

# Package ‘PCL’

April 10, 2021

**Type** Package

**Title** Proximal Causal Learning

**Version** 1.0

**Date** 2021-04-04

**Maintainer** Andrew Ying <aying9339@gmail.com>

**Description** We fit causal models using proxies. We implement two stage proximal least squares estimator. E.J. Tchetgen Tchetgen, A. Ying, Y. Cui, X. Shi, and W. Miao. (2020). An Introduction to Proximal Causal Learning. arXiv e-prints, arXiv-2009 <arXiv:2009.10982>.

**License** GPL (>= 2)

**Depends** R (>= 4.0)

**RoxygenNote** 7.1.1

**Encoding** UTF-8

**NeedsCompilation** no

**Author** Andrew Ying [aut, cre],  
Yifan Cui [ctb],  
AmirEmad Ghassami [ctb]

**Repository** CRAN

**Date/Publication** 2021-04-10 07:50:10 UTC

## R topics documented:

pcl . . . . .	2
pclfit . . . . .	2

<b>Index</b>	<b>4</b>
--------------	----------

---

pcl *Create a Proximal Causal Learning Object*

---

**Description**

Create a proximal causal learning object, usually used as a variable in a model function. Argument matching

**Usage**

```
pcl(outcome, trt, trt_pxy, out_pxy, covariates)
```

**Arguments**

outcome	the outcome variable
trt	the binary treatment variable
trt_pxy	the treatment-inducing proxies
out_pxy	the outcome-inducing proxies
covariates	the observed confounders

**Value**

pcl returns an object of class "pcl", which wraps the treatment, outcome, treatment inducing confounding proxies, outcome inducing confounding proxies and other covariates

**Examples**

```
n <- 100
outcome <- rnorm(n, 0, 1)
trt <- rbinom(n, 1, 0.5)
trt_pxy <- rnorm(n, 0, 1)
out_pxy <- rnorm(n, 0, 1)
covariates <- rnorm(n, 0, 1)
pcl_object <- pcl(outcome, trt, trt_pxy, out_pxy, covariates)
```

---

pclfit *Fit a Proximal Causal Learning Model*

---

**Description**

Fit a proximal causal learning model

**Usage**

```
pclfit(pcl_object, method = "POR")
```

**Arguments**

<code>pcl_object</code>	an <code>pcl</code> object
<code>method</code>	method used to fit

**Value**

returns the average causal effect

**Examples**

```
n <- 100
outcome <- rnorm(n, 0, 1)
trt <- rbinom(n, 1, 0.5)
trt_pxy <- matrix(rnorm(n, 0, 1), ncol = 1)
out_pxy <- matrix(rnorm(n, 0, 1), ncol = 1)
covariates <- matrix(rnorm(n, 0, 1), ncol = 1)
pcl_object <- pcl(outcome, trt, trt_pxy, out_pxy, covariates)
fit <- pclfit(pcl_object)
```

# Index

pcl, 2  
pclfit, 2