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## COMPUTATIONAL APPROACHES FOR TRANSCRIPTOME CANCER ANALYSIS BY RNA-SEQ



Yuxiang Tan  
Computational Approaches  
for Transcriptome Cancer  
Analysis by RNA-Seq



Condition: New. Publisher/Verlag: LAP Lambert Academic Publishing | RNA-Seq provides an ideal platform to study the complete set of transcripts for a specific developmental stage or physiological condition. It reveals not only expression-level changes, but also structural changes in the coding sequences, including gene rearrangements. In this dissertation, I present my contributions to the development of computational tools for the robust and efficient analysis of RNA-Seq data to support cancer research. To automate the laborious and computationally intensive procedure of...

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