

# Package ‘rd2d’

May 23, 2026

**Type** Package

**Title** Estimation and Inference for Boundary Discontinuity Designs

**Version** 0.2.0

**URL** <https://rdpackages.github.io/>, <https://github.com/rdpackages/rd2d>

**BugReports** <https://github.com/rdpackages/rd2d/issues>

**Description** Provides pointwise and uniform estimation and inference methods for boundary discontinuity (BD) designs, a causal inference design that generalizes univariate regression discontinuity (RD) designs to settings with bivariate scores. Implements local polynomial methods for location-based and distance-based analyses, including sharp and fuzzy designs, data-driven bandwidth selection, pointwise confidence intervals, and uniform confidence bands. Methodology is developed in Cattaneo, Titiunik, and Yu (2026) <[doi:10.48550/arXiv.2505.05670](https://doi.org/10.48550/arXiv.2505.05670)> for location-based methods and Cattaneo, Titiunik, and Yu (2026) <[doi:10.48550/arXiv.2510.26051](https://doi.org/10.48550/arXiv.2510.26051)> for distance-based methods. For an overview and empirical guidance, see Cattaneo, Titiunik, and Yu (2026) <[doi:10.48550/arXiv.2511.06474](https://doi.org/10.48550/arXiv.2511.06474)>. The companion software article is Cattaneo, Titiunik, and Yu (2025) <[doi:10.48550/arXiv.2505.07989](https://doi.org/10.48550/arXiv.2505.07989)>.

**Imports** MASS, expm, ggplot2

**Suggests** testthat (>= 3.0.0)

**License** GPL-3

**Encoding** UTF-8

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**NeedsCompilation** no

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**Config/testthat/edition** 3

**Config/roxygen2/version** 8.0.0

Repository CRAN

Date/Publication 2026-05-23 05:20:02 UTC

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rd2d-package	<i>rd2d: Estimation and Inference for Boundary Discontinuity Designs</i>
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## Description

**rd2d** implements pointwise and uniform estimation and inference procedures for boundary discontinuity (BD) designs using local polynomial methods. The package includes location-based and distance-based methods, sharp and fuzzy designs, automatic bandwidth selection, pointwise confidence intervals, and uniform confidence bands. Distance-based methods in this package target level effects at two-dimensional boundary points.

Included functions are: [rd2d](#) for location-based estimation and inference, [rdbw2d](#) for location-based bandwidth selection, [rd2d.distance](#) for distance-based estimation and inference, and [rdbw2d.distance](#) for distance-based bandwidth selection.

`print()` and `summary()` methods are available for all four functions.

Related Stata, R, and Python packages useful for inference in RD designs are described at:

<https://rdpackages.github.io/>

For an introduction to regression discontinuity designs, see Cattaneo and Titiunik (2022, [doi:10.1146/annureveconomics051520021409](https://doi.org/10.1146/annureveconomics051520021409)) and references therein.

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## References

- Cattaneo, M. D., and Titiunik, R. (2022). Regression Discontinuity Designs. [doi:10.1146/annureveconomics051520021409](https://doi.org/10.1146/annureveconomics051520021409).
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- Cattaneo, M. D., Titiunik, R., and Yu, R. R. (2026). Estimation and Inference in Boundary Discontinuity Designs: Distance-Based Methods.
- Cattaneo, M. D., Titiunik, R., and Yu, R. R. (2026). Boundary Discontinuity Designs: Theory and Practice.
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## See Also

Useful links:

- <https://rdpackages.github.io/>
- <https://github.com/rdpackages/rd2d>
- Report bugs at <https://github.com/rdpackages/rd2d/issues>

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print.rd2d

*Print Method for 2D Local Polynomial RD Estimation*

---

## Description

Prints the results of a 2D local polynomial regression discontinuity (RD) estimation, as obtained from [rd2d](#).

## Usage

```
## S3 method for class 'rd2d'  
print(x, ...)
```

## Arguments

x                    An object of class rd2d, returned by [rd2d](#).  
...                   Additional arguments passed to the method (currently ignored).

## Value

No return value. This function is called for its side effects, which are to print the [rd2d](#) results.

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**See Also**

[rd2d](#) for conducting 2D local polynomial RD estimation.

Supported methods: [print.rd2d](#), [summary.rd2d](#).

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<code>print.rd2d.distance</code>	<i>Print Method for 2D Local Polynomial RD Estimation (Distance-Based)</i>
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**Description**

Prints the results of a 2D local polynomial regression discontinuity (RD) estimation using distance-based evaluation, as obtained from [rd2d.distance](#).

**Usage**

```
## S3 method for class 'rd2d.distance'  
print(x, ...)
```

**Arguments**

<code>x</code>	An object of class <code>rd2d.distance</code> , returned by <a href="#">rd2d.distance</a> .
<code>...</code>	Additional arguments passed to the method (currently ignored).

**Value**

No return value. This function is called for its side effects: it prints the [rd2d.distance](#) results.

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**See Also**

[rd2d.distance](#) for estimation using distance-based methods in 2D local polynomial RD designs.

Supported methods: [print.rd2d.distance](#), [summary.rd2d.distance](#).

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print.rdbw2d	<i>Print Method for Bandwidth Selection for 2D Local Polynomial RD Design</i>
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**Description**

The print method for bandwidth selection for 2D local polynomial RD design

**Usage**

```
## S3 method for class 'rdbw2d'  
print(x, ...)
```

**Arguments**

x	Class rdbw2d objects, obtained by calling <a href="#">rdbw2d</a> .
...	Additional arguments passed to the method (currently ignored).

**Value**

No return value, called to print [rdbw2d](#) results.

**Author(s)**

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**See Also**

[rdbw2d](#) for bandwidth selection for 2D local polynomial RD design  
Supported methods: [print.rdbw2d](#), [summary.rdbw2d](#).

---

print.rdbw2d.distance	<i>Print Method for Bandwidth Selection (Distance-Based) in 2D Local Polynomial RD Design</i>
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**Description**

Print method for displaying summary information from distance-based bandwidth selection in 2D local polynomial regression discontinuity (RD) designs, as produced by [rdbw2d.distance](#).

**Usage**

```
## S3 method for class 'rdbw2d.distance'  
print(x, ...)
```

**Arguments**

`x` An object of class `rdbw2d.distance`, returned by `rdbw2d.distance`.  
`...` Additional arguments passed to the method (currently ignored).

**Value**

No return value. This function is called for its side effects: it prints summary information of `rdbw2d.distance`.

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**See Also**

`rdbw2d.distance` for distance-based bandwidth selection in 2D local polynomial RD design.  
 Supported methods: `print.rdbw2d.distance`, `summary.rdbw2d.distance`.

---

 rd2d

---

*Location-Based Methods for Boundary Discontinuity Design*


---

**Description**

`rd2d` implements location-based local polynomial boundary discontinuity (BD) point estimators with robust bias-corrected pointwise confidence intervals and uniform confidence bands. See [Cattaneo, M. D., Titiunik, R., and Yu, R. R. \(2026\)](#) for methodological background.

Companion commands are: `rdbw2d` for data-driven bandwidth selection.

