sMAP:
Standard Microarray Analysis Pipeline

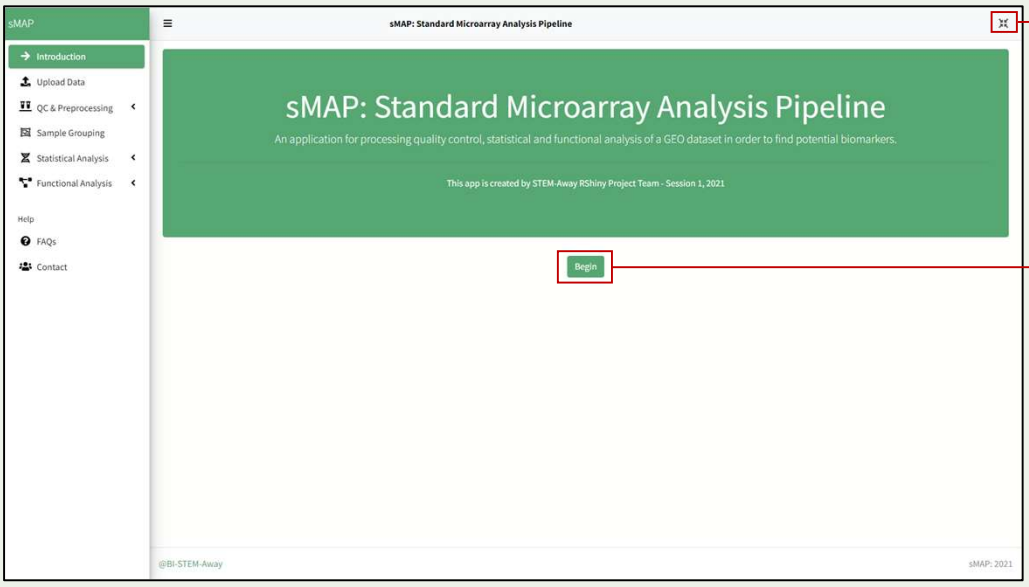
An R Shiny Educational App for Transcriptomic Analysis

