

# Package ‘doseSens’

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**Title** Conduct Sensitivity Analysis with Continuous Exposures and Binary Outcomes

**Version** 0.1.0

**Description** Performs sensitivity analysis for the sharp null and attributable effects in matched studies with continuous exposures and binary outcomes as described in Zhang, Small, Heng (2024) <[arXiv:2401.06909](https://arxiv.org/abs/2401.06909)>. Two of the functions require installation of the 'Gurobi' optimizer. Please see <[https://www.gurobi.com/documentation/9.0/refman/ins\\_the\\_r\\_package.html](https://www.gurobi.com/documentation/9.0/refman/ins_the_r_package.html)> for guidance.

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binary\_thresh\_attribute

*Separable algorithm for threshold attributable effect in a sensitivity analysis with at most one over-exposed unit in each matched set. For a greater than alternative, finds the 'a' matched sets that most decrease the mean and/or variance.*

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### Description

Separable algorithm for threshold attributable effect in a sensitivity analysis with at most one over-exposed unit in each matched set. For a greater than alternative, finds the 'a' matched sets that most decrease the mean and/or variance.

### Usage

```
binary_thresh_attribute(
  Z,
  Q,
  index,
  gamma,
  thresh = 0,
  a = 1,
  trans = identity,
  mc = 50000
)
```

### Arguments

Z	A length N vector of (nonnegative) observed doses.
Q	A length N vector of observed binary outcomes.
index	A length N vector of indices indicating matched set membership.
gamma	The nonnegative sensitivity parameter; gamma = 0 means no unmeasured confounding.
thresh	The dose threshold for the TAE.
a	The number of attributable effects to test for.
trans	The transformation of the doses to use for the test statistic. Default is the identity function.
mc	Number of monte-carlo samples if testing the sharp null, i.e. a = 0.

### Value

Either "reject" if the value a is deemed not plausible/compatible, "feasible" if the value a is deemed so, else a list containing a p-value and dataframe of matched sets that have contribution to the test statistic sorted in order of smallest mean reduction followed by smallest variance reduction.

**Examples**

```
# Load the data
data <- treat_out_match
# Solve by the separable algorithm
solution <- binary_thresh_attribute(data$treat, data$complain, data$match_ind,
gamma = 0, thresh = log(3.5), a = 5, trans = identity)
```

---

change_Delta	<i>A helper that takes a gurobi model object outputted from dose_attributable_general or dose_thresh_attributable_one_sided and changes the Delta parameter. Saves computation time by directly editing the constraint involving Delta without having to reinitialize the other constraints that are kept the same. Outputs a list analogous to output from dose_attributable_general or dose_thresh_attributable_one_sided.</i>
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**Description**

A helper that takes a gurobi model object outputted from `dose_attributable_general` or `dose_thresh_attributable_one_sided` and changes the Delta parameter. Saves computation time by directly editing the constraint involving Delta without having to reinitialize the other constraints that are kept the same. Outputs a list analogous to output from `dose_attributable_general` or `dose_thresh_attributable_one_sided`.

**Usage**

```
change_Delta(model, Delta, direction = "equal", TT)
```

**Arguments**

model	A gurobi model object outputted from <code>dose_attributable_general</code> .
Delta	The new Delta to test for.
direction	The new direction to test
TT	The observed test statistic.

**Value**

A gurobi model and solution.

---

dev_TV	<i>Computes deviation from uniform distribution in total variation distance for a given amount of unmeasured confounding and a greater than alternative with a binary outcome.</i>
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### Description

Computes deviation from uniform distribution in total variation distance for a given amount of unmeasured confounding and a greater than alternative with a binary outcome.

### Usage

```
dev_TV(Z, Q, index, gamma, direct = "upper")
```

### Arguments

Z	A length N vector of (nonnegative) observed doses.
Q	A length N vector of observed binary outcomes.
index	A length N vector of indices indicating matched set membership.
gamma	The nonnegative sensitivity parameter; gamma = 0 means no unmeasured confounding.
direct	The direction of the test - "upper" or "lower"; default is upper.