For other packages of RD designs, visit <https://rdpackages.github.io/>

**Usage**

```
rd2d(
  Y,
  X,
  assignment,
  b,
  h = NULL,
  deriv = c(0, 0),
  tangvec = NULL,
  p = 1,
  q = NULL,
  kernel = c("tri", "triangular", "epa", "epanechnikov", "uni", "uniform", "gau",
    "gaussian"),
  kernel_type = c("prod", "rad"),
```

```

vce = c("hc1", "hc0", "hc2", "hc3"),
masspoints = c("check", "adjust", "off"),
cluster = NULL,
level = 95,
params.other = NULL,
params.cov = NULL,
side = c("two", "left", "right"),
bwselect = c("mserd", "cerrd", "imserd", "icerrd", "msetwo", "certwo", "imsetwo",
"icertwo", "user provided"),
bwparam = c("main", "itt"),
method = c("dpi", "rot"),
bwcheck = 50 + p + 1,
scaleregul = 3,
scalebiascrct = 1,
stdvars = TRUE,
fuzzy = NULL
)

```

### Arguments

Y	Dependent variable; a numeric vector of length $N$ , where $N$ is the sample size.
X	Bivariate running variable (a.k.a score variable); a numeric matrix or data frame of dimension $N \times 2$ , with each row $\mathbf{X}_i = (X_{1i}, X_{2i})$ .
assignment	Treatment assignment indicator; a logical or binary vector indicating assignment to the treated side.
b	Evaluation points; a matrix or data frame specifying boundary points $\mathbf{b}_j = (b_{1j}, b_{2j})$ , of dimension $J \times 2$ .
h	Bandwidths. Either a positive scalar (same bandwidth for all dimensions and groups), or a matrix/data frame of size $J \times 4$ , corresponding to $h_{\text{control},1}$ , $h_{\text{control},2}$ , $h_{\text{treated},1}$ , $h_{\text{treated},2}$ at each evaluation point. If not specified, bandwidth $h$ is computed by the companion command <code>rdbw2d</code> ; for fuzzy designs, <code>bwparam</code> determines whether automatic bandwidths target the fuzzy Wald ratio or the reduced-form outcome discontinuity. Default is <code>h = NULL</code> .
deriv	The order of the derivatives of the regression functions to be estimated; a non-negative integer vector of length 2 specifying the number of derivatives in each coordinate (e.g., <code>c(1, 2)</code> corresponds to $\partial_1 \partial_2^2$ ).
tangvec	Tangent vectors; a matrix or data frame of dimension $J \times 2$ specifying directional derivatives. Overrides <code>deriv</code> if provided.
p	Polynomial order for point estimation ( $p = 1$ by default).
q	Polynomial order for robust confidence interval construction. Must satisfy $q \geq p$ ; default is $q = p + 1$ .
kernel	Kernel function to use. Options are "tri" or "triangular" (triangular, default), "epa" or "epanechnikov" (Epanechnikov), "uni" or "uniform" (uniform), and "gau" or "gaussian" (Gaussian).
kernel_type	Kernel structure. Either "prod" for product kernels (default) or "rad" for radial kernels.

vce	<p>Variance-covariance estimation method. Options are:</p> <ul style="list-style-type: none"> <li>• "hc0": heteroskedasticity-robust plug-in residual variance estimator without small-sample adjustment.</li> <li>• "hc1": heteroskedasticity-robust plug-in residual variance estimator with HC1 small-sample adjustment (default).</li> <li>• "hc2": heteroskedasticity-robust plug-in residual variance estimator with HC2 adjustment.</li> <li>• "hc3": heteroskedasticity-robust plug-in residual variance estimator with HC3 adjustment.</li> </ul> <p>Default is "hc1".</p>
masspoints	<p>Handling of mass points in the running variable. Options are:</p> <ul style="list-style-type: none"> <li>• "check": detects presence of mass points and reports the number of unique observations (default).</li> <li>• "adjust": adjusts preliminary bandwidths to ensure a minimum number of unique observations within each side of the cutoff.</li> <li>• "off": ignores presence of mass points.</li> </ul>
cluster	<p>Cluster ID variable used for cluster-robust variance estimation with degrees-of-freedom weights. Default is <code>cluster = NULL</code>.</p>
level	<p>Nominal confidence level for intervals/bands, between 0 and 100 (default is 95).</p>
params.other	<p>Optional character vector requesting companion-side result tables. Options are "main.0", "main.1" for sharp fits, and "itt.0", "itt.1", "fs.0", "fs.1" for fuzzy fits. Unrequested companion tables are returned as NA. Default is NULL.</p>
params.cov	<p>Optional character vector requesting covariance matrices to store for later use by <code>summary.rd2d</code>. Options are "main", "main.0", "main.1", "itt", "itt.0", "itt.1", "fs", "fs.0", and "fs.1", subject to the sharp/fuzzy design and <code>params.other</code>. Default is NULL, which computes no covariance matrices.</p>
side	<p>Type of confidence interval. Options: "two" (two-sided, default), "left" (left tail), or "right" (right tail).</p>
bwselect	<p>Bandwidth selection strategy. Options:</p> <ul style="list-style-type: none"> <li>• "mserd". One common MSE-optimal bandwidth selector for the boundary RD treatment effect estimator for each evaluation point (default).</li> <li>• "cerrd". CER-optimal counterpart of "mserd".</li> <li>• "imserd". IMSE-optimal bandwidth selector for the boundary RD treatment effect estimator based on all evaluation points.</li> <li>• "icerrd". CER-optimal counterpart of "imserd".</li> <li>• "msetwo". Two different MSE-optimal bandwidth selectors (control and treatment) for the boundary RD treatment effect estimator for each evaluation point.</li> <li>• "certwo". CER-optimal counterpart of "msetwo".</li> <li>• "imsetwo". Two IMSE-optimal bandwidth selectors (control and treatment) for the boundary RD treatment effect estimator based on all evaluation points.</li> <li>• "icertwo". CER-optimal counterpart of "imsetwo".</li> </ul>

- "user provided". User-provided bandwidths. If `h` is not NULL, then `bwselect` is overwritten to "user provided".

<code>bwparam</code>	Target parameter used for fuzzy automatic bandwidth selection. Options are "main" (default), which selects bandwidths for the linearized fuzzy Wald ratio, and "itt", which selects bandwidths for the reduced-form outcome discontinuity. This option is ignored in sharp designs and when <code>h</code> is supplied.
<code>method</code>	Bandwidth selection method for bias estimator based on local polynomials. Either "dpi" (default) for data-driven plug-in MSE optimal bandwidth selector or "rot" for rule-of-thumb bandwidth selector.
<code>bwcheck</code>	If a positive integer is provided, the preliminary bandwidth used in the calculations is enlarged so that at least <code>bwcheck</code> unique observations are used. Default is $50 + p + 1$ .
<code>scaleregul</code>	Scaling factor for the regularization term in bandwidth selection. Default is 3.
<code>scalebiasrcrt</code>	Scaling factor used for bias correction based on higher order expansions. Default is 1.
<code>stdvars</code>	Logical. If TRUE, the running variables $X_{1i}$ and $X_{2i}$ are standardized before computing automatic bandwidths. Default is TRUE. Standardization only affects automatic bandwidth selection when bandwidths are not manually provided through <code>h</code> .
<code>fuzzy</code>	Optional treatment receipt/status variable used for fuzzy RD estimation. The default is NULL, which estimates the sharp RD design.

