**Manual for t-SNE Visualization Interactive app**

This manual describes the functionality of a MATLAB-based GUI designed for visualizing gene expression data using t-distributed Stochastic Neighbor Embedding (t-SNE), a machine learning algorithm for dimensionality reduction. This interactive GUI allows users to perform t-SNE computations on their dataset, visualize the results in 3D, cluster data using K-means, and explore gene correlations and proximities. Start the t-SNE app GUI from by clicking t-SNE button on main IVCCA GUI.

## GUI Components and Features

### 1. Data Input and Initialization

Upon starting, the GUI initializes and prompts the user to input their dataset through MATLAB's workspace. The dataset should include gene expression data with genes as variables.

### 2. t-SNE Computation

The GUI performs t-SNE on the input data, visualizing the data points in a 3D scatter plot. It preprocesses the data by filling missing values, performing PCA for dimensionality reduction, and then applying t-SNE.

### 3. Visualization Controls

3D Scatter Plot: Displays the t-SNE results. Users can interact with the plot, brush points, visualize gene expression, rotate and zoom to explore data points. Buttons for Analysis:

**Cluster:** Performs K-means clustering on the t-SNE results and visualizes clusters.

**Clear Clusters:** Removes clustering results from the visualization.

**Select Pathway(s):** Allows users to highlight specific genes or pathways by selecting files with gene lists.

**Clear Highlights**: Removes any highlighted genes from the visualization.

**Visualize Gene:** Searches for and highlights a specific gene entered in the adjacent input field.

**Find proximity genes**: Highlights a gene and its nearest neighbors based on the number specified by the user.

**Connect to STRING:** Opens a connection or visualizes the selected from the table gene in the STRING database for network analysis.

### 4. Data Interaction and Exploration

Gene Selection: Users can select genes directly from the scatter plot or through the gene list to view specific information or highlight them.

Brushing and Linking: Allows users to brush (select) points on the scatter plot to see their gene names in a table, facilitating detailed analysis of selected genes.

**Saving and Exporting Results:**

The GUI offers functionality to save clustering results and highlighted genes for further analysis, either programmatically or through user interaction with the GUI.

### 5. Advanced Features

Customization and Extensions: Users with programming knowledge can modify the GUI to add new features, integrate with other databases, or adapt the visualization to other types of data.