

Canadian Bioinformatics Workshops

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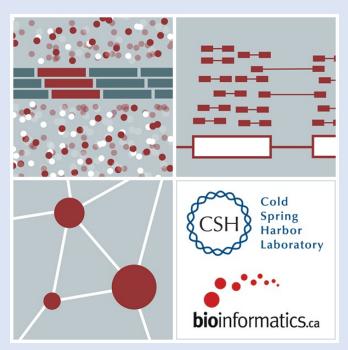
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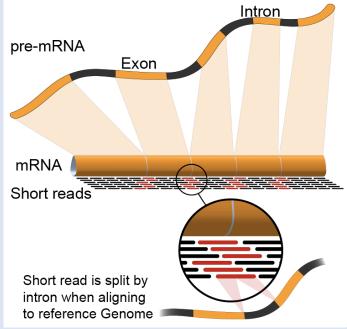
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RNA-Seq Module 3: HTSeq



Malachi Griffith, Obi Griffith, Isabel Risch, Nicolas Ho, Melisa Acun, Varinder Verma, Mobin Khoramjoo RNA-seq Analysis 2025. July 7-9, 2025







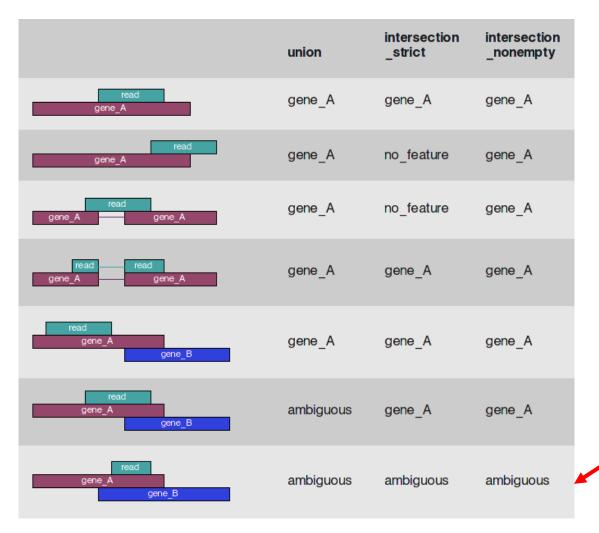
Alternatives to FPKM

- Raw read counts for differential expression analysis
 - Assign reads/fragments to defined genes/transcripts, get "raw counts"
 - Transcript structures could still be defined by something like Stringtie
- HTSeq (htseq-count)
 - https://htseq.readthedocs.io/

```
htseq-count --mode intersection-strict --stranded no --minaqual 1 --type
exon --idattr transcript_id accepted_hits.sam chr22.gff >
transcript_read_counts_table.tsv
```

- Caveats of 'transcript' analysis by htseq-count:
 - Designed for genes ambiguous reads from overlapping transcripts may not be handled!
 - http://seqanswers.com/forums/showthread.php?t=18068

HTSeq-count basically counts reads supporting a feature (exon, gene) by assessing overlapping coordinates



Note, if gene_A and gene_B on opposite strands, sequence data is stranded, and correct HTSeq parameter set then this read may not be ambiguous

Whether a read is counted depends on the nature of overlap and "mode" selected

We are on a Coffee Break & Networking Session

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