


PLATFORM INSTRUCTION

Patients RNA-seq and Clinic data Explorer

Data CollectionData ProcessingEDADEGALASSO FeatureSelectGo Enrichment

Upload Gene Expression files

Browse...

7 files selected.

Upload

GSE114286.csv

Index	ID_REF	3.8-1.3	3.8-1.4	...	ZYX	ZZEP1	ZZZ3
0	NN1	0	0	...	1401	1161	140
1	NN5	0	0	...	2321	708	47
2	NN7	0	0	...	1005	637	34
3	NN8	0	0	...	6091	2165	54
4	NN10	0	0	...	1978	1274	103

GSE54456.csv

Index	ID_REF	A2ML1	AAGALT	...	ZNF90	ZNRH2	ZP1
0	M3209	115.8440018	8.863999825	...	0.081	9.093000412	0.0
1	M3171	32.24000108	9.506999969	...	0.022	13.3760004	0.0
2	M3418	83.30000305	13.27200031	...	0.097999997	5.861999989	0.046999998
3	M3878	104.4179993	11.137799953	...	0.024	7.485000153	0.0
4	M4208	138.1970062	9.092000008	...	0.149000004	10.6170002	0.057

AGSE121212.csv

Index	ID_REF	SS_rRNA	75K	...	snoU2-30	snoU2-19	sno25
0	AD_004_lesional	0	9	...	30	28	4
1	AD_004_non-lesional	3	6	...	37	19	3
2	AD_005_lesional	9	25	...	21	38	14
3	AD_005_non-lesional	12	25	...	18	32	14
4	AD_006_lesional	2	7	...	20	25	3

ADGSE157194.csv

Index	ID_REF	NIPAL3	ANKK1	...	AL590434.1	AC009093.10	AF228730.6
0	Patient1AL	733	1182	...	0	0	0
1	Patient1AN	557	596	...	0	0	0
2	Patient2AN	962	792	...	1	0	0
3	Patient2AL	873	1050	...	1	0	0
4	Patient3AN	1129	1299	...	0	2	0

Upload Meta-data files

Browse...

meta_general.csv

UploadNext

Data Preview

metaFile

Index	ID_REF	LABEL
0	Patient1AL	AD_LESION
1	Patient1AN	AD_NONLESION
2	Patient2AN	AD_NONLESION
3	Patient2AL	AD_LESION
4	Patient3AN	AD_NONLESION

Navigator Tab:DataCollection

Upload RNA-seq Files, each file needs to include ID_REF

- Demonstration skin datasets (RPKM):
- GSE54456** psoriasis
 - GSE114286** psoriasis
 - GSE121212** psoriasis
 - GSE157194** atopic dermatitis(AD)
 - GSE186476** Cutaneous lupus erythematosus
 - GSE179633** DLE (discoid lupus erythematosus, a main type of CLE) ,SLE(systemic lupus erythematosus)
 - GSE 130955** Prospective Registry for Early Systemic Sclerosis (PRESS)

Upload meta-data Files, each file needs to include ID_REF and LABEL, may include some clinic data

