

## “SCALE”: A Web-Based Tool For Mapping Gene Expression Patterns And Cell Types In The Developmental Lung At Single Cell Level

Y. Du<sup>a</sup>, M. Guo<sup>ab</sup>, J.A. Whitsett<sup>a</sup> and Y. Xu<sup>ac</sup> on behalf of NHLBI LungMap Consortium

<sup>a</sup>The Perinatal Institute and Section of Neonatology, Perinatal and Pulmonary Biology, and the <sup>c</sup>Division of Biomedical Informatics, Cincinnati Children's Hospital Medical Center, Cincinnati, OH. <sup>b</sup>Department of Electrical Engineering and Computing Systems, University of Cincinnati.

**Rationale:** The lung is a complex, multicellular organ containing a diversity of distinct cell types. Knowledge regarding the proliferation, differentiation and functions of individual cells and the mechanisms by which multiple cell types interact to form the normal lung provide scientific basis to understand the processes of lung development and repair. Recent advances in single cell isolation and massive parallel DNA sequencing make it possible to resolve cell behaviors and cell-to-cell variation in gene expression (cell states) by mapping the lung transcriptome at single cell level. Processing and interpreting large amounts of single cell genomic data presents a major challenge for most investigators. Herein we present “SCALE” (Single Cell Application of Lung Gene-Expression), a user-friendly web-tool for mapping gene expression patterns in specific pulmonary cells at single cell level.

**Methods:** We developed “SCALE” in Java IDE using Eclipse (<http://www.eclipse.org/>), an integrated development environment. MySQL relational database management system was used for data-storage and querying. Highchart (<http://www.highcharts.com/>) an interactive charting library was used to provide dynamic and interactive data visualization for prospective users.

**Results:** With “SCALE”, users are able to query a single cell RNA expression database by inputting either a gene symbol or selecting a specific pulmonary cell type of interest. “Gene query” will extract a detailed gene expression pattern across individual lung cell types, provide a list of genes highly correlated with the input gene, and display the dynamic expression pattern of the given gene during lung development (E15-PN0). The “cell type query” provides the cell type selective gene signatures, associated cell surface markers and transcription factors. After execution, “SCALE” displays query results in tables, heatmaps, bar charts and profile charts on the web page. All charts are dynamic and interactive for users to explore. Gene Links to external databases and resources such as NCBI, GeneCard, MGI, and Protein Atlas are provided.

**Availability:** The web-tool is freely available for non-commercial use at <http://research.cchmc.org/pbqe/scale> (Supported by R01HL105433 and U01HL110964-Lungmap).