Package ‘adaptest’

October 14, 2018

Title Data-Adaptive Statistics for High-Dimensional Multiple Testing

Version 1.0.0

Author Weixin Cai [aut, cre, cph], Nima Hejazi [aut], Alan Hubbard [ctb, ths]

Maintainer Weixin Cai <wcai@berkeley.edu>

Description Data-adaptive test statistics represent a general methodology for performing multiple hypothesis testing on effects sizes while maintaining honest statistical inference when operating in high-dimensional settings (<doi here>). The utilities provided here extend the use of this general methodology to many common data analytic challenges that arise in modern computational and genomic biology.

Depends R (>= 3.5.0)

License GPL-2


Encoding UTF-8

LazyData true

Imports origami (>= 1.0.0), tmle, calibrate, methods, graphics, stats, utils, SummarizedExperiment

Suggests testthat, Matrix, SuperLearner, earth, gam, nlns, airway, rmarkdown, knitr, BiocStyle

VignetteBuilder knitr

RoxygenNote 6.0.1.9000

biocViews Genetics, GeneExpression, DifferentialExpression, Sequencing, Microarray, Regression, DimensionReduction, MultipleComparison

git_url https://github.com/wilsoncai1992/adaptest

git_branch RELEASE_3_7

git_last_commit bb90fa5

git_last_commit_date 2018-04-30

Date/Publication 2018-10-14
Computes marginal average treatment effects of a binary point treatment on multi-dimensional outcomes, adjusting for baseline covariates, using Targeted Minimum Loss-Based Estimation. A data-mining algorithm is used to perform biomarker selection before multiple testing to increase power.

Usage

```r
adaptest(Y, A, W = NULL, n_top, n_fold, parameter_wrapper = rank_DE, learning_library = c("SL.glm", "SL.step", "SL.glm.interaction", "SL.gam", "SL.earth"), absolute = FALSE, negative = FALSE, p_cutoff = 0.05, q_cutoff = 0.05)
```

Arguments

- **Y** (numeric vector) - A data.frame or matrix of binary or continuous biomarker measures (outcome variables). Alternatively, this will be an object of class adapTMLE if the wrapper bioadaptest is invoked (n.b., the wrapper is the preferred interface for standard data analytic use-cases arising in computational and genomic biology).
- **A** (numeric vector) - binary treatment indicator: 1 = treatment, 0 = control
- **W** (numeric vector, numeric matrix, or numeric data.frame) - matrix of baseline covariates where each column correspond to one baseline covariate and each row corresponds to one observation.
- **n_top** (integer vector) - value for the number of candidate covariates to generate using the data-adaptive estimation algorithm
- **n_fold** (integer vector) - number of cross-validation folds.
parameter_wrapper
(function) - user-defined function that takes input (Y, A, W, absolute, negative) and outputs a (integer vector) containing ranks of biomarkers (outcome variables). For details, please refer to the documentation for rank_DE

learning_library
(character vector) - library of learning algorithms to be used in fitting the "Q" and "g" step of the standard TMLE procedure.

absolute (logical) - whether or not to test for absolute effect size. If FALSE, test for directional effect. This overrides argument negative.

negative (logical) - whether or not to test for negative effect size. If FALSE = test for positive effect size. This is effective only when absolute = FALSE.

p_cutoff (numeric) - p-value cutoff (default as 0.05) at and below which to be considered significant. Used in inference stage.

q_cutoff (numeric) - q-value cutoff (default as 0.05) at and below which to be considered significant. Used in multiple testing stage.

Value
S4 object of class data_adapt, sub-classed from the container class SummarizedExperiment, with the following additional slots containing data-mining selected biomarkers and their TMLE-based differential expression and inference, as well as the original call to this function (for user reference), respectively.

top_index (integer vector) - indices for the data-mining selected biomarkers
top_colname (character vector) - names for the data-mining selected biomarkers
top_colname_significant_q (character vector) - names for the data-mining selected biomarkers, which are significant after multiple testing stage

DE (numeric vector) - differential expression effect sizes for the biomarkers in top_colname

p_value (numeric vector) - p-values for the biomarkers in top_colname

q_value (numeric vector) - q-values for the biomarkers in top_colname

significant_q (integer vector) - indices of top_colname which is significant after multiple testing stage.

mean_rank_top (numeric vector) - average ranking across folds of cross-validation folds for the biomarkers in top_colname

folds (origami::folds class) - cross validation object

Examples
set.seed(1234)
data(simpleArray)
simulated_array <- simulated_array
simulated_treatment <- simulated_treatment

adaptest(Y = simulated_array,
         A = simulated_treatment,
         W = NULL,
         n_top = 5,
         n_fold = 3,
         learning_library = 'SL.glm',
         parameter_wrapper = adaptest::rank_DE,
         absolute = FALSE,
         negative = FALSE)
Description

Constructor for class adaptmle

Value

class adaptmle object, sub-classed from SummarizedExperiment.