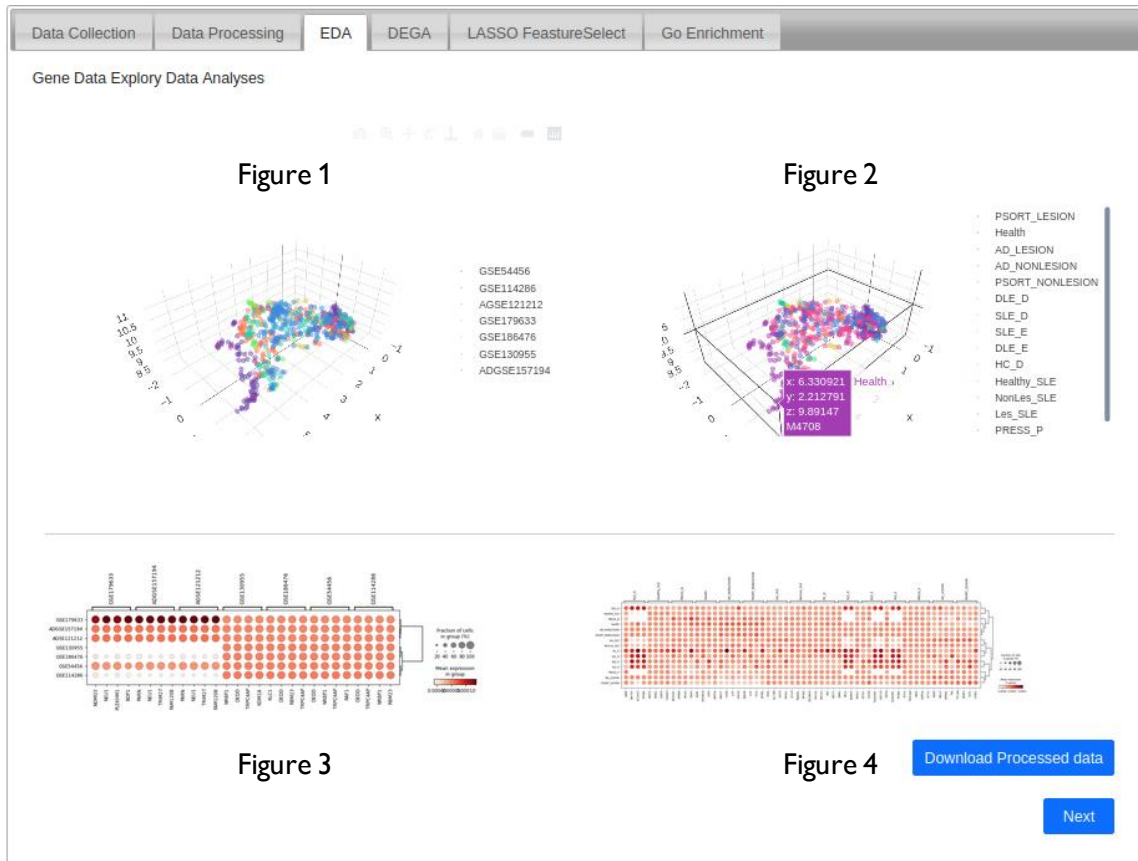
The screenshot shows a software interface with a horizontal tab bar at the top. The tabs are labeled 'Data Collection', 'Data Processing', 'EDA', 'DEGA', 'LASSO FeatureSelect', and 'Go Enrichment'. The 'Data Processing' tab is currently selected and highlighted. Below the tab bar, the interface is divided into three sections: 'Combined Options', 'Log2 Transformation', and 'Feature Reduction Method'. In the 'Combined Options' section, there are two radio buttons: 'Combat' (which is selected) and 'Harmony'. In the 'Log2 Transformation' section, there are two radio buttons: 'Yes' and 'No' (which is selected). In the 'Feature Reduction Method' section, there are two radio buttons: 'TSNE' and 'UMAP' (which is selected). At the bottom center of the interface, there is a blue button labeled 'Next'.

Combined Options	Log2 Transformation	Feature Reduction Method
<input checked="" type="radio"/> Combat	<input type="radio"/> Yes	<input type="radio"/> TSNE
<input type="radio"/> Harmony	<input checked="" type="radio"/> No	<input checked="" type="radio"/> UMAP

