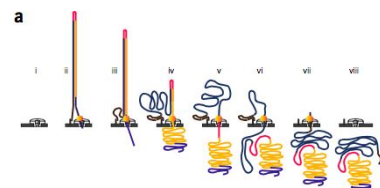
- Clinical microbiology
- Precision medicine
- In field *de novo* assembly
- Epigenomics
- Structural variation analysis

**PacBio**

# ONT Sequencing Mechanism



...CGATC



# Project Concept

## **Primary:**

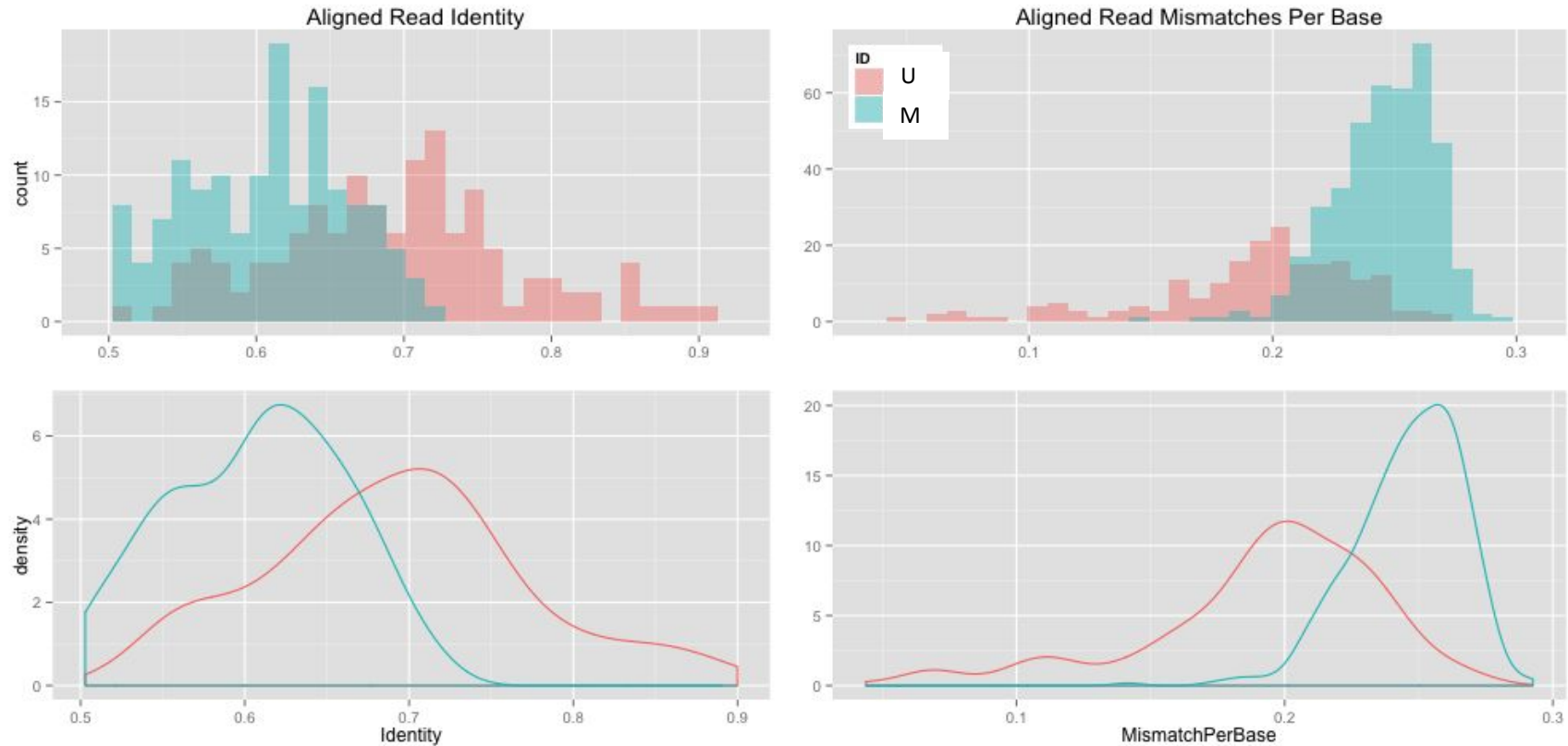
Use ONT to analyze modified DNA to determine feasibility of pre-sequencing modification of substrates for 'error mitigation'.

