Package ‘bbo’

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Type Package

Title Biogeography-Based Optimization

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Description This package provides an R implementation of Biogeography-Based Optimization (BBO), originally invented by Prof. Dan Simon, Cleveland State University, Ohio. This method is an application of the concept of biogeography, a study of the geographical distribution of biological organisms, to optimization problems. More information about this method can be found here: http://academic.csuohio.edu/simond/bbo/.

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LazyLoad yes

Repository CRAN

Depends

Suggests

NeedsCompilation no

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R topics documented:

`bbo` *Biogeography-Based Optimization*

Description

Solves global optimization problems via Biogeography-Based Optimization method.

Usage

```
bbo(fn, lower, upper, DisplayFlag = TRUE, RandSeed, control = bbo.control(), ...)
```

Arguments

`fn`	the function to be optimized (minimized).
`lower, upper`	two vectors specifying scalar real lower and upper bounds on each parameter to be optimized, so that the i-th element of `lower` and `upper` applied to the i-th parameter. The implementation searches between `lower` and `upper` for the global optimum (minimum) of `fn`.
`DisplayFlag`	TRUE or FALSE, whether or not to display, default is `TRUE`
`RandSeed`	random number seed
`control`	a list of control parameters; see `bbo.control`.
`...`	further arguments to be passed to `fn`

Details

Given an objective function, this method performs biogeography-based optimization and returns the minimum cost for the given objective function.

Value

The output of the function bbo is a list containing the following elements:
`prop`, a list of control parameters for BBO for the current run:

- `pModify`
- `pMutate`
- `KEEP`
- `popSize`
- `maxGen`
- `numVar`
- `orderDep`

`minCost`, a list containing the following elements:

- `bestMember`: the best set of parameters found.
- `bestValue`: the value of `fn` corresponding to `bestMember`.

`bestHabitat` a list containing the following elements:

- `itersBestValue`: the best value of `fn` at each iteration.
- `itersBestMember`: the best member at each iteration.
- `itersAvg`: the average population cost at each iteration.

Author(s)

For package **bbo**: Sarvesh Nikumbh<snikumbh@mpi-inf.mpg.de> Maintainer: Sarvesh Nikumbh<snikumbh@mpi-inf.mpg.de>

For BBO method: Prof. D. Simon, Cleveland State University, Ohio.

References

D. Simon, "Biogeography-Based Optimization", IEEE Transactions on Evolutionary Computation, vol. 12, no. 6, pp. 702-713, December 2008.

See Also

`bbo.control` for control arguments

Examples

```
## --------------------
## Rosenbrock function:
## --------------------
## It has a global minimum f(x) = 0 at (1,1).
## Kindly note that the first parameter passed to the
## objective function should be the vector of parameters
## to be optimized.
Rosenbrock <- function(x){
  x1 <- x[1]
  x2 <- x[2]
  return(  100 * (x2 - x1 * x1)^2 + (1 - x1)^2 )
   }

bbo(Rosenbrock, -5, 5, control =
bbo.control(pMutate = 0.4,
numVar = 2,
popSize = 50,
KEEP = 5,
maxGen = 20))
```

`bbo-methods` *bbo-methods*

Description

Methods for bbo objects.

Usage

```
## S3 method for class 'bbo'
summary(object, ...)
## S3 method for class 'bbo'
plot(x, plot.type = c("itersAvg", "itersBestValue"), ...)
```

Arguments

`object`	an object of class bbo; usually, a result of a call to `bbo`.
`x`	an object of class bbo; usually, a result of a call to `bbo`.
`plot.type`	should we plot the best member at each iteration, the best value at each iteration or the intermediate populations?
`...`	any additional arguments to be passed to plot function

Details

Members of the class `bbo` have a `plot` method that accepts the argument `plot.type`. `plot.type = "itersAvg"` results in a plot of the parameter values that represent the lowest value of the objective function at each generation. `plot.type = "itersBestValue"` plots the best value of the objective function each generation.

A summary method also exists and returns the best parameter vector (habitat), the best value of the objective function, average cost of all habitats in the population at each iteration, best habitat at each iteration and the cost of the best habitats.

Note

Further details and examples of the R package **bbo** can be found look at the package's vignette by typing `vignette("bbo")`.

Please cite the package in publications. Use `citation("bbo")`.

Author(s)

For package **bbo**: Sarvesh Nikumbh<snikumbh@mpi-inf.mpg.de> Maintainer: Sarvesh Nikumbh<snikumbh@mpi-inf.mpg.de>

For BBO method: Prof. D. Simon, Cleveland State University, Ohio.

References

D. Simon, "Biogeography-Based Optimization", IEEE Transactions on Evolutionary Computation, vol. 12, no. 6, pp. 702-713, December 2008.

See Also

`bbo` and `bbo.control`.

Examples

```
        ## --------------------
        ## Rosenbrock function:
        ## --------------------
        ## It has a global minimum f(x) = 0 at (1,1).
        ## Kindly note that the first parameter passed to the
        ## objective function should be the vector of parameters
        ## to be optimized.
        Rosenbrock <- function(x){
          x1 <- x[1]
          x2 <- x[2]
          return(  100 * (x2 - x1 * x1)^2 + (1 - x1)^2 )
        }

        sample.output.of.bbo <- bbo(Rosenbrock, -5, 5,
DisplayFlag = FALSE,
control = bbo.control(pMutate = 0.4,
numVar = 2,
popSize = 50,
KEEP = 5,
maxGen = 20))

## print the output information
bbo:::summary.bbo(sample.output.of.bbo)

## plot
bbo:::plot.bbo(sample.output.of.bbo, plot.type = "itersBestValue")
```

`bbo.control` *Control various aspects of the BBO implementation*

Description

Allow the user to set some characteristics of the Biogeography-based optimization algorithm implemented in bbo.

Usage

```
bbo.control(pModify = 1, pMutate = 0.3, KEEP = 5,
popSize = 20,
maxGen = 20,
numVar = 2,
orderDep = TRUE)
```

Arguments

`pModify`	habitat modification probability, between 0 and 1; default = 1
`pMutate`	mutation probability; default = 0.3
`KEEP`	elitism parameter: how many of the best habitats to keep from one generation to the next; default = 5
`popSize`	population size (i.e., number of candidate solutions for every generation) default = 20. Kindly make sure that `KEEP` is never greater than `popSize` and not <= 0
`maxGen`	number of generations; default = 20
`numVar`	number of variables in each population member (i.e., problem dimension); default = 2
`orderDep`	TRUE/FALSE; whether order of the parameters of the habitat is to be maintained; default = TRUE

Details

Control parameters for the `bbo`

Value

Returns a list with all the BBO algorithm parameters set

Author(s)

For package **bbo**: Sarvesh Nikumbh<snikumbh@mpi-inf.mpg.de> Maintainer: Sarvesh Nikumbh<snikumbh@mpi-inf.mpg.de>

For BBO method: Prof. D. Simon, Cleveland State University, Ohio.

References

D. Simon, "Biogeography-Based Optimization", IEEE Transactions on Evolutionary Computation, vol. 12, no. 6, pp. 702-713, December 2008.

See Also

`bbo.control` for control arguments

Examples

```
ct <- bbo.control(pMutate = 0.4, popSize = 50, KEEP = 10, maxGen = 50, numVar = 2)
```

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