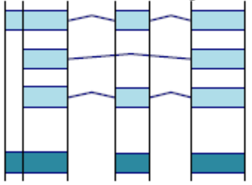
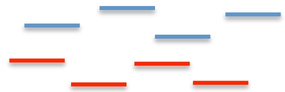
How does DEXSeq work?

Annotation .gtf file



Create counting bins for each gene

Alignment and .gtf files

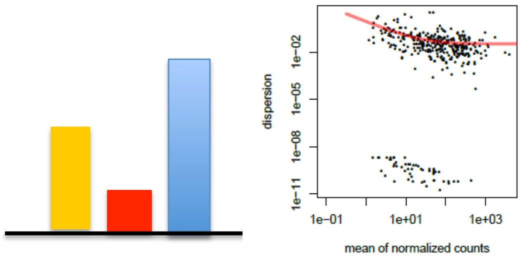


Counts # of reads that map to each exon counting bin

Read data in R

16M vs 23M

Normalize: estimate size factors



Variance: estimate dispersion

Null model vs Alternative Model

Test for DEU: differential expression of each bin