Semiparametric Least Squares Inference for Causal Effects with R

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Abstract

This vignette explains how to use the causalSLSE package to estimate causal effects using the semiparametric least squares methods developed by Giurcanu et al. (2023). We describe the classes and methods implemented in the package as well as how they can be used to analyze synthetic and real data.

1 Introduction

This document presents the `causalSLSE` package describing the functions implemented in the package. It is intended for users interested in the details about the methods presented in Giurcanu et al. (2023) and how they are implemented. We first present the theory and will present the package in the following sections.

The general causal semiparametric additive regression model is

$$\begin{aligned} Y &= \beta_0(1-Z) + \beta_1 Z + \sum_{l=1}^{q} f_{l,0}(X_l)(1-Z) + \sum_{l=1}^{q} f_{l,1}(X_l)Z + \xi \\ &\equiv \beta_0(1-Z) + \beta_1 Z + f_0(X)(1-Z) + f_1(X)Z + \xi\,, \end{aligned} \tag{1}$$

where $Y \in \mathbb{R}$ is the response variable, Z is the treatment indicator defined as $Z=1$ for the treated and $Z=0$ for the nontreated, and $X \in \mathbb{R}^q$ is a q-vector of confounders. We approximate this model by the following regression model:

$$\begin{aligned} Y &= \beta_0(1-Z) + \beta_1 Z + \sum_{l=1}^{q} \psi_{l,0}^T U_{l,0}(1-Z) + \sum_{l=1}^{q} \psi_{l,1}^T U_{l,1} Z + \zeta \\ &\equiv \beta_0(1-Z) + \beta_1 Z + \psi_0^T U_0(1-Z) + \psi_1^T U_1 Z + \zeta\,, \end{aligned} \tag{2}$$

where $U_{l,k} = u_{l,k}(X_l) = (u_{j,l,k}(X_l) \,:\, 1 \le j \le p_{l,k}) \in \mathbb{R}^{p_{l,k}}$ is a vector of basis functions corresponding to the l^{th} nonparametric component of the k^{th} group $f_{l,k}(X_l)$, $\psi_{l,k} \in \mathbb{R}^{p_{l,k}}$ is an unknown vector of regression coefficients, $U_k = u_k(X) = (u_{l,k}(X_l) \,:\, 1 \le l \le q) \in \mathbb{R}^{p_k}$ and $\psi_k = (\psi_{l,k} \,:\, 1 \le l \le q) \in \mathbb{R}^{p_k}$, with $p_k = \sum_{l=1}^q p_{l,k}$. In this paper, we propose a data-driven method for selecting the vectors of basis functions $u_0(X)$ and $u_1(X)$. Note that we allow the number of basis functions ($p_{l,k}$) to differ across confounders and groups.

Let the following be the regression model estimated by least squares:

$$Y_i = \beta_0(1-Z_i) + \beta_1 Z_i + \psi_0^T U_{i,0}(1-Z_i) + \psi_1^T U_{i,1} Z_i + \zeta_i \text{ for } i = 1, ..., n\,, \tag{3}$$

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and $\hat\beta_0$, $\hat\beta_1$, $\hat\psi_0$ and $\hat\psi_1$ be the least squares estimators of the regression parameters. Then, the semiparametric least squares estimators (SLSE) of the average causal effect (ACE), causal effect on the treated (ACT) and causal effect on the non-treated (ACN) are defined respectively as follows:

$$\begin{aligned}\text{ACE} &= \hat\beta_1 - \hat\beta_0 + \hat\psi_1^T\bar U_1 - \hat\psi_0^T\bar U_0\\ \text{ACT} &= \hat\beta_1 - \hat\beta_0 + \hat\psi_1^T\bar U_{1,1} - \hat\psi_0^T\bar U_{0,1}\\ \text{ACN} &= \hat\beta_1 - \hat\beta_0 + \hat\psi_1^T\bar U_{1,0} - \hat\psi_0^T\bar U_{0,0}\,,\end{aligned} \tag{4}$$

where $\bar U_k = \frac{1}{n}\sum_{i=1}^n U_{i,k}$, $\bar U_{k,1} = \frac{1}{n_1}\sum_{i=1}^n U_{i,k}Z_i$, $\bar U_{k,0} = \frac{1}{n_0}\sum_{i=1}^n U_{i,k}(1-Z_i)$, for $k=0,1$, and n_0 and n_1 are the sample sizes of the nontreated and treated groups respectively. As shown by Giurcanu et al. (2023), under some regularity conditions these estimators are consistent and asymptotically normal.

To derive the variance of these causal effect estimators, note that they can be expressed as a linear combination of the vector of least squares estimates. Let $\hat\theta = \{\hat\beta_0, \hat\beta_1, \hat\psi_0^T, \hat\psi_1^T\}^T$. Then, the causal effect estimators can be written as $\hat D_{\text{c}}^T\hat\theta$ for c=ACE, ACT or ACN, with $\hat D_{\text{ACE}} = \{-1, 1, -\bar U_0^T, \bar U_1^T\}^T$, $\hat D_{\text{ACT}} = \{-1, 1, -\bar U_{0,1}^T, \bar U_{1,1}^T\}^T$ and $\hat D_{\text{ACN}} = \{-1, 1, -\bar U_{0,0}^T, \bar U_{1,0}^T\}^T$. Since $\hat D_{\text{c}}$ is random, we need a first order Taylor expansion to derive the variance of the estimators. Assuming that the data set is iid and using the asymptotic properties of least squares estimators, we can show that the variance of ACE=$\hat D_{\text{ACE}}^T\hat\theta$ can be consistently estimated as follows (we can derive a similar expression for the ACT and ACN):

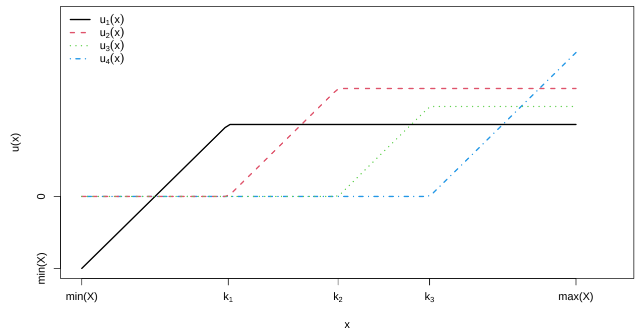
$$\hat V_{\text{ACE}} = \begin{pmatrix}-\hat\beta_0 & \hat\beta_1 & \hat D_{\text{ACE}}^T\end{pmatrix}\begin{pmatrix}\hat\Sigma_0 & \hat\Sigma_{0,1} & \hat\Sigma_{0,\hat\theta}\\ \hat\Sigma_{1,0} & \hat\Sigma_1 & \hat\Sigma_{1,\hat\theta}\\ \hat\Sigma_{\hat\theta,0} & \hat\Sigma_{\hat\theta,1} & \hat\Sigma_{\hat\theta}\end{pmatrix}\begin{pmatrix}-\hat\beta_0\\ \hat\beta_1\\ \hat D_{\text{ACE}}\end{pmatrix}, \tag{5}$$

where $\hat\Sigma_k = \widehat{\text{var}(\bar U_k)}$, $\hat\Sigma_{k,l} = \widehat{\text{cov}(\bar U_k, \bar U_l)}$, $\hat\Sigma_{k,\hat\theta} = \hat\Sigma_{\hat\theta,k}^T = \widehat{\text{cov}(\bar U_k, \hat\theta)}$, for $k,l=0,1$, and $\hat\Sigma_{\hat\theta}$ is a consistent estimator of the variance of $\hat\theta$. We will discuss the choice of the covariance matrix estimator $\hat\Sigma_{\hat\theta}$ in the next section.

To understand the package, it is important to know how the $u_{l,k}(X_l)$'s are defined. For clarity, let's write $U_{l,k} = u_{l,k}(X_l)$ as $U = u(X) = (u_j(X)\ :\ 1\le j\le p)\in\mathbb{R}^p$. We just need to keep in mind that it is different for the treated and nontreated groups and also for different confounders. We describe here how to construct the local linear splines for a given confounder X in a given group. To this end, let $\{\kappa_1,\ldots,\kappa_{p-1}\}$ be a set of $p-1$ knots strictly inside the support of X satisfying $\kappa_1<\kappa_2<\ldots<\kappa_{p-1}$. In the case of local linear splines described in the paper, we have:

$$\begin{aligned}u_1(x) &= xI(x\le\kappa_1) + \kappa_1 I(x>\kappa_1)\\ u_j(x) &= (x-\kappa_{j-1})I(\kappa_{j-1}\le x\le\kappa_j) + (\kappa_j-\kappa_{j-1})I(x>\kappa_j)\,,\quad 2\le j\le p-1\\ u_p(x) &= (x-\kappa_{p-1})I(x>\kappa_{p-1})\end{aligned} \tag{6}$$

Therefore, if the number of knots is equal to 1, we only have two local linear splines. Since the knots must be strictly inside the support of X, for any categorical variable with two levels, the number of knots must be equal to zero. In this case, $u(x)=x$. For general ordinal variables, the number of knots cannot exceed the number of levels minus two. The following illustrates local spline functions when the number of knots is equal to 3:



Note that for the sample regression, the knots of X_l for group k, $l = 1, ..., q$, must be strictly inside the sample range of $(X_{i,l} \; : \; 1 \leq i \leq n, \; Z_i = k) \in \mathbb{R}^{n_k}$, where n_k is the sample size in group k, instead of inside the support of X_l.

The following section explains in details how to use the package to estimate the causal effects using this method, and the last section summarizes the package by providing a list of all objects and methods.

2 The `causalSLSE` package

2.1 The Semiparametric LSE model

Note that the regression model presented by Equation (3) can expressed as:

$$\begin{aligned} Y_i &= \beta_0 + \psi_0^T U_{i,0} + \zeta_{i,0} \text{ for } i \text{ s.t. } Z_i = 0 \\ Y_i &= \beta_1 + \psi_1^T U_{i,1} + \zeta_{i,1} \text{ for } i \text{ s.t. } Z_i = 1\,. \end{aligned} \tag{7}$$

Estimating Equation (3) is identical to estimating the previous two models separately. The latter may even be numerically more accurate since it avoids many unnecessary operations. Also, as mentioned in the previous section, the knots and basis functions are obtained separately for the treated and nontreated. Therefore, we can see the model from Equation (3) as two semiparametric LSE (SLSE) models, one for the treated and one for the nontreated, and this is the approach that we take in the package. One benefit of this approach is to allow an extension to multiple treatment models. For example, a two treatment model is like a one treatment model with one more SLSE model.

Since our causal SLSE model is a collection of SLSE models, we start by presenting how SLSE models are defined in the package. We ignore for now that our objective is to estimate causal effects and consider the following SLSE model:

$$\begin{aligned} Y &= \beta + \sum_{l=1}^{q} \psi_l^T U_l + \zeta \\ Y &= \beta + \psi^T U + \zeta\,, \end{aligned} \tag{8}$$

where $U_l = u_l(X_l) = (u_{j,l}(X_l) \; : \; 1 \leq j \leq p_l) \in \mathbb{R}^{p_l}$, $\psi_l \in \mathbb{R}^{p_l}$ is an unknown vector of regression coefficients, $U = u(X) = (u_l(X_l) \; : \; 1 \leq l \leq q) \in \mathbb{R}^p$ and $\psi = (\psi_l \; : \; 1 \leq l \leq q) \in \mathbb{R}^p$, with $p = \sum_{l=1}^{q} p_l$. The next section explains how the knots are determined.

2.1.1 The starting knots

The starting knots are automatically generated by the function `slseKnots`. The following is the list of arguments of the function:

- **form**: A formula with the right-hand side being the list of covariates. If a left-hand side is provided, the `slseKnots` function will ignore it, because its purpose is only to generate the knots.
- **data**: A `data.frame` containing all variables included in the formula.
- **X**: Alternatively, we can input directly the matrix of covariates. If a matrix `X` is provided, the arguments `form` and `data` are ignored.
- **nbasis**: A function that determines the number of basis functions as explained in the procedure below. The default is `nbasis=function(n) n^0.3`.
- **knots**: This argument is used to set the knots manually. We will explain how to use this argument in the next section.

The following is the procedure implemented by the function `slseKnots`. It explains the procedure for any covariate X.

1. The starting number of knots, also equal to the number of basis functions minus 1, depends on the type of covariate. Unless it has a type that restricts the number of knots, which is explained below, it is determined by the argument `nbasis`. This is a function of one argument, the same size, and it returns the default number of basis functions. This number cannot be smaller than 2 (we will see other ways of forcing the number of basis functions to be equal to 1 below) and must be an integer. To be more specific, the number of basis functions is set to the maximum between 2 and the ceiling of what the `nbasis` function returns. For example, if the sample size is 500, the default starting number of basis functions is 7=`ceiling(500^0.3)`, which implies a starting number of knots of 6. It is possible to have a number of knots that does not depend on the sample size. All we need is to set the argument `nbasis` to a function that returns an integer, e.g., `nbasis=function(n) 4` for 4 basis functions or 3 knots.
2. Let $(p-1)$ be the number of knots determined in the previous step. The default knots are obtained by computing $p+1$ quantiles of X for equally spaced probabilities from 0 to 1, and by dropping the first and last quantiles. For example, if the number of knots is 3, then the initial knots are given by quantiles for the probabilities 0.25, 0.5 and 0.75.
3. We drop any duplicated knots and any knots equal to either the max or the min of X. If the resulting number of knots is equal to 0, the vector of knots is set to `NULL`. When the knots is equal to `NULL` for a variable X, it means that $u(x) = x$.

