

Title: Optimization of Liver RNA-Seq Analysis through HRNet: Bridging Computational Techniques and Biological Understanding

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Abstract: In the digital era, the rapid proliferation of RNA sequencing (RNA-Seq) has uncovered vast datasets, particularly in liver-specific gene expression, yet the complexity of such high-dimensional data often obscures actionable insights. This research focuses on optimizing the analysis of liver RNA-Seq data through the innovative application of the Human RNA Network (HRNet) architecture, renowned for its proficiency in handling complex image and data patterns. Employing a refined dataset from the All RNA-seq and ChIP-seq sample and signature search (ARCHS4) platform, this study evaluates the effectiveness of HRNet alongside traditional machine learning and emerging deep learning techniques. The introduction of enhanced preprocessing, feature selection, and dimensionality reduction methods tailored to the intricacies of liver RNA-Seq data marks a pivotal advance in computational biology. Rigorous testing against conventional models demonstrates the superior capability of HRNet, achieving remarkable precision in identifying and analyzing gene expressions critical to understanding liver functions and disorders. The results showcase not only HRNet's robust performance, with accuracy rates exceeding 98.5% in complex gene expression patterns, but also its potential in transforming the landscape of genomic research, facilitating more precise diagnostic and therapeutic strategies. This study underscores the necessity of integrating advanced computational models to effectively decipher the voluminous data generated by RNA-Seq, thereby enhancing the accuracy and applicability of genomic analyses in medical research.

Keywords: RNA-Seq, Liver gene expression, HRNet, High-dimensional data analysis, Computational biology, Feature selection

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