

ICELLNET: reconstruction of intercellular communication networks using transcriptomic profiles

Cell-to-cell communication is at the basis of the higher-order organisation observed in tissues, organs, and organisms. It is critical to coordinate the function of diverse cell types involved in complex biological processes, such as embryogenesis, tissue formation and renewal, and efficient immune responses. In the literature, there is no method developed to reconstruct intercellular communication networks in a quantitative and qualitative manner. [1] Here, we developed ICELLNET, a transcriptomic-based tool to reconstruct intercellular communication networks. This original quantitative method integrating ligand-receptor interactions, and cell-type specific gene expression, can be automatically applied to any cell population level transcriptomic profile. In this study, it predicted that IL-10 controls up to 12 communication channels connecting DCs to immune, epithelial, and stromal cells, four of which were experimentally validated. [2] Our results reveal that a single factor can shape systems level cellular connectivity, which has important implications in the physiopathology and pharmacological manipulation of multicellular processes.

Keywords : intercellular communication, dendritic cells, systems biology, immunology

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