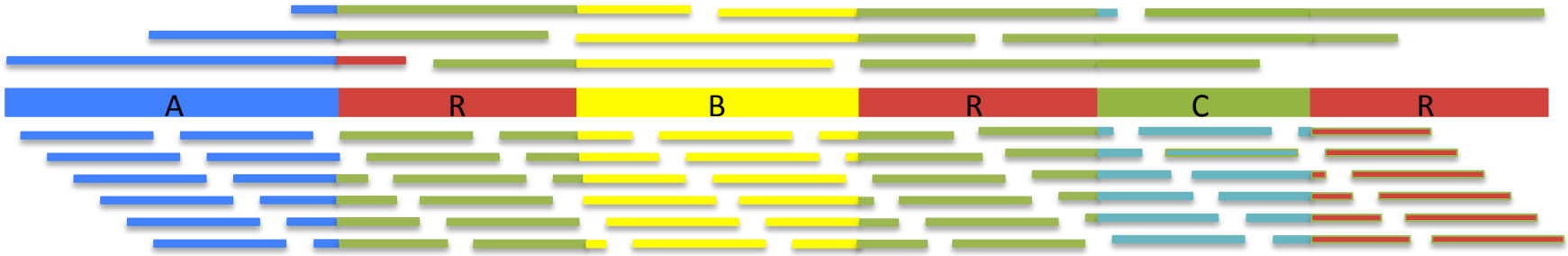
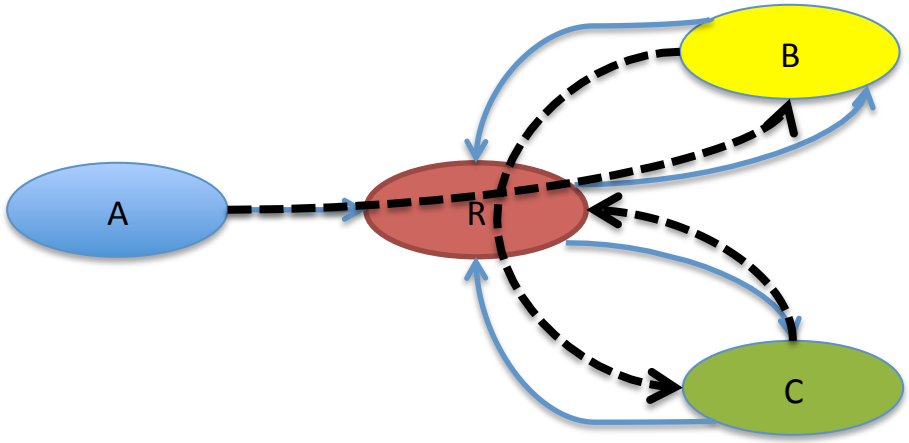
Error Correction and Assembly of Single Molecule Sequencing Data

