## CellCraft: a web-based platform for single cell analysis for reconstructing gene regulatory network

Jeonghwan Henry Kim<sup>1</sup>, Dongmin Shin<sup>2</sup>, Hyeonkyu Kim<sup>1</sup>, Sean Cho<sup>2</sup>, Chanho Park<sup>1</sup>, Beomsu Park<sup>1</sup>, Jungyoung Kim<sup>1</sup>, Daewon Lee<sup>2</sup>, and Junil Kim<sup>1</sup>

<sup>1</sup>School of Systems Biomedical Science, Soongsil University, 369 Sangdo-Ro, Dongjak-Gu, Seoul 06978, Republic of Korea, <sup>2</sup>School of Art and Technology, Chung-Ang University, 4726 Seodong-daero, Anseong-si, Gyeonggi-do 17546, Republic of Korea

## **Abstract**

Reconstruction of gene regulatory network (GRN) is a key step in understanding of single cell RNA sequencing (scRNAseq) analysis. Here, we introduce a web-based platform 'CellCraft' that helps researchers conduct TENET, a GRN reconstructor based on pseudotime-ordered scRNAseq dataset. CellCraft is composed of backend for TENET, frontend for graphical user interface (GUI), and database. It features a GUI equipped with visual programming that simplify complex steps of data analysis, making it easier for researchers to visualize and interpret their results. Furthermore, the tool is designed to handle advanced types of data that can reveal more about how genes are regulated and how they influence each other in space and time using single-cell multi-omics data and spatial transcriptomics data. By providing these capabilities, CellCraft aims to offer novel perspectives and insights to researchers working with single cell multi-omics and spatial transcriptomics.