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Inferring Tissue-Specific Alternative Splicing from Blood Samples

This study explores an innovative, less invasive approach to diagnosing complex diseases like dilated cardiomyopathy (DCM) by predicting target tissue expression profiles using gene expression and alternative splicing profiles from blood samples. Machine learning approaches, specifically dimensionality reduction and linear regression, are utilized. Preliminary results indicate that while this approach is insufficient for robust tissue splicing factor expression predictions, it holds significant promise. The study suggests that incorporating additional data types (e.g., proteomics, RNA-Seq on exosomes) or alternative methods (e.g., deep learning techniques) may yield stronger predictions. Despite limitations, this study emphasizes the potential of this approach and encourages further research.

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Keywords

Systems biology, tissue expression prediction, linear regression, dimensionality reduction

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