

Canadian Bioinformatics Workshops

www.bioinformatics.ca

bioinformaticsdotca.github.io

Supported by



This page is available in the following languages:

Afrikaans Ελληνικά Català Dansk Deutsch Ελληνικά English English (CA) English (GB) English (US) Esperanto
 Castellano Castellano (AR) Español (CL) Castellano (CO) Español (Ecuador) Castellano (MX) Castellano (PE)
 Euskara Suomi français français (CA) Galego עברית hrvatski Magyar Italiano 日本語 한국어 Macedonian Melayu
 Nederlands Norsk Sesotho sa Leboa polski Português română slovenski jezik срpski (latinica) Sotho svenska
 中文 華語 (台灣) isiZulu



Attribution-Share Alike 2.5 Canada

You are free:



to **Share** — to copy, distribute and transmit the work



to **Remix** — to adapt the work



Under the following conditions:



Attribution. You must attribute the work in the manner specified by the author or licensor (but not in any way that suggests that they endorse you or your use of the work).



Share Alike. If you alter, transform, or build upon this work, you may distribute the resulting work only under the same or similar licence to this one.

- For any reuse or distribution, you must make clear to others the licence terms of this work.
- Any of the above conditions can be waived if you get permission from the copyright holder.
- The author's moral rights are retained in this licence.

[Disclaimer](#)

Your fair dealing and other rights are in no way affected by the above.
 This is a human-readable summary of the Legal Code (the full licence) available in the following languages:
[English](#) [French](#)

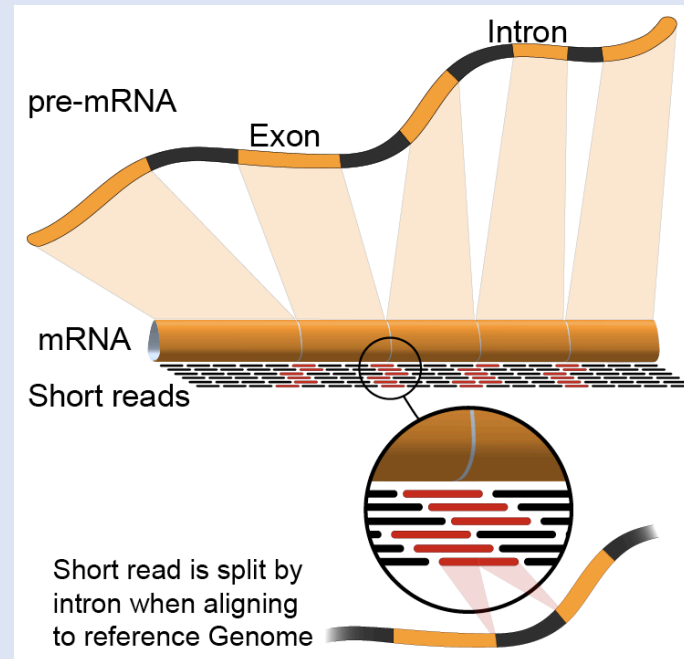
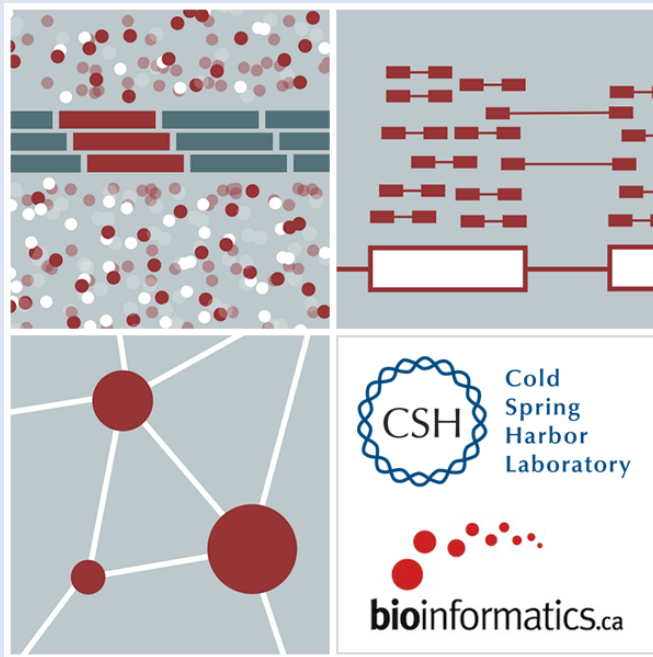
[Learn how to distribute your work using this licence](#)

