Package ‘endoSwitch’

February 21, 2020

Type Package
Title Endogenous Switching Regression Models
Version 1.0.0
Encoding UTF-8
License GPL (>= 2)
LazyData true
RoxygenNote 7.0.2
Depends R (>= 3.6.0)
URL https://github.com/cbw1243/endoSwitch
Imports data.table (>= 1.12.2), maxLik (>= 1.3-6), stats (>= 3.6.1), msm (>= 1.6.7)
NeedsCompilation no
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Repository CRAN
Date/Publication 2020-02-21 10:20:02 UTC

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**calcPar**

*Endogenous switching regression*

**Description**

This R function provides estimates of original distribution parameters (sigma and rho) from the estimates of transformed distribution parameters using the delta method.

**Usage**

```r
calcPar(Results)
```

**Arguments**

- `Results` A maxLik object that is estimated by the `endoSwitch` function.

**Value**

A matrix that reports the estimates of original distribution parameters. sigma is standard deviation, and rho is correlation coefficient.

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**endoSwitch**

*Endogenous Switching Regression Models*

**Description**

This is the main interface for the endoSwitch package to estimate the endogenous switching regression models (Heckman, 1979).

**Usage**

```r
endoSwitch(
  data,
  OutcomeDep,
  SelectDep,
  OutcomeCov,
  SelectCov,
  Weight = NA,
  treatEffect = TRUE,
  method = "BFGS",
  start = NULL,
  verbose = FALSE,
  ...
)
```
### Arguments

- **data**
  a data frame. Data for running the regression analysis.

- **OutcomeDep**
  character. Dependent variable in the outcome equation.

- **SelectDep**
  character. Dependent variable in the Selection model. The variable must be binary (0 or 1).

- **OutcomeCov**
  character vector. Covariates in the outcome equation.

- **SelectCov**
  character vector. Covariates in the selection equation.

- **Weight**
  optional character. Name of the weight variable in the dataset, or NA (equal weight).

- **treatEffect**
  TRUE/FALSE. If TRUE, average treatment effects will be calculated and returned. If FALSE, expected outcome values will be calculated and returned.

- **method**
  character. Maximization method to be used. The default is "BFGS" (for Broyden-Fletcher-Goldfarb-Shanno). Other methods can also be used. See maxLik.

- **start**
  optional numeric vector. Used as initial values of parameters for maximization purpose. If NULL, the coefficient estimates from the two-stage estimation will be used.

- **verbose**
  TRUE/FALSE. Choose to show the status of optimization or not.

- **...**
  Other parameters to be passed to the selected maximization routine. See maxLik.

### Details

This function estimates the endogenous switching regression model using the full maximum likelihood estimation method. In this model, a selection equation sorts observation units over two different regimes (e.g., treated and not-treated, or adopter and non-adopter), and two outcome equations that determine the outcome. Estimation of the model relies on joint normality of the error terms in the three-equation system (the selection equation plus two outcome equations). The model is estimated by maximizing the joint likelihood function that is provided in Lokshin and Sajaia (2004).

The endoSwitch uses the maxLik function in the maxLik package to do the optimization. The function automatically searches for starting values for maximization using the results from two-stage estimation following Maddala (1986, chapter 8). Though not recommended, users may provide starting values manually. Assume that you have M variables (including the constant) in the selection equation, and N variables (including the constant) in each outcome equation. Then you need (M + 2*N + 4) starting values. The first M values are for the variables in the selection equation (last value for the constant), followed by N values for the outcome equation for the non-treated individuals (SelectDep = 0), and another N values for the outcome equation for the treated individuals (SelectDep = 1). The last four values are: sigma in outcome equation for the non-treated, sigma in outcome equation for the treated, rho in outcome equation for the non-treated, rho in outcome equation for the treated.

If treatEffect = TRUE, the endoSwitch function will report average treatment effects (for the treated or untreated) as well as heterogeneity effects. A detailed description of these effects is provided in Di Falco, Veronesi, and Yesuf (2011, p.837). If treatEffect = FALSE, the endoSwitch function will report expected outcome values in a list of two dataframes: dataframe EY A1 reports actual (column EY1.A1) and counterfactual (column EY0.A1) expected outcome values for the treated; dataframe EY A0 reports actual (column EY0.A0) and counterfactual (column EY1.A0) expected outcome values for the untreated.
endoSwitch2Stage

**Value**

A list containing three elements. The first element is an object of class "maxLik", which includes parameters in the selection equation, parameters in the outcome equations, and the transformed distributional parameters (parameters are transformed to facilitate maximization, as recommended by Lokshin and Sajaia (2004)). The second element contains the estimates of original distributional parameters (transformed back via the delta method). The third element contains a table reporting average treatment effects or a list of expected outcome values, depending on users’ choice of treatEffect.

**References**


**Examples**

```r
data(ImpactData) # Data are from Abdulai (2016)
OutcomeDep <- 'Output'
SelectDep <- 'CA'
OutcomeCov <- c('Age')
SelectCov <- c('Age', 'Perception')
endoReg <- endoSwitch(ImpactData, OutcomeDep, SelectDep, OutcomeCov, SelectCov)
summary(endoReg) # Summarize the regression results
```

**Description**

This function estimates the endogenous switching regression model via two-stage estimations (Maddala, 1986)

**Usage**

```r
endoSwitch2Stage(data, OutcomeDep, SelectDep, OutcomeCov, SelectCov)
```
**ImpactData**

**Arguments**

- **data**: a data frame. Data for running the regression analysis.
- **OutcomeDep**: character. Dependent variable in the outcome equation.
- **SelectDep**: character. Dependent variable in the Selection model. The variable must be binary (0 or 1).
- **OutcomeCov**: character vector. Covariates in the outcome equation.
- **SelectCov**: character vector. Covariates in the selection equation.

**Details**

The first stage uses a probit model to estimate the selection equation. The second stage uses ordinary least squares including the inverse mills ratios computed from the first stage estimation results to estimate the outcome equations.

**Value**

A list containing regression results.

**References**


**Examples**

```r
data(ImpactData)
OutcomeDep <- 'Output'
SelectDep <- 'CA'
OutcomeCov <- c('Age')
SelectCov <- c('Age', 'Perception')
Results <- endoSwitch2Stage(ImpactData, OutcomeDep, SelectDep, OutcomeCov, SelectCov)
# First stage regression results
summary(Results$FirstStageReg)
# Second stage regression results -- non-adopter
summary(Results$SecondStageReg.0)
# Second stage regression results -- adopter
summary(Results$SecondStageReg.1)
```

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**ImpactData**

A dataset on adoption of conservation agriculture in Zambia

**Description**

A dataset on adoption of conservation agriculture in Zambia
Summary

EndoSwitch

Usage

data(ImpactData)

Format

An object of class data.table (inherits from data.frame) with 408 rows and 31 columns.

Source


References


Examples

data(ImpactData)
summary(ImpactData)

summary.endoSwitch

Summarize the endogenous switching regression results.

Description

Summarize the endogenous switching regression results.

Usage

## S3 method for class 'endoSwitch'
summary(object, ...)

Arguments

object Estimated endogenous switching regression model.

... Other elements.

Value

A list containing the key regression results.
treatmentEffect

Endogenous switching regression

Description
This function calculates average treatment effects and heterogeneity effects from an estimated endogenous switching regression model.

Usage
treatmentEffect(
  Results,
  data,
  OutcomeDep,
  SelectDep,
  OutcomeCov,
  SelectCov,
  treatEffect
)

Arguments
Results    Estimated endogenous switching regression model.
data       a data frame. Data for running the regression analysis.
OutcomeDep character. Dependent variable in the outcome equation.
SelectDep character. Dependent variable in the Selection model. The variable must be binary (0 or 1).
OutcomeCov character vector. Covariates in the outcome equation.
SelectCov character vector. Covariates in the selection equation.
treatEffect TRUE/FALSE. Show average treatment effects or expected outcome values.

Value
A data table that reports the average treatment effects or a list of two tables reporting expected outcome values.
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