Improvement of human interactome with de novo network inference from single-cell atlas

Eui Jeong Sung[1], JunHa Cha[1], and Insuk Lee[1,*]

[1] *Department of Biotechnology, Yonsei University*
**Corresponding author: insuklee@yonsei.ac.kr*

The investigation of gene-gene relationships using network analysis has been a longstanding practice. However, due to variations in gene expression levels across tissue types and cell types, it is essential to observe cell type-specific networks to discern accurate gene associations. To address this, we used single-cell RNA sequencing (scRNA) data to construct networks and utilized three existing single-cell imputation/transformation tools known for effectively reflecting gene-gene correlations. These individual networks were then integrated to create a more robust network through a dedicated pipeline. We confirmed that the links derived from such scRNA data were indeed cell type-specific, and the addition of these links to the reference network resulted in improved disease predictability. Leveraging this approach allows us to observe gene-gene correlations that are more context-specific.