## Value

An object of class "rd2d", a list with components:

<code>main</code>	A data frame with point estimates, standard errors, t-statistics, p-values, confidence intervals, and bandwidths at each evaluation point.
<code>b1, b2</code>	First and second coordinate of evaluation points $\mathbf{b} = (b_1, b_2)$ .
<code>estimate.p</code>	Point estimate $\hat{\tau}_p(\mathbf{b})$ .
<code>std.err.p</code>	Standard error of $\hat{\tau}_p(\mathbf{b})$ .
<code>estimate.q</code>	Bias-corrected point estimate $\hat{\tau}_q(\mathbf{b})$ .
<code>std.err.q</code>	Standard error of the bias-corrected estimate $\hat{\tau}_q(\mathbf{b})$ .
<code>t.value, p.value</code>	t-statistic and p-value based on the bias-corrected estimate.
<code>ci.lower, ci.upper</code>	Pointwise confidence intervals.
<code>h01, h02, h11, h12</code>	Bandwidths used in each coordinate and group.
<code>N.Co, N.Tr</code>	Effective sample size for the control and treatment sides, respectively.
<code>main.0, main.1</code>	For sharp RD only, companion-side outcome tables requested through <code>params.other</code> ; otherwise NA.
<code>bw</code>	Bandwidth and effective sample size table.
<code>itt</code>	For fuzzy RD only, same structure as <code>main</code> but for the reduced-form or intention-to-treat outcome discontinuity.
<code>itt.0, itt.1</code>	For fuzzy RD only, outcome summaries for the control and treated sides requested through <code>params.other</code> ; otherwise NA.

`fs` For fuzzy RD only, same structure as `main` but for the first-stage treatment receipt/status discontinuity.  
`fs.0`, `fs.1` For fuzzy RD only, first-stage summaries for the control and treated sides requested through `params.other`; otherwise NA.  
`tau.hat` Point estimates at each evaluation point.  
`tau.hat.q` Bias-corrected estimates at each evaluation point.  
`se.hat` Standard errors corresponding to `tau.hat`.  
`se.hat.q` Standard errors corresponding to `tau.hat.q`.  
`params.cov` List of covariance matrices for aggregate inference in [summary.rd2d](#). Contains only entries requested through `params.cov`.  
`ci` List with pointwise confidence intervals.  
`pvalues` Two-sided p-values based on bias-corrected estimates.  
`tvalues` t-statistics based on bias-corrected estimates.  
`tau.itt`, `tau.itt.q` For fuzzy RD, reduced-form outcome estimates using polynomial orders  $p$  and  $q$ ; otherwise NA.  
`tau.fs`, `tau.fs.q` For fuzzy RD, first-stage treatment receipt/status estimates using polynomial orders  $p$  and  $q$ ; otherwise NA.  
`rdmodel` Character label describing the fitted RD model.  
`call` Matched function call.  
`opt` List of options used in the function call.

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### References

- Cattaneo, M. D., and Titiunik, R. (2022). Regression Discontinuity Designs. [doi:10.1146/annureveconomics051520021409](#).
- Cattaneo, M. D., Titiunik, R., and Yu, R. R. (2026). Estimation and Inference in Boundary Discontinuity Designs: Location-Based Methods.
- Cattaneo, M. D., Titiunik, R., and Yu, R. R. (2026). Boundary Discontinuity Designs: Theory and Practice.
- Cattaneo, M. D., Titiunik, R., and Yu, R. R. (2025). rd2d: Causal Inference in Boundary Discontinuity Designs.

### See Also

[rdbw2d](#), [print.rd2d](#), [summary.rd2d](#)

**Examples**

```

# Simulated example
set.seed(123)
n <- 800
X1 <- rnorm(n)
X2 <- rnorm(n)
assignment <- as.numeric(X1 > 0)
Y <- 3 + 2 * X1 + 1.5 * X2 + assignment + rnorm(n)
X <- cbind(X1, X2)
b <- matrix(c(0, 0, 0, 1), ncol = 2)

# Estimate treatment effect using rd2d
result <- rd2d(Y, X, assignment, b, params.cov = "main",
              masspoints = "off", bwcheck = 10)
print(result)
summary(result, cbands = "main", repp = 49)

# Fuzzy RD example
fuzzy <- as.numeric(runif(n) < ifelse(assignment == 1, 0.8, 0.2))
Y.fuzzy <- 3 + 2 * X1 + 1.5 * X2 + 1.5 * fuzzy + rnorm(n)
result.fuzzy <- rd2d(Y.fuzzy, X, assignment, b, fuzzy = fuzzy,
                    bwparam = "main", masspoints = "off",
                    bwcheck = 10)
print(result.fuzzy)
summary(result.fuzzy, output = "itt")

```

---

rd2d.distance

*Distance-Based Methods for Boundary Discontinuity Design*


---

**Description**

rd2d.distance implements distance-based local polynomial boundary discontinuity (BD) point estimators with robust bias-corrected pointwise confidence intervals and uniform confidence bands. The command targets level effects at two-dimensional boundary points. See [Cattaneo, M. D., Titiunik, R., and Yu, R. R. \(2026\)](#) for methodological background.

Companion commands are: rdbw2d.distance for data-driven bandwidth selection.

For other packages of RD designs, visit <https://rdpackages.github.io/>

**Usage**

```

rd2d.distance(
  Y,
  distance,
  h = NULL,
  b = NULL,
  p = 1,
  q = NULL,
  kink.unknown = c(FALSE, FALSE),

```

```

kink.position = NULL,
kernel = c("tri", "triangular", "epa", "epanechnikov", "uni", "uniform", "gau",
"gaussian"),
level = 95,
cbands = TRUE,
side = c("two", "left", "right"),
bwselect = c("mserd", "cerrd", "imserd", "icerrd", "msetwo", "certwo", "imsetwo",
"icertwo", "user provided"),
bwparam = c("main", "itt"),
params.other = NULL,
params.cov = NULL,
vce = c("hc1", "hc0", "hc2", "hc3"),
bwcheck = 50 + p + 1,
masspoints = c("check", "adjust", "off"),
cluster = NULL,
scaleregul = 1,
cqt = 0.5,
fuzzy = NULL
)