GitHub: https://github.com/BI-STEM-Away/sMAP

Documentation: https://bi-stem-away.github.io/sMAP_doc/

sMAP Website: https://bi-stem-away.github.io/sMAP/

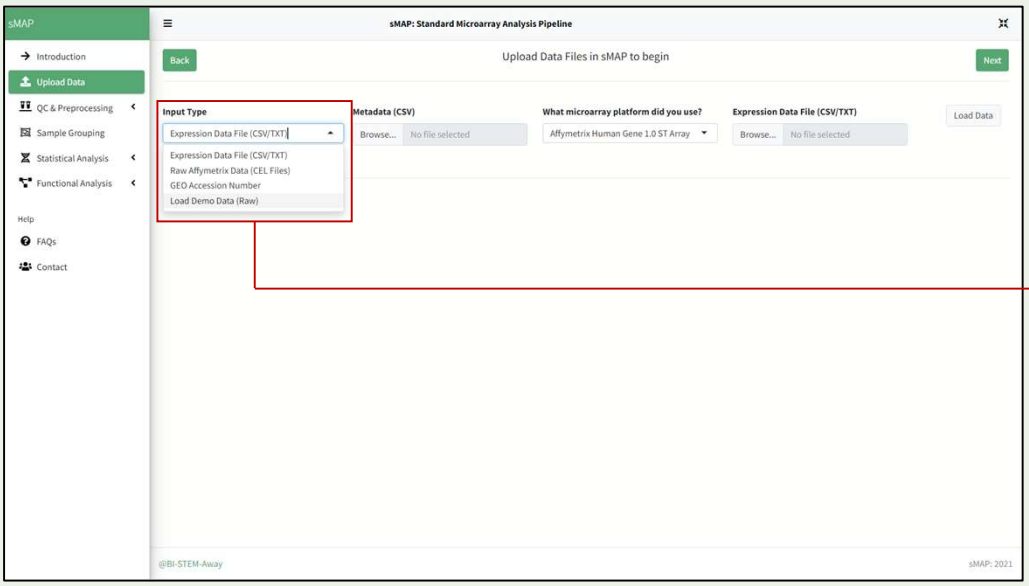
Welcome screen of sMAP



Click on Fullscreen mode for better visualization

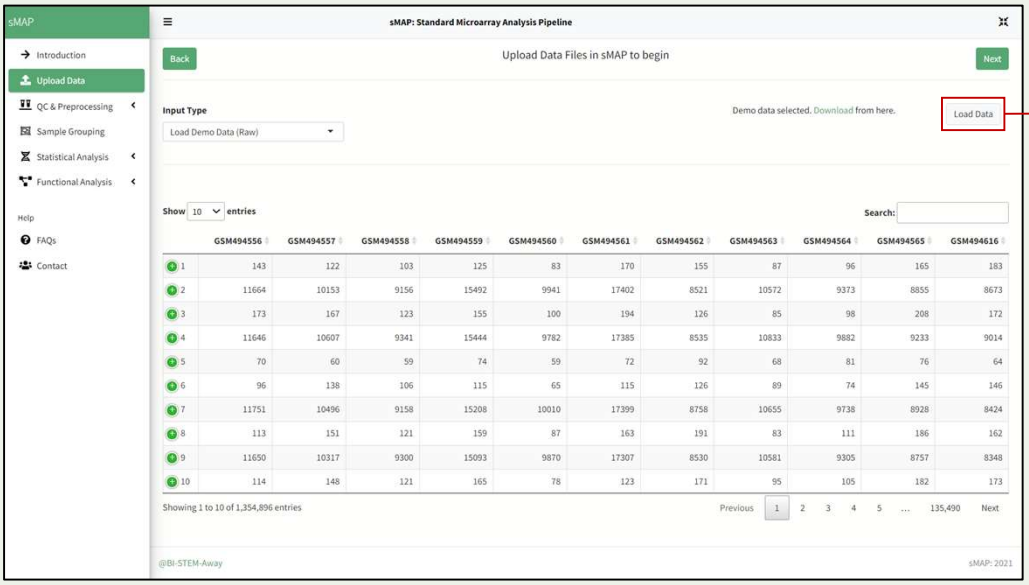
Click on Begin to get started with sMAP.

Data Importation



Select one of the 3 data input methods sMAP provides or get started with an installed demo dataset.

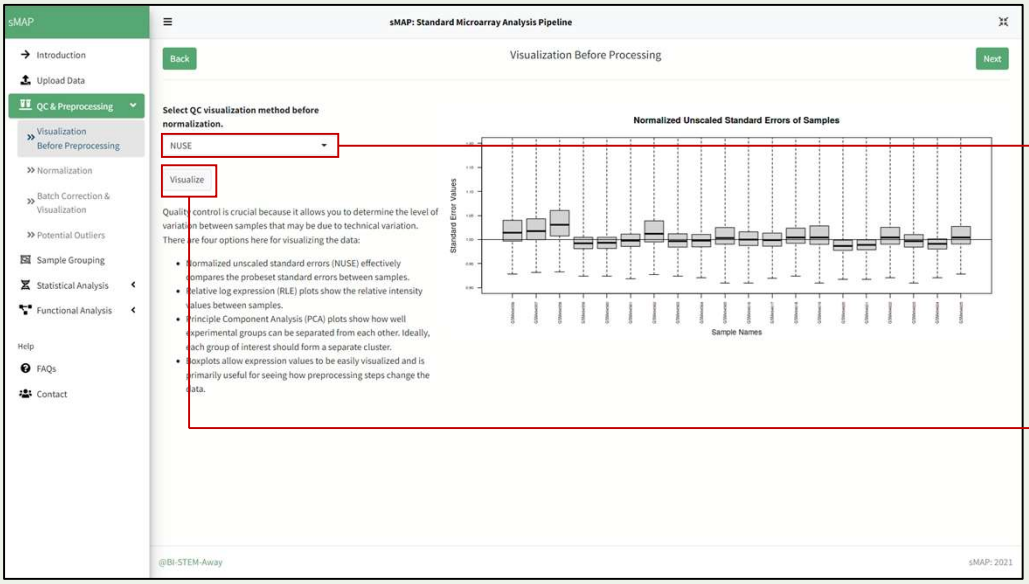
Data Loading



Click on load data after selecting input method and uploading datasets.

