Package ‘mco’

January 11, 2024

Version 1.16
Title Multiple Criteria Optimization Algorithms and Related Functions
Description A collection of function to solve multiple criteria optimization problems using genetic algorithms (NSGA-II). Also included is a collection of test functions.
Language en-US
Depends R (>= 3.0.0)
Suggests scatterplot3d, testthat
License GPL-2
URL https://github.com/olafmersmann/mco
Encoding UTF-8
LazyData yes

R topics documented:

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Description

Collection of functions implementing various MCO test problems.
Usage

belegundu(x)
belegundu.constr(x)
binh1(x)
binh2(x)
binh2.constr(x)
binh3(x)
deb3(x)
fonseca1(x)
fonseca2(x)
gianna(x)
hanne1(x)
hanne1.constr(x)
hanne2(x)
hanne2.constr(x)
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hanne4.constr(x)
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hanne5.constr(x)
jimenez(x)
jimenez.constr(x)
vnt(x)
zdt1(x)
zdt2(x)
zdt3(x)

Arguments

x     Input vector

Value

Function value.

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Examples

## Not run:
nsga2(belegundu, 2, 2,
    constraints=belegundu.constr, cdim=2,
    lower.bounds=c(0, 0), upper.bounds=c(5, 3))
nsga2(binh1, 2, 2,
    lower.bounds=c(-5, -5), upper.bounds=c(10, 10))
nsga2(binh2, 2, 2,
    lower.bounds=c(0, 0), upper.bounds=c(5, 3),
    constraints=binh2.constr, cdim=2)
nsga2(binh3, 2, 3, lower.bounds=c(10e-6, 10e-6), upper.bounds=c(10e6, 10e6))
nsga2(deb3, 2, 2, lower.bounds=c(0, 0), upper.bounds=c(1, 1), generations=500)
nsga2(fonseca1, 2, 2, lower.bounds=c(-100, -100), upper.bounds=c(100, 100))
nsga2(fonseca2, 2, 2, lower.bounds=c(-4, -4), upper.bounds=c(4, 4))
nsga2(gianna, 1, 2, lower.bounds=5, upper.bounds=10)
nsga2(hanne1, 2, 2, lower.bounds=c(0, 0), upper.bounds=c(10, 10), constraints=hanne1.constr, cdim=1)
nsga2(hanne2, 2, 2, lower.bounds=c(0, 0), upper.bounds=c(10, 10), constraints=hanne2.constr, cdim=1)
nsga2(hanne3, 2, 2, lower.bounds=c(0, 0), upper.bounds=c(10, 10), constraints=hanne3.constr, cdim=1)
nsga2(hanne4, 2, 2, lower.bounds=c(0, 0), upper.bounds=c(10, 10), constraints=hanne4.constr, cdim=1)
nsga2(hanne5, 2, 2, lower.bounds=c(0, 0), upper.bounds=c(10, 10), constraints=hanne5.constr, cdim=1)
nsga2(jimenez, 2, 2, lower.bounds=c(0, 0), upper.bounds=c(100, 100), constraints=jimenez.constr, cdim=4)
nsga2(vnt, 2, 3, lower.bounds=rep(-3, 2), upper.bounds=rep(3, 2))
nsga2(zdt1, 30, 2, lower.bounds=rep(0, 30), upper.bounds=rep(1, 30))
nsga2(zdt2, 30, 2, lower.bounds=rep(0, 30), upper.bounds=rep(1, 30))
nsga2(zdt3, 30, 2, lower.bounds=rep(0, 30), upper.bounds=rep(1, 30))

## End(Not run)
Description

Functions to evaluate the quality of the estimated pareto front.

Usage

generationalDistance(x, o)
generalizedSpread(x, o)
epsilonIndicator(x, o)
dominatedHypervolume(x, ref)

Arguments

x Estimated pareto front or an object which has a paretoFront method
o True pareto front or an object which has a paretoFront method
ref Reference point (may be omitted).

Details

Instead of the pareto front, one can also pass an object for which a paretoFront method exists to both methods.

For dominatedHypervolume, if no reference point is given, the maximum in each dimension is used as the reference point.

Value

The respective quality measure.

Note

This code uses version 1.3 of the hypervolume code available from https://lopez-ibanez.eu/hypervolume. For a description of the algorithm see


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References


Examples

```r
## Estimate true front:
## Not run:
tf <- nsga2(fonseca2, 2, 2,
    lower.bounds=c(-4, -4), upper.bounds=c(4, 4),
    popsize=1000, generations=100)
res <- nsga2(fonseca2, 2, 2,
    lower.bounds=c(-4, -4), upper.bounds=c(4, 4),
    popsize=16, generations=c(2, 4, 6, 8, 10, 20, 50))
n <- length(res)
sapply(1:n, function(i) dominatedHypervolume(res[[i]], c(1, 1)))
sapply(1:n, function(i) generationalDistance(res[[i]], tf))
sapply(1:n, function(i) generalizedSpread(res[[i]], tf))
sapply(1:n, function(i) epsilonIndicator(res[[i]], tf))
## End(Not run)
```

### normalizeFront

**normalizeFront**

Normalize a pareto front

#### Description

Rescales a pareto front to be in the unit hypercube

#### Usage

```r
normalizeFront(front, minval, maxval)
```

#### Arguments

- `front` Matrix containing the pareto front
- `minval` Vector containing the minimum value of each objective. May be omitted.
- `maxval` Vector containing the maximum value of each objective. May be omitted.

