Package 'EffectTreat'

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Type Package

Title Prediction of Therapeutic Success

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Description In personalized medicine, one wants to know, for a given patient and his or her outcome for a predictor (pre-treatment variable), how likely it is that a treatment will be more beneficial than an alternative treatment. This package allows for the quantification of the predictive causal association (i.e., the association between the predictor variable and the individual causal effect of the treatment) and related metrics. Part of this software has been developed using funding provided from the European Union's 7th Framework Programme for research, technological development and demonstration under Grant Agreement no 602552.

Depends

Imports methods

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`CausalPCA.ContCont` *Show a causal diagram of the median correlation between the counterfactuals in the continuous-continuous setting*

Description

This function provides a diagram that depicts the estimable correlations $\rho(_{T_0,S})$ and $\rho(_{T_1,S})$, and median of the correlation $\rho(_{T_0,T_1})$ for a specified range of values of the predictive causal association (PCA; ρ_ψ).

Usage

```
CausalPCA.ContCont(x, Min=-1, Max=1, Cex.Letters=3, Cex.Corrs=2,
Lines.Rel.Width=TRUE, Col.Pos.Neg=TRUE)
```

Arguments

`x`	An object of class `PCA.ContCont`. See `PCA.ContCont`.
`Min`	The minimum values of the PCA that should be considered. Default=-1.
`Max`	The maximum values of the PCA that should be considered. Default=1.
`Cex.Letters`	The size of the symbols for S, T_0, and T_1 in the diagram. Default=3.
`Cex.Corrs`	The size of the text depicting the (median) correlations in the diagram. Default=2.
`Lines.Rel.Width`	Logical. When `Lines.Rel.Width=TRUE`, the widths of the lines that represent the correlations in the diagram are relative to the size of the correlations (i.e., a smaller line is used for correlations closer to zero whereas a thicker line is used for (absolute) correlations closer to 1). When `Lines.Rel.Width=FALSE`, the width of all lines representing the correlations between the counterfactuals is identical. Default=`TRUE`.
`Col.Pos.Neg`	Logical. When `Col.Pos.Neg=TRUE`, the color of the lines that represent the correlations in the diagram is red for negative correlations and black for positive ones. When `Col.Pos.Neg=FALSE`, all lines are in black. Default=`TRUE`.

Author(s)

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

References

Alonso, A., Van der Elst, W., & Molenberghs, G. (submitted). Validating predictors of therapeutic success: a causal inference approach.

See Also

PCA.ContCont

Examples

```
# Generate the vector of PCA.ContCont values when rho_T0S=.3, rho_T1S=.9,
# sigma_T0T0=2, sigma_T1T1=2,sigma_SS=2, and the grid of values {-1, -.99,
# ..., 1} is considered for the correlations between T0 and T1:
PCA <- PCA.ContCont(T0S=.3, T1S=.9, T0T0=2, T1T1=2, SS=2,
T0T1=seq(-1, 1, by=.01))

# Obtain causal diagram for PCA score range [-1; 1]:
CausalPCA.ContCont(PCA,  Min=-1, Max=1)

# Obtain causal diagram for PCA score range [0.5; 1]:
CausalPCA.ContCont(PCA,  Min=0.5, Max=1)
```

Example.Data *An example dataset*

Description

Example.Data is a hypothetical dataset constructed to demonstrate some of the functions in the package.

Usage

```
data(Example.Data)
```

Format

A `data.frame` with 181 observations on 4 variables.

`Id` The Patient ID.

`Treat` The treatment indicator, coded as -1 = control and 1 = experimental.

`T` The most credible outcome to assess therapeutic success.

`S` The potential pretreatment predictor.

GoodPretreatContCont *Examine the plausibility of finding a good pretreatment predictor in the Continuous-continuous case*

Description

The function GoodPretreatContCont examines the plausibility of finding a good pretreatment predictor in the continuous-continuous setting. For details, see Alonso et al. (submitted).

Usage

```
GoodPretreatContCont(T0T0, T1T1, Delta, T0T1=seq(from=0, to=1, by=.01))
```

Arguments

T0T0	A scalar that specifies the variance of the true endpoint in the control treatment condition.
T1T1	A scalar that specifies the variance of the true endpoint in the experimental treatment condition.
Delta	A scalar that specifies an upper bound for the prediction mean squared error when predicting the individual causal effect of the treatment on the true endpoint based on the pretreatment predictor.
T0T1	A scalar or vector that contains the correlation(s) between the counterfactuals T_0 and T_1 that should be considered in the computation of ρ^2_{min}. Default seq(0,1,by=.01), i.e., the values $0, 0.01, 0.02, \ldots, 1$.

Value

An object of class GoodPretreatContCont with components,

T0T1	A scalar or vector that contains the correlation(s) between the counterfactuals T0 and T1 that were considered (i.e., $\rho(_{T_0,T_1})$).
Sigma.Delta.T	A scalar or vector that contains the standard deviations of the individual causal treatment effects on the true endpoint as a function of $\rho(_{T_0,T_1})$.
Rho2.Min	A scalar or vector that contains the ρ^2_{min} values as a function of $\rho(_{T_0,T_1})$.

Author(s)

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

References

Alonso, A., Van der Elst, W., & Molenberghs, G. (submitted). Validating predictors of therapeutic success: a causal inference approach.

See Also

PCA.ContCont

Examples

```
# Assess the plausibility of finding a good pretreatment predictor when
# sigma_T0T0 = sigma_T1T1 = 8 and Delta = 1
MinPred <- GoodPretreatContCont(T0T0 = 8, T1T1 = 8, Delta = 1)
summary(MinPred)
plot(MinPred)
```

Min.Max.Multivar.PCA *Minimum and maximum values for the multivariate predictive causal association (PCA) in the continuous-continuous case*

Description

The function Min.Max.Multivar.PCA computes the minimum and maximum values for the multivariate predictive causal association (PCA) in the continuous-continuous case.

Usage

```
Min.Max.Multivar.PCA(gamma, Sigma_SS, Sigma_T0T0, Sigma_T1T1)
```

Arguments

gamma	The vector of regression coefficients for the S by treatment interactions.
Sigma_SS	The variance-covariance matrix of the pretreatment predictors. For example, when there are 2 pretreatment predictors $\mathbf{\Sigma}_{SS} = \begin{pmatrix} \sigma_{S1S1} & \sigma_{S1S2} \\ \sigma_{S1S2} & \sigma_{S2S2} \end{pmatrix}$.
Sigma_T0T0	The variance of T in the control treatment group.
Sigma_T1T1	The variance of T in the experimental treatment group.

Author(s)

Wim Van der Elst & Ariel Alonso

References

Alonso, A., & Van der Elst, W. (submitted). Evaluating multivariate predictors of therapeutic success: a causal inference approach.

Examples

```
# Specify vector of S by treatment interaction coefficients
gamma <- matrix(data = c(-0.006, -0.002, 0.045), ncol=1)
# Specify variances
Sigma_SS = matrix(data=c(882.352, 49.234, 6.420,
49.234, 411.964, -26.205, 6.420, -26.205, 95.400),
byrow = TRUE, nrow = 3)
Sigma_T0T0 <- 82.274
Sigma_T1T1 <- 96.386

# Compute min and max PCA
Min.Max.Multivar.PCA(gamma=gamma, Sigma_SS=Sigma_SS,
Sigma_T0T0=Sigma_T0T0, Sigma_T1T1=Sigma_T1T1)
```

`Min.R2.delta` *Compute minimum $R\hat{}2\_\delta$ for desired prediction accuracy*

Description

Computes the minimum R^2_δ needed to achieve the desired prediction accuracy for the set of pre-treatment predictors.

Usage

```
Min.R2.delta(delta, Sigma_T0T0, Sigma_T1T1)
```

Arguments

`delta`	The vector of δ values to be considered.
`Sigma_T0T0`	The variance of T in the control treatment group.
`Sigma_T1T1`	The variance of T in the experimental treatment group.

Author(s)

Wim Van der Elst, Ariel Alonso & Geert Molenberghs

References

Alonso, A., Van der Elst, W., Luaces, P., Sanchez, L., & Molenberghs, G. (submitted). Evaluating multivariate predictors of therapeutic success: a causal inference approach.

Examples

```
Fit <- Min.R2.delta(delta = seq(from = 0, to = 250, by=50),
  Sigma_T0T0 = 38.606, Sigma_T1T1 = 663.917)

# Explore the results
summary(Fit)
plot(Fit)
```

`Multivar.PCA.ContCont` *Compute the multivariate predictive causal association (PCA) in the Continuous-continuous case*

Description

The function `Multivar.PCA.ContCont` computes the predictive causal association (PCA) when S = the vector of pretreatment predictors and T = the True endpoint. All S and T should be continuous normally distributed endpoints. See **Details** below.

Usage

```
Multivar.PCA.ContCont(Sigma_TT, Sigma_TS, Sigma_SS, T0T1=seq(-1, 1, by=.01), M=NA)
```

Arguments

`Sigma_TT`	The variance-covariance matrix $\mathbf{\Sigma}_{TT} = \begin{pmatrix} \sigma_{T0T0} & \sigma_{T0T1} \\ \sigma_{T0T1} & \sigma_{T1T1} \end{pmatrix}$.
`Sigma_TS`	The matrix that contains the covariances σ_{T0Sr}, σ_{T1Sr}. For example, when there are 2 pretreatment predictors $\mathbf{\Sigma}_{TS} = \begin{pmatrix} \sigma_{T0S1} & \sigma_{T0S2} \\ \sigma_{T1S1} & \sigma_{T1S2} \end{pmatrix}$.
`Sigma_SS`	The variance-covariance matrix of the pretreatment predictors. For example, when there are 2 pretreatment predictors $\mathbf{\Sigma}_{SS} = \begin{pmatrix} \sigma_{S1S1} & \sigma_{S1S2} \\ \sigma_{S1S2} & \sigma_{S2S2} \end{pmatrix}$.
`T0T1`	A scalar or vector that contains the correlation(s) between the counterfactuals T_0 and T_1 that should be considered in the computation of R^2_ψ. Default `seq(-1,1,by=.01)`, i.e., the values -1, -0.99, -0.98, $\ldots$, 1.
`M`	If `M=NA`, all correlation(s) between the counterfactuals T_0 and T_1 specified in the argument `T0T1` are used to compute R^2_ψ. If `M=m`, random draws are taken from `T0T1` until `m` R^2_ψ are found. Default `M=NA`.

Value

An object of class `Multivar.PCA.ContCont` with components,

`Total.Num.Matrices`
: An object of class `numeric` that contains the total number of matrices that can be formed as based on the user-specified correlations in the function call.

`Pos.Def`
: A `data.frame` that contains the positive definite matrices that can be formed based on the user-specified correlations. These matrices are used to compute the vector of the R^2_ψ values.

`PCA`
: A scalar or vector that contains the PCA (R^2_ψ) value(s).

`R2_psi_g`
: A `Data.frame` that contains $R^2_{\psi g}$.

Author(s)

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

References

Alonso, A., & Van der Elst, W. (submitted). Evaluating multivariate predictors of therapeutic success: a causal inference approach.

Examples

```
# First specify the covariance matrices to be used
Sigma_TT = matrix(c(177.870, NA, NA, 162.374), byrow=TRUE, nrow=2)
Sigma_TS = matrix(data = c(-45.140, -109.599, 11.290, -56.542,
-106.897, 20.490), byrow = TRUE, nrow = 2)
Sigma_SS = matrix(data=c(840.564, 73.936, -3.333, 73.936, 357.719,
-30.564, -3.333, -30.564, 95.063), byrow = TRUE, nrow = 3)

# Compute PCA
Results <- Multivar.PCA.ContCont(Sigma_TT = Sigma_TT,
Sigma_TS = Sigma_TS, Sigma_SS = Sigma_SS)

# Evaluate results
summary(Results)
plot(Results)
```

`PCA.ContCont` *Compute the predictive causal association (PCA) in the Continuous-continuous case*

Description

The function `PCA.ContCont` computes the predictive causal association (PCA) when S=pretreatment predictor and T=True endpoint are continuous normally distributed endpoints. See **Details** below.

Usage

```
PCA.ContCont(T0S, T1S, T0T0=1, T1T1=1, SS=1, T0T1=seq(-1, 1, by=.01))
```

Arguments

`T0S`	A scalar or vector that specifies the correlation(s) between the pretreatment predictor and the true endpoint in the control treatment condition that should be considered in the computation of ρ_ψ.
`T1S`	A scalar or vector that specifies the correlation(s) between the pretreatment predictor and the true endpoint in the experimental treatment condition that should be considered in the computation of ρ_ψ.
`T0T0`	A scalar that specifies the variance of the true endpoint in the control treatment condition that should be considered in the computation of ρ_ψ. Default 1.
`T1T1`	A scalar that specifies the variance of the true endpoint in the experimental treatment condition that should be considered in the computation of ρ_ψ. Default 1.

SS — A scalar that specifies the variance of the pretreatment predictor endpoint. Default 1.

T0T1 — A scalar or vector that contains the correlation(s) between the counterfactuals T_0 and T_1 that should be considered in the computation of ρ_ψ. Default `seq(-1,1,by=.01)`, i.e., the values -1, -0.99, -0.98, ..., 1.

Details

Based on the causal-inference framework, it is assumed that each subject *j* has two counterfactuals (or potential outcomes), i.e., T_{0j} and T_{1j} (the counterfactuals for the true endpoint (T) under the control ($Z = 0$) and the experimental ($Z = 1$) treatments of subject *j*, respectively). The individual causal effects of Z on T for a given subject *j* is then defined as $\Delta_{T_j} = T_{1j} - T_{0j}$.

The correlation between the individual causal effect of Z on T and S_j (the pretreatment predictor) equals (for details, see Alonso et al., submitted):

$$\rho_\psi = \frac{\sqrt{\sigma_{T1T1}}\rho_{T1S} - \sqrt{\sigma_{T0T0}}\rho_{T0S}}{\sqrt{\sigma_{T0T0} + \sigma_{T1T1} - 2\sqrt{\sigma_{T0T0}\sigma_{T1T1}}\rho_{T0T1}}},$$

where the correlation $\rho_{T_0T_1}$ is not estimable. It is thus warranted to conduct a sensitivity analysis (by considering vectors of possible values for the correlations between the counterfactuals – rather than point estimates).

When the user specifies a vector of values that should be considered for $\rho_{T_0T_1}$ in the above expression, the function `PCA.ContCont` constructs all possible matrices that can be formed as based on these values and the estimable quantities ρ_{T_0S}, ρ_{T_1S}, identifies the matrices that are positive definite (i.e., valid correlation matrices), and computes ρ_ψ for each of these matrices. The obtained vector of ρ_ψ values can subsequently be used to e.g., conduct a sensitivity analysis.

Notes

A single ρ_ψ value is obtained when all correlations in the function call are scalars.

Value

An object of class `PCA.ContCont` with components,

`Total.Num.Matrices` — An object of class `numeric` that contains the total number of matrices that can be formed as based on the user-specified correlations in the function call.

`Pos.Def` — A `data.frame` that contains the positive definite matrices that can be formed based on the user-specified correlations. These matrices are used to compute the vector of the ρ_ψ values.

`PCA` — A scalar or vector that contains the PCA (ρ_ψ) value(s).

`GoodSurr` — A `data.frame` that contains the PCA (ρ_ψ), σ_{ψ_T}, and δ.

Author(s)

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

References

Alonso, A., Van der Elst, W., & Molenberghs, G. (submitted). Validating predictors of therapeutic success: a causal inference approach.

Examples

```
# Based on the example dataset
    # load data in memory
data(Example.Data)
    # compute corr(S, T) in control treatment, gives .77
cor(Example.Data$S[Example.Data$Treat==-1],
Example.Data$T[Example.Data$Treat==-1])
   # compute corr(S, T) in experimental treatment, gives .71
cor(Example.Data$S[Example.Data$Treat==1],
Example.Data$T[Example.Data$Treat==1])
   # compute var T in control treatment, gives 263.99
var(Example.Data$T[Example.Data$Treat==-1])
   # compute var T in experimental treatment, gives 230.64
var(Example.Data$T[Example.Data$Treat==1])
   # compute var S, gives 163.65
var(Example.Data$S)

# Generate the vector of PCA.ContCont values using these estimates
# and the grid of values {-1, -.99, ..., 1} for the correlations
# between T0 and T1:
PCA <- PCA.ContCont(T0S=.77, T1S=.71, T0T0=263.99, T1T1=230.65,
                    SS=163.65, T0T1=seq(-1, 1, by=.01))

# Examine and plot the vector of generated PCA values:
summary(PCA)
plot(PCA)


# Other example

# Generate the vector of PCA.ContCont values when rho_T0S=.3, rho_T1S=.9,
# sigma_T0T0=2, sigma_T1T1=2,sigma_SS=2, and
# the grid of values {-1, -.99, ..., 1} is considered for the correlations
# between T0 and T1:
PCA <- PCA.ContCont(T0S=.3, T1S=.9, T0T0=2, T1T1=2, SS=2,
T0T1=seq(-1, 1, by=.01))

# Examine and plot the vector of generated PCA values:
summary(PCA)
plot(PCA)

# Obtain the positive definite matrices than can be formed as based on the
# specified (vectors) of the correlations (these matrices are used to
# compute the PCA values)
PCA$Pos.Def
```

plot GoodPretreatContCont

Graphically illustrates the theoretical plausibility of finding a good pretreatment predictor in the continuous-continuous case

Description

This function provides a plot that displays the frequencies, percentages, or cumulative percentages of ρ^2_{min} for a fixed value of δ (given the observed variances of the true endpoint in the control and experimental treatment conditions and a specified grid of values for the unidentified parameter $\rho(_{T_0,T_1})$; see GoodPretreatContCont). For details, see the online appendix of Alonso et al., submitted.

Usage

```
## S3 method for class 'GoodPretreatContCont'
plot(x, main, col, Type="Percent", Labels=FALSE,
Par=par(oma=c(0, 0, 0, 0), mar=c(5.1, 4.1, 4.1, 2.1)), ...)
```

Arguments

x	An object of class GoodPretreatContCont. See GoodPretreatContCont.
main	The title of the plot.
col	The color of the bins.
Type	The type of plot that is produced. When Type=Freq or Type=Percent, the Y-axis shows frequencies or percentages of ρ^2_{min}. When Type=CumPerc, the Y-axis shows cumulative percentages of ρ^2_{min}. Default "Percent".
Labels	Logical. When Labels=TRUE, the percentage of ρ^2_{min} values that are equal to or larger than the midpoint value of each of the bins are displayed (on top of each bin). Only applies when Type=Freq or Type=Percent. Default FALSE.
Par	Graphical parameters for the plot. Default par(oma=c(0,0,0,0),mar=c(5.1,4.1,4.1,2.1)).
...	Extra graphical parameters to be passed to hist().

Author(s)

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

References

Alonso, A., Van der Elst, W., & Molenberghs, G. (submitted). Validating predictors of therapeutic success: a causal inference approach.

See Also

GoodPretreatContCont

Examples

```
# compute rho^2_min in the setting where the variances of T in the control
# and experimental treatments equal 100 and 120, delta is fixed at 50,
# and the grid G={0, .01, ..., 1} is considered for the counterfactual
# correlation rho_T0T1:

MinPred <- GoodPretreatContCont(T0T0 = 100, T1T1 = 120, Delta = 50,
T0T1 = seq(0, 1, by = 0.01))

# Plot the results (use percentages on Y-axis)
plot(MinPred, Type="Percent")

# Same plot, but add the percentages of ICA values that are equal to or
# larger than the midpoint values of the bins
plot(MinPred, Labels=TRUE)
```

`plot Min.R2.delta` *Plot R^2_δ as a function of δ.*

Description

This function plots R^2_δ as a function of δ (in the multivariate case).

Usage

```
## S3 method for class 'Min.R2.delta'
plot(x, Ylab, Main="", Ylim=c(0, 1), ...)
```

Arguments

`x`	An object of class `plot.Min.R2.delta`. See `Min.R2.delta`.
`Ylab`	The legend of the Y-axis of the PCA plot. Default R^2_δ.
`Main`	The title of the plot. Default " " (no title).
`Ylim`	The limits of the Y-axis. Default `Ylim=c(0,1)`.
`...`	Extra graphical parameters to be passed to `plot()`.

Author(s)

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

References

Alonso, A., Van der Elst, W., Luaces, P., Sanchez, L., & Molenberghs, G. (submitted). Evaluating multivariate predictors of therapeutic success: a causal inference approach.

See Also

Min.R2.delta

Examples

```
Fit <- Min.R2.delta(delta = seq(from = 0, to = 250, by=50),
  Sigma_T0T0 = 38.606, Sigma_T1T1 = 663.917)

# Explore the results
summary(Fit)
plot(Fit)
```

`plot PCA.ContCont` *Plots the Predictive Causal Association in the continuous-continuous case*

Description

This function provides a plot that displays the frequencies, percentages, or cumulative percentages of the Predictive Causal Association (PCA; ρ_ψ, R^2_ψ). These figures are useful to examine the sensitivity of the obtained results with respect to the assumptions regarding the correlations between the counterfactuals (for details, see Alonso et al., submitted). Optionally, it is also possible to obtain plots that are useful in the examination of the plausibility of finding a good pretreatment predictor (in the univariate case).

Usage

```
## S3 method for class 'PCA.ContCont'
plot(x, Xlab.PCA, Main.PCA, Type="Percent",
Labels=FALSE, PCA=TRUE, Good.Pretreat=FALSE, EffectT0T1=FALSE,
R2_psi_g=FALSE, Main.Good.Pretreat, Par=par(oma=c(0, 0, 0, 0),
mar=c(5.1, 4.1, 4.1, 2.1)), col, ...)
```

Arguments

`x`	An object of class `PCA.ContCont` or `Multivar.PCA.ContCont`. See `PCA.ContCont` and `Multivar.PCA.ContCont`.
`Xlab.PCA`	The legend of the X-axis of the PCA plot. Default ρ_ψ (univariate predictor case) or R^2_ψ (multivariate predictor case).
`Main.PCA`	The title of the PCA plot. Default "PCA".
`Type`	The type of plot that is produced. When `Type=Freq` or `Type=Percent`, the Y-axis shows frequencies or percentages of PCA and/or δ. When `Type=CumPerc`, the Y-axis shows cumulative percentages of PCA and/or δ. Default "Percent".
`Labels`	Logical. When `Labels=TRUE`, the percentage of ρ_ψ, R^2_ψ and/or δ values that are equal to or larger than the midpoint value of each of the bins are displayed (on top of each bin). Default `FALSE`.

PCA	Logical. When PCA=TRUE, a plot of the PCA is provided. Default TRUE.
Good.Pretreat	Logical. When Good.Pretreat=TRUE, a plot of δ is provided. This plot is useful in the context of examinating the plausibility of finding a good pretretment predictor endpoint. For details, see Alonso et al. (submitted). Can only be requested for fitted objects of class object of class PCA.ContCont. Default FALSE.
EffectT0T1	Logical. When EffectT0T1=TRUE, a plot depicting the relation between $\rho[T0T1]$ and PCA is provided. Default FALSE.
R2_psi_g	Logical. When R2_psi_g=TRUE, a plot depicting the relation between $\rho[T0T1]$ and $R^2_{\psi g}$ is provided. Default FALSE.
Main.Good.Pretreat	The title of the plot of δ. For details, see Alonso et al. (submitted).
Par	Graphical parameters for the plot. Default par(oma=c(0,0,0,0),mar=c(5.1,4.1,4.1,2.1)).
col	The color of the bins. Default col <-c(8).
...	Extra graphical parameters to be passed to hist() or plot().

Author(s)

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

References

Alonso, A., Van der Elst, W., & Molenberghs, G. (submitted). Validating predictors of therapeutic success: a causal inference approach.

See Also

PCA.ContCont

Examples

```
# Generate the vector of PCA.ContCont values when rho_T0S=.3, rho_T1S=.9,
# sigma_T0T0=2, sigma_T1T1=2,sigma_SS=2, and
# the grid of values {-1, -.99, ..., 1} is considered for the correlations
# between T0 and T1:
PCA <- PCA.ContCont(T0S=.3, T1S=.9, T0T0=2, T1T1=2, SS=2,
T0T1=seq(-1, 1, by=.01))

# Plot the results:
plot(PCA)

# Same plot but add the percentages of PCA values that are equal to or larger
# than the midpoint values of the bins
plot(PCA, Labels=TRUE)

# Plot of the cumulative distribution of PCA
plot(PCA, Typ="CumPerc")
```

plot.Predict.Treat.ContCont *Plots the distribution of the individual causal effect based on S.*

Description

Plots the distribution of $\Delta T_j | S_j$ and the $1 - \alpha\%$ CIs for the mean and median ρ_{T0T1} values (and optionally, for other user-requested ρ_{T0T1} values).

Usage

```
## S3 method for class 'Predict.Treat.ContCont'
plot(x, Xlab, Main, Mean.T0T1=FALSE, Median.T0T1=TRUE,
Specific.T0T1="none", alpha=0.05, Cex.Legend=1, ...)
## S3 method for class 'Predict.Treat.Multivar.ContCont'
plot(x, Xlab, Main, Mean.T0T1=FALSE, Median.T0T1=TRUE,
Specific.T0T1="none", alpha=0.05, Cex.Legend=1, ...)
```

Arguments

x	An object of class Predict.Treat.ContCont or Predict.Treat.Multivar.ContCont. See Predict.Treat.ContCont or Predict.Treat.Multivar.ContCont.
Xlab	The legend of the X-axis of the plot. Default "$\Delta T_j \mid S_j$".
Main	The title of the PCA plot. Default " ".
Mean.T0T1	Logical. When Mean.T0T1=TRUE, the $1 - \alpha\%$ CI for the mean ρ_{T0T1} value (i.e., the mean of all valid ρ_{T0T1} values in x) is shown. Default FALSE.
Median.T0T1	Logical. When Median.T0T1=TRUE, the $1 - \alpha\%$ CI for the median ρ_{T0T1} value is shown. Default TRUE.
Specific.T0T1	Optional. A scalar that specifies a particular value ρ_{T0T1} for which the $1 - \alpha\%$ CI is shown. Default "none".
alpha	The α level to be used in the computation of the CIs. Default 0.05.
Cex.Legend	The size of the legend of the plot. Default 1.
...	Other arguments to be passed to the $plot()$ function.

Author(s)

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

References

Alonso, A., Van der Elst, W., & Molenberghs, G. (submitted). Validating predictors of therapeutic success: a causal inference approach.

See Also

Predict.Treat.ContCont

Examples

```
# Generate the vector of PCA.ContCont values when rho_T0S=.3, rho_T1S=.9,
# sigma_T0T0=2, sigma_T1T1=2,sigma_SS=2, and the grid of values {-1, -.99,
# ..., 1} is considered for the correlations between T0 and T1:
PCA <- PCA.ContCont(T0S=.3, T1S=.9, T0T0=2, T1T1=2, SS=2,
T0T1=seq(-1, 1, by=.01))

# Obtain the predicted value T for a patient who scores S = 10, using beta=5,
# SS=2, mu_S=4
Predict <- Predict.Treat.ContCont(x=PCA, S=10, Beta=5, SS=2, mu_S=4)

# examine the results
summary(Predict)

# plot Delta_T_j given S_T and 95% CI  based on
# the mean value of the valid rho_T0T1 results
plot(Predict, Mean.T0T1=TRUE, Median.T0T1=FALSE,
xlim=c(4, 13))

# plot Delta_T_j given S_T and 99% CI  using
#  rho_T0T1=.8
plot(Predict, Mean.T0T1=FALSE, Median.T0T1=FALSE,
Specific.T0T1=.6, alpha=0.01, xlim=c(4, 13))
```

`plot.Predict.Treat.T0T1.ContCont`

Plots the distribution of the individual causal effect based on S for a specific assumed correlation between the counterfactuals.

Description

Plots the distribution of $\Delta T_j|S_j$ and the $1-\alpha\%$ CIs for a user-requested ρ_{T0T1} value). The function is similar to `plot.Predict.Treat.ContCont`, but it is applied to an object of class `Predict.Treat.T0T1.ContCont` (rather than to an object of class `Predict.Treat.ContCont`). This object contains only one ρ_{T0T1} value (rather than a vector of ρ_{T0T1} values), and thus the plot automatically uses the considered ρ_{T0T1} value in the object `x` to compute the $1-\alpha\%$ CI for $\Delta T_j|S_j$.

Usage

```
## S3 method for class 'Predict.Treat.T0T1.ContCont'
plot(x, Xlab, Main, alpha=0.05, Cex.Legend=1, ...)
```

Arguments

`x`	An object of class `Predict.Treat.T0T1.ContCont`. See `Predict.Treat.T0T1.ContCont`.
`Xlab`	The legend of the X-axis of the plot. Default "$\Delta T_j|S_j$".
`Main`	The title of the PCA plot. Default " ".
`alpha`	The α level to be used in the computation of the CIs. Default 0.05.

Cex.Legend	The size of the legend of the plot. Default 1.
...	Other arguments to be passed to the $plot()$ function.

Author(s)

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

References

Alonso, A., Van der Elst, W., & Molenberghs, G. (submitted). Validating predictors of therapeutic success: a causal inference approach.

See Also

Predict.Treat.T0T1.ContCont

Examples

```
# Generate the vector of PCA.ContCont values when rho_T0S=.3, rho_T1S=.9,
# sigma_T0T0=2, sigma_T1T1=2,sigma_SS=2, and the grid of values {-1, -.99,
# ..., 1} is considered for the correlations between T0 and T1:
PCA <- PCA.ContCont(T0S=.3, T1S=.9, T0T0=2, T1T1=2, SS=2,
T0T1=seq(-1, 1, by=.01))

# Obtain the predicted value T for a patient who scores S = 10, using beta=5,
# SS=2, mu_S=4, assuming rho_T0T1=.6
indiv <- Predict.Treat.T0T1.ContCont(x=PCA, S=10, Beta=5, SS=2, mu_S=4, T0T1=.6)
summary(indiv)

# obtain a plot with the 95% CI around delta T_j | S_j (assuming rho_T0T1=.6)
plot(indiv, xlim=c(5, 12))
```

Predict.Treat.ContCont

Compute the predicted treatment effect on the true endpoint of a patient based on his or her observed pretreatment predictor value in the continuous-continuous setting

---

Description

This function computes the predicted ΔT_j of a patient based on the pretreatment value S_j of a patient in the continuous-continuous setting.

Usage

```
Predict.Treat.ContCont(x, S, Beta, SS, mu_S)
```

Arguments

x	An object of class PCA.ContCont. See PCA.ContCont.
S	The observed pretreatment value S_j for a patient.
Beta	The estimated treatment effect on the true endpoint (in the validation sample).
SS	The estimated variance of the pretreatment predictor endpoint.
mu_S	The estimated mean of the pretreatment predictor (in the validation sample).

Value

An object of class PCA.Predict.Treat.ContCont with components,

Pred_T	The predicted ΔT_j.
Var_Delta.T	The variance σ_{Δ_T}.
T0T1	The correlation between the counterfactuals T_0, T_1.
PCA	The vector of ρ_ψ values.
Var_Delta.T_S	The variance σ_{Δ_T}|S_j.

Author(s)

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

References

Alonso, A., Van der Elst, W., & Molenberghs, G. (submitted). Validating predictors of therapeutic success: a causal inference approach.

See Also

PCA.ContCont

Examples

```
# Generate the vector of PCA.ContCont values when rho_T0S=.3, rho_T1S=.9,
# sigma_T0T0=2, sigma_T1T1=2,sigma_SS=2, and the grid of values {-1, -.99,
# ..., 1} is considered for the correlations between T0 and T1:
PCA <- PCA.ContCont(T0S=.3, T1S=.9, T0T0=2, T1T1=2, SS=2,
T0T1=seq(-1, 1, by=.01))

# Obtain the predicted value T for a patient who scores S = 10, using beta=5,
# SS=2, mu_S=4
Predict <- Predict.Treat.ContCont(x=PCA, S=10, Beta=5, SS=2, mu_S=4)

# examine the results
summary(Predict)

# plot Delta_T_j given S_T, for the mean value of the valid rho_T0T1
plot(Predict, Mean.T0T1=TRUE, Median.T0T1=FALSE)
```

`Predict.Treat.Multivar.ContCont` *Compute the predicted treatment effect on the true endpoint of a patient based on his or her observed vector of pretreatment predictor values in the continuous-continuous setting*

Description

This function computes the predicted ΔT_j of a patient based on the vector of pretreatment values $\boldsymbol{S}_j$ of a patient in the continuous-continuous setting.

Usage

```
Predict.Treat.Multivar.ContCont(Sigma_TT, Sigma_TS, Sigma_SS, Beta,
S, mu_S, T0T1=seq(-1, 1, by=.01))
```

Arguments

`Sigma_TT`	The variance-covariance matrix $\boldsymbol{\Sigma}_{TT} = \begin{pmatrix} \sigma_{T0T0} & \sigma_{T0T1} \\ \sigma_{T0T1} & \sigma_{T1T1} \end{pmatrix}$.
`Sigma_TS`	The matrix that contains the covariances σ_{T0Sr}, σ_{T1Sr}. For example, when there are 2 pretreatment predictors $\boldsymbol{\Sigma}_{TS} = \begin{pmatrix} \sigma_{T0S1} & \sigma_{T0S2} \\ \sigma_{T1S1} & \sigma_{T1S2} \end{pmatrix}$.
`Sigma_SS`	The variance-covariance matrix of the pretreatment predictors. For example, when there are 2 pretreatment predictors $\boldsymbol{\Sigma}_{SS} = \begin{pmatrix} \sigma_{S1S1} & \sigma_{S1S2} \\ \sigma_{S1S2} & \sigma_{S2S2} \end{pmatrix}$.
`Beta`	The estimated treatment effect on the true endpoint (in the validation sample).
`S`	The vector of observed pretreatment values $\boldsymbol{S}_j$ for a patient.
`mu_S`	The vector of estimated means of the pretreatment predictor (in the validation sample).
`T0T1`	A scalar or vector that contains the correlation(s) between the counterfactuals T_0 and T_1 that should be considered in the computation of ρ_ψ. Default `seq(-1,1,by=.01)`, i.e., the values -1, -0.99, -0.98, $\ldots$, 1.