Here we will use demo dataset that comes installed in sMAP.

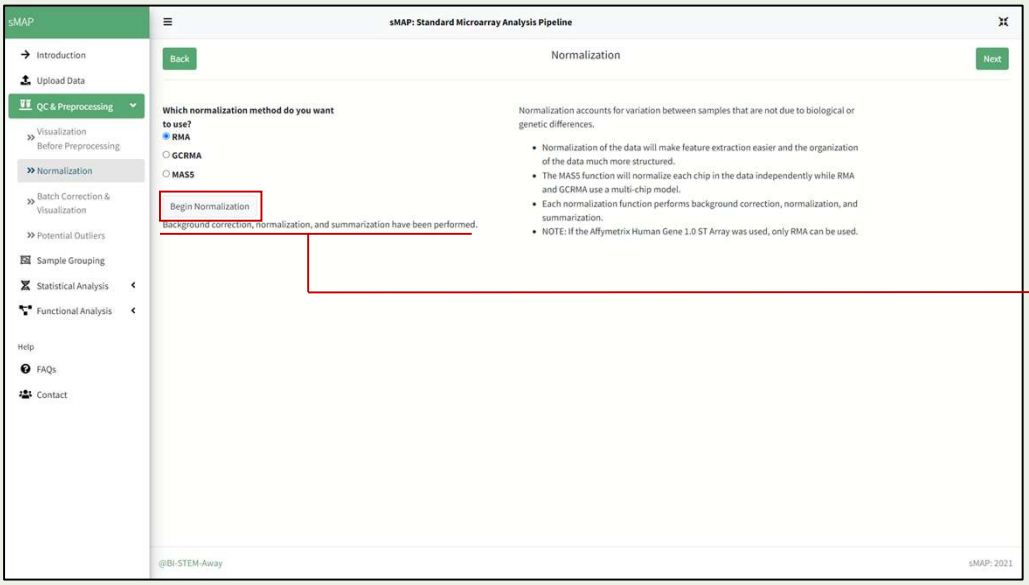
QC: Visualization of raw data before normalization



Select one of the 4 visualization methods.

Click on visualize to load the plot.

