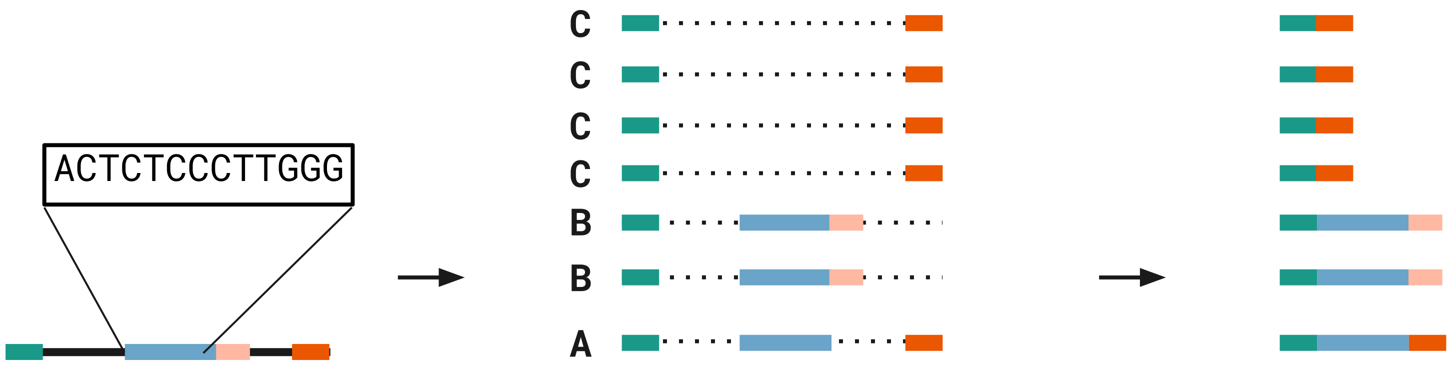
Visualizing Transcriptomic Long-read Sequencing Artifacts

