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at Washington University

GenViz Module 4: Expression profiling, visualization, and interpretation

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Genomic Data Visualization and Interpretation
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Learning objectives of the course

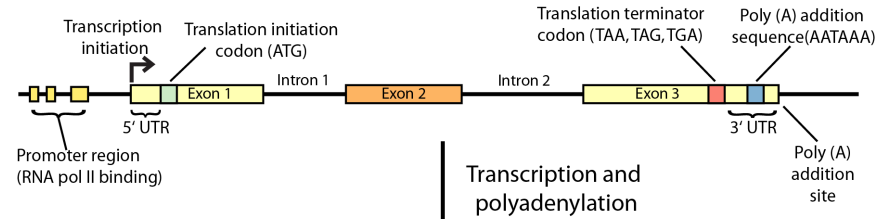
- Module 1: Introduction to genomic data visualization and interpretation
- Module 2: Using R for genomic data visualization and interpretation
- Module 3: Introduction to GenVisR
- **Module 4: Expression profiling, visualization, and interpretation**
- Module 5: Variant annotation and interpretation
- Module 6: Q & A, discussion, integrated assignments, and working with your own data
- Tutorials
 - Provide working examples of data visualization and interpretation
 - Self contained, self explanatory, portable

Learning objectives of module 4

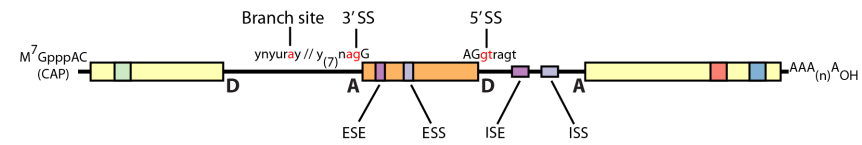
- Expression profiling, visualization, and interpretation
 - Expression estimation for known genes (concepts)
 - FPKM' expression estimates vs. 'raw' counts
 - Differential expression methods (DESeq2)
 - Downstream interpretation of expression and differential estimates

Gene expression

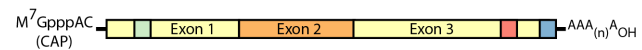
Double-stranded genomic DNA template



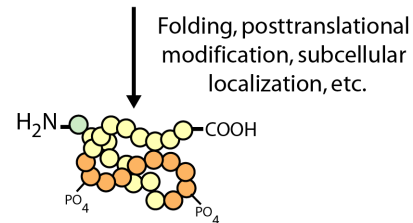
Single-stranded pre-mRNA (nuclear RNA)



