Politechnika Wrocławska

Inteligencja Obliczeniowa i jej zastosowania

Badanie algorytmu genetycznego z zakresu optymalizacji globalnej dla wybranych funkcji testowych

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Spis treści

1 Wprowadzenie

Wstęp

1.1 Opis zadania projektowego

1.2 Środowisko testowe i narzędzia

2 Implementacja

Listing 1: Skrypt w języku R wykorzystany do badań

```

rm(list=ls())

require("GA")
require("globalOptTests")
require("rgl")

# Params ----

n <- 5             # default 7
GAPopulation <- 10 # default 500
GAIterations <- 10 # default 50
GAMutations <- 0.1 # % (def 0.1)
GACrossovers <- 0.8 # % (def 0.8)

isSingleTest <- FALSE
graphs <- TRUE
quality <- 100 #graph probes

mutationTests <- seq(0, 1, 0.05)
crossoverTests <- seq(0, 1, 0.05)
elitismTests <- seq(0, 1, 0.05)
populationTests <- seq(10, 200, 10)
iterationTests <- seq(1, 20, 1)

# Functions ----

funcName <- "Branin" #2d
#funcName <- "Gulf" #3d
#funcName <- "CosMix4" #4d
#funcName <- "EMichalewicz" #5d
#funcName <- "Hartman6" #6d
#funcName <- "PriceTransistor" #9d
#funcName <- "Schwefel" #10d
#funcName <- "Zeldasine20" #20d

# Processing ----

dim <- getProblemDimen(funcName)
B <- matrix(unlist(getDefaultBounds(funcName)),ncol=dim,byrow=TRUE)
f <- function(xx) goTest(par=c(xx, rep(0, dim-length(xx))), fnName=funcName,
    checkDim = TRUE)
globalOpt <- getGlobalOpt(funcName)

if (graphs) {
  xprobes <- abs(B[2,1] - B[1,1]) / quality
  yprobes <- abs(B[2,2] - B[1,2]) / quality
  x <- seq(B[1,1], B[2,1], by = xprobes)
  y <- seq(B[1,2], B[2,2], by = yprobes)
  z <- outer(x, y, Vectorize(function(x,y) f(c(x,y))))
  nbcol = 100
  color = rev(rainbow(nbcol, start = 0/6, end = 4/6))
  zcol  = cut(z, nbcol)
  persp3d(x, y, z, theta=50, phi=25, expand=0.75, col=color[zcol],
          ticktype="detailed",axes=TRUE)
  persp3D(x, y, z, theta = -45, phi = 20, color.palette = jet.colors)
}

if (isSingleTest) {

  vector <- rep(NA,n)
  for (i in 1:n) {
    GAmin <- ga(type = "real-valued", fitness = function(xx) -f(xx),
              min = c(B[1,]), max = c(B[2,]),
              popSize = GAPopulation, maxiter = GAIterations,
              pmutation = GAMutations, pcrossover = GACrossovers)
    solution <- matrix(unlist(GAmin@solution),ncol=dim,byrow=TRUE)
    vector[i] <- f(solution[1,])
  }
  result <- matrix(c(vector),nrow = n,ncol = 1)
  write.table(result, file = "resultsSingle.csv", row.names=FALSE, na="", col.names=FALSE, sep=";")

} else {

  gMin <- .Machine$integer.max
  gBest <- NA

  temp <- c()
  values <- mutationTests
  averages <- c()
  for (mutation in values) {
    sum <- 0
    vector <- rep(NA,n)
    for (i in 1:n) {
      GAmin <- ga(type = "real-valued",
                fitness = function(xx) -f(xx),
                min = c(B[1,]), max = c(B[2,]),