Alignment

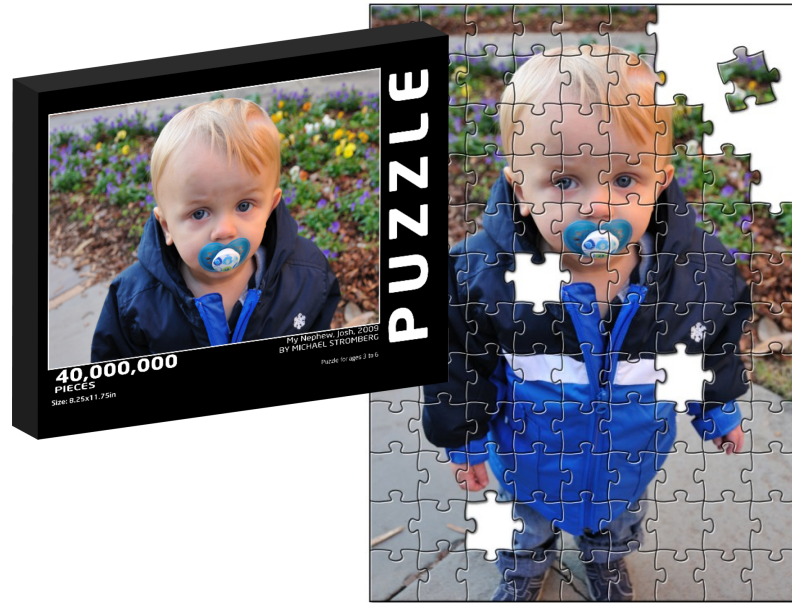
Emma Bell, Felicia Gomez, Obi Griffith, Malachi Griffith, Huiming Xia

RNA-Seq Analysis

Sep 8th-10th, 2021



Alignment - How does it work?



- Alignment is about fitting individual pieces (reads) into the correct part of the puzzle
- The human genome project gave us the picture on the box cover (the reference genome)
- Imperfections in how the pieces fit can indicate changes to a copy of the picture

Reference: AGCCTGAGACCGTAAAAAA**A**GTCAAG

|||||

A read sequence:

GAGACCGTAAAAAA**C**GTC

↑
A variant!

RNA-seq alignment challenges

- Computational cost
 - 100's of millions of reads
- Introns!
 - Spliced vs. unspliced alignments
- Can I just align my data once using one approach and be done with it?
 - Unfortunately probably not

