



Applied DEGBOE computational framework for the dynamics of LUAD. We acquired scRNA-seq data from an individual with a pathological diagnosis of lung adenocarcinoma (LUAD) [18]. The sample includes data on primary LUAD and LUAD with metastasis. I used t-distributed stochastic neighbor embedding (t-SNE) to reduce the high-dimensional single-cell data. I compared cell growth in LUAD to a normal lung sample.

Here, I present a part of results of the project I proposed earlier for the identification of single cancer drivers. As shown in this figure, I characterized epithelial cells as cell types with an increased population, which led to the designation of epithelial cells as promoters of LUAD growth. To depict driver genes of epithelial cells, I used DEGBOE to evaluate the driver coefficients of genes in epithelial cells. Among the 15 genes with the highest coefficients, the gene *TP53INP1* was shown as the most influential cancer driver that promotes LUAD. The driver coefficients of the 15 genes in epithelial cells were the lowest compared to their coefficients in the remaining identified cell types. In particular, NK cells had the highest driver coefficients of all the 15 genes, indicating the absence or death of NK cells and a decrease in other cell populations at metastasis. Based on this initial result, I hypothesize that the 15 designated cancer drivers play an immunosuppressive role in promoting LUAD.