Package 'BCEA'

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Type Package

Title Bayesian Cost Effectiveness Analysis

Version 2.4

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ggplot2,
graphics,
INLA,
knitr,
ldr,
MASS,
plotly,
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rlang,
rmarkdown,
withr,
gridExtra

Depends R (>= 3.5.0)

Suggests RColorBrewer,
grid,
mgcv,
R2jags,
R2OpenBUGS,
splancs,
testthat (>= 2.1.0),
vdiffr

Additional_repositories https://inla.r-inla-download.org/R/stable/

Description Produces an economic evaluation of a sample of suitable variables of
cost and effectiveness / utility for two or more interventions,
e.g. from a Bayesian model in the form of MCMC simulations.
This package computes the most cost-effective alternative and
produces graphical summaries and probabilistic sensitivity analysis.

License GPL-3

URL http://www.statistica.it/gianluca/BCEA,
http://www.statistica.it/gianluca,

https://github.com/giabaio/BCEA

NeedsCompilation no

RoxygenNote 7.1.1

Encoding UTF-8

VignetteBuilder knitr

R **topics documented:**

BCEA-package	*BCEA: A package for Bayesian Cost-Effectiveness Analysis*

Description

A package to post-process the results of a Bayesian health economic model and produce standardised output for the analysis of the results.

Details

Package:	BCEA
Type:	Package
Version:	2.4
Date:	2020-07-21
License:	GPL2
LazyLoad:	Yes

BCEA produces a health economic evaluation given a random sample of suitable variables of costs and clinical benefits for two or more interventions, e.g. using results of a Bayesian model (possibly

based on MCMC) in the form of simulations from the posterior distributions. Compares one of the interventions (the "reference") to the others ("comparators"). Produces many summaries and plots to analyse the results.

Author(s)

Gianluca Baio, Andrea Berardi, Anna Heath

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London.

Baio G., Berardi A., Heath A. (2017). Bayesian Cost Effectiveness Analysis with the R package BCEA. Springer

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| bcea | *Create Bayesian Cost-Effectiveness Analysis Object* |

Description

Cost-effectiveness analysis based on the results of a simulation model for a variable of clinical benefits (e) and of costs (c). Produces results to be post-processed to give the health economic analysis. The output is stored in an object of the class "bcea".

Usage

```
bcea(
  eff,
  cost,
  ref = 1,
  interventions = NULL,
  .comparison = NULL,
  Kmax = 50000,
  wtp = NULL,
  plot = FALSE
)

## Default S3 method:
bcea(
  eff,
  cost,
  ref = 1,
  interventions = NULL,
  .comparison = NULL,
  Kmax = 50000,
  wtp = NULL,
  plot = FALSE
)
```

Arguments

eff	An object containing nsim simulations for the variable of clinical effectiveness for each intervention being considered. In general it is a matrix with nsim rows and nint columns. This are partially matched with 'e' from previous version of 'BCEA' for back-compatibility.
cost	An object containing nsim simulations for the variable of cost for each intervention being considered. In general it is a matrix with nsim rows and nint columns. This are partially matched with 'c' from previous version of 'BCEA' for back-compatibility.
ref	Defines which intervention (columns of e or c) is considered to be the reference strategy. The default value ref = 1 means that the intervention associated with the first column of e or c is the reference and the one(s) associated with the other column(s) is(are) the comparators.
interventions	Defines the labels to be associated with each intervention. By default and if NULL, assigns labels in the form "Intervention1", ... , "InterventionT".
.comparison	Selects the comparator, in case of more than two interventions being analysed. Default as NULL plots all the comparisons together. Any subset of the possible comparisons can be selected (e.g., comparison=c(1,3) or comparison = 2).
Kmax	Maximum value of the willingness to pay to be considered. Default value is k = 50000. The willingness to pay is then approximated on a discrete grid in the interval [0,Kmax]. The grid is equal to wtp if the parameter is given, or composed of 501 elements if wtp = NULL (the default).
wtp	A(n optional) vector including the values of the willingness to pay grid. If not specified then BCEA will construct a grid of 501 values from 0 to Kmax. This option is useful when performing intensive computations (e.g. for the EVPPI).
plot	A logical value indicating whether the function should produce the summary plot or not.

Value

An object of the class "bcea" containing the following elements

n_sim	Number of simulations produced by the Bayesian model
n.comparators	Number of interventions being analysed
n.comparisons	Number of possible pairwise comparisons
delta.e	For each possible comparison, the differential in the effectiveness measure
delta.c	For each possible comparison, the differential in the cost measure
ICER	The value of the Incremental Cost-Effectiveness Ratio
Kmax	The maximum value assumed for the willingness to pay threshold
k	The vector of values for the grid approximation of the willingness to pay
ceac	The value for the Cost-Effectiveness Acceptability Curve, as a function of the willingness to pay
ib	The distribution of the Incremental Benefit, for a given willingness to pay
eib	The value for the Expected Incremental Benefit, as a function of the willingness to pay
kstar	The grid approximation of the break even point(s)

best	A vector containing the numeric label of the intervention that is the most cost-effective for each value of the willingness to pay in the selected grid approximation
U	An array including the value of the expected utility for each simulation from the Bayesian model, for each value of the grid approximation of the willingness to pay and for each intervention being considered
vi	An array including the value of information for each simulation from the Bayesian model and for each value of the grid approximation of the willingness to pay
Ustar	An array including the maximum "known-distribution" utility for each simulation from the Bayesian model and for each value of the grid approximation of the willingness to pay
ol	An array including the opportunity loss for each simulation from the Bayesian model and for each value of the grid approximation of the willingness to pay
evi	The vector of values for the Expected Value of Information, as a function of the willingness to pay
interventions	A vector of labels for all the interventions considered
ref	The numeric index associated with the intervention used as reference in the analysis
comp	The numeric index(es) associated with the intervention(s) used as comparator(s) in the analysis
step	The step used to form the grid approximation to the willingness to pay
e	The e matrix used to generate the object (see Arguments)
c	The c matrix used to generate the object (see Arguments)

Author(s)

Gianluca Baio, Andrea Berardi

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research. doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London.

Examples

```
# See Baio G., Dawid A.P. (2011) for a detailed description of the
# Bayesian model and economic problem

# Load the processed results of the MCMC simulation model
data(Vaccine)

# Runs the health economic evaluation using BCEA
m <- bcea(
      e=e,
      c=c,                  # defines the variables of
                            #  effectiveness and cost
      ref=2,                # selects the 2nd row of (e, c)
                            #  as containing the reference intervention
      interventions=treats, # defines the labels to be associated
                            #  with each intervention
      Kmax=50000,           # maximum value possible for the willingness
```

```
                                # to pay threshold; implies that k is chosen
                                # in a grid from the interval (0, Kmax)
      plot=TRUE                 # plots the results
)

# Creates a summary table
summary(
      m,          # uses the results of the economic evaluation
                  # (a "bcea" object)
      wtp=25000 # selects the particular value for k
)



# Plots the cost-effectiveness plane using base graphics
ceplane.plot(
      m,              # plots the Cost-Effectiveness plane
      comparison=1,   # if more than 2 interventions, selects the
                      #  pairwise comparison
      wtp=25000,      # selects the relevant willingness to pay
                      #  (default: 25,000)
      graph="base"    # selects base graphics (default)
)

# Plots the cost-effectiveness plane using ggplot2
if (requireNamespace("ggplot2")) {
ceplane.plot(
      m,              # plots the Cost-Effectiveness plane
      comparison=1,   # if more than 2 interventions, selects the
                      #  pairwise comparison
      wtp=25000,      # selects the relevant willingness to pay
                      #  (default: 25,000)
      graph="ggplot2"# selects ggplot2 as the graphical engine
)

# Some more options
ceplane.plot(
      m,
      graph="ggplot2",
      pos="top",
      size=5,
      ICER_size=1.5,
      label.pos=FALSE,
      opt.theme=ggplot2::theme(text=ggplot2::element_text(size=8))
)
}

# Plots the contour and scatterplot of the bivariate
# distribution of (Delta_e,Delta_c)
contour(
      m,              # uses the results of the economic evaluation
                      #  (a "bcea" object)
      comparison=1, # if more than 2 interventions, selects the
                      #  pairwise comparison
      nlevels=4,      # selects the number of levels to be
                      #  plotted (default=4)
      levels=NULL,  # specifies the actual levels to be plotted
```

```
                         #  (default=NULL, so that R will decide)
        scale=0.5,       # scales the bandwidths for both x- and
                         #  y-axis (default=0.5)
        graph="base"     # uses base graphics to produce the plot
)

# Plots the contour and scatterplot of the bivariate
#   distribution of (Delta_e,Delta_c)
contour2(
        m,              # uses the results of the economic evaluation
                        #  (a "bcea" object)
        wtp=25000,      # selects the willingness-to-pay threshold
        xlim=NULL,      # assumes default values
        ylim=NULL       # assumes default values
)

# Using ggplot2
if (requireNamespace("ggplot2")) {
contour2(
        m,                  # uses the results of the economic evaluation
                            #  (a "bcea" object)
        graph="ggplot2",# selects the graphical engine
        wtp=25000,          # selects the willingness-to-pay threshold
        xlim=NULL,          # assumes default values
        ylim=NULL,          # assumes default values
        label.pos=FALSE # alternative position for the wtp label
)
}

# Plots the Expected Incremental Benefit for the "bcea" object m
eib.plot(m)

# Plots the distribution of the Incremental Benefit
ib.plot(
    m,              # uses the results of the economic evaluation
                    #  (a "bcea" object)
    comparison=1, # if more than 2 interventions, selects the
                    #  pairwise comparison
    wtp=25000,      # selects the relevant willingness
                    #  to pay (default: 25,000)
    graph="base"  # uses base graphics
)

# Produces a plot of the CEAC against a grid of values for the
# willingness to pay threshold
ceac.plot(m)

# Plots the Expected Value of Information for the "bcea" object m
evi.plot(m)
```

---

best_interv_given_k   *Select Best Option For Each Value Of Willingness To Pay*

Description

Select Best Option For Each Value Of Willingness To Pay

Usage

```
best_interv_given_k(eib, ref, comp)
```

Arguments

eib	Expected incremental benefit
ref	Reference group number
comp	Comparison group number(s)

Value

Group index

---

ceac.plot.bcea   *Cost-Effectiveness Acceptability Curve (CEAC) Plot*

Description

Produces a plot of the Cost-Effectiveness Acceptability Curve (CEAC) against the willingness to pay threshold.

Usage

```
## S3 method for class 'bcea'
ceac.plot(
  he,
  comparison = NULL,
  pos = c(1, 0),
  graph = c("base", "ggplot2", "plotly"),
  ...
)

ceac.plot(he, ...)
```

Arguments

he	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
comparison	Selects the comparator, in case of more than two interventions being analysed. Default as NULL plots all the comparisons together. Any subset of the possible comparisons can be selected (e.g., comparison=c(1,3) or comparison=2).
pos	Parameter to set the position of the legend (only relevant for multiple interventions, ie more than 2 interventions being compared). Can be given in form of a string (bottom|top)(right|left) for base graphics and bottom, top, left or right for *ggplot2*. It can be a two-elements vector, which specifies the relative position on the x and y axis respectively, or alternatively in form of a

logical variable, with FALSE indicating to use the default position and TRUE to
place it on the bottom of the plot. Default value is c(1,0), that is the bottom
right corner inside the plot area.

graph   A string used to select the graphical engine to use for plotting. Should (partial-
)match the three options "base", "ggplot2" or "plotly". Default value is
               "base".

...   If graph = "ggplot2" and a named theme object is supplied, it will be added to
               the ggplot object. Additional arguments:

               - line_colors: specifies the line colour(s) - all graph types.
               - line_types: specifies the line type(s) as lty numeric values - all graph
                 types.
               - area_include: logical, include area under the CEAC curves - plotly only.
               - area_color: specifies the AUC colour - plotly only.