The last step implies that the number of knots for all categorical variables with two levels is equal to 0. For nominal variables with a small number of levels, the number of knots, a subset of the levels, may be smaller than the ones defined by `nbasis`. For example, when the number of levels for a nominal variable is 3, the number of knots cannot exceed 1.

To illustrate how to use the package, we are using the dataset from Lalonde (1986). The purpose of this dataset is to measure the causal effect of a training program on real income, but we ignore it for the moment. The dataset is included in the `causalSLSE` package and can be loaded as follows.

```
library(causalSLSE)
data(nsw)
```

The dependent variable is the real income in 1978 (`re78`) and the dataset contains the following covariates: the continuous variables age (`age`), education (`ed`) and the 1975 real income (`re75`), and the binary variables `black`, `hisp`, `married` and `nodeg`. We start by considering a model that includes the covariates `age`, `re75`, `ed`, and `married`. Since we do not need to specify the left-hand side, we can create the initial knots as follows

```
k <- slseKnots(form = ~ age + re75 + ed + married, data = nsw)
```

The function returns an object of class `slseKnots` and its `print` method produces a nice display separating confounders with and without knots. For example, the following are the starting knots:

```
print(k)
```

```
Covariates with no knots:
    married

Covariates with knots:
age :
      12.5% 25% 37.5% 50% 62.5% 75% 87.5%
Knots    18  19    21  23    25  27    31

re75 :
        50% 62.5%  75% 87.5%
Knots 936.2  2037 4023  8015

ed :
      12.5% 25% 37.5% 62.5% 87.5%
Knots     8   9    10    11    12
```

The sample size is equal to 722 and the default `nbasis` is $n^{0.3}$, which implies a default number of starting knots equal to $7 =$ `ceiling(`$722^{0.3}$`)-1`. This is the number of knots we have for `age`. However, the number of knots for `ed` is 5 and it is 4 for `re75`. To understand why, the following shows the 7 default quantiles for `re75` and `ed` (the `type` argument of the `quantile` function is the same as it is implemented in the package):

```
p <- seq(0,1,len=9)[c(-1,-9)] # these are the probabilities with 7 knots
quantile(nsw[,'re75'], p, type=1)
```

```
    12.5%       25%     37.5%       50%     62.5%       75%     87.5%
   0.0000    0.0000    0.0000  936.1773 2036.7900 4023.2110 8015.4420
```

```
quantile(nsw[,'ed'], p, type=1)
```

```
12.5%   25% 37.5%   50% 62.5%   75% 87.5%
    8     9    10    10    11    11    12
```

We can see that the first three quantiles of `re75` are equal to its minimum, so they are removed. For the `ed` variable, 10 and 11 appear twice, so one 10 and one 11 must be removed.

Note that each object in the package is S3-class, so the elements can be accessed using the operator $. For example, we can extract the knots for `age` as follows:

```
k$age
```

```
12.5%   25% 37.5%   50% 62.5%   75% 87.5%
   18    19    21    23    25    27    31
```

Note that the covariates are listed in the “no knots” section when their values are set to `NULL`. In the above example, it is the case of `married` because it is a binary variable. As we can see its list of knots it set to `NULL`:

```
k$married
```

```
NULL
```

2.1.2 Creating a SLSE model

The SLSE model is created by the function `slseModel`. The arguments of the function are the same as for the `slseknots` function except for the argument `X`, which is not needed. The difference is that `form` must include the left-hand side variable. For example, we can create a SLSE model using `re78` as dependent variance and the same covariates used in the previous section as follows:

```
mod1 <- slseModel(form = re78 ~ age + re75 + ed + married, data = nsw)
```

The function returns an object of class `slseModel` and its print method provides a summary of its specification:

```
print(mod1)
```

```
Semiparametric LSE Model
************************

Number of observations:  722
Selection method: Default

Covariates approximated by SLSE:
    age, re75, ed
Covariates not approximated by SLSE:
    married
```

Note that the selection method is set to `Default` when the knots are selected using the procedure described in the previous section. The function selects the knots using the `slseKnots` and stores them in the object under `knots`. We can print them using the $ operator as follows and compare them with the ones obtained in the previous section:

```
mod1$knots
```

```


Covariates with no knots:
    married

Covariates with knots:
age :
      12.5% 25% 37.5% 50% 62.5% 75% 87.5%
Knots    18  19    21  23    25  27    31

re75 :
        50% 62.5%  75% 87.5%
Knots 936.2  2037 4023  8015

ed :
      12.5% 25% 37.5% 62.5% 87.5%
Knots     8   9    10    11    12
```

Note that we can also print the knots by running the command `print(mod, which="selKnots")`.

In order to present another example with different types of covariates, the dataset `simDat4` is included in the package. This is a simulated dataset which contains special types of covariates. It helps to further illustrate how the knots are determined. The dataset contains a continuous variable `X1` with a large proportion of zeros, the categorical variable `X2` with 3 levels, an ordinal variable `X3` with 3 levels, and a binary variable `X4`. The levels for `X2` are {“first”,“second”,“third”} and for `X3` the levels are {1,2,3}.

```
data(simDat4)
mod2 <- slseModel(Y ~ X1 + X2 + X3 + X4, data = simDat4)
print(mod2, which="selKnots")
```

```
Semiparametric LSE Model: Selected knots
****************************************
Selection method: Default

Covariates with no knots:
    X2second, X2third, X4

Covariates with knots:
X1 :
      42.86% 57.14% 71.43% 85.71%
Knots 0.4258  2.304  7.911  17.58

X3 :
      42.86%
Knots      2
```

Character-type variables are automatically converted into factors. It is also possible to define a numerical variable like `X3` as a factor by using the function `as.factor` in the formula. We see that the 2 binary variables

`X2second` and `X2third` are created and `X2first` is omitted to avoid multicollinearity. For the binary variable `X4`, the number of knots is set to 0, and for the ordinal variable `X3`, the number of knots is set to 1 because the min and max values 1 and 3 cannot be selected.

2.1.3 Selecting the knots manually

The user has control over the selection of knots through the argument `knots`. When the argument is missing (the default), all knots are set automatically as described above. One way to set the number of knots to 0 for all variables is to set the argument to `NULL`.

```
slseModel(~ age + re75 + ed + married, data = nsw, knots = NULL)
```

```
Semiparametric LSE Model
************************

Number of observations:  722
Selection method: User Based

Covariates approximated by SLSE:
    None
Covariates not approximated by SLSE:
    age, re75, ed, married
```

Notice that the selection method is defined as "User Based" whenever the knots are provided manually by the user. The other option is to provide a list of knots. For each variable, we have three options:

- `NA`: The knots are set automatically for this variable only.
- `NULL`: The number of knots is set to 0 for this variable only.
- A numeric vector: The vector cannot contain missing or duplicated values and must be strictly inside the range of the variable.

In the following, we describe all possible formats for the list of knots.

Case 1: An unnamed list of length equal to the number of covariates.

In that case, the knots must be defined in the same order of variables implied by the formula. For example, if we want to set an automatic selection for `age`, no knots for `ed` and the knots $\{1000, 5000, 10000\}$ for `re75`, we proceed as follows. Note that setting the value to `NA` or `NULL` has the same effect for the binary variable `married`.

```
selK <- list(NA, c(1000,5000,10000), NULL, NA)
mod <- slseModel(re78 ~ age + re75 + ed + married, data = nsw,
                 knots = selK)
print(mod, which = "selKnots")
```

```
Semiparametric LSE Model: Selected knots
****************************************
Selection method: User Based

Covariates with no knots:
    ed, married

Covariates with knots:
age :
      12.5% 25% 37.5% 50% 62.5% 75% 87.5%
Knots    18  19    21  23    25  27    31

re75 :
        k1   k2    k3
Knots 1000 5000 10000
```

Case 2: A named list of length equal to the number of covariates.

In that case, the order of the list of variables does not matter. The `slseModel` function will automatically reorder the variables to match the order implied by the formula. The names must match perfectly the variable names generated by R. In the following example, we want to add the interaction between `ed` and `age`. We want the same set of knots as in the previous example and no knots for the interaction term. The name of the interaction depends on how we enter it in the formula. For example, it is "age:ed" if we enter `age*ed` in the formula and "ed:age" if we enter `ed*age`. For factors, the names depend on which binary variable is omitted. Using the above example with the `simDat4` model, if we interact `X2` and `X4` by adding `X2*X4` to the formula, the names of the interaction terms are "X2second:X4" and "X2third:X4". When we are uncertain about the names, we can print the knots of a model with the default sets of knots. In the following, we change the order of variables to show that the order does not matter.

```
selK <- list(married = NA, ed = NULL, 'age:ed' = NULL, re75 = c(1000,5000,10000), age = NA)
model <- slseModel(re78 ~ age * ed + re75 + married, data = nsw, knots = selK)
print(model, which="selKnots")
```

```
Semiparametric LSE Model: Selected knots
****************************************
Selection method: User Based

Covariates with no knots:
    ed, married, age:ed

Covariates with knots:
age :
      12.5% 25% 37.5% 50% 62.5% 75% 87.5%
Knots    18  19    21  23    25  27    31

re75 :
        k1   k2    k3
Knots 1000 5000 10000
```

Case 3: A named list of length strictly less than the number of confounders.

The names of the selected variables must match perfectly the names generated by R and the order does not matter. This is particularly useful when the number of covariates is large. If we consider the previous example, the knots are set manually only `age`. By default, all names not included in the list of knots are set to `NA`. Therefore, we can create the same model from the previous example as follows:

```
selK <- list(ed = NULL, 'age:ed' = NULL, re75 = c(1000,5000,10000))
model <- slseModel(re78 ~ age * ed + re75 + married, data = nsw, knots = selK)
print(model, which="selKnots")
```

```
Semiparametric LSE Model: Selected knots
****************************************
Selection method: User Based

Covariates with no knots:
    ed, married, age:ed

Covariates with knots:
age :
      12.5% 25% 37.5% 50% 62.5% 75% 87.5%
Knots    18  19    21  23    25  27    31

re75 :
        k1   k2    k3
Knots 1000 5000 10000
```

Note that the previous case offers an easy way of setting the number of knots to 0 for a subset of the covariates. For example, suppose we want to add more interaction terms and set the knots to 0 for all of them. We can proceed as follows.

```
selK <- list('age:ed' = NULL, 'ed:re75' = NULL, 'ed:married' = NULL)
model <- slseModel(re78 ~ age * ed + re75 * ed + married * ed,
                   data = nsw, knots = selK)
```

```r
model
```

```
Semiparametric LSE Model
************************

Number of observations:  722
Selection method: User Based

Covariates approximated by SLSE:
    age, ed, re75
Covariates not approximated by SLSE:
    married, age:ed, ed:re75, ed:married
```

Note also that `slseModel` deals with interaction terms as any other variable. For example, `ed:black` is like a continuous variable with a large proportion of zeros. The following shows the default selected knots for `ed:black`.

```r
model <- slseModel(re78 ~ age + ed * black, data = nsw)
model$knots[["ed:black"]]
```

```
  25% 37.5%   50% 62.5% 87.5%
    8     9    10    11    12
```

We can see that the number of knots is smaller than 7. This is because `ed:black` has many zeros and the quantiles equal to 0 are removed.

2.1.4 Methods for `slseModel` objects

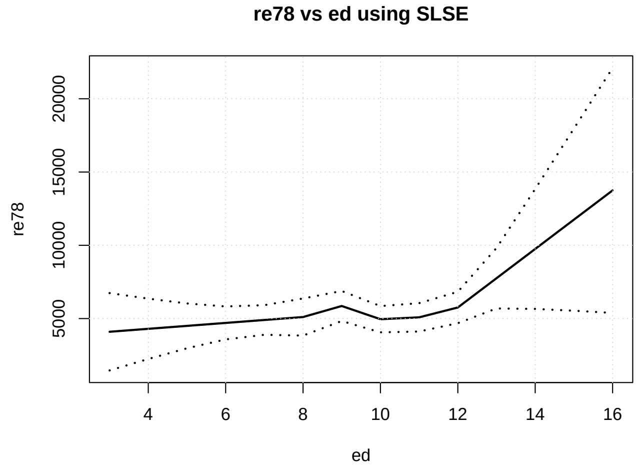
Other methods are registered for `slseModel` objects. For example, we can estimate `slseModel` objects using the `estSLSE` method and summarize the results using the `summary` method. The following is an example using a simpler model:

```r
mod2 <- slseModel(form = re78 ~ ed + married, data = nsw)
fit2 <- estSLSE(mod2)
summary(fit2)
```

```
Semiparametric LSE
******************
Selection method: Default

Residuals:
   Min     1Q Median     3Q    Max
-11472  -4846  -1548   3195  55335

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   3384.7     2304.0   1.469   0.1418
U.ed_1         201.2      328.0   0.613   0.5396
U.ed_2         752.2      824.6   0.912   0.3616
U.ed_3        -900.4      695.0  -1.296   0.1951
U.ed_4         126.5      672.5   0.188   0.8508
U.ed_5         672.8      735.9   0.914   0.3605
U.ed_6        1997.6     1105.1   1.808   0.0707 .
U.married      674.2      652.5   1.033   0.3015
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 6212 on 714 degrees of freedom
Multiple R-squared:  0.02276,	Adjusted R-squared:  0.01317
```

We can also plot the predicted dependent variable as a function of education using the `plot` method and add a confidence region:

```r
plot(fit2, "ed", interval="confidence", level=0.95)
```



In the next section, we present the `cslseModel` class which represents the causal-SLSE model of Equation (3). We will see that it is just a list of `slseModel` objects. Therefore, the methods registered for `cslseModel` objects are derived from `slseModel` methods. Since this paper is about causal-SLSE, we choose to present these methods through the `cslseModel` object.

