Package ‘bbo’

February 19, 2015

Type Package

Title Biogeography-Based Optimization

Version 0.2

Date 2013-02-28

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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/.

License GPL (>= 3)

LazyLoad yes

Repository CRAN

Depends

Suggests

NeedsCompilation no

Date/Publication 2014-09-18 17:26:25

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**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


See Also

bbo.control for control arguments

Examples

```r
## --------------------------
## 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))
```
Description

Methods for bbo objects.

Usage

```r
## 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.
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.

References


See Also

bbo and bbo.control.

Examples

```r
## ----------------------
## 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")
```
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); de-
          fault = 2
orderDep TRUE/FALSE; whether order of the parameters of the habitat is to be main-
          tained; default = TRUE

Details

Control parameters for the bbo

Value

Returns a list with all the BBO algorithm parameters set

Author(s)

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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

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