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기타소속:

강연제목: 단일세포전사체 데이터를 이용한 질병의 다세포적 특성 분석

Unraveling multicellular responses of human diseases using single-cell transcriptomics

Abstract:

Diseases affect various cell types within the lesions. However, the overall landscape of the multicellular responses in human diseases remains largely unexplored. We categorize the multicellular responses of human diseases based on a remapped atlas of human cells, incorporating 12 million cellular transcriptome profiles acquired from an automated data processing pipeline. We constructed a hierarchical cell classification framework comprising 32 major cell types and 165 cellular subtype annotations. Using this annotation framework, we explored an extensive atlas of human cells that includes 46 million cells from 160 diseases across 49 organs. Systematic profiling of disease and organ association patterns of cellular subtypes reveals core archetypes of human diseases repeatedly found across organs.

Brief Biosketch

* Education/Career

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| Sep 2024 ~ present | Postdoctoral fellow | KAIST |
| Mar 2020 ~ Aug 2024 | Doctor of Philosophy | KAIST |
| Mar 2016 ~ Feb 2020 | Doctor of Medicine | The Catholic University of Korea |
| Mar 2011 ~ Feb 2016 | Bachelor of Science | Seoul National University |

* Publications

Kim S*, Jeon JH*, ..., Park J-E#, Yeo J#. (2024) Innate immune responses against the mRNA vaccine promote cellular immunity through IFN- β at the injection site. ***Nat. Commun.***

Kim S*, Leem G*, ..., Kang CM#, Bang S#, Park J-E#. (2024) Integrative analysis of spatial and single-cell transcriptome data from human pancreatic cancer reveals an intermediate cancer cell population associated with poor prognosis. ***Genome Med.***