                popSize = GAPopulation, maxiter = GAIterations,
                pmutation = mutation, pcrossover = GACrossovers)
      solution <- matrix(unlist(GAmin@solution),ncol=dim,byrow=TRUE)
      eval <- f(solution[1,])
      if (eval < gMin) {
        gMin <- eval
        gBest <- GAmin
      }
      sum <- sum + eval
      vector[i] <- eval
    }
    temp <- c(temp, vector)
    averages <- c(averages, (sum / n))
  }
  result <- matrix(c(temp),nrow = n,ncol = length(values))
  write.table(result, file = "resultsMutations.csv", row.names=FALSE, na="", col.names=FALSE, sep=";")

  if (graphs) {
```

```
  plot(values, averages,
      main="Goal function value for different mutation probabilities",
      ylim=c(min(c(averages,globalOpt)),max(c(averages,globalOpt))),
      type="l", col="red", xlab="params", ylab="value")
  abline(globalOpt,0, col="green")
}

temp <- c()
values <- crossoverTests
averages <- c()
for (crossover in values) {
  sum <- 0
  vector <- rep(NA,n)
  for (i in 1:n) {
    GAmin <- ga(type = "real-valued",
              fitness = function(xx) -f(xx),
              min = c(B[1,]), max = c(B[2,]),
              popSize = GAPopulation, maxiter = GAIterations,
              pmutation = GAMutations, pcrossover = crossover)
    solution <- matrix(unlist(GAmin@solution),ncol=dim,byrow=TRUE)
    eval <- f(solution[1,])
    if (eval < gMin) {
      gMin <- eval
      gBest <- GAmin
    }
    sum <- sum + eval
    vector[i] <- eval
  }
  temp <- c(temp, vector)
  averages <- c(averages, (sum / n))
}
result <- matrix(c(temp),nrow = n,ncol = length(values))
write.table(result, file = "resultsCrossover.csv", row.names=FALSE, na="",
    col.names=FALSE, sep=";")

if (graphs) {
  plot(values, averages,
      main="Goal function value for different crossover probabilities",
      ylim=c(min(c(averages,globalOpt)),max(c(averages,globalOpt))),
      type="l", col="red", xlab="params", ylab="value")
  abline(globalOpt,0, col="green")
}

temp <- c()
values <- elitismTests
averages <- c()
for (elitism in values) {
  sum <- 0
  vector <- rep(NA,n)
  for (i in 1:n) {
    GAmin <- ga(type = "real-valued",
              fitness = function(xx) -f(xx),
              min = c(B[1,]), max = c(B[2,]),
              popSize = GAPopulation, maxiter = GAIterations,
              pmutation = GAMutations, pcrossover = GACrossovers, elitism =
                  elitism)
    solution <- matrix(unlist(GAmin@solution),ncol=dim,byrow=TRUE)
    eval <- f(solution[1,])
    if (eval < gMin) {
      gMin <- eval
      gBest <- GAmin
    }
    sum <- sum + eval
    vector[i] <- eval
  }
  temp <- c(temp, vector)
  averages <- c(averages, (sum / n))
}
result <- matrix(c(temp),nrow = n,ncol = length(values))
write.table(result, file = "resultsElitism.csv", row.names=FALSE, na="",
    col.names=FALSE, sep=";")

