

Package: sjofun (via r-universe)

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Type Package

Title Misc package for Daniel Sjoberg

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Description Misc package for Daniel Sjoberg.

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Imports dplyr, purrr, rlang, tibble, tidyr

Suggests gtsummary, covr

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RemoteUrl <https://github.com/ddsjoberg/sjofun>

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golden_search

One-dimensional Search Algorithm

Description

Find the minimum of a function using the Golded-section search algorithm

Usage

```
golden_search(x, a, b, tol = 1e-04)
```

Arguments

x	function with one argument
a	min value of search values
b	max value of search values
tol	tolerance level. Default is 1e-04

Examples

```
contfunc = function(x){
  -exp(-x) * sin(x)
}
golden_search(contfunc, a = 0, b = 1.5)
```

model_diff

Model-based test for treatment efficacy

Description

The model-based sinlge-arm comparison addresses the fundamental question of whether the current treatment provides a clinically significant improvement over prior treatments in the population. The proposed test statistic computes the difference between the observed outcome from the current treatment and the covariate-specific predicted outcome based on a model of the historical data. Thus, the difference between the observed and predicted quantities is attributed to the current treatment.

Usage

```
model_diff(
  data,
  outcome,
  covars,
  model,
  cov,
  coef,
```

```

    type = "logistic",
    output.details = FALSE
  )

```

Arguments

data	a data frame containing the outcome and the outcome predictions.
outcome	the outcome, or response variable name. Must be a variable contained within the data frame specified in data=.
covars	vector of covariate/predictor variable(s) names. Must be a variable(s) contained within the data frame specified in data=. If model includes an intercept, user must include the column of ones in the covars vector
model	glm object of the predictive model estimated on historical cohort. If specified, the outcome, covars, cov, and coef objects will be extracted from object.
cov	Variance-covariance matrix of the beta coefficients from predictive model.
coef	Vector of the beta coefficients from predictive model. If model includes an intercept, a vector of ones must appear in data.
type	Type of predictive model used. logistic is currently the only valid input.
output.details	Save additional information. Default is FALSE.

Details

Heller, Glenn, Michael W. Kattan, and Howard I. Scher. "Improving the decision to pursue a phase 3 clinical trial by adjusting for patient-specific factors in evaluating phase 2 treatment efficacy data." Medical Decision Making 27.4 (2007): 380-386.

Value

Returns a list of results from analysis.

Author(s)

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Examples

```

set.seed(23432)
#simulating historic dataset and creating prediction model.
marker=rnorm(500, sd = 2)
respond=runif(500)<plogis(marker)
historic.data=data.frame(respond,marker)
model.fit=glm(data=historic.data, formula = respond ~ marker, family = binomial(logit))

#simulating new data, with higher response rate
new.data = marker=rnorm(50, sd = 2)
respond=runif(50)<plogis(marker + 1)
new.data=data.frame(respond,marker)

```

```
#comparing outcomes in new data to those predicted in historic data
# z-statistic = 2.412611 indicates significant difference
model_diff(data = new.data, model = model.fit)

#comparing model based difference with binomial test
#p-value of 0.3222 indicates we fail to reject null hypothesis
binom.test(x=sum(new.data$respond), n=nrow(new.data), p = 0.5, alternative = c("two.sided"))
```

ph2_single_bayes_seq_sim

Simulate results from a single arm Bayesian Phase 2 Trial

Description

Trial is a single arm Bayesian phase 2 trial with sequential stopping boundaries as outlined in Thall, Peter F., and Richard Simon. "Practical Bayesian guidelines for phase IIB clinical trials." *Biometrics* (1994): 337-349.

Usage

```
ph2_single_bayes_seq_sim(
  theta_s_mu,
  theta_s_width,
  theta_s_w_conf_level = 0.9,
  theta_e_c,
  delta_0,
  n_min,
  n_max,
  sim_n = 1,
  pr_low = 0.05,
  pr_high = 0.95,
  mu_e = theta_s_mu + delta_0,
  verbose = FALSE,
  quiet = FALSE
)
```

Arguments

theta_s_mu	Mean of prior distribution on theta_s
theta_s_width	Width of the probability interval (set by w_conf_level=) running from the (1 + w_conf_level) / 2 to the (1 - w_conf_level) / 2 percentiles
theta_s_w_conf_level	Confidence level of width of probability specified
theta_e_c	Concentration parameter for prior distribution on theta_e
delta_0	Targeted improvement of treatment for treatment E over S

n_min	Minimum number of patients that may be enrolled
n_max	Maximum number of patients that may be enrolled
sim_n	Number of simulated trials to create
pr_low	Lower probability limit for concluding treatment not promising
pr_high	Upper probability limit for concluding treatment promising
mu_e	True rate of success with experimental treatment in theta_s_width
verbose	When TRUE, additional information is returned as an attribute
quiet	Run with no notes, progress bars, etc.

Examples

```
# simulate trial results
sim_results <- ph2_single_bayes_seq_sim(
  # setting priors for standard treatment
  theta_s_mu = 0.2, theta_s_width = 0.20, theta_s_w_conf_level = 0.90,
  # setting priors for experimental treatment
  theta_e_c = 2, delta_0 = 0.15,
  # other trial parameters
  n_min = 10, n_max = 65,
  pr_low = 0.05, pr_high = 0.95,
  # true effect of experimental tx
  mu_e = 0.35,
  # number of simulations
  sim_n = 1000
)

# tabulate summary
library(gtsummary)
sim_results %>%
  dplyr::select(-sim_id) %>%
  tbl_summary(
    label = list(result ~ "Trial Result",
                  n_enrolled ~ "No. Enrolled in Trial")
  ) %>%
  add_stat_label() %>%
  as_kable()
```

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