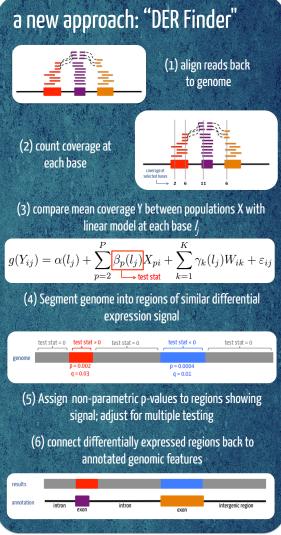
background what is RNA-seq data? cell transcril of DNA into RNA how is the data currently analyzed? (1) align reads back to genome (2) choose between: read counting by transcript assembly annotated feature (3) perform statistical tests compare exon- or abundance estimation assembled-transcriptlevel measurements between populations

detecting differential expression with

RNA-seq data alyssa frazee, sarven sabunciyan, kasper hansen, rafa irizarry, jeff leek problems with current methods assembly-based: read alignments support all three of these assemblies poor statistical results inherent ambiguity annotation-based: cannot detect differential complex regions require downstream counting decisions, expression outside of known which affect results features



reference & acknowledgments

Frazee AC, Sabunciyan S, Hansen KD, Irizarry RA, and Leek JT (2013). "Differential expression analysis of RNA-seq data at single-base resolution." Biostatistics, under review.

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