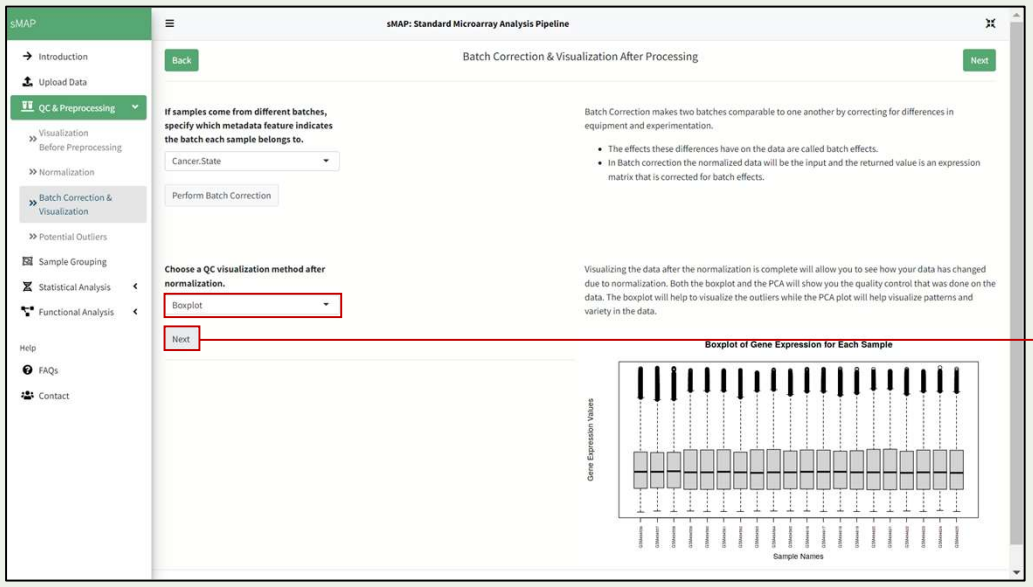
QC: Normalization of raw data



Select one of the 3 methods for normalization of raw data.

Click on begin normalization to normalize and wait for the message to appear below indicating completion..

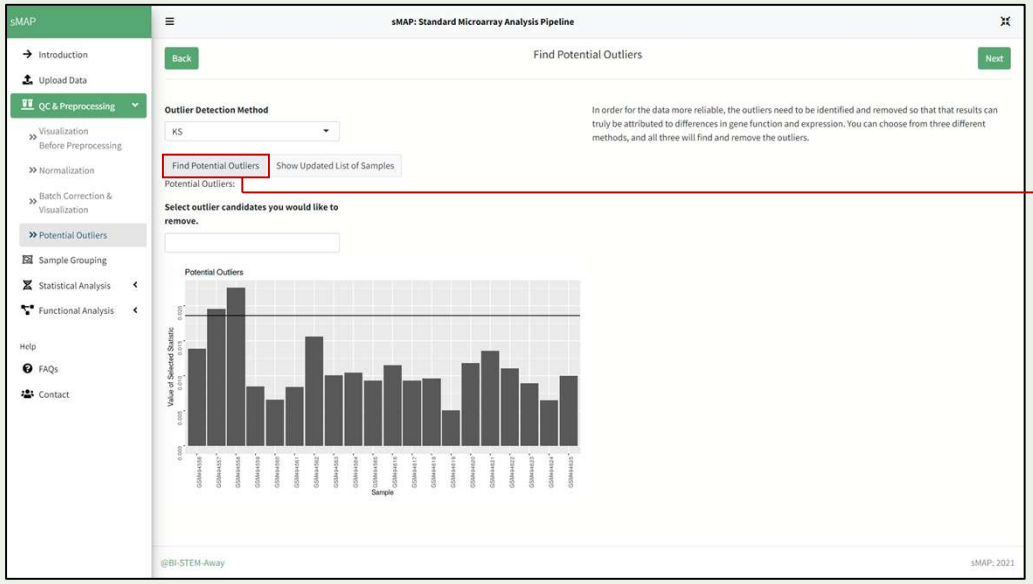
QC: Batch Correction + Visualization of normalized data



Here we will not use batch correction since demo dataset is from single batch.

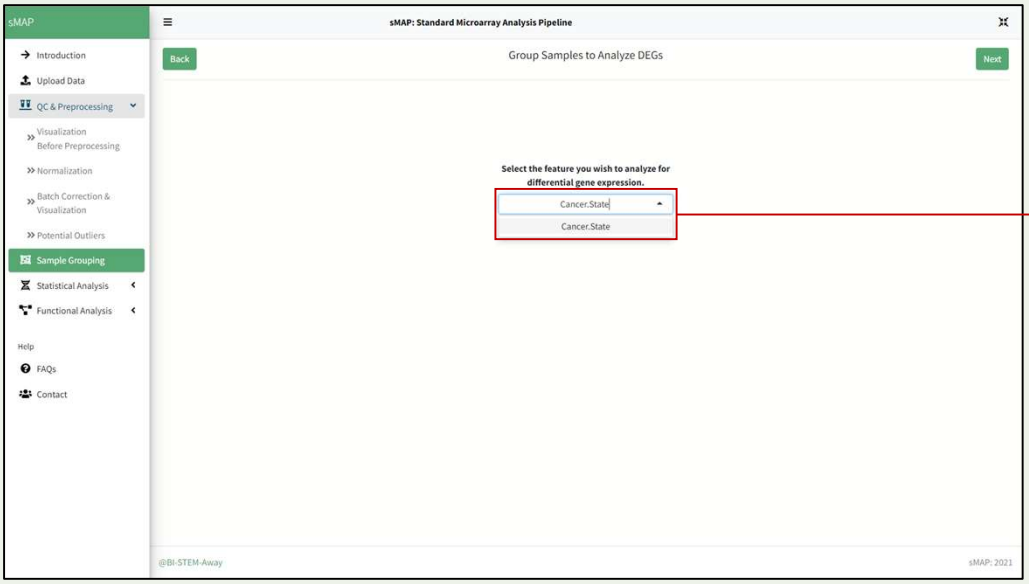
Select visualization method to check data after normalization and click next to generate plot.

