

Package: mt.surv (via r-universe)

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Type Package

Title Multi-Threshold Survival Analysis

Version 1.1.1

Description Implements survival analyses across multiple abundance thresholds, repeatedly partitioning samples into groups and evaluating survival differences to assess taxonomic associations with outcomes.

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Suggests testthat, rmarkdown, survminer

Imports dplyr, survival, broom, forcats, purrr, tidyr, ggplot2, magrittr

NeedsCompilation no

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butterfly_input	<i>Generate input for butterfly plot</i>
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Description

Generate input for butterfly plot

Usage

```
butterfly_input(area.input, subtype, num_micro)
```

Arguments

area.input	a dataframe with area for all taxonomy level generated by 'calculateArea'
subtype	a string object specifying what cancer subtype to be included
num_micro	an integer indicating how many microbes should be included for zoomed up version

Value

a list with two ggplot2 objects. One for all taxonomy level and another for selected number specified in 'num_micro'

Examples

```
# Create mock area input data
area.input <- data.frame(
  type = c("T_DDLPS", "T_DDLPS", "T_DDLPS",
           "T_LMS", "T_LMS",
           "O_DDLPS", "O_DDLPS", "O_DDLPS",
           "O_LMS", "O_LMS"),
  species = c("Proteobacteria", "Firmicutes", "Bacteroidetes",
             "Proteobacteria", "Firmicutes",
             "Proteobacteria", "Firmicutes", "Bacteroidetes",
             "Proteobacteria", "Firmicutes"),
  area = c(0.45, 0.30, 0.25,
           0.60, 0.40,
           0.35, 0.40, 0.25,
```

```

    0.50, 0.50)
  )

# Run for DDLPS subtype, showing top 3 microbes
result <- butterfly_input(area.input, subtype = "DDLPS", num_micro = 3)

# Result is a list with two ggplot objects
# result$common.taxarea.all - stacked bar chart of all shared taxa
# result$common.taxarea.head - dodged bar chart of top num_micro taxa

```

calculateArea

Quantify taxonomy significance using multi-threshold results

Description

This function calculates the distance between alpha (default 0.05) and p-values below the significance threshold as an indicator of area under the curve.

Usage

```
calculateArea(taxlev, threshold.mat, alpha = 0.05)
```

Arguments

taxlev	a character object specifying which subject survival analysis is applying to.
threshold.mat	output from function survivalByQuantile. It includes information about survival under various threshold
alpha	a numeric value representing the statistically significant p-value

Value

A data frame containing the calculated area values for the specified taxonomy level.

Examples

```

# Create mock threshold matrix for two taxonomy levels
threshold.mat <- list(
  Phylum = data.frame(
    pval = c(0.01, 0.04, 0.10, 0.02, 0.50),
    hazard.direction = c("<1", "<1", ">1", ">1", "<1")
  ),
  Family = data.frame(
    pval = c(0.03, 0.20, 0.001, 0.04, 0.08),
    hazard.direction = c(">1", "<1", "<1", ">1", ">1")
  )
)

# Calculate area for Phylum level at default alpha = 0.05
result <- calculateArea(taxlev = "Phylum", threshold.mat = threshold.mat)

```

```
# Calculate area for Family level with stricter alpha
result_strict <- calculateArea(
  taxlev      = "Family",
  threshold.mat = threshold.mat,
  alpha       = 0.01
)
```

StackBarinput

Generate input objects for stacked bar plots

Description

Generate input objects for stacked bar plots

Usage

```
StackBarinput(TCGA.list, ORIEN.list)
```

Arguments

TCGA.list a list object containing survival and taxonomy information for TCGA
 ORIEN.list a list object containing survival and taxonomy information for ORIEN

Value

a dataframe that can be used to make stacked bar plot

Examples

```
# Create mock TCGA taxonomic data
tcga_tax <- data.frame(
  ID = c("S1", "S2", "S3"),
  p__Proteobacteria = c(0.4, 0.3, 0.5),
  p__Firmicutes     = c(0.2, 0.4, 0.1),
  p__Bacteroidetes  = c(0.2, 0.1, 0.2),
  p__Actinobacteria = c(0.1, 0.1, 0.1),
  p__Chordata       = c(0.1, 0.1, 0.1)
)

# Create mock TCGA clinical data
tcga_clin <- data.frame(
  ID           = c("S1", "S2", "S3"),
  diagnosis    = c("Dedifferentiated liposarcoma",
                  "Leiomyosarcoma, NOS",
                  "Other sarcoma"),
  vitalstatus  = c(1, 0, 1),
  days        = c(365, 200, 500)
)
```

```

# Create mock ORIEN taxonomic data
orien_tax <- data.frame(
  ID = c("P1", "P2", "P3"),
  p__Proteobacteria = c(0.5, 0.2, 0.3),
  p__Firmicutes     = c(0.1, 0.5, 0.2),
  p__Bacteroidetes = c(0.2, 0.2, 0.3),
  p__Actinobacteria = c(0.1, 0.0, 0.1),
  p__Chordata       = c(0.1, 0.1, 0.1)
)

# Create mock ORIEN clinical data
orien_clin <- data.frame(
  ID                = c("P1", "P2", "P3"),
  diagnosis         = c("Dedifferentiated liposarcoma",
                       "Leiomyosarcoma, NOS",
                       "Other sarcoma"),
  AgeCollect       = c(55, 62, 48),
  AvatarKey        = c("A1", "A2", "A3"),
  AgeAtLastContact = c(57, 63, 50),
  PrimaryMet       = c("Primary", "Met", "Primary"),
  vitalstatus      = c(1, 0, 1),
  days             = c(400, 150, 600)
)

# Bundle into lists and run
TCGA.list <- list(tcga_tax, tcga_clin)
ORIEN.list <- list(orien_tax, orien_clin)

result <- StackBarinput(TCGA.list, ORIEN.list)