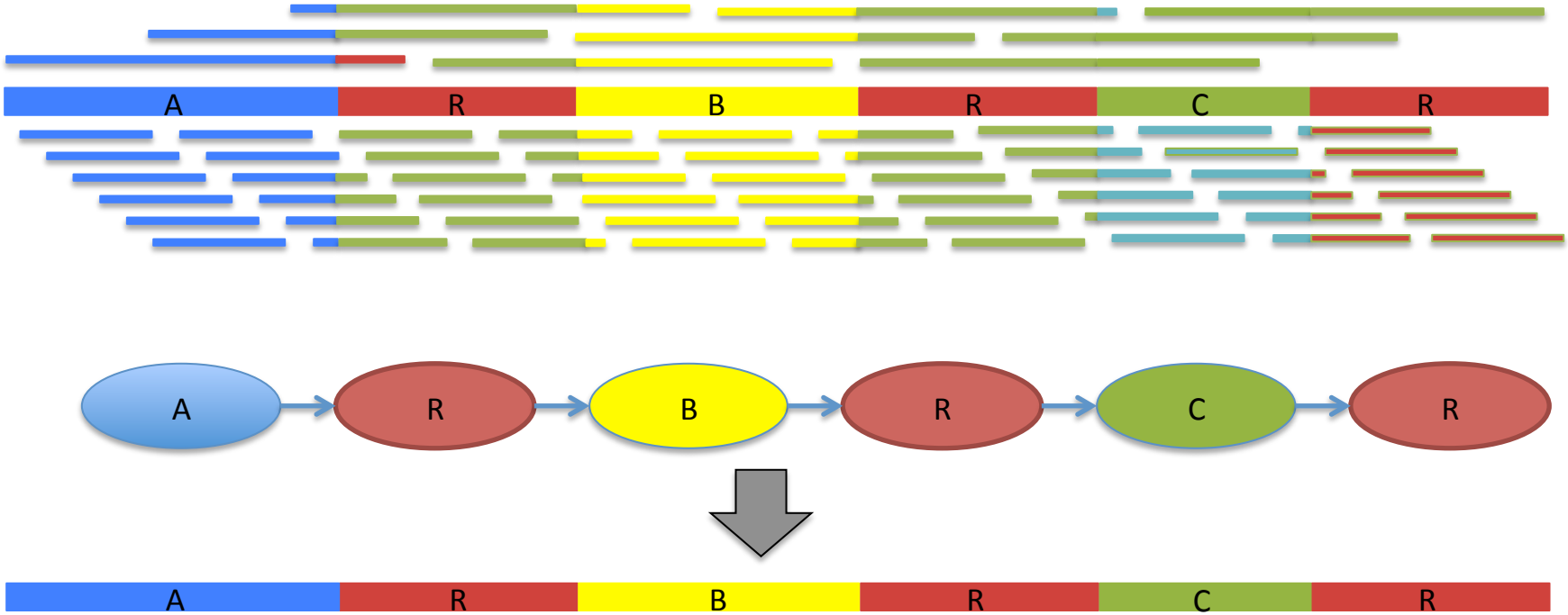
James Gurtowski

Assembly Complexity





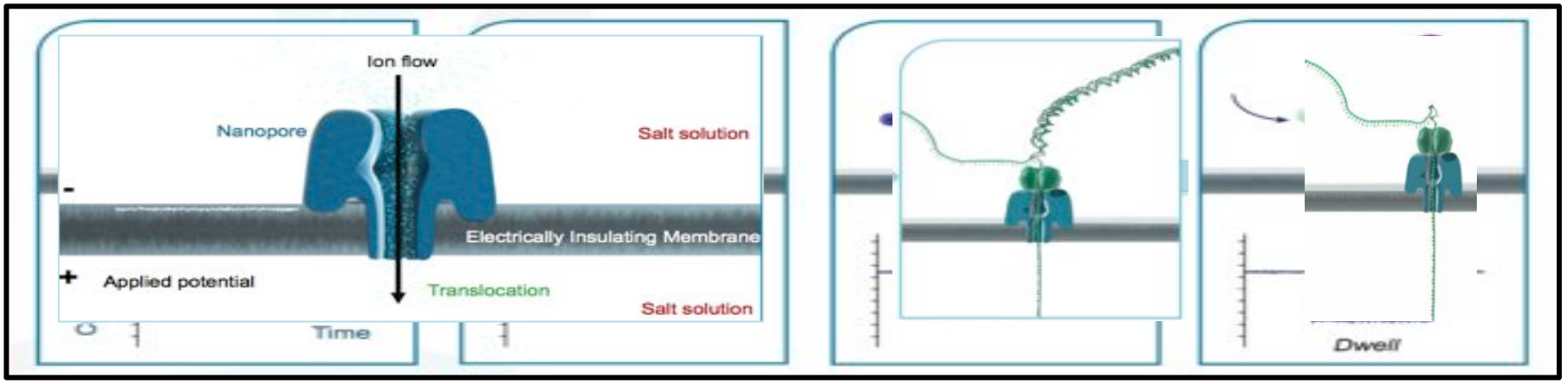
Assembly Complexity



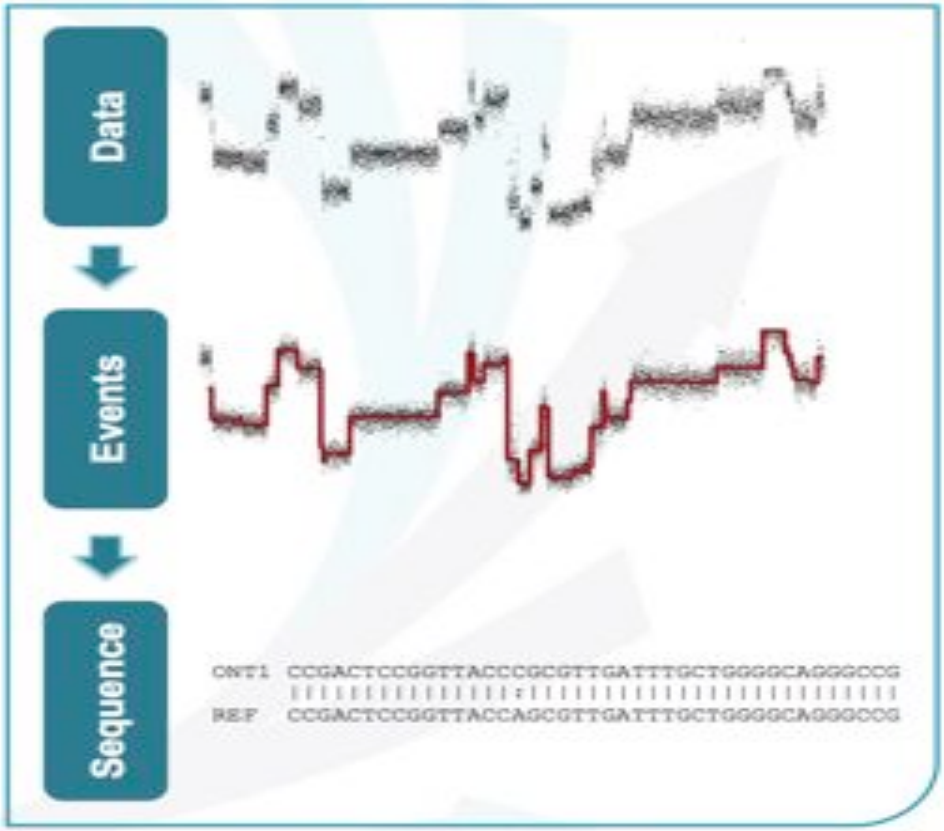
The advantages of SMRT sequencing