CPSC547 peer review presentation

By Baraa Orabi and Nico Ritschel

RNA Sequencing

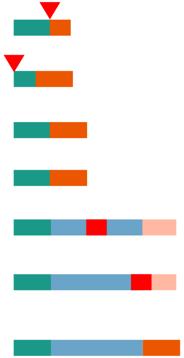


One gene

Multiple (different) transcript

Reads sequencing each transcript

RNA Sequencing is noisy



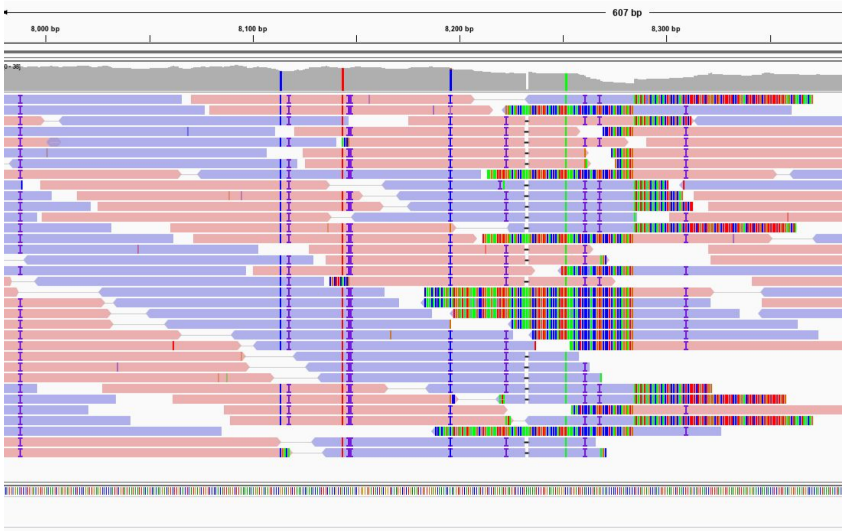
Reads have high error rate

Gene reference sequence

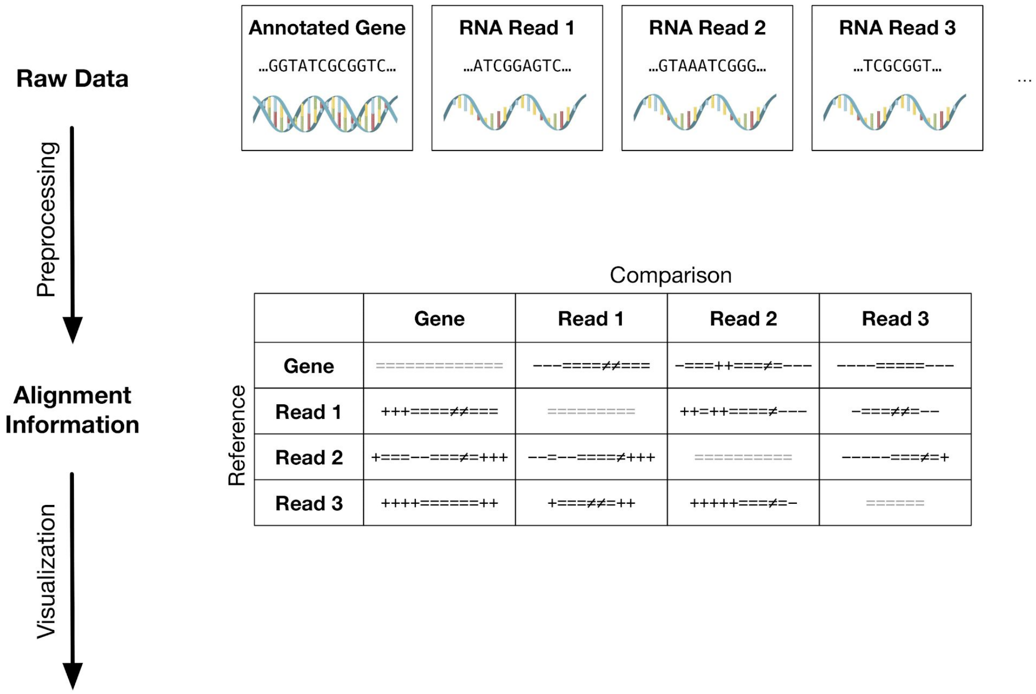
Sample might contain *novel* transcripts

