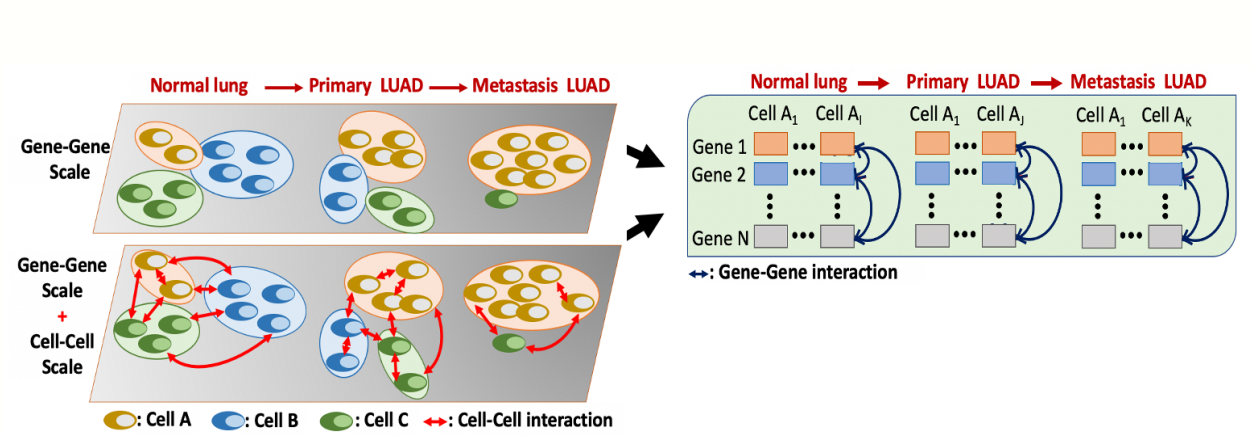


**Overview of principles for interpreting cancer drivers.** Visual representation of cancer drivers in terms of cell-cell communication (e.g., *Cell A*, *Cell B*, and *Cell C*), and gene-gene interaction. For example, with the total number of genes *N* that interact with each other, Cell A type presents *I*, *J*, and *K* total population in the normal lung, primary, and metastasis LUAD, respectively.

For *N* number of genes in a single cell data, the DEGBOE method is expected to give a tractable form of the density of the dynamics of gene expression in each cell of a cluster in terms of the observation (normalized single cell data), and (*N-1*) possible interactions of genes. Since a variation in gene expression in a cell convey the greatest information about the relationship between expression and disease severity, I plan to relate the density of gene expression to gene expression level in a cell. Finally, I defined the gene driver coefficient as the rate of a gene expression level over the total number of cells in a specific cluster. The results can be used to identify a single cancer driver and distinguish driver mutations from passenger mutations, since passenger mutations have low driver coefficients and thus a non-significant effect on new driver mutations for lung cancer progression.