```

### Arguments

<code>Y</code>	Dependent variable; a numeric vector of length $N$ , where $N$ is the sample size.
<code>distance</code>	Signed distance scores; a numeric matrix or data frame of dimension $N \times J$ , where $N$ is the sample size and $J$ is the number of evaluation points. Non-negative values identify observations on the treated side and negative values identify observations on the control side.
<code>h</code>	Bandwidths. A positive scalar uses the same bandwidth for both groups and all evaluation points. A matrix/data frame of size $J \times 2$ uses row-specific control and treated bandwidths. If not specified, bandwidths are selected by <a href="#">rdbw2d.distance</a> .
<code>b</code>	Optional evaluation points; a matrix or data frame specifying boundary points $\mathbf{b}_j = (b_{1j}, b_{2j})$ , dimension $J \times 2$ .
<code>p</code>	Polynomial order for point estimation. Default is $p = 1$ .
<code>q</code>	Polynomial order for bias-corrected estimation. Must satisfy $q \geq p$ . Default is $q = p + 1$ , except when <code>kink.unknown[1] = TRUE</code> , where the default is $q = p$ .
<code>kink.unknown</code>	Logical value or vector of length 2 controlling unknown-kink bandwidth adjustments. A scalar TRUE is expanded to <code>c(TRUE, TRUE)</code> , and a scalar FALSE is expanded to <code>c(FALSE, FALSE)</code> . With the vector form, the first element controls whether the point-estimation bandwidth is shrunk to the unknown-kink rate; the second controls whether the inference bandwidth is further shrunk. Default is <code>c(FALSE, FALSE)</code> . The second element can be TRUE only when the first element is TRUE.
<code>kink.position</code>	Optional boundary positions of known kink points. Either a logical vector with one entry per boundary point, where TRUE identifies a kink point, or an integer vector with indices between 1 and the number of boundary points. Requires <code>b</code> so

distances between boundary points can be computed. This option applies only to automatic bandwidth selection.

kernel	Kernel function to use. Options are "tri" or "triangular" (triangular, default), "epa" or "epanechnikov" (Epanechnikov), "uni" or "uniform" (uniform), and "gau" or "gaussian" (Gaussian).
level	Nominal confidence level for intervals/bands, between 0 and 100 (default is 95).
cbands	Logical. If TRUE, stores the covariance matrix needed for uniform confidence bands and aggregate inference computed by <code>summary(..., cbands = "main")</code> , <code>summary(..., WBATE = weights)</code> , or <code>summary(..., LBATE = TRUE)</code> . Default is TRUE.
side	Type of confidence interval. Options: "two" (two-sided, default), "left" (left tail), or "right" (right tail).
bwselect	Bandwidth selection strategy. Options: <ul style="list-style-type: none"> <li>• "mserd". One common MSE-optimal bandwidth selector for the boundary RD treatment effect estimator for each evaluation point (default).</li> <li>• "cerrd". CER-optimal counterpart of "mserd".</li> <li>• "imserd". IMSE-optimal bandwidth selector for the boundary RD treatment effect estimator based on all evaluation points.</li> <li>• "icerrd". CER-optimal counterpart of "imserd".</li> <li>• "msetwo". Two different MSE-optimal bandwidth selectors (control and treatment) for the boundary RD treatment effect estimator for each evaluation point.</li> <li>• "certwo". CER-optimal counterpart of "msetwo".</li> <li>• "imsetwo". Two IMSE-optimal bandwidth selectors (control and treatment) for the boundary RD treatment effect estimator based on all evaluation points.</li> <li>• "icertwo". CER-optimal counterpart of "imsetwo".</li> <li>• "user provided". User-provided bandwidths. If <code>h</code> is not NULL, then <code>bwselect</code> is overwritten to "user provided".</li> </ul>
bwparam	Target parameter used for fuzzy automatic bandwidth selection. Options are "main" (default), which selects bandwidths for the linearized fuzzy Wald ratio, and "itt", which selects bandwidths for the reduced-form outcome. Ignored in sharp designs.
params.other	Optional character vector requesting companion output tables. In sharp designs, available values are "main.0" and "main.1". In fuzzy designs, available values are "itt.0", "itt.1", "fs.0", and "fs.1".
params.cov	Optional character vector requesting covariance matrices for aggregate inference or confidence bands. Available values are "main" for sharp and fuzzy main effects, plus "main.0" and "main.1" for sharp side-specific effects, and "itt", "itt.0", "itt.1", "fs", "fs.0", and "fs.1" for fuzzy reduced-form and first-stage effects. If <code>cbands = TRUE</code> , "main" is added automatically.
vce	Variance-covariance estimator for standard errors. Options: <ul style="list-style-type: none"> <li>"hc0" Heteroskedasticity-robust variance estimator without small sample adjustment (White robust).</li> </ul>

	"hc1" Heteroskedasticity-robust variance estimator with degrees-of-freedom correction. (default)
	"hc2" Heteroskedasticity-robust variance estimator using leverage adjustments.
	"hc3" More conservative heteroskedasticity-robust variance estimator (similar to jackknife correction).
bwcheck	If a positive integer is provided, the preliminary bandwidth used in the calculations is enlarged so that at least bwcheck unique observations are used. Default is $50 + p + 1$ .
masspoints	Strategy for handling mass points in the running variable. Options: "check" (default) Check for repeated values and adjust inference if needed. "adjust" Adjust bandwidths to guarantee a sufficient number of unique support points. "off" Ignore mass points completely.
cluster	Cluster ID variable used for cluster-robust variance estimation with degrees-of-freedom weights. Default is <code>cluster = NULL</code> .
scaleregul	Scaling factor for the regularization term in bandwidth selection. Default is 1.
cqt	Constant controlling subsample fraction for initial bias estimation. Default is 0.5.
fuzzy	Optional treatment receipt/status variable for fuzzy RD designs. If supplied, <code>main</code> reports the fuzzy Wald treatment effect, <code>itt</code> reports the reduced-form outcome discontinuity, and <code>fs</code> reports the first-stage treatment receipt/status discontinuity.

## Value

An object of class "rd2d.distance", a list containing:

`main` Data frame of point estimates, standard errors, confidence intervals, and bandwidths:

- `b1` First coordinate of the evaluation point.
- `b2` Second coordinate of the evaluation point.
- `estimate.p` Point estimate with polynomial order  $p$ .
- `std.err.p` Standard error for `estimate.p`.
- `estimate.q` Bias-corrected estimate with polynomial order  $q$ .
- `std.err.q` Standard error for `estimate.q`.
- `t.value` t-statistic based on  $\hat{\tau}_{\text{distance},q}(\mathbf{b})$ .
- `p.value` Two-sided p-value based on  $T_{\text{distance},q}(\mathbf{b})$ .
- `ci.lower` Lower bound of confidence interval.
- `ci.upper` Upper bound of confidence interval.
- `h0` Bandwidth used for the control group (negative signed distance).
- `h1` Bandwidth used for the treatment group (non-negative signed distance).
- `h0.rbc` Bandwidth used for control-side inference.
- `h1.rbc` Bandwidth used for treated-side inference.
- `N.Co` Effective sample size for the control side.
- `N.Tr` Effective sample size for the treatment side.

