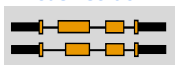
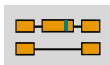


Characterize transcripts

cdsInsertion

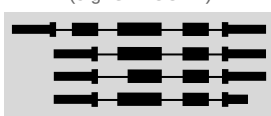


Couple events to functional effects
findSwitchEvents



Transcriptome annotation

(e.g. GENCODE)



Binary AS event annotation

(splice_lib_events.gtf)



RNA-seq data

(FASTQ)



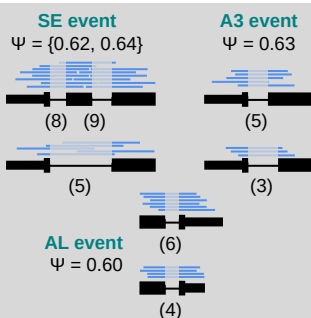
Map reads to genome

(e.g. STAR)



Count junction reads

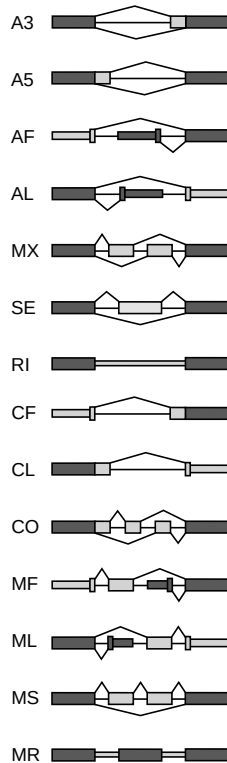
calculate percent spliced in (Ψ)



Statistical testing
DEXSeq

Event-level output

Cross-condition
mean $\Delta\Psi$, FDR



included form excluded form

JC
junctionCounts