if (graphs) {
  plot(values, averages,
      main="Goal function value for different elitism",
      ylim=c(min(c(averages,globalOpt)),max(c(averages,globalOpt))),
      type="l", col="red", xlab="params", ylab="value")
  abline(globalOpt,0, col="green")
}

temp <- c()
values <- populationTests
averages <- c()
for (population in values) {
  sum <- 0
  vector <- rep(NA,n)
  for (i in 1:n) {
    GAmin <- ga(type = "real-valued",
               fitness = function(xx) -f(xx),
               min = c(B[1,]), max = c(B[2,]),
               popSize = population, maxiter = GAIterations,
               pmutation = GAMutations, pcrossover = GACrossovers)
    solution <- matrix(unlist(GAmin@solution),ncol=dim,byrow=TRUE)
    eval <- f(solution[1,])
    if (eval < gMin) {
      gMin <- eval
      gBest <- GAmin
    }
    sum <- sum + eval
    vector[i] <- eval
  }
  temp <- c(temp, vector)
  averages <- c(averages, (sum / n))
}
result <- matrix(c(temp),nrow = n,ncol = length(values))
write.table(result, file = "resultsPopulation.csv", row.names=FALSE, na="",
    col.names=FALSE, sep=";")

if (graphs) {
  plot(values, averages,
      main="Goal function value for different population sizes",
      ylim=c(min(c(averages,globalOpt)),max(c(averages,globalOpt))),
         type="l", col="red", xlab="params", ylab="value")
    abline(globalOpt,0, col="green")
  }

  temp <- c()
  values <- iterationTests
  averages <- c()
  for (iterations in values) {
    sum <- 0
    vector <- rep(NA,n)
    for (i in 1:n) {
      GAmin <- ga(type = "real-valued",
                  fitness = function(xx) -f(xx),
                  min = c(B[1,]), max = c(B[2,]),
                  popSize = GAPopulation, maxiter = iterations,
                  pmutation = GAMutations, pcrossover = GACrossovers)
      solution <- matrix(unlist(GAmin@solution),ncol=dim,byrow=TRUE)
      eval <- f(solution[1,])
      if (eval < gMin) {
        gMin <- eval
        gBest <- GAmin
      }
      sum <- sum + eval
      vector[i] <- eval
    }
    temp <- c(temp, vector)
    averages <- c(averages, (sum / n))
  }
  result <- matrix(c(temp),nrow = n,ncol = 10)
  write.table(result, file = "resultsIterations.csv", row.names=FALSE, na="",
      col.names=FALSE, sep=";")

  if (graphs) {
    plot(values, averages,
         main="Goal function value for different iteration quantities",
         ylim=c(min(c(averages,globalOpt)),max(c(averages,globalOpt))),
         type="l", col="red", xlab="params", ylab="value")
    abline(globalOpt,0, col="green")
  }

}

if (graphs) {
  summary(GAmin)
  filled.contour(x, y, z, color.palette = jet.colors, nlevels = 24,
     plot.axes = {
       axis(1);
       axis(2);
       points(solution[1,1], solution[1,2], pch = 3, cex = 5, col = "black", lwd
           = 2)
     }
  )
  plot(GAmin)
}
```