Examples

```r
library(SummarizedExperiment)
library(airway)
data(airway)

example_adaptmle_class <- function(se, n_top = 20, n_fold = 10) {
  call <- match.call(expand.dots = TRUE)
adaptmle <- .adaptmle(
    SummarizedExperiment::SummarizedExperiment(
      assays = SummarizedExperiment::assay(se),
      colData = SummarizedExperiment::colData(se)
    ),
    call = call,
folds = list(), # folds (from origami)
plot_ingredients = list(), # top_colname
diff_exp = as.numeric(rep(NaN, n_top)), # DE
p_value = as.numeric(rep(NaN, n_top)), # p_value
q_value = as.numeric(rep(NaN, n_top)), # q_value
q_sig = as.numeric(rep(NaN, n_top)), # significant_q
q_sig_names = list(), # top_colname_significant_q
rank_mean = as.numeric(rep(NaN, n_top * n_fold)), # mean_rank_top
prob_top = as.numeric(rep(NaN, n_top * n_fold)), # prob_in_top
top_index = as.numeric(rep(NaN, n_top * n_fold)) # top_index
  )
return(adaptmle)
}

example_class <- example_adaptmle_class(se = airway)
```

Description

A thin wrapper that implements the main data-adaptive multiple hypothesis testing strategy for data structures commonly found in computational biology experiments, using the popular SummarizedExperiment container class.
Usage

bioadaptest(data_in, var_int, cntrl_set = NULL, n_top = 25, n_fold = 10,
            parameter_wrapper = rank.DE, learning_library = c("SL.mean", "SL.glm"),
            absolute = FALSE, negative = FALSE, p_cutoff = 0.05, q_cutoff = 0.05)

Arguments

data_in
An object of class SummarizedExperiment, a common container class for computational biology and bioinformatics. This object is used to construct the output object of class adaptmle.

var_int
A numeric vector of binary treatment assignment whose effect on the biological units is to be assessed. The data-adaptive target parameter approach finds any biological sites strongly impacted by this quantity across the observed experimental units (subjects).

cntrl_set
A matrix of discrete variables representing baseline covariates that are controlled for in the estimation of the data-adaptive target parameter via targeted maximum likelihood estimation. If NULL, an identity vector is generated internally.

n_top
(integer vector) - value for the number of candidate covariates to generate using the data-adaptive estimation algorithm.

n_fold
(integer vector) - number of cross-validation folds.

parameter_wrapper
(function) - user-defined function that takes input (Y, A, W, absolute, negative) and outputs a (integer vector) containing ranks of biomarkers (outcome variables). For detail, please refer to the documentation for rank.DE.

learning_library
(character vector) - library of learning algorithms to be used in fitting the "Q" and "g" step of the standard TMLE procedure.

absolute
(logical) - whether or not to test for absolute effect size. If FALSE, test for directional effect. This overrides argument negative.

negative
(logical) - whether or not to test for negative effect size. If FALSE = test for positive effect size. This is effective only when absolute = FALSE.

p_cutoff
The minimum p-value required to evaluate a given biological unit (e.g., gene) as statistically significant.

q_cutoff
The minimum p-value required to evaluate a given biological unit (e.g., gene) as statistically significant after applying a correction for multiple hypothesis testing.

Value

An object of class adaptmle, sub-classed from the popular container class SummarizedExperiment, containing information about the experiment being analyzed as well as results from applying the TMLE for the data-adaptive target parameter as produced by adaptest.

Examples

library(SummarizedExperiment)
library(airway)
set.seed(5678)
data(airway)
cv_param_est <- order(sample(seq_len(100)))
air_reduced <- airway[, genes_sub,]
simple_air <- cbind(air_reduced, air_reduced)
dex_var = as.numeric(as.matrix(colData(simple_air))[, 3] - 1)
airway_out <- bioadaptest(data_in = simple_air,
var_int = dex_var,
cntrl_set = NULL,
 n_top = 5,
n_fold = 2,
 parameter_wrapper = rank_DE)

---

**cv_param_est**

*Compute data-adaptive parameter estimate for a single cross-validation fold*

**Description**

Compute data-adaptive parameter estimate for a single cross-validation fold

**Usage**

`cv_param_est(fold, data, parameter_wrapper, absolute, negative, n_top, learning_library, Y_name, A_name, W_name)`