main.0 Sharp-design summary table for the control side only.  
 main.1 Sharp-design summary table for the treated side only.  
 itt Fuzzy-design reduced-form outcome summary table.  
 itt.0, itt.1 Optional fuzzy-design side-specific reduced-form outcome summary tables requested through params.other.  
 fs Fuzzy-design first-stage treatment receipt/status summary table.  
 fs.0, fs.1 Optional fuzzy-design side-specific first-stage treatment receipt/status summary tables requested through params.other.  
 bw Bandwidth and effective-sample-size table.  
 tau.hat Vector of point estimates  $\hat{\tau}_p(\mathbf{b})$ .  
 tau.hat.q Vector of bias-corrected estimates  $\hat{\tau}_q(\mathbf{b})$ .  
 se.hat Standard errors corresponding to  $\hat{\tau}_p(\mathbf{b})$ .  
 se.hat.q Standard errors corresponding to  $\hat{\tau}_q(\mathbf{b})$ .  
 params.cov List containing covariance matrices requested for aggregate or uniform inference.  
 ci Pointwise confidence interval endpoints.  
 pvalues Two-sided p-values based on bias-corrected estimates.  
 tvalues t-statistics based on bias-corrected estimates.  
 tau.itt, tau.itt.q, tau.fs, tau.fs.q Fuzzy reduced-form and first-stage point estimates with polynomial orders  $p$  and  $q$ ; these are NULL in sharp designs.  
 rdmodel Character label describing the fitted RD model.  
 call Matched function call.  
 opt A list of estimation options (e.g., p, q, kernel, level, etc.) and internal variables such as sample size  $N$ .

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### References

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### See Also

[rdbw2d.distance](#), [rd2d](#), [print.rd2d.distance](#), [summary.rd2d.distance](#)

**Examples**

```

set.seed(123)
n <- 800

# Generate running variables x1 and x2
x1 <- rnorm(n)
x2 <- rnorm(n)

# Define treatment assignment: treated if x1 >= 0
assignment <- as.numeric(x1 >= 0)

# Generate outcome variable Y with some treatment effect
Y <- 3 + 2 * x1 + 1.5 * x2 + 1.5 * assignment + rnorm(n, sd = 0.5)

# Define evaluation points (e.g., at the origin and another point)
eval <- data.frame(x.1 = c(0, 0), x.2 = c(0, 1))

# Compute Euclidean distances to evaluation points
distance.a <- sqrt((x1 - eval$x.1[1])^2 + (x2 - eval$x.2[1])^2)
distance.b <- sqrt((x1 - eval$x.1[2])^2 + (x2 - eval$x.2[2])^2)

# Combine distances into a matrix
distance <- as.data.frame(cbind(distance.a, distance.b))

# Assign positive distances for treatment group, negative for control
assignment_expanded <- matrix(rep(2 * assignment - 1, times = ncol(distance)),
                             nrow = nrow(distance), ncol = ncol(distance))
distance <- distance * assignment_expanded

# Run the rd2d.distance function
result <- rd2d.distance(Y, distance = distance, b = eval, cbands = FALSE,
                       masspoints = "off", bwcheck = 10)

# View the estimation results
print(result)
summary(result)

# Fuzzy distance-based fit with a user-supplied bandwidth
fuzzy <- as.numeric(runif(n) < ifelse(assignment == 1, 0.8, 0.2))
Y.fuzzy <- 3 + 2 * x1 + 1.5 * x2 + 1.5 * fuzzy + rnorm(n, sd = 0.5)
fuzzy.result <- rd2d.distance(Y.fuzzy, distance = distance, h = 0.8, b = eval, fuzzy = fuzzy,
                             cbands = FALSE, masspoints = "off")
summary(fuzzy.result)

```

## Description

rdbw2d implements bandwidth selectors for location-based local polynomial boundary discontinuity (BD) estimation and inference. See [Cattaneo, M. D., Titiunik, R., and Yu, R. R. \(2026\)](#) for methodological background.

Companion commands are: rd2d for point estimation and inference procedures.

For other packages of RD designs, visit <https://rdpackages.github.io/>

## Usage

```
rdbw2d(
  Y,
  X,
  assignment,
  b,
  p = 1,
  deriv = c(0, 0),
  tangvec = NULL,
  kernel = c("tri", "triangular", "epa", "epanechnikov", "uni", "uniform", "gau",
    "gaussian"),
  kernel_type = c("prod", "rad"),
  bwselect = c("mserd", "cerrd", "imserd", "icerrd", "msetwo", "certwo", "imsetwo",
    "icertwo"),
  bwparam = c("main", "itt"),
  method = c("dpi", "rot"),
  vce = c("hc1", "hc0", "hc2", "hc3"),
  bwcheck = 20,
  masspoints = c("check", "adjust", "off"),
  cluster = NULL,
  scaleregul = 1,
  scalebiascrct = 1,
  stdvars = TRUE,
  fuzzy = NULL
)
```

## Arguments

Y	Dependent variable; a numeric vector of length $N$ , where $N$ is the sample size.
X	Bivariate running variable (a.k.a score variable); a numeric matrix or data frame of dimension $N \times 2$ , with each row $\mathbf{X}_i = (X_{1i}, X_{2i})$ .
assignment	Treatment assignment indicator; a logical or binary vector indicating assignment to the treated side.
b	Evaluation points; a matrix or data frame specifying boundary points $\mathbf{b}_j = (b_{1j}, b_{2j})$ , of dimension $J \times 2$ .
p	Polynomial order of the local polynomial estimator. Default is $p = 1$ .
deriv	The order of the derivatives of the regression functions to be estimated; a non-negative integer vector of length 2 specifying the number of derivatives in each coordinate (e.g., $c(1, 2)$ corresponds to $\partial_1 \partial_2^2$ ).

tangvec	Tangent vectors; a matrix or data frame of dimension $J \times 2$ specifying directional derivatives. Overrides deriv if provided.
kernel	Kernel function to use. Options are "tri" or "triangular" (triangular, default), "epa" or "epanechnikov" (Epanechnikov), "uni" or "uniform" (uniform), and "gau" or "gaussian" (Gaussian).
kernel_type	Kernel structure. Either "prod" for product kernels (default) or "rad" for radial kernels.
bwselect	Bandwidth selection strategy. Options: <ul style="list-style-type: none"> <li>• "mserd". One common MSE-optimal bandwidth selector for the boundary RD treatment effect estimator for each evaluation point (default).</li> <li>• "cerrd". CER-optimal counterpart of "mserd".</li> <li>• "imserd". IMSE-optimal bandwidth selector for the boundary RD treatment effect estimator based on all evaluation points.</li> <li>• "icerrd". CER-optimal counterpart of "imserd".</li> <li>• "msetwo". Two different MSE-optimal bandwidth selectors (control and treatment) for the boundary RD treatment effect estimator for each evaluation point.</li> <li>• "certwo". CER-optimal counterpart of "msetwo".</li> <li>• "imsetwo". Two IMSE-optimal bandwidth selectors (control and treatment) for the boundary RD treatment effect estimator based on all evaluation points.</li> <li>• "icertwo". CER-optimal counterpart of "imsetwo".</li> </ul>
bwparam	Target parameter used for fuzzy bandwidth selection. Options are "main" (default), which selects bandwidths for the linearized fuzzy Wald ratio, and "itt", which selects bandwidths for the reduced-form outcome discontinuity. This option is ignored in sharp designs, where only "main" is used.
method	Bandwidth selection method for bias estimator based on local polynomials. Either "dpi" (default) for data-driven plug-in MSE optimal bandwidth selector or "rot" for rule-of-thumb bandwidth selector.
vce	Variance-covariance estimation method. Options are: <ul style="list-style-type: none"> <li>• "hc0": heteroskedasticity-robust plug-in residual variance estimator without small-sample adjustment.</li> <li>• "hc1": heteroskedasticity-robust plug-in residual variance estimator with HC1 small-sample adjustment (default).</li> <li>• "hc2": heteroskedasticity-robust plug-in residual variance estimator with HC2 adjustment.</li> <li>• "hc3": heteroskedasticity-robust plug-in residual variance estimator with HC3 adjustment.</li> </ul> Default is "hc1".
bwcheck	If a positive integer is provided, the preliminary bandwidth used in the calculations is enlarged so that at least bwcheck unique observations are used. Default is 20.
masspoints	Handling of mass points in the running variable. Options are:

	<ul style="list-style-type: none"> <li>• "check": detects presence of mass points and reports the number of unique observations (default).</li> <li>• "adjust": adjusts preliminary bandwidths to ensure a minimum number of unique observations within each side of the cutoff.</li> <li>• "off": ignores presence of mass points.</li> </ul>
cluster	Cluster ID variable used for cluster-robust variance estimation with degrees-of-freedom weights. Default is <code>cluster = NULL</code> .
scaleregul	Scaling factor for the regularization term in bandwidth selection. Default is 1.
scalebiasrcrt	Scaling factor used for bias correction based on higher order expansions. Default is 1.
stdvars	Logical. If TRUE, the running variables $X_{1i}$ and $X_{2i}$ are standardized before computing the bandwidths. Default is TRUE.
fuzzy	Optional treatment receipt/status variable used to construct bandwidth selectors for fuzzy RD estimation. If supplied, <code>bwparam</code> controls whether the selector targets the fuzzy Wald ratio or the reduced-form outcome discontinuity.

## Value

A list of class "rdbw2d" containing:

`bws` Data frame of estimated bandwidths for each evaluation point:

- `b1` First coordinate of the evaluation point.
- `b2` Second coordinate of the evaluation point.
- `h01` Estimated bandwidth for  $X_{1i}$  in the control group ( $\mathcal{A}_0$ ).
- `h02` Estimated bandwidth for  $X_{2i}$  in the control group ( $\mathcal{A}_0$ ).
- `h11` Estimated bandwidth for  $X_{1i}$  in the treatment group ( $\mathcal{A}_1$ ).
- `h12` Estimated bandwidth for  $X_{2i}$  in the treatment group ( $\mathcal{A}_1$ ).

`mseconsts` Data frame of intermediate quantities used in bandwidth calculation:

- `N.Co` Effective sample size for the control group  $\mathcal{A}_0$ .
- `N.Tr` Effective sample size for the treatment group  $\mathcal{A}_1$ .
- `bias.0` Bias constant estimate for the control group.
- `bias.1` Bias constant estimate for the treatment group.
- `var.0` Variance constant estimate for the control group.
- `var.1` Variance constant estimate for the treatment group.
- `reg.bias.0` Bias correction adjustment for the control group.
- `reg.bias.1` Bias correction adjustment for the treatment group.
- `reg.var.0` Variance of the bias estimate for the control group.
- `reg.var.1` Variance of the bias estimate for the treatment group.

`opt` List containing:

- `p` Polynomial order used for estimation.
- `kernel` Kernel function used.
- `kernel_type` Type of kernel (product or radial).
- `stdvars` Logical indicating if standardization was applied.

**bwselect** Bandwidth selection strategy used.  
**bwparam** Target parameter for fuzzy bandwidth selection.  
**method** Bandwidth estimation method.  
**vce** Variance estimation method.  
**scaleregul** Scaling factor for regularization.  
**scalebiascrct** Scaling factor for bias correction.  
**N** Total sample size  $N$ .  
**call** Matched function call.

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### References

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- Cattaneo, M. D., Titiunik, R., and Yu, R. R. (2025). rd2d: Causal Inference in Boundary Discontinuity Designs.

### See Also

[rd2d](#), [print.rdbw2d](#), [summary.rdbw2d](#)

### Examples

```

# Simulated example
set.seed(123)
n <- 800
X1 <- rnorm(n)
X2 <- rnorm(n)
assignment <- as.numeric(X1 > 0)
Y <- 3 + 2 * X1 + 1.5 * X2 + assignment + rnorm(n)
X <- cbind(X1, X2)
b <- matrix(c(0, 0, 0, 1), ncol = 2)

# MSE optimal bandwidth for rd2d
bws <- rdbw2d(Y, X, assignment, b, masspoints = "off", bwcheck = 10)

# View the bandwidth selection results
print(bws)
summary(bws)

```

```
# Fuzzy bandwidth selection can target the Wald ratio or the reduced form
fuzzy <- as.numeric(runif(n) < ifelse(assignment == 1, 0.8, 0.2))
Y.fuzzy <- 3 + 2 * X1 + 1.5 * X2 + 1.5 * fuzzy + rnorm(n)
bws.fuzzy <- rdbw2d(Y.fuzzy, X, assignment, b, fuzzy = fuzzy, bwparam = "main",
                    masspoints = "off", bwcheck = 10)
print(bws.fuzzy)
```

---

rdbw2d.distance	<i>Bandwidth Selection for Distance-Based Methods for Boundary Discontinuity Design</i>
-----------------	---

---

### Description

rdbw2d.distance implements bandwidth selectors for distance-based local polynomial boundary discontinuity (BD) estimation and inference. The command targets level effects at two-dimensional boundary points. See [Cattaneo, M. D., Titiunik, R., and Yu, R. R. \(2026\)](#) for methodological background.

### Usage

```
rdbw2d.distance(
  Y,
  distance,
  b = NULL,
  p = 1,
  kink.unknown = c(FALSE, FALSE),
  kink.position = NULL,
  kernel = c("tri", "triangular", "epa", "epanechnikov", "uni", "uniform", "gau",
            "gaussian"),
  bwselect = c("mserd", "cerrd", "imserd", "icerrd", "msetwo", "certwo", "imsetwo",
            "icertwo"),
  bwparam = c("main", "itt"),
  vce = c("hc1", "hc0", "hc2", "hc3"),
  bwcheck = 20 + p + 1,
  masspoints = c("check", "adjust", "off"),
  cluster = NULL,
  scaleregul = 1,
  cqt = 0.5,
  fuzzy = NULL
)
```

### Arguments

Y	Dependent variable; a numeric vector of length $N$ , where $N$ is the sample size.
distance	Signed distance scores; a numeric matrix or data frame of dimension $N \times J$ , where $N$ is the sample size and $J$ is the number of evaluation points. Non-negative values identify observations on the treated side and negative values identify observations on the control side.