### Value

A vector of length equaling the number of matched sets consisting of the TV distance from the uniform for each matched set at gamma level of unmeasured confounding for the worst-case.

### Examples

```
# Load the data
data <- treat_out_match
# compute total variation distances.
total_variation <- dev_TV(data$treat, data$complain,
data$match_ind, gamma = log(1.5))
```

---

dose\_attributable\_general

*Inference for general attributable effects in sensitivity analysis with continuous exposures and binary outcomes. Gurobi must be installed to use this function.*

---

### Description

Inference for general attributable effects in sensitivity analysis with continuous exposures and binary outcomes. Gurobi must be installed to use this function.

**Usage**

```
dose_attributable_general(
  Z,
  Q,
  index,
  gamma,
  alpha = 0.05,
  monotone = TRUE,
  Delta,
  sign = "positive",
  trans = identity,
  direction = "equal",
  M = 10000,
  eps = 0.01,
  alternative = "both",
  mv_threshold = NA,
  baseline = 0,
  relax = FALSE,
  feasible = TRUE,
  MIPgap = 0.01,
  WorkLimit = 1000,
  OutputFlag = 0
)
```

**Arguments**

Z	A length N vector of (nonnegative) observed doses.
Q	A length N vector of observed binary outcomes.
index	A length N vector of indices indicating matched set membership.
gamma	The nonnegative sensitivity parameter; gamma = 0 means no unmeasured confounding.
alpha	Level of the test.
monotone	Whether to impose a monotonicity constraint on the potential outcomes
Delta	A numeric for the attributable effect to be tested for.
sign	The sign of monotonicity - "positive" or "negative".
trans	The transformation of the doses to use for the test statistic. Default is the identity function.
direction	A string indicating the direction of testing the attributable effect with respect to Delta; "greater", "equal", or "less"
M	The numeric penalty parameter to ensure correct sign relationship.
eps	precision parameter for the objective function if solving feasible = "Yes"
alternative	For constraining the rejection region using the test statistic with baseline potential outcomes, should it be constructed with "lower" alternative, "upper" alternative, or "both."

<code>mv_threshold</code>	The number of allowed monotonicity violations.
<code>baseline</code>	The baseline dose level for defining the threshold attributable effect.
<code>relax</code>	Whether to solve the continuous relaxation.
<code>feasible</code>	Whether to look for a feasible solution or to find the optimal solution.
<code>MIPgap</code>	Gurobi parameter specifying the precision of the mixed integer program solution; default is 0.01.
<code>WorkLimit</code>	Gurobi parameter specifying the maximum work units before stopping; default is 1000.
<code>OutputFlag</code>	0 if Gurobi print output is desired, 1 otherwise; default 0.

**Value**

A list containing the following:

<code>sol</code>	A gurobi object containing the solution to the optimization. If <code>feasible</code> is TRUE, then failing to find a solution indicates rejection. If <code>feasible</code> is FALSE, then optimal value greater than zero indicates rejection.
<code>attribut</code>	The attributable effect attained by the least rejectable allocation of potential outcomes and unmeasured confounders.
<code>search</code>	A list of length the number of matched sets containing the matrix of compatible baseline potential outcomes in each matched set.
<code>null_exp</code>	The null expectation of the pivot attained by the least rejectable allocation of potential outcomes and unmeasured confounders.
<code>obsT</code>	The value of the pivot attained by the least rejectable allocation of potential outcomes and unmeasured confounders.
<code>nps</code>	A vector with length the number of matched sets containing the size of each matched set.
<code>start.ind</code>	A vector with length the number of matched sets containing the starting index of the decision variables pertaining to each matched set in the optimization program.
<code>exp_upper</code>	The expectation of the pivot attained by the unmeasured confounders equalling the baseline potential outcome.
<code>exp_lower</code>	The expectation of the pivot attained by the unmeasured confounders equalling 1 minus the baseline potential outcome.
<code>var_upper</code>	The variance of the pivot attained by the unmeasured confounders equalling the baseline potential outcome.
<code>var_lower</code>	The variance of the pivot attained by the unmeasured confounders equalling 1 minus the baseline potential outcome.
<code>dose</code>	A list of length the number of matched sets containing the vector of doses observed in each matched set.
<code>model</code>	The initialized gurobi model.

