

# Package ‘opdisDownsampling’

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**Type** Package

**Title** Optimal Distribution Preserving Down-Sampling of Bio-Medical Data

**Version** 0.6.1

**Description** An optimized method for distribution-preserving class-proportional down-sampling of bio-medical data.

**Depends** R (>= 3.5.0)

**Imports** parallel, graphics, methods, stats, caTools, pracma, twosamples, utils, pbmcapply, benchmarkme

**LazyData** true

**Suggests** testthat

**License** GPL-3

**URL** <https://github.com/JornLotsch/opdisDownsampling>

**Encoding** UTF-8

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**NeedsCompilation** no

**Repository** CRAN

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FlowcytometricData     *Example data of hematologic marker expression.*

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**Description**

Data set of 6 flow cytometry-based lymphoma makers from 55,843 cells from healthy subjects (class 1) and 55,843 cells from lymphoma patients (class 2).

**Usage**

```
data("FlowcytometricData")
```

**Details**

Size 111686 x 6 , stored in FlowcytometricData\$[Var\_1,Var\_2,Var\_3,Var\_4,Var\_5,Var\_6]  
Classes 2, stored in FlowcytometricData\$Cls

**Examples**

```
data(FlowcytometricData)  
str(FlowcytometricData)
```

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GMMartificialData     *Example data an artificial Gaussioan mixture.*

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**Description**

Dataset of 30000 instances with 10 variables that are Gaussian mixtures and belong to classes Cls = 1, 2, or 3, with different means and standard deviations and equal weights of 0.5, 0.4, and 0.1, respectively.

**Usage**

```
data("GMMartificialData")
```

**Details**

Size 30000 x 10, stored in GMMartificialData\$[X1,X2,X3,X4,X5,X6,X7,X8,X9,X10]  
Classes 3, stored in GMMartificialData\$Cls

**Examples**

```
data(GMMartificialData)  
str(GMMartificialData)
```

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opdisDownsampling      *Optimal Distribution Preserving Down-Sampling of Bio-Medical Data*

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## Description

The package provides the necessary functions for optimal distribution-preserving down-sampling of large (bio-medical) data sets.

## Usage

```
opdisDownsampling(Data, Cls, Size, Seed, nTrials = 1000, TestStat = "ad", MaxCores = 2048,  
  JobSize = 1000, PCAimportance = FALSE)
```

## Arguments

Data	the data as a vector, matrix or data frame.
Cls	the class information, if any, as a vector of similar length as instances in the data.
Size	the percentage of instances per class to be drawn.
Seed	a predefined seed to modify the results.
nTrials	how many samples to choose from should be randomly drawn.
TestStat	statistical criterion for similarity judgment.
MaxCores	maximum number of cpu cores to use for parallel computing.
JobSize	how many samples can be drawn at once.
PCAimportance	PCA based feature selection; only variables important in PCA projection are considered.

## Value

Returns a list of data containing the drawn samples and the omitted data.

ReducedData	the selected sample data and class information.
RemucedData	the not-selected sample data and class information.

## Author(s)

Jorn Lotsch

## References

Lotsch, J. (2021): opdisDownsampling – an R Package for optimal distribution-preserving down-sampling of large (bio-medical) data sets.

## Examples

```
## example 1  
data(iris)  
Iris50percent <- opdisDownsampling(Data = iris[,1:4], Cls = as.integer(iris$Species),  
  Size = 50, MaxCores = 1)
```

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