Roberts, RJ, Carneiro, MO, Schatz, MC (2013) *Genome Biology*. 14:405

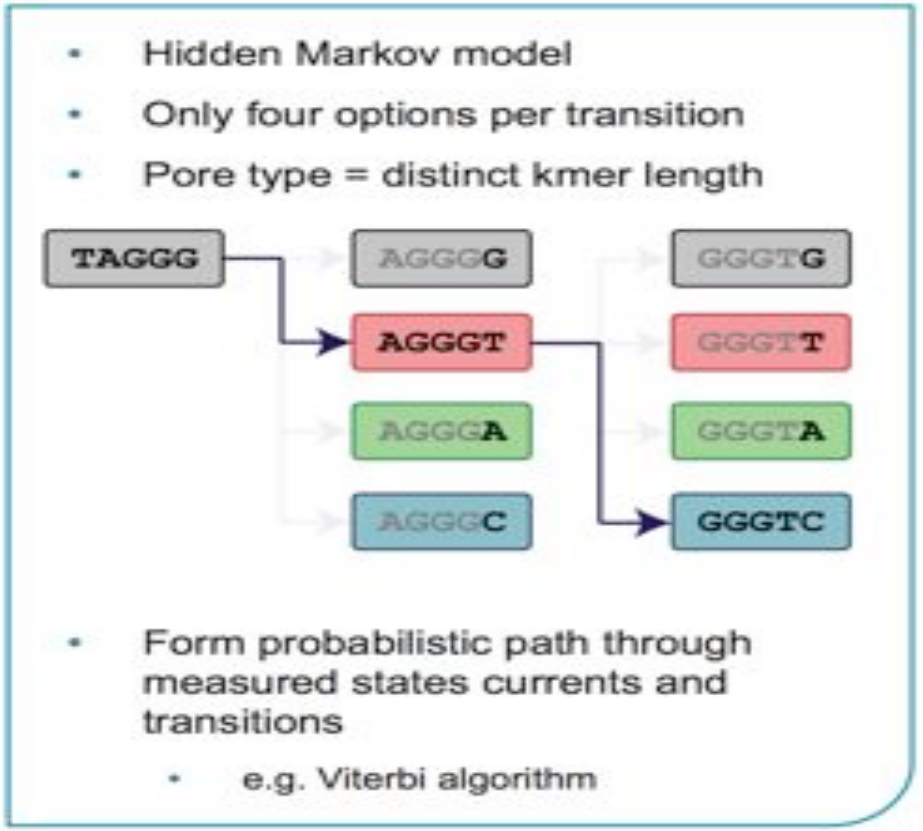
Oxford Nanopore MinION

- Thumb drive sized sequencer powered over USB
- Senses DNA by measuring changes to ion flow
- Reads both DNA Strands (2D)



