POLITECHNIKA WROCŁAWSKA

Inteligencja Obliczeniowa i jej zastosowania

Badanie algorytmu genetycznego z zakresu optymalizacji globalnej dla wybranych funkcji testowych

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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
10
   GAPopulation <- 10 # default 500
11
   GAIterations <- 10 # default 50
   GAMutations <- 0.1 # % (def 0.1)
   GACrossovers <- 0.8 # % (def 0.8)
14
15
   isSingleTest <- FALSE
16
   graphs <- TRUE</pre>
17
   quality <- 100 #graph probes
18
19
   mutationTests <- seq(0, 1, 0.05)</pre>
   crossoverTests <- seq(0, 1, 0.05)</pre>
21
   elitismTests \leftarrow seq(0, 1, 0.05)
22
   populationTests <- seq(10, 200, 10)
23
   iterationTests <- seq(1, 20, 1)</pre>
24
   # Functions ----
26
27
   funcName <- "Branin" #2d</pre>
   #funcName <- "Gulf" #3d</pre>
29
   #funcName <- "CosMix4" #4d</pre>
30
   #funcName <- "EMichalewicz" #5d</pre>
31
   #funcName <- "Hartman6" #6d</pre>
   #funcName <- "PriceTransistor" #9d</pre>
33
   #funcName <- "Schwefel" #10d</pre>
34
   #funcName <- "Zeldasine20" #20d</pre>
35
   # Processing ----
37
38
   dim <- getProblemDimen(funcName)</pre>
39
   B <- matrix(unlist(getDefaultBounds(funcName)),ncol=dim,byrow=TRUE)</pre>
   f <- function(xx) goTest(par=c(xx, rep(0, dim-length(xx))), fnName=funcName,
41
        checkDim = TRUE)
   globalOpt <- getGlobalOpt(funcName)</pre>
43
    if (graphs) {
44
     xprobes \leftarrow abs(B[2,1] - B[1,1]) / quality
45
     yprobes \leftarrow abs(B[2,2] - B[1,2]) / quality
46
     x \leftarrow seq(B[1,1], B[2,1], by = xprobes)
47
     y \le seq(B[1,2], B[2,2], by = yprobes)
48
     z <- outer(x, y, Vectorize(function(x,y) f(c(x,y))))</pre>
49
     nbcol = 100
```

```
color = rev(rainbow(nbcol, start = 0/6, end = 4/6))
      zcol = cut(z, nbcol)
52
      persp3d(x, y, z, theta=50, phi=25, expand=0.75, col=color[zcol],
53
              ticktype="detailed",axes=TRUE)
54
      persp3D(x, y, z, theta = -45, phi = 20, color.palette = jet.colors)
56
57
    if (isSingleTest) {
58
      vector <- rep(NA,n)</pre>
60
      for (i in 1:n) {
61
        GAmin <- ga(type = "real-valued", fitness = function(xx) -f(xx),
62
                    \min = c(B[1,]), \max = c(B[2,]),
                    popSize = GAPopulation, maxiter = GAIterations,
64
                    pmutation = GAMutations, pcrossover = GACrossovers)
        solution <- matrix(unlist(GAmin@solution),ncol=dim,byrow=TRUE)</pre>
        vector[i] <- f(solution[1,])</pre>
67
68
      result <- matrix(c(vector), nrow = n, ncol = 1)
      write.table(result, file = "resultsSingle.csv", row.names=FALSE, na="",
          col.names=FALSE, sep=";")
71
    } else {
72
73
      gMin <- .Machine$integer.max
74
      gBest <- NA
76
      temp \leftarrow c()
77
      values <- mutationTests</pre>
78
      averages <- c()
79
      for (mutation in values) {
80
        sum <- 0
        vector <- rep(NA,n)</pre>
82
        for (i in 1:n) {
83
          GAmin <- ga(type = "real-valued",</pre>
84
                      fitness = function(xx) - f(xx),
85
                      \min = c(B[1,]), \max = c(B[2,]),
86
                      popSize = GAPopulation, maxiter = GAIterations,
87
                      pmutation = mutation, pcrossover = GACrossovers)
89
          solution <- matrix(unlist(GAmin@solution),ncol=dim,byrow=TRUE)</pre>
          eval <- f(solution[1,])</pre>
90
          if (eval < gMin) {</pre>
91
            gMin <- eval
92
            gBest <- GAmin
93
          }
94
          sum <- sum + eval
95
          vector[i] <- eval</pre>
97
        temp <- c(temp, vector)</pre>
98
        averages <- c(averages, (sum / n))</pre>
99
100
101
      result <- matrix(c(temp),nrow = n,ncol = length(values))</pre>
      write.table(result, file = "resultsMutations.csv", row.names=FALSE, na="",
102
          col.names=FALSE, sep=";")
      if (graphs) {
104
```