Details

The CEAC estimates the probability of cost-effectiveness, with respect to a given willingness to
pay threshold. The CEAC is used mainly to evaluate the uncertainty associated with the decision-
making process, since it enables the quantification of the preference of the compared interventions,
defined in terms of difference in utilities. Formally, the CEAC is defined as:

$$\text{CEAC} = P(\text{IB}(\theta) > 0)$$

If the net benefit function is used as utility function, the definition can be re-written as

$$\text{CEAC} = P(k \cdot \Delta_e - \Delta_c > 0)$$

effectively depending on the willingness to pay value k.

Value

ceac   If graph = "ggplot2" a ggplot object, or if graph = "plotly" a plotly object
               containing the requested plot. Nothing is returned when graph = "base", the
               default.

The function produces a plot of the cost-effectiveness acceptability curve against the discrete grid
of possible values for the willingness to pay parameter. Values of the CEAC closer to 1 indicate
that uncertainty in the cost-effectiveness of the reference intervention is very low. Similarly, values
of the CEAC closer to 0 indicate that uncertainty in the cost-effectiveness of the comparator is very
low.

Author(s)

Gianluca Baio, Andrea Berardi

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical
Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London.

See Also

bcea, plot.bcea

ceac.plot.bcea

Examples

```
data("Vaccine")
he <- BCEA::bcea(e, c)
ceac.plot(he)

ceac.plot(he, graph = "base")
ceac.plot(he, graph = "ggplot2")
ceac.plot(he, graph = "plotly")

ceac.plot(he, graph = "ggplot2",
          title = "my title",
          line = list(colors = "green"),
          theme = ggplot2::theme_dark())

## more interventions
he2 <- BCEA::bcea(cbind(e, e - 0.0002), cbind(c, c + 5))
mypalette <- RColorBrewer::brewer.pal(3, "Accent")
ceac.plot(he2, graph = "ggplot2",
          title = "my title",
          theme = ggplot2::theme_dark(),
          pos = TRUE,
          line = list(colors = mypalette))
ceac.plot(he, graph = "base", title = "my title", line = list(colors = "green"))
ceac.plot(he2, graph = "base")

ceac.plot(he2, graph = "plotly", pos = "bottom")
```

---

ceac_matplot *CEAC Matrix Plot*

Description

CEAC plot using 'matplot' in Base R.

Usage

```
ceac_matplot(he, pos_legend, graph_params, ceac)
```

Arguments

he	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
pos_legend	Legend position
graph_params	Aesthetic ggplot parameters
ceac	'ceac' index in 'he'

---

ceac_plot_graph   *Cost-Effectiveness Acceptability Curve (CEAC) Plot By Graph Device*

Description

Choice of base R, ggplot2 or plotly.

Usage

```
ceac_plot_base(he, pos_legend, graph_params, ...)

## S3 method for class 'pairwise'
ceac_plot_base(he, pos_legend, graph_params, ...)

## S3 method for class 'bcea'
ceac_plot_base(he, pos_legend, graph_params, ...)

ceac_plot_ggplot(he, pos_legend, graph_params, ...)

## S3 method for class 'pairwise'
ceac_plot_ggplot(he, pos_legend, graph_params, ...)

## S3 method for class 'bcea'
ceac_plot_ggplot(he, pos_legend, graph_params, ...)

ceac_ggplot(he, pos_legend, graph_params, ceac, ...)

ceac_plot_plotly(he, pos_legend = "left", graph_params)
```

Arguments

he	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
pos_legend	Legend position
graph_params	Aesthetic ggplot parameters
...	Additional arguments
ceac	ceac index in he

---

ceaf.plot.pairwise   *Cost-Effectiveness Acceptability Frontier (CEAF) plot*

Description

Produces a plot the Cost-Effectiveness Acceptability Frontier (CEAF) against the willingness to pay threshold.

Usage

```
## S3 method for class 'pairwise'
ceaf.plot(mce, graph = c("base", "ggplot2"), ...)

ceaf.plot(mce, ...)
```

Arguments

mce	The output of the call to the function `multi.ce`
graph	A string used to select the graphical engine to use for plotting. Should (partial-) match the two options "base" or "ggplot2". Default value is "base".
...	Additional arguments

Value

ceaf	A ggplot object containing the plot. Returned only if graph="ggplot2".

Author(s)

Gianluca Baio, Andrea Berardi

References

Baio G, Dawid AP. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London.

See Also

bcea, multi.ce

Examples

```
# See Baio G., Dawid A.P. (2011) for a detailed description of the
# Bayesian model and economic problem

# Load the processed results of the MCMC simulation model
data(Vaccine)

# Runs the health economic evaluation using BCEA
m <- bcea(
     e=e,
     c=c,                   # defines the variables of
                            #  effectiveness and cost
     ref=2,                 # selects the 2nd row of (e, c)
                            #  as containing the reference intervention
     interventions=treats,  # defines the labels to be associated
                            #  with each intervention
     Kmax=50000,            # maximum value possible for the willingness
                            #  to pay threshold; implies that k is chosen
                            #  in a grid from the interval (0, Kmax)
     plot=FALSE             # inhibits graphical output
)
```

```
mce <- multi.ce(m)          # uses the results of the economic analysis



ceaf.plot(mce)              # plots the CEAF



ceaf.plot(mce, graph = "g") # uses ggplot2



# Use the smoking cessation dataset
data(Smoking)
m <- bcea(e, c, ref = 4, intervention = treats, Kmax = 500, plot = FALSE)
mce <- multi.ce(m)
ceaf.plot(mce)
```

---

ceef.plot.bcea   *Cost-Effectiveness Efficiency Frontier (CEAF) Plot*

Description

Back compatibility with BCEA previous versions: The bcea objects did not include the generating
e and c matrices in BCEA versions <2.1-0. This function is not compatible with objects created
with previous versions. The matrices can be appended to bcea objects obtained using previous
versions, making sure that the class of the object remains unaltered.

Usage

```
## S3 method for class 'bcea'
ceef.plot(
  he,
  comparators = NULL,
  pos = c(1, 1),
  start.from.origins = TRUE,
  threshold = NULL,
  flip = FALSE,
  dominance = TRUE,
  relative = FALSE,
  print.summary = TRUE,
  graph_type = c("base", "ggplot2"),
  ...
)

ceef.plot(he, ...)
```

Arguments

he	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
comparators	Vector specifying the comparators to be included in the frontier analysis. It must have a length > 1. Default as NULL includes all the available comparators.
pos	Parameter to set the position of the legend. Can be given in form of a string (bottom|top)(right|left) for base graphics and bottom, top, left or right for ggplot2. It can be a two-elements vector, which specifies the relative position on the x and y axis respectively, or alternatively it can be in form of a logical variable, with FALSE indicating to use the default position and TRUE to place it on the bottom of the plot. Default value is c(1,1), that is the topright corner inside the plot area.
start.from.origins	Logical. Should the frontier start from the origins of the axes? The argument is reset to FALSE if the average effectiveness and/or costs of at least one comparator are negative.
threshold	Specifies if the efficiency should be defined based on a willingness-to-pay threshold value. If set to NULL (the default), no conditions are included on the slope increase. If a positive value is passed as argument, to be efficient an intervention also requires to have an ICER for the comparison versus the last efficient strategy not greater than the specified threshold value. A negative value will be ignored with a warning.
flip	Logical. Should the axes of the plane be inverted?
dominance	Logical. Should the dominance regions be included in the plot?
relative	Logical. Should the plot display the absolute measures (the default as FALSE) or the differential outcomes versus the reference comparator?
print.summary	Logical. Should the efficiency frontier summary be printed along with the graph? See Details for additional information.
graph_type	A string used to select the graphical engine to use for plotting. Should (partial-)match the two options "base" or "ggplot2". Default value is "base".
...	If graph_type="ggplot2" and a named theme object is supplied, it will be added to the ggplot object. Ignored if graph_type="base". Setting the optional argument include.ICER to TRUE will print the ICERs in the summary tables, if produced.

Details

The argument print.summary allows for printing a brief summary of the efficiency frontier, with default to TRUE. Two tables are plotted, one for the interventions included in the frontier and one for the dominated interventions. The average costs and clinical benefits are included for each intervention. The frontier table includes the slope for the increase in the frontier and the non-frontier table displays the dominance type of each dominated intervention. Please note that the slopes are defined as the increment in the costs for a unit increment in the benefits even if flip = TRUE for consistency with the ICER definition. The angle of increase is in radians and depends on the definition of the axes, i.e. on the value given to the flip argument.

If the argument relative is set to TRUE, the graph will not display the absolute measures of costs and benefits. Instead the axes will represent differential costs and benefits compared to the reference intervention (indexed by ref in the bcea function).

Value

ceplane   A ggplot object containing the plot. Returned only if graph_type="ggplot2".

The function produces a plot of the cost-effectiveness efficiency frontier. The dots show the simulated values for the intervention-specific distributions of the effectiveness and costs. The circles indicate the average of each bivariate distribution, with the numbers referring to each included intervention. The numbers inside the circles are black if the intervention is included in the frontier and grey otherwise. If the option dominance is set to TRUE, the dominance regions are plotted, indicating the areas of dominance. Interventions in the areas between the dominance region and the frontier are in a situation of extended dominance.

Author(s)

Andrea Berardi, Gianluca Baio

References

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London.

IQWIG (2009). General methods for the Assessment of the Relation of Benefits to Cost, Version 1.0. IQWIG, November 2009.

See Also

bcea

Examples

```
## create the bcea object m for the smoking cessation example
data(Smoking)
m <- bcea(e, c, ref = 4, Kmax = 500, interventions = treats)

## produce plot
ceef.plot(m, graph_type = "base")


## tweak the options
## flip axis
ceef.plot(m,
          flip = TRUE,
          dominance = FALSE,
          start.from.origins = FALSE,
          print.summary = FALSE,
          graph_type = "base")

## or use ggplot2 instead
if(require(ggplot2)){
ceef.plot(m,
          dominance = TRUE,
          start.from.origins = FALSE,
          pos = TRUE,
          print.summary = FALSE,
          graph_type = "ggplot2")
 }
```

ceplane.plot.bcea   *Cost-effectiveness Plane Plot*

Description

Produces a scatter plot of the cost-effectiveness plane, together with the sustainability area, as a function of the selected willingness to pay threshold.

Usage

```
## S3 method for class 'bcea'
ceplane.plot(
  he,
  comparison = NULL,
  wtp = 25000,
  pos = c(0, 1),
  graph = c("base", "ggplot2", "plotly"),
  ...
)

ceplane.plot(he, ...)
```

Arguments

he	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
comparison	Selects the comparator, in case of more than two interventions being analysed. Default as NULL plots all the comparisons together. Any subset of the possible comparisons can be selected (e.g., comparison = c(1,3) or comparison = 2).
wtp	The value of the willingness to pay parameter. Not used if graph = "base" for multiple comparisons.
pos	Parameter to set the position of the legend; for a single comparison plot, the ICER legend position. Can be given in form of a string (bottom|top)(right|left) for base graphics and bottom|top|left|right for ggplot2. It can be a two-elements vector, which specifies the relative position on the x and y axis respectively, or alternatively it can be in form of a logical variable, with FALSE indicating to use the default position and TRUE to place it on the bottom of the plot. Default value is c(1,1), that is the topright corner inside the plot area.
graph	A string used to select the graphical engine to use for plotting. Should (partial-) match the two options "base" or "ggplot2". Default value is "base".
...	If graph = "ggplot2" and a named theme object is supplied, it will be added to the ggplot object. Additional graphical arguments:

- label.pos = FALSE: will place the willingness to pay label in a different position at the bottom of the graph - base and ggplot2 only (no label in plotly).
- point_colors: a vector of colours specifying the colour(s) associated to the cloud of points. Should be of length 1 or equal to the number of comparisons.

- point_size: a vector of colours specifying the size(s) of the points. Should be of length 1 or equal to the number of comparisons.
- ICER_colors: a vector of colours specifying the colour(s) of the ICER points. Should be of length 1 or equal to the number of comparisons.
- ICER_size: a vector of colours specifying the size(s) of the ICER points. Should be of length 1 or equal to the number of comparisons.
- area_include: logical, include or exclude the cost-effectiveness acceptability area (default is TRUE).
- area_color: a colour specifying the colour of the cost-effectiveness acceptability area.

