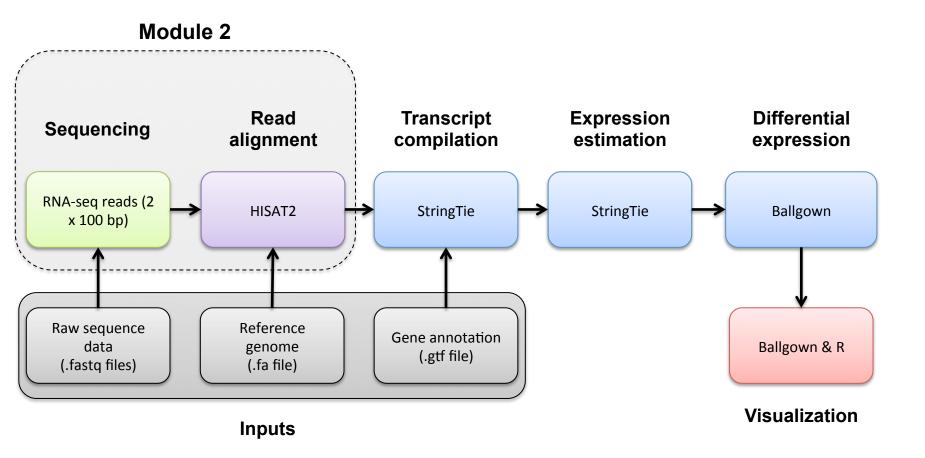
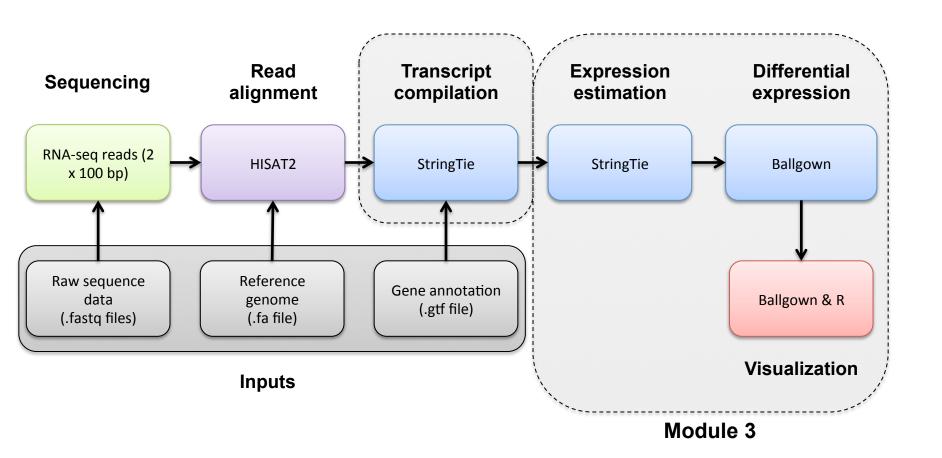


Module 1





Module 4 – Rerun StringTie in alternative 'modes' Read **Transcript Expression Alternative** Sequencing estimate alignment compilation expression RNA-seq reads (2 HISAT2 StringTie StringTie Ballgown x 100 bp) Raw sequence Reference Gene annotation data Ballgown & R genome (.gtf file) (.fastq files) (.fa file) Inputs