

# Package ‘baggedcv’

July 26, 2019

**Type** Package

**Title** Bagged Cross-Validation for Kernel Density Bandwidth Selection

**Version** 1.0

**Date** 2019-07-03

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**Description** Bagged cross-validation for bandwidth selection

in kernel density estimation (Hall and Marron (1987) <doi:10.1007/BF00363516>). This bandwidth selector can achieve greater statistical precision than standard cross-validation while being computationally fast.

**License** GPL-3

**Encoding** UTF-8

**Imports** parallel, foreach, doParallel, mclust, kedd, stats

**RoxygenNote** 6.1.1

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2019-07-26 07:50:02 UTC

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bagcv	<i>Bagged CV bandwidth selector</i>
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### Description

Bagged CV bandwidth selector

**Usage**

```
bagcv(x, r, s, h0, h1, nb = r, ncores = parallel::detectCores())
```

**Arguments**

x	Vector. Sample.
r	Positive integer. Size of the subsamples.
s	Positive integer. Number of subsamples.
h0	Positive real number. Range over which to minimize, left bound.
h1	Positive real number. Range over which to minimize, right bound.
nb	Positive integer. Number of bins to use in the <code>bw.ucv</code> function.
ncores	Positive integer. Number of cores with which to parallelize the computations.

**Details**

Bagged cross-validation bandwidth for kernel density estimation.

**Value**

Bagged CV bandwidth.

**Examples**

```
set.seed(1)
x <- rnorm(10^6)
bagcv(x, 5000, 100, 0.01, 1, 5000, 2)
```

*mopt*

*Estimation of the optimal subsample size for bagged CV*

**Description**

Estimation of the optimal subsample size for bagged CV

**Usage**

```
mopt(x, N, r = 1000, s = 100, ncores = parallel::detectCores())
```

**Arguments**

x	Vector. Sample.
N	Positive integer. Number of subsamples for the bagged bandwidth.
r	Positive integer. Size of the subsamples.
s	Positive integer. Number of subsamples.
ncores	Positive integer. Number of cores with which to parallelize the computations.

**Details**

Estimates the optimal size of the subsamples for the bagged CV bandwidth selector.

**Value**

Estimate of the optimal subsample size.

**Examples**

```
set.seed(1)
x <- rt(10^5, 5)
mopt(x, 500, 500, 10, 2)
```