Details

In the plotly version, point_colors, ICER_colors and area_color can also be specified as rgba colours using either the toRGB function or a rgba colour string, e.g. 'rgba(1,1,1,1)'.

Value

If graph = "ggplot2" a ggplot object, or if graph = "plotly" a plotly object containing the requested plot. Nothing is returned when graph = "base", the default.

Grey dots show the simulated values for the joint distribution of the effectiveness and cost differentials. The larger red dot shows the ICER and the grey area identifies the sustainability area, i.e. the part of the plan for which the simulated values are below the willingness to pay threshold. The proportion of points in the sustainability area effectively represents the CEAC for a given value of the willingness to pay. If the comparators are more than 2 and no pairwise comparison is specified, all scatterplots are graphed using different colours.

Author(s)

Gianluca Baio, Andrea Berardi

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research. doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London.

See Also

bcea, ceplane_plot_graph

Examples

```
## create the bcea object for the smoking cessation example
data(Smoking)

m <- bcea(e, c, ref = 4, Kmax = 500, interventions = treats)

## produce the base plot
ceplane.plot(m, wtp = 200, graph = "base")

## select only one comparator
ceplane.plot(m, wtp = 200, graph = "base", comparison = 3)
```

```
## use ggplot2
if (requireNamespace("ggplot2")) {
   ceplane.plot(m, wtp = 200, pos = "right", ICER_size = 2, graph = "ggplot2")
}

## plotly
ceplane.plot(m, wtp = 200, graph = "plotly")
ceplane.plot(m, wtp = 200, comparison = 1, graph = "plotly")
```

---

ceplane_geom_params   *Extract Separate Parameter Sets*

Description

Extract Separate Parameter Sets

Usage

```
ceplane_geom_params(...)
```

Arguments

`...`	Additional arguments

---

ceplane_ggplot_params   *CE-plane ggplot Parameters*

Description

CE-plane ggplot Parameters

Usage

```
ceplane_ggplot_params(he, wtp, pos_legend, graph_params, ...)
```

Arguments

`he`	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
`wtp`	Willingness to pay
`pos_legend`	Position of legend
`graph_params`	Other graphical parameters
`...`	Additional arguments

---

ceplane_plot_base.bcea

Cost-Effectiveness Plane Plot By Graph Device

Description

Choice of base R, ggplot2 or plotly.

Usage

```
## S3 method for class 'bcea'
ceplane_plot_base(he, wtp = 25000, pos_legend, graph_params, ...)

ceplane_plot_base(he, ...)

## S3 method for class 'bcea'
ceplane_plot_ggplot(he, wtp = 25000, pos_legend, graph_params, ...)

ceplane_plot_ggplot(he, ...)

## S3 method for class 'bcea'
ceplane_plot_plotly(he, wtp = 25000, pos_legend, graph_params, ...)

ceplane_plot_plotly(he, ...)
```

Arguments

he	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
wtp	Willingness to pay threshold; default 25,000
pos_legend	Legend position
graph_params	Graph parameters in ggplot format
...	Additional arguments

Value

For base R returns a plot

For ggplot2 returns ggplot2 object

For plotly returns a plot in the Viewer

Examples

```
data(Vaccine)
he <- bcea(e, c)

ceplane.plot(he, graph = "ggplot2")

data(Smoking)
he <- bcea(e, c, ref = 4, Kmax = 500, interventions = treats)
```

```
ceplane.plot(he, graph = "ggplot2")

ceplane.plot(he,
             wtp = 200,
             pos = "right",
             ICER_size = 2,
             graph = "ggplot2")

ceplane.plot(he,
             wtp = 200,
             pos = TRUE,
             graph = "ggplot2")

ceplane.plot(he,
             graph = "ggplot2",
             wtp=200,
             theme = ggplot2::theme_linedraw())

# single comparator
data(Vaccine)

he <- bcea(e,c)

# need to provide all the defaults because thats what
# ceplane.plot() does

graph_params <-  list(xlab = "x-axis label",
                      ylab = "y-axis label",
                      title = "my title",
                      xlim = c(-0.002, 0.001),
                      ylim = c(-13, 5),
                      point = list(sizes = 1,
                                   colors = "darkgrey"),
                      area = list(color = "lightgrey"))

he$delta_e <- as.matrix(he$delta_e)
he$delta_c <- as.matrix(he$delta_c)

ceplane_plot_base(he, graph_params = graph_params)

## single non-default comparator


## multiple comparators
data(Smoking)

graph_params <-  list(xlab = "x-axis label",
                      ylab = "y-axis label",
                      title = "my title",
                      xlim = c(-1, 2.5),
                      ylim = c(-1, 160),
                      point = list(sizes = 0.5,
                                   colors = grey.colors(3, start = 0.1, end = 0.7)),
                      area = list(color = "lightgrey"))

he <- bcea(e, c, ref = 4, Kmax = 500, interventions = treats)
ceplane_plot_base(he,
```

```
                wtp = 200,
                pos_legend = FALSE,
                graph_params = graph_params)
```

CEriskav   *Cost-effectiveness Analysis Including a Parameter of Risk Aversion*

Description

Extends the standard cost-effectiveness analysis to modify the utility function so that risk aversion of the decision maker is explicitly accounted for.

Usage

```
CEriskav(he, r = NULL, comparison = 1)
```

Arguments

he	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
r	A vector of values for the risk aversion parameter. If NULL, default values are assigned by R. The first (smallest) value (r -> 0) produces the standard analysis with no risk aversion.
comparison	In case of more than 2 interventions being analysed, selects which plot should be made. By default the first possible choice is selected as the comparator.

Value

An object of the class CEriskav containing the following elements:

Ur	An array containing the simulated values for all the "known-distribution" utilities for all interventions, all the values of the willingness to pay parameter and for all the possible values of r
Urstar	An array containing the simulated values for the maximum "known-distribution" expected utility for all the values of the willingness to pay parameter and for all the possible values of r
IBr	An array containing the simulated values for the distribution of the Incremental Benefit for all the values of the willingness to pay and for all the possible values of r
eibr	An array containing the Expected Incremental Benefit for each value of the willingness to pay parameter and for all the possible values of r
vir	An array containing all the simulations for the Value of Information for each value of the willingness to pay parameter and for all the possible values of r
evir	An array containing the Expected Value of Information for each value of the willingness to pay parameter and for all the possible values of r
R	The number of possible values for the parameter of risk aversion r
r	The vector containing all the possible values for the parameter of risk aversion r

Author(s)

Gianluca Baio

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London.

See Also

bcea

Examples

```
# See Baio G., Dawid A.P. (2011) for a detailed description of the
# Bayesian model and economic problem

# Load the processed results of the MCMC simulation model
data(Vaccine)

# Runs the health economic evaluation using BCEA
m <- bcea(e=e,c=c,           # defines the variables of
                             #  effectiveness and cost
      ref=2,                 # selects the 2nd row of (e, c)
                             #  as containing the reference intervention
      interventions=treats,  # defines the labels to be associated
                             #  with each intervention
      Kmax=50000             # maximum value possible for the willingness
                             #  to pay threshold; implies that k is chosen
                             #  in a grid from the interval (0, Kmax)
)

# Define the vector of values for the risk aversion parameter, r, eg:
r <- c(1e-10, 0.005, 0.020, 0.035)

# Run the cost-effectiveness analysis accounting for risk aversion

cr <- CEriskav(m,      # uses the results of the economic evalaution
                       #  (a "bcea" object)
         r=r,          # defines the vector of values for the risk
                       #  aversion parameter
         comparison=1  # if more than 2 interventions, selects the
                       #  pairwise comparison
)
```

---

compute_CEAC   *Compute Cost-Effectiveness Acceptability Curve*

Description

Compute Cost-Effectiveness Acceptability Curve

Usage

```
compute_CEAC(ib)
```

Arguments

ib   Incremental benefit

Value

Array with dimensions (interv x k)

See Also

ceac.plot

---

compute_EIB   *Compute Expected Incremental Benefit*

Description

A summary measure useful to assess the potential changes in the decision under different scenarios.

Usage

```
compute_EIB(ib)
```

Arguments

ib   Incremental benefit

Details

When considering a pairwise comparison (e.g. in the simple case of a reference intervention $t = 1$ and a comparator, such as the status quo, $t = 0$), it is defined as the difference between the expected utilities of the two alternatives:

$$eib := \mathrm{E}[u(e, c; 1)] - \mathrm{E}[u(e, c; 0)] = \mathcal{U}^1 - \mathcal{U}^0.$$

Analysis of the expected incremental benefit describes how the decision changes for different values of the threshold. The EIB marginalises out the uncertainty, and does not incorporate and describe explicitly the uncertainty in the outcomes. To overcome this problem the tool of choice is the CEAC.

Value

Array with dimensions (interv x k)

See Also

ceac.plot, compute_CEAC, compute_IB

---

compute_IB *Compute Incremental Benefit*

Description

Sample of incremental net monetary benefit for each willingness-to-pay threshold, k, and comparator.

Usage

```
compute_IB(df_ce, k)
```

Arguments

df_ce   Dataframe of cost and effectiveness deltas

k   Vector of willingness to pay values

Details

Defined as:

$$IB = u(e, c; 1) - u(e, c; 0).$$

If the net benefit function is used as utility function, the definition can be re-written as

$$IB = k \cdot \Delta_e - \Delta_c.$$

Value

Array with dimensions (k x sim x ints)

See Also

compute_EIB

---

compute_ICER *Compute Incremental Cost-Effectiveness Ratio*

Description

Defined as

Usage

```
compute_ICER(df_ce)
```

Arguments

df_ce   Cost-effectiveness dataframe

Details

$$ICER = \Delta_c / \Delta_e$$

Value

ICER for all comparisons

---

compute_kstar   *Compute kstar*

Description

Find willingness-to-pay threshold when optimal decision changes.

Usage

```
compute_kstar(k, best, ref)
```

Arguments

k	Willingness-to-pay vector
best	Best intervention for each 'k'
ref	Reference intervention

Value

Array with dimensions

See Also

[ceac.plot](#)

---

compute_ol   *Compute Opportunity Loss*

Description

The difference between the maximum utility computed for the current parameter configuration (e.g. at the current simulation) U^* and the current utility of the intervention associated with the maximum utility overall.

Usage

```
compute_ol(Ustar, U, best)
```

Arguments

Ustar	Maximum utility value (sim x k)
U	Net monetary benefit (sim x k x interv)
best	Best intervention for given willingness-to-pay (k)

Details

In mathematical notation,

$$\text{OL}(\theta) := U^*(\theta) - U(\theta^\tau)$$

where τ is the intervention associated with the overall maximum utility and $U^*(\theta)$ is the maximum utility value among the comparators in the given simulation. The opportunity loss is a non-negative quantity, since $U(\theta^\tau) \leq U^*(\theta)$.

In all simulations where the intervention is more cost-effective (i.e. when incremental benefit is positive), then $\text{OL}(\theta) = 0$ as there would be no opportunity loss, if the parameter configuration were the one obtained in the current simulation.

Value

Array with dimensions (sim x k)

See Also

compute_vi

---

compute_U   *Compute U Statistic*

Description

Sample of net monetary benefit for each willingness-to-pay threshold and intervention.

Usage

```
compute_U(df_ce, k)
```

Arguments

df_ce	Cost-effectiveness dataframe
k	Willingness to pay vector

Value

Array with dimensions (sim x k x ints)

---

compute_Ustar   *Compute Ustar Statistic*

Description

The maximum utility value among the comparators, indicating which intervention produced the most benefits at each simulation.

Usage

```
compute_Ustar(U)
```

Arguments

U   Net monetary benefit (sim x k x intervs)

Value

Array with dimensions (sim x k)

---

compute_vi   *Compute Value of Information*

Description

The difference between the maximum utility computed for the current parameter configuration U^* and the utility of the intervention which is associated with the maximum utility overall.

