

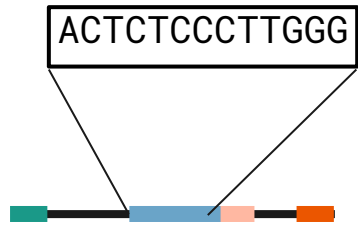


Visualizing Transcriptomic Long-read Sequencing Artifacts

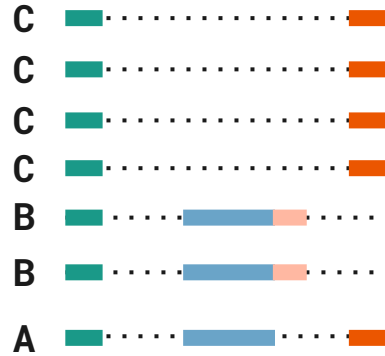
CPSC547 peer review presentation

By Baraa Orabi and Nico Ritschel

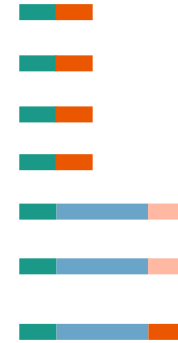
RNA Sequencing



One gene



Multiple
(different)
transcript



Reads sequencing
each transcript

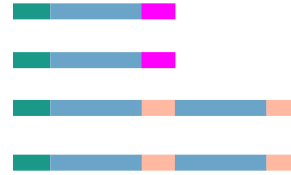
RNA Sequencing is noisy



Reads have high
error rate



