

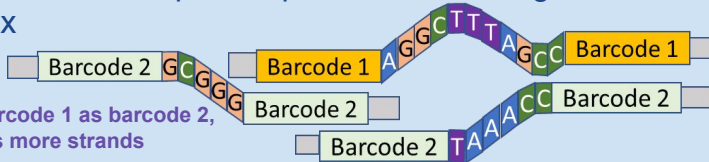
Real-Time Adaptive Sequencing of HIV DNA using the Nanopore

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1. Problem

HIV sequencing is complicated by inconsistent strand lengths, which are sequenced at unequal frequencies interfering with the ability to multiplex



Same # of bases with barcode 1 as barcode 2,
but barcode 2 has more strands

Objective - Create a software that improves multiplexing abilities by correcting the base pair per barcode ratio:

$$\frac{\# \text{ of Bases}}{\text{Barcode}} = \frac{1}{\# \text{ of Barcodes}}$$

2. Solution

Approach - Evenize the base pair counts of each barcoded strand in order to save both time and information

$N = \#$ of Unique barcodes

$BP_{1:N} =$ # of Base Pairs associated with Barcodes 1:N	$Total \ BP \ Read =$ $\Sigma(\# \text{ of Base Pairs associated with Barcodes } 1:N)_{1:N}$
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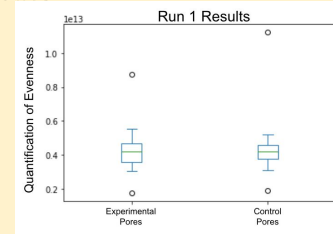
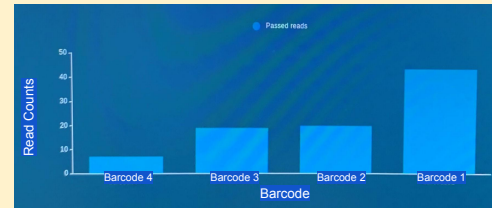
After Every 2 minutes:

Recalculate $BP_{1:N}$	Recalculate Total BP Read	Calculate: $\frac{BP_N}{Total \ BP \ Read}$
If: $\frac{BP_N}{Total \ BP \ Read} \geq \frac{1}{N}$	$\frac{1}{N}$	Eject all strands of Barcode N
Else: $\frac{BP_N}{Total \ BP \ Read} < \frac{1}{N}$	$\frac{1}{N}$	Accept all strands of Barcode N

3. Testing/Results

Testing - Quantify evenness of base pairs per barcode. Compare between experimental and controlled pores.

$$Score = \frac{\Sigma[(\# \text{ of bases} - \text{average \# of bases per barcode})^2]}{\# \text{ of barcodes}}$$



4. Conclusions and Impact

This program will **better sample** DNA strands in a **time-efficient** manner to **reduce waste** caused by oversampled and undersampled sequences.

The time and money saved can be reinvested into research.

This expedites the progress to a cure for HIV/AIDS.