Usage

```
compute_vi(Ustar, U)
```

Arguments

Ustar   Maximum utility value (sim x k)
U   Net monetary benefit (sim x k x interv)

Details

The value of obtaining additional information on the parameter θ to reduce the uncertainty in the decisional process. It is defined as:

$$\text{VI}(\theta) := U^*(\theta) - \mathcal{U}^*$$

with $U^*(\theta)$ the maximum utility value for the given simulation among all comparators and $\mathcal{U}^*(\theta)$ the expected utility gained by the adoption of the cost-effective intervention.

Value

Array with dimensions (sim x k)

See Also

compute_ol

---

comp_names_from_   *Comparison Names From*

Description

Comparison Names From

Usage

```
comp_names_from_(df_ce)
```

Arguments

df_ce   Cost-effectiveness dataframe

---

contour.bcea   *Contour Plots for the Cost-Effectiveness Plane*

Description

Contour method for objects in the class bcea. Produces a scatterplot of the cost-effectiveness plane, with a contour-plot of the bivariate density of the differentials of cost (y-axis) and effectiveness (x-axis).

Usage

```
## S3 method for class 'bcea'
contour(
  he,
  comparison = 1,
  scale = 0.5,
  nlevels = 4,
  levels = NULL,
  pos = c(1, 0),
  xlim = NULL,
  ylim = NULL,
  graph = c("base", "ggplot2"),
  ...
)

contour(he, ...)
```

Arguments

he	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
comparison	In case of more than 2 interventions being analysed, selects which plot should be made. By default the first comparison among the possible ones will be plotted. If graph="ggplot2" any subset of the possible comparisons can be selected, and comparison=NULL will yield a plot of all the possible comparisons together.
scale	Scales the plot as a function of the observed standard deviation.
nlevels	Number of levels to be plotted in the contour.
levels	Numeric vector of levels at which to draw contour lines. Will be ignored using graph="ggplot2".
pos	Parameter to set the position of the legend. Can be given in form of a string (bottom|top)(right|left) for base graphics and bottom, top, left or right for ggplot2. It can be a two-elements vector, which specifies the relative position on the x and y axis respectively, or alternatively it can be in form of a logical variable, with FALSE indicating to use the default position and TRUE to place the legend on the bottom of the plot. Default value is c(1,0), that is the bottomright corner inside the plot area.
xlim	The range of the plot along the x-axis. If NULL (default) it is determined by the range of the simulated values for delta_e
ylim	The range of the plot along the y-axis. If NULL (default) it is determined by the range of the simulated values for delta_c
graph	A string used to select the graphical engine to use for plotting. Should (partial-) match the two options "base" or "ggplot2". Default value is "base".
...	Additional arguments to 'plot.window', 'title', 'Axis' and 'box', typically graphical parameters such as 'cex.axis'. Will be ignored if graph="ggplot2".

Value

ceplane	A ggplot object containing the plot. Returned only if graph="ggplot2".

Plots the cost-effectiveness plane with a scatterplot of all the simulated values from the (posterior) bivariate distribution of (Δ_e, Δ_c), the differentials of effectiveness and costs; superimposes a contour of the distribution and prints the estimated value of the probability of each quadrant (combination of positive/negative values for both Δ_e and Δ_c)

Author(s)

Gianluca Baio, Andrea Berardi

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London.

See Also

bcea, ceplane.plot, contour2

Examples

```
data(Vaccine)

# Runs the health economic evaluation using BCEA
m <- bcea(e=e,
          c=c,                # defines the variables of
                              #  effectiveness and cost
        ref=2,                # selects the 2nd row of (e,c)
                              #  as containing the reference intervention
        interventions=treats, # defines the labels to be associated
                              #  with each intervention
        Kmax=50000,           # maximum value possible for the willingness
                              #  to pay threshold; implies that k is chosen
                              #  in a grid from the interval (0,Kmax)
        plot=TRUE             # plots the results
)

contour(m)
contour(m, graph = "ggplot2")

# Plots the contour and scatterplot of the bivariate
# distribution of (Delta_e, Delta_c)
contour(m,            # uses the results of the economic evaluation
                      #  (a "bcea" object)
      comparison=1, # if more than 2 interventions, selects the
                      #  pairwise comparison
      nlevels=4,    # selects the number of levels to be
                      #  plotted (default=4)
      levels=NULL,  # specifies the actual levels to be plotted
                      #  (default=NULL, so that R will decide)
      scale=0.5,    # scales the bandwidths for both x- and
                      #  y-axis (default=0.5)
      graph="base"  # uses base graphics to produce the plot
)
```

---

contour2.bcea   *Specialised CE-plane Contour Plot*

Description

Produces a scatterplot of the cost-effectiveness plane, with a contour-plot of the bivariate density of the differentials of cost (y-axis) and effectiveness (x-axis). Also adds the sustainability area (i.e. below the selected value of the willingness-to-pay threshold).

Usage

```
## S3 method for class 'bcea'
contour2(
  he,
  wtp = 25000,
  xlim = NULL,
  ylim = NULL,
```

```
  comparison = NULL,
  graph_type = c("base", "ggplot2"),
  ...
)

contour2(he, ...)
```

Arguments

he	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
wtp	The selected value of the willingness-to-pay. Default is 25000.
xlim	Limits on the x-axis (default=NULL, so that R will select appropriate limits).
ylim	Limits on the y-axis (default=NULL, so that R will select appropriate limits).
comparison	The comparison being plotted. Default to NULL chooses the first comparison if graph_type="base". If graph_type="ggplot2" the default value will choose all the possible comparisons. Any subset of the possible comparisons can be selected (e.g., comparison=c(1,3)).
graph_type	A string used to select the graphical engine to use for plotting. Should (partial-)match the two options "base" or "ggplot2". Default value is "base".
...	Arguments to be passed to `ceplane.plot`. See the relative manual page for more details.

Value

contour	A ggplot item containing the requested plot. Returned only if graph_type="ggplot2".

Plots the cost-effectiveness plane with a scatterplot of all the simulated values from the (posterior) bivariate distribution of (Δ_e, Δ_c), the differentials of effectiveness and costs; superimposes a contour of the distribution and prints the value of the ICER, together with the sustainability area.

Author(s)

Gianluca Baio, Andrea Berardi

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London.

See Also

`bcea`, `ceplane.plot`, `contour.bcea`

Examples

```
## create the bcea object m for the smoking cessation example
data(Smoking)
m <- bcea(e, c, ref = 4, interventions = treats, Kmax = 500)

## produce the plot
contour2(m,
```

```
             wtp = 200,
             graph_type = "base")


## or use ggplot2 to plot multiple comparisons
contour2(m,
             wtp = 200,
             ICER_size = 2,
             graph_type = "ggplot2")
```

---

convert_pts_to_mm   *Use from Base R to ggplot*

Description

Use from Base R to ggplot

Usage

```
convert_pts_to_mm(x)
```

Arguments

x   points

---

create_inputs_evpi   *Create Inputs for EVPI Calculation*

Description

Creates an object containing the matrix with the parameters simulated using the MCMC procedure (using JAGS, BUGS or Stan) and a vector of parameters (strings) that can be used to perform the expected value of partial information analysis. In the process, CreateInputs also checks for linear dependency among columns of the PSA samples or columns having constant values and removes them to only leave the fundamental parameters (to run VoI analysis). This also deals with simulations stored in a .csv or .txt file (eg as obtained using bootstrapping from a non-Bayesian model).

Usage

```
create_inputs_evpi(inputs, print_is_linear_comb = TRUE)

createInputs(inputs, print_is_linear_comb = TRUE)

## S3 method for class 'rjags'
createInputs(inputs, print_is_linear_comb = TRUE)

## S3 method for class 'bugs'
```

```
createInputs(inputs, print_is_linear_comb = TRUE)

## S3 method for class 'stanfit'
createInputs(inputs, print_is_linear_comb = TRUE)

## S3 method for class 'data.frame'
createInputs(inputs, print_is_linear_comb = TRUE)

## S3 method for class 'matrix'
createInputs(inputs, print_is_linear_comb = TRUE)

## S3 method for class 'numeric'
createInputs(inputs, print_is_linear_comb = TRUE)

## Default S3 method:
createInputs(inputs, print_is_linear_comb)
```

Arguments

inputs   A rjags, bugs or stanfit object, containing the results of a call to either JAGS,
                      (under R2jags), BUGS (under R2WinBUGS or R2OpenBUGS), or Stan (under rstan).
print_is_linear_comb
                      A TRUE/FALSE indicator. If set to TRUE (default) then prints the output of the
                      procedure trying to assess whether there are some parameters that are a linear
                      combination of others (in which case they are removed).

Value

mat   A data.frame containing all the simulations for all the monitored parameters
parameters   A character vectors listing the names of all the monitored parameters

Author(s)

Gianluca Baio and Mark Strong

See Also

bcea, evppi

---

  diag.evppi   *Diagnostic Plots For The Results Of The EVPPI*

Description

The function produces either a residual plot comparing the fitted values from the INLA-SPDE
Gaussian Process regression to the residuals. This is a scatter plot of residuals on the y axis and
fitted values (estimated responses) on the x axis. The plot is used to detect non-linearity, unequal
error variances, and outliers. A well-behaved residual plot supporting the appropriateness of the
simple linear regression model has the following characteristics: 1) The residuals bounce randomly
around the 0 line. This suggests that the assumption that the relationship is linear is reasonable. 2)
The residuals roughly form a horizontal band around the 0 line. This suggests that the variances
of the error terms are equal. 3) None of the residual stands out from the basic random pattern of
residuals. This suggests that there are no outliers.

Usage

```
diag.evppi(evppi, he, plot_type = c("residuals", "qqplot"), interv = 1)
```

Arguments

evppi	A evppi object obtained by running the function evppi on a bcea model.
he	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
plot_type	The type of diagnostics to be performed. It can be the 'residual plot' or the 'qqplot plot'.
interv	Specifies the interventions for which diagnostic tests should be performed (if there are many options being compared)

Details

The second possible diagnostic is the qqplot for the fitted value. This is a graphical method for comparing the fitted values distributions with the assumed underlying normal distribution by plotting their quantiles against each other. First, the set of intervals for the quantiles is chosen. A point (x,y) on the plot corresponds to one of the quantiles of the second distribution (y-coordinate) plotted against the same quantile of the first distribution (x-coordinate). If the two distributions being compared are identical, the Q-Q plot follows the 45 degrees line.

Value

Plot

Author(s)

Gianluca Baio, Anna Heath

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London.

See Also

bcea, evppi

---

eib.plot.bcea	*Expected Incremental Benefit (EIB) Plot*

Description

Produces a plot of the Expected Incremental Benefit (EIB) as a function of the willingness to pay.

Usage

```
## S3 method for class 'bcea'
eib.plot(
  he,
  comparison = NULL,
  pos = c(1, 0),
  size = NULL,
  plot.cri = NULL,
  graph = c("base", "ggplot2", "plotly"),
  ...
)

eib.plot(he, ...)
```

Arguments

he	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
comparison	Selects the comparator, in case of more than two interventions being analysed. Default as NULL plots all the comparisons together. Any subset of the possible comparisons can be selected (e.g., comparison=c(1,3) or comparison=2).
pos	Parameter to set the position of the legend; for a single comparison plot, the ICER legend position. Can be given in form of a string (bottom|top)(right|left) for base graphics and bottom|top|left|right for ggplot2. It can be a two-elements vector, which specifies the relative position on the x and y axis respectively, or alternatively it can be in form of a logical variable, with FALSE indicating to use the default position and TRUE to place it on the bottom of the plot. Default value is c(1,0), that is the bottomright corner inside the plot area.
size	Value (in millimetres) of the size of the willingness to pay label. Used only if graph="ggplot2", otherwise it will be ignored with a message. If set to NA, the break-even point line(s) and label(s) are suppressed, with both base graphics and ggplot2.
plot.cri	Logical value. Should the credible intervals be plotted along with the expected incremental benefit? Default as NULL draws the 95% credible intervals if only one comparison is selected, and does not include them for multiple comparisons. Setting plot.cri=TRUE or plot.cri=FALSE forces the function to add the intervals or not. The level of the intervals can be also set, see ... for more details.
graph	A string used to select the graphical engine to use for plotting. Should (partial-)match the three options "base", "ggplot2" or "plotly". Default value is "base".
...	If graph="ggplot2" and a named theme object is supplied, it will be added to the ggplot object. Additional arguments:

- alpha can be used to set the CrI level when plot.cri=TRUE, with a default value of alpha=0.05.
- cri.quantile controls the the method of calculation of the credible intervals. The default value cri.quantile=TRUE defines the CrI as the interval between the alpha/2-th and 1-alpha/2-th quantiles of the IB distribution. Setting cri.quantile=FALSE will use a normal approximation on the IB distribution to calculate the intervals.
- line_colors: specifies the line colour(s) - all graph types.

