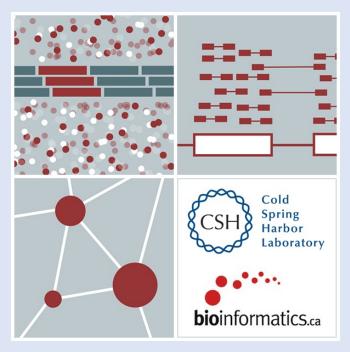
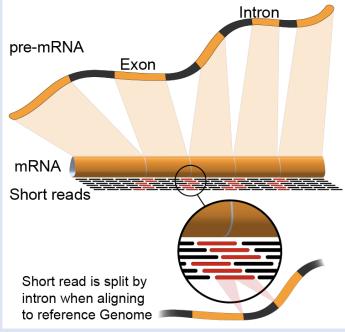


RNA-Seq Module 2: Alignment vs Assembly vs Pseudoalignment

Arpad Danos, Felicia Gomez, Obi Griffith, Malachi Griffith, My Hoang, Mariam Khanfar, Chris Miller, Kartik Singhal Advanced Sequencing Technologies & Bioinformatics Analysis November 5-19, 2023

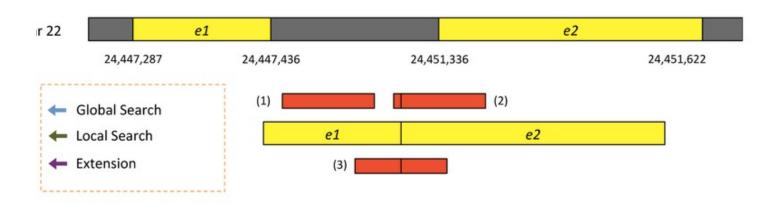






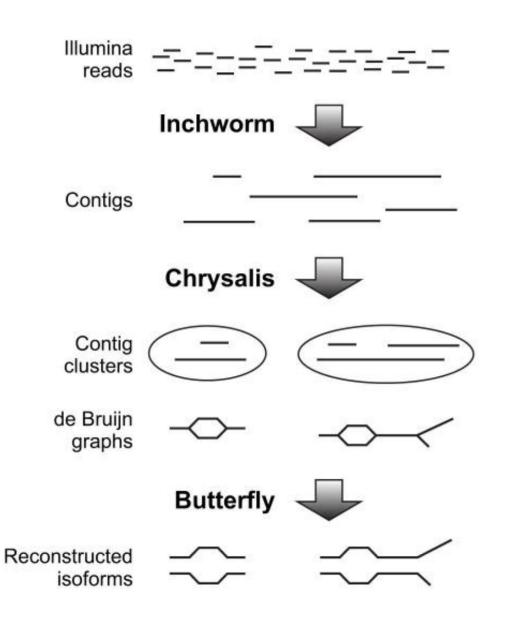
Alignment

- Uses a reference genome/transcriptome to map reads
- Capable of some novel transcript inference
- Relatively fast runtime
- Tools: HISAT2, STAR, GSNAP



Assembly

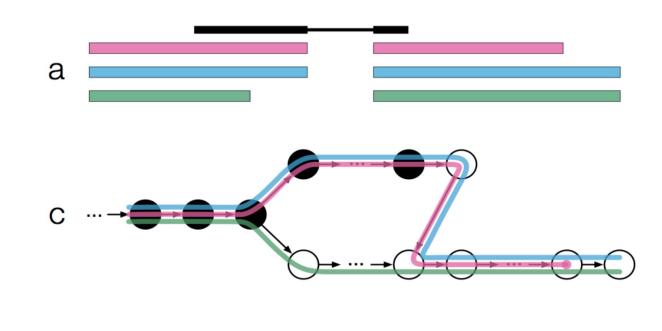
- Infer transcript structure directly from the data
- Useful when you do not have a reference sequence
- Other uses highly rearranged genomes (some cancers)
- Computationally expensive
- Tools: Trinity, Velvet, SPAdes



Haas, et al (2013) doi: 10.1038/nprot.2013.084

Pseudoalignment

- Does not determine where in the genome a read lies, only which transcripts it is compatible with
- Very fast!
- Does not produce a bam by default (though pseudo-bams can be created), not useful for variant detection.
- Tools: Kallisto, Sailfish



Bray, 2016 doi:10.1038/nbt.3519

https://tinyheero.github.io/2015/09/02/pseudoalignments-kallisto.html

We are on a Coffee Break & Networking Session