

Supplementary Fig. S1. Screenshots of scGEApp.

scGEApp - GUI of scGEAToolbox

Load Data | Filter | Normalization | Batch Correction | Imputation | Feature Selection | Visualization | Clustering | Pseudotime | Network

Data 1

File Name:

Data 2

File Name:

Data Source:

☐ Your Own
☐ Example 1 Data
☒ Example 2 Data

Data 1: [6044 genes x 644 cells]

Genes	Cell 1	Cell 2	Cell 3		
AP006222.2	3	0	2	0	
NOC2L	3	4	3	0	
HES4	38	29	4	18	
ISG15	558	358	172	514	
AGRN	3	3	6	6	

Data 2: [7757 genes x 835 cells]

Genes	Cell 1	Cell 2	Cell 3		
FO538757.2	1	1	0	0	
AP006222.2	2	0	2	0	
NOC2L	1	1	2	3	
HES4	50	15	19	50	
ISG15	279	312	425	180	

Data | Result | About

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Filter 1

Minimal # of nonzeros (per gene)
Minimal # of nonzeros (per cell)

Select Genes with at least
 cells having >=
 read(s) per cell.

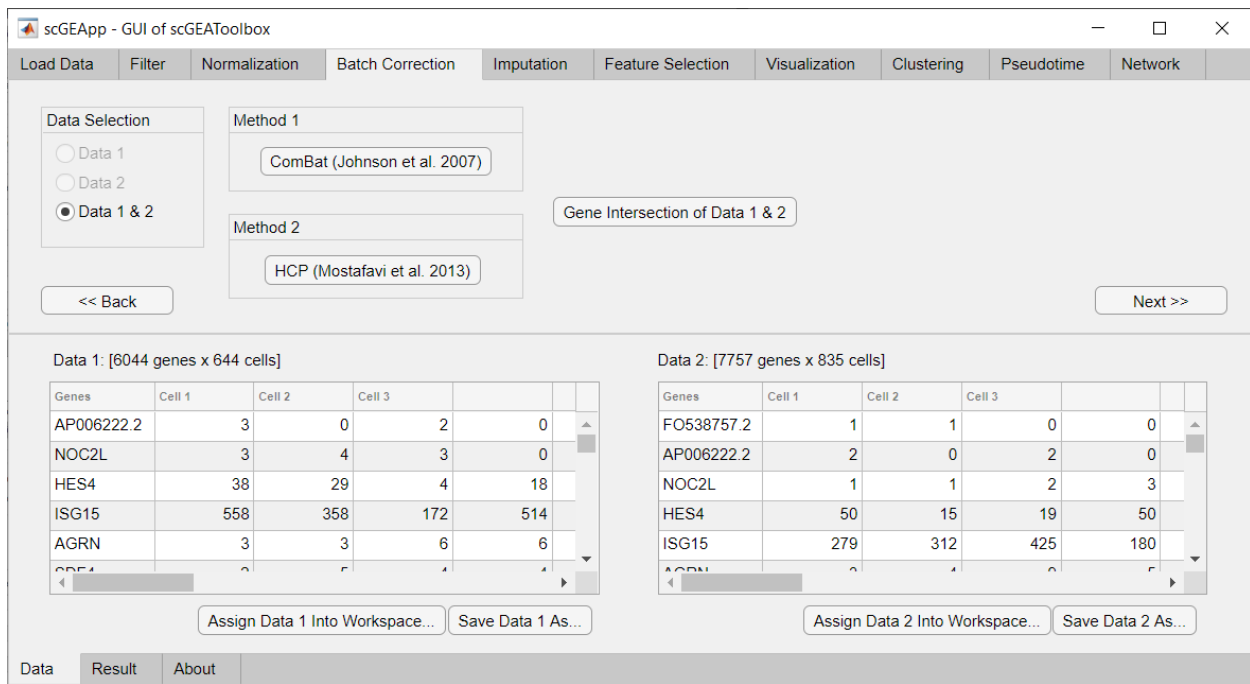
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☒ Data 1

☐ Data 2

☐ Data 1 & 2

All Cells

PCA...

t-SNE...

Diffusion Map...

PHATE 3D...

Featured Genes

Expression Landscape (3D Stem)...

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All Genes

Mean-CV 2D Scatter...

Mean(log)-Var(log) 2D Scatter...

Mean-Dropout 2D Scatter...

Mean-CV-Dropout 3D Scatter...

Combined Embedding...

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Assign Data 1 Into Workspace...

Save Data 1 As...

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Assign Data 2 Into Workspace...

Save Data 2 As...

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☒ Data 1

☐ Data 2

☐ Data 1 & 2

Cell Clustering Method 1

SC3: consensus clustering

Cell Clustering Method 2

SIMLR: multi-kernel learning

Cell Clustering Method 3

SOPTSC: symmetric NMF

of Clusters

☒ Automatic Estimation

☐ Predefine k= 3

☐ Show Clusters in t-SNE Plot

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Assign Data 2 Into Workspace...

Save Data 2 As...

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