- line_types: specifies the line type(s) as lty numeric values - all graph types.
- area_include: include area under the EIB curve - plotly only.
- area_color: specifies the AUC curve - plotly only.

Value

eib   If graph="ggplot2" a ggplot object, or if graph="plotly" a plotly object containing the requested plot. Nothing is returned when graph="base", the default.

The function produces a plot of the Expected Incremental Benefit as a function of the discrete grid approximation of the willingness to pay parameter. The break even point (i.e. the point in which the EIB = 0, i.e. when the optimal decision changes from one intervention to another) is also showed by default. The value 'k*' is the discrete grid approximation of the ICER.

Author(s)

Gianluca Baio, Andrea Berardi

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London.

See Also

bcea, ib.plot, ceplane.plot

Examples

```
data(Vaccine)

# Runs the health economic evaluation using BCEA
m <- bcea(
     e=e,
     c=c,                  # defines the variables of
                           #  effectiveness and cost
     ref=2,                # selects the 2nd row of (e, c)
                           #  as containing the reference intervention
     interventions=treats, # defines the labels to be associated
                           #  with each intervention
     Kmax=50000,           # maximum value possible for the willingness
                           #  to pay threshold; implies that k is chosen
                           #  in a grid from the interval (0, Kmax)
     plot=TRUE             # plots the results
)
eib.plot(m)
eib.plot(m, graph = "ggplot2") + ggplot2::theme_linedraw()
```

---

eib.plot.cri *Calculate Credible Intervals*

Description

Calculate Credible Intervals

Usage

```
## S3 method for class 'cri'
eib.plot(he, alpha = 0.05, cri.quantile)
```

Arguments

he   A bcea object containing the results of the Bayesian modelling and the economic evaluation.

alpha   Significance level, 0 - 1

cri.quantile   Credible interval quantile?; logical

Value

cri

---

evi.plot.bcea *Expected Value of Information (EVI) Plot*

Description

Plots the Expected Value of Information (EVI) against the willingness to pay.

Usage

```
## S3 method for class 'bcea'
evi.plot(he, graph = c("base", "ggplot2", "plotly"), ...)

evi.plot(he, ...)
```

Arguments

he   A bcea object containing the results of the Bayesian modelling and the economic evaluation.

graph   A string used to select the graphical engine to use for plotting. Should (partial-)match the three options "base", "ggplot2" or "plotly". Default value is "base".

...   Additional graphical arguments:

- line_colors to specify the EVPI line colour - all graph types.
- line_types to specify the line type (lty) - all graph types.
- area_include to specify whether to include the area under the EVPI curve - plotly only.
- area_color to specify the area under the colour curve - plotly only.

Value

eib   If graph="ggplot2" a ggplot object, or if graph="plotly" a plotly object
             containing the requested plot. Nothing is returned when graph="base", the
             default.

The function produces a plot of the Expected Value of Information as a function of the discrete
grid approximation of the willingness to pay parameter. The break even point(s) (i.e. the point in
which the EIB=0, ie when the optimal decision changes from one intervention to another) is(are)
also showed.

Author(s)

Gianluca Baio, Andrea Berardi

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical
Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London.

See Also

bcea, ceac.plot, ceplane.plot

---

evppi   *Expected Value of Perfect Partial Information (EVPPI) for Selected*
                         Parameters

Description

Calculates the Expected Value of Perfect Partial Information (EVPPI) for subsets of parameters.
Uses GAM non-parametric regression for single parameter EVPPI and the SPDE-INLA method for
larger parameter subsets.

Usage

```
evppi(he, param_idx, input, N = NULL, plot = FALSE, residuals = TRUE, ...)

## Default S3 method:
evppi(he, ...)
```

Arguments

he   A bcea object containing the results of the Bayesian modelling and the economic
             evaluation.

param_idx   A vector of parameters for which the EVPPI should be calculated. This can be
             given as a string (or vector of strings) of names or a numeric vector, corresponding
             to the column numbers of important parameters.

input   A matrix containing the simulations for all the parameters monitored by the call
             to JAGS or BUGS. The matrix should have column names matching the names
             of the parameters and the values in the vector parameter should match at least
             one of those values.

N	The number of PSA simulations used to calculate the EVPPI. The default uses all the available samples.
plot	A logical value indicating whether the triangular mesh for SPDE-INLA should be plotted. Default set to 'FALSE'.
residuals	A logical value indicating whether the fitted values for the SPDE-INLA method should be outputted. Default set to 'TRUE'.
...	Additional arguments. The default methods to compute the EVPPI are: - For single-parameter: GAM regression. - For multi-parameter: INLA/SPDE. However, it is possible (mainly for backward compatibility) to use different methods. For single-parameter, the user can specify the method of Sadatsafavi et al or the method of Strong & Oakley. In order to do so, it is necessary to include the extra parameter `method` which takes as value a string `"sad"` in the former case and a string `"so"` in the latter. In case "sal" is selected, then it is possible to also specify the number of "separators" (e.g. `n.seps=3`). If none is specified, the default value `n.seps=1` is used. If `"so"` is used as method for the calculation of the EVPPI, then the user *needs* to also specify the number of "blocks" (e.g. `n.blocks=20`).

Details

The single parameter EVPPI has been calculated using the non-parametric GAM regression developed by Strong et al. (2014). The multi-parameter EVPPI is calculated using the SPDE-INLA regression method for Gaussian Process regression developed by Heath et al. (2015).

Value

evppi	The computed values of evppi for all values of the parameter of willingness to pay.
index	A numerical vector with the index associated with the parameters for which the EVPPI was calculated.
k	The vector of values for the willingness to pay.
evi	The vector of values for the overall EVPPI.
fitted.costs	The fitted values for the costs.
fitted.effects	The fitted values for the effects.
parameters	A single string containing the names of the parameters for which the EVPPI was calculated, used for plotting the EVPPI.
time	Computational time (in seconds).
fit.c	The object produced by the model fit for the costs.
fit.e	The object produced by the model fit for the effects.
formula	The formula used to fit the model.
method	A string indicating the method used to estimate the EVPPI.

GAM regression

For multi-parameter, the user can select 3 possible methods. If `method = "GAM"` (BCEA will accept also `"gam"`, `"G"` or `"g"`), then the computations are based on GAM regression. The user can also specify the formula for the regression. The default option is to use a tensor product (e.g. if there are two main parameters, p1 and p2, this amounts to setting `formula = "te(p1,p2)"`, which indicates that the two parameters interact). Alternatively, it is possible to specify a model in which the parameters are independent using the notation `formula = "s(p1) + s(p2)"`. This may lead to worse accuracy in the estimates.

Strong et al. GP regression

This is used if `method="GP"` (BCEA will also accept the specification `method="gp"`). In this case, the user can also specify the number of PSA runs that should be used to estimate the hyperparameters of the model (e.g. `n.sim=100`). This value is set by default to 500.

INLA-related options

These are all rather technical and are described in detail in Baio et al. (2017). The optional parameter vector `int.ord` can take integer values (c(1,1) is default) and will force the predictor to include interactions: if `int.ord = c(k,h)`, then all k-way interactions will be used for the effects and all h-way interactions will be used for the costs. Also, the user can specify the feature of the mesh for the "spatial" part of the model. The optional parameter `cutoff` (default 0.3) controls the density of the points inside the mesh. Acceptable values are typically in the interval (0.1, 0.5), with lower values implying more points (and thus better approximation and greater computational time). The construction of the boundaries for the mesh can be controlled by the optional inputs `convex.inner` (default = -0.4) and `convex.outer` (default = -0.7). These should be negative values and can be decreased (say to -0.7 and -1, respectively) to increase the distance between the points and the outer boundary, which also increases precision and computational time. The optional argument `robust` can be set to TRUE, in which case INLA will use a t prior distribution for the coefficients of the linear predictor. Finally, the user can control the accuracy of the INLA grid-search for the estimation of the hyperparameters. This is done by setting a value `h.value` (default = 0.00005). Lower values imply a more refined search (and hence better accuracy), at the expense of computational speed. The method argument can also be given as a list allowing different regression methods for the effects and costs, and the different incremental decisions. The first list element should contain a vector of methods for the incremental effects and the second for the costs, for example `method = list(c("GAM"),c("INLA"))`. The `int.ord` argument can also be given as a list to give different interaction levels for each regression curve.

By default, when no method is specified by the user, `evppi` will use GAM if the number of parameters is <5 and INLA otherwise.

Author(s)

Anna Heath, Gianluca Baio

References

Strong M., Oakley J. and Brennan A. (2014). Estimating multi-parameter partial Expected Value of Perfect Information from a probabilistic sensitivity analysis sample: a non-parametric regression approach. Medical Decision Making.

Sadatsafavi M., Bansback N., Zafari Z., Najafzadeh M., Marra C. (2013). Need for speed: an efficient algorithm for calculation of single-parameter expected value of partial perfect information. Value in Health.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London.

Baio, G, A Berardi, and A Heath. 2017. Bayesian Cost-Effectiveness Analysis with the R package BCEA. New York, NY: Springer. doi:10.1007/978-3-319-55718-2.

Heath A., Manolopoulou I., Baio G. (2016). Estimating the Expected Value of Partial Perfect Information in Health Economic Evaluations using Integrated Nested Laplace Approximation. Statistics in Medicine. http://onlinelibrary.wiley.com/doi/10.1002/sim.6983/full

See Also

bcea, plot.evppi,

Examples

```
# See Baio G., Dawid A.P. (2011) for a detailed description of the
# Bayesian model and economic problem

# Load the processed results of the MCMC simulation model
data(Vaccine)

# Run the health economic evaluation using BCEA
m <- bcea(e, c, ref = 2, interventions = treats)

# Compute the EVPPI for a bunch of parameters
inp <- createInputs(vaccine)

# Compute the EVPPI using INLA/SPDE
x0 <- evppi(he = m, param_idx = 39:40, input = inp$mat)

# using GAM regression
x1 <- evppi(he = m, param_idx = 39:40, input = inp$mat, method = "GAM")

# using GP regression
x2 <- evppi(he = m, param_idx = 39:40, input = inp$mat, method = "GP")

# plot results
plot(x0)
points(x0$k, x0$evppi, type = "l", lwd = 2, lty = 2)
points(x1$k, x1$evppi, type = "l", col = "red")
points(x2$k, x2$evppi, type = "l", col = "blue")

plot(x0$k, x0$evppi, type = "l", lwd = 2, lty = 2)
points(x1$k, x1$evppi, type = "l", col = "red")
points(x2$k, x2$evppi, type = "l", col = "blue")
```

---

fit.gam   *Gaussian Additive Model Fitting*

Description

Gaussian Additive Model Fitting

Usage

```
fit.gam(parameter, inputs, x, form)
```

Arguments

parameter	Parameter
inputs	Inputs
x	Response variable
form	Formula

Value

List

`fit.gp` *Fit Gaussian Process*

Description

Fit Gaussian Process

Usage

```
fit.gp(parameter, inputs, x, n.sim)
```

Arguments

parameter	Parameters
inputs	Inputs
x	x
n.sim	Number of simulations

`fit.inla` *Fit INLA*

Description

Fit INLA

Usage

```
fit.inla(
  parameter,
  inputs,
  x,
  mesh,
  data.scale,
  int.ord,
  convex.inner,
  convex.outer,
  cutoff,
  max.edge,
  h.value,
  family
)
```

Arguments

parameter	Parameters
inputs	Inputs
x	x
mesh	Mesh
data.scale	data.scale
int.ord	int.ord
convex.inner	convex.inner
convex.outer	convex.outer
cutoff	Cut-off
max.edge	Maximum edge
h.value	h.value
family	family

---

ib.plot.bcea   *Incremental Benefit (IB) Distribution Plot*

Description

Plots the distribution of the Incremental Benefit (IB) for a given value of the willingness to pay
threshold.