b	Optional evaluation points; a matrix or data frame specifying boundary points $\mathbf{b}_j = (b_{1j}, b_{2j})$ , dimension $J \times 2$ .
p	Polynomial order for point estimation. Default is $p = 1$ .
kink.unknown	Logical value or vector of length 2 controlling unknown-kink bandwidth adjustments. A scalar TRUE is expanded to $c(\text{TRUE}, \text{TRUE})$ , and a scalar FALSE is expanded to $c(\text{FALSE}, \text{FALSE})$ . With the vector form, the first element controls whether the point-estimation bandwidth is shrunk to the unknown-kink rate; the second controls whether the inference bandwidth is further shrunk in <a href="#">rd2d.distance</a> . For bandwidth selection, only the first element is used. Default is $c(\text{FALSE}, \text{FALSE})$ .
kink.position	Optional boundary positions of known kink points. Either a logical vector with one entry per boundary point, where TRUE identifies a kink point, or an integer vector with indices between 1 and the number of boundary points. Requires b so distances between boundary points can be computed.
kernel	Kernel function to use. Options are "tri" or "triangular" (triangular, default), "epa" or "epanechnikov" (Epanechnikov), "uni" or "uniform" (uniform), and "gau" or "gaussian" (Gaussian).
bwselect	Bandwidth selection strategy. Options: <ul style="list-style-type: none"> <li>• "mserd". One common MSE-optimal bandwidth selector for the boundary RD treatment effect estimator for each evaluation point (default).</li> <li>• "cerrd". CER-optimal counterpart of "mserd".</li> <li>• "imserd". IMSE-optimal bandwidth selector for the boundary RD treatment effect estimator based on all evaluation points.</li> <li>• "icerrd". CER-optimal counterpart of "imserd".</li> <li>• "msetwo". Two different MSE-optimal bandwidth selectors (control and treatment) for the boundary RD treatment effect estimator for each evaluation point.</li> <li>• "certwo". CER-optimal counterpart of "msetwo".</li> <li>• "imsetwo". Two IMSE-optimal bandwidth selectors (control and treatment) for the boundary RD treatment effect estimator based on all evaluation points.</li> <li>• "icertwo". CER-optimal counterpart of "imsetwo".</li> </ul>
bwparam	Target parameter used for fuzzy automatic bandwidth selection. Options are "main", which selects bandwidths for the linearized fuzzy Wald ratio, and "itt", which selects bandwidths for the reduced-form outcome. Ignored in sharp designs.
vce	Variance-covariance estimator for standard errors. Options: <ul style="list-style-type: none"> <li>"hc0" Heteroskedasticity-robust variance estimator without small sample adjustment (White robust).</li> <li>"hc1" Heteroskedasticity-robust variance estimator with degrees-of-freedom correction. (default)</li> <li>"hc2" Heteroskedasticity-robust variance estimator using leverage adjustments.</li> <li>"hc3" More conservative heteroskedasticity-robust variance estimator (similar to jackknife correction).</li> </ul>

bwcheck	If a positive integer is provided, the preliminary bandwidth used in the calculations is enlarged so that at least bwcheck unique observations are used. Default is $2\theta + p + 1$ .
masspoints	Strategy for handling mass points in the running variable. Options: "check" (default) Check for repeated values and adjust inference if needed. "adjust" Adjust bandwidths to guarantee a sufficient number of unique support points. "off" Ignore mass points completely.
cluster	Cluster ID variable used for cluster-robust variance estimation with degrees-of-freedom weights. Default is <code>cluster = NULL</code> .
scaleregul	Scaling factor for the regularization term in bandwidth selection. Default is 1.
cqt	Constant controlling subsample fraction for initial bias estimation. Default is 0.5.
fuzzy	Optional treatment receipt/status variable used for fuzzy RD bandwidth selection. If supplied, bwparam controls whether the selector targets the fuzzy Wald ratio or the reduced-form outcome.

### Value

An object of class "rdbw2d.distance", containing:

`bws` Data frame of optimal bandwidths for each evaluation point:

- `b1` First coordinate of the evaluation point  $b1$ .
- `b2` Second coordinate of the evaluation point  $b2$ .
- `h0` Bandwidth for observations with negative signed distance.
- `h1` Bandwidth for observations with non-negative signed distance.

`mseconsts` Data frame of intermediate bias and variance constants used for MSE/IMSE calculations, including `N.Co` and `N.Tr`, the effective sample sizes for observations with negative and non-negative signed distances, respectively.

`opt` A list of options and settings used in estimation, including `p`, `kernel`, sample size  $N$ , and user-specified choices.

`call` Matched function call.

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### See Also

[rd2d.distance](#), [rd2d](#), [summary.rdbw2d.distance](#), [print.rdbw2d.distance](#)

### Examples

```
set.seed(123)
n <- 800

# Generate running variables x1 and x2
x1 <- rnorm(n)
x2 <- rnorm(n)

# Define treatment assignment: treated if x1 >= 0
assignment <- as.numeric(x1 >= 0)

# Generate outcome variable Y with some treatment effect
Y <- 3 + 2 * x1 + 1.5 * x2 + 1.5 * assignment + rnorm(n, sd = 0.5)

# Define evaluation points (e.g., at the origin and another point)
eval <- data.frame(x.1 = c(0, 0), x.2 = c(0, 1))

# Compute Euclidean distances to evaluation points
distance.a <- sqrt((x1 - eval$x.1[1])^2 + (x2 - eval$x.2[1])^2)
distance.b <- sqrt((x1 - eval$x.1[2])^2 + (x2 - eval$x.2[2])^2)

# Combine distances into a matrix
distance <- as.data.frame(cbind(distance.a, distance.b))

# Assign positive distances for treatment group, negative for control
assignment_expanded <- matrix(rep(2 * assignment - 1, times = ncol(distance)),
                              nrow = nrow(distance), ncol = ncol(distance))
distance <- distance * assignment_expanded

# Run the rdbw2d.distance function
bws <- rdbw2d.distance(Y, distance = distance, b = eval, masspoints = "off", bwcheck = 10)

# View the estimation results
print(bws)
summary(bws)

# Fuzzy distance-based bandwidths
fuzzy <- as.numeric(runif(n) < ifelse(assignment == 1, 0.8, 0.2))
Y.fuzzy <- 3 + 2 * x1 + 1.5 * x2 + 1.5 * fuzzy + rnorm(n, sd = 0.5)
bws.fuzzy <- rdbw2d.distance(Y.fuzzy, distance = distance, b = eval, fuzzy = fuzzy,
                             bwparam = "main", masspoints = "off",
                             bwcheck = 10)
```

```
print(bws.fuzzy)
```

---

summary.rd2d

*Summary Method for 2D Local Polynomial RD Estimation*


---

## Description

Summarizes estimation and bandwidth results from a 2D local polynomial regression discontinuity (RD) design, as produced by [rd2d](#).