QC: Detection and remove of outliers



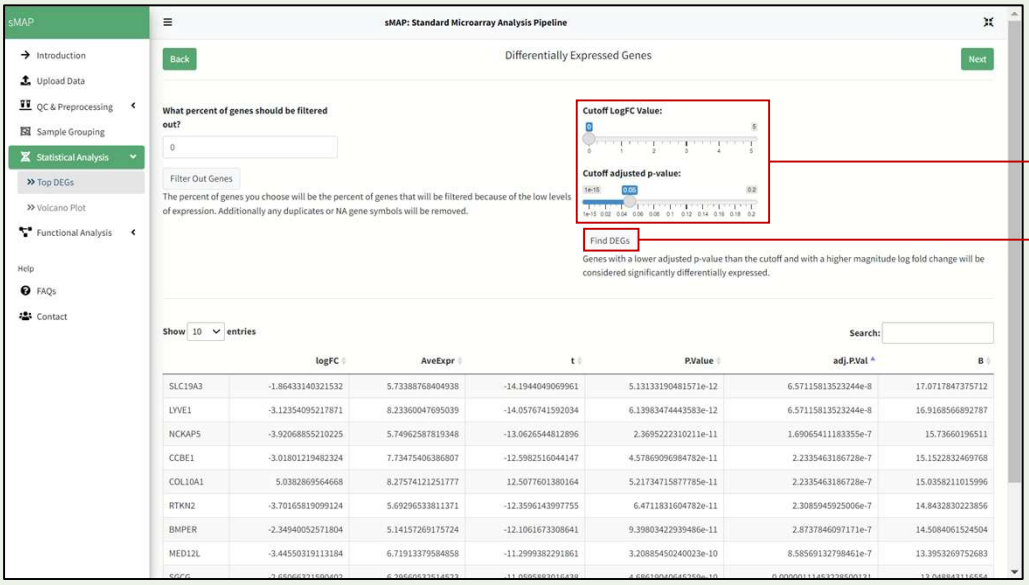
Find potential outliers and if need remove them from dataset.

Sample Grouping for DEG Analysis



Select column name in metadata file which contains sample grouping information.

