visGSEA

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visGSEA   *Function to visualise running enrichment score for a given sample and*
                                  a gene set

Description

visGSEA is supposed to visualise running enrichment score for a given sample and a gene set. To help understand the underlying running enrichment score, the input gene scores are also displayed. Positions for members in the given gene set are color-coded in both displays (red line for the positive gene scores, and green line for the negative).

Usage

```
visGSEA(eTerm, which_sample = 1, which_term = "GO:0006281", weight = 1,
orientation = c("vertical", "horizontal"), newpage = T)
```

Arguments

eTerm   an object of class "eTerm"

which_sample   which sample will be used. It can be index or sample names

which_term   which term will be used. It can be index or term ID or term names

weight   type of score weigth. It can be "0" for unweighted (an equivalent to Kolmogorov-Smirnov, only considering the rank), "1" for weighted by input gene score (by default), and "2" for over-weighted, and so on

orientation   the orientation of the plots. It can be either "vertical" (default) or "horizontal"

newpage   logical to indicate whether to open a new page. By default, it sets to true for opening a new page

Value

invisible

Note

See Also

dGSEA, dGSEAview

Examples

```
#visGSEA(eTerm, which_sample=1, which_term=1)
```