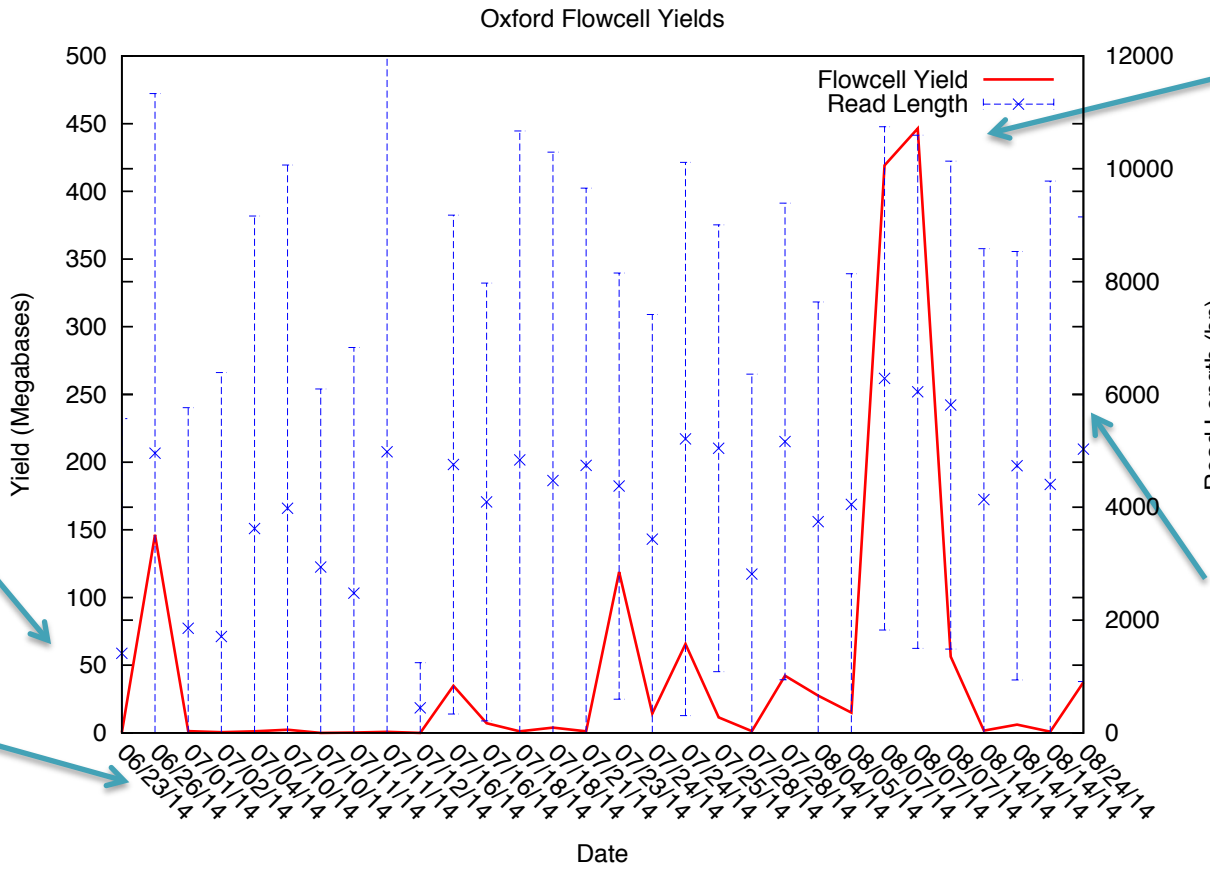
Nanopore Basecalling





Basecalling currently performed at Amazon with frequent updates to algorithm

Our Data - Yeast W303



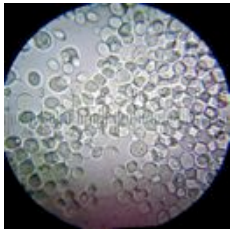
Best: 446Mb

Mean: 50Mb

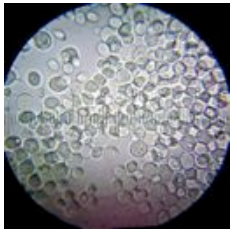
Mean Read Length: ~6kb (10kb shear)