Usage

```
## S3 method for class 'bcea'
ib.plot(
  he,
  comparison = NULL,
  wtp = 25000,
  bw = nbw,
  n = 512,
  xlim = NULL,
  graph = c("base", "ggplot2"),
  ...
)

ib.plot(he, ...)
```

Arguments

he	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
comparison	In the case of multiple interventions, specifies the one to be used in comparison with the reference. Default value of NULL forces R to consider the first non-reference intervention as the comparator.
wtp	The value of the willingness to pay threshold. Default value at 25000.

bw	Identifies the smoothing bandwidth used to construct the kernel estimation of the IB density.
n	The number of equally spaced points at which the density is to be estimated.
xlim	The limits of the plot on the x-axis.
graph	A string used to select the graphical engine to use for plotting. Should (partial-) match the two options "base" or "ggplot2". Default value is "base".
...	Additional arguments

Value

ib	A ggplot object containing the requested plot. Returned only if graph="ggplot2".

The function produces a plot of the distribution of the Incremental Benefit for a given value of the willingness to pay parameter. The dashed area indicates the positive part of the distribution (i.e. when the reference is more cost-effective than the comparator).

Author(s)

Gianluca Baio, Andrea Berardi

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London.

See Also

bcea, ib.plot, ceplane.plot

---

info.rank   *Information-Rank Plot*

Description

Produces a plot similar to a Tornado-plot, but based on the analysis of the EVPPI. For each parameter and value of the willingness-to-pay threshold, a barchart is plotted to describe the ratio of EVPPI (specific to that parameter) to EVPI. This represents the relative 'importance' of each parameter in terms of the expected value of information.

Usage

```
info.rank(he, ...)
```

Arguments

he	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
...	Additional options. These include graphical parameters that the user can specify:

- xlim = limits of the x-axis; ca = font size for the axis label (default = 0.7 of full size).
- cn = font size for the parameter names vector (default = 0.7 of full size) - base graphics only.
- mai = margins of the graph (default = c(1.36, 1.5, 1,1)) - base graphics only.
- rel = logical argument that specifies whether the ratio of EVPPI to EVPI (rel=TRUE, default) or the absolute value of the EVPPI should be used for the analysis.

Value

Bar plot

---

is.bcea   *Check bcea Class*

Description

Check bcea Class

Usage

```
is.bcea(he)
```

Arguments

he	A bcea object containing the results of the Bayesian modelling and the economic evaluation.

Value

is.bcea returns TRUE or FALSE depending on whether its argument is a bcea class object.

---

line_labels   *Create Labels for Plot*

Description

Create Labels for Plot

Usage

```
line_labels(he, ...)

## Default S3 method:
line_labels(he, ...)

## S3 method for class 'pairwise'
line_labels(he, ...)
```

Arguments

he	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
...	Additional arguments

---

make.mesh   *Make Mesh*

Description

Make Mesh

Usage

```
make.mesh(data, convex.inner, convex.outer, cutoff, max.edge)
```

Arguments

data	Data
convex.inner	convex.inner
convex.outer	convex.outer
cutoff	Cut-off
max.edge	Maximum edge

---

make.proj   *INLA Fitting*

Description

INLA Fitting

Usage

```
make.proj(parameter, inputs, x, k, l)
```

Arguments

    `parameter`   Parameter

    `inputs`   Inputs

    `x`   x

    `k`   k

    `l`   l

`make.report`	*Make Report*

Description

Constructs the automated report from the output of the BCEA.

Usage

```
make.report(he, evppi = NULL, ext = "pdf", echo = FALSE, ...)
```

Arguments

`he`	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
`evppi`	An object obtained as output to a call to evppi (default is NULL, so not essential to producing the report).
`ext`	A string of text to indicate the extension of the resulting output file. Possible options are "pdf", "docx". This requires the use of pandoc, knitr and rmarkdown.
`echo`	A string (default to FALSE) to instruct whether the report should also include the BCEA commands used to produce the analyses. If the optional argument echo is set to TRUE (default = FALSE), then the commands are also printed.
`...`	Additional parameters. For example, the user can specify the value of the willingness to pay wtp, which is used in some of the resulting analyses (default at the break even point). Another additional parameter that the user can specify is the name of the file to which the report should be written. This can be done by simply passing the optional argument filename="NAME". The user can also specify an object including the PSA simulations for all the relevant model parameters. If this is passed to the function (in the object psa_sims), then make.report will automatically construct an "Info-rank plot", which is a probabilistic form of tornado plot, based on the Expected Value of Partial Information. The user can also specify the optional argument show.tab (default=FALSE); if set to TRUE, then a table with the values of the Info-rank is also shown.

Author(s)

Gianluca Baio

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London.

See Also

[bcea](#)

Examples

```
## Not run:
  data(Vaccine)
  m <- bcea(e, c, ref = 2)
  make.report(m)

## End(Not run)
```

---

make_legend_plotly   *Legend Positioning*

Description

Legend Positioning

Usage

```
make_legend_plotly(pos_legend)
```

Arguments

pos_legend   Position of legend

Value

String

---

mixedAn   *Cost-Effectiveness Analysis When Multiple (Possibly Non-Cost-Effective) Interventions are Present on the Market*

Description

Runs the cost-effectiveness analysis, but accounts for the fact that more than one intervention is present on the market.

Usage

```
mixedAn(he, mkt.shares = NULL, plot = FALSE)

## Default S3 method:
mixedAn(he, mkt.shares = NULL, plot = FALSE)
```

Arguments

he	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
mkt.shares	A vector of market shares associated with the interventions. Its size is the same as the number of possible comparators. By default, assumes uniform distribution for each intervention.
plot	Logical value indicating whether the function should produce graphical output, via plot.mixedAn, or not. Default is set to FALSE.

Value

Creates an object in the class mixedAn which contains the results of the health economic evaluation in the mixed analysis case:

Ubar	An array with the simulations of the "known-distribution" mixed utilities, for each value of the discrete grid approximation of the willingness to pay parameter
OL.star	An array with the simulations of the distribution of the Opportunity Loss for the mixed strategy, for each value of the discrete grid approximation of the willingness to pay parameter
evi.star	The Expected Value of Information for the mixed strategy, for each value of the discrete grid approximation of the willingness to pay parameter
k	The discrete grid approximation of the willingness to pay parameter used for the mixed strategy analysis
Kmax	The maximum value of the discrete grid approximation for the willingness to pay parameter
step	The step used to form the grid approximation to the willingness to pay
ref	The numeric index associated with the intervention used as reference in the analysis
comp	The numeric index(es) associated with the intervention(s) used as comparator(s) in the analysis
mkt.shares	The vector of market shares associated with each available intervention
n.comparisons	The total number of pairwise comparisons available
interventions	A vector of labels for all the interventions considered
evi	The vector of values for the "optimal" Expected Value of Information, as a function of the willingness to pay

The function can also produce a graph showing the difference between the "optimal" version of the EVPI (when only the most cost-effective intervention is included in the market) and the mixed strategy one (when more than one intervention is considered in the market).

Author(s)

Gianluca Baio

References

Baio, G. and Russo, P. (2009). A decision-theoretic framework for the application of cost-effectiveness analysis in regulatory processes. Pharmacoeconomics 27(8), 645-655 doi:10.2165/11310250

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London.

See Also

bcea

Examples

```
# See Baio G., Dawid A.P. (2011) for a detailed description of the
# Bayesian model and economic problem

# Load the processed results of the MCMC simulation model
data(Vaccine)

# Runs the health economic evaluation using BCEA
m <- bcea(e=e,c=c,          # defines the variables of
                            #  effectiveness and cost
      ref=2,                # selects the 2nd row of (e, c)
                            #  as containing the reference intervention
      interventions=treats, # defines the labels to be associated
                            #  with each intervention
      Kmax=50000,           # maximum value possible for the willingness
                            #  to pay threshold; implies that k is chosen
                            #  in a grid from the interval (0, Kmax)
      plot=FALSE)           # inhibits graphical output

ma <- mixedAn(m,       # uses the results of the mixed strategy
                       #  analysis (a "mixedAn" object)
      mkt.shares=NULL,  # the vector of market shares can be defined
                       #  externally. If NULL, then each of the T
                       #  interventions will have 1/T market share
      plot=TRUE)       # produces the plots
```

---

multi.ce *Cost-effectiveness Analysis With Multiple Comparison*

Description

Computes and plots the probability that each of the 'n_int' interventions being analysed is the most cost-effective and the cost-effectiveness acceptability frontier.

Usage

```
multi.ce(he)
```

Arguments

he   A bcea object containing the results of the Bayesian modelling and the economic evaluation.

Value

Original bcea object (list) of class "pairwise" with additional:

p_best_interv A matrix including the probability that each intervention is the most cost-effective for all values of the willingness to pay parameter

ceaf   A vector containing the cost-effectiveness acceptability frontier

Author(s)

Gianluca Baio

See Also

bcea, mce.plot, ceaf.plot

Examples

```
# See Baio G., Dawid A.P. (2011) for a detailed description of the
# Bayesian model and economic problem

# Load the processed results of the MCMC simulation model
data(Vaccine)

# Runs the health economic evaluation using BCEA

m <- bcea(e=e,c=c,          # defines the variables of
                            #  effectiveness and cost
      ref=2,                # selects the 2nd row of (e,c)
                            #  as containing the reference intervention
      interventions=treats, # defines the labels to be associated
                            #  with each intervention
      Kmax=50000,           # maximum value possible for the willingness
                            #  to pay threshold; implies that k is chosen
                            #  in a grid from the interval (0,Kmax)
      plot=FALSE            # inhibits graphical output
)

mce <- multi.ce(m)          # uses the results of the economic analysis
```

---

multiplot   *Plot Multiple bcea Graphs*

Description

Arrange plots in grid. Sourced from R graphics cookbook.

Usage

```
multiplot(plotlist = NULL, cols = 1, layout_config = NULL)
```

Arguments

plotlist	List of ggplot objects
cols	Number of columns
layout_config	Matrix of plot configuration

Value

ggplot TableGrob object

---

new_bcea   *Constructor for bcea*

Description

Constructor for bcea

Usage

```
new_bcea(df_ce, k)
```

Arguments

df_ce   Dataframe of all simulation eff and cost

k   Vector of willingness to pay values

Value

List object of class bcea.

See Also

bcea

---

openPDF   *Automatically open pdf output using default pdf viewer*

Description

Automatically open pdf output using default pdf viewer

Usage

```
openPDF(file_name)
```

Arguments

file_name   String file names for pdf

plot.bcea   *Summary Plot of the Health Economic Analysis*

Description

Plots in a single graph the Cost-Effectiveness plane, the Expected Incremental Benefit, the CEAC
and the EVPI.

