

Package ‘SurvBal’

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Type Package

Title Selection of Compositional Microbiome Balances for Survival Outcomes

Version 1.1.0

Description Enables the selection of microbiome balances in relation to censored survival and time-to-event outcomes which are of considerable interest, particularly in many biomedical studies. The most common Cox proportional hazards and standard parametric survival (including accelerated failure time) models are included in the package, which are used in combination with step-wise selection procedures to identify the optimal associated ratio of the geometric means of two groups of taxa’s relative abundances.

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URL <https://github.com/yinglia/SurvBal>

BugReports <https://github.com/yinglia/SurvBal/issues>

Depends R (>= 3.5.0)

Imports boot,
ggplot2,
nonnestcox,
survival (>= 3.5.7),
survminer,
zCompositions (<= 1.4.0.1)

Suggests knitr,
rmarkdown

VignetteBuilder knitr

License GPL (>= 3)

Encoding UTF-8

LazyData true

RoxygenNote 7.2.3

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bacteria	<i>Raw Taxon Count Table</i>
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Description

The data is a raw taxon count table consisting of 63 samples and 139 taxa

Usage

```
bacteria
```

Format

An object of class `data.frame` with 63 rows and 139 columns.

balance_selection	<i>Selection of the optimal balance of microbiome associated with survival outcomes</i>
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Description

`balances_selection()` identifies the log-ratio of geometric means of two sets of taxa that is most associated with the survival outcome using a greedy forward stepwise selection approach

Usage

```
balance_selection(
  Surv_obj,
  data,
  covariates = NULL,
  min_prevalence = 0.1,
  mult_repl = TRUE,
  model = "coxph",
  dist = "weibull",
  stopping_pvalue = 0.15,
  sequential_test = FALSE,
  sequential_alpha = 0.25,
  selection_criterion = "min_decrement_pvalue",
  selection_threshold = 0.15,
  quantile_plotted = c(0.25, 0.5, 0.75),
  alpha = 0.05
)
```

Arguments

<code>Surv_obj</code>	An object of class <code>Surv</code> generated by <code>survival:Surv</code>
<code>data</code>	A $n \times p$ matrix which is the raw taxon count table, where rows are the samples, columns are the taxa
<code>covariates</code>	A $n \times q$ data frame containing important covariates for adjustment, which could be a mixture of q continuous and discrete (pre-defined as factor) variables. The default value is <code>NULL</code>
<code>min_prevalence</code>	The minimum prevalence of taxa that could be considered in the selection procedure. The default value is <code>0.1</code>
<code>mult_repl</code>	A logical variable indicating which algorithm is used to process the raw taxon count table. If <code>TRUE</code> then the geometric Bayesian Multiplicative Replacement (<code>zCompositions:cmultRepl</code>) is used to impute the inflated zeros. Otherwise, a small pseudo count (<code>0.5</code>) will be added to all raw counts. Finally, either processed data will be converted to relative abundance, then log of relative abundance will be used in the selection procedure. The default value is <code>TRUE</code>
<code>model</code>	Specifies which kind of survival regression model is built. The options are “ <code>coxph</code> ” (<code>survival:coxph</code>) and “ <code>parametric</code> ” (<code>survival:survreg</code>). Make sure there is no zero survival time if choose “ <code>parametric</code> ”. The default value is “ <code>coxph</code> ”.
<code>dist</code>	Specifies which kind of parametric distribution is used if <code>model</code> is “ <code>parametric</code> ”. The options include “ <code>weibull</code> ”, “ <code>exponential</code> ”, “ <code>gaussian</code> ”, “ <code>logistic</code> ”, “ <code>lognormal</code> ” and “ <code>loglogistic</code> ”. For more details, please see <code>survival:survreg</code> . The default value is “ <code>weibull</code> ”
<code>stopping_pvalue</code>	The threshold of p-value to stop the forward search. The forward search where, at each step, a new taxon is added to the existing balance, will be stopped if the resulting p-value is larger than <code>stopping_pvalue</code> . The default value is <code>0.15</code>
<code>sequential_test</code>	A logical variable indicating whether sequential testing, in addition to <code>stopping_pvalue</code> , is used to stop the forward search. If <code>TRUE</code> , the forward search where, at each step, a new taxon is added to the existing balance, will be stopped if the new balance is not significantly different from the current one in the survival regression model. The default value is <code>FALSE</code>
<code>sequential_alpha</code>	The level of significance for the sequential testing if <code>sequential_test</code> is <code>TRUE</code> . The default value is <code>0.25</code>
<code>selection_criterion</code>	The criterion to select balance in the final model. The options include “ <code>min_pvalue</code> ” and “ <code>min_decrement_pvalue</code> ”. If “ <code>min_pvalue</code> ” is used, the balance that has the smallest p-value along the forward selection path will be selected. If “ <code>min_decrement_pvalue</code> ” is used, the decrement of p-value along the forward selection path will be calculated, the balance before the first decrement that is smaller than <code>selection_threshold</code> will be selected. The default value is “ <code>min_decrement_pvalue</code> ”
<code>selection_threshold</code>	A threshold of p-value decrement used for balance selection in the final model if <code>selection_criterion</code> is “ <code>min_decrement_pvalue</code> ”. The default value is <code>0.15</code>
<code>quantile_plotted</code>	A vector specifies the quantiles of the final selected balance that will be shown in the survival plot. The default value is <code>c(0.25, 0.5, 0.75)</code>

alpha The level of significance for survival plot of the final selected balance. The corresponding confidence intervals will be shown in the survival plot. The default value is 0.05

Value

`balance_selection` return a list containing the following components:

selection_path A matrix showing the forward selection path. If `sign` is 1, the corresponding taxon is in the numerator of the balance; If `sign` is 0, the corresponding taxon is in the denominator of the balance. `p_value` is the p-value of the balance consisting of taxa up to the current taxon

survival_model An object of class `coxph` or `survreg` depending on the user's input, which is the final model with the final selected balance of microbiome

balance_name A list containing names of the taxa in the numerator and the denominator of the final selected balance

balance The value of the final selected balance of microbiome for each sample

survival_plot A plot of survival curves with confidence intervals, stratified by chosen quantiles of the final selected balance of microbiome

References

Rivera-Pinto, J., Egozcue, J. J., Pawlowsky-Glahn, V., Paredes, R., Noguera-Julian, M., & Calle, M. L. "Balances: a new perspective for microbiome analysis". *MSystems* 3.4 (2018): 10-1128

Fine, J. P. "Comparing nonnested Cox models". *Biometrika* 89.3 (2002): 635-648

Wahrendorf, J., Becher, H., & Brown, C. C. "Bootstrap comparison of non-nested generalized linear models: applications in survival analysis and epidemiology". *Journal of the Royal Statistical Society: Series C (Applied Statistics)* 36.1 (1987): 72-81

Examples

```
balance_selection(Surv_obj = gvhd, data = bacteria, mult_repl = TRUE,
  model = "coxph", selection_criterion = "min_pvalue")

balance_selection(Surv_obj = gvhd, data = bacteria, mult_repl = FALSE,
  model = "parametric", dist = "weibull", selection_criterion = "min_decrement_pvalue")
```

gvhd

Survival Data

Description

The data is a survival object containing survival time and censoring/event information for 63 samples

Usage

gvhd

Format

An object of class `Surv` with 63 rows and 2 columns.

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