

# Package ‘adaptest’

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**Title** Data-Adaptive Statistics for High-Dimensional Multiple Testing

**Version** 1.2.0

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**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

**URL** <https://github.com/wilsoncai1992/adaptest>

**BugReports** <https://github.com/wilsoncai1992/adaptest/issues>

**Encoding** UTF-8

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adaptest	<i>Data-adaptive Statistics for High-Dimensional Multiple Testing</i>
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### Description

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

```
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)
```

---

 adapTMLE-class

*Constructor for class adaptmle*


---

### Description

Constructor for class adaptmle

### Value

class adaptmle object, sub-classed from SummarizedExperiment.

### Examples

```
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)
```

---

 bioadptest

*Data Adaptive Multiple Testing for Computational Biology*


---

### 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**

```
bioadapttest(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**

<code>data_in</code>	An object of class <code>SummarizedExperiment</code> , a common container class for computational biology and bioinformatics. This object is used to construct the output object of class <code>adaptmle</code> .
<code>var_int</code>	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).
<code>cntrl_set</code>	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 <code>NULL</code> , an identity vector is generated internally.
<code>n_top</code>	(integer vector) - value for the number of candidate covariates to generate using the data-adaptive estimation algorithm.
<code>n_fold</code>	(integer vector) - number of cross-validation folds.
<code>parameter_wrapper</code>	(function) - user-defined function that takes input ( <code>Y</code> , <code>A</code> , <code>W</code> , <code>absolute</code> , <code>negative</code> ) and outputs a (integer vector) containing ranks of biomarkers (outcome variables). For detail, please refer to the documentation for <code>rank_DE</code> .
<code>learning_library</code>	(character vector) - library of learning algorithms to be used in fitting the "Q" and "g" step of the standard TMLE procedure.
<code>absolute</code>	(logical) - whether or not to test for absolute effect size. If <code>FALSE</code> , test for directional effect. This overrides argument <code>negative</code> .
<code>negative</code>	(logical) - whether or not to test for negative effect size. If <code>FALSE</code> = test for positive effect size. This is effective only when <code>absolute</code> = <code>FALSE</code> .
<code>p_cutoff</code>	The minimum p-value required to evaluate a given biological unit (e.g., gene) as statistically significant.
<code>q_cutoff</code>	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 `adpatetest`.

**Examples**

```
library(SummarizedExperiment)
library(airway)
set.seed(5678)
```

```

data(airway)
genes_sub <- 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 <- bioadapttest(data_in = simple_air,
                           var_int = dex_var,
                           cntrl_set = NULL,
                           n_top = 5,
                           n_fold = 2,
                           parameter_wrapper = rank_DE)

```

---

cv_param_est	<i>Compute data-adaptive parameter estimate for a single cross-validation fold</i>
--------------	--

---

### 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.

---

 get\_composition

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


---

**Description**

Customized informative tables for examining data-adaptive statistics.

**Usage**

```
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**

```

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	<i>Plot method for data_adapt objects</i>
-----------------	---

---

**Description**

Customized plotting method for easily examining data-adaptive statistics

**Usage**

```

## 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

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

### Arguments

x (data\_adapt) - object of class data\_adapt as returned by adapttest  
 ... 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 effect sizes, which are computed by Targeted Minimum Loss-Based Estimation. This function is designed to be called inside adapttest; it should not be run by itself outside of that context.

### Usage

```
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 correspond 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**

```
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)
```

---

rank\_ttest

*Compute ranking of biomarkers by sorting t-test p-values*

---

**Description**

Compute ranking of biomarkers by sorting t-test p-values

**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**

```
set.seed(1234)
data(simpleArray)
rank_ttest(Y = simulated_array,
          A = simulated_treatment,
          W = rep(1, length(A)))
```

---

simulated_array	<i>Simulated differential expression data with one exposure</i>
-----------------	---

---

**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 adapttest procedure. Consult the vignettes for how to use this data.

**Value**

A matrix simulated\_array

---

simulated_treatment	<i>Simulated differential expression data with one exposure</i>
---------------------	---

---

**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 adapttest 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: 'biomarkers', 'mean rank', 'appear in top'

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