Usage

```
## S3 method for class 'bcea'
plot(
  x,
  comparison = NULL,
  wtp = 25000,
  pos = FALSE,
  graph = c("base", "ggplot2"),
  ...
)
```

Arguments

x	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
comparison	Selects the comparator, in case of more than two interventions being analysed. Default as NULL plots all the comparisons together. Any subset of the possible comparisons can be selected (e.g., comparison=c(1,3) or comparison=2).
wtp	The value of the willingness to pay parameter. It is passed to ceplane.plot.
pos	Parameter to set the position of the legend. Can be given in form of a string, a single logical value, or a two-element vector with the respective relative positions on the x and y axis. Default as FALSE sets the legend position to the default one for each plot (see the details section), while TRUE puts it on the bottom of each plot. Changes will affect all the individual plots.
graph	A string used to select the graphical engine to use for plotting. Should (partial-)match the two options "base" or "ggplot2". Default value is "base".
...	Arguments to be passed to the methods ceplane.plot and eib.plot. Please see the manual pages for the individual functions. Arguments like size, ICER.size and plot.cri can be supplied to the functions in this way. In addition if graph="ggplot2" and the arguments are named theme objects they will be added to each plot.

Details

The default position of the legend for the cost-effectiveness plane (produced by ceplane.plot) is
set to c(1,1.025) overriding its default for pos=FALSE, since multiple ggplot2 plots are rendered
in a slightly different way than single plots.

Value

A plot with four graphical summaries of the health economic evaluation.

Author(s)

Gianluca Baio, Andrea Berardi

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London.

See Also

bcea, ceplane.plot, eib.plot, ceac.plot, evi.plot

Examples

```
# See Baio G., Dawid A.P. (2011) for a detailed description of the
# Bayesian model and economic problem

# Load the processed results of the MCMC simulation model
data(Vaccine)

# Runs the health economic evaluation using BCEA
he <- bcea(
        e=e, c=c,             # defines the variables of
                              #  effectiveness and cost
        ref=2,                # selects the 2nd row of (e,c)
                              #  as containing the reference intervention
        interventions=treats, # defines the labels to be associated
                              #  with each intervention
        Kmax=50000,           # maximum value possible for the willingness
                              #  to pay threshold; implies that k is chosen
                              #  in a grid from the interval (0,Kmax)
        plot=FALSE            # does not produce graphical outputs
     )

# Plots the summary plots for the "bcea" object m using base graphics
plot(he, graph = "base")

# Plots the same summary plots using ggplot2
if(require(ggplot2)){
plot(he, graph = "ggplot2")

##### Example of a customized plot.bcea with ggplot2
plot(he,
  graph = "ggplot2",                                 # use ggplot2
  theme = theme(plot.title=element_text(size=rel(1.25))), # theme elements must have a name
  ICER_size = 1.5,                                   # hidden option in ceplane.plot
  size = rel(2.5)                                    # modifies the size of k = labels
  )                                                  # in ceplane.plot and eib.plot
}
```

---

plot.CEriskav   *Plots EIB for the Risk Aversion Case*

Description

Summary plot of the health economic analysis when risk aversion is included.

Usage

```
## S3 method for class 'CEriskav'
plot(x, pos = c(0, 1), graph = c("base", "ggplot2"), ...)
```

Arguments

x   An object of the class CEriskav, containing the results of the economic analysis
             performed accounting for a risk aversion parameter (obtained as output of the
             function CEriskav).

pos   Parameter to set the position of the legend. Can be given in form of a string
             (bottom|top)(right|left) for base graphics and bottom|top|left|right
             for ggplot2. It can be a two-elements vector, which specifies the relative position
             on the x and y axis respectively, or alternatively it can be in form of a logical
             variable, with FALSE indicating to use the default position and TRUE to place it
             on the bottom of the plot. Default value is c(0,1), that is in the topleft corner
             inside the plot area.

graph   A string used to select the graphical engine to use for plotting. Should (partial-
)match the two options "base" or "ggplot2". Default value is "base".

...   Arguments to be passed to methods, such as graphical parameters (see par).

Details

Plots the EIB and the EVPI when risk aversion is included in the utility function.

Value

list(eib,evi) A two-elements named list of the ggplot objects containing the requested plots.
               Returned only if graph="ggplot2".

The function produces two plots for the risk aversion analysis. The first one is the EIB as a function
of the discrete grid approximation of the willingness parameter for each of the possible values of
the risk aversion parameter, r. The second one is a similar plot for the EVPI.

Author(s)

Gianluca Baio, Andrea Berardi

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical
Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London

See Also

bcea, CEriskav

Examples

```
# See Baio G., Dawid A.P. (2011) for a detailed description of the
# Bayesian model and economic problem
#
# Load the processed results of the MCMC simulation model
data(Vaccine)
#
# Runs the health economic evaluation using BCEA
m <- bcea(e=e,c=c,           # defines the variables of
                             #  effectiveness and cost
     ref=2,                  # selects the 2nd row of (e,c)
                             #  as containing the reference intervention
     interventions=treats,   # defines the labels to be associated
                             #  with each intervention
     Kmax=50000,             # maximum value possible for the willingness
                             #  to pay threshold; implies that k is chosen
                             #  in a grid from the interval (0,Kmax)
     plot=FALSE              # inhibits graphical output
)
#
# Define the vector of values for the risk aversion parameter, r, eg:
r <- c(0.000000000001,0.005,0.020,0.035)
#
# Run the cost-effectiveness analysis accounting for risk aversion

cr <- CEriskav(m,      # uses the results of the economic evalaution
                       #  (a "bcea" object)
        r=r,           # defines the vector of values for the risk
                       #  aversion parameter
        comparison=1   # if more than 2 interventions, selects the
                       #  pairwise comparison
)

#
# Now produce the plots

plot(cr # uses the results of the risk aversion
        #  analysis (a "CEriskav" object)
)

### Alternative options, using ggplot2

plot(cr,
  graph="ggplot2",
  plot="ask"           # plot option can be specified as
                       #  "dev.new" (default), "x11" or "ask"
  )
```

plot.evppi   *Plot Expected Value of Partial Information With Respect to a Set of*
                          Parameters

Description

Plot Expected Value of Partial Information With Respect to a Set of Parameters

Usage

```
## S3 method for class 'evppi'
plot(x, pos = c(0, 0.8), graph = c("base", "ggplot2"), col = NULL, ...)
```

Arguments

x   An object in the class evppi, obtained by the call to the function evppi.

pos   Parameter to set the position of the legend. Can be given in form of a string
              (bottom|top)(right|left) for base graphics and bottom|top|left|right
              for ggplot2. It can be a two-elements vector, which specifies the relative position
              on the x and y axis respectively, or alternatively it can be in form of a logical
              variable, with FALSE indicating to use the default position and TRUE to place it
              on the bottom of the plot. Default value is c(0,1), that is in the topleft corner
              inside the plot area.

graph   A string used to select the graphical engine to use for plotting. Should (partial-
)match the two options "base" or "ggplot2". Default value is "base".

col   Sets the color for the lines depicted in the graph.

...   Arguments to be passed to methods, such as graphical parameters (see par).

Value

Plot with base R or ggplot 2.

Author(s)

Gianluca Baio, Andrea Berardi

References

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London.

See Also

bcea, evppi

---

plot.mesh *Plot Mesh*

Description

Plot Mesh

Usage

```
## S3 method for class 'mesh'
plot(mesh, data, plot)
```

Arguments

mesh	Mesh
data	Data
plot	Plot; logical

---

plot.mixedAn *Summary Plot of the Health Economic Analysis For Mixed Analysis*

Description

Compares the optimal scenario to the mixed case in terms of the EVPI.

Usage

```
## S3 method for class 'mixedAn'
plot(x, y.limits = NULL, pos = c(0, 1), graph = c("base", "ggplot2"), ...)
```

Arguments

x	An object of class mixedAn, given as output of the call to the function mixedAn.
y.limits	Range of the y-axis for the graph. The default value is NULL, in which case the maximum range between the optimal and the mixed analysis scenarios is considered.
pos	Parameter to set the position of the legend. Can be given in form of a string (bottom|top)(right|left) for base graphics and bottom|top|left|right for ggplot2. It can be a two-elements vector, which specifies the relative position on the x and y axis respectively, or alternatively it can be in form of a logical variable, with FALSE indicating to use the default position and TRUE to place it on the bottom of the plot. Default value is c(0,1), that is in the topleft corner inside the plot area.
graph	A string used to select the graphical engine to use for plotting. Should (partial-)match the two options "base" or "ggplot2". Default value is "base".
...	Arguments to be passed to methods, such as graphical parameters (see par).

Value

evi   A ggplot object containing the plot. Returned only if `graph="ggplot2"`.

The function produces a graph showing the difference between the "optimal" version of the EVPI (when only the most cost-effective intervention is included in the market) and the mixed strategy one (when more than one intervention is considered in the market).

Author(s)

Gianluca Baio, Andrea Berardi

References

Baio, G. and Russo, P. (2009). A decision-theoretic framework for the application of cost-effectiveness analysis in regulatory processes. Pharmacoeconomics 27(8), 645-655 doi:10.2165/11310250

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London

See Also

`bcea`, `mixedAn`

Examples

```
# See Baio G., Dawid A.P. (2011) for a detailed description of the
# Bayesian model and economic problem
#
# Load the processed results of the MCMC simulation model
data(Vaccine)

# Runs the health economic evaluation using BCEA
m <- bcea(e=e,c=c,          # defines the variables of
                            #  effectiveness and cost
        ref=2,              # selects the 2nd row of (e,c)
                            #  as containing the reference intervention
        interventions=treats, # defines the labels to be associated
                            #  with each intervention
        Kmax=50000,         # maximum value possible for the willingness
                            #  to pay threshold; implies that k is chosen
                            #  in a grid from the interval (0,Kmax)
        plot=FALSE          # inhibits graphical output
)

ma <- mixedAn(m,         # uses the results of the mixed strategy
                         #  analysis (a "mixedAn" object)
        mkt.shares=NULL  # the vector of market shares can be defined
                         #  externally. If NULL, then each of the T
                         #  interventions will have 1/T market share
)

# Can also plot the summary graph
plot(ma,graph="base")

# Or with ggplot2
```

```
if(require(ggplot2)){
plot(ma,graph="ggplot2")
}
```

---

post.density   *Gaussian Process Fitting*

Description

Gaussian Process Fitting

Usage

```
post.density(hyperparams, parameter, x, input.matrix)
```

Arguments

hyperparams	Hyperparameters
parameter	Parameters
x	Response variable
input.matrix	Input data matrix

---

prep.x   *Prepare Delta arrays*

Description

Prepare Delta arrays

Usage

```
prep.x(he, seq_rows, k, l)
```

Arguments

he	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
seq_rows	Rows of (e,c) to keep
k	e or c? 1 or 2.
l	Columns of (e,c) to keep

---

prep_ceplane_params   *Prepare CE-plane Parameters*

Description

In ggplot format, combine user-supplied parameters with defaults.

Usage

```
prep_ceplane_params(he, wtp, ...)
```

Arguments

he	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
wtp	Willingness-to-pay
...	Additional arguments

Value

List pf graph parameters

---

print.bcea   *bcea Print Method*

Description

bcea Print Method

Usage

```
## S3 method for class 'bcea'
print(x, digits = getOption("digits"), give.attr = FALSE, no.list = TRUE, ...)
```

Arguments

x	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
digits	Minimal number of significant digits, see `print.default`.
give.attr	Logical; if TRUE (default), show attributes as sub structures.
no.list	Logical; if TRUE, no 'list of ...' nor the class are printed.
...	Potential further arguments.

Examples

```
data("Vaccine")
he <- BCEA::bcea(e, c)
```

quiet   *Allow disabling of the cat messages*

Description

Allow disabling of the cat messages

Usage

```
quiet(x)
```

Arguments

x   Object to quietly return

select_plot_type   *Choose Graphical Engine*

Description

From base R, ggplot2 or plotly.

Usage

```
select_plot_type(graph)
```

Arguments

graph   Type names; string

Value

Plot ID integer 1:base R; 2:ggplot2; 3:plotly

setComparisons   *Set Comparisons Group*

Description

One of the alternative way to set (e,c) comparison group.

Usage

```
setComparisons(he, comparison)
```

Arguments

he	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
comparison	Selects the comparator, in case of more than two interventions being analysed. Default as NULL plots all the comparisons together. Any subset of the possible comparisons can be selected (e.g., comparison=c(1,3) or comparison=2).

