dEnricherView

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dEnricherView | *Function to view enrichment results of dEnricher*

Description

dEnricherView is supposed to view results of enrichment analysis by dEnricher.

Usage

```
dEnricherView(eTerm, top_num = 10, sortBy = c("adjp", "pvalue",
"zscore",
"nAnno", "nOverlap", "none"), decreasing = NULL, details = F)
```

Arguments

eTerm
: an object of class "eTerm"

top_num
: the maximum number of gene sets (terms) will be viewed

sortBy
: which statistics will be used for sorting and viewing gene sets (terms). It can be "adjp" for adjusted p value, "pvalue" for p value, "zscore" for enrichment z-score, "nAnno" for the number of sets (terms), "nOverlap" for the number in overlaps, and "none" for ordering according to ID of gene sets (terms)

decreasing
: logical to indicate whether to sort in a decreasing order. If it is null, it would be true for "zscore", "nAnno" or "nOverlap"; otherwise it would be false

details
: logical to indicate whether the detailed information of gene sets (terms) is also viewed. By default, it sets to false for no inclusion

Value

a data frame with following components:

- setID: term ID; as rownames
- name: term name
- nAnno: number in gene members annotated by a term
- nOverlap: number in overlaps
- zscore: enrichment z-score
- pvalue: nominal p value

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- `adjp`: adjusted p value
- `namespace`: term namespace; optional, it is only appended when "details" is true
- `distance`: term distance; optional, it is only appended when "details" is true
- `members`: members (represented as Gene Symbols) in overlaps; optional, it is only appended when "details" is true

Note

See Also

dEnricher

Examples

```
#dEnricherView(eTerm, top_num=10, sortBy="adjp", decreasing=FALSE, details=TRUE)
```