Gene Filtering and Differentially Expressed Gene Analysis

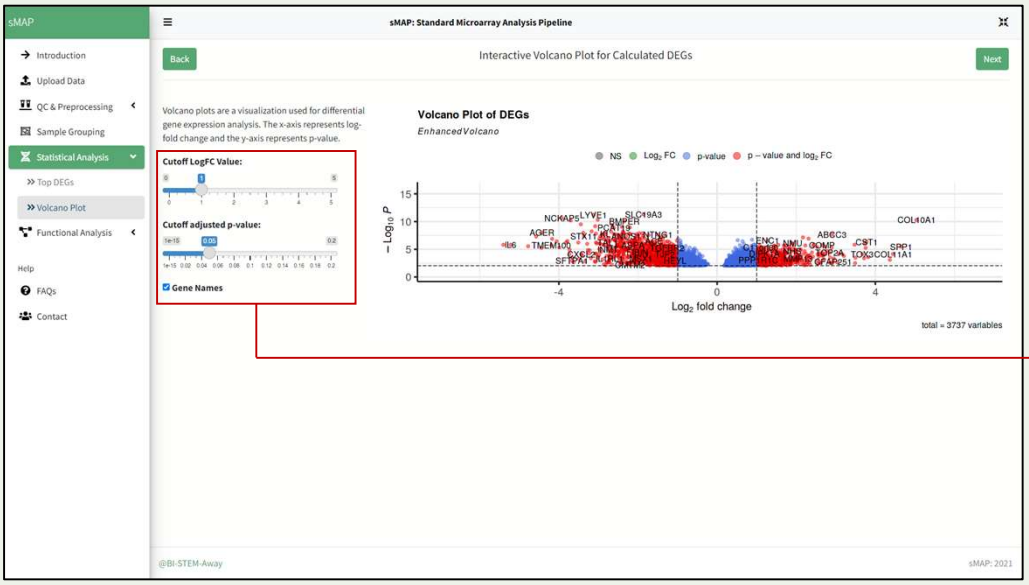


Adjust required parameters for DEG analysis.

Click on find DEGs to start analysis.

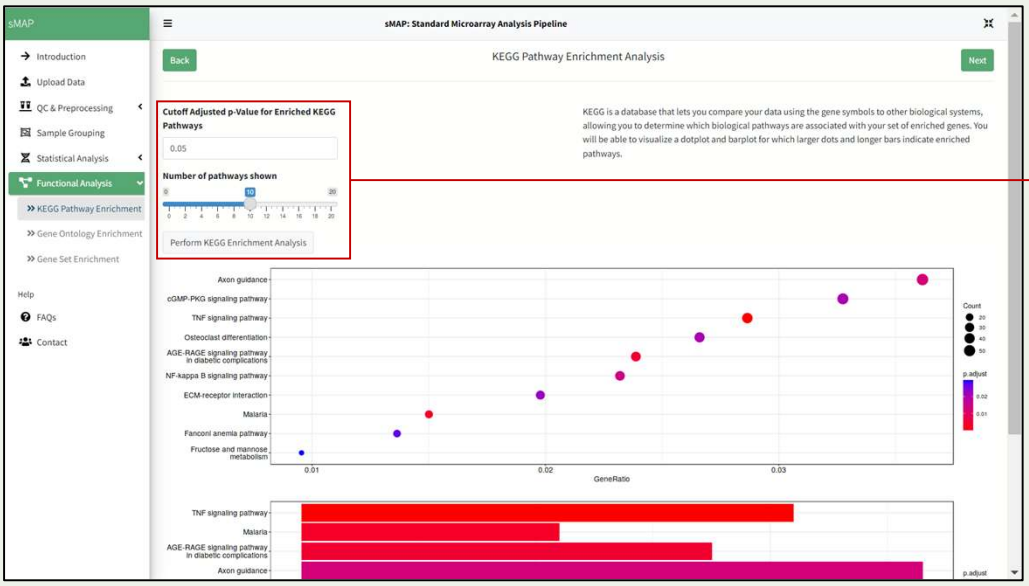
* We didn't use gene filtering option for this demo but can be used as per requirement of user.