**Arguments**

- **fold**: fold output from origami
- **data**: entire training data
- **parameter_wrapper**: user-defined function
- **absolute**: boolean: TRUE = test for absolute effect size. This FALSE = test for directional effect. This overrides argument negative.
- **negative**: boolean: TRUE = test for negative effect size, FALSE = test for positive effect size
- **n_top**: integer value for the number of candidate covariates to generate using the data-adaptive estimation algorithm
- **learning_library**: character of SuperLearner library
- **Y_name**: (character) colnames of all biomarkers
- **A_name**: (character) colnames of treatment
- **W_name**: (character) colnames of all baseline covariates

**Value**

- **data_adaptive_index** (integer vector) rank for each gene
- **index_grid** (integer matrix) gene index from rank 1 to rank K
- **psi_est** estimand of DE for rank 1 to rank K genes
- **EIC_est** estimand of EIC for rank 1 to rank K genes
data_adapt

S3-Style Constructor for Data Adaptive Parameter Class

Description
S3-Style Constructor for Data Adaptive Parameter Class

Usage
data_adapt(Y, A, W = NULL, n_top, n_fold, absolute, negative,
parameter_wrapper, learning_library)

Arguments
Y (numeric vector) - continuous or binary biomarkers outcome variables
A (numeric vector) - binary treatment indicator: 1 = treatment, 0 = control
W (numeric vector, numeric matrix, or numeric data.frame) - matrix of baseline covariates where each column correspond to one baseline covariate. Each row correspond to one observation
n_top (integer vector) - value for the number of candidate covariates to generate using the data-adaptive estimation algorithm.
n_fold (integer vector) - number of cross-validation folds.
absolute (logical) - whether or not to test for absolute effect size. If FALSE, test for directional effect. This overrides argument negative.
negative (logical) - whether or not to test for negative effect size. If FALSE = test for positive effect size. This is effective only when absolute = FALSE.
parameter_wrapper (function) - user-defined function that takes input (Y, A, W, absolute, negative) and outputs a (integer vector) containing ranks of biomarkers (outcome variables). For detail, please refer to the documentation for rank_DE.
learning_library (character vector) - library of learning algorithms to be used in fitting the "Q" and "g" step of the standard TMLE procedure.

Value
S3 object of class "data_adapt" for data-adaptive multiple testing.

generate_composition
Decomposition tables of the data-adaptive parameter after data-mining

Description
Customized informative tables for examining data-adaptive statistics.
get_composition(object, type = "small")

Arguments

object (data_adapt) - object of class data_adapt as returned by adaptest
type (character) - 'small' or 'big'. 'small' mode returns composition of data-adaptive parameters after multiple testing stage. 'big' mode returns composition of data-adaptive parameters before multiple testing stage.

Value

(numeric matrix) containing what fraction of the data-adaptive parameter comes from which biomarker in the original dataset.

Examples

set.seed(1234)
data(simpleArray)
simulated_array <- simulated_array
simulated_treatment <- simulated_treatment

adaptest_out <- adaptest(Y = simulated_array,
                          A = simulated_treatment,
                          W = NULL,
                          n_top = 5,
                          n_fold = 3,
                          learning_library = "SL.glm",
                          parameter_wrapper = adaptest::rank_DE,
                          absolute = FALSE,
                          negative = FALSE)

get_composition(adaptest_out, type = "small")

get_significant_biomarker

Extract statistically significant biomarkers

Description

Extract statistically significant biomarkers

Usage

get_significant_biomarker(object, cutoff = 0.5)

Arguments

object data_adapt object
cutoff cut-off value for composition percentage

Value

(integer vector) of significant gene index
**Examples**

```r
set.seed(1234)
data(simpleArray)
simulated_array <- simulated_array
simulated_treatment <- simulated_treatment

adaptest_out <- adaptest(Y = simulated_array,
A = simulated_treatment,
W = NULL,
n_top = 5,
n_fold = 3,
learning_library = 'SL.glm',
parameter_wrapper = adaptest::rank_DE,
absolute = FALSE,
negative = FALSE)
get_significant_biomarker(adaptest_out)
```

---

**plot.data_adapt**  
*Plot method for data_adapt objects*

**Description**

Customized plotting method for easily examining data-adaptive statistics

**Usage**

```r
## S3 method for class 'data_adapt'
plot(x, ..., plot_type = c("biomarker", "adapt_param"))
```

**Arguments**

- `x`  
  (data_adapt) - object of class data_adapt as returned by adaptest

- `...`  
  additional arguments passed to plot as necessary

- `plot_type`  
  character vector specifying which of the two types of plots to generate: "biomarker" for a plot sorted average CV-rank, or "adapt_param" for a plot sorted by q-values with labels corresponding to indices

