

RNA-Seq and Alternative Splicing

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RNA-Seq

- ▶ De novo assembly of RNA-seq data
 - SOAPdenovo-Trans (CLI)
 - Oases (CLI)
 - Trinity (Galaxy and CLI)
 - Trans-Abyss
- ▶ Different from genomic de novo assembler
 - Needs to expect coverage differences

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RNA-seq

- ▶ Reference based
 - TopHat
 - Align reads to reference genome
 - Discover transcript splice sites
 - Cufflinks
 - Assemble transcript models
 - Compare different datasets to identify differential expression

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Trapnell et al., 2012

Nature Protocols 7:562-578

PROTOCOL

Differential gene and transcript expression analysis of RNA-seq experiments with TopHat and Cufflinks

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The Tuxedo Suite

- ▶ Bowtie
- ▶ TopHat (uses Bowtie)
- ▶ Cufflinks package
 - Cufflinks
 - Assembles transcripts
 - Cuffcompare
 - Compares transcript assemblies to annotation
 - Cuffmerge
 - Merges two or more transcript assemblies
 - Cuffdiff
 - Finds differentially expressed genes and transcripts
 - Detects differential splicing and promoter use
- ▶ CummeRbund

Bowtie
Extremely fast, general purpose short read aligner

TopHat
Aligns RNA-Seq reads to the genome using Bowtie
Discovers splice sites

Cufflinks package

Cufflinks
Assembles transcripts

Cuffcompare
Compares transcript assemblies to annotation

Cuffmerge
Merges two or more transcript assemblies

Cuffdiff
Finds differentially expressed genes and transcripts
Detects differential splicing and promoter use

