dGSEAwrite

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dGSEAwrite   *Function to write out enrichment results*

Description

dGSEAwrite is supposed to write out enrichment results.

Usage

```
dGSEAwrite(eTerm, which_content = c("gadjp", "adjp", "pvalue", "FWER",
"FDR",
"qvalue", "nES", "ES"), which_score = c("gadjp", "adjp", "FWER", "FDR",
"qvalue", "nES"), cutoff = 0.1, filename = NULL, keep.significance = T)
```

Arguments

eTerm   an object of class "eTerm"

which_content   the content will be written out. It includes two categories: i) based on "adjp" for adjusted p value, "gadjp" for globally adjusted p value, "pvalue" for p value, "FWER" for family-wise error rate, "FDR" for false discovery rate, "qvalue" for q value; ii) based on "ES" for enrichment score, "nES" for normalised enrichment score. For the former, the content is : first -1*log10-transformed, and then multiplied by -1 if nES is negative.

which_score   which statistics/score will be used for declaring the significance. It can be "adjp" for adjusted p value, "gadjp" for globally adjusted p value, "FWER" for family-wise error rate, "FDR" for false discovery rate, "qvalue" for q value

cutoff   a cutoff to declare the signficance. It should be used together with 'which_score'

filename   a character string naming a filename

keep.significance

     logical to indicate whether or not to mask those insignfiicant by NA. By default, it sets to true to mask those insignfiicant by NA

Value

a data frame with following components:

- `setID`: term ID
- `setSize`: the number of genes in the set
- `name`: term name
- `namespace`: term namespace
- `distance`: term distance
- `sample names`: sample names in the next columns

Note

If "filename" is not NULL, a tab-delimited text file will be also written out.

See Also

[dGSEA](#)

Examples

```
#output <- dGSEAwrite(eTerm, which_content="gadjp", which_score="gadjp", filename="eTerm.txt")
```