2.2 The causal-SLSE model (`cslseModel`)

The function `cslseModel` returns an object of class `cslseModel` (or causal-SLSE model). It is a list of `slseModel` objects, one for each treatment group. The object also contains names of the variable representing the treatment indicator (Z) and what values of this indicator is associated with the treated and the nontreated. The function has the same arguments as `slseModel`, plus the argument `groupInd` that specifies which value of Z is associated with the treated and which one is associated with the nontreated. The default is `groupInd=c(treated = 1, nontreated = 0)`. It is possible to have other values or even characters as indicator, but the names must be treated and nontreated. We will allow more names in future version of the package once the multiple treatment method is implemented.

The argument `form` must include a formula linking the outcome and the treatment indicator and a formula listing the confounders, separated by the operator `|`. In the following example, we see the formula linking the outcome `re78` and the treatment indicator `treat`, and a list of confounders:

```
model1 <- cslseModel(re78 ~ treat | ~ age + re75 + ed + married, data = nsw)
```

Its print method summarizes the characteristics of the model. It is like the `slseModel` object, but the information is provided by group

```
model1
```

```
Causal Semiparametric LSE Model
*******************************

Number of  treated :  297
Number of  nontreated :  425
Selection method: Default

Confounders approximated by SLSE:
    treated: age, re75, ed
    nontreated: age, re75, ed
Confounders not approximated by SLSE:
    treated: married
    nontreated: married
```

Since `model1` is a list of `slseModel` objects, stored as `treated` and `nontreated`, we can access the knots of a specific group as follows

```
model1$treated$knots
```

```
Covariates with no knots:
    married

Covariates with knots:
age :
      16.67% 33.33% 50% 66.67% 83.33%
Knots     19     21  23     26     29

re75 :
       50% 66.67% 83.33%
Knots 1117   2657   6511

ed :
      16.67% 33.33% 50% 83.33%
Knots      9     10  11     12
```

Alternatively, we can use the print method for `slseModel` objects and print the knots of a specific gropup using the command 'print(model1$treated, which="selKnots")'. To print the list of knots for both groups, we can proceed as follows:

```r
print(model1, which="selKnots")
```

```
treated
*******
Selection method: Default

Covariates with no knots:
    married

Covariates with knots:
age :
      16.67% 33.33% 50% 66.67% 83.33%
Knots     19     21  23     26     29

re75 :
       50% 66.67% 83.33%
Knots 1117   2657   6511

ed :
      16.67% 33.33% 50% 83.33%
Knots      9     10  11     12

nontreated
**********
Selection method: Default

Covariates with no knots:
    married

Covariates with knots:
age :
      14.29% 28.57% 42.86% 57.14% 71.43% 85.71%
Knots     18     20     22     25     27     31

re75 :
      42.86% 57.14% 71.43% 85.71%
Knots  240.1   1406   2856   7667

ed :
      14.29% 42.86% 57.14% 85.71%
Knots      9     10     11     12
```

To understand how to create a `cslseModel` when the treatment indicator is not binary, consider the dataset `simDat4` that we described in Section 2.1.2. In the following we create the treatment indicator variable `treat` equal to "treat" for the treated and "notreat" for the nontreated.

```r
simDat4$treat <- ifelse(simDat4$Z==1, "treat", "notreat")
```

We can create a `cslseModel` object by specifying the value associated with each group in the argument `groupInd`:

```
model2 <- cslseModel(Y ~ treat | ~ X1 + X2 + X3 + X4, data = simDat4,
                     groupInd = c(treated = "treat", nontreated = "notreat"))
model2
```

```
Causal Semiparametric LSE Model
*******************************

Number of  treated :  246
Number of  nontreated :  254
Selection method: Default

Confounders approximated by SLSE:
    treated: X1, X3
    nontreated: X1, X3
Confounders not approximated by SLSE:
    treated: X2second, X2third, X4
    nontreated: X2second, X2third, X4
```

If some values in the treatment indicator variable differ from the values in `groupInd`, the function will return an error message.

2.2.1 Setting the knots manually

As for SLSE models, we can select the knots using the argument `knots`. The procedure is the same, but we need to specified the name of the group associated with the knots. If `knots` is set to `NULL`, the number of knots it set to 0 for all confounders and all groups. If we only want the number of knots to be 0 for one group, we need to specify the group. For example, the number of knots is set to 0 for the treated only in the following:

```
selK <- list(treated=NULL)
cslseModel(re78 ~ treat | ~ age + re75 + ed + married, data = nsw,
           knots = selK)
```

```
Causal Semiparametric LSE Model
*******************************

Number of  treated :  297
Number of  nontreated :  425
Selection method for the treated: User Based
Selection method for the nontreated: Default

Confounders approximated by SLSE:
    treated: None
    nontreated: age, re75, ed
Confounders not approximated by SLSE:
    treated: age, re75, ed, married
    nontreated: married
```

The 3 cases presented in Section 2.1.3 are the same, but it applies group by group. If a group is missing from the argument `knots`, the knots of the missing group are set automatically. For example, if we want to set the knots as in Case 1, but only for the nontreated and let `cslseModel` choose them for the treated, we would proceed as follows:

```
selK <- list(nontreated=list(NA, c(1000,5000,10000), NULL, NA))
model <- cslseModel(re78 ~ treat | ~ age + re75 + ed + married, data = nsw,
                    knots = selK)
print(model, which = "selKnots")
```

```
treated
*******
Selection method: Default

Covariates with no knots:
    married
```

```
Covariates with knots:
age :
      16.67% 33.33% 50% 66.67% 83.33%
Knots     19     21  23     26     29

re75 :
       50% 66.67% 83.33%
Knots 1117   2657   6511

ed :
      16.67% 33.33% 50% 83.33%
Knots      9     10  11     12

nontreated
**********
Selection method: User Based

Covariates with no knots:
    ed, married

Covariates with knots:
age :
      14.29% 28.57% 42.86% 57.14% 71.43% 85.71%
Knots     18     20     22     25     27     31

re75 :
        k1   k2    k3
Knots 1000 5000 10000
```

2.2.2 Estimating the model

Given the set of knots from the model object, the estimation is just a least squares method applied to the extended set of confounders defined as the local linear splines corresponding to the set of knots. The regression model is given by:

$$Y = \beta_0(1-Z) + \beta_1 Z + \psi_0^T U_0(1-Z) + \psi_1^T U_1 Z + \zeta\,,$$

where $U_0 = u_0(X)$ and $U_1 = u_1(X)$ are defined above (which depend on the knots of the model). The method that estimates the model is `estSLSE` which has three arguments, but two of them are mainly used internally by other functions. We present them in case they are needed. The arguments are:

- `model`: A model created by the function `cslseModel`.
- `selKnots`: It is a list of one or two elements, one for each group. Each element is a list of integers to select knots for the associated group. For example, suppose we have 2 confounders with 5 knots each. If we want to estimate the model with only the first knot for the first confounder and knots 3 and 5 for the second for the treated and all knots for the nontreated, we set `selKnots` to `list(treated=list(1L,c(3L, 5L)))`. By default it is missing and all the knots from the model are used.

Note that the `cslseModel` object is a list of slseModel objects. Also, we saw that the above model can be written as two regression models, one for each group. Therefore, the `estSLSE` method is simply estimating the `slseModel` objects separately. We illustrate the use of `estSLSE` with a simple model containing 2 confounders and one knot per variable.

```
model <- cslseModel(re78 ~ treat | ~ age + married, data = nsw,
                    nbasis = function(n) 2)
fit <- estSLSE(model)
fit
```

```
Causal Semiparametric LSE
*************************
Selection method: Default
```

```
treated
*******
(Intercept)      U.age_1      U.age_2    U.married
    3754.98        89.25        22.22      1435.28

nontreated
**********
(Intercept)      U.age_1      U.age_2    U.married
    4558.28        27.80       -12.51      -115.82
```

We see that the coefficients are separated by group. The coefficients for the treated correspond to $\{\hat{\beta}_1, \hat{\psi}_1\}$ and the coefficients for the nontreated correspond to $\{\hat{\beta}_0, \hat{\psi}_0\}$. Note that the `cslseFit` object returned by the method is a list of `slseFit`, which is the object returned by `estSLSE` when it is applied to `slseModel`. We can access the estimated SLSE model for each group using the $ operator. For example, the following is the estimated model for the treated:

```
fit$treated
```

```
Semiparametric LSE
******************
Selection method: Default


(Intercept)      U.age_1      U.age_2    U.married
    3754.98        89.25        22.22      1435.28
```

A more detailed presentation of the results can be obtained using the `summary` method. The only arguments of `summary` is the `cslseFit` object and `vcov.`. The latter is a function that returns the estimated covariance matrix of the LSE. By default, it is equal to the `vcovHC` function of the `sandwich` package (Zeileis (2006)) with its default `type="HC3"`. The following is an example with the previous model using and the HC0 type:

```
s <- summary(fit, type="HC0")
```

The object `s` is an object of class `summary.cslseFit`, which is a list of objects of class `summary.slseFit`, one for each group. By default, if we print `s`, we will see the two LSE summary tables, one for each group. Alternatively, we can print the result for one group using the $ operator. For example, the following is the result for the nontreated:

```
s$nontreated
```

```
Semiparametric LSE
******************
Selection method: Default

Residuals:
   Min     1Q Median     3Q    Max
 -5198  -5031  -1364   3216  34341

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  4558.28    2711.20   1.681   0.0927 .
U.age_1        27.80     135.20   0.206   0.8371
U.age_2       -12.51      54.80  -0.228   0.8194
U.married    -115.82     782.92  -0.148   0.8824
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 5738 on 421 degrees of freedom
Multiple R-squared:  0.0001584, Adjusted R-squared:  -0.006966
```

We can see that the only knot for `age` in the nontreated group is 23:

```
model$nontreated$knots$age
```

```
50%
 23
```

Therefore, the coefficient of `U.age_1` is the effect of age for the nontreated on `re78` when `age`$\leq$ 23 and

U.age_2 is the effect when age> 23.

2.2.3 The predict method

The predict method is very similar to predict.lm. We use the same arguments: object, interval, se.fit, newdata and level. The difference is that it returns the predicted outcome for the treated and nontreated separately, and the argument vcov. provides a way of changing how the least squares covariance matrix is computed. By default, it is computed using vcovHC from the sandwich package. The function returns a list of 2 elements, treated and nontreated. By default (se.fit=FALSE and interval="none"), each element contains a vector of predictions. Here is an example with the previously fitted model fit:

```
predict(fit,
        newdata = data.frame(treat = c(1,1,0,0),age = 20:23, married = 1))
```

```
$treated
[1] 6975.337 7064.591

$nontreated
[1] 5054.036 5081.834
```

If interval is set to "confidence", but se.fit remains equal to FALSE, each element contains a matrix containing the prediction, and the lower and upper confidence limits, with the confidence level determined by the argument level (set to 0.95 by default). Here is an example with the same fitted model:

```
predict(fit,
        newdata = data.frame(treat = c(1,1,0,0),age = 20:23, married = 1),
        interval = "confidence")
```

```
$treated
       fit    lower    upper
1 6975.337 4646.673 9304.001
2 7064.591 4741.653 9387.528

$nontreated
       fit    lower    upper
3 5054.036 3574.096 6533.975
4 5081.834 3544.849 6618.820
```

If se.fit is set to TRUE, each element, treated or nontreated, is a list with the elements pr, containing the predictions, and se.fit, containing the standard errors. In the following, we show the result for the same fitted model:

```
predict(fit, newdata = data.frame(treat = c(1,1,0,0),age = 20:23, married = 1),
        se.fit = TRUE)
```

```
$treated
$treated$fit
[1] 6975.337 7064.591

$treated$se.fit
       1        2
1188.116 1185.194


$nontreated
$nontreated$fit
[1] 5054.036 5081.834

$nontreated$se.fit
       3        4
755.0851 784.1907
```

2.2.4 The plot method

The predict method is called by the plot method to visually assess the predicted outcome for the treated and nontreated with respect to a given confounder, controlling for the other variables in the model. Note that this method is very close to the `plot` method for `slseFit` objects. In fact, the arguments are the same with some exceptions that we briefly explain below. Since the predicted outcome is obtained separately for the treated and nontreated the method for `cslseFit` objects simply apply the method for `slseFit` objects on each group. The following is the list of arguments:

- **x**: An object of class `cslseFit` (or 'slseFit').
- **y**: An alias for `which` for compatibility with the generic `plot` function.
- **which**: confounder to plot against the outcome variable. It could be an integer (the position of the confounder) or a character (the name of the confounder)
- **interval**: The type of confidence interval to display. The default is "none". The alternative is "confidence".
- **level**: The confidence level when `interval="confidence"`. The default is 0.95.
- **fixedCov**: Optional named lists of fixed values for some or all other confounders in each group. The values of the confounders not specified are determined by the argument `FUN`. To fix some covariates for both groups, `fixedCov` is just a named list with the names being the variable names. To fix them to different values for the treated and nontreated, `fixedCov` is a named list of 1 or 2 elements (for the treated, nontreated or both), each element being a named list of values for the covariates. See the examples below. When applied to `slseFit` objects, it is just a named list with the variables names.
- **vcov.**: An optional function to compute the estimated matrix of covariance of the least squares estimators. This argument only affects the confidence intervals. The default is `vcovHC` with `type="HC3"`.
- **add**: Should the curves be added to an existing plot? The default is `FALSE`.
- **addToLegend**: An optional character string to add to the legend next to "treated" and "nontreated". Note that a legend is added when applied to `slseFit` objects, so this argument has no effect in this case.
- **addPoints**: Should we include the scatterplot of the outcome and confounder to the graph? The default is `FALSE`.
- **FUN**: A function to determine how the other confounders are fixed. The default is `mean`. Note that the function is applied to each group separately (obviously since the plot is applied to each group separately).
- **plot**: By default, the method produces a graph. Alternatively, we can set this argument to `FALSE` and it returns one `data.frame` per group with the variable selected by `which` and the prediction.
- **graphPar**: A list of graphical parameters if not satisfied with the default ones.
- `...`: Other arguments are passed to the `vcov.` function. For example, it is possible to change the type of `vcovHC` from the default HC3 to any available methods included in the `sandwich` package (Zeileis (2006)).