#### Value

Matrix containing the rescaled pareto front.

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NSGA II MOEA

Description

The NSGA-II algorithm minimizes a multidimensional function to approximate its Pareto front and Pareto set. It does this by successive sampling of the search space, each such sample is called a population. The number of samples taken is governed by the generations parameter, the size of the sample by the popsize parameter. Each population is obtained by creating so called offspring search points from the best individuals in the previous population. The best individuals are calculated by non-dominated sorting breaking ties using the crowding distance. The total number of function evaluations used is

\[ n_{eval} = \text{popsize} \times (\text{generations} + 1) \]

when generations is a single number and

\[ n_{eval} = \text{popsize} \times (\max(\text{generations}) + 1) \]

when generations is a vector of numbers. Note the additional generation of evaluations in the above equation. These stem from the initial population which must be evaluated before the algorithm can start evolving new individuals.

While the algorithm supports unbounded minimization, it will throw a warning and best results are obtained when a sensible upper and lower bound are given. No attempt is made to find such a sensible region of interest, instead if any element of the upper or lower bound is infinite, it is replace with a very large number (currently +/-4.49423283715579e+307).

Usage

```r	nsga2(fn, idim, odim, ..., constraints = NULL, cdim = 0,
    lower.bounds = rep(-Inf, idim), upper.bounds = rep(Inf, idim),
    popsize = 100, generations = 100,
    cprob = 0.7, cdist = 5,
    mprob = 0.2, mdist = 10,
    vectorized=FALSE)
```

Arguments

- **fn** Function to be minimized
- **idim** Input dimension
- **odim** Output dimension
- **...** Arguments passed through to 'fn'
- **constraints** Constraint function
- **cdim** Constraint dimension
- **lower.bounds** Lower bound of parameters
- **upper.bounds** Upper bound of parameters
- **popsize** Size of population
generations    Number of generations to breed. If a vector, then the result will contain the population at each given generation.
cprob         Crossover probability
cdist         Crossover distribution index
mprob         Mutation probability
mdist         Mutation distribution index
vectorized    If TRUE, the objective and constraint functions must be vectorized, i.e. accept a matrix instead of a vector and return a matrix instead of a vector. The matrix is structured such that one individual parameter combination is contained in each row (the matrix has shape \text{popsise} \times \text{idim}) and each objective is stored in a row of the returned matrix (the returned matrix must have shape \text{odim} \times \text{popsise}). A vectorized of a function \text{fn} should behave like \text{apply}(x, 1, f) for a population stored in the matrix \text{x}.

Value

If generation is an integer, a list describing the final population with components \text{par}, \text{value} and \text{pareto.optimal}. If generations is a vector, a list is returned. The i-th element of the list contains the population after \text{generations[i]} generations, this is not necessarily the set of new individuals that were evaluated in this generation. Some of the new individuals might have been eliminated in the selection phase.

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References


See Also

\code{zdt1} for more examples and a list of multiobjective test functions.

Examples

```r
## Binh 1 problem:
binh1 <- function(x) {
  y <- numeric(2)
  y[1] <- crossprod(x, x)
  y[2] <- crossprod(x - 5, x - 5)
  return (y)
}
r1 <- nsga2(binh1, 2, 2,
            generations=150, popsize=100,
            cprob=0.7, cdist=20,
            mprob=0.2, mdist=20,
            lower.bounds=rep(-5, 2),
            upper.bounds=rep(10, 2))
plot(r1)
```
## VNT problem:

```r
vnt <- function(x) {
  y <- numeric(3)
  xn <- crossprod(x, x)
  y[1] <- xn/2 + sin(xn);
  y[2] <- (crossprod(c(3, -2), x) + 4)^2/8 + (crossprod(c(1, -1), x) + 1)^2/27 + 15
  y[3] <- 1/(xn + 1) - 1.1*exp(-xn)
  return (y)
}
```

```r
r2 <- nsga2(vnt, 2, 3,
  generations=150, popsize=100,
  lower.bounds=rep(-3, 2),
  upper.bounds=rep(3, 2))
plot(r2)
```

## Example using constraints:

```r
## minimize f(x) = (x[1]^2, x[2]^2)
## subject to  g(x) = (sum(x) - 5) >= 0
f <- function(x) { x^2 }
g <- function(x) { sum(x) - 5 }
res <- nsga2(f, 2, 2, generations=500,
  lower.bounds=c(0, 0), upper.bounds=c(10, 10),
  constraints=g, cdim=1)
opar <-par(mfrow=c(1,2))
plot(res, xlab='y1', ylab='y2', main='Objective space')
plot(res$par, xlab='x1', ylab='x2', main='Parameter space')
par(opar)
```

---

### paretoFront

**Pareto Front and pareto set getters**

**Description**

Extract the pareto front or pareto set from an mco result object.

Filter an mco result and extract the pareto-optimal solutions.

**Usage**

```r
paretoFront(x, ...)
paretoSet(x, ...)
paretoFilter(x, ...)
```

**Arguments**

- `x` matrix or mco result object
- `...` Ignored

**Value**

A matrix containing the pareto front or pareto set.

`paretoFilter` returns those values in `x` which are not dominated by any other solution.
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