Package 'Oncofilterfast'

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Type Package

Title Aids in the Analysis of Genes Influencing Cancer Survival

Version 1.0.0

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Description Aids in the analysis of genes influencing cancer survival by including a principal function, calculator(), which calculates the P-value for each provided gene under the optimal cutoff in cancer survival studies. Grounded in methodologies from significant works, this package references Therneau's 'survival' package (Therneau, 2024; <https://CRAN.R-project.org/package=survival>) and the survival analysis extensions by Therneau and Grambsch (2000, ISBN 0-387-98784-3). It also integrates the 'survminer' package by Kassambara et al. (2021; <https://CRAN.R-project.org/package=survminer>), enhancing survival curve visualizations with 'ggplot2'.

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RoxygenNote 7.3.1

Depends survival, survminer

NeedsCompilation no

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R topics documented:

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calculator   *calculator of Pvalue*

Description

By using this function, you can calculate the Pvalue of all genes you have provided.

Usage

```
calculator(survival, RNA, result)
```

Arguments

survival	the dataframe that contains survival data
RNA	the dataframe that contains the expression data of genes
result	the dataframe which will contains the outcome

Value

this function will return a dataframe that contains either the gene's ensemble IDs and it's Pvalue.

Examples

```
library(Oncofilterfast)
result <- data.frame(gene = c("A"),Pvalue = c(1))
RNA_all_path=system.file("extdata", "TCGA-LGG.htseq_fpkm.tsv", package = "Oncofilterfast")
RNA_all=read.csv(RNA_all_path,header=TRUE,sep="\t")
rows_to_keep <- apply(RNA_all[, -1], 1, function(row) {
  non_zero_count <- sum(row != 0)
  total_elements <- length(row)
  (non_zero_count / total_elements) >= 0.5
  })
RNA <- RNA_all[rows_to_keep, ]
survival_path=system.file("extdata", "TCGA-LGG.survival.tsv", package = "Oncofilterfast")
survival=read.csv(survival_path,header=TRUE,sep="\t")
final=calculator(survival=survival,RNA=RNA,result=result)
print(nrow(final))
filtered_result <- final[final$Pvalue < 0.01, ]
print(nrow(filtered_result))
print(filtered_result)
```

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