```

survival_plot

Make survival curve

Description

Make survival curve

Usage

```
survival_plot(modified_input, taxlev, title.input)
```

Arguments

`modified_input` the output list from 'generate_surv_input' function

`taxlev` an output string object from 'generate_surv_input' specifying a taxonomy level to be plotted

`title.input` a string object to specify the title of the plot

Value

a ggplot object

Examples

```
## Example requires survival and survminer
set.seed(123)

## Simulated survival data
surv_df <- data.frame(
  days = runif(60, min = 100, max = 4000),
  vitalstatus = sample(c(0, 1), 60, replace = TRUE)
)

## Simulated taxonomic matrix (one column per taxonomic level)
tax_mat <- data.frame(
  "k__Bacteria" = rlnorm(60, meanlog = -2, sdlog = 0.5),
  "p__Firmicutes" = rlnorm(60, meanlog = -1.8, sdlog = 0.6)
)

## Simulated threshold table for each taxonomic level
thresh_k <- data.frame(
  percentile = c(0.25, 0.50, 0.75),
  pval = c(0.01, 0.05, 0.10)
)

thresh_p <- data.frame(
  percentile = c(0.30, 0.60, 0.90),
  pval = c(0.02, 0.04, 0.08)
)

## Assemble modified_input list
modified_input <- list(
  tresh = list(
    "k__Bacteria" = thresh_k,
    "p__Firmicutes" = thresh_p
  ),
  tax.mat = tax_mat,
  surv = surv_df
)

## Run survival plot
p <- survival_plot(
  modified_input = modified_input,
  taxlev = "k__Bacteria",
  title.input = "Example Cohort"
)

## View plot
p
```

survivalByQuantile *Compute cox model p-value under various threshold*

Description

Compute cox model p-value under various threshold

Usage

```
survivalByQuantile(  
  input.var,  
  input.tax,  
  surv.dat,  
  percentiles = seq(0.01, 0.99, 0.01)  
)
```

Arguments

input.var	a character object specifying which subject survival analysis is applying to.
input.tax	data frame containing information about an object to be tested. The sample order must agree with surv.dat's sample order
surv.dat	a data frame containing all survival information. The sample order must agree with input.dat's sample order
percentiles	a list of numeric values specifying all of the percentiles to be tested on

Details

The threshold used in this function is to categorize data into two groups

Value

The function will generate a data frame containing hazard ratio, lower bound, upper bound, percentile, cutoff threshold, and p-value. This data frame can then be manipulated for various plots

Examples

```
set.seed(123)  
  
## Simulated survival data  
surv.dat <- data.frame(  
  ID = paste0("S", 1:50),  
  days = runif(50, 100, 3000),  
  vitalstatus = sample(c(0, 1), 50, replace = TRUE)  
)  
  
## Simulated taxonomic abundance matrix  
input.tax <- data.frame(  
  genus_A = rlnorm(50, meanlog = -2, sdlog = 0.5),
```

```

    genus_B = rlnorm(50, meanlog = -1.5, sdlog = 0.6)
  )

  ## Compute hazard ratios across quantiles
  res <- survivalByQuantile(
    input.var = "genus_A",
    input.tax = input.tax,
    surv.dat = surv.dat,
    percentiles = seq(0.2, 0.8, 0.2)
  )

  res

```

 ToWide

Change data frame into wide format and match survival data

Description

Change data frame into wide format and match survival data

Usage

```

ToWide(
  data.long,
  surv.dat,
  taxalevels = c("domain", "kingdom", "phylum", "class", "order", "family", "genus",
    "species")
)

```

Arguments

<code>data.long</code>	input taxonomy matrix in long format
<code>surv.dat</code>	survival information for the <code>data.long</code>
<code>taxalevels</code>	character vector representing every taxonomy level to be changed into wide format

Value

a long format of the taxonomy data with matching survival information

Examples

```

## Reproducible example
set.seed(123)

## Simulated long-format exogenous relative abundance data
data.long <- data.frame(
  ID = rep(paste0("S", 1:10), each = 4),

```

```
exo.ra = runif(40),
domain = rep("d_Bacteria", 40),
kingdom = rep("k_Bacteria", 40),
phylum = rep(c("p_Firmicutes", "p_Proteobacteria"), each = 20),
class = rep(c("c_Bacilli", "c_Gammaproteobacteria"), each = 20),
order = rep("o_TestOrder", 40),
family = rep("f_TestFamily", 40),
genus = rep(c("g_A", "g_B"), times = 20),
species = rep(c("s_A1", "s_B1"), times = 20)
)

## Simulated survival metadata
surv.dat <- data.frame(
  ID = paste0("S", 1:10),
  days = runif(10, 500, 3000),
  vitalstatus = sample(c(0, 1), 10, replace = TRUE)
)

## Convert to wide format across taxonomic levels
wide_list <- ToWide(
  data.long = data.long,
  surv.dat = surv.dat
)

## Inspect output
names(wide_list)
wide_list$phylum
```

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