```
plot(values, averages,
             main="Goal function value for different mutation probabilities",
106
             ylim=c(min(c(averages,globalOpt)),max(c(averages,globalOpt))),
             type="1", col="red", xlab="params", ylab="value")
108
        abline(globalOpt,0, col="green")
109
112
      temp <- c()
      values <- crossoverTests</pre>
      averages <- c()
114
      for (crossover in values) {
        sum <- 0
116
        vector <- rep(NA,n)</pre>
117
        for (i in 1:n) {
118
          GAmin <- ga(type = "real-valued",</pre>
119
                      fitness = function(xx) - f(xx),
120
                      \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)</pre>
124
          eval <- f(solution[1,])</pre>
          if (eval < gMin) {</pre>
126
            gMin <- eval
            gBest <- GAmin
128
          sum <- sum + eval</pre>
130
          vector[i] <- eval</pre>
131
        temp <- c(temp, vector)</pre>
133
        averages <- c(averages, (sum / n))</pre>
134
135
      result <- matrix(c(temp),nrow = n,ncol = length(values))</pre>
136
      write.table(result, file = "resultsCrossover.csv", row.names=FALSE, na="",
137
          col.names=FALSE, sep=";")
138
      if (graphs) {
        plot(values, averages,
140
             main="Goal function value for different crossover probabilities",
141
             ylim=c(min(c(averages,globalOpt)),max(c(averages,globalOpt))),
142
             type="1", col="red", xlab="params", ylab="value")
        abline(globalOpt,0, col="green")
144
145
146
      temp <- c()
147
      values <- elitismTests</pre>
148
      averages <- c()
149
      for (elitism in values) {
        sum <- 0
        vector <- rep(NA,n)</pre>
        for (i in 1:n) {
          GAmin <- ga(type = "real-valued",</pre>
154
                      fitness = function(xx) - f(xx),
                      \min = c(B[1,]), \max = c(B[2,]),
156
                      popSize = GAPopulation, maxiter = GAIterations,
157
                      pmutation = GAMutations, pcrossover = GACrossovers, elitism =
                          elitism)
```

```
solution <- matrix(unlist(GAmin@solution),ncol=dim,byrow=TRUE)
159
          eval <- f(solution[1,])</pre>
160
          if (eval < gMin) {</pre>
161
            gMin <- eval
162
            gBest <- GAmin
163
164
          sum <- sum + eval</pre>
165
166
          vector[i] <- eval</pre>
        temp <- c(temp, vector)</pre>
168
        averages <- c(averages, (sum / n))</pre>
169
170
      result <- matrix(c(temp),nrow = n,ncol = length(values))</pre>
171
      write.table(result, file = "resultsElitism.csv", row.names=FALSE, na="",
172
          col.names=FALSE, sep=";")
      if (graphs) {
        plot(values, averages,
175
176
             main="Goal function value for different elitism",
             ylim=c(min(c(averages,globalOpt)),max(c(averages,globalOpt))),
177
             type="1", col="red", xlab="params", ylab="value")
178
        abline(globalOpt,0, col="green")
179
180
      temp <- c()
182
      values <- populationTests</pre>
183
      averages <- c()
184
      for (population in values) {
        sum <- 0
186
        vector <- rep(NA,n)</pre>
187
        for (i in 1:n) {
          GAmin <- ga(type = "real-valued",</pre>
                      fitness = function(xx) - f(xx),
190
                      \min = c(B[1,]), \max = c(B[2,]),
191
                      popSize = population, maxiter = GAIterations,
192
                      pmutation = GAMutations, pcrossover = GACrossovers)
193
          solution <- matrix(unlist(GAmin@solution),ncol=dim,byrow=TRUE)</pre>
194
          eval <- f(solution[1,])</pre>
195
          if (eval < gMin) {</pre>
            gMin <- eval
            gBest <- GAmin
198
199
          sum <- sum + eval</pre>
200
          vector[i] <- eval</pre>
201
202
        temp <- c(temp, vector)</pre>
203
        averages <- c(averages, (sum / n))</pre>
204
205
      result <- matrix(c(temp),nrow = n,ncol = length(values))</pre>
206
      write.table(result, file = "resultsPopulation.csv", row.names=FALSE, na="",
207
          col.names=FALSE, sep=";")
      if (graphs) {
209
        plot(values, averages,
210
             main="Goal function value for different population sizes",
             ylim=c(min(c(averages,globalOpt)),max(c(averages,globalOpt))),
212
```

```
type="1", col="red", xlab="params", ylab="value")
213
        abline(globalOpt,0, col="green")
214
216
217
      temp <- c()
      values <- iterationTests</pre>
218
      averages <- c()
219
      for (iterations in values) {
220
        sum <- 0
        vector <- rep(NA,n)</pre>
222
        for (i in 1:n) {
223
          GAmin <- ga(type = "real-valued",</pre>
224
                      fitness = function(xx) - f(xx),
225
                      \min = c(B[1,]), \max = c(B[2,]),
226
                      popSize = GAPopulation, maxiter = iterations,
227
                      pmutation = GAMutations, pcrossover = GACrossovers)
          solution <- matrix(unlist(GAmin@solution),ncol=dim,byrow=TRUE)</pre>
          eval <- f(solution[1,])</pre>
230
          if (eval < gMin) {</pre>
231
232
            gMin <- eval
            gBest <- GAmin
233
          }
234
          sum <- sum + eval</pre>
235
          vector[i] <- eval</pre>
236
237
        temp <- c(temp, vector)</pre>
238
        averages <- c(averages, (sum / n))</pre>
239
      result <- matrix(c(temp), nrow = n, ncol = 10)
241
      write.table(result, file = "resultsIterations.csv", row.names=FALSE, na="",
242
          col.names=FALSE, sep=";")
243
      if (graphs) {
244
        plot(values, averages,
245
             main="Goal function value for different iteration quantities",
246
             ylim=c(min(c(averages,globalOpt)),max(c(averages,globalOpt))),
247
             type="1", col="red", xlab="params", ylab="value")
248
        abline(globalOpt,0, col="green")
249
      }
251
252
253
    if (graphs) {
254
      summary(GAmin)
255
      filled.contour(x, y, z, color.palette = jet.colors, nlevels = 24,
256
         plot.axes = {
257
           axis(1);
           axis(2);
259
           points(solution[1,1], solution[1,2], pch = 3, cex = 5, col = "black", lwd
260
261
262
      )
      plot(GAmin)
263
264
```

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 "global OptTests".

3 Przebieg badań

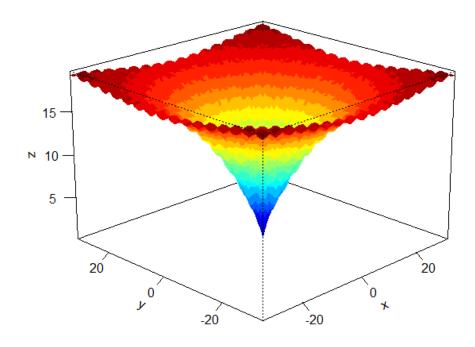
Do badań zostały wybrane funkcje o różnych wymiarach zaczynając na 2 kończąc na 20. Poniżej wymieniono te funkcje wraz z ilością wymiarów podaną w nawiasie.

• Branin (2) • Gulf (3) • CosMix4 (4) • EMichalewicz (5) • Hartman6 (6) • PriceTransistor (9) • Schwefel (10) • Zeldasine20 (20) 3.1 Branin (wariant 2D) Test Gulf (wariant 3D) 3.2 Test CosMix4 (wariant 4D) 3.3 Test 3.4 EMichalewicz (wariant 5D) Test 3.5 Hartman6 (wariant 6D) Test PriceTransistor (wariant 9D) 3.6 Test Schwefel (wariant 10D) 3.7 Test 3.8 Zeldasine20 (wariant 20D) Test

3.9 Test

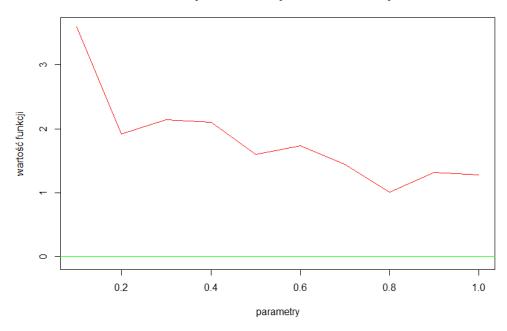
Test

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



Rysunek 1: Wykres funkcji Ackleys (d=3)

Wartość funkcji celu dla różnych wartości P. krzyżowania



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

4 Podsumowanie

Test

Akapit

Literatura

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