

ChimeraLM: A genomic language model to detect chimer artifacts

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Abstract

Non-colinear Transcript (NLT) arising from structural variations challenge conventional linear analysis approaches in transcriptomics. Here we introduce the concept of **Transcriptome Segment Graph (TSG)** and present the first comprehensive infrastructure for graph-based transcript analysis. We develop the TSG file format as the first standardized encoding for transcript segment graphs, enabling systematic representation of **NLT**, and complex splicing patterns impossible to capture with linear methods. Our command-line toolkit provides the first comprehensive suite for **TSG** manipulation, analysis, and format conversion, while Aurora offers the first interactive visualization platform for transcript segment graphs. Together with our companion TSG caller **scannls**, this work establishes the foundational infrastructure for a new paradigm in transcriptomic analysis, providing the essential tools for systematic investigation of **NLT** structures.

Keywords: Transcriptomics, Graph-based analysis, Non-colinear transcripts, TSG caller, TSG visualization

1 main

Transcriptomic structural variations, including gene fusions, circular RNAs, and complex alternative splicing, play critical roles in cancer, development, and disease.

2 Methods

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Supplementary information. This separation aligns with how many transcript assembly algorithms work:

1. First, chains of exons and splice junctions are identified from the data
2. Then, potential transcripts are derived by traversing the graph in different ways
3. Finally, relationships between different transcript graphs are established

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Appendix A Section title of first appendix

An appendix contains supplementary information that is not an essential part of the text itself but which may be helpful in providing a more comprehensive understanding of the research problem or it is information that is too cumbersome to be included in the body of the paper.

References