**scRNA-Seq data analysis ICA guidance**

**Background:**

Mammary gland (MG) is a unique organ in mammals, whose development relies on the precise control of differentiation of mammary epithelial cells and the interaction between epithelial cells and other types of cells in the tissue. It is known that a specific type of diet will affect the development of mammary gland, but the detailed molecular and cellular alteration is unclear. To unveil this, scRNA-Seq is performed in mammary gland from normal mice (Control) and mice fed with specific diet (Treatment).

Please use the data to explore the following two questions.

1. Does the diet change the cell-type composition of mammary gland?
2. What are the gene expression alterations in luminal cells, basal cells and adipocytes in the mammary gland?

You can explore different ways to exhibit the data. The presented results should be accompanied with biological interpretation. And the answers to the questions should be supported by the results from your analysis.

(Reference: https://journals.biologists.com/dev/article/142/6/1028/47198/Mammary-gland-development-cell-fate-specification)

**The following raw data are provided in ZJE server** (/public/workspace/chaochenwang/Course/GP2\_ICA\_scRNASeq\_data/2023)

1. Control\_MG\_10X\_Matrix
2. Treatment\_MG\_10X\_Matrix