

# Package: Rpcop (via r-universe)

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**Type** Package

**Title** Principal Curves of Oriented Points

**Version** 1.3

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**Description** Principal curves generalize the notion of a first principal component to the case in which it is a nonlinear smooth curve. This package provides a function `pcop(X)` to compute principal curves with the algorithm defined in Delicado (2001) <[doi:10.1006/jmva.2000.1917](https://doi.org/10.1006/jmva.2000.1917)> from a data matrix `X`.

**License** GPL (>= 2)

**Depends** R (>= 3.5.0)

**Imports** Rcpp (>= 1.0.7), princurve

**Suggests** knitr, rmarkdown, testthat (>= 3.0.0)

**LinkingTo** Rcpp

**VignetteBuilder** knitr

**Encoding** UTF-8

**Roxygen** list(markdown = TRUE, roclets = c("` namespace", "` rd", "` srr::srr\_stats\_roclet"))

**URL** <https://github.com/kmfrick/Rpcop>

**BugReports** <https://github.com/kmfrick/Rpcop/issues>

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**Repository** <https://kmfrick.r-universe.dev>

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## Contents

pcop . . . . .	2
pcop-methods . . . . .	3
<b>Index</b>	<b>5</b>

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pcop *Principal Curve of Oriented Points*

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### Description

Computes a principal curve as defined in Delicado and Huerta (2003) [doi:10.1007/s001800300145](https://doi.org/10.1007/s001800300145).

### Usage

```
pcop(x, Ch = 1.5, Cd = 0.3, plot.true = FALSE, ...)
```

### Arguments

x	A finite numeric matrix or data frame of $n$ points in dimension $p$ . Missing and infinite values are rejected.
Ch	The smoothing parameter $h$ is $C_H$ times the value given by the normal reference rule. Default value 1.5. Constraints $0.5 \leq C_H \leq 1.5$ .
Cd	The distance between two consecutive principal oriented points in a PCOP is about $C_D$ times the value of the smoothing parameter $h$ . Default value 0.3. Constraints $0.25 \leq C_D \leq 0.5$ .
plot.true	If TRUE, produce a two-dimensional plot of the resulting curve. Plotting requires at least two columns in x.
...	Additional parameters passed to lines.

### Value

A list with two elements:

**pcop.f1** Data frame storing the principal curve of oriented points in the original format, with columns param, dens, span, orth.var, pop1, pop2, ..., pr.dir1, pr.dir2, ...

**pcop.f2** List conforming to the format used in **princurve**; see that package for details.

**parameters** List of algorithm parameters used for the fit.

**input\_names** Input row and column names, if present. Other input attributes are not used by the algorithm and are not propagated.

**call** Matched function call.

## Examples

```
n <- 500
p <- 3
x <- matrix(rnorm(n * p), ncol = p) %*% diag(p:1)
pcop(x, plot.true = FALSE)

x <- runif(100, -1, 1)
x <- cbind(x, x ^ 2 + rnorm(100, sd = 0.1))
pcop(x, plot.true = FALSE)
if (interactive()) {
  pcop(x, plot.true = TRUE, lwd = 4, col = 2)
}
```

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pcop-methods

*Methods for pcp objects*

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## Description

Print, summary, and plot methods for objects returned by `pcop()`.

## Usage

```
## S3 method for class 'pcop'
print(x, ...)
## S3 method for class 'pcop'
summary(object, ...)
## S3 method for class 'summary.pcop'
print(x, ...)
## S3 method for class 'pcop'
plot(x, ...)
```

## Arguments

<code>x</code>	A <code>pcop</code> or <code>summary.pcop</code> object.
<code>object</code>	A <code>pcop</code> object.
<code>...</code>	Additional arguments passed to methods. For <code>plot.pcop()</code> , arguments are passed to <code>graphics::plot</code> .

## Value

`print.pcop()`, `print.summary.pcop()`, and `plot.pcop()` return their input invisibly. `summary.pcop()` returns a compact summary object.

**Examples**

```
set.seed(1)
x <- runif(100, -1, 1)
x <- cbind(x, x ^ 2 + rnorm(100, sd = 0.1))
fit <- pcop(x, plot.true = FALSE)

print(fit)
summary(fit)
if (interactive()) {
  plot(fit)
}
```

# Index

`pcop`, [2](#)  
`pcop-methods`, [3](#)  
`plot.pcop (pcop-methods)`, [3](#)  
`print.pcop (pcop-methods)`, [3](#)  
`print.summary.pcop (pcop-methods)`, [3](#)  
`summary.pcop (pcop-methods)`, [3](#)