**Examples**

```
# To run the following example, Gurobi must be installed.
# Load the data
data <- treat_out_match
# Make a threshold at log(3.5) transformation function.
above = function(Z) { return(Z > log(3.5)) }
# Solve the mixed-integer program.
solution = dose_attributable_general(data$treat,
data$complain, data$match_ind, gamma=log(1),
alpha = 0.1, monotone = TRUE, trans = above,
Delta = 5, direction = "less", M = 10000, eps = 0.0001,
alternative = "upper", relax = FALSE, feasible = FALSE)
```

---

dose\_sensitivity\_mc\_gen

*Sharp null monte-carlo sensitivity analysis for continuous exposures and binary outcomes.*

---

**Description**

Sharp null monte-carlo sensitivity analysis for continuous exposures and binary outcomes.

**Usage**

```
dose_sensitivity_mc_gen(
  Z,
  Q,
  index,
  mc,
  gamma,
  weights = NA,
  obsT = NULL,
  trans = identity,
  direct = "upper",
  seed = 1,
  verbose = FALSE
)
```

**Arguments**

Z	A length N vector of (nonnegative) observed doses.
Q	A length N vector of observed binary outcomes.
index	A length N vector of indices indicating matched set membership.
mc	An integer for the total number of Monte-Carlo samples desired.
gamma	The nonnegative sensitivity parameter; gamma = 0 means no unmeasured confounding.

weights	Weights for each stratum to apply for the test statistic
obsT	The observed value of the test statistic; default is NULL
trans	The transformation of the doses to use for the test statistic. Default is the identity function.
direct	The direction of the test - "upper" or "lower"; default is upper.
seed	seed for random number generation.
verbose	Whether to print status updates or not; default is FALSE.

### Value

A list containing two objects:

mc	A length mc vector containing the monte-carlo samples of the test statistic.
p	The monte-carlo p-value.

### Examples

```
# Load the data
data <- treat_out_match
# Make a threshold at log(3.5) transformation function.
above = function(Z) { return(Z > log(3.5)) }
# Conduct randomization test.
solution <- dose_sensitivity_mc_gen(data$treat, data$complain, data$match_ind,
mc = 250, gamma = 0, trans = above)
```

---

dose\_thresh\_attributable\_one\_sided

*Inference for threshold attributable effects in sensitivity analysis with continuous exposures and binary outcomes. Gurobi must be installed to use this function.*

---

### Description

Inference for threshold attributable effects in sensitivity analysis with continuous exposures and binary outcomes. Gurobi must be installed to use this function.

### Usage

```
dose_thresh_attributable_one_sided(
  Z,
  Q,
  index,
  gamma,
  alpha = 0.05,
  monotone = TRUE,
```



```

Delta,
sign = "positive",
direction = "equal",
threshold = 0,
M = 10000,
eps = 0.01,
mv_threshold = NA,
baseline = 0,
relax = FALSE,
feasible = TRUE,
MIPgap = 0.01,
WorkLimit = 1000,
OutputFlag = 0
)

```

### Arguments

Z	A length N vector of (nonnegative) observed doses.
Q	A length N vector of observed binary outcomes.
index	A length N vector of indices indicating matched set membership.
gamma	The nonnegative sensitivity parameter; gamma = 0 means no unmeasured confounding.
alpha	Level of the test.
monotone	Whether to impose a monotonicity constraint on the potential outcomes
Delta	A numeric for the attributable effect to be tested for.
sign	The sign of monotonicity - "positive" or "negative".
direction	A string indicating the direction of testing the attributable effect with respect to Delta; "greater", "equal", or "less"
threshold	The threshold for the TAE.
M	The numeric penalty parameter to ensure correct sign relationship.
eps	precision parameter for the objective function if solving feasible = "Yes"
mv_threshold	The number of allowed monotonicity violations.
baseline	The baseline dose level for defining the threshold attributable effect.
relax	Whether to solve the continuous relaxation.
feasible	Whether to look for a feasible solution or to find the optima.
MIPgap	Gurobi parameter specifying the precision of the mixed integer program solution; default is 0.01.
WorkLimit	Gurobi parameter specifying the maximum work units before stopping; default is 1000.
OutputFlag	0 if Gurobi print output is desired, 1 otherwise; default 0.

