



Computational Approaches for Transcriptome Cancer Analysis by RNA -Seq

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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 RNA-Seq data management, I worked on the development of Hydra, an RNA-Seq pipeline for the parallel processing and quality control of large numbers of samples. I then present QueryFuse, a novel gene-specific fusion-detection algorithm for aligned RNA-Seq data. It is designed to help biologists find and/or computationally validate fusions of interest quickly, and to annotate the detected events with visualization and detailed properties of the supporting reads. Finally, I contributed to the identification of a novel fusion event in lymphoma, with potential therapeutic implications in clinical samples. I validated this fusion in silico and by experimental validation. | Format: Paperback | Language/Sprache: english | 108 pp.

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