- (1) Do base modifications affect ONT read distributions?
- (2) Can modifications produce more easily distinguishable signal patterns?

## **Secondary:**

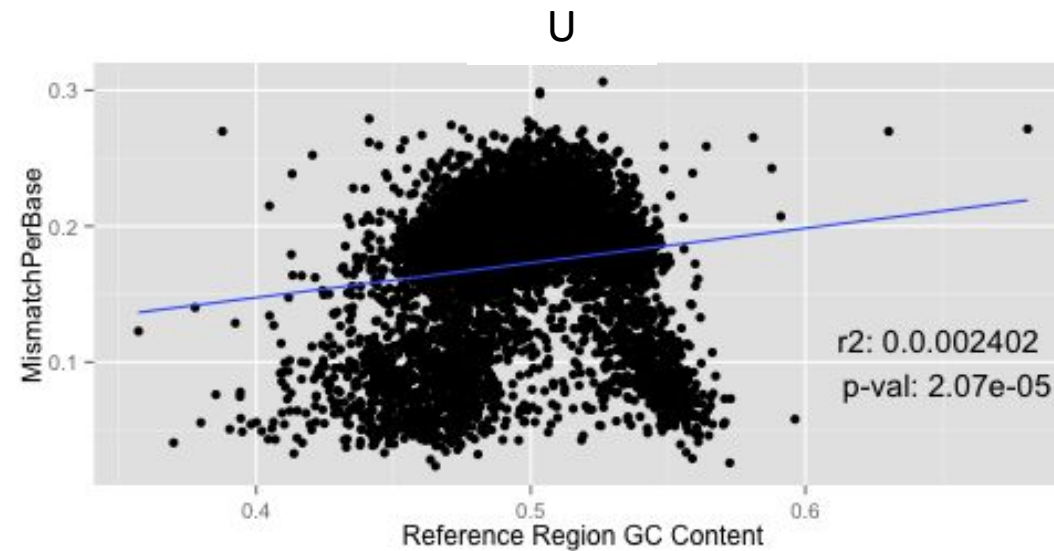
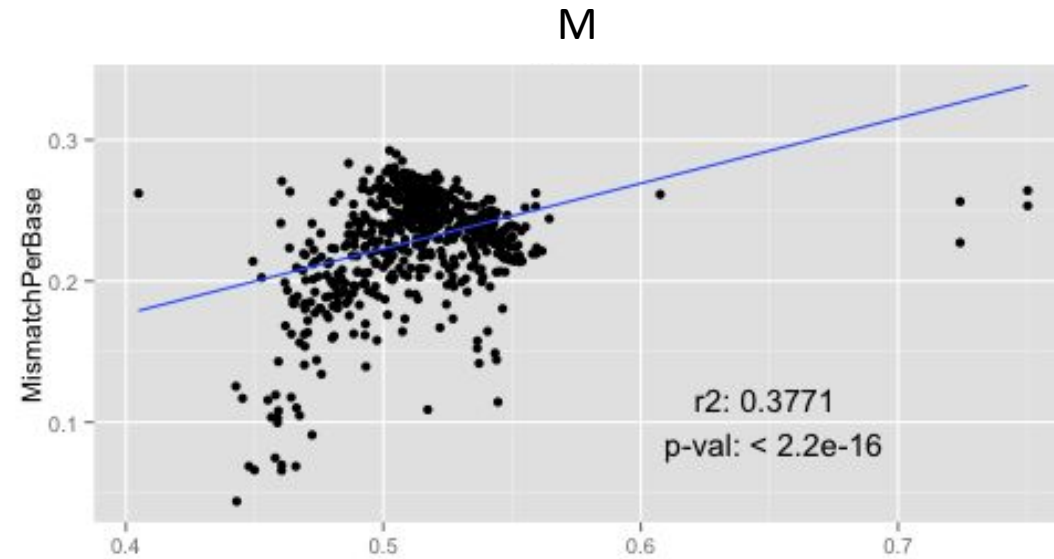
- Assess computational tools available for ONT data
- Build pipeline for future ONT data processing/ analysis