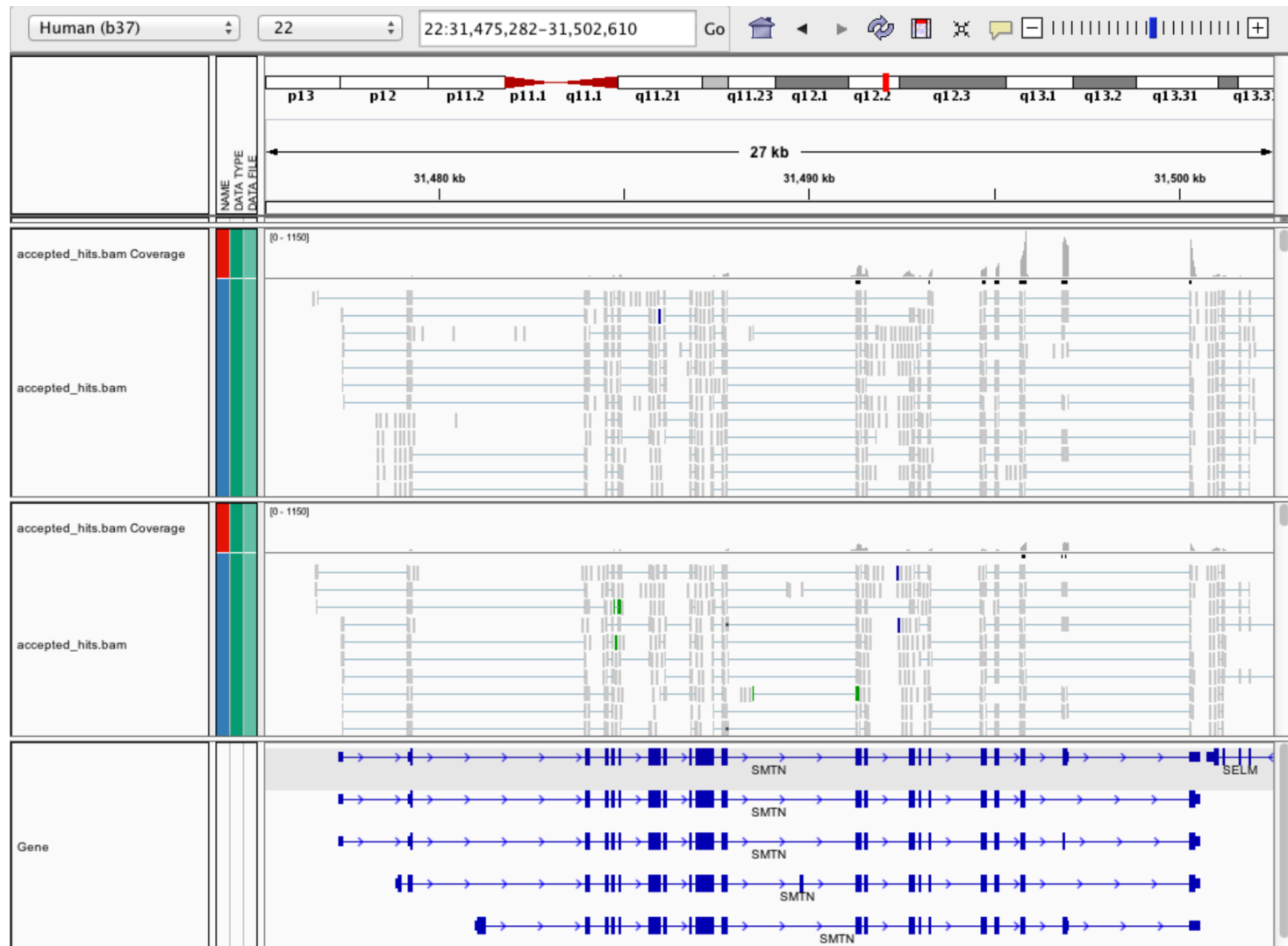
Mature mRNA



Protein (amino acid sequence)



Expression estimation for known genes and transcripts



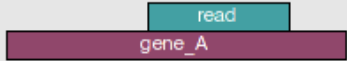
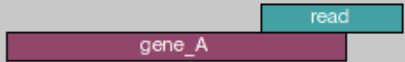




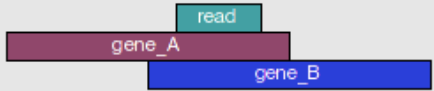
What is FPKM (RPKM)

- RPKM: Reads Per Kilobase of transcript per Million mapped reads.
- FPKM: Fragments Per Kilobase of transcript per Million mapped reads.
- In RNA-Seq, the relative expression of a transcript is proportional to the number of cDNA fragments that originate from it. However:
 - The number of fragments is also biased towards larger genes
 - The total number of fragments is related to total library depth
- FPKM (RPKM) attempt to normalize for gene size and library depth
- $$\text{FPKM (RPKM)} = (10^9 * C) / (N * L)$$
 - C = number of mappable reads/fragments for a gene/transcript/exon/etc
 - N = total number of mappable reads/fragments in the library
 - L = number of base pairs in the gene/transcript/exon/etc
- <http://www.biostars.org/p/11378/>
- <http://www.biostars.org/p/68126/>

What are raw counts?

- Raw read counts as an alternate for differential expression analysis
 - Instead of calculating FPKM, simply assign reads/fragments to a defined set of genes/transcripts and determine “raw counts”
 - Transcript structures could still be defined by something like cufflinks
- HTSeq (htseq-count)
 - <http://www-huber.embl.de/users/anders/HTSeq/doc/count.html>
 - `htseq-count --mode intersection-strict --stranded no --minqual 1 --type exon --idattr transcript_id accepted_hits.sam chr22.gff > transcript_read_counts_table.tsv`
 - Important caveat of ‘transcript’ analysis by htseq-count:
 - <http://seqanswers.com/forums/showthread.php?t=18068>

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

	union	intersection_strict	intersection_nonempty
	gene_A	gene_A	gene_A
	gene_A	no_feature	gene_A
	gene_A	no_feature	gene_A
	gene_A	gene_A	gene_A
	gene_A	gene_A	gene_A
	ambiguous	gene_A	gene_A
	ambiguous	ambiguous	ambiguous

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

Alternative differential expression methods

- Raw count approaches
 - DESeq2 - <http://www-huber.embl.de/users/anders/DESeq/>
 - edgeR - <http://www.bioconductor.org/packages/release/bioc/html/edgeR.html>
 - Others...

'FPKM' expression estimates vs. 'raw' counts

- Which should I use?
 - Long running debate with countless blogs and analyses arguing the advantages of each. The general consensus:
- FPKM
 - Isoform deconvolution
 - Good for straight visualization (e.g., heatmaps)
 - Calculating fold changes, etc.
- Counts
 - More robust statistical methods for differential expression
 - Accommodates more sophisticated experimental designs with appropriate statistical tests

Multiple approaches advisable

