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SCANET for single-cell network-based drug repurposing candidate extraction

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Abstract

Reconstructing small regulatory networks is essential for understanding cellular functions and mechanisms. Performing this task with single-cell RNA sequencing data poses a substantial computational challenge.
In response, we present SCANet (single-cell co-expression network analysis) [1], a comprehensive tool designed for single-cell profiling. SCANet encompasses the entire workflow of differential mechanotyping, from identifying trait/cell-type-specific gene co-expression modules to predicting mechanistic drug repurposing candidates [2]. To showcase SCANet's efficacy, we examined two distinct datasets. Firstly, we uncovered monocytic drivers associated with cytokine storms in patients with acute respiratory illness, elucidating potential targets for intervention. Secondly, in obese mice, we identified 20 drugs targeting 8 potential pharmacological targets within metabolic driver mechanisms in intestinal stem cells. In another study [3], SCANet efficiently deciphers cell- and disease-specific co-expression gene modules across lesion types in patients with multiple sclerosis.
SCANet is available as a free, open-source Python package, facilitating its integration into single-cell-based systems medicine research and mechanistic drug discovery.

Keywords

Single-cell RNA, Regulatory networks, Mechanistic drug repurposing

References

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