2.1 Parametryzacja skryptu

Parametryzacji podlega jedynie algorytm genetyczny. Wybór funkcji do optymalizacji odbywa się przez podanie jej nazwy. Pozostałe dane są odczytywane z pakietu „globalOptTests”.

3 Przebieg badań

Do badań zostały wybrane funkcje o różnych wymiarach zaczynając na 2 kończąc na 20. Poniżej wymieniono te funkcje wraz z ilością wymiarów podaną w nawiasie.

- Branin (2)
- Gulf (3)
- CosMix4 (4)
- EMichalewicz (5)
- Hartman6 (6)
- PriceTransistor (9)
- Schwefel (10)
- Zeldasine20 (20)

3.1 Branin (wariant 2D)

Test

3.2 Gulf (wariant 3D)

Test

3.3 CosMix4 (wariant 4D)

Test

3.4 EMichalewicz (wariant 5D)

Test

3.5 Hartman6 (wariant 6D)

Test

3.6 PriceTransistor (wariant 9D)

Test

3.7 Schwefel (wariant 10D)

Test

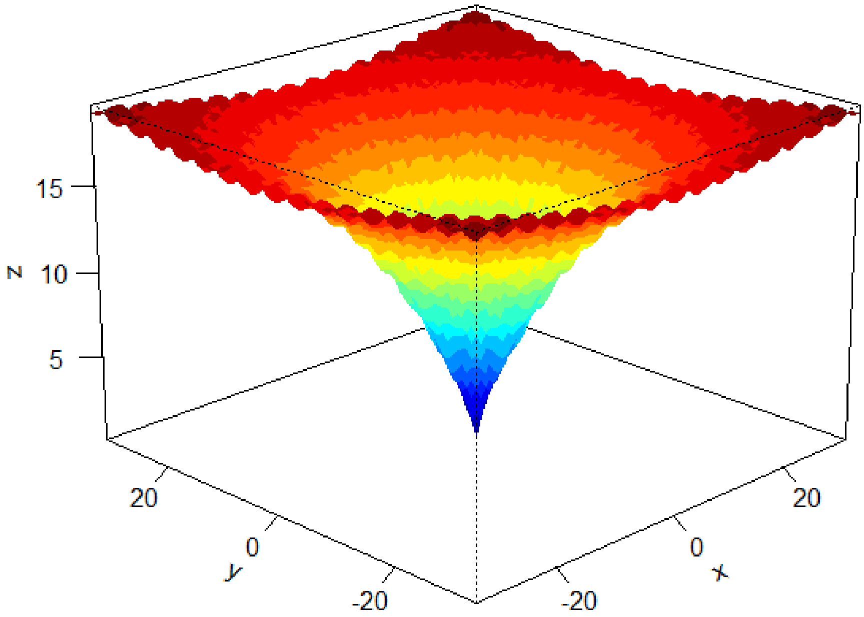
3.8 Zeldasine20 (wariant 20D)

Test

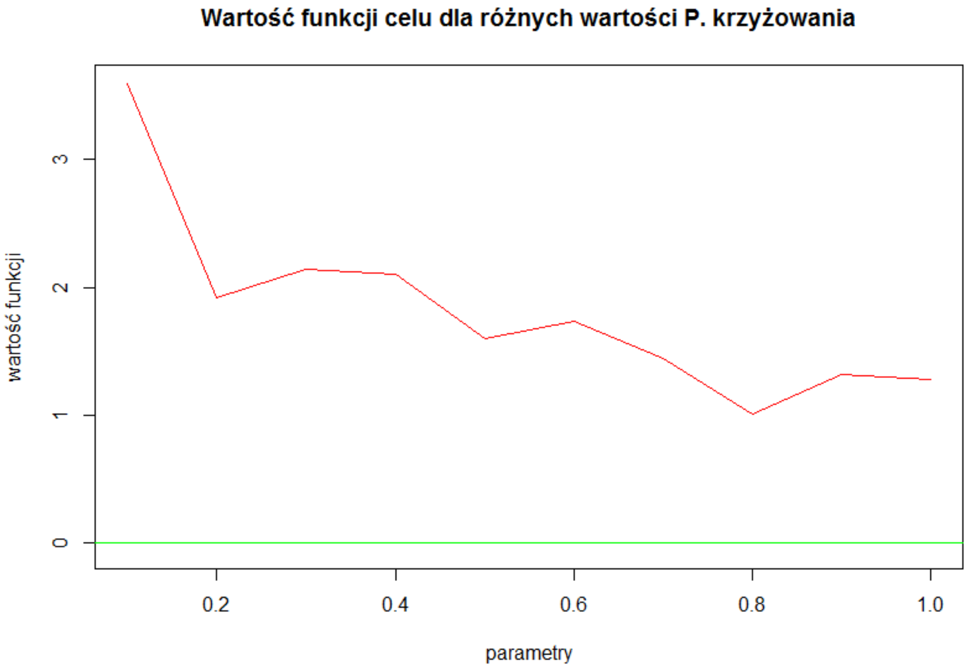
3.9 Test

Test

Na ilustracji (rys. 1) przedstawiono wykres omawianej funkcji.



Rysunek 1: Wykres funkcji Ackleys (d=3)



Rysunek 2: Wartość znalezionego minimum funkcji w zależności od P. krzyżowania

4 Podsumowanie

Test

Akapit

Literatura

[1] Artur Suchwałko “Wprowadzenie do R dla programistów innych języków” https://cran.r-project.org/doc/contrib/R-dla-programistow-innych-jezykow.pdf