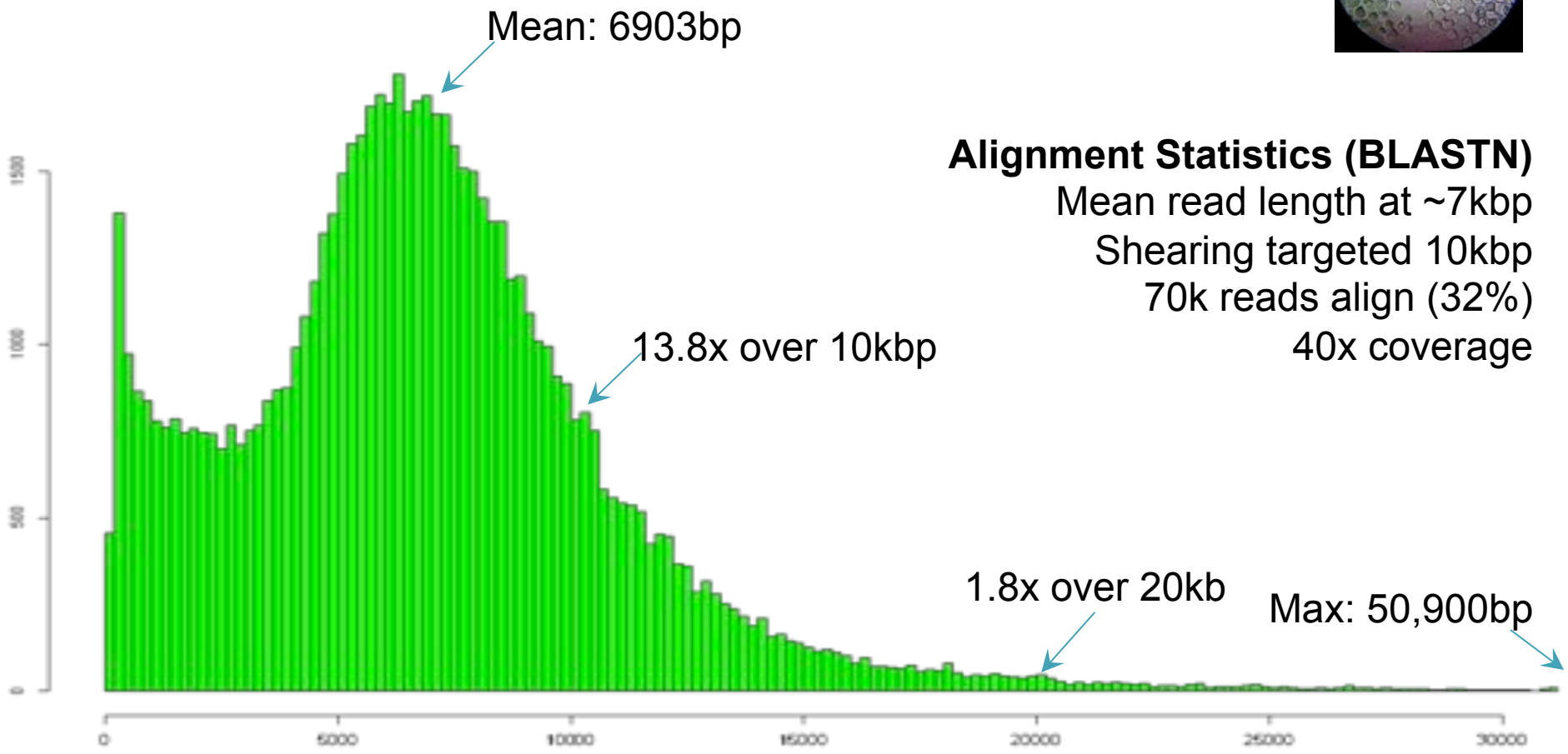
30 Flowcells

Nanopore Readlengths



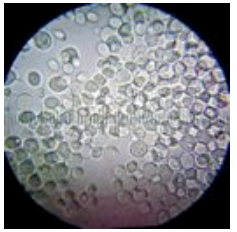
Nanopore Alignments



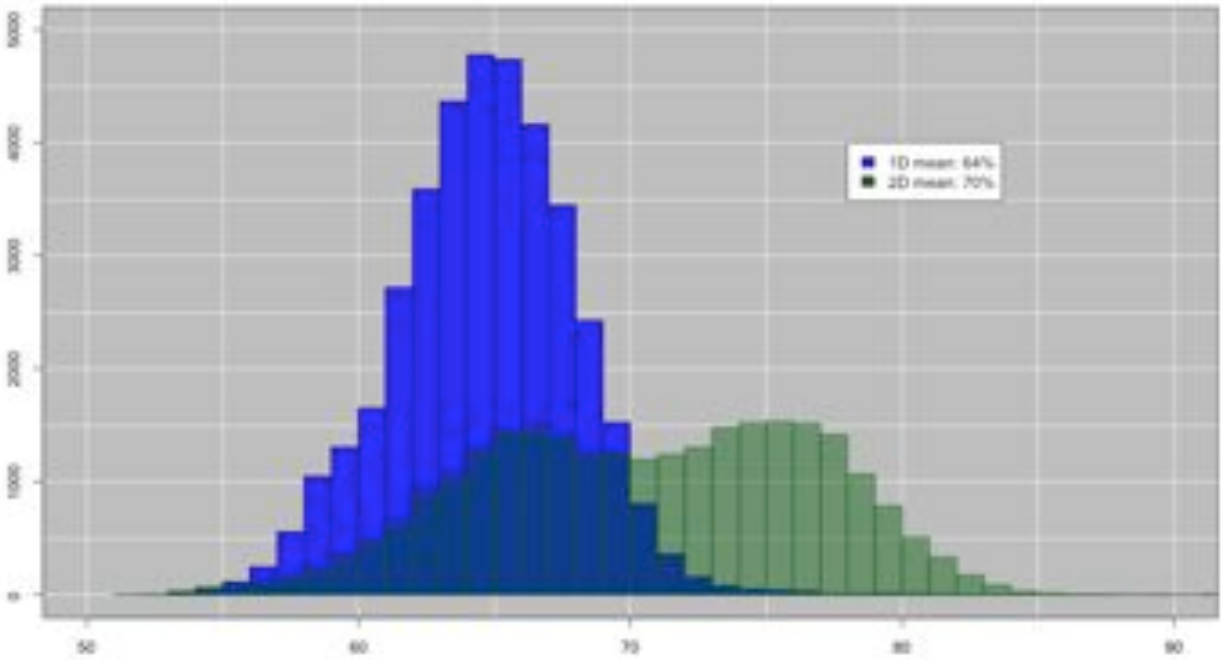


Alignment Statistics (BLASTN)
Mean read length at ~7kbp
Shearing targeted 10kbp
70k reads align (32%)
40x coverage

Nanopore Accuracy



Alignment Quality (BLASTN)
Of reads that align, average ~64% identity
“2D base-calling” improves to ~70% identity