**Value**

A list containing the following:

<code>sol</code>	A gurobi object containing the solution to the optimization. If <code>feasible</code> is <code>TRUE</code> , then failing to find a solution indicates rejection. If <code>feasible</code> is <code>FALSE</code> , then optimal value greater than zero indicates rejection.
<code>attribut</code>	The attributable effect attained by the least rejectable allocation of potential outcomes and unmeasured confounders.
<code>search</code>	A list of length the number of matched sets containing the matrix of compatible baseline potential outcomes in each matched set.
<code>null_exp</code>	The null expectation of the pivot attained by the least rejectable allocation of potential outcomes and unmeasured confounders.
<code>obsT</code>	The value of the pivot attained by the least rejectable allocation of potential outcomes and unmeasured confounders.
<code>nps</code>	A vector with length the number of matched sets containing the size of each matched set.
<code>start.ind</code>	A vector with length the number of matched sets containing the starting index of the decision variables pertaining to each matched set in the optimization program.
<code>exp_upper</code>	The expectation of the pivot attained by the unmeasured confounders equalling the baseline potential outcome.
<code>var_upper</code>	The variance of the pivot attained by the unmeasured confounders equalling the baseline potential outcome.
<code>dose</code>	A list of length the number of matched sets containing the vector of doses observed in each matched set.
<code>model</code>	The initialized gurobi model.

**Examples**

```
# To run the following example, Gurobi must be installed.
# Load the data
data <- treat_out_match
# Solve the mixed-integer program.
solution = dose_thresh_attributable_one_sided(data$treat,
data$complain, data$match_ind,
gamma=log(1), alpha = 0.1, monotone = TRUE, Delta = 5,
direction = "less", threshold = log(3.5),M = 10000,
eps = 0.0001,relax = FALSE, feasible = FALSE)
```

---

normal_test_gen	<i>Sharp null sensitivity analysis for continuous exposures and binary outcomes using normal approximation.</i>
-----------------	---

---

### Description

Sharp null sensitivity analysis for continuous exposures and binary outcomes using normal approximation.

### Usage

```
normal_test_gen(
  Z,
  Q,
  index,
  gamma,
  trans = identity,
  weights = NA,
  obsT = NULL,
  direct = "upper"
)
```

### Arguments

Z	A length N vector of (nonnegative) observed doses.
Q	A length N vector of observed binary outcomes.
index	A length N vector of indices indicating matched set membership.
gamma	The nonnegative sensitivity parameter; gamma = 0 means no unmeasured confounding.
trans	The transformation of the doses to use for the test statistic. Default is the identity function.
weights	Weights to apply for the test statistic
obsT	The observed value of the test statistic; default is NULL.
direct	The direction of the test - "upper" or "lower"; default is upper.

### Value

A list containing the following:

obsT	The observed value of the test statistic
exp	The worst-case expectation
var	The worst-case variance.
deviate	The normal approximation deviate.

### Examples

```
# Load the data
data <- treat_out_match
# Make a threshold at log(3.5) transformation function.
above = function(Z) { return(Z > log(3.5)) }
# Conduct randomization test using normal approximation.
solution <- normal_test_gen(data$treat, data$complain, data$match_ind,
gamma = 0, trans = above)
```

---

treat_out_match	<i>Matched lead dataset</i>
-----------------	-----------------------------

---

### Description

A matched, trimmed dataset of early life lead exposure and juvenile delinquency. There are 2007 matched sets.

### Usage

```
treat_out_match
```

### Format

treat\_out\_match:

A data frame with 4,134 rows and 4 columns:

**treat** The log of lead exposure level measured in micrograms per deciliter.

**serious** Whether the juvenile committed a serious offense.

**complain** Whether the juvenile committed an offense worthy of complaint.

**match\_ind** Matched set membership. ...

### Source

<https://scholarworks.iu.edu/dspace/handle/2022/25638>

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