

Visualizing gene expression:

Instructions for uploading the sample files into the visgenex software

The human_embryo_data zip contains the following files:

HG-U133A.na29.annot.csv
human_embryo_2148genes_6clusters.csv
HG-U133A.na29.annot.csv_Annotation.mat
human_embryo_2148genes-Repository.mat
human_embryo_2148genes-Study.mat
human_embryo_2148genes-Exported-tSNEmap.mat
human_embryo_2148genes-6clusters-Supplement.mat

Transfer files to visgenex folders

Transfer all raw data files to the folder "raw data" contained in the visgenex-matlab zip (visgenex_matlab/data/raw data). This step is not required, but we recommend it.

Transfer HG-U133A.na29.annot.csv_Annotation.mat and human_embryo_2148genes-6clusters-Supplement.mat to visgenex_matlab/data/libraries.

Transfer human_embryo_2148genes-Repository.mat to visgenex_matlab/data/repositories.

Transfer human_embryo_2148genes-Study.mat and human_embryo_2148genes-Exported-tSNEmap.mat to visgenex_matlab/data/studies.

Set directory

To use the visgenex software, set the current directory in Matlab to the "utils" folder contained in the visgenex_matlab folder (visgenex_matlab/utils).

Transform raw data files into Matlab files

The .csv files are raw data files and need to be transformed into Matlab files. This is done by entering the following commands into the Matlab command window and following the instructions in the graphical user interface.

1. Create a Matlab **Annotation file** from a .csv file:
Type "gui_annotation" and follow the instructions in the GUI, selecting HG-U133A.na29.annot.csv as the raw annotation file.
2. Create Matlab **Repository and Supplement files** from a .csv file:

Type "gui_repository" and follow the instructions in the GUI:

Step 1:

Import human_embryo_2148genes_6clusters.csv as the raw repository file.

Step 2:

- Scroll down and assign "Comment" from the pull-down menu to columns 19 - 25, which are labelled "Cluster...". These columns contain information about the cluster membership of individual genes and will be saved in a separate supplemental file.
- Set the number of groups (pull-down menu on the right, above the "Done" button) to 6, and columns 1 - 18 will be automatically assigned to groups 1 - 6.
- Click "Done".

Step 3:

Click "Skip" (The data in the sample file has already been log2 transformed).

Step 4:

Enter a repository name and click "Done".

Step 5:

Delete the suggested prefix and click "Remove prefix" (nothing needs to be removed).

Final Step - Save:

- Click "Save Comments file" to save the supplemental file.
- Click "Process and Save Repository" to save the repository file.

Create a Study

Type "gui_study" and follow the instructions in the GUI:

- Click "Load repository" and select either the repository file provided (human_embryo_2148genes-Repository.mat) or the one you have created.
- Click "Save without filtering".
- Save.

Create a t-SNE map

Type "gui_analysis".

- Click "Load Study" and select either the study file provided (human_embryo_2148genes-Study.mat) or the one you have created (It will be in a newly created folder with the name of your study).

- Click "Load Primary Annotation" and select either the annotation file provided (HG-U133A.na29.annot.csv_Annotation.mat) or the one you have created.
- Click "Plot t-SNE (z scores)". Rendering of the plot will take several minutes.

Export a t-SNE map

- To save a t-SNE map that you have generated (above) click "Export t-SNE data" and save.

Import an existing t-SNE map

Type "gui_analysis".

- Click "Load Primary Annotation" and select either the annotation file provided (HG-U133A.na29.annot.csv_Annotation.mat) or the one you have created.
- Click "Import t-SNE data" and select either the exported-tSNE file provided (human_embryo_2148genes-Exported-tSNEmap.mat) or the one you have created.

Import additional information from a supplement file

- Follow the instructions to create or import a t-SNE map (above).
- Click "Load Supplementary Annotation" and select either the supplement file provided (human_embryo_2148genes-6clusters-Supplement.mat) or the one you have created.
- Click "Pre-process".

For instructions on how to analyse and manipulate the plot, please refer to the general user guide.