Digital Assignment – I

Course Code: BBIT327L

Course Title: Data Analytics in Bioinformatics

Slot: G1+TG1

Question: Write a review on available single cell RNA-seq (scRNA-seq) data integration methods. Describe their use with example code and output as screenshot. Use any example scRNA-seq dataset.

After integration using one such method, find the differentially expressed genes (markers) of the cell types across conditions and provide some analytical hypothesis from the list of marker genes.

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