Current genome vis

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



Solution: Overview

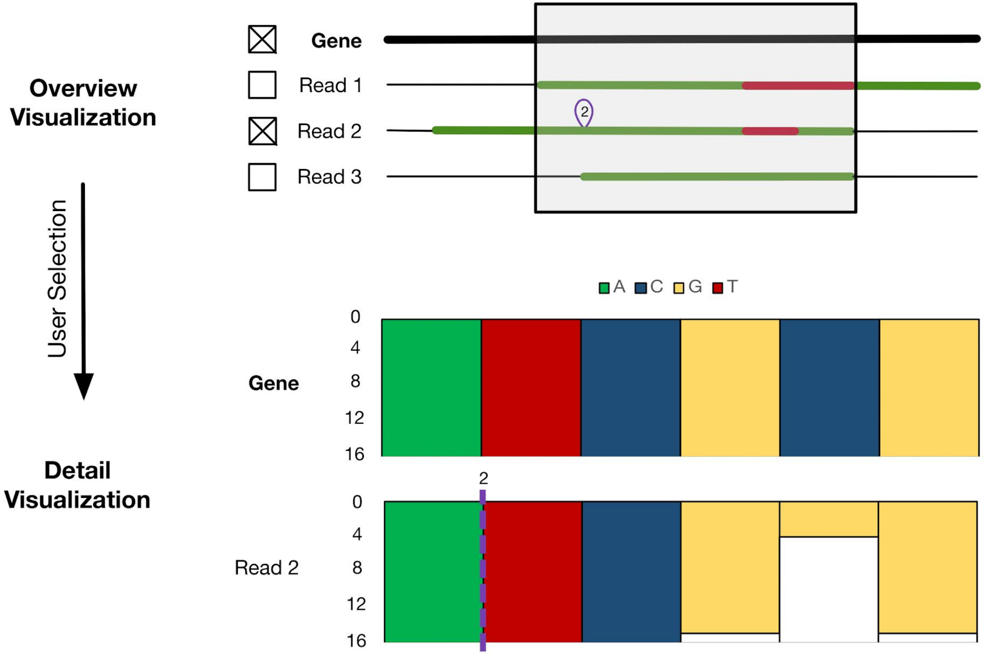


Comparison

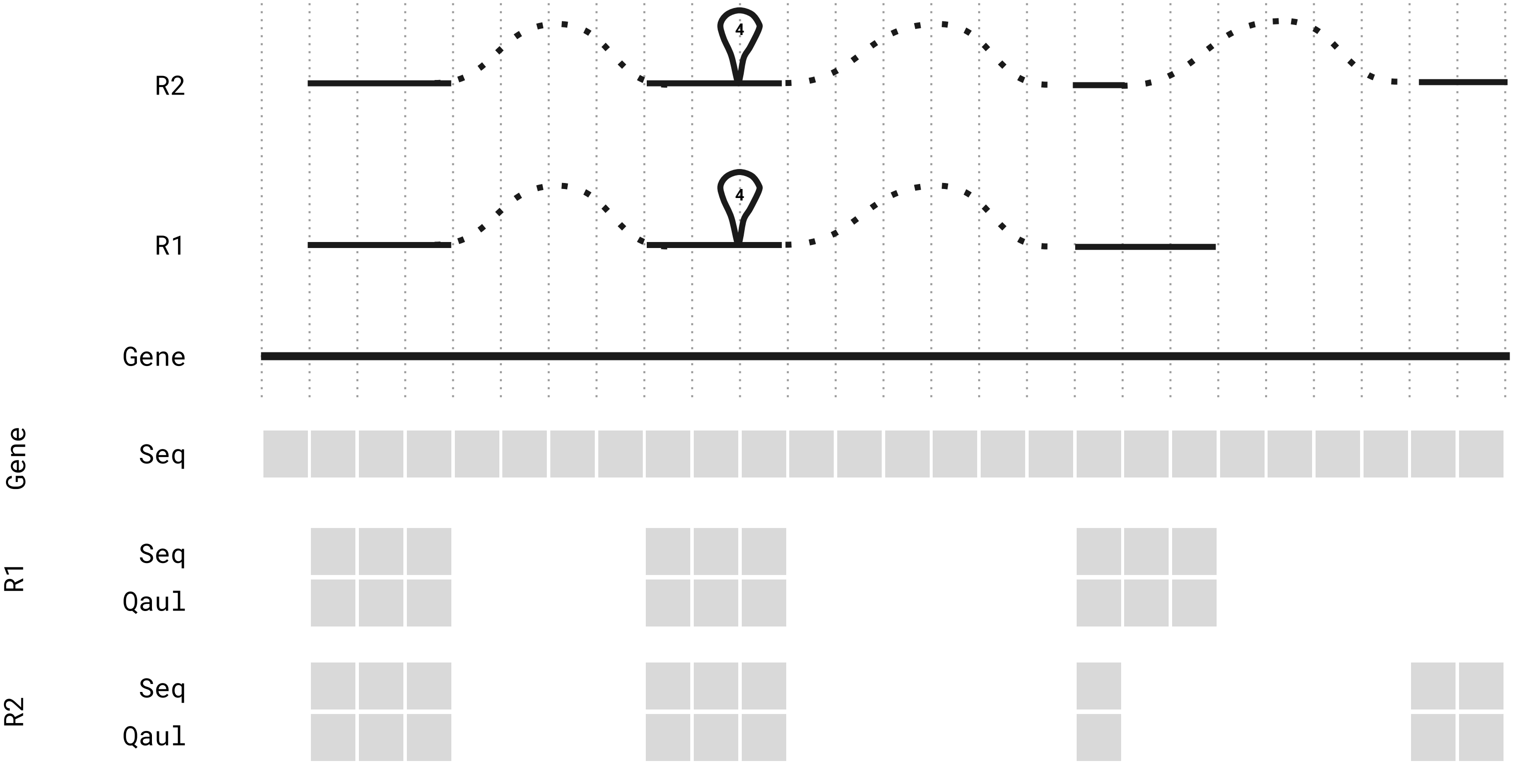
Reference

	Gene	Read 1	Read 2	Read 3
Gene	==============	–––====≠≠====	–===++===≠=–––	––––=====–––
Read 1	+++====≠≠====	==========	++=++====≠–––	–===≠≠=––
Read 2	+===––===≠=+++	––=––====≠+++	===========	–––––===≠=+
Read 3	++++======++	+===≠≠=++	+++++===≠=–	======

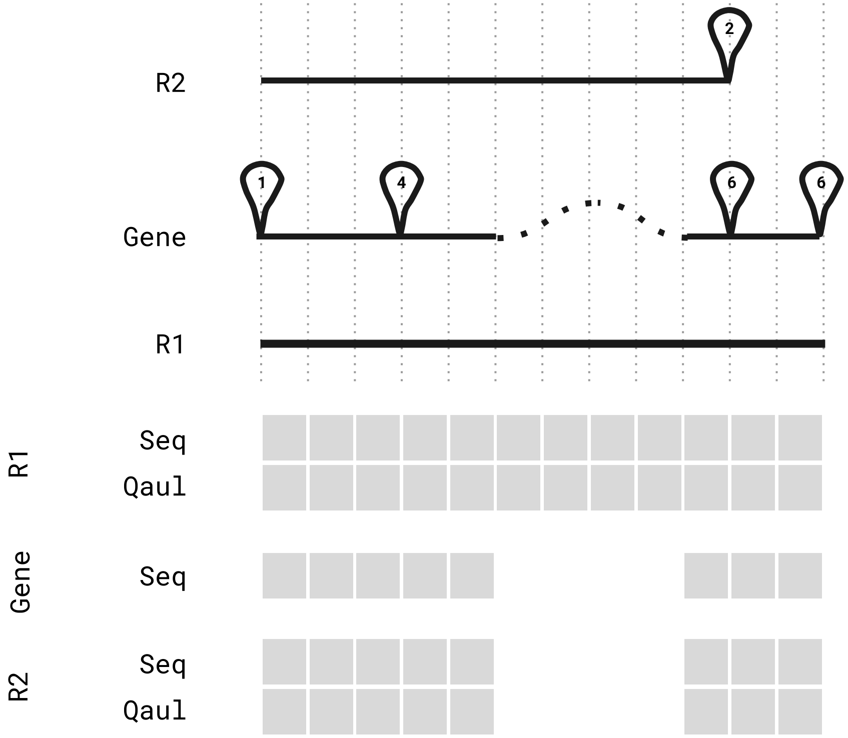
Solution: Overview



Solution: reference switching



Solution: reference switching



Code