gsa_FUN {AffyPipelineHG2ST} R Documentation

CAMERA Gene Set Analysis

Description

This finction performs gene set test using the method implemented in the camera function of th limma package

Usage

gsa_FUN(top_t = NULL, rma_obj, exprmnt, cntrst = "simple", msig.data.lists, cnt_mat = NULL, d_m = NULL, msigs = NULL, wts = NULL, pltfrm = "AFFY", res_path)

Arguments

top_t toptable

rma_obj an rma object or an MAList

exprmnt character vector for the short experiment expression

cntrst character, defaults to simple, which denotes a simple treatment-control design, otherwise pairwise contrasts are used as described in the contrast matrix

cnt_mat contrast matrix
d_m design matrix

msigs only used if platform != affy, numeric for the number of MSigDB gene lists

wts numeric weights of different samples pltfrm defaults to AFFY, but could be others

res_path path to save files

Author(s)

Ahmed Sadik

[Package AffyPipelineHG2ST version 2.0 Index]