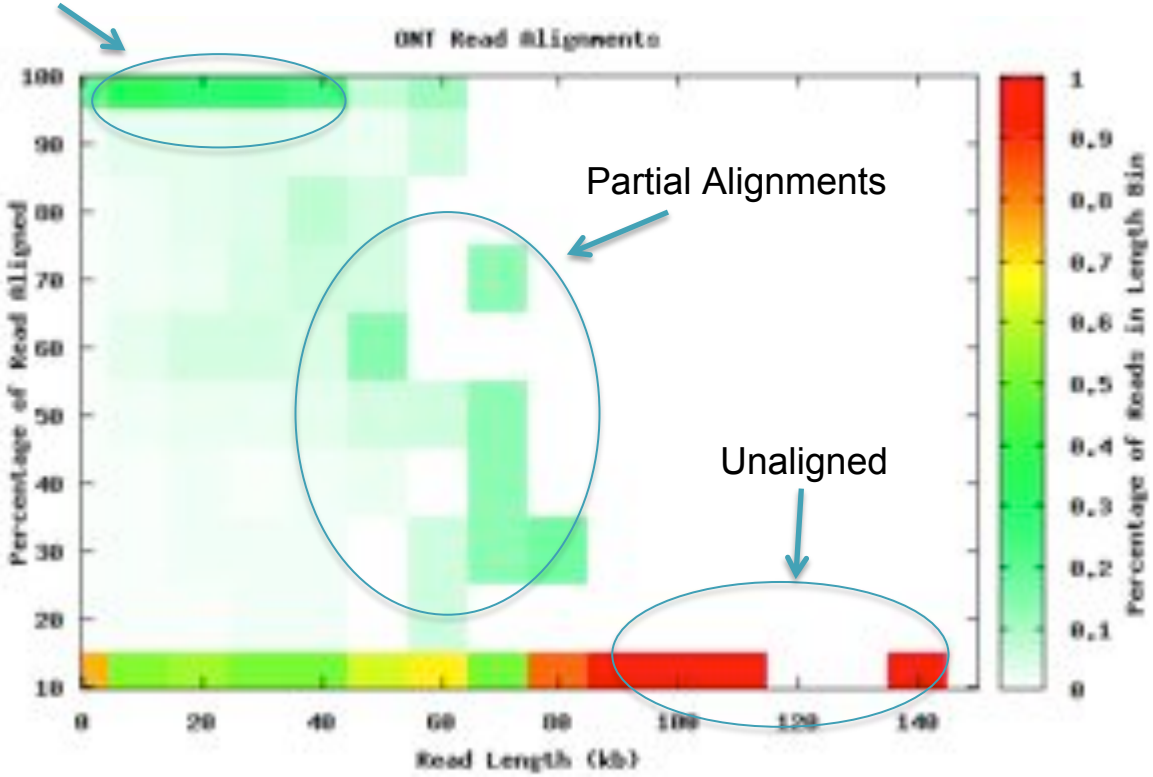


57% Mismatches
32% Deletions
11% Insertions

Nanopore Alignment Summary

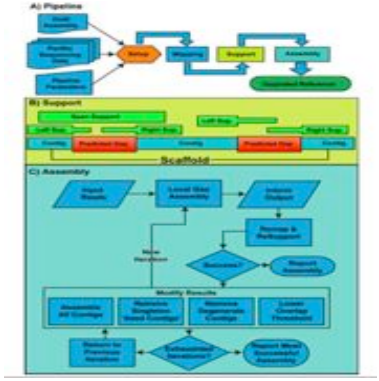
32% of the data map using BLASTN

Full Length Alignments



Long Read Correction Algorithms

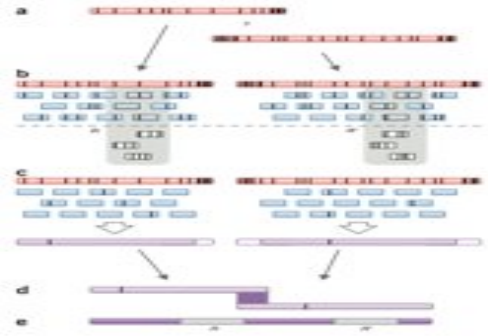
PBJelly



Gap Filling and Assembly Upgrade

English *et al* (2012)
PLOS One. 7(11): e47768

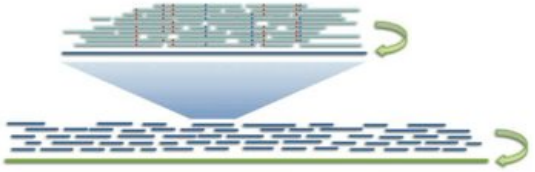
PacBioToCA & ECTools



Hybrid Error Correction

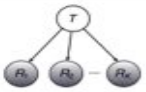
Koren, Schatz, *et al* (2012)
Nature Biotechnology. 30:693–700

HGAP & Quiver



$$\Pr(\mathbf{R} \mid T)$$

$$\Pr(\mathbf{R} \mid T) = \prod_k \Pr(R_k \mid T)$$



Quiver Performance Results
Comparison to Reference Genome
(M. ruber ; 3.1 MB ; SMRT® Cells)

	Initial Assembly	Quiver Consensus
QV	43.4	54.5
Accuracy	99.99540%	99.99964%
Differences	141	11