The default set of graphical parameters can be obtained by running the function `causalSLSE:::.initParCSLSE()` (or `causalSLSE:::.initParSLSE()` for `slseFit` objects). The function returns a list of four elements: `treated`, `nontreated`, `common`, `legend`. The first two are lists of two elements: `points` for the list of parameters of the scatterplot produced when `addPoints=TRUE` and `lines` for the line parameters. For example, we can see that the type of points for the treated is initially set to `pch=21` and their colour to `2`:

```
causalSLSE:::.initParCSLSE()$treated$points
```

```
$pch
[1] 21

$col
[1] 2
```

The element `common` are for parameters not specific to a group like the main title or the axis labels and `legend` are the parameters that control the legend. Note, however, that the colour and line shapes for the legend are automatically determined by the lines and points parameters of the `treated` and `nontreated` elements.

The default parameters can be modified by the argument `graphPar`. This argument must follow the structure of `causalSLSE:::.initParCSLSE()` (or `causalSLSE:::.initParSLSE()` for `slseFit` objects). For example, if we want a new title, new x-axis label, new type of lines for the treated, new type of points for the nontreated and a different position for the legend, we create the following `graphPar`:

```
graphPar <- list(treated = list(lines = list(lty=5, col=4)),
                 nontreated = list(points = list(pch=25, col=3)),
                 common = list(xlab = "MyNewLab", main="My New Title"),
                 legend = list(x = "top"))
```

In the following, we illustrate some examples.

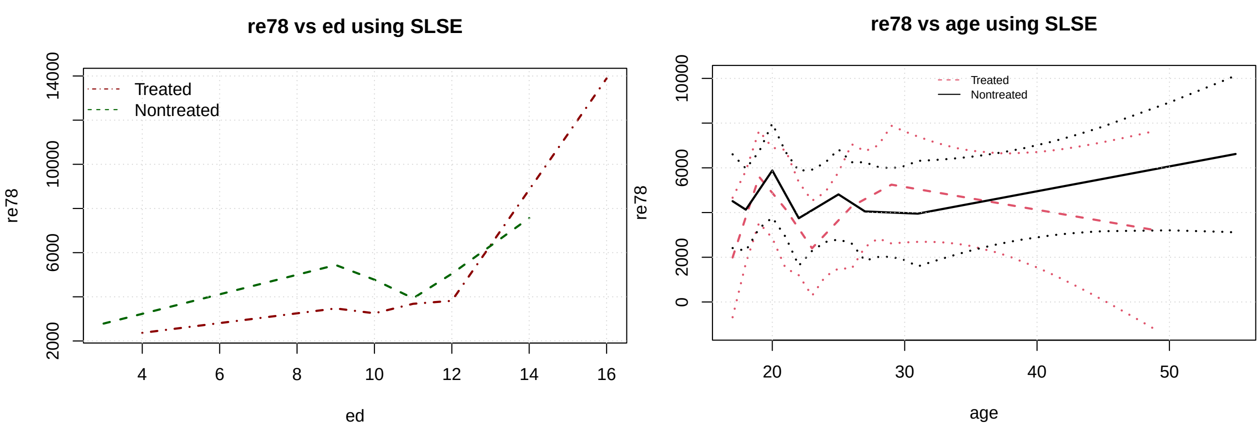
Example 1:

Consider the model:

```
model1 <- cslseModel(re78 ~ treat | ~ age + re75 + ed + married, data = nsw)
fit1 <- estSLSE(model1)
```

Suppose we want to compare the predicted income between the two treatment groups with respect to age or education, holding the other variables fixed to their group means (the default). The following are two examples with some of the default arguments modified. Note that `vcov.lm` is used in the first plot function and `vcovHC` (the default) of type HC1 in the second plot.

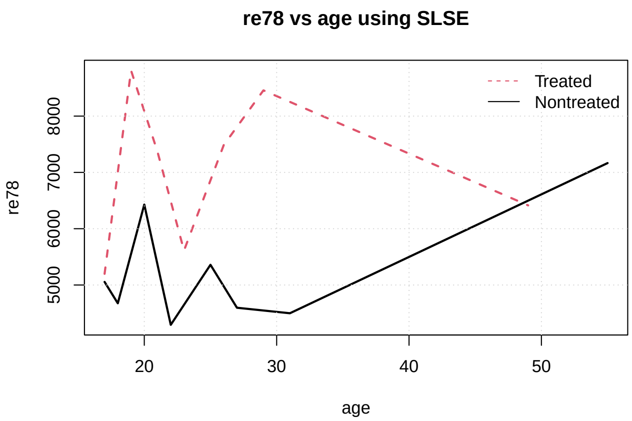
```
library(sandwich)
arg1 <- list(treated = list(lines = list(col = "darkred", lty = 4)),
             nontreated = list(lines = list(col = "darkgreen", lty = 2)),
             legend = list(x = "topleft"))
arg2 <- list(legend = list(x = "top", cex=0.7))
plot(fit1, "ed", vcov. = vcov, graphPar=arg1)
plot(fit1, "age", interval = 'confidence', level = 0.9, type = "HC1", graphPar=arg2)
```

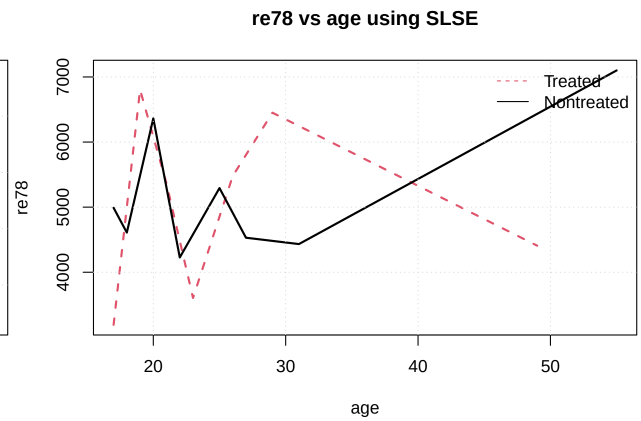


Example 2:

If we want to fix the other confounders using another function, we can change the argument `FUN`. The new function must be a function of one argument. For example, if we want to fix the other confounders to their group medians, we set `FUN` to `median` (no quotes). We proceed the same way for any function that requires only one argument. If the function requires more than one argument, we have to create a new function. For example, if we want to fix them to their 20% group empirical quantiles, we can set the argument to `function(x) quantile(x, .20)`. The following illustrates the two cases:

```
plot(fit1, "age", FUN = median)
plot(fit1, "age", FUN = function(x) quantile(x, 0.20))
```

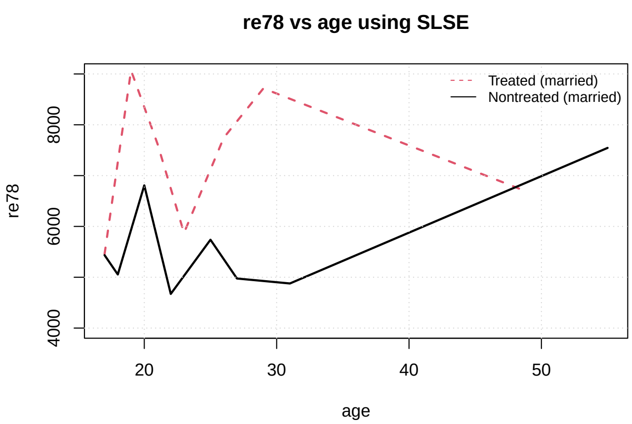


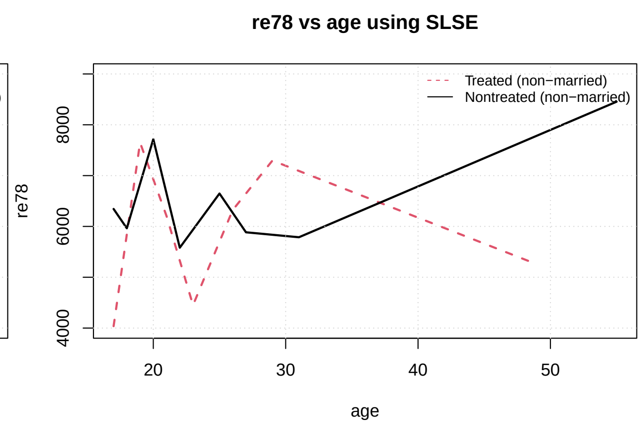


Example 3:

It is also possible to set some of the other confounders to a specific value by changing the argument `fixedCov`. To fix some variables to the same values for both groups, `fixedCov` must be a named list with the names corresponding to the variables you want to fix. You can also add a description to the legend with the argument `addToLegend`. In the following `re75` is fixed at 10,000 and we compare the predicted outcome for the married individuals (the left graph) with the non-married ones (the right graph)

```
arg2 <- list(legend = list(cex = 0.8), common=list(ylim=c(4000,9000)))
plot(fit1, "age", fixedCov = list(married = 1, re75 = 10000),
     addToLegend = "married", graphPar = arg2)
plot(fit1, "age", fixedCov = list(married = 0, re75 = 10000),
     addToLegend = "non-married", graphPar = arg2)
```

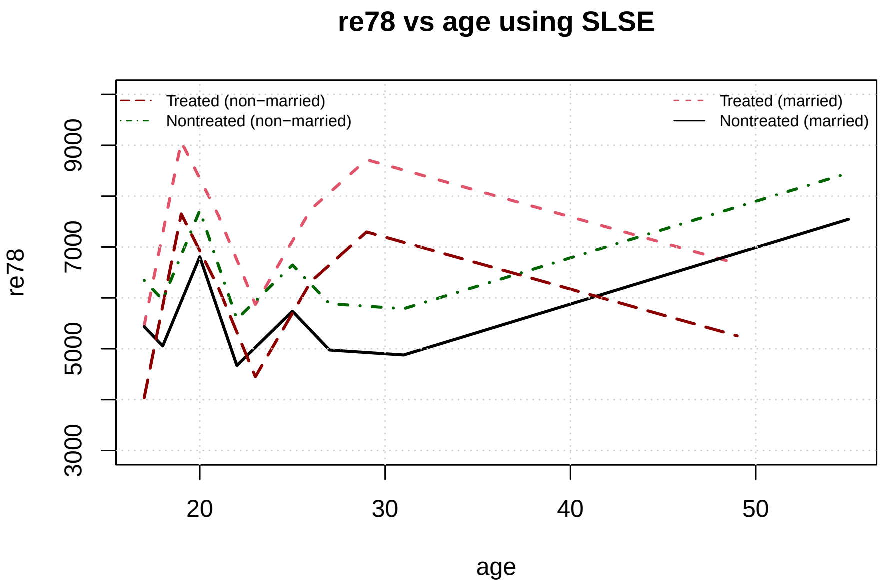




Example 4:

To better compare the two groups, it is also possible to have them plotted on the same graph by setting the argument `add.` to `TRUE`. We just need to adjust some of the arguments to better distinguish the different curves. In the following example, we set the colors and line shapes to different values and change the position of the legend for the second set of lines.