Volcano plot



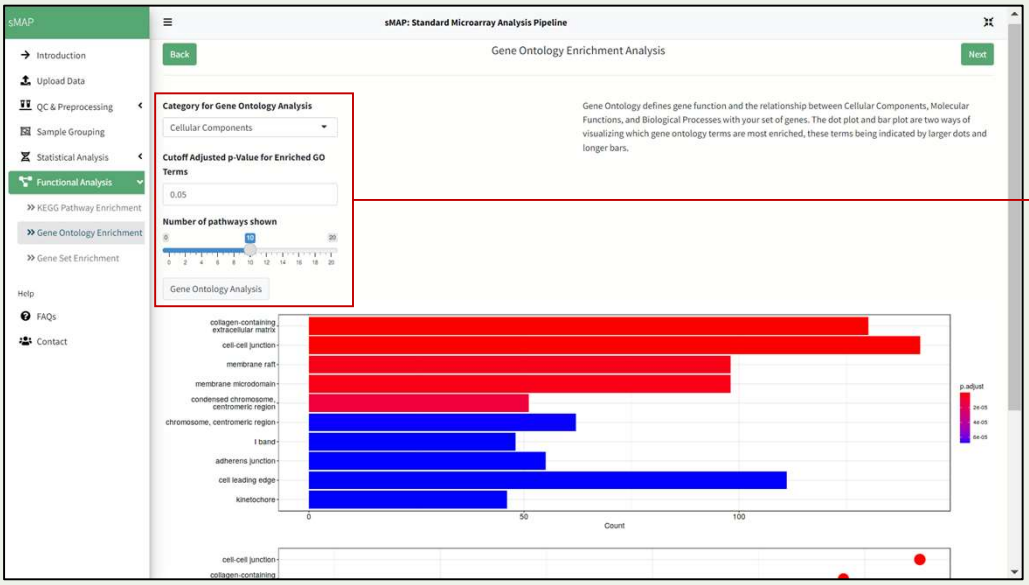
Adjust parameters for volcano plot visualization and use check box to show/hide gene symbols.

Enrichment Analysis: KEGG Pathway Enrichment Analysis



Adjust P-value and other parameters for KEGG pathway enrichment analysis.

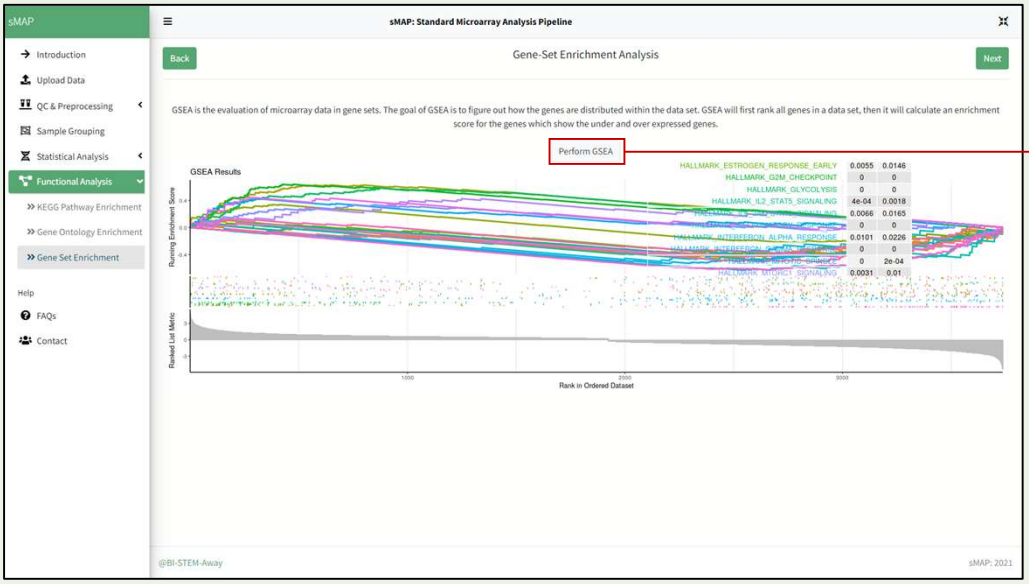
Enrichment Analysis: Gene Ontology Enrichment Analysis



Select one of the three GO categories.