Three RNA-seq mapping strategies

De novo assembly

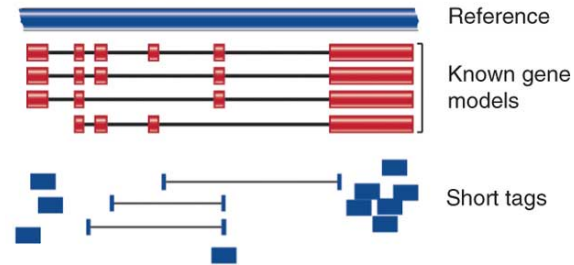


Assemble transcripts from overlapping tags



Optional: align to genome to get exon structure

Align to transcriptome



Use known and/or predicted gene models to examine individual features

Align to reference genome



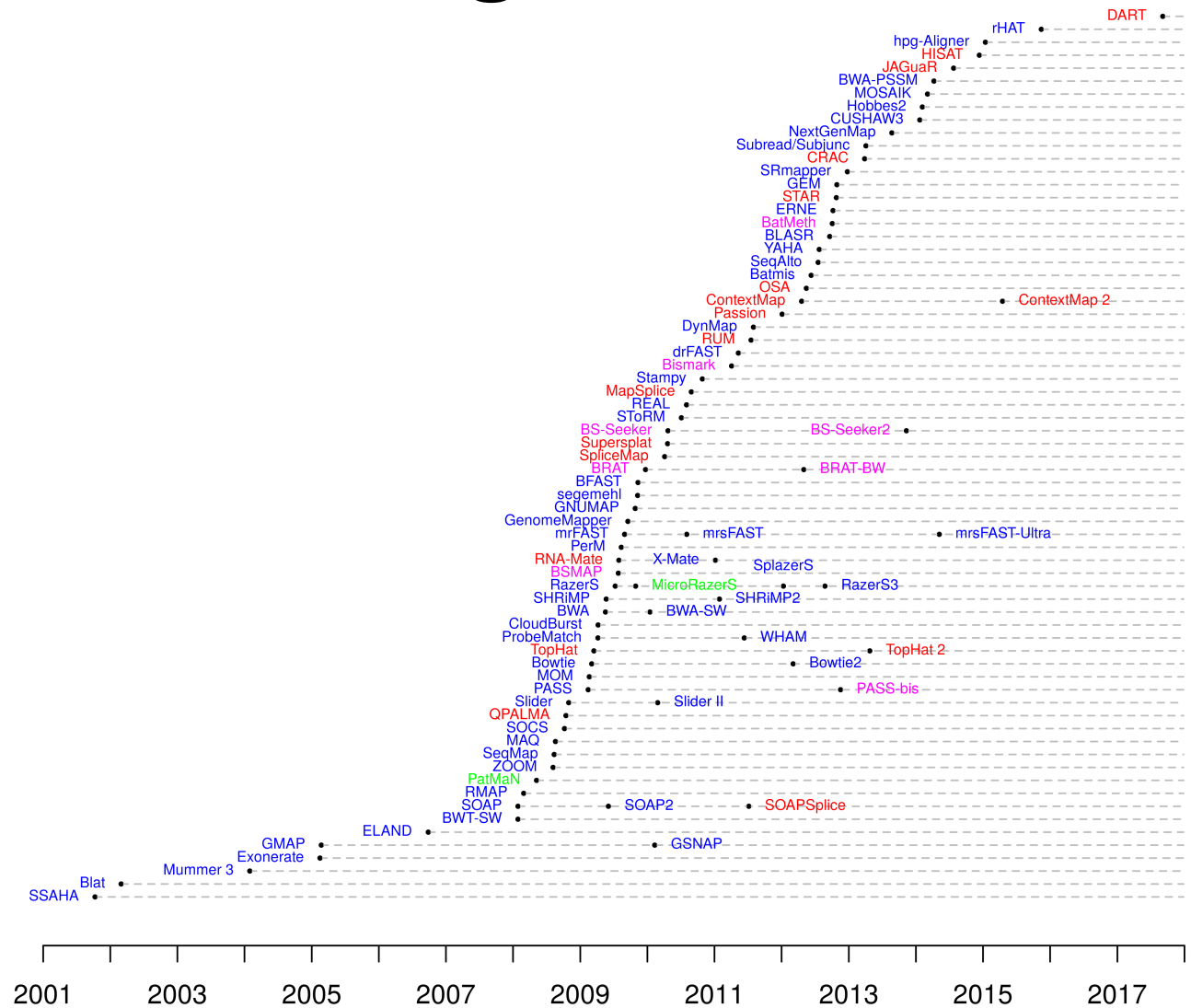
Infer possible transcripts and abundance

Diagrams from Cloonan & Grimmond, Nature Methods 2010

Which alignment strategy is best?

- De novo assembly
 - If a reference genome does not exist for the species being studied
 - If complex polymorphisms/mutations/haplotypes might be missed by comparing to the reference genome
- Align to transcriptome
 - If you have short reads (< 50bp)
- Align to reference genome
 - All other cases
- Each strategy involves different alignment/assembly tools

Which read aligner should I use?