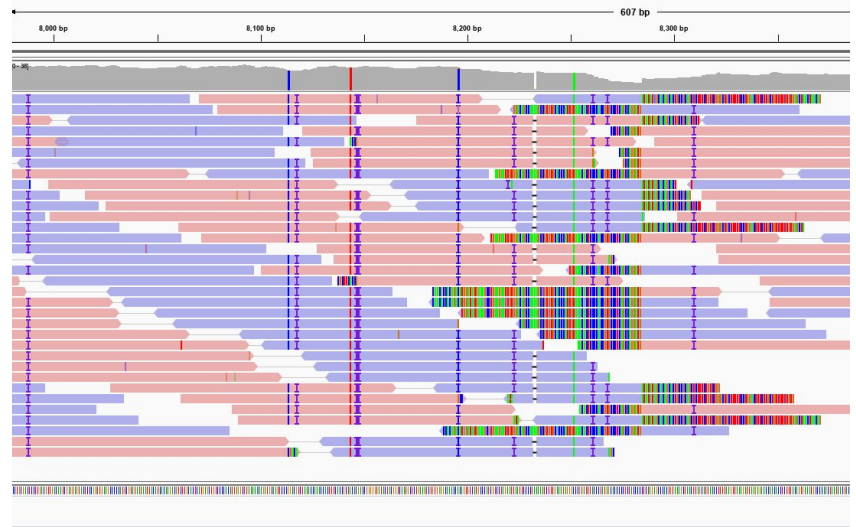
Gene reference
sequence



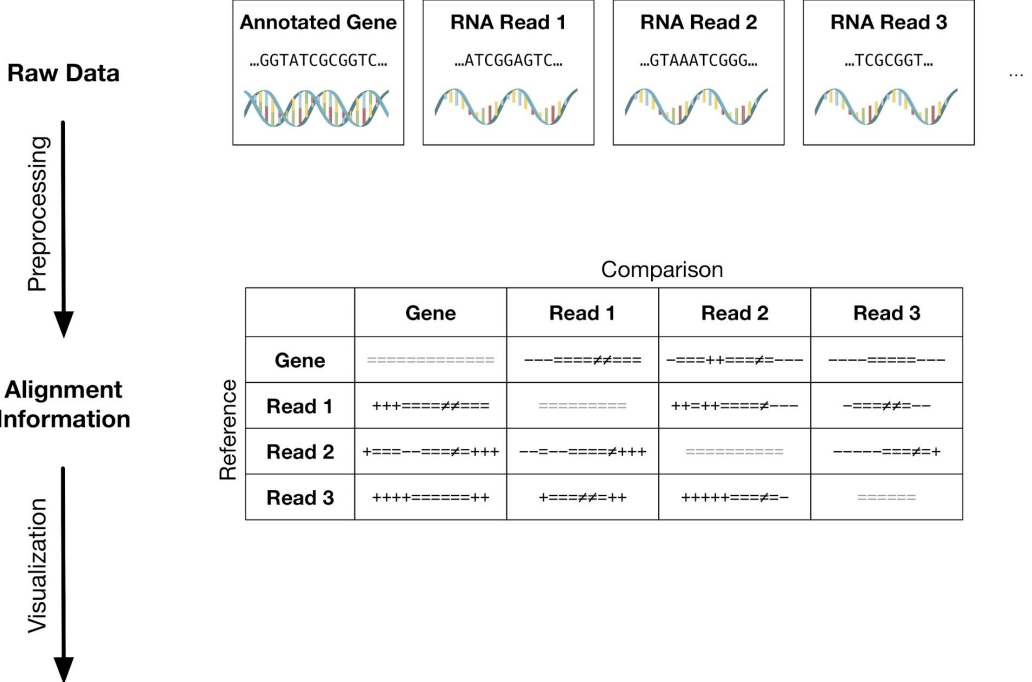
Sample might
contain *novel*
transcripts

Current genome vis

- Designed for *short-reads*
- Fit as many as possible in view
- Reference is fixed
 - Cannot view novel sequences

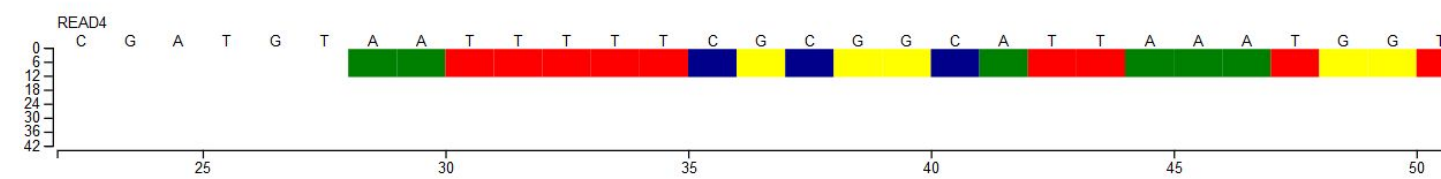
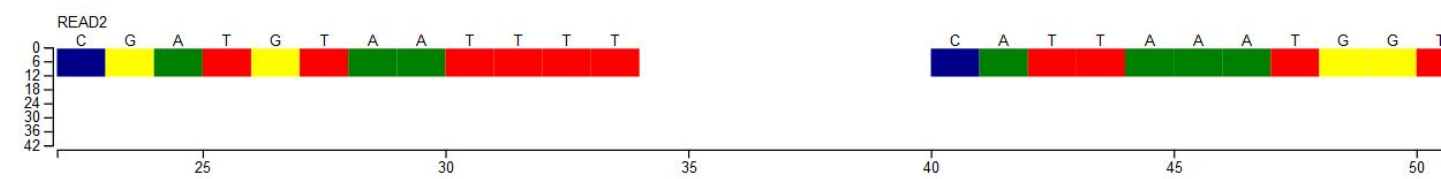
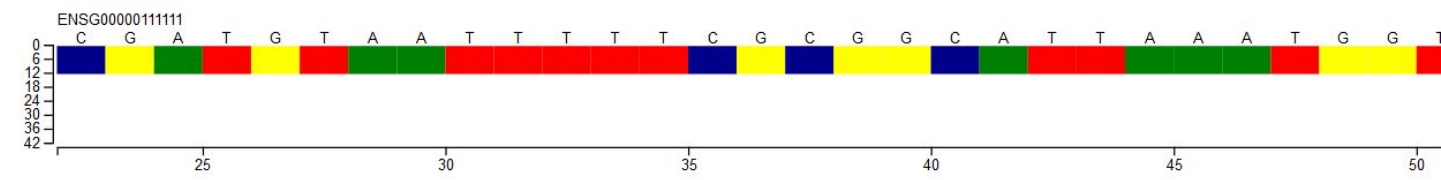
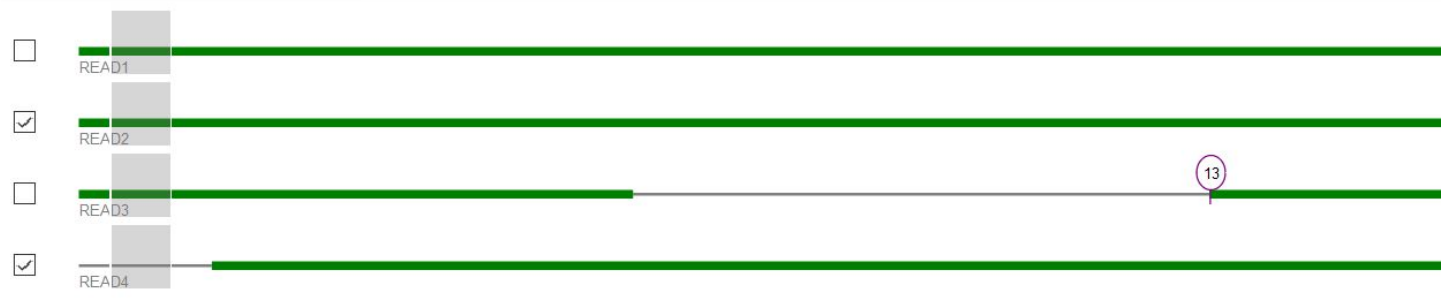