**Value**

plot of model statistics
print.data_adapt  

*Print method for data_adapt objects*

**Description**

Customized informative print method for examining data-adaptive statistics

**Usage**

```r
## S3 method for class 'data_adapt'
print(x, ...)
```

**Arguments**

- `x` (data_adapt) - object of class data_adapt as returned by adaptest
- `...` additional arguments passed to print as necessary

**Value**

strings into stdout; containing information of the fitted model

---

**rank.DE**  

*Compute ranking of biomarkers by sorting effect sizes*

**Description**

Computes ranking of biomarkers based on effect sizes, which are computed by Targeted Minimum Loss-Based Estimation. This function is designed to be called inside `adaptest`; it should not be run by itself outside of that context.

**Usage**

```r
rank_DE(Y, A, W, absolute = FALSE, negative = FALSE,
        learning_library = c("SL.glm", "SL.step", "SL.glm.interaction", "SL.gam"))
```

**Arguments**

- `Y` (numeric vector) - continuous or binary biomarkers outcome variables
- `A` (numeric vector) - binary treatment indicator: 1 = treatment, 0 = control
- `W` (numeric vector, numeric matrix, or numeric data.frame) - matrix of baseline covariates where each column corresponds to one baseline covariate. Each row correspond to one observation
- `absolute` (logical) - whether or not to test for absolute effect size. If FALSE, test for directional effect. This overrides argument negative.
- `negative` (logical) - whether or not to test for negative effect size. If FALSE = test for positive effect size. This is effective only when absolute = FALSE.
- `learning_library` (character vector) - library of learning algorithms to be used in fitting the "Q" and "g" step of the standard TMLE procedure.
Value

an integer vector containing ranks of biomarkers.

Examples

```r
set.seed(1234)
data(simpleArray)
simulated_array <- simulated_array
simulated_treatment <- simulated_treatment
rank_DE(Y = simulated_array,
        A = simulated_treatment,
        W = rep(1, length(simulated_treatment)),
        absolute = FALSE,
        negative = FALSE)
```

### Usage

`rank_ttest(Y, A, W)`

### Arguments

- **Y** `(numeric vector)` - continuous or binary biomarkers outcome variables
- **A** `(numeric vector)` - binary treatment indicator: 1 = treatment, 0 = control
- **W** `(numeric vector, numeric matrix, or numeric data.frame)` - matrix of baseline covariates where each column correspond to one baseline covariate and each row correspond to one observation.

### Value

an integer vector containing ranks of biomarkers.

### Examples

```r
set.seed(1234)
data(simpleArray)
rank_ttest(Y = simulated_array,
           A = simulated_treatment,
           W = rep(1, length(A)))
```
**simulated_array**  
*Simulated differential expression data with one exposure*

**Description**
A dataset containing 1e4 biomarkers and one exposure

**Usage**
simulated_array

**Format**
A numeric matrix containing 1e4 biomarkers of 1e2 subjects.
This is example data to be used in testing the `adaptest` procedure. Consult the vignettes for how to use this data.

**Value**
A matrix simulated_array

**simulated_treatment**  
*Simulated differential expression data with one exposure*

**Description**
A dataset containing 1e4 biomarkers and one exposure

**Usage**
simulated_treatment

**Format**
A numeric vector containing binary exposures
This is example data to be used in testing the `adaptest` procedure. Consult the vignettes for how to use this data.

**Value**
A numeric vector simulated_treatment.
summary.data_adapt

Summary tables for data_adapt objects

Description

Summary tables for data_adapt objects

Usage

## S3 method for class 'data_adapt'
summary(object, type = "adapt_param", ...)

Arguments

- object: (data_adapt) object as returned by adapttest
- type: (character) - 'adapt_param' or 'biomarker'. 'adapt_param' mode summarizes the data-adaptive target parameter. 'biomarker' mode summarizes characteristics of the biomarkers from the original data
- ...: not implemented

Value

(data.frame) of the summary statistics

- type = 'adapt_param' with columns: 'data-adaptive parameters', 'Differential expression', 'p-values', 'q-values'
- type = 'biomarker' with columns: 'biomakers', 'mean rank', 'appear in top'
## Index

**Topic datasets**
- simulated_array, 12
- simulated_treatment, 12
- .adaptmle(adapTMLE-class), 4

adapttest, 2
adapTMLE-class, 4
bioadapttest, 4
cv_param_est, 6
data_adapt, 7
get_composition, 7
get_significant_biomarker, 8
plot.data_adapt, 9
print.data_adapt, 10
rank_DE, 10
rank_ttest, 11
simulated_array, 12
simulated_treatment, 12
summary.data_adapt, 13