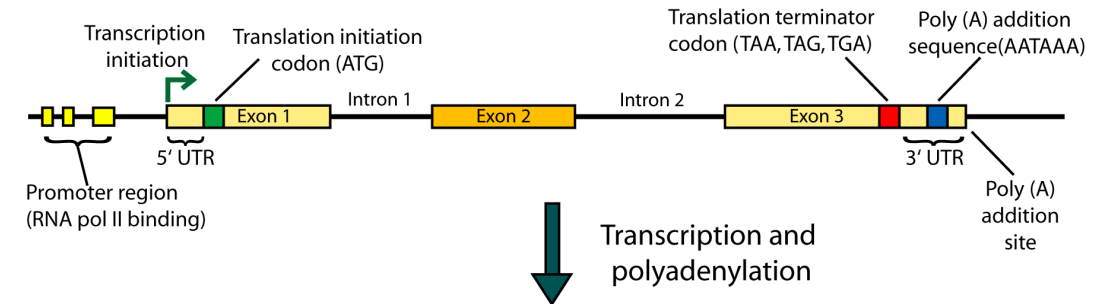
RNA
Bisulfite
DNA
microRNA

http://wwwdev.ebi.ac.uk/fg/hts_mappers/

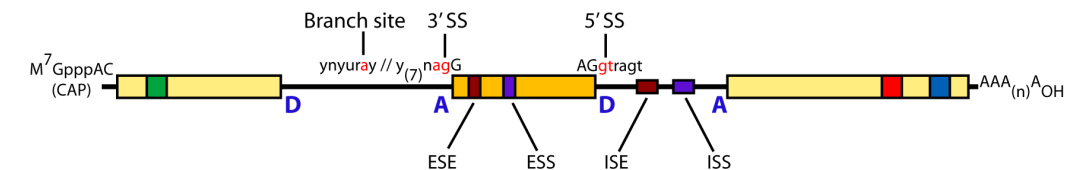
Should I use a splice-aware or unspliced mapper?

- RNA-seq reads may span large introns
- The fragments being sequenced in RNA-seq represent mRNA - introns are removed
- But we are usually aligning these reads back to the reference genome
- Unless your reads are short (<50bp) you should use a splice-aware aligner
 - HISAT2, STAR, MapSplice, etc.

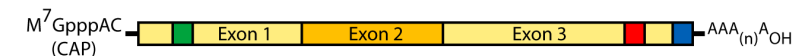
Double-stranded genomic DNA template



Single-stranded pre-mRNA (nuclear RNA)



Mature mRNA



HISAT/HISAT2

- HISAT is a 'splice-aware' RNA-seq read aligner
- Requires a reference genome
- Very fast

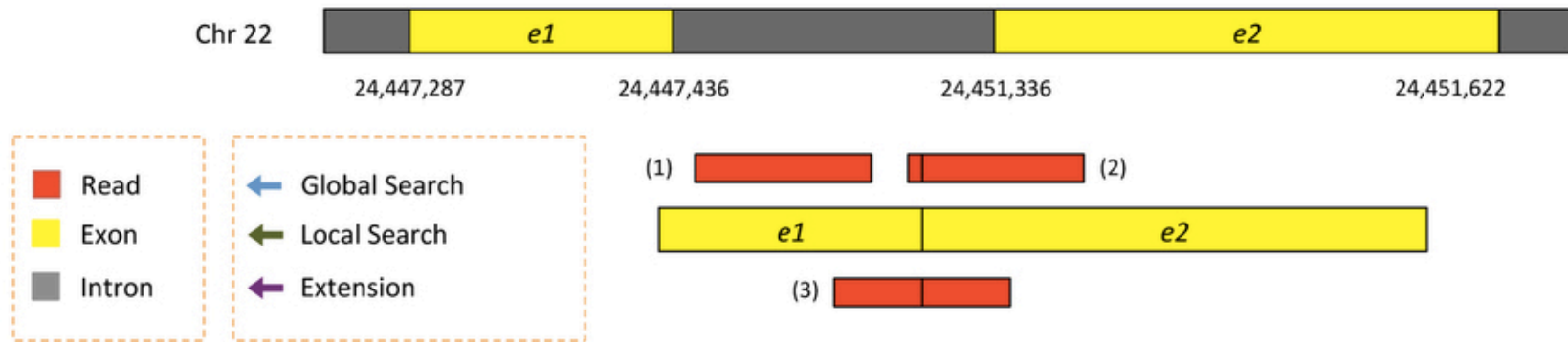
- Uses an indexing scheme based on the Burrows-Wheeler transform and the Ferragina-Manzini (FM) index
- Multiple types of indexes for alignment
 - a whole-genome FM index to anchor each alignment
 - numerous local FM indexes for very rapid extensions of these alignments.
 - Whole-genome indices with SNPs and known transcript structures accounted for

Kim et al. 2015. Nat Methods 12:357–360

HISAT/HISAT2 algorithm

- Uses a hierarchical indexing algorithm + several adaptive strategies
 - based on the position of a read with respect to splice sites
- 1) Find candidate locations across the whole genome first
 - mapping part of each read using the global FM index
 - Generally identifies one or a small number of candidates.
- 2) Do local alignment
 - selects one of ~48,000 local indexes for each candidate
 - uses it to align the remainder of the read.
- For paired reads, each mate is separately aligned
 - If a read fails to align, then the alignments of its mate are used as anchors to map the unaligned mate

