Package 'Oncofilterfast'

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Type Package

Title Aids in the Analysis of Genes Influencing Cancer Survival

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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'.

Encoding UTF-8

RoxygenNote 7.3.1

Depends survival, survminer

NeedsCompilation no

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Contents

`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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