Visualizing Transcriptomic Long-read Sequencing Artifacts

CPSC547 peer review presentation

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RNA Sequencing

One gene

ACTCTCCCTTTGGG

Multiple (different) transcript

Reads sequencing each transcript
RNA Sequencing is noisy

**Reads have high error rate**

**Sample might contain novel transcripts**

**Gene reference sequence**
Current genome vis

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

Preprocessing → Alignment Information → Visualization

- Raw Data
- Annotated Gene
- RNA Read 1
- RNA Read 2
- RNA Read 3
...
Solution: Overview
Solution: reference switching
Solution: reference switching