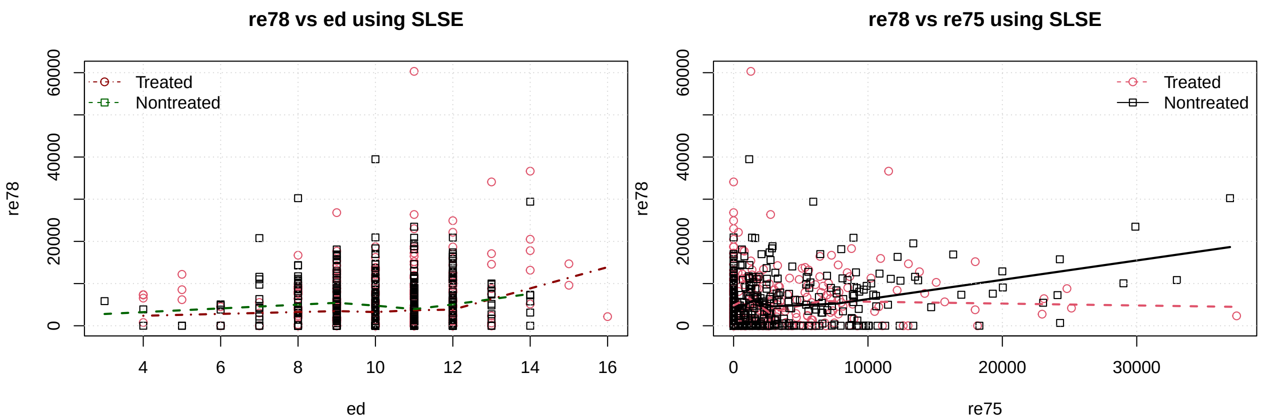
```
arg3 <- list(legend = list(cex = 0.7),
             common = list(ylim = c(3000, 10000)))
plot(fit1, "age", fixedCov = list(married = 1, re75 = 10000),
     addToLegend = "married", graphPar = arg3)
arg4 <- list(treated = list(lines = list(col = "darkred", lty = 5)),
             nontreated = list(lines = list(col = "darkgreen", lty = 4)),
             legend = list(x = "topleft", cex = 0.7))
plot(fit1, "age", fixedCov = list(married = 0, re75 = 10000),
     addToLegend = "non-married", add = TRUE, graphPar = arg4)
```



Example 5:

Finally, it is also possible to add the observed points to the graph.

```
arg5 <- list(treated = list(lines = list(col = "darkred", lty = 4)),
             nontreated = list(lines = list(col = "darkgreen", lty = 2)),
             legend = list(x = "topleft"))
plot(fit1, "ed", addPoints = TRUE, graphPar = arg5)
plot(fit1, "re75", addPoints = TRUE)
```



2.2.5 Factors, interactions and functions of confounders

The package allows some of the confounders to be factors, functions of other confounders or interactions. For example, the dataset `simDat4` includes one factor, `X2`, with levels equal to "first", "second" and "third". We can include this confounder directly to the list of confounders. For example,

```
data(simDat4)
mod <- cslseModel(Y ~ Z | ~ X1 + X2 + X4, data = simDat4)
mod
```

```
Causal Semiparametric LSE Model
*******************************

Number of  treated :  246
Number of  nontreated :  254
Selection method: Default

Confounders approximated by SLSE:
```

```
    treated: X1
    nontreated: X1
Confounders not approximated by SLSE:
    treated: X2second, X2third, X4
    nontreated: X2second, X2third, X4
```

We see that R has created 2 binary variables, one for `X2="second"` and one for `X2="third"`. These two variables are automatically included in the group of confounders not approximated by SLSE because they are binary variables like `X4`. If we want to plot `Y` against `X1`, the binary variables `X2second`, `X2third` and `X4` are fixed to their group averages which, in case of binary variables, represent the proportions of ones in each group.

For interaction terms or functions of confounders, `FUN` is applied to the functions of confounders. This is how we have to proceed to obtain the average prediction in regression models. For example, if we interact `X2` and `X4`, we obtain:

```
data(simDat4)
mod <- cslseModel(Y ~ Z | ~ X1 + X2 * X4, data = simDat4)
mod
```

```
Causal Semiparametric LSE Model
*******************************

Number of  treated :  246
Number of  nontreated :  254
Selection method: Default

Confounders approximated by SLSE:
    treated: X1
    nontreated: X1
Confounders not approximated by SLSE:
    treated: X2second, X2third, X4, X2second:X4, X2third:X4
    nontreated: X2second, X2third, X4, X2second:X4, X2third:X4
```

In this case, when `FUN=mean`, `X2second:X4` is replaced by the proportion of ones in `X2second`×`X4` for each group. It is not replaced by the proportion of ones in `X2second` times the proportion of ones in `X4`. The same applies to functions of confounders. For functions of confounders, which can be defined in the formula using a built-in function like `log` or using the identity function `I()` (e.g. we can interact `X1` and `X4` by using `I(X1*X4)`), `FUN` is applied to the function (e.g. the average `log(X)` or the average `I(X1*X4)`).

To fix a factor to a specific level, we just set its value in the `fixedCov`. In the following example, we fix `X2` to "first", so `X2second` and `X2third` are set to 0.

```
fit <- estSLSE(mod)
plot(fit, "X1", fixedCov = list(X2 = "first"))
```

Note that if a function of confounders (or an interaction) involves the confounder we want to plot the outcome against, we factorize the confounder out, apply `FUN` to the remaining of the function and add the confounder back. For example, if we interact `X1` with `X4` and `FUN=mean`, `X1:X4` is replaced by `X1` times the proportion of ones in `X4` for each group.

2.3 Optimal selection of the knots

We have implemented two methods for selecting the knots: the backward semiparametric LSE (BLSE) and the forward semiparametric LSE (FLSE) methods. For each method, we have 3 criteria: the p-value threshold (PVT), the Akaike Information criterion (AIC), and the Bayesian Information criterion (BIC). Note that the consistency of the causal effect estimators has only been proved for the last two in Giurcanu et al. (2023). The two selection methods can be summarized as follows:

> We first compute one p-value per knot using either the BLSE or FLSE method:
>
> **BLSE**:
>
> 1. We estimate the model with all knots included in the model.

2. For each knot, we test if the slopes of the basis functions adjacent to the knot are the same, and return the p-value.

FLSE:

1. We estimate the model by including a subset of the knots, one variable at the time. When we test a knot for one confounder, the number of knots is set to 0 for all other variables.
2. For each knot, we test if the adjacent slopes to the knot is the same, and return the p-value. The set of knots used for each test depends on the following:
   - Variables with 1 knot: we return the p-value of the test of equality of the slopes adjacent to the knot.
   - Variables with 2 knots: we include the two knots and return the p-values of the test of equality of the slopes adjacent to each knot.
   - Variables with p knots ($p > 2$): We test the equality of the slopes adjacent to knot i, for $i = 1, ..., p$, using the sets of knots $\{1, 2\}$, $\{1, 2, 3\}$, $\{2, 3, 4\}$, ..., $\{p-2, p-1, p\}$ and $\{p-1, p\}$ respectively.

Once we have the p-values, we proceed to step 3:

3. The knots are selected using one of the following criteria
   - **PVT**: We remove all knots with a p-value greater than a specified threshold.
   - **AIC** or **BIC**: We order the p-values in ascending order. Then, starting with a model with no knots and going from the smallest to the highest highest p-value, we add the knot associated with the smallest remaining p-value one by one, estimate the model and return the information criterion. We keep the model with the smallest information citerion.

The knot selection is done using the `selSLSE` method. The arguments are:

- **model**: An object of class `cslseModel`.
- **selType**: This is the selection method. We have the choice between "FLSE" and "BLSE" (the default).
- **selCrit**: This is the criterion used by the selection method. We have the choice between "AIC" (the default), "BIC" or "PVT".
- **pvalT**: This is a function that returns the p-value threshold. It is a function of one argument, the average number of basis functions per confounder. The default is `function(p) 1/log(p)` and it is applied to each group separately. Therefore, the threshold may be different for the treated and non-treated. It is also possible to set it to a fix threshold. For example, `function(p) 0.20` sets the threshold to 0.2. This argument affects the result only when `selCrit` is set to "PVT".
- **vcov.**: An optional function to compute the least squares standard errors. By default, the p-values are computed using the `vcovHC` method from the `sandwich` package with `type="HC3"` (Zeileis (2006)).
- **...**: This is used to pass arguments to the `vcov.` function.

The function returns a model of class `cslseModel` with the optimal selection of knots. For example, we can compare the starting knots of `model1`, with the model selected by the default arguments.

```
print(model1, which = "selKnots")
```

```
treated
*******
Selection method: Default

Covariates with no knots:
    married

Covariates with knots:
```

```
age :
      16.67% 33.33% 50% 66.67% 83.33%
Knots     19     21  23     26     29

re75 :
       50% 66.67% 83.33%
Knots 1117   2657   6511

ed :
      16.67% 33.33% 50% 83.33%
Knots      9     10  11     12

nontreated
**********
Selection method: Default

Covariates with no knots:
    married

Covariates with knots:
age :
      14.29% 28.57% 42.86% 57.14% 71.43% 85.71%
Knots     18     20     22     25     27     31

re75 :
      42.86% 57.14% 71.43% 85.71%
Knots  240.1   1406   2856   7667

ed :
      14.29% 42.86% 57.14% 85.71%
Knots      9     10     11     12
```

```r
model2 <- selSLSE(model1)
print(model2,  which = "selKnots")
```

```
treated
*******
Selection method: BLSE-JAIC

Covariates with no knots:
    married

Covariates with knots:
age :
      16.67% 50%
Knots     19  23

re75 :
       50% 66.67% 83.33%
Knots 1117   2657   6511

ed :
      83.33%
Knots     12

nontreated
**********
Selection method: BLSE-JAIC

Covariates with no knots:
    married

Covariates with knots:
age :
      14.29% 28.57% 42.86%
Knots     18     20     22

re75 :
      57.14% 85.71%
```

```
Knots   1406   7667

ed :
      14.29% 57.14%
Knots      9     11
```

For example, the BLSE-AIC method has removed all knots from `re75` for the treated and kept two knots for the nontreated. The print method indicates which method was used to select the knots. It is possible to recover the p-values of all original knots by setting the argument `which` to `Pvalue`.

```
print(model2, which="Pvalues")
```

```
No p-values are available. You must apply a selection methods first.
```

In the following example, we see BLSE as selection method and BIC as criterion. Note that the BIC selects 0 knots for all confounders.

```
model3 <- selSLSE(model1, selType = "BLSE", selCrit = "BIC")
model3
```

```
Causal Semiparametric LSE Model
*******************************

Number of  treated :  297
Number of  nontreated :  425
Selection method: BLSE-BIC

Confounders approximated by SLSE:
    treated: None
    nontreated: None
Confounders not approximated by SLSE:
    treated: age, re75, ed, married
    nontreated: age, re75, ed, married
```

Since the `selSLSE` method returns a new model, we can apply the `estSLSE` to it:

```
estSLSE(selSLSE(model1, selType = "FLSE", selCrit = "BIC"))
```

```
Causal Semiparametric LSE
**************************
Selection method: FLSE-BIC

treated
*******
(Intercept)       U.age       U.re75        U.ed    U.married
 -388.96789    41.05403      0.02676   484.91610   1417.29125

nontreated
**********
(Intercept)       U.age       U.re75        U.ed    U.married
  4825.8776    -20.1057       0.2982      2.5002   -1094.0844
```

2.4 The `causalSLSE` method for `slseFit` objects

The method `causalSLSE` estimates the causal effects from `slseFit` objects using the knots included in the estimated model. The arguments of the method are:

- **object**: An object of class `slseFit`.
- **causal**: What causality measure should the function compute? We have the choice between "ALL" (the default), "ACE", "ACT" or "ACN".
- **vcov.**: An alternative function used to compute the covariance matrix of the least squares estimates. This is the $\hat{\Sigma}_{\hat{\theta}}$ defined in the Introduction section. By default, `vcovHC` is used with `type="HC3"`. Simulations show that using `vcovHC` with `type="HC3"` produces the most accurate estimate of the variance of ACE, ACT and ACN in small and large samples.
- `...`: This is used to pass arguments to the `vcov.` function.

In the following example, we estimate the causal effect with the initial knots (without selection).

```
model1 <- cslseModel(re78 ~ treat | ~ age + re75 + ed + married, data=nsw)
fit1 <- estSLSE(model1)
causalSLSE(fit1)
```

```
Causal Effect using Semiparametric LSE
**************************************
Selection method: Default


ACE = 825.4
ACT = 843.7
ACN = 812.6
```

We see that the selection method used to select the knots are set to `Default` because the knots were first selected by the default method and no additional selection method was used. The method returns an object of class `cslse` and its `print` method only prints the causal effect estimates. For more details about the estimation, which includes standard errors and significance tests, we can use the `summary` method:

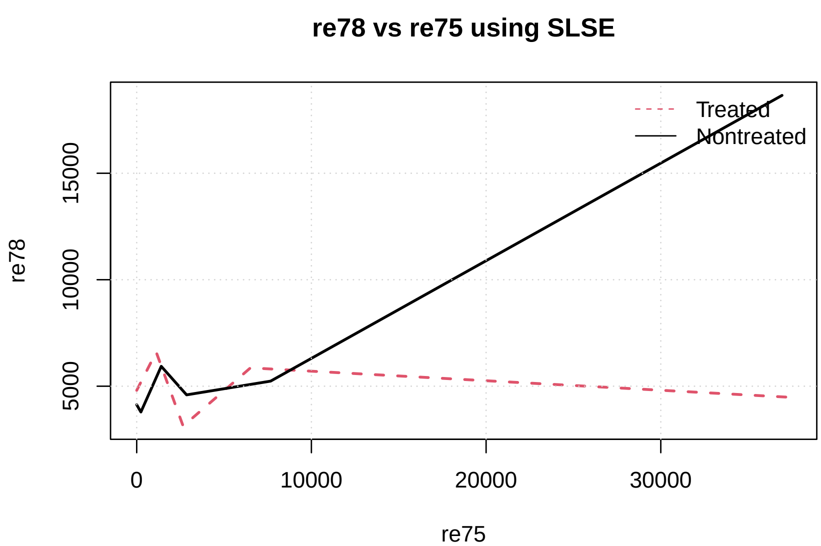
```
ce <- causalSLSE(fit1)
sce <- summary(ce)
sce
```

```
Causal Effect using Semiparametric LSE
**************************************
Selection method: Default

    Estimate Std. Error t value Pr(>|t|)
ACE    825.4      505.7   1.632    0.103
ACT    843.7      527.9   1.598    0.110
ACN    812.6      513.7   1.582    0.114
```

The `summary` method returns an object of class `summary.cslse` and the above output is produced by its `print` method. If needed, we can extract the above table using `$causal`, the least squares coefficients table using `$beta` or the list of knots using `$knots`.