CummeRbund
Plots abundance and differential expression results from Cuffdiff

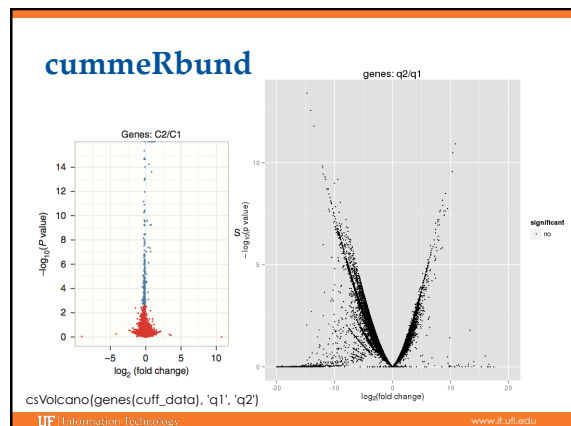
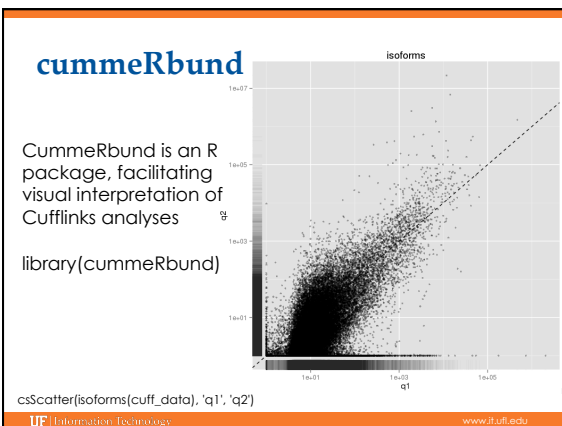
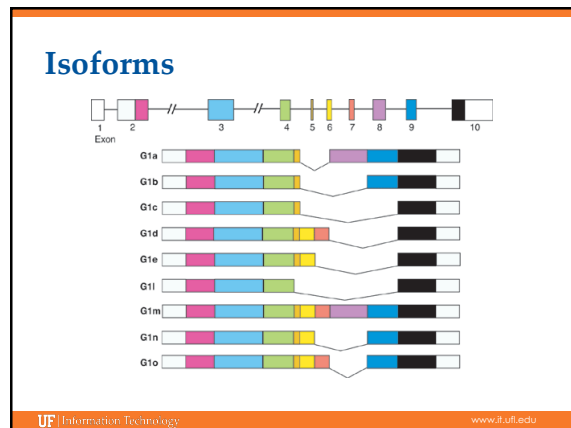
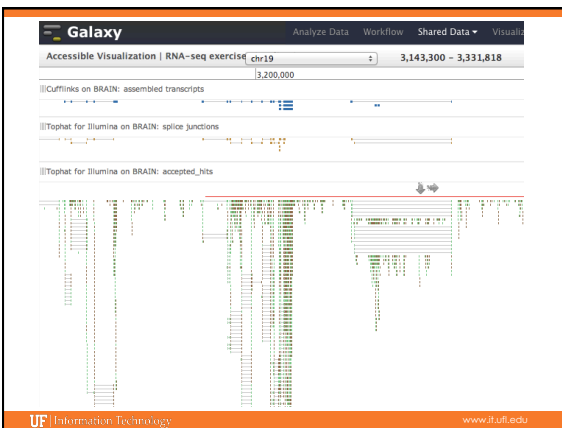
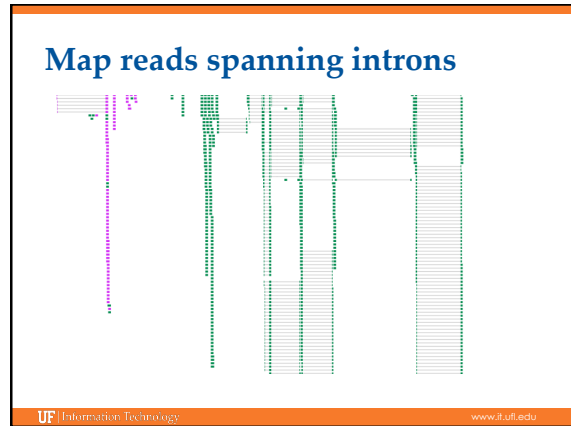
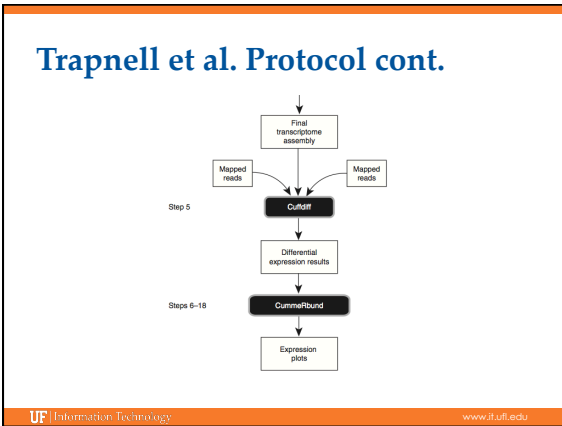
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Trapnell et al. Protocol

```

    graph TD
        A[Condition A Reads] --> TopHat
        B[Condition B Reads] --> TopHat
        subgraph Step 1
            TopHat --> MR1[Mapped reads]
            TopHat --> MR2[Mapped reads]
        end
        subgraph Step 2
            MR1 --> AT1[Assembled transcripts]
            MR2 --> AT2[Assembled transcripts]
        end
        subgraph Steps 3-4
            AT1 --> Cuffmerge
            AT2 --> Cuffmerge
        end
    
```

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Miso

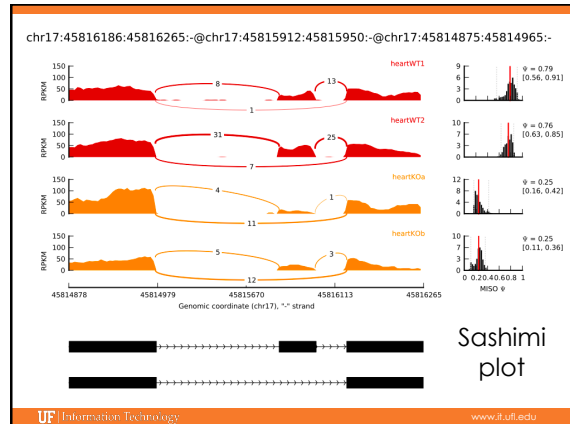


MISO / Probabilistic analysis and design of RNA-Seq experiments for identifying isoform regulation

Home | Paper | Software | Documentation | Datasets | Contact

- ▶ Improved accuracy in isoform frequencies
- ▶ Takes TopHat output (or other SAM file)

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UF HPC Training: Spring 2013

- ▶ Mondays 11:00-noon
- ▶ Starts January 14th
- ▶ Session topics needed

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