Solution: Overview





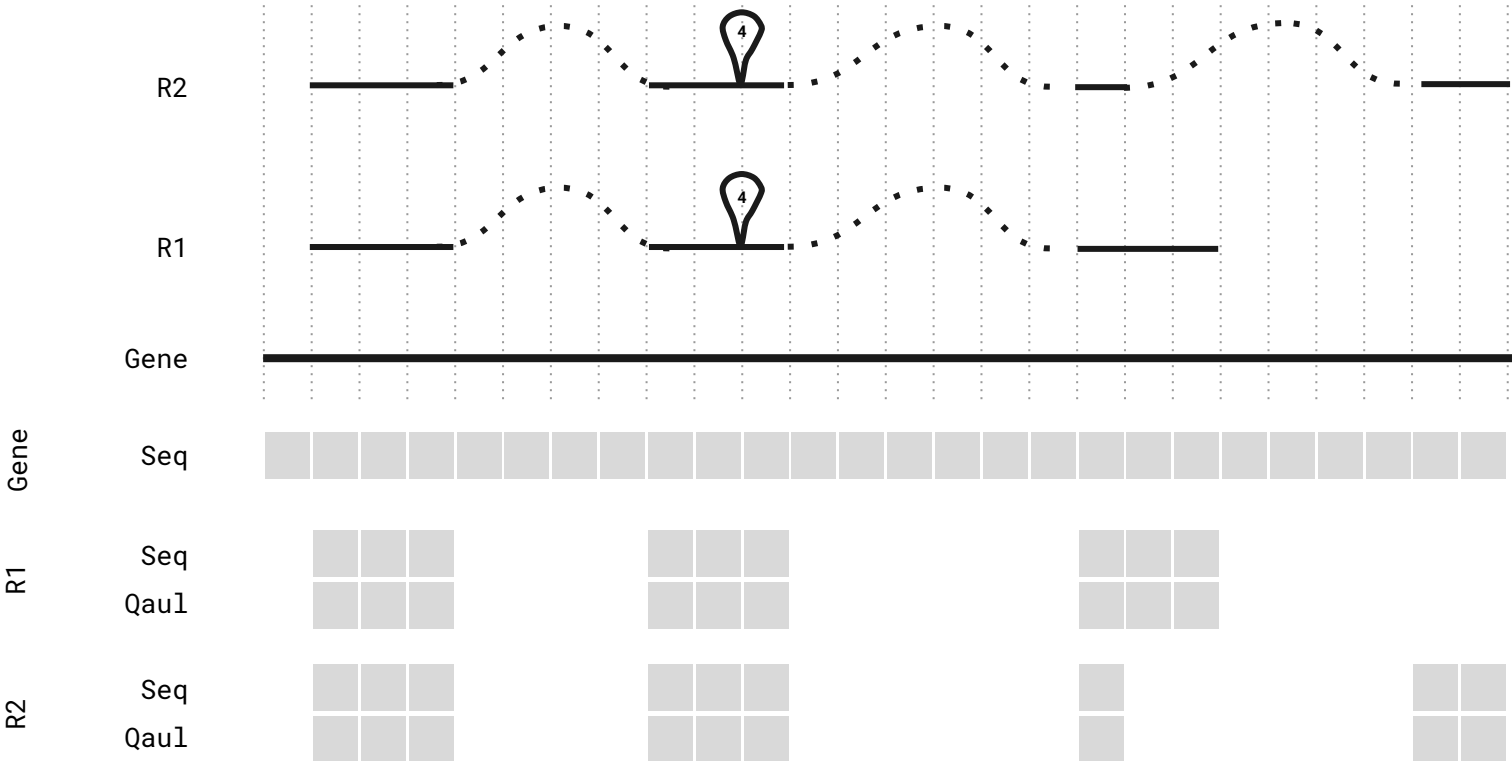
Solution



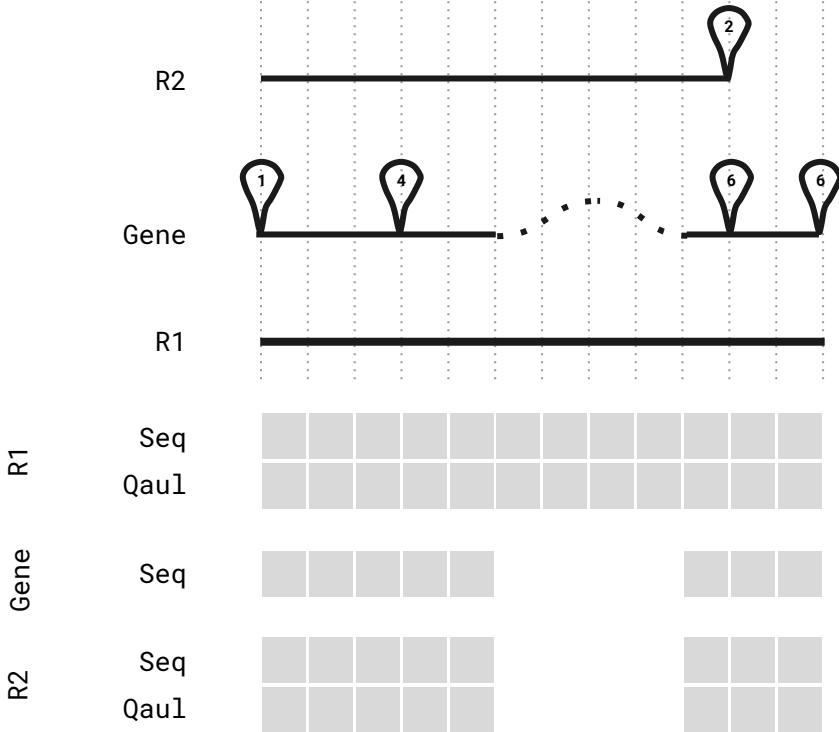


Target switching

Solution: reference switching



Solution: reference switching



Code