Next

Navigator Tab:DataProcessing

Options for preprocessing the data



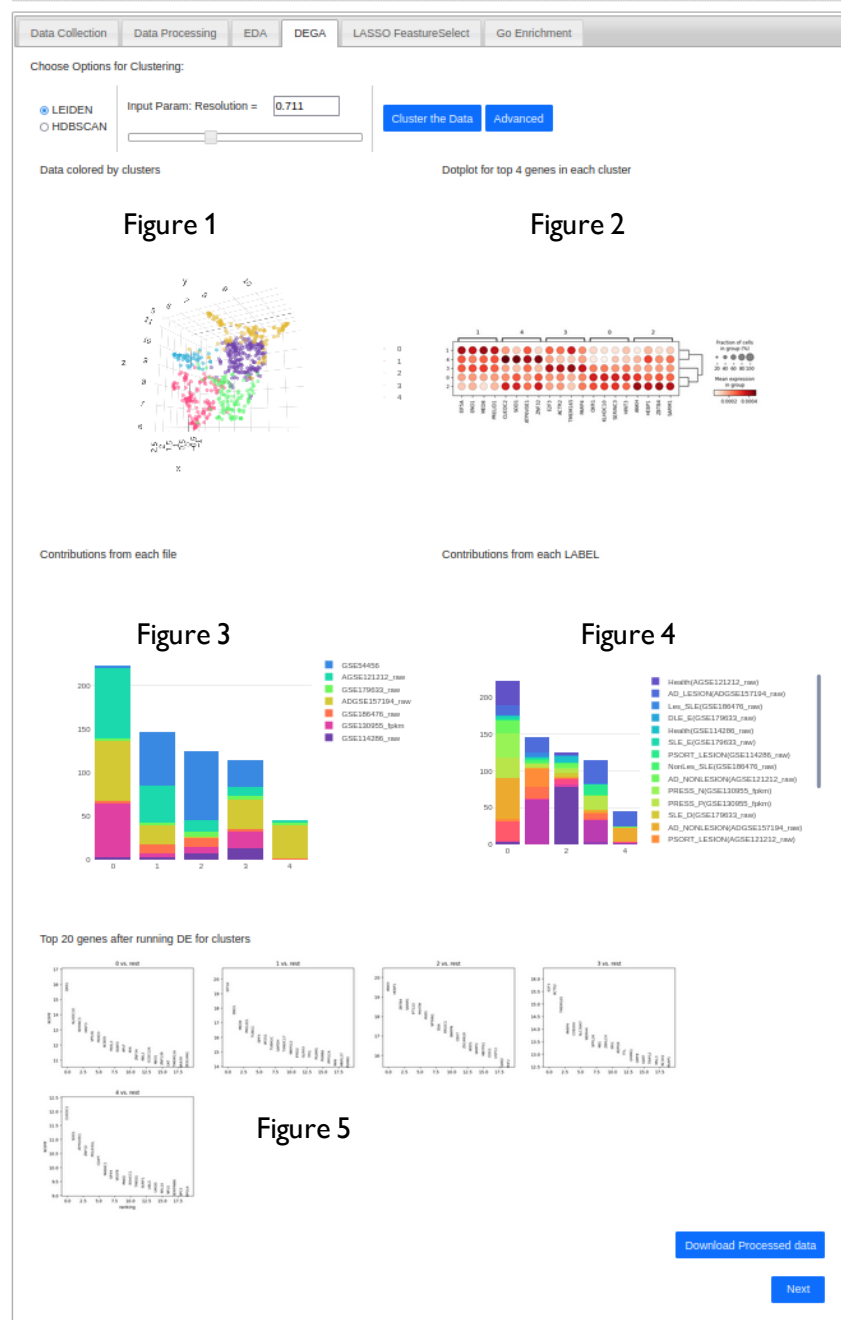
Navigator Tab: EDA

Figure 1: plotted data colored by FileNames

Figure 2: plotted data colored by LABEL in meta file

Figure 3: Dotplot for top 4 genes in each file

Figure 4: Dotplot for top 4 genes in each LABEL



Navigator Tab: DEDA

User can choose options for clustering with parameters:

Figure 1: plotted data colored by clusters

Figure 2: Dotplot for top 4 genes in each cluster

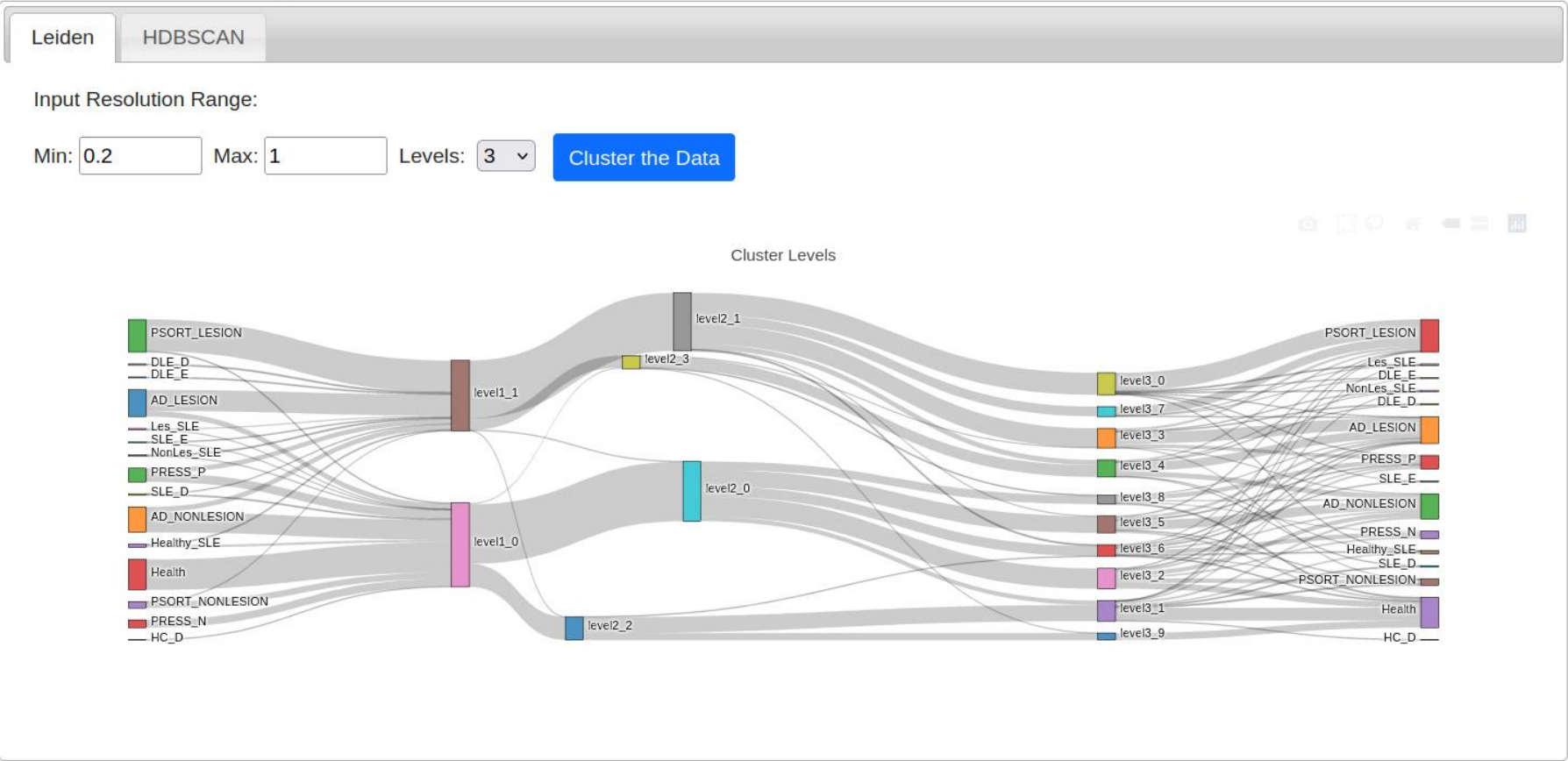
Figure 3: contributions from each file

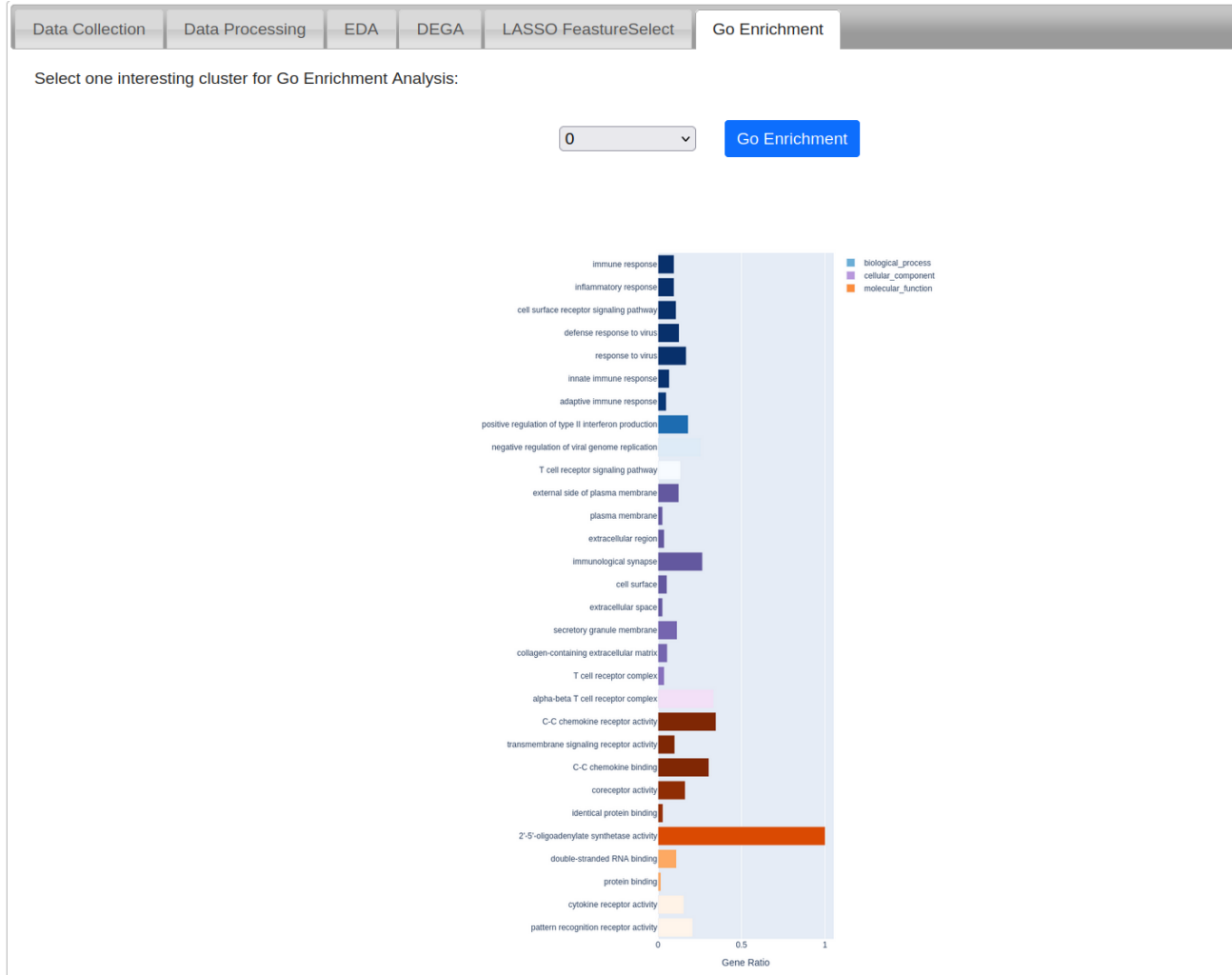
Figure 4: contributions from each LABEL

Figure 5: top 20 genes after running DE for clusters

Advanced Clustering

Advanced Clustering





Navigator Tab: Go Enrichment
User can specify a cluster for Go Enrichment: