ALMOND

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Type Package

Title Bayesian Analysis of Late (Local Average Treatment Effect) for Missing Or/and Nonnormal Data (ALMOND)

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Description
Using Bayesian robust two-stage causal models with instrumental variables to estimate the Local Average Treatment Effect and simultaneously handle the nonnormal and missing data.

License GPL (>= 3.0)

Encoding UTF-8

LazyData true

Imports R2OpenBUGS, coda, Formula

Suggests knitr, rmarkdown

RoxygenNote 6.1.1

R topics documented:

`gts.nnormal` *Apply the generalized Bayesian two-stage normal-based causal model with instrumental variables.*

Description

The `gts.nnormal` function applies the generalized Bayesian two-stage normal-based causal model to the categorical treatment data. The model best suits the normally-distributed outcome data that are complete or ignorably missing (i.e., missing completely at random or missing at random).

Usage

```
gts.nnormal(formula, data, advanced = FALSE, adv.model, b0 = 1,
  B0 = 1e-06, g0 = 0, G0 = 1e-06, e0 = 0.001, E0 = 0.001,
  beta.start = NULL, gamma.start = NULL, e.start = NULL,
  n.chains = 1, n.burnin = floor(n.iter/2), n.iter = 10000,
  n.thin = 1, DIC, debug = FALSE, codaPkg = FALSE)
```

Arguments

`formula`	An object of class formula: a symbolic description of the model to be fitted. The details of the model specification are given under "Details".
`data`	A dataframe with the variables to be used in the model.
`advanced`	Logical; if FALSE (default), the model is specified using the formula argument, if TRUE, self-defined models can be specified using the adv.model argument.
`adv.model`	Specify the self-defined model. Used when advanced=TRUE.
`b0`	The mean hyperparameter of the normal distribution (prior distribution) for the first-stage generalized causal model coefficients, i.e., coefficients for the instrumental variables. This can either be a numerical value or a vector with dimensions equal to the number of coefficients for the instrumental variables. If this takes a numerical value, then that values will serve as the mean hyperparameter for all of the coefficients for the instrumental variables. Default value of 0 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.
`B0`	The precision hyperparameter of the normal distribution (prior distribution) for the first stage generalized causal model coefficients. This can either be a numerical value or a vector with dimensions equal to the number of coefficients for the instrumental variables. If this takes a numerical value, then that values will serve as the precision hyperparameter for all of the coefficients for the instrumental variables. Default value of 1.0E-6 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.
`g0`	The mean hyperparameter of the normal distribution (prior distribution) for the second-stage generalized causal model coefficients, i.e., coefficients for the treatment variable and other regression covariates). This can either be a numerical value if there is only one treatment variable in the model, or a if there is a treatment variable and multiple regression covariates, with dimensions equal to the

total number of coefficients for the treatment variable and covariates. Default value of 0 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.

`G0` The precision hyperparameter of the normal distribution (prior distribution) for the second-stage generalized causal model coefficients. This can either be a numerical value if there is only one treatment variable in the model, or a vector if there is a treatment variable and multiple regression covariates, with dimensions equal to the total number of coefficients for the treatment variable and covariates. Default value of 1.0E-6 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.

`e0` The location hyperparameter of the inverse Gamma distribution (prior for the variance of the normal distribution on the model residual). Default of 0.001 is equivalent to the noninformative prior for the inverse Gamma distribution.

`E0` The shape hyperparameter of the inverse Gamma distribution (prior for the variance of the normal distribution on the model residual). Default of 0.001 is equivalent to the noninformative prior for the inverse Gamma distribution.

`beta.start` The starting values for the first-stage generalized causal model coefficients, i.e., coefficients for the instrumental variables. This can either be a numerical value or a column vector with dimensions equal to the number of first-stage coefficients. The default value of NA will use the IWLS (iteratively reweighted least squares) estimate of first-stage coefficients as the starting value. If this is a numerical value, that value will serve as the starting value mean for all the first-stage beta coefficients.

`gamma.start` The starting values for the second-stage generalized causal model coefficients, i.e., coefficients for the treatment variable and the model covariates. This can either be a numerical value or a column vector with dimensions equal to the number of second-stage coefficients. The default value of NA will use the IWLS (iteratively reweighted least squares) estimate of second-stage coefficients as the starting value. If this is a numerical value, that value will serve as the starting value mean for all the second-stage gamma coefficients.

`e.start` The starting value for the precision hyperparameter of the inverse gamma distribution (prior for the scale parameter of Student's t distribution of the model residual). The default value of NA will use the inverse of the residual variance from the IWLS (iteratively reweighted least square) estimate of the second-stage model.

`n.chains` The number of Markov chains. The default is 1.

`n.burnin` Length of burn in, i.e., number of iterations to discard at the beginning. Default is n.iter/2, that is, discarding the first half of the simulations.

`n.iter` The number of total iterations per chain (including burnin). The default is 10000.

`n.thin` The thinning rate. Must be a positive integer. The default is 1.

`DIC` Logical; if TRUE (default), compute deviance, pD, and DIC. The rule pD=Dbar-Dhat is used.

`codaPkg` Logical; if FALSE (default), an object is returned; if TRUE, file names of the output are returned.

Details

1. Bayesian two-stage causal models are specified symbolically. A typical model has the form *reponse ~ terms|instrumental_variables*, where response is the (numeric) response vector and

terms is a series of terms which specifies a linear predictor (i.e., the treatment variable and the covariates) for the response. The first specification in the term is always the treatment variable and the remaining specifications are always the covariates for the response.

2. DIC is computed as *mean(deviance)+pD*.
3. Prior distributions used in ALMOND.
   - Generalized causal model coefficients at both stages: normal distributions.
   - The generalized causal model residual term: normal distribution.

Value

If *codaPkg=FALSE*(default), returns an object containing summary statistics of the saved parameters, including

`s1.intercept`	Estimate of the intercept from the first stage.
`s1.slopeP`	Estimate of the pth slope from the first stage.
`s2.intercept`	Estimate of the intercept from the second stage.
`s2.slopeP`	Estimate of the pth slope from the second stage (the first slope is always the **LATE**).
`var.e.s2`	Estimate of the residual variance at the second stage.
`DIC`	Deviance Information Criterion.

If *codaPkg=TRUE*, the returned value is the path for the output file containing the Markov chain Monte Carlo output.

References

Gelman, A., Carlin, J.B., Stern, H.S., Rubin, D.B. (2003). *Bayesian data analysis*, 2nd edition. Chapman and Hall/CRC Press.

Spiegelhalter, D. J., Thomas, A., Best, N. G., Gilks, W., & Lunn, D. (1996). BUGS: Bayesian inference using Gibbs sampling.

Examples

```
# Run the model
model1 <- gts.nnormal(outcome~treatment|instrument,data=simCatNormMCAR)

# Run the model with the self-defined advanced feature

model2 <- gts.nnormal(outcome~treatment|instrument,data=simCatNormMCAR,
advanced=TRUE, adv.model=my.model)

# Extract the model DIC
model1$DIC

# Extract the MCMC output
model3 <- gts.nnormal(outcome~treatment|instrument,data=simCatNormMCAR,codaPkg=TRUE)
```

gts.nnormal.s *Apply the generalized Bayesian two-stage normal-selection causal model with instrumental variables.*

Description

The gts.nnormal.s function applies the generalized Bayesian two-stage normal-selection causal model to the categorical treatment data. The model best suits the normally-distributed outcome data that are normally-distributed and nonignorably missing (i.e., MNAR) (e.g., dropout, attrition).

Usage

```
gts.nnormal.s(formula, data, m.ind, advanced = FALSE, adv.model,
  b0 = 0, B0 = 1e-06, g0 = 0, G0 = 1e-06, e0 = 0.001,
  E0 = 0.001, beta.start = NULL, gamma.start = NULL,
  e.start = NULL, lambda0.start = 1, lambda1.start = 1,
  n.chains = 1, n.burnin = floor(n.iter/2), n.iter = 50000,
  n.thin = 1, DIC, debug = FALSE, codaPkg = FALSE)
```

Arguments

formula	An object of class formula: a symbolic description of the model to be fitted. The details of the model specification are given under "Details".
data	A dataframe with the variables to be used in the model.
advanced	Logical; if FALSE (default), the model is specified using the formula argument, if TRUE, self-defined models can be specified using the adv.model argument.
adv.model	Specify the self-defined model. Used when advanced=TRUE.
b0	The mean hyperparameter of the normal distribution (prior distribution) for the first-stage generalized causal model coefficients, i.e., coefficients for the instrumental variables. This can either be a numerical value or a vector with dimensions equal to the number of coefficients for the instrumental variables. If this takes a numerical value, then that values will serve as the mean hyperparameter for all of the coefficients for the instrumental variables. Default value of 0 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.
B0	The precision hyperparameter of the normal distribution (prior distribution) for the first stage generalized causal model coefficients. This can either be a numerical value or a vector with dimensions equal to the number of coefficients for the instrumental variables. If this takes a numerical value, then that values will serve as the precision hyperparameter for all of the coefficients for the instrumental variables. Default value of 1.0E-6 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.
g0	The mean hyperparameter of the normal distribution (prior distribution) for the second-stage generalized causal model coefficients, i.e., coefficients for the treatment variable and other regression covariates. This can either be a numerical value if there is only one treatment variable in the model, or a if there is a treatment variable and multiple regression covariates, with dimensions equal to the total number of coefficients for the treatment variable and covariates. Default value of 0 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.

`G0` The precision hyperparameter of the normal distribution (prior distribution) for the second-stage generalized causal model coefficients. This can either be a numerical value if there is only one treatment variable in the model, or a vector if there is a treatment variable and multiple regression covariates, with dimensions equal to the total number of coefficients for the treatment variable and covariates. Default value of 1.0E-6 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.

`e0` The location hyperparameter of the inverse Gamma distribution (prior for the variance of the normal distribution on the model residual). Default of 0.001 is equivalent to the noninformative prior for the inverse Gamma distribution.

`E0` The shape hyperparameter of the inverse Gamma distribution (prior for the variance of the normal distribution on the model residual). Default of 0.001 is equivalent to the noninformative prior for the inverse Gamma distribution.

`beta.start` The starting values for the first-stage generalized causal model coefficients, i.e., coefficients for the instrumental variables. This can either be a numerical value or a column vector with dimensions equal to the number of first-stage coefficients. The default value of NA will use the IWLS (iteratively reweighted least squares) estimate of first-stage coefficients as the starting value. If this is a numerical value, that value will serve as the starting value mean for all the first-stage beta coefficients.

`gamma.start` The starting values for the second-stage generalized causal model coefficients, i.e., coefficients for the treatment variable and the model covariates. This can either be a numerical value or a column vector with dimensions equal to the number of second-stage coefficients. The default value of NA will use the IWLS (iteratively reweighted least squares) estimate of second-stage coefficients as the starting value. If this is a numerical value, that value will serve as the starting value mean for all the second-stage gamma coefficients.

`e.start` The starting value for the precision hyperparameter of the inverse gamma distribution (prior for the variance of the normal distribution on the model residual). The default value of NA will use the inverse of the residual variance from the IWLS (iteratively reweighted least square) estimate of the second-stage model.

`lambda0.start` The starting value for the intercept of the coefficient of the added-on selection model.

`lambda1.start` The starting value for the slope of the coefficient of the added-on selection model.

`n.chains` The number of Markov chains. The default is 1.

`n.burnin` Length of burn in, i.e., number of iterations to discard at the beginning. Default is n.iter/2, that is, discarding the first half of the simulations.

`n.iter` The number of total iterations per chain (including burnin). The default is 50000.

`n.thin` The thinning rate. Must be a positive integer. The default is 1.

`DIC` Logical; if TRUE (default), compute deviance, pD, and DIC. The rule pD=Dbar-Dhat is used.

`codaPkg` Logical; if FALSE (default), an object is returned; if TRUE, file names of the output are returned.

`l0` The mean hyperparameter of the normal distribution (prior for the added-on selection model coefficients). This can either be a numerical value or a vector with dimensions equal to the number of coefficients for the instrumental variables. If this takes a numerical value, then that values will serve as the mean hyperparameter for all of the coefficients for the instrumental variables. Default value

of 0 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.

`L0` The precision hyperparameter of the normal distribution (prior for the added-on selection model coefficients). This can either be a numerical value or a vector with dimensions equal to the number of coefficients for the instrumental variables. If this takes a numerical value, then that values will serve as the precision hyperparameter for all of the coefficients for the instrumental variables. Default value of 1.0E-6 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.

Details

1. The formula takes the form *response ~ terms|instrumental_variables*. `gts.nnormal` provides a detailed description of the formula rule.
2. DIC is computed as *mean(deviance)+pD*.
3. Prior distributions used in ALMOND.
   - Generalized causal model coefficients at both stages: normal distributions.
   - Added-on selection model coefficients: normal distributions.

Value

If *codaPkg=FALSE*(default), returns an object containing summary statistics of the saved parameters, including

`s1.intercept` Estimate of the intercept from the first stage.

`s1.slopeP` Estimate of the pth slope from the first stage.

`s2.intercept` Estimate of the intercept from the second stage.

`s2.slopeP` Estimate of the pth slope from the second stage (the first slope is always the **LATE**).

`select.intercept` Estimate of the intercept from the added-on selection model.

`select.slope` Estimate of the slope from the added-on selection model.

`var.e.s2` Estimate of the residual variance at the second stage.

`DIC` Deviance Information Criterion.

If *codaPkg=TRUE*, the returned value is the path for the output file containing the Markov chain Monte Carlo output.

References

Gelman, A., Carlin, J.B., Stern, H.S., Rubin, D.B. (2003). *Bayesian data analysis*, 2nd edition. Chapman and Hall/CRC Press.

Spiegelhalter, D. J., Thomas, A., Best, N. G., Gilks, W., & Lunn, D. (1996). BUGS: Bayesian inference using Gibbs sampling.

Examples

```
# Run the model
model1 <- gts.nnormal.s(outcome~treatment|instrument,data=simCatNormMNAR,
m.ind=simCatNormMNAR$indicator,n.iter=100000)

# Run the model with the self-defined advanced feature
my.normal.s.model<- function(){
  for (i in 1:N){
    logit(p[i]) <- beta0 + beta1*z[i]
    x[i] ~ dbern(p[i])
    muY[i] <- gamma0 + gamma1*p[i]
    y[i] ~ dnorm(muY[i], pre.u2)

    m[i] ~ dbern(q[i])
    q[i] <- phi(lambda0 + lambda1*y[i])
  }

  beta0 ~ dnorm(0,1)
  beta1 ~ dnorm(1, 1)
  gamma0 ~ dnorm(0, 1)
  gamma1 ~ dnorm(.5, 1)
  lambda0 ~ dnorm(0, 1.0E-6)
  lambda1 ~ dnorm(0, 1.0E-6)

  pre.u2 ~ dgamma(.001, .001)

  s1.intercept <- beta0
  s1.slope1 <- beta1
  s2.intercept <- gamma0
  s2.slope1 <- gamma1
  select.intercept <- lambda0
  select.slope <- lambda1
  var.e.s2 <- 1/pre.u2
}

model2 <- gts.nnormal.s(outcome~treatment|instrument,data=simCatNormMNAR,
m.ind=simCatNormMNAR$indicator, advanced=TRUE, adv.model=my.normal.s.model,n.iter=100000)

# Extract the model DIC
model1$DIC

# Extract the MCMC output
model3 <- gts.nnormal.s(outcome~treatment|instrument,data=simCatNormMNAR,
m.ind=simCatNormMNAR$indicator,n.iter=100000,codaPkg=TRUE)
```

`gts.nrobust` *Apply the generalized Bayesian two-stage robust-based causal model with instrumental variables.*

Description

The gts.nrobust function applies the generalized Bayesian two-stage robust-based causal model to the categorical treatment data. The model best suits the outcome data that contain outliers and are ignorably missing (i.e., MCAR or MAR).

Usage

```
gts.nrobust(formula, data, advanced = FALSE, adv.model, b0 = 1,
  B0 = 1e-06, g0 = 0, G0 = 1e-06, e0 = 0.001, E0 = 0.001,
  v0 = 0, V0 = 100, beta.start = NULL, gamma.start = NULL,
  e.start = NULL, df.start = 5, n.chains = 1,
  n.burnin = floor(n.iter/2), n.iter = 10000, n.thin = 1, DIC,
  debug = FALSE, codaPkg = FALSE)
```

Arguments

formula	An object of class formula: a symbolic description of the model to be fitted. The details of the model specification are given under "Details".
data	A dataframe with the variables to be used in the model.
advanced	Logical; if FALSE (default), the model is specified using the formula argument, if TRUE, self-defined models can be specified using the adv.model argument.
adv.model	Specify the self-defined model. Used when advanced=TRUE.
b0	The mean hyperparameter of the normal distribution (prior distribution) for the first-stage generalized causal model coefficients, i.e., coefficients for the instrumental variables. This can either be a numerical value or a vector with dimensions equal to the number of coefficients for the instrumental variables. If this takes a numerical value, then that values will serve as the mean hyperparameter for all of the coefficients for the instrumental variables. Default value of 0 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.
B0	The precision hyperparameter of the normal distribution (prior distribution) for the first stage generalized causal model coefficients. This can either be a numerical value or a vector with dimensions equal to the number of coefficients for the instrumental variables. If this takes a numerical value, then that values will serve as the precision hyperparameter for all of the coefficients for the instrumental variables. Default value of 1.0E-6 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.
g0	The mean hyperparameter of the normal distribution (prior distribution) for the second-stage generalized causal model coefficients, i.e., coefficients for the treatment variable and other regression covariates. This can either be a numerical value if there is only one treatment variable in the model, or a if there is a treatment variable and multiple regression covariates, with dimensions equal to the total number of coefficients for the treatment variable and covariates. Default value of 0 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.
G0	The precision hyperparameter of the normal distribution (prior distribution) for the second-stage generalized causal model coefficients. This can either be a numerical value if there is only one treatment variable in the model, or a vector if there is a treatment variable and multiple regression covariates, with dimensions equal to the total number of coefficients for the treatment variable and covariates.

Default value of 1.0E-6 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.

`e0` The location hyperparameter of the inverse Gamma distribution (prior for the scale parameter of Student's t distribution on the model residual). Default of 0.001 is equivalent to the noninformative prior for the inverse Gamma distribution.

`E0` The shape hyperparameter of the inverse Gamma distribution (prior for the scale parameter of Student's t distribution on the model residual). Default of 0.001 is equivalent to the noninformative prior for the inverse Gamma distribution.

`v0` The lower boundary hyperparameter of the uniform distribution (prior for the degrees of freedom parameter of Student's t distribution).

`V0` The upper boundary hyperparameter of the uniform distribution (prior for the degrees of freedom parameter of Student's t distribution).

`beta.start` The starting values for the first-stage generalized causal model coefficients, i.e., coefficients for the instrumental variables. This can either be a numerical value or a column vector with dimensions equal to the number of first-stage coefficients. The default value of NA will use the IWLS (iteratively reweighted least squares) estimate of first-stage coefficients as the starting value. If this is a numerical value, that value will serve as the starting value mean for all the first-stage beta coefficients.

`gamma.start` The starting values for the second-stage generalized causal model coefficients, i.e., coefficients for the treatment variable and the model covariates. This can either be a numerical value or a column vector with dimensions equal to the number of second-stage coefficients. The default value of NA will use the IWLS (iteratively reweighted least squares) estimate of second-stage coefficients as the starting value. If this is a numerical value, that value will serve as the starting value mean for all the second-stage gamma coefficients.

`e.start` The starting value for the precision hyperparameter of the inverse gamma distribution (prior for the scale parameter of Student's t distribution of the model residual). The default value of NA will use the inverse of the residual variance from the IWLS (iteratively reweighted least square) estimate of the second-stage model.

`df.start` The starting value for the degrees of freedom of Student's t distribution.

`n.chains` The number of Markov chains. The default is 1.

`n.burnin` Length of burn in, i.e., number of iterations to discard at the beginning. Default is n.iter/2, that is, discarding the first half of the simulations.

`n.iter` The number of total iterations per chain (including burnin). The default is 10000.

`n.thin` The thinning rate. Must be a positive integer. The default is 1.

`DIC` Logical; if TRUE (default), compute deviance, pD, and DIC. The rule pD=Dbar-Dhat is used.

`codaPkg` Logical; if FALSE (default), an object is returned; if TRUE, file names of the output are returned.

Details

1. The formula takes the form *response ~ terms|instrumental_variables*. `gts.nnormal` provides a detailed description of the formula rule.
2. DIC is computed as *mean(deviance)+pD*.

3. Prior distributions used in ALMOND.
    - Generalized causal model coefficients at both stages: normal distributions.
    - The generalized causal model residual: Student's t distribution.

Value

If *codaPkg=FALSE*(default), returns an object containing summary statistics of the saved parameters, including

`s1.intercept`	Estimate of the intercept from the first stage.
`s1.slopeP`	Estimate of the pth slope from the first stage.
`s2.intercept`	Estimate of the intercept from the second stage.
`s2.slopeP`	Estimate of the pth slope from the second stage (the first slope is always the **LATE**).
`var.e.s2`	Estimate of the residual variance at the second stage.
`df.est`	Estimate of the degrees of freedom for the Student's t distribution.
`DIC`	Deviance Information Criterion.

If *codaPkg=TRUE*, the returned value is the path for the output file containing the Markov chain Monte Carlo output.

References

Gelman, A., Carlin, J.B., Stern, H.S., Rubin, D.B. (2003). *Bayesian data analysis*, 2nd edition. Chapman and Hall/CRC Press.

Spiegelhalter, D. J., Thomas, A., Best, N. G., Gilks, W., & Lunn, D. (1996). BUGS: Bayesian inference using Gibbs sampling.

Examples

```
# Run the model
model1 <- gts.nrobust(neighborhoodRating~voucherProgram|extraBedroom,data=simVoucher)

# Run the model with the self-defined advanced feature
my.robust.model<- function(){
  for (i in 1:N){
    logit(p[i]) <- beta0 + beta1*z[i]
    x[i] ~ dbern(p[i])
    muY[i] <- gamma0 + gamma1*p[i]
    y[i] ~ dt(muY[i], pre.u2, df)
  }

  beta0 ~ dnorm(0,1)
  beta1 ~ dnorm(1, 1)
  gamma0 ~ dnorm(0, 1)
  gamma1 ~ dnorm(.5, 1)

  pre.u2 ~ dgamma(.001, .001)

  df ~ dunif(0,100)

  s1.intercept <- beta0
```

```
  s1.slope1 <- beta1
  s2.intercept <- gamma0
  s2.slope1 <- gamma1
  df.est <- df
  var.e.s2 <- 1/pre.u2
}

model2 <- gts.nrobust(neighborhoodRating~voucherProgram|extraBedroom,data=simVoucher,
advanced=TRUE, adv.model=my.robust.model)

# Extract the model DIC
model1$DIC

# Extract the MCMC output
model3 <- gts.nrobust(neighborhoodRating~voucherProgram|extraBedroom,data=simVoucher,
codaPkg=TRUE)
```

`gts.nrobust.s` *Apply the generalized Bayesian two-stage robust-selection causal model with instrumental variables.*

Description

The `gts.nrobust.s` function applies the generalized Bayesian two-stage robust-selection causal model to the categorical treatment data. The model best suits the outcome data that contain outliers and are nonignorably missing (i.e., MNAR) (e.g., dropout, attrition).

Usage

```
gts.nrobust.s(formula, data, m.ind, advanced = FALSE, adv.model,
  b0 = 1, B0 = 1e-06, g0 = 0, G0 = 1e-06, e0 = 0.001,
  E0 = 0.001, l0 = 0, L0 = 1e-06, v0 = 0, V0 = 100,
  beta.start = NULL, gamma.start = NULL, e.start = NULL,
  lambda0.start = 1, lambda1.start = 1, df.start = 5, n.chains = 1,
  n.burnin = floor(n.iter/2), n.iter = 50000, n.thin = 1, DIC,
  debug = FALSE, codaPkg = FALSE)
```

Arguments

`formula`	An object of class formula: a symbolic description of the model to be fitted. The details of the model specification are given under "Details".
`data`	A dataframe with the variables to be used in the model.
`advanced`	Logical; if FALSE (default), the model is specified using the formula argument, if TRUE, self-defined models can be specified using the adv.model argument.
`adv.model`	Specify the self-defined model. Used when advanced=TRUE.
`b0`	The mean hyperparameter of the normal distribution (prior distribution) for the first-stage generalized causal model coefficients, i.e., coefficients for the instrumental variables. This can either be a numerical value or a vector with dimensions equal to the number of coefficients for the instrumental variables. If this

takes a numerical value, then that values will serve as the mean hyperparameter for all of the coefficients for the instrumental variables. Default value of 0 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.

B0 The precision hyperparameter of the normal distribution (prior distribution) for the first stage generalized causal model coefficients. This can either be a numerical value or a vector with dimensions equal to the number of coefficients for the instrumental variables. If this takes a numerical value, then that values will serve as the precision hyperparameter for all of the coefficients for the instrumental variables. Default value of 1.0E-6 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.

g0 The mean hyperparameter of the normal distribution (prior distribution) for the second-stage generalized causal model coefficients, i.e., coefficients for the treatment variable and other regression covariates. This can either be a numerical value if there is only one treatment variable in the model, or a if there is a treatment variable and multiple regression covariates, with dimensions equal to the total number of coefficients for the treatment variable and covariates. Default value of 0 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.

G0 The precision hyperparameter of the normal distribution (prior distribution) for the second-stage generalized causal model coefficients. This can either be a numerical value if there is only one treatment variable in the model, or a vector if there is a treatment variable and multiple regression covariates, with dimensions equal to the total number of coefficients for the treatment variable and covariates. Default value of 1.0E-6 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.

e0 The location hyperparameter of the inverse Gamma distribution (prior for the scale parameter of Student's t distribution on the model residual). Default of 0.001 is equivalent to the noninformative prior for the inverse Gamma distribution.

E0 The shape hyperparameter of the inverse Gamma distribution (prior for the scale parameter of Student's t distribution on the model residual). Default of 0.001 is equivalent to the noninformative prior for the inverse Gamma distribution.

l0 The mean hyperparameter of the normal distribution (prior for the added-on selection model coefficients). This can either be a numerical value or a vector with dimensions equal to the number of coefficients for the instrumental variables. If this takes a numerical value, then that values will serve as the mean hyperparameter for all of the coefficients for the instrumental variables. Default value of 0 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.

L0 The precision hyperparameter of the normal distribution (prior for the added-on selection model coefficients). This can either be a numerical value or a vector with dimensions equal to the number of coefficients for the instrumental variables. If this takes a numerical value, then that values will serve as the precision hyperparameter for all of the coefficients for the instrumental variables. Default value of 1.0E-6 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.

v0 The lower boundary hyperparameter of the uniform distribution (prior for the degrees of freedom parameter of Student's t distribution).

V0 The upper boundary hyperparameter of the uniform distribution (prior for the degrees of freedom parameter of Student's t distribution).

`beta.start` The starting values for the first-stage generalized causal model coefficients, i.e., coefficients for the instrumental variables. This can either be a numerical value or a column vector with dimensions equal to the number of first-stage coefficients. The default value of NA will use the IWLS (iteratively reweighted least squares) estimate of first-stage coefficients as the starting value. If this is a numerical value, that value will serve as the starting value mean for all the first-stage beta coefficients.

`gamma.start` The starting values for the second-stage generalized causal model coefficients, i.e., coefficients for the treatment variable and the model covariates. This can either be a numerical value or a column vector with dimensions equal to the number of second-stage coefficients. The default value of NA will use the IWLS (iteratively reweighted least squares) estimate of second-stage coefficients as the starting value. If this is a numerical value, that value will serve as the starting value mean for all the second-stage gamma coefficients.

`e.start` The starting value for the precision hyperparameter of the inverse gamma distribution (prior for the scale parameter of Student's t distribution of the model residual). The default value of NA will use the inverse of the residual variance from the IWLS (iteratively reweighted least square) estimate of the second-stage model.

`lambda0.start` The starting value for the intercept of the coefficient of the added-on selection model.

`lambda1.start` The starting value for the slope of the coefficient of the added-on selection model.

`df.start` The starting value for the degrees of freedom of Student's t distribution.

`n.chains` The number of Markov chains. The default is 1.

`n.burnin` Length of burn in, i.e., number of iterations to discard at the beginning. Default is n.iter/2, that is, discarding the first half of the simulations.

`n.iter` The number of total iterations per chain (including burnin). The default is 50000.

`n.thin` The thinning rate. Must be a positive integer. The default is 1.

`DIC` Logical; if TRUE (default), compute deviance, pD, and DIC. The rule pD=Dbar-Dhat is used.

`codaPkg` Logical; if FALSE (default), an object is returned; if TRUE, file names of the output are returned.

Details

1. The formula takes the form *response ~ terms|instrumental_variables*. `gts.nnormal` provides a detailed description of the formula rule.
2. DIC is computed as *mean(deviance)+pD*.
3. Prior distributions used in ALMOND.
   - Generalized causal model coefficients at both stages: normal distributions.
   - The generalized causal model residual: Student's t distribution.
   - Added-on selection model coefficients: normal distributions.

Value

If *codaPkg=FALSE*(default), returns an object containing summary statistics of the saved parameters, including

s1.intercept	Estimate of the intercept from the first stage.
s1.slopeP	Estimate of the pth slope from the first stage.
s2.intercept	Estimate of the intercept from the second stage.
s2.slopeP	Estimate of the pth slope from the second stage (the first slope is always the **LATE**).
select.intercept	Estimate of the intercept from the added-on selection model.
select.slope	Estimate of the slope from the added-on selection model.
var.e.s2	Estimate of the residual variance at the second stage.
df.est	Estimate of the degrees of freedom for the Student's t distribution.
DIC	Deviance Information Criterion.

If *codaPkg=TRUE*, the returned value is the path for the output file containing the Markov chain Monte Carlo output.

References

Gelman, A., Carlin, J.B., Stern, H.S., Rubin, D.B. (2003). *Bayesian data analysis*, 2nd edition. Chapman and Hall/CRC Press.

Spiegelhalter, D. J., Thomas, A., Best, N. G., Gilks, W., & Lunn, D. (1996). BUGS: Bayesian inference using Gibbs sampling.

Examples

```
# Run the model
model1 <- gts.nrobust.s(outcome~treatment|instrument,data=simCatOutMNAR,
m.ind=simCatOutMNAR$indicator,n.iter=100000)

# Run the model with the self-defined advanced feature
my.model <- function(){
  for (i in 1:N){
    logit(p[i]) <- beta0 + beta1*z[i]
    x[i] ~ dbern(p[i])
    muY[i] <- gamma0 + gamma1*p[i]
    y[i] ~ dt(muY[i], pre.u2, df)

    m[i] ~ dbern(q[i])
    q[i] <- phi(lambda0 + lambda1*y[i])
  }

  beta0 ~ dnorm(0,1)
  beta1 ~ dnorm(1, 1)
  gamma0 ~ dnorm(0, 1)
  gamma1 ~ dnorm(.5, 1)
  lambda0 ~ dnorm(0, 1.0E-6)
  lambda1 ~ dnorm(0, 1.0E-6)

  pre.u2 ~ dgamma(.001, .001)

  df ~ dunif(0,50)

  s1.intercept <- beta0
```

```
  s1.slope1 <- beta1
  s2.intercept <- gamma0
  s2.slope1 <- LATE
  select.intercept <- lambda0
  select.slope <- lambda1
  df.est <- df
  var.e.s2 <- 1/pre.u2
}

model2 <- ts.nrobust.s(outcome~treatment|instrument,m.ind=simCatOutMNAR$indicator,data=simCatOutMNAR,
advanced=TRUE, adv.model=my.model,n.iter=100000)

# Extract the model DIC
model1$DIC

# Extract the MCMC output
model3 <- gts.nrobust.s(outcome~treatment|instrument,data=simCatOutMNAR,
m.ind=simCatOutMNAR$indicator,n.iter=100000, codaPkg=TRUE)
```

`simCatNormMCAR` *A simulated dataset 1.*

Description

A simulated dataset with the categorical treatment variable. The outcome variable is normally-distributed and is missing completely at random (MCAR). The dataset contains a data frame with 600 rows (participants) and 4 columns (variables). The variables are as follows.

Usage

```
data(simCatNormMCAR)
```

Format

A data frame with 600 rows and 4 columns .

Details

- outcome. The hypothetical causal outcome variable.
- treatment. The hypothetical causal treatment variable.
- instrument. The hypothetical instrumental variable.
- mis.ind. Is the outcome variable value missing? 1=Yes, 0=No.

Examples

```
data(simCatNormMCAR)
```

simCatNormMNAR *A simulated dataset 2.*

Description

A simulated dataset with the categorical treatment variable. The outcome variable is normally-distributed and is missing not at random (MNAR, e.g., dropout or attrition). The dataset contains a data frame with 600 rows (participants) and 4 columns (variables). The variables are as follows.

Usage

```
data(simCatNormMNAR)
```

Format

A data frame with 600 rows and 4 columns .

Details

- outcome. The hypothetical causal outcome variable.
- treatment. The hypothetical causal treatment variable.
- instrument. The hypothetical instrumental variable.
- mis.ind. Is the outcome variable value missing? 1=Yes, 0=No.

Examples

```
data(simCatNormMNAR)
```

simCatOutMCAR *A simulated dataset 3.*

Description

A simulated dataset with the categorical treatment variables. The outcome variable contains outliers and is missing completely at random (MCAR). The dataset contains a data frame with 600 rows (participants) and 4 columns (variables). The variables are as follows.

Usage

```
data(simCatOutMCAR)
```

Format

A data frame with 600 rows and 4 columns .

Details

- outcome. The hypothetical causal outcome variable.
- treatment. The hypothetical causal treatment variable.
- instrument. The hypothetical instrumental variable.
- mis.ind. Is the outcome variable value missing? 1=Yes, 0=No.

Examples

```
data(simCatOutMCAR)
```

`simCatOutMNAR` *A simulated dataset 4.*

Description

A simulated dataset with the categorical treatment variable. The outcome variable contains outliers and is missing not at random (MNAR, e.g., dropout or attrition). The dataset contains a data frame with 600 rows (participants) and 4 columns (variables). The variables are as follows.

Usage

```
data(simCatOutMNAR)
```

Format

A data frame with 600 rows and 4 columns .

Details

- outcome. The hypothetical causal outcome variable.
- treatment. The hypothetical causal treatment variable.
- instrument. The hypothetical instrumental variable.
- mis.ind. Is the outcome variable value missing? 1=Yes, 0=No.

Examples

```
data(simCatOutMNAR)
```

simNormMCAR *A simulated dataset 5.*

Description

A simulated dataset with the continous treatment variable. The outcome variable is normally-distributed and is missing completely at random (MCAR). The dataset contains a data frame with 600 rows (participants) and 4 columns (variables). The variables are as follows.

Usage

```
data(simNormMCAR)
```

Format

A data frame with 600 rows and 4 columns .

Details

- outcome. The hypothetical causal outcome variable.
- treatment. The hypothetical causal treatment variable.
- instrument. The hypothetical instrumental variable.
- mis.ind. Is the outcome variable value missing? 1=Yes, 0=No.

Examples

```
data(simNormMCAR)
```

simNormMNAR *A simulated dataset 6.*

Description

A simulated dataset with the continuous treatment variable. The outcome variable is normally-distributed and is missing not at random (MNAR, e.g., dropout or attrition). The dataset contains a data frame with 600 rows (participants) and 4 columns (variables). The variables are as follows.

Usage

```
data(simNormMNAR)
```

Format

A data frame with 600 rows and 4 columns .

Details

- outcome. The hypothetical causal outcome variable.
- treatment. The hypothetical causal treatment variable.
- instrument. The hypothetical instrumental variable.
- mis.ind. Is the outcome variable value missing? 1=Yes, 0=No.

Examples

```
data(simNormMNAR)
```

`simOutMCAR` *A simulated dataset 7.*

Description

A simulated dataset with the continuous treatment variables. The outcome variable contains outliers and is missing completely at random (MCAR). The dataset contains a data frame with 600 rows (participants) and 4 columns (variables). The variables are as follows.

Usage

```
data(simOutMCAR)
```

Format

A data frame with 600 rows and 4 columns .

Details

- outcome. The hypothetical causal outcome variable.
- treatment. The hypothetical causal treatment variable.
- instrument. The hypothetical instrumental variable.
- mis.ind. Is the outcome variable value missing? 1=Yes, 0=No.

Examples

```
data(simOutMCAR)
```

simOutMNAR *A simulated dataset 8.*

Description

A simulated dataset with the continuous treatment variable. The outcome variable contains outliers and is missing not at random (MNAR, e.g., dropout or attrition). The dataset contains a data frame with 600 rows (participants) and 4 columns (variables). The variables are as follows.

Usage

```
data(simOutMNAR)
```

Format

A data frame with 600 rows and 4 columns .

Details

- outcome. The hypothetical causal outcome variable.
- treatment. The hypothetical causal treatment variable.
- instrument. The hypothetical instrumental variable.
- mis.ind. Is the outcome variable value missing? 1=Yes, 0=No.

Examples

```
data(simOutMNAR)
```

simVoucher *Simulated data of a public voucher program.*

Description

The dataset is simulated from a study of the effect of a public voucher program (Currie and Yelowitz, 2000). The dataset contains the status of the public voucher program participation and other attributes. The variables are as follows.

Usage

```
data(simVoucher)
```

Format

A data frame with 1954 rows (participants) and 10 columns (variables).

References

Currie, J., & Yelowitz, A. (2000). Are public housing projects good for kids? *Journal of public economics*, *75*(1), 99-124.

Examples

```
data(simVoucher)
```

---

subECLSK *A subset of the ECLSK (Early Childhood Longitudinal Study – Kindergarten) cohort data.*

Description

The dataset contains the reading and mathematics scores and other attributes of 600 kindergarteners. The variables are as follows.

Usage

```
data(subECLSK)
```

Format

A data frame with 600 rows (participants) and 11 columns (variables).

Details

- dobmm. The date of birth measured in months.
- gender. 1=Male; 2=Female
- race.
  - 1 = White,non-Hispanic
  - 2 = Black or African American, non-Hispanic
  - 3 = Hispanic, race specified
  - 4 = Hispanic, race no specified
  - 5 = Asian
  - 6 = Native Hawaiin, other Pacific islander
  - 7 = American Indian or Alaska native
  - 8 = More than one race, non-Hispanic
- readingIRT. Reading IRT (Item Response Theory) scaled score.
- mathIRT. Mathematics IRT (Item Response Theory) scaled score.
- numsib. Number of siblings in household.
- parentedu. Parent highest education level.
- ses. Continuous socioeconomic status measure.
- relAge. The relative age of the participant entering kindergarten measured in months.
- PredEnt. The predicted relative kindergarten entrance age.
- mis.ind.read. Is the reading IRT score missing? 1=Yes, 0=No.
- mis.ind.math. Is the math IRT score missing? 1=Yes, 0=No.

References

Zhong, S. Y., & Hoxby, C. M. (2012). The effects of relative age on early childhood academic achievement: how they differ between gender and change across time. (Unpublished Honors Thesis) Stanford University, Stanford, CA. (Tourangeau, K., Nord, C., Lê, T., Sorongon, A. G., & Najarian, M. (2009). Early childhood longitudinal study, kindergarten class of 1998–99 (ECLS-K), combined User's manual for the ECLS-K eighth-grade and K–8 full sample data files and electronic codebooks (NCES2009–004). National Center for Education Statistics, Institute of Education Sciences, U.S. Departmentof Education. Washington DC.

Examples

```
data(subECLSK)
```

`ts.nnormal` *Apply the normal-based Bayesian two-stage causal model with instrumental variables.*

Description

The `ts.nnormal` function applies the normal-based Bayesian two-stage causal model to the continuous treatment data. The model best suits the normally-distributed outcome data that are complete or ignorably missing (i.e., missing completely at random or missing at random).

Usage

```
ts.nnormal(formula, data, advanced = FALSE, adv.model, b0 = 1,
  B0 = 1e-06, g0 = 0, G0 = 1e-06, u0 = 0.001, U0 = 0.001,
  e0 = 0.001, E0 = 0.001, beta.start = NULL, gamma.start = NULL,
  u.start = NULL, e.start = NULL, n.chains = 1,
  n.burnin = floor(n.iter/2), n.iter = 10000, n.thin = 1, DIC,
  debug = FALSE, codaPkg = FALSE)
```

Arguments

`b0`	The mean hyperparameter of the normal distribution (prior distribution) for the first-stage causal model coefficients, i.e., coefficients for the instrumental variables. This can either be a numerical value or a vector with dimensions equal to the number of coefficients for the instrumental variables. If this takes a numerical value, then that values will serve as the mean hyperparameter for all of the coefficients for the instrumental variables. Default value of 0 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.
`B0`	The precision hyperparameter of the normal distribution (prior distribution) for the first stage causal model coefficients. This can either be a numerical value or a vector with dimensions equal to the number of coefficients for the instrumental variables. If this takes a numerical value, then that values will serve as the precision hyperparameter for all of the coefficients for the instrumental variables. Default value of 10E+6 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.

`g0` The mean hyperparameter of the normal distribution (prior distribution) for the second-stage causal model coefficients, i.e., coefficients for the treatment variable and other regression covariates). This can either be a numerical value if there is only one treatment variable in the model, or a if there is a treatment variable and multiple regression covariates, with dimensions equal to the total number of coefficients for the treatment variable and covariates. Default value of 0 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.

`G0` The precision hyperparameter of the normal distribution (prior distribution) for the second-stage causal model coefficients. This can either be a numerical value if there is only one treatment variable in the model, or a vector if there is a treatment variable and multiple regression covariates, with dimensions equal to the total number of coefficients for the treatment variable and covariates. Default value of 10E+6 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.

`u0` The location hyperparameter of the inverse Gamma distribution (prior for the variance of the normal distribution on the model residuals at the first stage). Default of 0.001 is equivalent to the noninformative prior for the inverse Gamma distribution.

`U0` The shape hyperparameter of the inverse Gamma distribution (prior for the variance of the normal distribution on the model residuals at the first stage). Default of 0.001 is equivalent to the noninformative prior for the inverse Gamma distribution.

`e0` The location hyperparameter of the inverse Gamma distribution (prior for the variance of the normal distribution on the model residuals at the second stage). Default of 0.001 is equivalent to the noninformative prior for the inverse Gamma distribution.

`E0` The shape hyperparameter of the inverse Gamma distribution (prior for the the variance of the normal distribution on the model residuals at the second stage). Default of 0.001 is equivalent to the noninformative prior for the inverse Gamma distribution.

`beta.start` The starting values for the first-stage causal model coefficients, i.e., coefficients for the instrumental variables. This can either be a numerical value or a column vector with dimensions equal to the number of first-stage coefficients. The default value of NA will use the OLS estimate of first-stage coefficients as the starting value. If this is a numerical value, that value will serve as the starting value mean for all the first-stage beta coefficients.

`gamma.start` The starting values for the second-stage causal model coefficients, i.e., coefficients for the treatment variable and the model covariates. This can either be a numerical value or a column vector with dimensions equal to the number of second-stage coefficients. The default value of NA will use the OLS estimate of second-stage coefficients as the starting value. If this is a numerical value, that value will serve as the starting value mean for all the second-stage gamma coefficients.

`u.start` The starting value for the precision hyperparameter of the inverse gamma distribution (prior for the variance of the normal distribution of the first-stage residual term). The default value of NA will use the inverse of the residual variance from the OLS estimate of the first-stage model.

`e.start` The starting value for the precision hyperparameter of the inverse gamma distribution (prior for the variance of the normal distribution of the second-stage

	residual term). The default value of NA will use the inverse of the residual variance from the OLS estimate of the second-stage model.
n.chains	Number of Markov chains. The default is 1.
n.burnin	Length of burn in, i.e., number of iterations to discard at the beginning. Default is n.iter/2, that is, discarding the first half of the simulations.
n.iter	The number of total iterations per chain (including burnin). The default is 10000.
n.thin	Thinning rate. Must be a positive integer. The default is 1.
DIC	Logical; if TRUE (default), compute deviance, pD, and DIC. The rule pD=Dbar-Dhat is used.
codaPkg	Logical; if FALSE (default), an object is returned; if TRUE, file names of the output are returned.

Details

1. Bayesian two-stage causal models are specified symbolically. A typical model has the form *reponse ~ terms|instrumental_variables*, where response is the (numeric) response vector and terms is a series of terms which specifies a linear predictor (i.e., the treatment variable and the covariates) for the response. The first specification in the term is always the treatment variable and the remaining specifications are always the covariates for the response.
2. DIC is computed as *mean(deviance)+pD*.
3. Prior distributions used in ALMOND.
   - Causal model coefficients at both stages: normal distributions.
   - Causal model residuals at both stages: normal distributions.

Value

If *codaPkg=FALSE*(default), returns an object containing summary statistics of the saved parameters, including

s1.intercept	Estimate of the intercept from the first stage.
s1.slopeP	Estimate of the pth slope from the first stage.
s2.intercept	Estimate of the intercept from the second stage.
s2.slopeP	Estimate of the pth slope from the second stage (the first slope is always the **LATE**).
var.e.s1	Estimate of the residual variance at the first stage.
var.e.s2	Estimate of the residual variance at the second stage.
DIC	Deviance Information Criterion.

If *codaPkg=TRUE*, the returned value is the path for the output file containing the Markov chain Monte Carlo output.

Examples

```
# Run the model
model1 <- ts.nnormal(readingIRT~relAge+gender+race+numsib+parentedu+ses|PredEnt,data=subECLSK)

# Run the model with the self-defined advanced feature
my.normal.model<- function(){
for (i in 1:N){
```

```
mu[i] <- beta0 + beta1*z[i]
x[i] ~ dnorm(mu[i], pre.u1)
muY[i] <- gamma0 + gamma1*mu[i]
y[i] ~ dnorm(muY[i], pre.u2)
}

beta0 ~ dnorm(0,1)
beta1 ~ dnorm(1, 1)
gamma0 ~ dnorm(0, 1)
gamma1 ~ dnorm(.5, 1)
pre.u1 ~ dgamma(.001, .001)
pre.u2 ~ dgamma(.001, .001)

s1.intercept <- beta0
s1.slope1 <- beta1
s2.intercept <- gamma0
s2.slope1 <- gamma1
var.e.s1 <- 1/pre.u1
var.e.s2 <- 1/pre.u2
}

model2 <- ts.nnormal(readingIRT~relAge+gender+race+numsib+parentedu+ses|PredEnt,data=subECLSK,
advanced=TRUE,adv.model=my.normal.model)

# Extract the model DIC
model1$DIC

# Extract the MCMC output
ts.nnormal(readingIRT~relAge+gender+race+numsib+parentedu+ses|PredEnt,data=subECLSK,codaPkg=TRUE)
```

`ts.nnormal.s` *Apply the Bayesian two-stage normal-selection causal model with instrumental variables.*

Description

The `ts.nnormal.s` function applies the Bayesian two-stage normal-selection causal model to the continuous treatment data. The model best suits the outcome data that are normally-distributed and nonignorably missing (i.e., MNAR) (e.g., dropout, attrition).

Usage

```
ts.nnormal.s(formula, data, m.ind, advanced = FALSE, adv.model, b0 = 0,
  B0 = 1e-06, g0 = 0, G0 = 1e-06, u0 = 0.001, U0 = 0.001,
  e0 = 0.001, E0 = 0.001, l0 = 0, L0 = 1e-06, beta.start = NULL,
  gamma.start = NULL, u.start = NULL, e.start = NULL,
  lambda0.start = 1, lambda1.start = 1, n.chains = 1,
  n.burnin = 5000, n.iter = 10000, n.thin = 1, DIC, debug = FALSE,
  codaPkg = FALSE)
```

Arguments

formula	An object of class formula: a symbolic description of the model to be fitted. The details of the model specification are given under "Details".
data	A dataframe with the variables to be used in the model.
advanced	Logical; if FALSE (default), the model is specified using the formula argument, if TRUE, self-defined models can be specified using the adv.model argument.
adv.model	Specify the self-defined model. Used when advanced=TRUE.
b0	The mean hyperparameter of the normal distribution (prior distribution) for the first-stage causal model coefficients, i.e., coefficients for the instrumental variables. This can either be a numerical value or a vector with dimensions equal to the number of coefficients for the instrumental variables. If this takes a numerical value, then that values will serve as the mean hyperparameter for all of the coefficients for the instrumental variables. Default value of 0 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.
B0	The precision hyperparameter of the normal distribution (prior distribution) for the first stage causal model coefficients. This can either be a numerical value or a vector with dimensions equal to the number of coefficients for the instrumental variables. If this takes a numerical value, then that values will serve as the precision hyperparameter for all of the coefficients for the instrumental variables. Default value of 10E+6 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.
g0	The mean hyperparameter of the normal distribution (prior distribution) for the second-stage causal model coefficients, i.e., coefficients for the treatment variable and other regression covariates). This can either be a numerical value if there is only one treatment variable in the model, or a if there is a treatment variable and multiple regression covariates, with dimensions equal to the total number of coefficients for the treatment variable and covariates. Default value of 0 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.
G0	The precision hyperparameter of the normal distribution (prior distribution) for the second-stage causal model coefficients. This can either be a numerical value if there is only one treatment variable in the model, or a vector if there is a treatment variable and multiple regression covariates, with dimensions equal to the total number of coefficients for the treatment variable and covariates. Default value of 10E+6 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.
u0	The location hyperparameter of the inverse Gamma distribution (prior for the variance of the normal distribution on the model residuals at the first stage). Default of 0.001 is equivalent to the noninformative prior for the inverse Gamma distribution.
U0	The shape hyperparameter of the inverse Gamma distribution (prior for the variance of the normal distribution on the model residuals at the first stage). Default of 0.001 is equivalent to the noninformative prior for the inverse Gamma distribution.
e0	The location hyperparameter of the inverse Gamma distribution (prior for the variance of the normal distribution on the model residuals at the second stage). Default of 0.001 is equivalent to the noninformative prior for the inverse Gamma distribution.

`E0` The shape hyperparameter of the inverse Gamma distribution (prior for the variance of the normal distribution on the model residuals at the second stage). Default of 0.001 is equivalent to the noninformative prior for the inverse Gamma distribution.

`l0` The mean hyperparameter of the normal distribution (prior for the added-on selection model coefficients). This can either be a numerical value or a vector with dimensions equal to the number of coefficients for the instrumental variables. If this takes a numerical value, then that values will serve as the mean hyperparameter for all of the coefficients for the instrumental variables. Default value of 0 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.

`L0` The precision hyperparameter of the normal distribution (prior for the added-on selection model coefficients). This can either be a numerical value or a vector with dimensions equal to the number of coefficients for the instrumental variables. If this takes a numerical value, then that values will serve as the precision hyperparameter for all of the coefficients for the instrumental variables. Default value of 10E+6 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.

`beta.start` The starting values for the first-stage causal model coefficients, i.e., coefficients for the instrumental variables. This can either be a numerical value or a column vector with dimensions equal to the number of first-stage coefficients. The default value of NA will use the OLS estimate of first-stage coefficients as the starting value. If this is a numerical value, that value will serve as the starting value mean for all the first-stage beta coefficients.

`gamma.start` The starting values for the second-stage causal model coefficients, i.e., coefficients for the treatment variable and the model covariates. This can either be a numerical value or a column vector with dimensions equal to the number of second-stage coefficients. The default value of NA will use the OLS estimate of second-stage coefficients as the starting value. If this is a numerical value, that value will serve as the starting value mean for all the second-stage gamma coefficients.

`u.start` The starting value for the precision hyperparameter of the inverse gamma distribution (prior for the variance of the normal distribution of the first-stage residual term). The default value of NA will use the inverse of the residual variance from the OLS estimate of the first-stage model.

`e.start` The starting value for the precision hyperparameter of the inverse gamma distribution (prior for the scale parameter of Student's t distribution of the second-stage residual term). The default value of NA will use the inverse of the residual variance from the OLS estimate of the second-stage model.

`lambda0.start` The starting value for the intercept of the coefficient of the added-on selection model.

`lambda1.start` The starting value for the slope of the coefficient of the added-on selection model.

`n.chains` Number of Markov chains. The default is 1.

`n.burnin` Length of burn in, i.e., number of iterations to discard at the beginning. Default is n.iter/2, that is, discarding the first half of the simulations.

`n.iter` Number of total iterations per chain (including burnin). The default is 50000.

`n.thin` Thinning rate. Must be a positive integer. The default is 1.

DIC	Logical; if TRUE (default), compute deviance, pD, and DIC. The rule pD=Dbar-Dhat is used.
codaPkg	Logical; if FALSE (default), an object is returned; if TRUE, file names of the output are returned.

Details

1. The formula takes the form *response ~ terms|instrumental_variables*. ts.nnormal provides a detailed description of the formula rule.
2. DIC is computed as *mean(deviance)+pD*.
3. Prior distributions used in ALMOND.
   - Causal model coefficients at both stages: normal distributions.
   - Causal model residuals at both stages: normal distributions.
   - Added-on selection model coefficients: normal distributions.

Value

If *codaPkg=FALSE*(default), returns an object containing summary statistics of the saved parameters, including

s1.intercept	Estimate of the intercept from the first stage.
s1.slopeP	Estimate of the pth slope from the first stage.
s2.intercept	Estimate of the intercept from the second stage.
s2.slopeP	Estimate of the pth slope from the second stage (the first slope is always the **LATE**).
select.intercept	Estimate of the intercept from the added-on selection model.
select.slope	Estimate of the slope from the added-on selection model.
var.e.s1	Estimate of the residual variance at the first stage.
var.e.s2	Estimate of the residual variance at the second stage.
DIC	Deviance Information Criterion.

If *codaPkg=TRUE*, the returned value is the path for the output file containing the Markov chain Monte Carlo output.

Examples

```
# Run the model
model1 <- ts.nnormal.s(readingIRT~relAge+gender+race+numsib+parentedu+ses|PredEnt,data=subECLSK,
m.ind=subECLSK$mis.ind.read, n.iter=100000)

# Run the model with the self-defined advanced feature
my.normal.s.model<- function(){
  for (i in 1:N){
    mu[i] <- beta0 + beta1*z[i]
    x[i] ~ dnorm(mu[i], pre.u1)
    muY[i] <- gamma0 + gamma1*mu[i]
    y[i] ~ dnorm(muY[i], pre.u2)

    m[i] ~ dbern(q[i])
```

```
    q[i] <- phi(lambda0 + lambda1*y[i])
  }

  beta0 ~ dnorm(0,1)
  beta1 ~ dnorm(1, 1)
  gamma0 ~ dnorm(0, 1)
  gamma1 ~ dnorm(.5, 1)
  lambda0 ~ dnorm(0, 1.0E-6)
  lambda1 ~ dnorm(0, 1.0E-6)

  pre.u1 ~ dgamma(.001, .001)
  pre.u2 ~ dgamma(.001, .001)

  s1.intercept <- beta0
  s1.slope1 <- beta1
  s2.intercept <- gamma0
  s2.slope1 <- gamma1
  select.intercept <- lambda0
  select.slope <- lambda1
  var.e.s1 <- 1/pre.u1
  var.e.s2 <- 1/pre.u2
}

model2 <- ts.nnormal.s(readingIRT~relAge+gender+race+numsib+parentedu+ses|PredEnt,
m.ind=subECLSK$mis.ind.read,data=subECLSK,advanced=TRUE, adv.model=my.normal.selection.model,
n.iter=100000)

# Extract the model DIC
model1$DIC

# Extract the MCMC output
ts.nnormal.s(readingIRT~relAge+gender+race+numsib+parentedu+ses|PredEnt,
m.ind=subECLSK$mis.ind.read,data=subECLSK,codaPkg=TRUE)
```

`ts.nrobust` *Apply the robust-based Bayesian two-stage causal model with instrumental variables.*

Description

The `ts.nrobust` function applies the robust-based Bayesian two-stage causal model to the continuous treatment data. The model best suits the outcome data that contain outliers and are complete or ignorably missing (i.e., missing completely at random or missing at random).

Usage

```
ts.nrobust(formula, data, advanced = FALSE, adv.model, b0 = 1,
  B0 = 1e-06, g0 = 0, G0 = 1e-06, u0 = 0.001, U0 = 0.001,
  e0 = 0.001, E0 = 0.001, v0 = 0, V0 = 100, beta.start = NULL,
  gamma.start = NULL, u.start = NULL, e.start = NULL, df.start = 5,
  n.chains = 1, n.burnin = floor(n.iter/2), n.iter = 10000,
  n.thin = 1, DIC, debug = FALSE, codaPkg = FALSE)
```

Arguments

formula	An object of class formula: a symbolic description of the model to be fitted. The details of the model specification are given under "Details".
data	A dataframe with the variables to be used in the model.
advanced	Logical; if FALSE (default), the model is specified using the formula argument, if TRUE, self-defined models can be specified using the adv.model argument.
adv.model	Specify the self-defined model. Used when advanced=TRUE.
b0	The mean hyperparameter of the normal distribution (prior distribution) for the first-stage causal model coefficients, i.e., coefficients for the instrumental variables. This can either be a numerical value or a vector with dimensions equal to the number of coefficients for the instrumental variables. If this takes a numerical value, then that values will serve as the mean hyperparameter for all of the coefficients for the instrumental variables. Default value of 0 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.
B0	The precision hyperparameter of the normal distribution (prior distribution) for the first stage causal model coefficients. This can either be a numerical value or a vector with dimensions equal to the number of coefficients for the instrumental variables. If this takes a numerical value, then that values will serve as the precision hyperparameter for all of the coefficients for the instrumental variables. Default value of 10E+6 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.
g0	The mean hyperparameter of the normal distribution (prior distribution) for the second-stage causal model coefficients, i.e., coefficients for the treatment variable and other regression covariates). This can either be a numerical value if there is only one treatment variable in the model, or a if there is a treatment variable and multiple regression covariates, with dimensions equal to the total number of coefficients for the treatment variable and covariates. Default value of 0 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.
G0	The precision hyperparameter of the normal distribution (prior distribution) for the second-stage causal model coefficients. This can either be a numerical value if there is only one treatment variable in the model, or a vector if there is a treatment variable and multiple regression covariates, with dimensions equal to the total number of coefficients for the treatment variable and covariates. Default value of 10E+6 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.
u0	The location hyperparameter of the inverse Gamma distribution (prior for the variance of the normal distribution on the model residuals at the first stage). Default of 0.001 is equivalent to the noninformative prior for the inverse Gamma distribution.
U0	The shape hyperparameter of the inverse Gamma distribution (prior for the variance of the normal distribution on the model residuals at the first stage). Default of 0.001 is equivalent to the noninformative prior for the inverse Gamma distribution.
e0	The location hyperparameter of the inverse Gamma distribution (prior for the scale parameter of Student's t distribution on the model residuals at the second stage). Default of 0.001 is equivalent to the noninformative prior for the inverse Gamma distribution.

E0	The shape hyperparameter of the inverse Gamma distribution (prior for the scale parameter of Student's t distribution on the model residuals at the second stage). Default of 0.001 is equivalent to the noninformative prior for the inverse Gamma distribution.
v0	The lower boundary hyperparameter of the uniform distribution (prior for the degrees of freedom parameter of Student's t distribution).
V0	The upper boundary hyperparameter of the uniform distribution (prior for the degrees of freedom parameter of Student's t distribution).
beta.start	The starting values for the first-stage causal model coefficients, i.e., coefficients for the instrumental variables. This can either be a numerical value or a column vector with dimensions equal to the number of first-stage coefficients. The default value of NA will use the OLS estimate of first-stage coefficients as the starting value. If this is a numerical value, that value will serve as the starting value mean for all the first-stage beta coefficients.
gamma.start	The starting values for the second-stage causal model coefficients, i.e., coefficients for the treatment variable and the model covariates. This can either be a numerical value or a column vector with dimensions equal to the number of second-stage coefficients. The default value of NA will use the OLS estimate of second-stage coefficients as the starting value. If this is a numerical value, that value will serve as the starting value mean for all the second-stage gamma coefficients.
u.start	The starting value for the precision hyperparameter of the inverse gamma distribution (prior for the variance of the normal distribution of the first-stage residual term). The default value of NA will use the inverse of the residual variance from the OLS estimate of the first-stage model.
e.start	The starting value for the precision hyperparameter of the inverse gamma distribution (prior for the scale parameter of Student's t distribution of the second-stage residual term). The default value of NA will use the inverse of the residual variance from the OLS estimate of the second-stage model.
df.start	The starting value for the degrees of freedom of Student's t distribution.
n.chains	Number of Markov chains. The default is 1.
n.burnin	Length of burn in, i.e., number of iterations to discard at the beginning. Default is n.iter/2, that is, discarding the first half of the simulations.
n.iter	Number of total iterations per chain (including burnin). The default is 10000.
n.thin	Thinning rate. Must be a positive integer. The default is 1.
DIC	Logical; if TRUE (default), compute deviance, pD, and DIC. The rule pD=Dbar-Dhat is used.
codaPkg	Logical; if FALSE (default), an object is returned; if TRUE, file names of the output are returned.

Details

1. The formula takes the form *response ~ terms|instrumental_variables*. `ts.nnormal` provides a detailed description of the formula rule.
2. DIC is computed as *mean(deviance)+pD*.
3. Prior distributions used in ALMOND.
   - Causal model coefficients at both stages: normal distributions.
   - The causal model residual at the first stage: normal distribution; the causal model residual at the second stage: Student's t distribution.

Value

If *codaPkg=FALSE*(default), returns an object containing summary statistics of the saved parameters, including

`s1.intercept`	Estimate of the intercept from the first stage.
`s1.slopeP`	Estimate of the pth slope from the first stage.
`s2.intercept`	Estimate of the intercept from the second stage.
`s2.slopeP`	Estimate of the pth slope from the second stage (the first slope is always the **LATE**).
`var.e.s1`	Estimate of the residual variance at the first stage.
`var.e.s2`	Estimate of the residual variance at the second stage.
`df.est`	Estimate of the degrees of freedom for the Student's t distribution.
`DIC`	Deviance Information Criterion.

If *codaPkg=TRUE*, the returned value is the path for the output file containing the Markov chain Monte Carlo output.

Examples

```
# Run the model
model1 <- ts.nrobust(outcome~treatment|instrument,data=subECLSK)

# Run the robust model with the self-defined advanced feature
my.robust.model<- function(){
  for (i in 1:N){
    mu[i] <- beta0 + beta1*z[i]
    x[i] ~ dnorm(mu[i], pre.u1)
    muY[i] <- gamma0 + gamma1*mu[i]
    y[i] ~ dt(muY[i], pre.u2, df)
  }

  beta0 ~ dnorm(0,1)
  beta1 ~ dnorm(1, 1)
  gamma0 ~ dnorm(0, 1)
  gamma1 ~ dnorm(.5, 1)

  pre.u1 ~ dgamma(.001, .001)
  pre.u2 ~ dgamma(.001, .001)

  df ~ dunif(0,50)

  s1.intercept <- beta0
  s1.slope1 <- beta1
  s2.intercept <- gamma0
  s2.slope1 <- gamma1
  df.est <- df
  var.e.s1 <- 1/pre.u1
  var.e.s2 <- 1/pre.u2
}

model2 <- ts.nrobust(outcome~treatment|instrument,data=subECLSK,
advanced=TRUE,adv.model=my.robust.model)
```

```
# Extract the model DIC
model1$DIC

# Extract the MCMC output
ts.nrobust(outcome~treatment|instrument,data=subECLSK,codaPkg=TRUE)
```

`ts.nrobust.s` *Apply the Bayesian two-stage robust-selection causal model with instrumental variables.*

Description

The `ts.nrobust.s` function applies the Bayesian two-stage robust-selection causal model to the continuous treatment data. The model best suits the outcome data that contain outliers and are nonignorably missing (i.e., MNAR) (e.g., dropout, attrition).

Usage

```
ts.nrobust.s(formula, data, m.ind, advanced = FALSE, adv.model, b0 = 1,
  B0 = 1e-06, g0 = 0, G0 = 1e-06, u0 = 0.001, U0 = 0.001,
  e0 = 0.001, E0 = 0.001, v0 = 0, V0 = 100, l0 = 0, L0 = 1e-06,
  beta.start = NULL, gamma.start = NULL, u.start = NULL,
  e.start = NULL, df.start = 5, lambda0.start = 1,
  lambda1.start = 1, n.chains = 1, n.burnin = floor(n.iter/2),
  n.iter = 50000, n.thin = 1, DIC, debug = FALSE, codaPkg = FALSE)
```

Arguments

`formula`	An object of class formula: a symbolic description of the model to be fitted. The details of the model specification are given under "Details".
`data`	A dataframe with the variables to be used in the model.
`advanced`	Logical; if FALSE (default), the model is specified using the formula argument, if TRUE, self-defined models can be specified using the adv.model argument.
`adv.model`	Specify the self-defined model. Used when advanced=TRUE.
`b0`	The mean hyperparameter of the normal distribution (prior distribution) for the first-stage causal model coefficients, i.e., coefficients for the instrumental variables. This can either be a numerical value or a vector with dimensions equal to the number of coefficients for the instrumental variables. If this takes a numerical value, then that values will serve as the mean hyperparameter for all of the coefficients for the instrumental variables. Default value of 0 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.
`B0`	The precision hyperparameter of the normal distribution (prior distribution) for the first stage causal model coefficients. This can either be a numerical value or a vector with dimensions equal to the number of coefficients for the instrumental variables. If this takes a numerical value, then that values will serve as the precision hyperparameter for all of the coefficients for the instrumental variables. Default value of 10E+6 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.

`g0` The mean hyperparameter of the normal distribution (prior distribution) for the second-stage causal model coefficients, i.e., coefficients for the treatment variable and other regression covariates). This can either be a numerical value if there is only one treatment variable in the model, or a if there is a treatment variable and multiple regression covariates, with dimensions equal to the total number of coefficients for the treatment variable and covariates. Default value of 0 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.

`G0` The precision hyperparameter of the normal distribution (prior distribution) for the second-stage causal model coefficients. This can either be a numerical value if there is only one treatment variable in the model, or a vector if there is a treatment variable and multiple regression covariates, with dimensions equal to the total number of coefficients for the treatment variable and covariates. Default value of 10E+6 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.

`u0` The location hyperparameter of the inverse Gamma distribution (prior for the variance of the normal distribution on the model residuals at the first stage). Default of 0.001 is equivalent to the noninformative prior for the inverse Gamma distribution.

`U0` The shape hyperparameter of the inverse Gamma distribution (prior for the variance of the normal distribution on the model residuals at the first stage). Default of 0.001 is equivalent to the noninformative prior for the inverse Gamma distribution.

`e0` The location hyperparameter of the inverse Gamma distribution (prior for the scale parameter of Student's t distribution on the model residuals at the second stage). Default of 0.001 is equivalent to the noninformative prior for the inverse Gamma distribution.

`E0` The shape hyperparameter of the inverse Gamma distribution (prior for the scale parameter of Student's t distribution on the model residuals at the second stage). Default of 0.001 is equivalent to the noninformative prior for the inverse Gamma distribution.

`v0` The lower boundary hyperparameter of the uniform distribution (prior for the degrees of freedom parameter of Student's t distribution).

`V0` The upper boundary hyperparameter of the uniform distribution (prior for the degrees of freedom parameter of Student's t distribution).

`l0` The mean hyperparameter of the normal distribution (prior for the added-on selection model coefficients). This can either be a numerical value or a vector with dimensions equal to the number of coefficients for the instrumental variables. If this takes a numerical value, then that values will serve as the mean hyperparameter for all of the coefficients for the instrumental variables. Default value of 0 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.

`L0` The precision hyperparameter of the normal distribution (prior for the added-on selection model coefficients). This can either be a numerical value or a vector with dimensions equal to the number of coefficients for the instrumental variables. If this takes a numerical value, then that values will serve as the precision hyperparameter for all of the coefficients for the instrumental variables. Default value of 10E+6 is equivalent to a noninformative prior for the normal distributions. Used when advanced=FALSE.

`beta.start`	The starting values for the first-stage causal model coefficients, i.e., coefficients for the instrumental variables. This can either be a numerical value or a column vector with dimensions equal to the number of first-stage coefficients. The default value of NA will use the OLS estimate of first-stage coefficients as the starting value. If this is a numerical value, that value will serve as the starting value mean for all the first-stage beta coefficients.
`gamma.start`	The starting values for the second-stage causal model coefficients, i.e., coefficients for the treatment variable and the model covariates. This can either be a numerical value or a column vector with dimensions equal to the number of second-stage coefficients. The default value of NA will use the OLS estimate of second-stage coefficients as the starting value. If this is a numerical value, that value will serve as the starting value mean for all the second-stage gamma coefficients.
`u.start`	The starting value for the precision hyperparameter of the inverse gamma distribution (prior for the variance of the normal distribution of the first-stage residual term). The default value of NA will use the inverse of the residual variance from the OLS estimate of the first-stage model.
`e.start`	The starting value for the precision hyperparameter of the inverse gamma distribution (prior for the scale parameter of Student's t distribution of the second-stage residual term). The default value of NA will use the inverse of the residual variance from the OLS estimate of the second-stage model.
`df.start`	The starting value for the degrees of freedom of Student's t distribution.
`lambda0.start`	The starting value for the intercept of the coefficient of the added-on selection model.
`lambda1.start`	The starting value for the slope of the coefficient of the added-on selection model.
`n.chains`	The number of Markov chains. The default is 1.
`n.burnin`	Length of burn in, i.e., number of iterations to discard at the beginning. Default is n.iter/2, that is, discarding the first half of the simulations.
`n.iter`	The number of total iterations per chain (including burnin). The default is 50000.
`n.thin`	The thinning rate. Must be a positive integer. The default is 1.
`DIC`	Logical; if TRUE (default), compute deviance, pD, and DIC. The rule pD=Dbar-Dhat is used.
`codaPkg`	Logical; if FALSE (default), an object is returned; if TRUE, file names of the output are returned.

Details

1. The formula takes the form *response ~ terms|instrumental_variables*. `ts.nnormal` provides a detailed description of the formula rule.
2. DIC is computed as *mean(deviance)+pD*.
3. Prior distributions used in ALMOND.
   - Causal model coefficients at both stages: normal distributions.
   - The causal model residual at the first stage: normal distribution; the causal model residual at the second stage: Student's t distribution.
   - Added-on selection model coefficients: normal distributions.

Value

If *codaPkg=FALSE*(default), returns an object containing summary statistics of the saved parameters, including

`s1.intercept`	Estimate of the intercept from the first stage.
`s1.slopeP`	Estimate of the pth slope from the first stage.
`s2.intercept`	Estimate of the intercept from the second stage.
`s2.slopeP`	Estimate of the pth slope from the second stage (the first slope is always the **LATE**).
`select.intercept`	Estimate of the intercept from the added-on selection model.
`select.slope`	Estimate of the slope from the added-on selection model.
`var.e.s1`	Estimate of the residual variance at the first stage.
`var.e.s2`	Estimate of the residual variance at the second stage.
`df.est`	Estimate of the degrees of freedom for the Student's t distribution.
`DIC`	Deviance Information Criterion.

If *codaPkg=TRUE*, the returned value is the path for the output file containing the Markov chain Monte Carlo output.

References

Gelman, A., Carlin, J.B., Stern, H.S., Rubin, D.B. (2003). *Bayesian data analysis*, 2nd edition. Chapman and Hall/CRC Press.

Spiegelhalter, D. J., Thomas, A., Best, N. G., Gilks, W., & Lunn, D. (1996). BUGS: Bayesian inference using Gibbs sampling.

Examples

```
# Run the model
model1 <- ts.nrobust.s(outcome~treatment|instrument,data=simOutMNAR,m.ind=subECLSK$mis.ind,
n.iter=100000)

# Run the model with the self-defined advanced feature
my.robust.s.model<- function(){
  for (i in 1:N){
    mu[i] <- beta0 + beta1*z[i]
    x[i] ~ dnorm(mu[i], pre.u1)
    muY[i] <- gamma0 + gamma1*mu[i]
    y[i] ~ dt(muY[i], pre.u2, df)

    m[i] ~ dbern(q[i])
    q[i] <- phi(lambda0 + lambda1*y[i])
  }

  beta0 ~ dnorm(0,1)
  beta1 ~ dnorm(1, 1)
  gamma0 ~ dnorm(0, 1)
  gamma1 ~ dnorm(.5, 1)
  lambda0 ~ dnorm(0, 1.0E-6)
  lambda1 ~ dnorm(0, 1.0E-6)
```

```
  pre.u1 ~ dgamma(.001, .001)
  pre.u2 ~ dgamma(.001, .001)

  df ~ dunif(0,50)

  s1.intercept <- beta0
  s1.slope1 <- beta1
  s2.intercept <- gamma0
  s2.slope1 <- gamma1
  select.intercept <- lambda0
  select.slope <- lambda1
  df.est <- df
  var.e.s1 <- 1/pre.u1
  var.e.s2 <- 1/pre.u2
}

model2 <- ts.nrobust.s(routcome~treatment|instrument,data=simOutMNAR,
m.ind=subECLSK$mis.ind, advanced=TRUE,adv.model=my.robust.s.model,n.iter=100000)

# Extract the model DIC
model1$DIC

# Extract the MCMC output
ts.nrobust.s(outcome~treatment|instrument,data=simOutMNAR,m.ind=subECLSK$mis.ind,
codaPkg=TRUE)
```

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