

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

- `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

none

See Also

[dEnricher](#)

Examples

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