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Transcriptomics data analysis unlocked: leveraging AI techniques for biomarker identification in COVID-19 and lupus use cases

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Biomarker identification is an essential task in the field of translational medicine and is crucial for predicting disease outcomes and guiding treatment decisions. Transcriptomic data is a valuable resource for identifying biomarkers due to its ability to capture changes in gene expression patterns that are associated with various diseases. Microarray, bulk RNA sequencing, and single-cell RNA sequencing are the three main methodologies used to obtain transcriptomic data. For instance, single-cell transcriptomics can identify cell type-specific biomarkers that cannot be obtained with bulk methods. However, this deeper biological insight comes with a tradeoff that the computational analysis of single-cell data is more challenging, and often more expensive to perform. Biomarker identification workflows typically rely on only one source of transcriptomic data, which can hamper the validation and generalization of results. For any given study, there is no guarantee that similar data from the same technology will be available in the literature. Relaxing the technology-specific constraint could increase the likelihood that an adequate dataset can be found for comparison and validation. However, if the biomarker identification workflow is not designed to flexibly handle multiple data technologies, then the user will be left without a straightforward means of validation. Furthermore, comparing results across two or more technology-specific workflows can be challenging as the analysis steps involved will almost certainly differ in each workflow. To address these limitations, at DeepLife we have developed a standardized workflow capable of analyzing transcriptomic data from microarray, bulk RNA sequencing, and single-cell RNA sequencing experiments to provide robust candidates for biomarkers. Our data-agnostic approach leverages both conventional statistical analyses and state-of-the-art explainable artificial intelligence (xAI) methods to provide specificity regarding biomarker candidates. Our standardized workflow has been deployed in multiple biomarker identification use cases, including data obtained from lupus and COVID-19 patients.

Biography

Katherine Driscoll's expertise lies in the simulation and modeling of complex systems. Her dissertation work focused on the development and analysis of models to study long-range electronic interactions in low-dimensional quantum systems. As a computational biologist DeepLife, she has leveraged her mathematical and computational skills to extract biologically relevant insights from complex data sources by developing an xAI-based workflow for identifying biomarkers from transcriptomic data.

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