SCANet: A Workflow for Single-Cell Co-Expression Based Analysis

Authors : Mhaned Oubounyt, Jan Baumbach

Abstract : Differences in co-expression networks between two or multiple cells (sub)types across conditions is a pressing problem in single-cell RNA sequencing (scRNA-seq). A key challenge is to define those co-variations that differ between or among cell types and/or conditions and phenotypes to examine small regulatory networks that can explain mechanistic differences. To this end, we developed SCANet, an all-in-one Python package that uses state-of-the-art algorithms to facilitate the workflow of a combined single-cell GCN (Gene Correlation Network) and GRN (Gene Regulatory Networks) pipeline, including inference of gene co-expression modules from scRNA-seq, followed by trait and cell type associations, hub gene detection, co-regulatory networks, and drug-gene interactions. In an example case, we illustrate how SCANet can be applied to identify regulatory drivers behind a cytokine storm associated with mortality in patients with acute respiratory illness. SCANet is available as a free, open-source, and user-friendly Python package that can be easily integrated into systems biology pipelines.

Keywords : single-cell, co-expression networks, drug-gene interactions, co-regulatory networks

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