HISAT2 Alignment



- Two exons from chr22
- Three reads

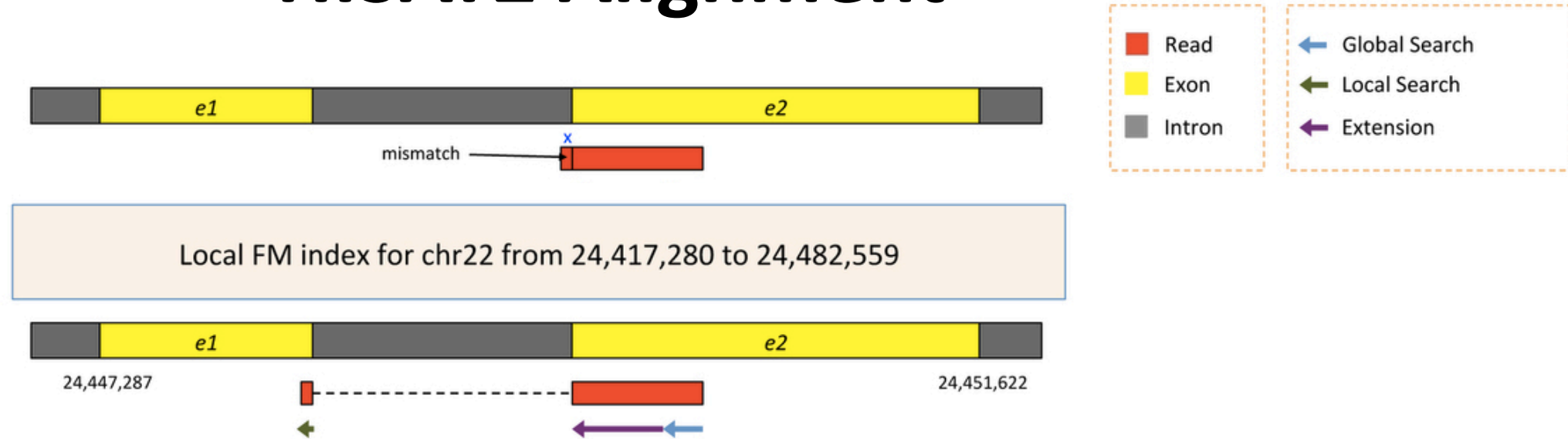
HISAT2 Alignment



- 1) Search for read position with global FM index (slower)
- 2) Once at least 28bp and exactly one location switch to extension mode against reference genome (faster)

Kim et al. 2015. Nat Methods 12:357–360

HISAT2 Alignment



- 1) Search for read position with global FM index (slower)
- 2) Extend until mismatch at 93bp (faster)
- 3) Switch to local FM index to align remaining 8bp
 - index covers only a small region, so we find just one match
- 4) Check for compatibility and combine into single spliced alignment

Kim et al. 2015. Nat Methods 12:357–360

HISAT2 Alignment



- 1) global search until exactly one match of at least 28bp (slower)
- 2) Extend until mismatch at 51bp (faster)
- 3) switch to local FM index to align first 8bp of remaining read
 - If too many matches increase prefix size
- 4) Extend again
- 5) Check for compatibility and combine into single spliced alignment

Kim et al. 2015. Nat Methods 12:357–360

What is the output of HISAT2?

- A SAM/BAM file
 - SAM stands for Sequence Alignment/Map format
 - BAM is the binary version of a SAM file
- Remember, compressed files require special handling compared to plain text files
- How can I convert BAM to SAM?
 - <http://www.biostars.org/p/1701/>
- Is HISAT2 the only mapper to consider for RNA-seq data?
 - <http://www.biostars.org/p/60478/>

We are on a Coffee Break & Networking Session

Workshop Sponsors:



Canadian Centre for
Computational
Genomics



neuro

Institut-Hôpital
neurologique de Montréal
Montreal Neurological
Institute-Hospital



OICR

Ontario Institute
for Cancer Research

MiC:M McGill initiative in
Computational Medicine



HPC4Health