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Characterization of cardiac fibrosis and identification of potential therapeutic targets through a large-scale single-cell atlas

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Cardiovascular diseases are among the leading causes of death worldwide, second only to cancer, and the number of deaths caused by them continues to rise. Despite advances in the treatment of cardiovascular diseases, the remodeling processes associated with heart failure remain poorly understood, limiting the effectiveness of therapies aimed at reducing mortality rates. Currently, various single-nucleus (or single-cell) RNA sequencing datasets related to cardiovascular diseases are accessible through public databases. However, datasets generated from independent studies often have limited sample sizes and are difficult to analyze comprehensively across multiple diseases. To facilitate a comprehensive understanding of cardiovascular diseases, I constructed a large-scale integrated dataset, I identified cellular trajectories of fibroblasts across the cardiac fibrosis process. By applying FastTENET, a tool that reconstructs gene regulatory networks based on trajectory, I identified transcription factors regulating the fibrosis processes. This study offers significant insights into the molecular mechanisms underlying cardiovascular diseases and highlights the potential to contribute to the development of novel therapeutic strategies.