

visGSEA

April 22, 2015

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| visGSEA | <i>Function to visualise running enrichment score for a given sample and a gene set</i> |
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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 weighth. 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

none

See Also

[dGSEA](#), [dGSEAView](#)

Examples

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