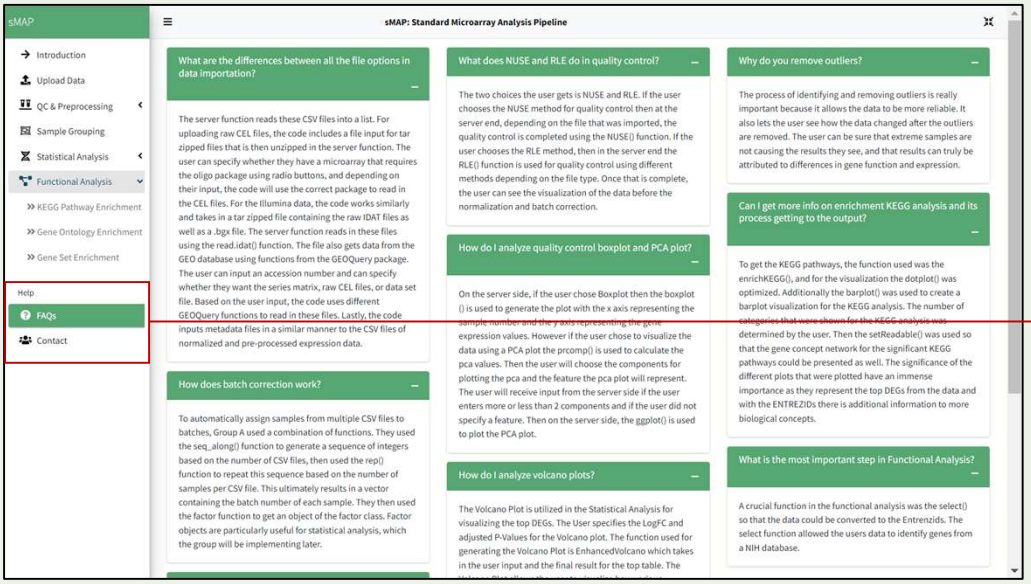
Adjust P-value and other parameters for GO enrichment analysis.

Enrichment Analysis: Gene Set Enrichment Analysis



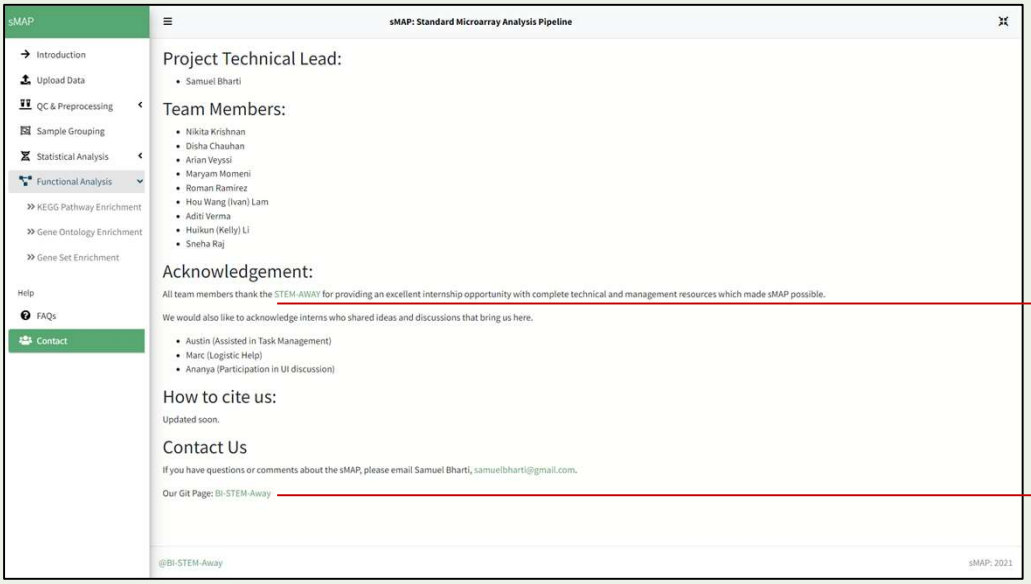
Perform GSEA analysis.

Help Sections: Frequently Asked Questions



Use this section for FAQs/help

Help section: Contact us and check out stemaway.com



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Visit out GitHub Page to clone repo and get docker image