The `cslse` object inherits from the class `slseFit`, so we can apply the `plot` (or the `predict`) method directly on this object as shown below:

```
plot(ce, "re75")
```



2.4.1 The extract method

The package comes with an `extract` method for objects of class `cslse`, which is a required method for creating Latex tables using the `texreg` package (Leifeld (2013)). For example, we can compare different methods in a single table. In the following example, we compare the SLSE, BLSE-AIC and FLSE-AIC:

```
library(texreg)
c1 <- causalSLSE(fit1)
fit2 <- estSLSE(selSLSE(model1, selType="BLSE"))
fit3 <- estSLSE(selSLSE(model1, selType="FLSE"))
c2 <- causalSLSE(fit2)
c3 <- causalSLSE(fit3)
texreg(list(SLSE=c1, BLSE=c2, FLSE=c3), table=FALSE, digits=4)
```

	SLSE	BLSE	FLSE
ACE	825.4222	785.8421	845.4417
	(505.7461)	(483.5174)	(496.1856)
ACT	843.7084	843.3745	855.8981
	(527.8792)	(516.7354)	(513.6188)
ACN	812.6434	745.6371	838.1346
	(513.6616)	(478.0473)	(501.8498)
Num. knots (Nontreated)	14	7	6
Num. knots (Treated)	12	6	5
Num. confounders	4	4	4
Num. obs. (Nontreated)	425	425	425
Num. obs. (Treated)	297	297	297
R^2	0.0925	0.0855	0.0839
Adj. R^2	0.0462	0.0567	0.0578

$^{***}p < 0.001$; $^{**}p < 0.01$; $^{*}p < 0.05$

Note that we refer to SLSE when no optimal selection method is used, which includes the `Default` and `User Based` methods. The option `table=FALSE`, from the `texreg` package, is used to remove the Latex floating table environment. With this option, the table appears right after the code instead of being placed somewhere else by Latex. The arguments of the `extract` methods, which control what is printed and can be modified through the `texreg` function, are:

- **include.nobs**: Include the number of observations. The default is `TRUE`.
- **include.nknots**: Include the number of knots. The default is `TRUE`.
- **include.rsquared**: Include the R^2. The default is `TRUE`.
- **include.adjrs**: Include the adjusted R^2. The default is `TRUE`.
- **which**: Which causal effects should be printed? The options are "ALL" (the default), "ACE", "ACT", "ACN", "ACE-ACT", "ACE-ACN" or "ACT-ACN".

Here is one example on how to change some arguments:

```
texreg(list(SLSE=c1, BLSE=c2, FLSE=c3), table=FALSE,
       which="ACE-ACT", include.adjrs=FALSE)
```

	SLSE	BLSE	FLSE
ACE	825.42	785.84	845.44
	(505.75)	(483.52)	(496.19)
ACT	843.71	843.37	855.90
	(527.88)	(516.74)	(513.62)
Num. knots (Nontreated)	14	7	6
Num. knots (Treated)	12	6	5
Num. confounders	4	4	4
Num. obs. (Nontreated)	425	425	425
Num. obs. (Treated)	297	297	297
R^2	0.09	0.09	0.08

$^{***}p < 0.001$; $^{**}p < 0.01$; $^{*}p < 0.05$

2.5 The `causalSLSE` method for `cslseModel` objects

When applied directly to `cslseModel` objects, the `causalSLSE` method offers the possibility to select the knots and estimate the causal effects all at once. The method also returns an object of class `cslse`. The arguments are the same as the method for `slseFit` objects, plus the necessary arguments for the knots selection. The following are the arguments not already defined for objects of class `slseFit`. The details of these arguments are presented in Section 2.3.

- **object**: An object of class `cslseModel`.
- **selType**: This is the selection method. We have the choice between "SLSE" (the default), "FLSE" and "BLSE". The SLSE method performs no selection, so all knots from the model are kept.
- **selCrit**: This is the criterion used by the selection method when `selType` is set to "FLSE" or "BLSE". The default is "AIC".
- **pvalT**: This is a function that returns the p-value threshold. We explained this argument when we presented the `selSLSE` method.

For example, we can generate the previous table as follows.

```
c1 <- causalSLSE(model1, selType="SLSE")
c2 <- causalSLSE(model1, selType="BLSE")
c3 <- causalSLSE(model1, selType="FLSE")
texreg(list(SLSE=c1, BLSE=c2, FLSE=c3), table=FALSE, digits=4)
```

	SLSE	BLSE	FLSE
ACE	825.4222	785.8421	845.4417
	(505.7461)	(483.5174)	(496.1856)
ACT	843.7084	843.3745	855.8981
	(527.8792)	(516.7354)	(513.6188)
ACN	812.6434	745.6371	838.1346
	(513.6616)	(478.0473)	(501.8498)
Num. knots (Nontreated)	14	7	6
Num. knots (Treated)	12	6	5
Num. confounders	4	4	4
Num. obs. (Nontreated)	425	425	425
Num. obs. (Treated)	297	297	297
R^2	0.0925	0.0855	0.0839
Adj. R^2	0.0462	0.0567	0.0578

$^{***}p < 0.001$; $^{**}p < 0.01$; $^{*}p < 0.05$

2.6 The `causalSLSE` method for `formula` objects

This last method, offers an alternative way of estimating the causal effects. It allows the estimation in one step without having to first create a model. The arguments are the same as for the `cslseModel` function and the `causalSLSE` method for `cslseModel` objects. It creates the model, selects the knots and estimates the causal effects in one step. For example, we can create the previous table as follows:

```
c1 <- causalSLSE(re78 ~ treat | ~ age + re75 + ed + married, data=nsw,
                 selType="SLSE")
c2 <- causalSLSE(re78 ~ treat | ~ age + re75 + ed + married, data=nsw,
                 selType="BLSE")
c3 <- causalSLSE(re78 ~ treat | ~ age + re75 + ed + married, data=nsw,
                 selType="FLSE")
texreg(list(SLSE=c1, BLSE=c2, FLSE=c3), table=FALSE, digits=4)
```

	SLSE	BLSE	FLSE
ACE	825.4222	785.8421	845.4417
	(505.7461)	(483.5174)	(496.1856)
ACT	843.7084	843.3745	855.8981
	(527.8792)	(516.7354)	(513.6188)
ACN	812.6434	745.6371	838.1346
	(513.6616)	(478.0473)	(501.8498)
Num. knots (Nontreated)	14	7	6
Num. knots (Treated)	12	6	5
Num. confounders	4	4	4
Num. obs. (Nontreated)	425	425	425
Num. obs. (Treated)	297	297	297
R^2	0.0925	0.0855	0.0839
Adj. R^2	0.0462	0.0567	0.0578

$^{***}p < 0.001$; $^{**}p < 0.01$; $^{*}p < 0.05$

Note that this method calls `cslseModel`, `selSLSE`, `estSLSE` and the method `causalSLSE` for `slseFit` objects sequentially. It is easier to simply work with this method, but manually going through all steps may be beneficial to better understand the procedure. Also, it is more convenient to work with a model when we want to compare the different selection methods, or if we want to compare estimations with different standard errors.

3 Examples

3.1 A simulated data set from Model 1

In the package, the data set `datSim1` is generated using the following data generating process with a sample size of 300.

$$\begin{aligned} Y(0) &= 1 + X + X^2 + \epsilon(0) \\ Y(1) &= 1 - 2X + \epsilon(1) \\ Z &= \text{Bernoulli}[\Lambda(1+X)] \\ Y &= Y(1)Z + Y(0)(1-Z) \end{aligned}$$

where X, $\epsilon(0)$ and $\epsilon(1)$ are independent standard normal and $\Lambda(x)$ is the CDF of the standard logistic distribution. The causal effects ACE, ACT and ACN are approximately equal to -1, -1.6903 and 0.5867 (estimated using a sample size of 10^7). We can start by building the starting model:

```
data(simDat1)
mod <- cslseModel(Y ~ Z | ~ X, data = simDat1)
```

Then we can compare three different methods:

```
c1 <- causalSLSE(mod, selType = "SLSE")
c2 <- causalSLSE(mod, selType = "BLSE", selCrit = "BIC")
c3 <- causalSLSE(mod, selType = "FLSE", selCrit = "BIC")
texreg(list(SLSE = c1, BLSE = c2, FLSE = c3), table = FALSE, digits = 4)
```

	SLSE	BLSE	FLSE
ACE	-1.4877^{***}	-1.4950^{***}	-1.4950^{***}
	(0.2723)	(0.2696)	(0.2696)
ACT	-1.9909^{***}	-1.9889^{***}	-1.9889^{***}
	(0.3143)	(0.3137)	(0.3137)
ACN	-0.1039	-0.1369	-0.1369
	(0.3322)	(0.3260)	(0.3260)
Num. knots (Nontreated)	3	2	2
Num. knots (Treated)	5	0	0
Num. confounders	1	1	1
Num. obs. (Nontreated)	80	80	80
Num. obs. (Treated)	220	220	220
R^2	0.7478	0.7431	0.7431
Adj. R^2	0.7381	0.7388	0.7388

$^{***}p < 0.001$; $^{**}p < 0.01$; $^{*}p < 0.05$

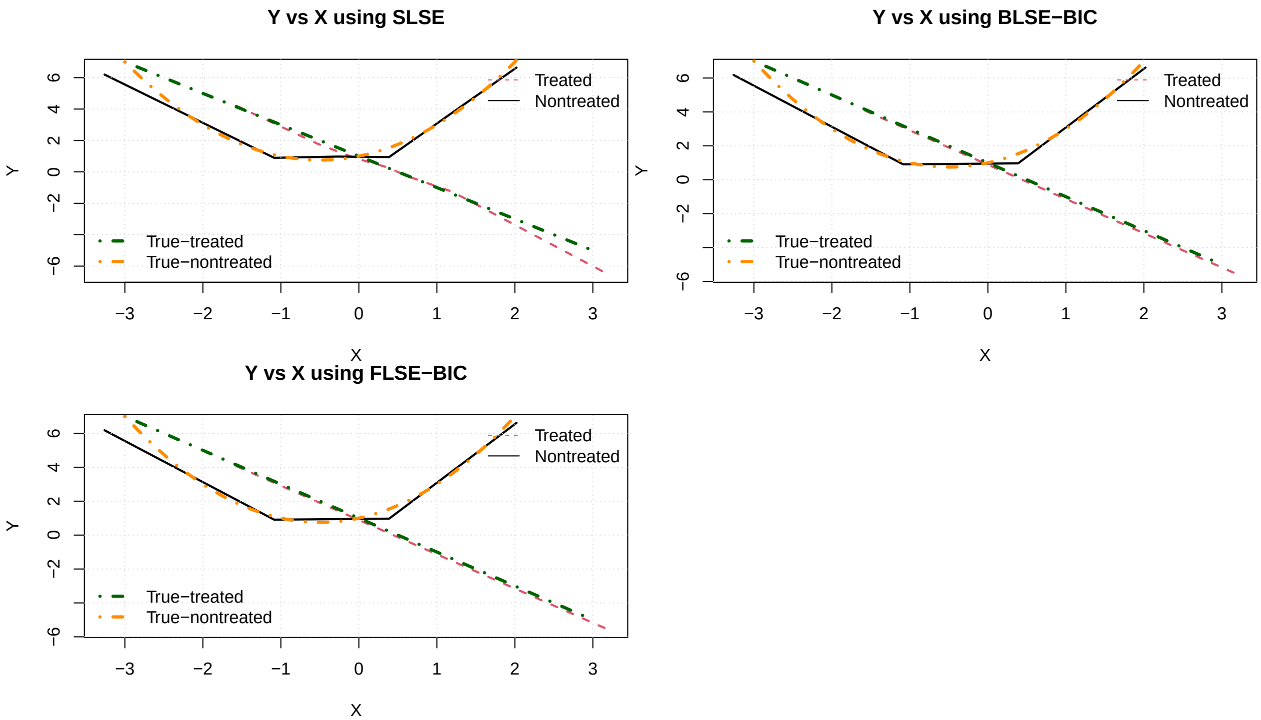
We see that both selection methods choose to assign 0 knots for the treated group, which is not surprising since the true $f_1(x)$ is linear. We can compare the different fits.

```
list(common = list(main = "Y vs X using BLSE-BIC"))
```

```
$common
$common$main
[1] "Y vs X using BLSE-BIC"
```

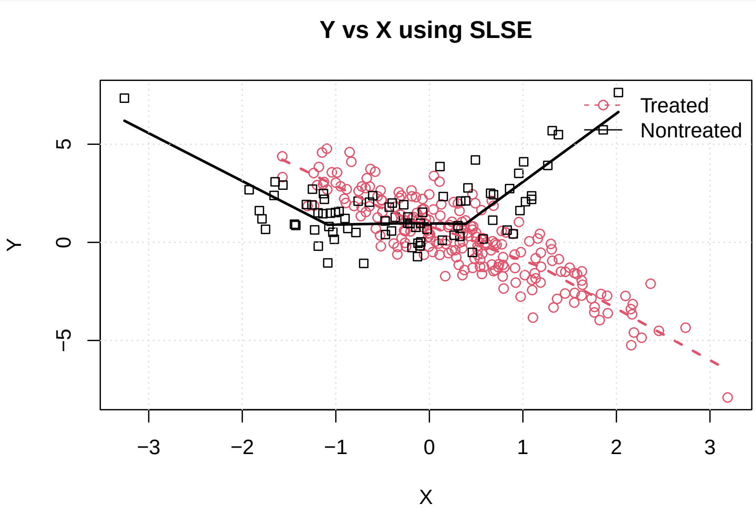
```
plot(c1, "X")
curve(1 - 2 * x, -3, 3, col = "darkgreen", lty = 4, lwd = 3, add = TRUE)
curve(1 + x + x^2, -3, 3, col = "darkorange", lty = 4, lwd = 3, add = TRUE)
legend("bottomleft", c("True-treated", "True-nontreated"),
       col=c("darkgreen", "darkorange"), lty = 4, lwd = 3, bty = 'n')
```

```r
plot(c2, "X", graphPar = list(common = list(main = "Y vs X using BLSE-BIC")))
curve(1 - 2 * x, -3, 3, col="darkgreen", lty = 4, lwd = 3, add = TRUE)
curve(1 + x + x^2, -3, 3, col = "darkorange", lty = 4, lwd = 3, add = TRUE)
legend("bottomleft", c("True-treated", "True-nontreated"),
       col = c("darkgreen", "darkorange"), lty = 4, lwd = 3, bty = 'n')
plot(c3, "X", graphPar = list(common = list(main = "Y vs X using FLSE-BIC")))
curve(1 - 2 * x, -3, 3, col="darkgreen", lty = 4, lwd = 3, add = TRUE)
curve(1 + x + x^2, -3, 3, col = "darkorange", lty = 4, lwd = 3, add = TRUE)
legend("bottomleft", c("True-treated", "True-nontreated"),
       col = c("darkgreen", "darkorange"), lty = 4, lwd = 3, bty = 'n')
```



