Please place files signature, exclusion.signature, and average.signature.exclusion in a known location.

Open a terminal window with the the directory where the scripts are located as working directory.

Please run the scripts as follows:

1. Script to calculate Dysfunction, Exclusion and TIDE scores. Input should be expression (FPKM log2(x+1) - average) data in matrix format as in the attached file format_examples>colon.expression.

./dysfunction_exclusion_patient_original_signatures.R [path to file signature] [path to file exclusion.signature] [path to file average.signature.exclusion] [path to gene expression file] [path to output file with name of output file]

2. Scripts to generate plots

./anti-correlation_plot.R [path to result of dysfunction_exclusion_patient_original_signatures.R] [path to output file containing the plot with name of file]

./average_correlation_exclusion_plot. [path to output of dysfunction_exclusion_patient_original_signatures.R] [path to output file containing the plot with f name of file]

./TAM_correlation_exclusion_plot.R [path to result of dysfunction_exclusion_patient_original_signatures.R] [path to output file containing the plot with name of file]

./CAF_correlation_exclusion_plot.R [path to result of dysfunction_exclusion_patient_original_signatures.R] [path to output file containing the plot with name of file]

./MDSC_correlation_exclusion_plot.R [path to result of dysfunction_exclusion_patient_original_signatures.R] [path to output file containing the plot with name of file]

2. Scripts to check gene expression and correlations with Dysfunction and Exclusion. Input file should be gene expression centered in csv format as in the attached file format_examples>expression_centered.csv.

./gene_expression_plot.R [path to gene expression file in csv format] [list of genes to check separated by commas] [path to output containing expressions of CTL genes with filename] [path to the directory where plots should be saved]

Examples:

./dysfunction_exclusion_patient_original_signatures.R   /Users/mesm/Desktop/

signature   /Users/mesm/Desktop/exclusion.signature   /Users/mesm/Desktop/average.signature.exclusion /Users/mesm/Desktop/colon.expression /Users/mesm/Desktop/colon_results.csv

/anti-correlation_plot.R   /Users/mesm/Desktop/colon_results.csv /Users/mesm/Desktop/colon_correlation_dysfunction_exclusion_plot.png

./average_correlation_exclusion_plot.R   /Users/mesm/Desktop/colon_results.csv /Users/mesm/Desktop/colon_Average_correlation_CTL_exclusion_plot.png

./TAM_correlation_exclusion_plot.R   /Users/mesm/Desktop/colon_results.csv /Users/mesm/Desktop/colon_TAM_correlation_CTL_exclusion_plot.png

./CAF_correlation_exclusion_plot.R /Users/mesm/Desktop/colon_results.csv /Users/mesm/Desktop/colon_CAF_correlation_CTL_exclusion_plot.png

./MDSC_correlation_exclusion_plot.R /Users/mesm/Desktop/colon_results.csv /Users/mesm/Desktop/colon_MDSC_correlation_CTL_exclusion_plot.png