# M and U give different distributions



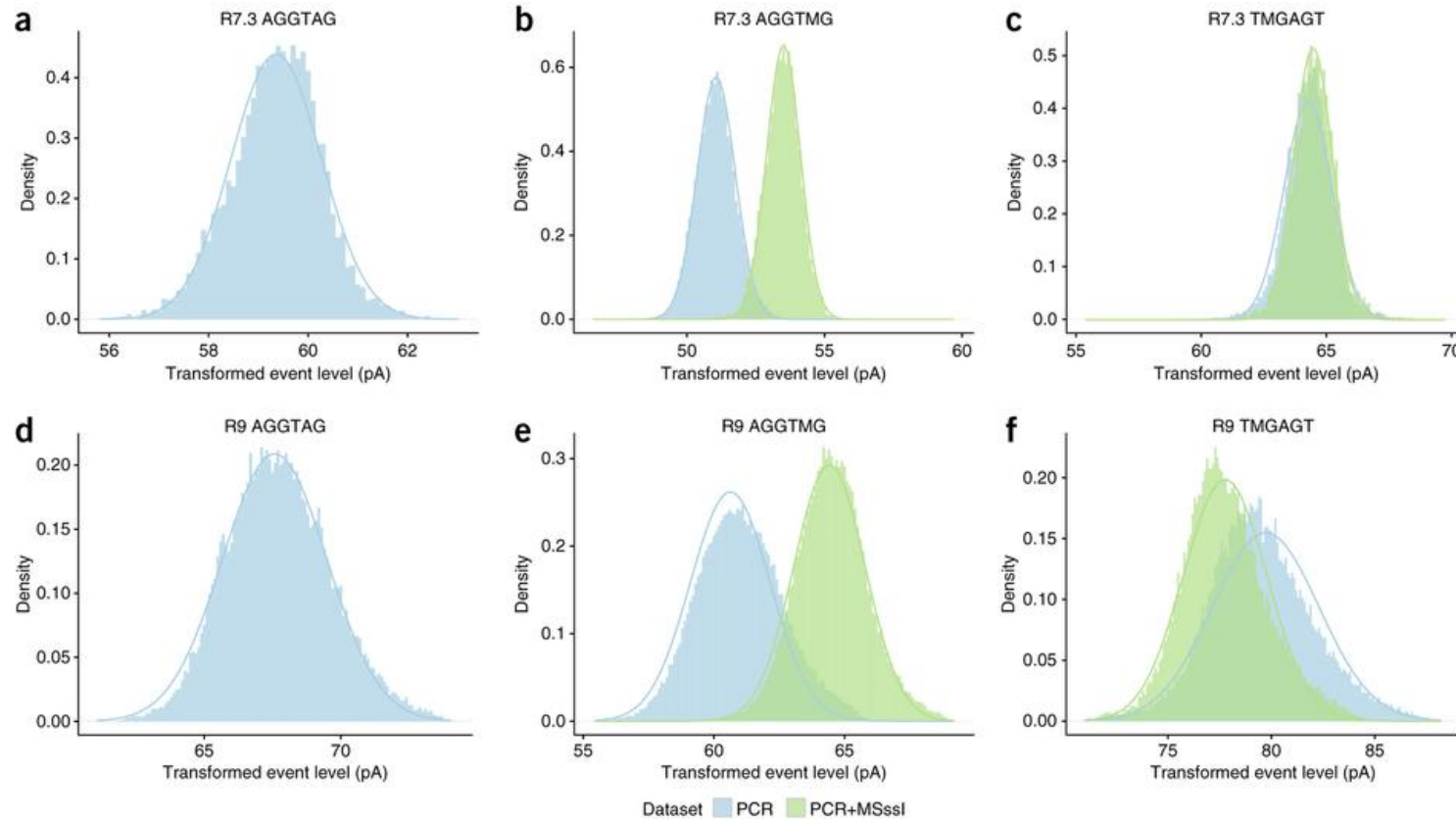
U	M	
55.6%	36.3%	Mean Identity
0.192	0.245	Mean MismatchPerBase

# M positively correlated with error



# More Recent Developments

Simpson JT, Workman RE, Zuzarte PC, David M, Dursi LJ, Timp W. 2017. **Detecting DNA cytosine methylation using nanopore sequencing.** *Nat Methods*, 14: 407–410. doi:10.1038/nmeth.4184.



# More Recent Developments

Rand AC, Jain M, Eizenga JM,  
Musselman-Brown A, Olsen HE,  
Akeson M, Paten B. 2017.

**Mapping DNA methylation with  
high-throughput nanopore  
sequencing.** *Nat Methods*, 14:  
407–410.

doi:10.1038/nmeth.4189.