We see that the piecewise polynomials are very close to the true $f_1(x)$ and $f_2(x)$ for SLSE and BLSE. However, the FLSE based on BIC does not do a good job. We can see from the folllowing graph how the lines are fit through the observations by group.

```r
plot(c1, "X", addPoints=TRUE)
```



3.2 A simulated data set from Model 2

The dataset `datSim2` is a change point regression model (with unknown location of change points) defined as follows:

$$\begin{aligned} Y(0) &= (1+X)I(X \leq -1) + (-1-X)I(X > -1) + \epsilon(0) \\ Y(1) &= (1-2X)I(X \leq 0) + (1+2X)I(X > 0) + \epsilon(1) \\ Z &= \text{Bernoulli}[\Lambda(1+X)] \\ Y &= Y(1)Z + Y(0)(1-Z) \end{aligned}$$

where $I(A)$ is the indicator function equal to 1 if A is true, and X, $\epsilon(0)$ and $\epsilon(1)$ are independent standard normal. The causal effects ACE, ACT and ACN are approximately equal to 3.763, 3.858 and 3.545 (estimated with a sample size of 10^7). We can compare the SLSE, BLSE-AIC and BLSE-BIC.

```
data(simDat2)
mod <- cslseModel(Y~Z | ~X, data=simDat2)
```

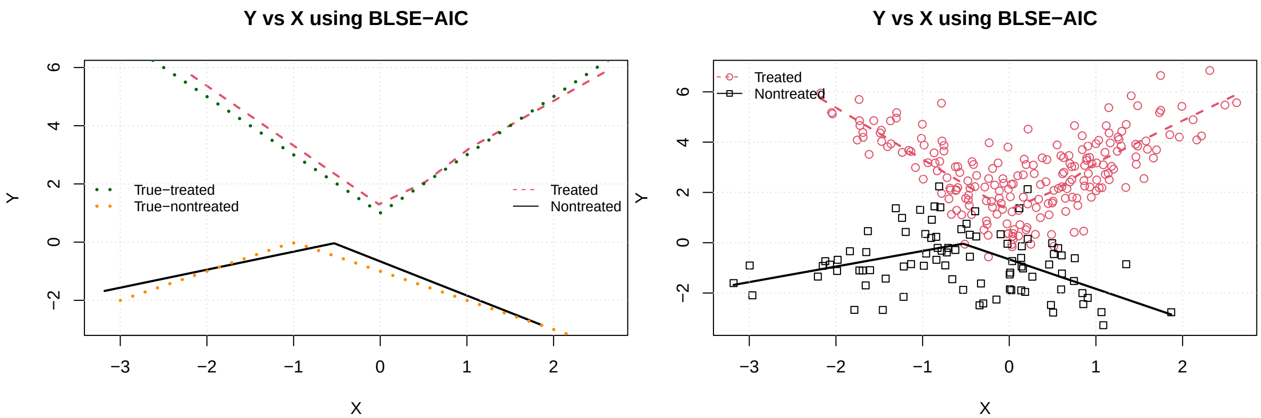
```
c1 <- causalSLSE(mod, selType = "SLSE")
c2 <- causalSLSE(mod, selType = "BLSE", selCrit = "BIC")
c3 <- causalSLSE(mod, selType = "BLSE", selCrit = "AIC")
texreg(list(SLSE = c1, BLSE.BIC = c2, BLSE.AIC = c3), table = FALSE, digits = 4)
```

	SLSE	BLSE.BIC	BLSE.AIC
ACE	3.9373^{***}	3.9268^{***}	3.9268^{***}
	(0.1791)	(0.1765)	(0.1765)
ACT	3.9679^{***}	3.9566^{***}	3.9566^{***}
	(0.2039)	(0.1992)	(0.1992)
ACN	3.8647^{***}	3.8560^{***}	3.8560^{***}
	(0.2310)	(0.2263)	(0.2263)
Num. knots (Nontreated)	3	1	1
Num. knots (Treated)	4	3	3
Num. confounders	1	1	1
Num. obs. (Nontreated)	89	89	89
Num. obs. (Treated)	211	211	211
R^2	0.7833	0.7827	0.7827
Adj. R^2	0.7758	0.7775	0.7775

$^{***}p < 0.001$; $^{**}p < 0.01$; $^{*}p < 0.05$

The following shows the fit of BLSE-AIC with the true $f_1(x)$ and $f_0(x)$, and the observations.

```
arg <-  list(common = list(main = "Y vs X using BLSE-AIC"),
             legend = list(x = "right", cex = 0.8))
plot(c2, "X", graphPar = arg)
curve((1 -2 * x) * (x <= 0) + (1 + 2 * x) * (x > 0), -3, 3,
      col = "darkgreen", lty = 3, lwd = 3, add = TRUE)
curve((1 + x) * (x <= -1) + (-1 - x) * (x > -1),
      -3, 3, col = "darkorange", lty = 3, lwd = 3, add = TRUE)
legend("left", c("True-treated", "True-nontreated"),
       col = c("darkgreen", "darkorange"), lty = 3, lwd = 3, bty = 'n', cex = .8)
arg$legend$x <- "topleft"
plot(c2, "X", addPoints = TRUE, graphPar = arg)
```



3.3 A simulated data set from Model 3

The data set `datSim3` is generated from model with multiple confounders defined as follows:

$$
\begin{aligned}
Y(0) &= [1 + X_1 + X_1^2] + [(1 + X_2)I(X_2 \leq -1) + (-1 - X_2)I(X_2 > -1)] + \epsilon(0) \\
Y(1) &= [1 - 2X_1] + [(1 - 2X_2)I(X_2 \leq 0) + (1 + 2X_2)I(X_2 > 0)] + \epsilon(1) \\
Z &= \text{Bernoulli}[\Lambda(1 + X_1 + X_2)] \\
Y &= Y(1)Z + Y(0)(1 - Z),
\end{aligned}
$$

where X_1, X_2, $\epsilon(0)$ and $\epsilon(1)$ are independent standard normal. The causal effects ACE, ACT and ACN are approximately equal to 2.762, 2.204 and 3.922 (estimated with a sample size of 10^7). We can compare the SLSE, FLSE with AIC and FLSE with BIC.

```
data(simDat3)
mod <- cslseModel(Y ~ Z | ~ X1 + X2, data = simDat3)
```

```
c1 <- causalSLSE(mod, selType = "SLSE")
c2 <- causalSLSE(mod, selType = "FLSE", selCrit = "BIC")
c3 <- causalSLSE(mod, selType = "FLSE", selCrit = "AIC")
texreg(list(SLSE = c1, FLSE.BIC = c2, FLSE.AIC = c3), table = FALSE, digits = 4)
```

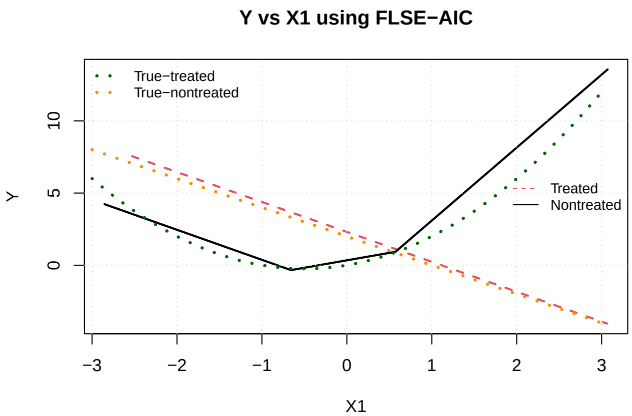
	SLSE	FLSE.BIC	FLSE.AIC
ACE	2.4685***	2.4810***	2.4685***
	(0.2729)	(0.2671)	(0.2727)
ACT	2.0634***	2.0554***	2.0634***
	(0.3443)	(0.3354)	(0.3442)
ACN	3.2319***	3.2832***	3.2319***
	(0.3475)	(0.3454)	(0.3465)
Num. knots (Nontreated)	8	4	8
Num. knots (Treated)	8	2	6
Num. confounders	2	2	2
Num. obs. (Nontreated)	104	104	104
Num. obs. (Treated)	196	196	196
R^2	0.8743	0.8662	0.8743
Adj. R^2	0.8648	0.8611	0.8658

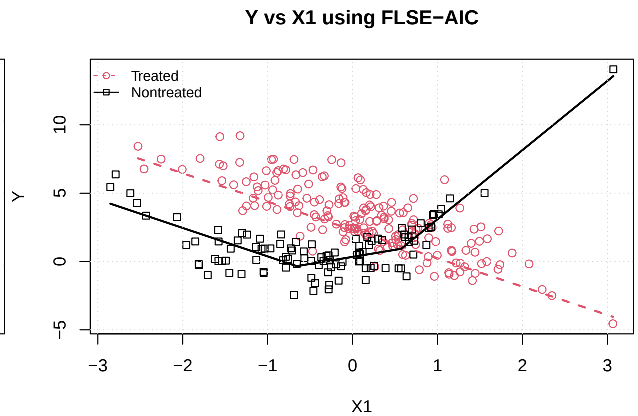
$^{***}p < 0.001$; $^{**}p < 0.01$; $^{*}p < 0.05$

To illustrate the method, since we have two confounders, we need to plot the outcome against one confounder holding the other fixed. The default is to fix it to its sample mean. For the true curve, we fix it to its population mean, which is 0. We first look at the outcome against X_1. By fixing X_2 to 0, the true curve is $X_1 + X_1^2$ for the untreated and $2 - 2X_1$ for the treated. The following graphs show how the FLSE-BIC method fits the curves.

```
arg <-  list(common = list(main = "Y vs X1 using FLSE-AIC"),
             legend = list(x = "right", cex = 0.8))
plot(c2, "X1", graphPar = arg)
```

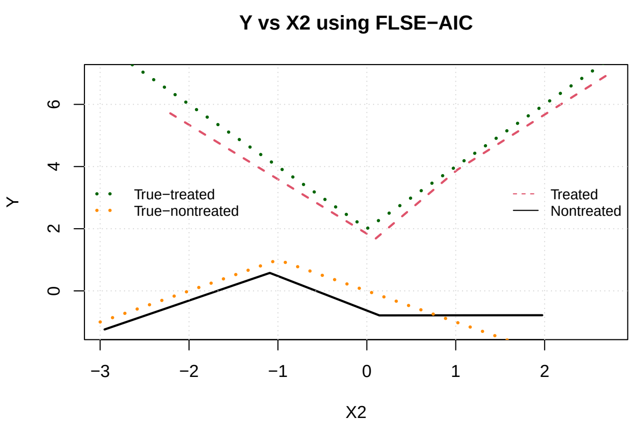
```
curve(x + x^2, -3, 3, col = "darkgreen", lty = 3, lwd = 3, add = TRUE)
curve(2 - 2 * x, -3, 3, col = "darkorange", lty = 3, lwd = 3, add = TRUE)
legend("topleft", c("True-treated", "True-nontreated"),
       col = c("darkgreen", "darkorange"), lty = 3, lwd = 3, bty = 'n', cex = .8)
arg$legend$x <- "topleft"
plot(c2, "X1", addPoints = TRUE, graphPar = arg)
```

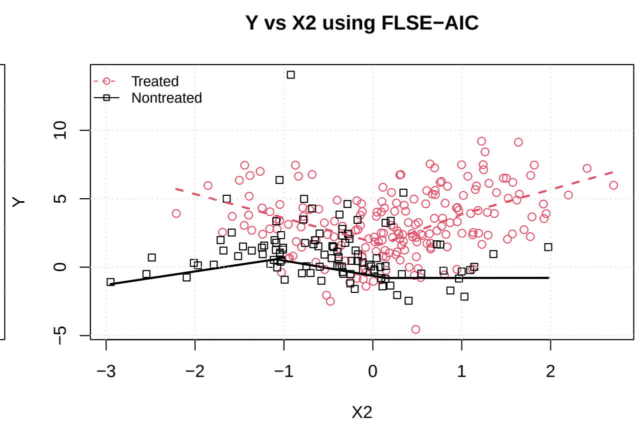




If we fix X_1 to 0, the true curve is $1 + [(1 + X_2)I(X_2 \leq -1) + (-1 - X_2)I(X_2 > -1)]$ for the nontreated and $1 + [(1 - 2X_2)I(X_2 \leq 0) + (1 + 2X_2)I(X_2 > 0)]$ for the treated. The following graphs illustrates how these curves are approximated by FLSE-AIC.

```
arg <-  list(common = list(main = "Y vs X2 using FLSE-AIC"),
             legend = list(x = "right", cex = 0.8))
plot(c2, "X2", graphPar = arg)
curve(1 + (1 - 2 * x) * (x <= 0) + (1 + 2 * x) * (x > 0), -3, 3,
      col = "darkgreen", lty = 3, lwd = 3, add = TRUE)
curve(1 + (1 + x) * (x <= -1) + (-1 - x) * (x > -1),
      -3, 3, col = "darkorange", lty = 3, lwd = 3, add = TRUE)
legend("left", c("True-treated", "True-nontreated"),
       col = c("darkgreen", "darkorange"), lty = 3, lwd = 3, bty = 'n', cex = .8)
arg$legend$x <- "topleft"
plot(c2, "X2", addPoints = TRUE, graphPar = arg)
```