LR-only Correction & Polishing

Chin *et al* (2013)
Nature Methods. 10:563–569

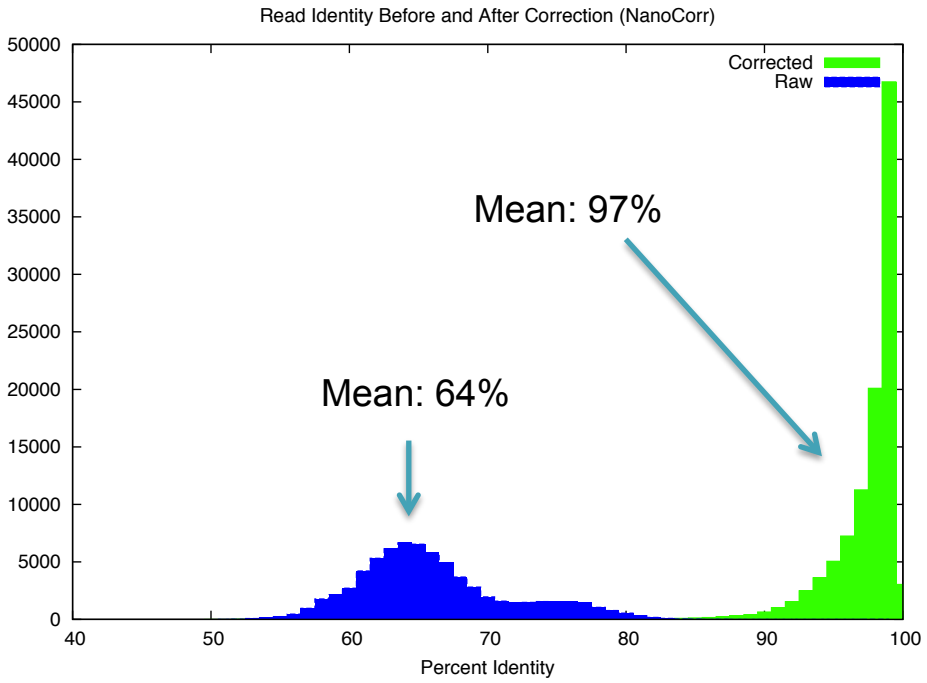
< 5x Long Read Coverage > 50x

NanoCorr: Nanopore-Illumina Hybrid Error Correction

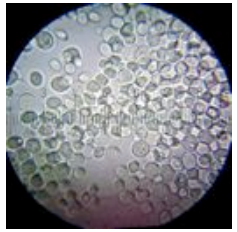
1. BLAST Miseq reads to all raw Oxford Nanopore reads

2. Select non-repetitive alignments
   - First pass scans to remove “contained” alignments
   - Second pass uses Dynamic Programming (LIS) to select set of high-identity alignments with minimal overlaps

3. Compute consensus of each Oxford Nanopore read
   - Currently using Pacbio’s pbdagcon



Long Read Assembly



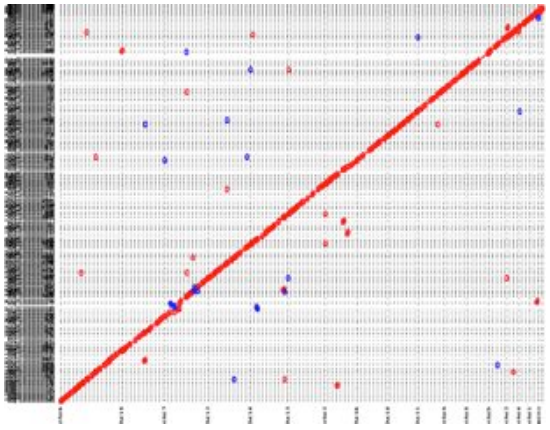
S288C Reference sequence

- 12.1Mbp; 16 chromo + mitochondria; N50: 924kbp

Illumina MiSeq

30x, 300bp PE (Flashed)
Celera Assembler

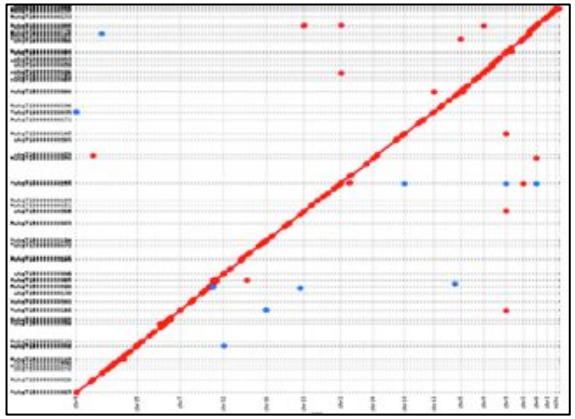
- 6953 non-redundant contigs
- N50: 59kb >99.9% id



Oxford Nanopore

30x corrected reads > 6kb
NanoCorr + Celera Assembler

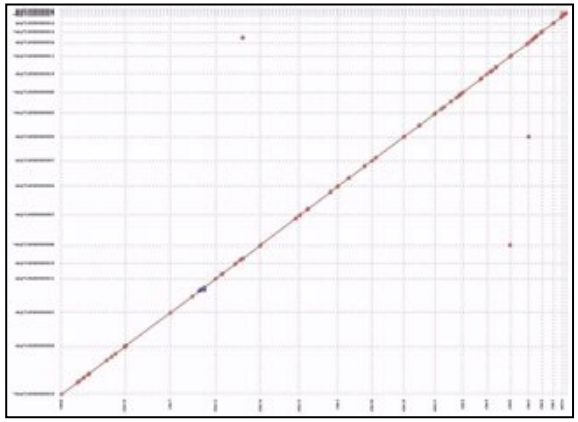
- 234 non-redundant contigs
- N50: 362kbp >99.78% id



Pacific Biosciences

25x corrected reads > 10kb
HGAP + Celera Assembler

- 21 non-redundant contigs
- N50: 811kb >99.8% id



Acknowledgements

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Schatz Lab