See Also

[setComparisons<-](#)

---

setComparisons<-   *Set Comparison Group*

Description

One of the alternative way to set (e,c) comparison group.

Usage

```
setComparisons(he) <- value
```

Arguments

he	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
value	Comparison

Value

bcea-type object

See Also

[setComparisons](#)

---

setKmax<-   *Set Maximum Willingness to Pay*

Description

Alternative way to define 'K' statistic.

Usage

```
setKmax(he) <- value
```

Arguments

he	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
value	Maximum willingness to pay

Value

bcea-type oject

---

setReferenceGroup<- *Set Reference Group*

Description

Alternative way to define (e,c) reference group.

Usage

```
setReferenceGroup(he) <- value
```

Arguments

he	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
value	Reference group number

Value

bcea-type objects

---

sim_table *Table of Simulation Statistics for the Health Economic Model*

Description

Using the input in the form of MCMC simulations and after having run the health economic model, produces a summary table of the simulations from the cost-effectiveness analysis.

Usage

```
sim_table(he, ...)

## S3 method for class 'bcea'
sim_table(he, wtp = 25000, ...)
```

Arguments

he	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
...	Additional arguments
wtp	The value of the willingness to pay threshold to be used in the summary table.

Value

Produces the following elements:

table	A table with simulation statistics from the economic model
names.cols	A vector of labels to be associated with each column of the table
wtp	The selected value of the willingness to pay
idx_wtp	The index associated with the selected value of the willingness to pay threshold in the grid used to run the analysis

Author(s)

Gianluca Baio

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London.

See Also

bcea

Examples

```
# See Baio G., Dawid A.P. (2011) for a detailed description of the
# Bayesian model and economic problem

# Load the processed results of the MCMC simulation model
data(Vaccine)

# Runs the health economic evaluation using BCEA
m <- bcea(e=e,                  # defines the variables of
          c=c,                  # effectiveness and cost
          ref=2,                # selects the 2nd row of (e, c)
                                # as containing the reference intervention
          interventions=treats, # defines the labels to be associated
                                # with each intervention
          Kmax=50000)           # maximum value possible for the willingness
                                # to pay threshold; implies that k is chosen
                                # in a grid from the interval (0, Kmax)

# Now can save the simulation exercise in an object using sim_table()
sim_table(m,         # uses the results of the economic evaluation
                     #  (a 'bcea' object)
          wtp=25000) # selects the particular value for k
```

| Smoking | *Data set for the Bayesian model for the cost-effectiveness of smoking cessation interventions* |

Description

This data set contains the results of the Bayesian analysis used to model the clinical output and the costs associated with the health economic evaluation of four different smoking cessation interventions.

Format

A data list including the variables needed for the smoking cessation cost-effectiveness analysis. The variables are as follows:

list("c") a matrix of 500 simulations from the posterior distribution of the overall costs associated with the four strategies

list("data") a dataset containing the characteristics of the smokers in the UK population

list("e") a matrix of 500 simulations from the posterior distribution of the clinical benefits associated with the four strategies

list("life.years") a matrix of 500 simulations from the posterior distribution of the life years gained with each strategy

list("pi") a matrix of 500 simulations from the posterior distribution of the event of smoking cessation with each strategy

list("smoking") a data frame containing the inputs needed for the network meta-analysis model. The data.frame object contains: nobs: the record ID number, s: the study ID number, i: the intervention ID number, r_i: the number of patients who quit smoking, n_i: the total number of patients for the row-specific arm and b_i: the reference intervention for each study

list("smoking_output") a rjags object obtained by running the network meta-analysis model based on the data contained in the smoking object

list("smoking_mat") a matrix obtained by running the network meta-analysis model based on the data contained in the smoking object

list("treats") a vector of labels associated with the four strategies

Source

Effectiveness data adapted from Hasselblad V. (1998). Meta-analysis of Multitreatment Studies. Medical Decision Making 1998;18:37-43.

Cost and population characteristics data adapted from various sources:

- Taylor, D.H. Jr, et al. (2002). Benefits of smoking cessation on longevity. American Journal of Public Health 2002;92(6)

- ASH: Action on Smoking and Health (2013). ASH fact sheet on smoking statistics, http://ash.org.uk/files/documents/ASH_106.pdf

- Flack, S., et al. (2007). Cost-effectiveness of interventions for smoking cessation. York Health Economics Consortium, January 2007

- McGhan, W.F.D., and Smith, M. (1996). Pharmacoeconomic analysis of smoking-cessation interventions. American Journal of Health-System Pharmacy 1996;53:45-52

References

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London

Examples

```
data(Smoking)


m <- bcea(e, c, ref = 4, interventions = treats, Kmax = 500)
```

---

struct.psa   *Structural Probability Sensitivity Analysis*

Description

Computes the weights to be associated with a set of competing models in order to perform structural PSA.

Usage

```
struct.psa(
  models,
  effect,
  cost,
  ref = 1,
  interventions = NULL,
  Kmax = 50000,
  plot = FALSE
)
```

Arguments

models	A list containing the output from either R2jags or R2OpenBUGS/R2WinBUGS for all the models that need to be combined in the model average
effect	A list containing the measure of effectiveness computed from the various models (one matrix with n.sim x n.ints simulations for each model)
cost	A list containing the measure of costs computed from the various models (one matrix with n.sim x n.ints simulations for each model)
ref	Which intervention is considered to be the reference strategy. The default value ref=1 means that the intervention appearing first is the reference and the other(s) is(are) the comparator(s)
interventions	Defines the labels to be associated with each intervention. By default and if NULL, assigns labels in the form "Intervention1", ... , "InterventionT"
Kmax	Maximum value of the willingness to pay to be considered. Default value is k=50000. The willingness to pay is then approximated on a discrete grid in the interval [0,Kmax]. The grid is equal to wtp if the parameter is given, or composed of 501 elements if wtp=NULL (the default)
plot	A logical value indicating whether the function should produce the summary plot or not

Details

The model is a list containing the output from either R2jags or R2OpenBUGS / R2WinBUGS for all the models that need to be combined in the model average effect is a list containing the measure of effectiveness computed from the various models (one matrix with n_sim x n_ints simulations for each model) cost is a list containing the measure of costs computed from the various models (one matrix with n_sim x n_ints simulations for each model).

Value

List object of bcea object, model weights and DIC

Author(s)

Gianluca Baio

References

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London.

See Also

bcea

---

summary.bcea   *Summary Method for Objects of Class* bcea

Description

Produces a table printout with some summary results of the health economic evaluation.

Usage

```
## S3 method for class 'bcea'
summary(object, wtp = 25000, ...)
```

Arguments

object	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
wtp	The value of the willingness to pay threshold used in the summary table.
...	Additional arguments affecting the summary produced.

Value

Prints a summary table with some information on the health economic output and synthetic information on the economic measures (EIB, CEAC, EVPI).

Author(s)

Gianluca Baio

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London.

See Also

bcea

Examples

```
data(Vaccine)

he <- bcea(e, c, interventions = treats, ref = 2)
summary(he)
```

---

summary.mixedAn   *Summary Methods For Objects in the Class* mixedAn *(Mixed Analysis)*

Description

Prints a summary table for the results of the mixed analysis for the economic evaluation of a given model.

Usage

```
## S3 method for class 'mixedAn'
summary(object, wtp = 25000, ...)
```

Arguments

object   An object of the class mixedAn, which is the results of the function mixedAn,
            generating the economic evaluation of a set of interventions, considering given
            market shares for each option.

wtp   The value of the willingness to pay choosen to present the analysis.

...   Additional arguments affecting the summary produced.

Value

Produces a table with summary information on the loss in expected value of information generated by the inclusion of non cost-effective interventions in the market.

Author(s)

Gianluca Baio

References

Baio, G. and Russo, P. (2009). A decision-theoretic framework for the application of cost-effectiveness analysis in regulatory processes. Pharmacoeconomics 27(8), 645-655 doi:10.2165/11310250

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London.

See Also

bcea, mixedAn

Examples

```
# See Baio G., Dawid A.P. (2011) for a detailed description of the
# Bayesian model and economic problem

# Load the processed results of the MCMC simulation model
data(Vaccine)

# Runs the health economic evaluation using BCEA
m <- bcea(e=e,c=c,          # defines the variables of
                            #  effectiveness and cost
      ref=2,                # selects the 2nd row of (e,c)
                            #  as containing the reference intervention
      interventions=treats, # defines the labels to be associated
                            #  with each intervention
      Kmax=50000            # maximum value possible for the willingness
                            #  to pay threshold; implies that k is chosen
                            #  in a grid from the interval (0,Kmax)
)

ma <- mixedAn(m,         # uses the results of the mixed strategy
                         #  analysis (a "mixedAn" object)
       mkt.shares=NULL   # the vector of market shares can be defined
                         #  externally. If NULL, then each of the T
                         #  interventions will have 1/T market share
)

# Prints a summary of the results
summary(ma,       # uses the results of the mixed strategy analysis
                  #  (a "mixedAn" object)
      wtp=25000   # selects the relevant willingness to pay
                  #  (default: 25,000)
)
```

| tabulate_means | *Calculate Dataset For ICERs From bcea Object* |

Description

Calculate Dataset For ICERs From bcea Object

Usage

```
tabulate_means(he, comp_label = NULL, ...)
```

Arguments

`he`	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
`comp_label`	Optional vector of strings with comparison labels
`...`	Additional arguments

Value

A data.frame object including mean outcomes, comparison identifier, comparison label and associated ICER

`Vaccine`	*Data set for the Bayesian model for the cost-effectiveness of influenza vaccination*

Description

This data set contains the results of the Bayesian analysis used to model the clinical output and the costs associated with an influenza vaccination.

Format

A data list including the variables needed for the influenza vaccination. The variables are as follows:

list("c") a matrix of simulations from the posterior distribution of the overall costs associated with the two treatments

list("c.pts")

list("cost.GP") a matrix of simulations from the posterior distribution of the costs for GP visits associated with the two treatments

list("cost.hosp") a matrix of simulations from the posterior distribution of the costs for hospitalisations associated with the two treatments

list("cost.otc") a matrix of simulations from the posterior distribution of the costs for over-the-counter medications associated with the two treatments

list("cost.time.off") a matrix of simulations from the posterior distribution of the costs for time off work associated with the two treatments

list("cost.time.vac") a matrix of simulations from the posterior distribution of the costs for time needed to get the vaccination associated with the two treatments

list("cost.travel") a matrix of simulations from the posterior distribution of the costs for travel to get vaccination associated with the two treatments

list("cost.trt1") a matrix of simulations from the posterior distribution of the overall costs for first line of treatment associated with the two interventions

list("cost.trt2") a matrix of simulations from the posterior distribution of the overall costs for second line of treatment associated with the two interventions

list("cost.vac") a matrix of simulations from the posterior distribution of the costs for vaccination

list("e") a matrix of simulations from the posterior distribution of the clinical benefits associated with the two treatments

list("e.pts")

list("N") the number of subjects in the reference population

list("N.outcomes") the number of clinical outcomes analysed

list("N.resources") the number of health-care resources under study

list("QALYs.adv") a vector from the posterior distribution of the QALYs associated with advert events

list("QALYs.death") a vector from the posterior distribution of the QALYs associated with death

list("QALYs.hosp") a vector from the posterior distribution of the QALYs associated with hospitalisation

list("QALYs.inf") a vector from the posterior distribution of the QALYs associated with influenza infection

list("QALYs.pne") a vector from the posterior distribution of the QALYs associated with pneumonia

list("treats") a vector of labels associated with the two treatments

list("vaccine") a `rjags` object containing the simulations for the parameters used in the original model

list("vaccine_mat") a matrix containing the simulations for the parameters used in the original model

Source

Adapted from Turner D, Wailoo A, Cooper N, Sutton A, Abrams K, Nicholson K. The cost-effectiveness of influenza vaccination of healthy adults 50-64 years of age. Vaccine. 2006;24:1035-1043.

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Examples

```
data(Vaccine)


m <- bcea(e, c, ref = 1, interventions = treats)
```

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