RNA-Seq Module 1 Indexing

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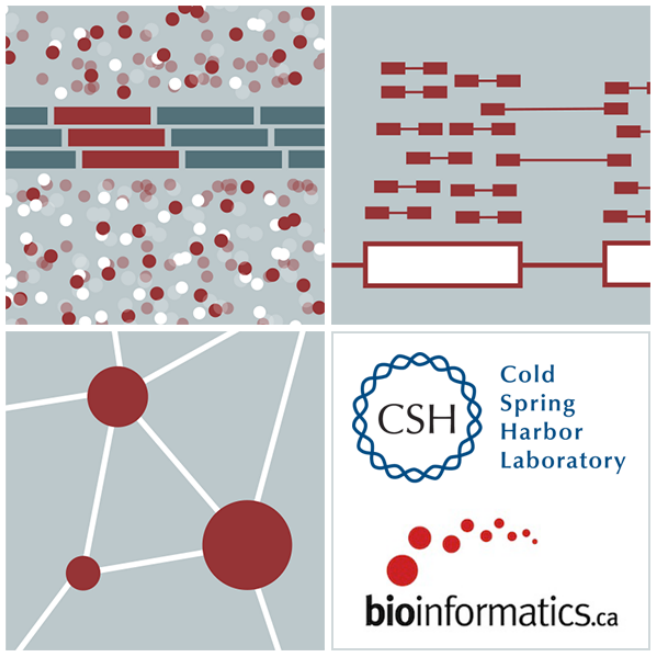

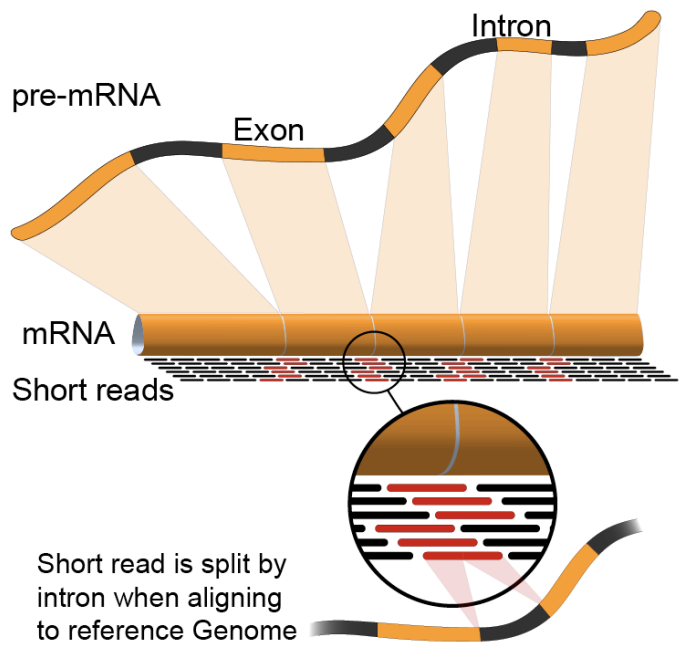

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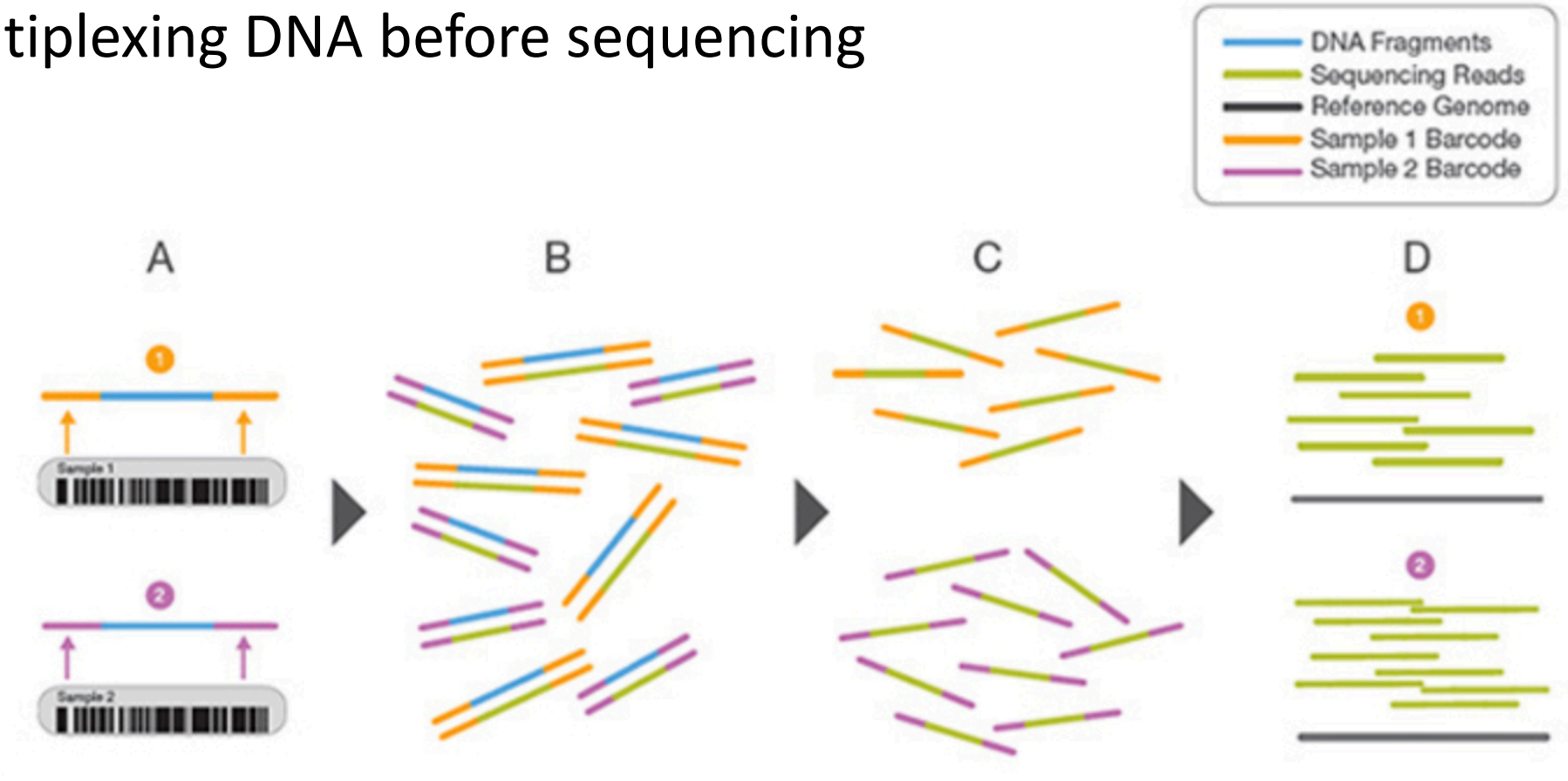
“Index” has many different meanings

- Indexes can refer to unique barcodes used for multiplexing DNA before sequencing



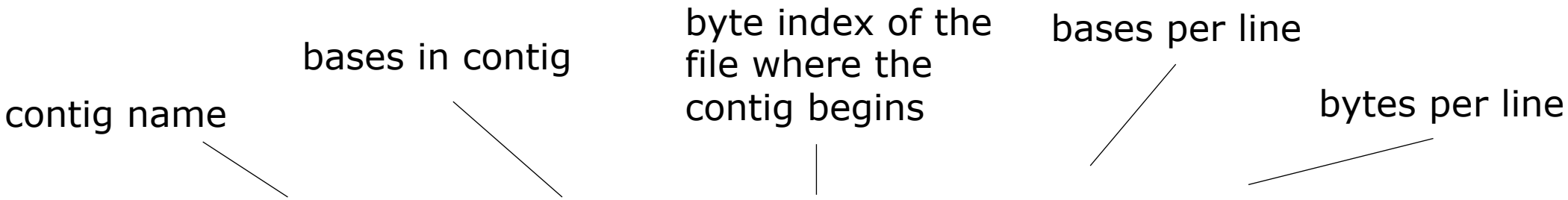
https://www.illumina.com/science/technology/next-generation-sequencing/multiplex-sequencing.html

Indexing in bioinformatics/CS enables rapid access

- Indexing is a recurring theme in genome analysis
- Files are *big* - scanning through them can take a long time
- Indexing builds a table-of-contents so that we can jump directly to specific positions

- Indexing may require significant compute/time but typically only occurs once
- Each application may require a different indexing strategy

What's inside a fasta's index file? (.fai)

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chr1    248956422   6            60   61
chr2    242193529   253105708    60   61
chr3    198295559   499335802    60   61
chr4    190214555   700936293    60   61
chr5    181538259   894321097    60   61
chr6    170805979   1078885000   60   61
chr7    159345973   1252537752   60   61
chr8    145138636   1414539498   60   61
chr9    138394717   1562097118   60   61
chr10   133797422   1702798421   60   61
```

Example index applications and associated files

Source file	Indexed file	Indexing tool	Use case
.bam	.bai	samtools index	Visualize bam in IGV
.fasta	.fai	faidx	Extract specific sequences from ref genome
.vcf	vcf.gz.tbi	bgzip/tabix	Pull out specific variants
.bed	.bed.gz.tbi	bgzip/tabix	extract specific genomic regions

Indexing is also essential for alignment

- Finding out where to place a read in the genome is impractical unless matches can be quickly found
- All read aligners use some kind of indexing
- These indices must be “built” once for a reference genome, but can then be used every time the aligner is run
- Different aligners use different indexing schemes that are not compatible

We are on a Coffee Break & Networking Session