3.4 A simulated data set with interactions

The data set `datSim5` is generated using the following data generating process with a sample size of 300.

$$
\begin{aligned}
Y(0) &= [1 + X_1 + X_1^2] + [(1 + X_2)I(X_2 \leq -1) + (-1 - X_2)I(X_2 > -1)] \\
&\quad +[1 + X_1X_2 + (X_1X_2)^2] + \epsilon(0) \\
Y(1) &= [1 - 2X_1] + [(1 - 2X_2)I(X_2 \leq 0) + (1 + 2X_2)I(X_2 > 0)] \\
&\quad +[1 - 2X_1X_2] + \epsilon(1) \\
Z &= \text{Bernoulli}[\Lambda(1 + X_1 + X_2 + X_1X_2)] \\
Y &= Y(1)Z + Y(0)(1 - Z)\,,
\end{aligned}
$$

whereX_1, X_2, e and u are independent standard normal. The causal effects ACE, ACT and ACN are approximately equal to 1.763, 0.998 and 3.194 (estimated with a sample size of 10^7). We can compare the SLSE, FLSE-AIC and FLSE-BIC.

```
data(simDat5)
mod <- cslseModel(Y ~ Z | ~ X1 * X2, data = simDat5)
```

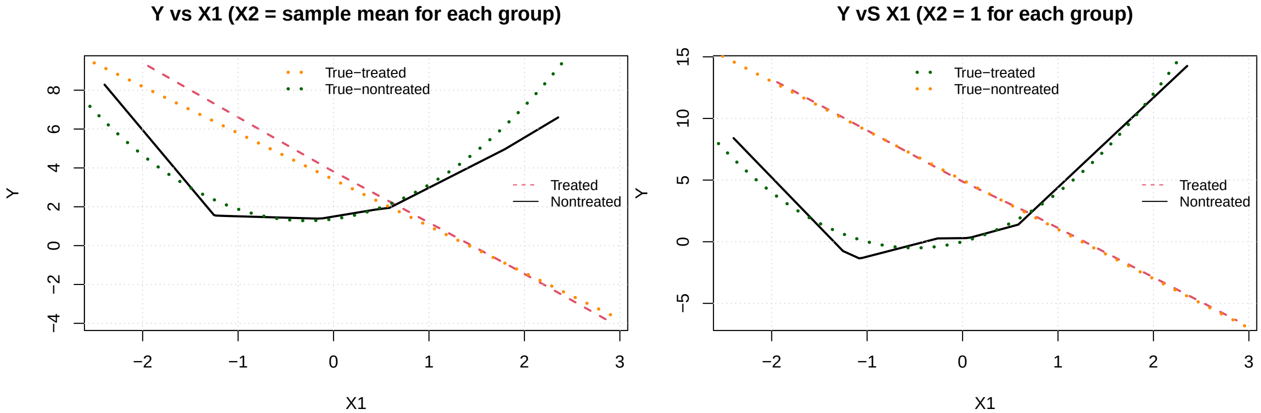
```
c1 <- causalSLSE(mod, selType = "SLSE")
c2 <- causalSLSE(mod, selType = "FLSE", selCrit = "BIC")
c3 <- causalSLSE(mod, selType = "FLSE", selCrit = "AIC")
texreg(list(SLSE = c1, FLSE.BIC = c2, FLSE.AIC = c3), table = FALSE, digits = 4)
```

	SLSE	FLSE.BIC	FLSE.AIC
ACE	1.8110***	1.7142***	1.7951***
	(0.3799)	(0.3815)	(0.3812)
ACT	1.2727*	1.1083*	1.2321*
	(0.4983)	(0.4956)	(0.4950)
ACN	2.8255***	2.8560***	2.8560***
	(0.4496)	(0.4478)	(0.4479)
Num. knots (Nontreated)	12	7	9
Num. knots (Treated)	12	6	6
Num. confounders	3	3	3
Num. obs. (Nontreated)	104	104	104
Num. obs. (Treated)	196	196	196
R^2	0.8963	0.8898	0.8928
Adj. R^2	0.8843	0.8819	0.8843

$^{***}p < 0.001$; $^{**}p < 0.01$; $^{*}p < 0.05$

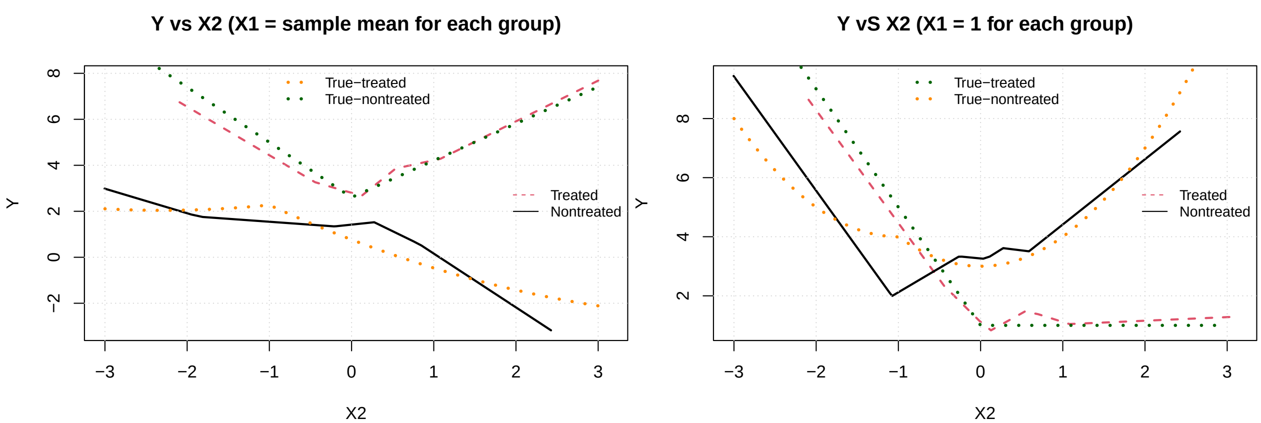
In the case of multiple confounders with interactions, the shape of the fitted outcome with respect to one confounder depends on the value of the other confounders. Without interaction, changing the value of the other confounders only shifts the fitted line without changing its shape. The following graphs compare the estimated relationship between Y and X_1 for X_2 equal to the group means (left graph) and 1 (right graph). Using a sample of 10^7, we obtain that $\mathrm{E}(X_2|Z = 1)$ and $\mathrm{E}(X_2|Z = 0)$ are approximately equal to 0.1982 and -0,3698, respectively. Therefore, the true curves are $(1.3698 + 0.6302x + 1.1368x^2)$ for the nontreated and $(3.3964 - 2.3964x)$ for the treated. If $X_2 = 1$, the true curves become $2x + 2x^2$ for the treated and $(5 - 4x)$ for the nontreated.

```
x20 <- mean(subset(simDat5, Z == 0)$X2)
x21 <- mean(subset(simDat5, Z == 1)$X2)
arg <-  list(common = list(main = "Y vs X1 (X2 = sample mean for each group)"),
             legend = list(x = "right", cex = 0.8))
plot(c2, "X1", fixedCov = list(nontreated = list(X2 = x20), treated = list(X2 = x21)),
     graphPar = arg)
curve(1.3698 + 0.6302 * x + 1.1368 * x^2, -3, 3,
      col = "darkgreen", lty = 3, lwd = 3, add = TRUE)
curve(3.3964 - 2.3964 * x, -3, 3, col = "darkorange", lty = 3, lwd = 3, add = TRUE)
legend("top", c("True-treated", "True-nontreated"),
       col=c("darkorange", "darkgreen"), lty = 3, lwd = 3, bty = 'n', cex = .8)
arg <-  list(common = list(main = "Y vS X1 (X2 = 1 for each group)"),
             legend = list(x = "right", cex = 0.8))
plot(c2, "X1", fixedCov = list(X2 = 1), graphPar = arg)
curve(2 * x + 2 * x^2, -3, 3, col = "darkgreen", lty = 3, lwd = 3, add = TRUE)
curve(5 - 4 * x, -3, 3, col = "darkorange", lty = 3, lwd = 3, add = TRUE)
legend("top", c("True-treated", "True-nontreated"),
       col = c("darkgreen", "darkorange"), lty = 3, lwd = 3, bty = 'n', cex = .8)
```



The following graphs illustrate the relationship between Y and X_2 for a given X_1. When X_1 is equal its population group means (they are equal to the population means of X_2), the true curves are $[1.6036 - 0.3964x)(x \leq 0) + (1+2x)(x > 0)]$ for the treated and $[(1.767 - 0.3698x + 0.1368x^2) + (1+x)(x \leq -1) + (-1 - x)(x > -1)]$ for the nontreated. If $X_1 = 1$, the true curves become $[-2x + (1-2x)(x \leq 0) + (1+2x)(x > 0)]$ for the treated and $[(4 + x + x^2) + (1+x)(x \leq -1) + (-1-x)(x > -1)]$ for the nontreated.

```
x10 <- mean(subset(simDat5, Z == 0)$X1)
x11 <- mean(subset(simDat5, Z == 1)$X1)
arg <-  list(common = list(main = "Y vs X2 (X1 = sample mean for each group)"),
             legend = list(x = "right", cex = 0.8))
plot(c2, "X2", fixedCov = list(nontreated = list(X1 = x10), treated = list(X1 = x11)),
     graphPar = arg)
curve(1.603900 - .3964 * x + (1 - 2 * x) * (x <= 0) + (1 + 2 * x) * (x > 0), -3, 3,
      col = "darkgreen", lty = 3, lwd = 3, add = TRUE)
curve(1.767 - 0.3698 * x + 0.1368 * x^2 + (1 + x) * (x <= -1) + (-1 - x) * (x > -1),
      -3, 3, col = "darkorange", lty = 3, lwd = 3, add = TRUE)
legend("top", c("True-treated", "True-nontreated"),
       col = c("darkorange", "darkgreen"), lty = 3, lwd = 3, bty = 'n', cex = .8)
arg$common$main <- "Y vS X2 (X1 = 1 for each group)"
plot(c2, "X2", fixedCov = list(X1 = 1), graphPar = arg)
curve(-2 * x + (1 - 2 * x) * (x <= 0) + (1 + 2 * x) * (x > 0), -3, 3,
      col = "darkgreen", lty = 3, lwd = 3, add = TRUE)
curve(4 + (1 + x) * (x <= -1) + (-1 - x) * (x > -1) + x + x^2,
      -3, 3, col = "darkorange", lty = 3, lwd = 3, add = TRUE)
legend("top", c("True-treated", "True-nontreated"),
       col = c("darkgreen", "darkorange"), lty = 3, lwd = 3, bty = 'n', cex = .8)
```



4 Summary of methods and objects

The following is a list of all objects from the package. For each object, we explain how it is constructed and give a list of the registered methods. For mode details about the arguments of the different methods, see the help files. Note, however, that no help files exist for non-exported methods and the latter must be called using `causalSLSE:::` before the method names.

- **slseKnots**: The object is created by the function `slseKnots` and the only exported registered method is `print`. The method `update`, which is used by `estSLSE` to select knots before estimating the model is not exported.
- **cslseKnots**: The object is created by the function `cslseKnots` and it is a list of `slseKnots` objects. As for `slseKnots` object, the only exported registered method is `print` and there is an non-exported method `update`.
- **cslseModel**: The object is created by the function `cslseModel` and the exported registered methods are `print`, `estSLSE` (estimate the regression model), `selSLSE` (optimal selection of knots) and `causalSLSE` (to compute the causal effects). There are two non-exported methods: `pvalSLSE` (used to compute the p-values) and `model.matrix` (to extract the matrix of confounders).
- **slseFit**: The object is created by the method `estSLSE` and the exported registered methods are `print`, `causalSLSE` (to compute the causal effects), `predict` (to predict the outcome), `plot` (to plot the outcome as a function of one confounder) and `summary` (to give more details about the least squares estimation)
- **summary.slseFit**: The object is created by the `summary` method for `slseFit` objects. The only exported registered method is `print`.
- **cslse**: The object is created by any `causalSLSE` method. It inherits from `slseFit` object. The methods that are common through this inheritance are `plot` and `predict`. The exported registered methods specific to `cslse` objects are `print`, `summary` (to give more details about the causal effect estimation) and `extract` (a method needed for `texreg`)

Note that the method `causalSLSE` is also registered for objects of class `formula`.

References

Giurcanu, M., M. Capanu, P. Chaussé, and G. Luta. 2023. “Efficient Semiparametric Inference for Causal Effects.” *Working Paper*.

Lalonde, R. 1986. “Evaluating the Econometric Evaluations of Training Programs.” *American Economic Review* 76: 604–20.

Leifeld, Philip. 2013. “texreg: Conversion of Statistical Model Output in R to LaTeX and HTML Tables.” *Journal of Statistical Software* 55 (8): 1–24. http://dx.doi.org/10.18637/jss.v055.i08.

Zeileis, Achim. 2006. “Object-Oriented Computation of Sandwich Estimators.” *Journal of Statistical Software* 16 (9): 1–16. https://doi.org/10.18637/jss.v016.i09.