pi0.mod	*Dependence adjusted estimator for the proportion of true null hypotheses*

Description

Estimates the proportion of true null hypotheses by modifying an existing estimator for the same under sparse dependence as described in the article "Estimation of the proportion of true null hypotheses under sparse dependence with application to colorectal cancer".

Usage

pi0.mod (pi0.est, data, f)

Arguments

pi0.est   A function estimating the proportion of true null hypotheses with only one argument being the dataset. For description of the dataset in its argument see description of the argument data.

data   A data (microarray) matrix with rows corresponding to the genes and columns corresponding to the samples.

f   A small fraction with no default choice.

Value

Estimate of the proportion of true null hypotheses.