## Usage

```
## S3 method for class 'rd2d'
summary(object, ...)
```

## Arguments

object	An object of class <code>rd2d</code> , typically returned by <a href="#">rd2d</a> .
...	Optional named arguments. Unsupported option names produce an error. Supported options include: <ul style="list-style-type: none"> <li><code>cbands</code>: Optional character vector requesting uniform confidence bands for displayed outputs. Options are "main", "main.0", "main.1", "itt", "itt.0", "itt.1", "fs", "fs.0", and "fs.1", subject to the sharp/fuzzy design and covariance matrices stored by <a href="#">rd2d</a>.</li> <li><code>repp</code>: Positive integer. Number of Gaussian simulation repetitions used for uniform confidence band and LBATE critical values. Default is 1000.</li> <li><code>WBATE</code>: Optional numeric weights for a weighted boundary average treatment effect row. The weights must match the full set of evaluation points for the selected output. The selected output must have a matching covariance matrix stored by <a href="#">rd2d</a>.</li> <li><code>LBATE</code>: Logical. If TRUE, prints a largest boundary average treatment effect row. The selected output must have a matching covariance matrix stored by <a href="#">rd2d</a>.</li> <li><code>subset</code>: Integer vector of indices of evaluation points to display. Aggregates and uniform-band critical values are still computed using all evaluation points. Defaults to all evaluation points.</li> <li><code>output</code>: Character. Use "main" to display sharp or fuzzy main results; "main.0" or "main.1" to display sharp control- or treatment-side main results; "itt", "itt.0", or "itt.1" to display fuzzy reduced-form or intention-to-treat results; "fs", "fs.0", or "fs.1" to display fuzzy first-stage treatment receipt/status results; and "bw" to display bandwidth information. If omitted, <code>summary()</code> prints all default and requested estimate tables and does not print "bw". Use <code>output = "bw"</code> to print bandwidth information.</li> </ul>

- `sep`: Integer vector of length three. Controls spacing in the output. `sep[1]` controls spacing for the columns of bandwidths, estimation, t-statistic, and p-value in the "main" table. `sep[2]` controls spacing for confidence intervals and confidence bands in the "main" table. `sep[3]` controls spacing for the columns in the "bw" table. Default is `c(7, 17, 8)`.

### Value

Invisibly returns a list with displayed tables and uniform confidence bands requested through `cbands`. Each returned estimate table has the same columns as the corresponding `rd2d` output, with pointwise confidence intervals always retained and `cb.lower` and `cb.upper` added only when uniform bands are requested. Requested WBATE and LBATE rows are appended to the corresponding returned table.

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### See Also

`rd2d` for estimation using 2D local polynomial RD design.  
 Supported methods: `print.rd2d`, `summary.rd2d`.

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summary.rd2d.distance *Summary Method for 2D Local Polynomial RD Estimation (Distance-Based)*

---

### Description

Summarizes estimation and bandwidth results from a 2D local polynomial regression discontinuity (RD) design using distance-based methods, as returned by `rd2d.distance`.

### Usage

```
## S3 method for class 'rd2d.distance'
summary(object, ...)
```

### Arguments

`object` An object of class `rd2d.distance`, returned by `rd2d.distance`.  
`...` Optional arguments. Supported options include:

- `cbands`: Character vector. Use `cbands = "main"` to display uniform confidence bands for the main distance-based estimates. Other stored outputs can be requested when their covariance matrices were stored through `params.cov`. The default displays pointwise confidence intervals.

- `repp`: Positive integer. Number of Gaussian simulation repetitions used for uniform confidence band and LBATE critical values. Default is 1000.
- `WBATE`: Optional numeric weights for a weighted boundary average treatment effect row. The weights must match the full set of evaluation points and are normalized internally. The fitted object must contain the covariance matrix stored by `rd2d.distance(cbands = TRUE)` or requested through `params.cov`.
- `LBATE`: Logical. If TRUE, prints a largest boundary average treatment effect row. The fitted object must contain the covariance matrix stored by `rd2d.distance(cbands = TRUE)` or requested through `params.cov`.
- `subset`: Integer vector of indices of evaluation points to display. Defaults to all evaluation points.
- `output`: Character vector. Use "main" to display treatment effect estimates or "bw" to display bandwidth information. In sharp designs, "main.0" and "main.1" display side-specific estimates. In fuzzy designs, "itt" and "fs" display reduced-form and first-stage estimates, and "itt.0", "itt.1", "fs.0", and "fs.1" display requested side-specific companion estimates.
- `sep`: Integer vector of length three. Controls spacing in the output. `sep[1]` controls spacing for the columns of boundary points, estimation, t-value, and p-value in the "main" table. `sep[2]` controls spacing for confidence intervals and confidence bands in the "main" table. `sep[3]` controls spacing for the columns in the "bw" table. Default is `c(7, 17, 8)`.

## Value

Invisibly returns an object of class "summary.rd2d.distance", a list with elements:

- `tables`: named list of returned summary tables. Estimate tables retain pointwise confidence intervals and add `cb.lower` and `cb.upper` only when uniform bands are requested.
- `cbands`: named list of confidence-band endpoints for outputs requested through `cbands`.
- `outputs`: character vector of summarized outputs.
- `call`: matched summary call.

Requested WBATE and LBATE rows are appended to the returned estimation table(s), except for `output = "bw"`. The function is also called for its side effect of printing a formatted summary.

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## See Also

[rd2d.distance](#) for estimation using distance-based 2D local polynomial RD design.

Supported methods: [print.rd2d.distance](#), [summary.rd2d.distance](#).

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summary.rdbw2d	<i>Summary Method for Bandwidth Selection for 2D Local Polynomial RD Design</i>
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## Description

Summary method for objects of class `rdbw2d`, displaying bandwidth selection results for 2D local polynomial regression discontinuity designs.

## Usage

```
## S3 method for class 'rdbw2d'  
summary(object, ...)
```

## Arguments

<code>object</code>	An object of class <code>rdbw2d</code> , typically returned by <a href="#">rdbw2d</a> .
<code>...</code>	Optional arguments. Supported options include: <ul style="list-style-type: none"><li>• <code>subset</code>: Integer vector of indices of evaluation points to display. Defaults to all evaluation points.</li><li>• <code>sep</code>: Integer. Controls spacing in the output. Default is 8.</li></ul>

## Value

No return value. Called for its side effects of printing a formatted summary of [rdbw2d](#) results.

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## See Also

[rdbw2d](#) for bandwidth selection in 2D local polynomial RD design.

Supported methods: [print.rdbw2d](#), [summary.rdbw2d](#).

---

summary.rdbw2d.distance

*Summary Method for Bandwidth Selection in 2D Local Polynomial RD Design (Distance-Based)*

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## Description

Summarizes bandwidth selection results from a 2D local polynomial regression discontinuity (RD) design using distance-based methods, as returned by [rdbw2d.distance](#).

## Usage

```
## S3 method for class 'rdbw2d.distance'
summary(object, ...)
```

## Arguments

**object** An object of class `rdbw2d.distance`, returned by [rdbw2d.distance](#).

**...** Optional arguments. Supported options include:

- **subset**: Integer vector of indices of evaluation points to display. Defaults to all evaluation points.
- **sep**: Integer vector of length two. Controls spacing in the output. `sep[1]` controls spacing for the columns of evaluation points in the table. `sep[2]` controls spacing for the columns of bandwidths in the table. Default is `c(8, 14)`.

## Value

No return value. This function is called for its side effects: it prints a formatted summary of [rdbw2d.distance](#) results.

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## See Also

[rdbw2d.distance](#) for bandwidth selection using 2D local polynomial RD design with distance-based methods.

Supported methods: [print.rdbw2d.distance](#), [summary.rdbw2d.distance](#).

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