Value

An object of class `PCA.Predict.Treat.Multivar.ContCont` with components,

`Pred_T`	The predicted ΔT_j.
`Var_Delta.T_S`	The variance σ_{Δ_T}|S_j.
`T0T1`	The correlation between the counterfactuals T_0, T_1.

Author(s)

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

References

Alonso, A., & Van der Elst, W. (submitted). Evaluating multivariate predictors of therapeutic success: a causal inference approach.

See Also

PCA.ContCont, Multivar.PCA.ContCont

Examples

```
# Specify the covariance matrices to be used
Sigma_TT = matrix(c(177.870, NA, NA, 162.374), byrow=TRUE, nrow=2)
Sigma_TS = matrix(data = c(-45.140, -109.599, 11.290, -56.542,
-106.897, 20.490), byrow = TRUE, nrow = 2)
Sigma_SS = matrix(data=c(840.564, 73.936, -3.333, 73.936, 357.719,
-30.564, -3.333, -30.564, 95.063), byrow = TRUE, nrow = 3)

# Specify treatment effect (Beta), means of vector S (mu_s), and
# observed pretreatment variable values for patient (S)
Beta <- -0.9581 # treatment effect
mu_S = matrix(c(66.8149, 84.8393, 25.1939), nrow=3) #means S_1--S_3
S = matrix(c(90, 180, 30), nrow=3) # S_1--S_3 values for a patient

# predict Delta_T based on S
Pred_S <- Predict.Treat.Multivar.ContCont(Sigma_TT=Sigma_TT, Sigma_TS=Sigma_TS,
Sigma_SS=Sigma_SS, Beta=Beta, S=S, mu_S=mu_S, T0T1=seq(-1, 1, by=.01))

# Explore results
summary(Pred_S)
plot(Pred_S)
```

`Predict.Treat.T0T1.ContCont`

Compute the predicted treatment effect on the true endpoint of a patient based on his or her observed pretreatment predictor value in the continuous-continuous setting for a particular (single) value of ρ_T0T1.

Description

This function computes the predicted ΔT_j of a patient based on the pretreatment value S_j of a patient in the continuous-continuous setting for a particular (single) value of rho_T0T1.

Usage

```
Predict.Treat.T0T1.ContCont(x, S, Beta, SS, mu_S, T0T1, alpha=0.05)
```

Arguments

`x`	An object of class `PCA.ContCont`. See `PCA.ContCont`.
`S`	The observed pretreatment value S_j for a patient.
`Beta`	The estimated treatment effect on the true endpoint (in the validation sample).
`SS`	The estimated variance of the pretreatment predictor endpoint.
`mu_S`	The estimated mean of the surrogate endpoint (in the validation sample).
`T0T1`	The ρ_{T0T1} value (used to compute the variance of $\Delta T_j | S_j$.
`alpha`	The α-level that is used to determine the confidence interval around $\Delta T_j | S_j$. Default 0.05.

Value

An object of class `PCA.Predict.Treat.T0T1.ContCont` with components,

`Pred_T`	The predicted ΔT_j.
`Var_Delta.T`	The variance σ_{Δ_T}.
`T0T1`	The correlation between the counterfactuals T_0, T_1.
`CI_low`	The lower border of the $1-\alpha\%$ confidence interval of $\Delta T_j | S_j$.
`CI_high`	The upper border of the $1-\alpha\%$ confidence interval of $\Delta T_j | S_j$.
`Var_Delta.T_S`	The variance $\sigma_{\Delta_T} | S_j$.
`alpha`	The α-level that is used to determine the confidence interval of $\Delta T_j | S_j$.

Author(s)

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

References

Alonso, A., Van der Elst, W., & Molenberghs, G. (submitted). Validating predictors of therapeutic success: a causal inference approach.

See Also

PCA.ContCont

Examples

```
# Generate the vector of PCA.ContCont values when rho_T0S=.3, rho_T1S=.9,
# sigma_T0T0=2, sigma_T1T1=2,sigma_SS=2, and the grid of values {-1, -.99,
# ..., 1} is considered for the correlations between T0 and T1:
PCA <- PCA.ContCont(T0S=.3, T1S=.9, T0T0=2, T1T1=2, SS=2,
T0T1=seq(-1, 1, by=.01))

# Obtain the predicted value T for a patient who scores S = 10, using beta=5,
# SS=2, mu_S=4, assuming rho_T0T1=.6
indiv <- Predict.Treat.T0T1.ContCont(x=PCA, S=10, Beta=5, SS=2, mu_S=4, T0T1=.6)
```

```
summary(indiv)

# obtain a plot with the 95% CI around delta T_j | S_j (assuming rho_T0T1=.6)
plot(indiv)
```

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