visGSEA

July 16, 2015

---

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)
```