732A90: Computational Statistics

Computer lab6 - Group11

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Question 1: Genetic algorithm

In this exercise we are going to perform one-dimensional maximization by using a genetic algorithm.

1.

Firstly, we define the function `f()` as

$$f(x) := \frac{x^2}{e^x} - 2\ \exp(-(9\sin\ x)/(x^2+x+1)).$$

2.

Secondly, we define the function `crossover()`, that takes two scalars x and y as inputs, and returns a child as $\frac{x+y}{2}$.

3.

Thirdly, we define the function `mutate()`, that performs the integer division x^2 mod 30, for a scalar input x.

4.

Further, we will create a function called `genetic()`, with the parameters `maxiter` and `mutprob`. The settings of this `genetic()` function, as well as its output results, are presented in (a)-(e). The code can be found in the Appendix.

(a). The function $f()$ is plotted in the range from 0 to 30 in Figure X, and we can observe that there is a maximum value located around $x = 1$.

(b). An initial population for the genetic algorithm is defined as $X = (0, 5, 10, 15, ..., 30)$.

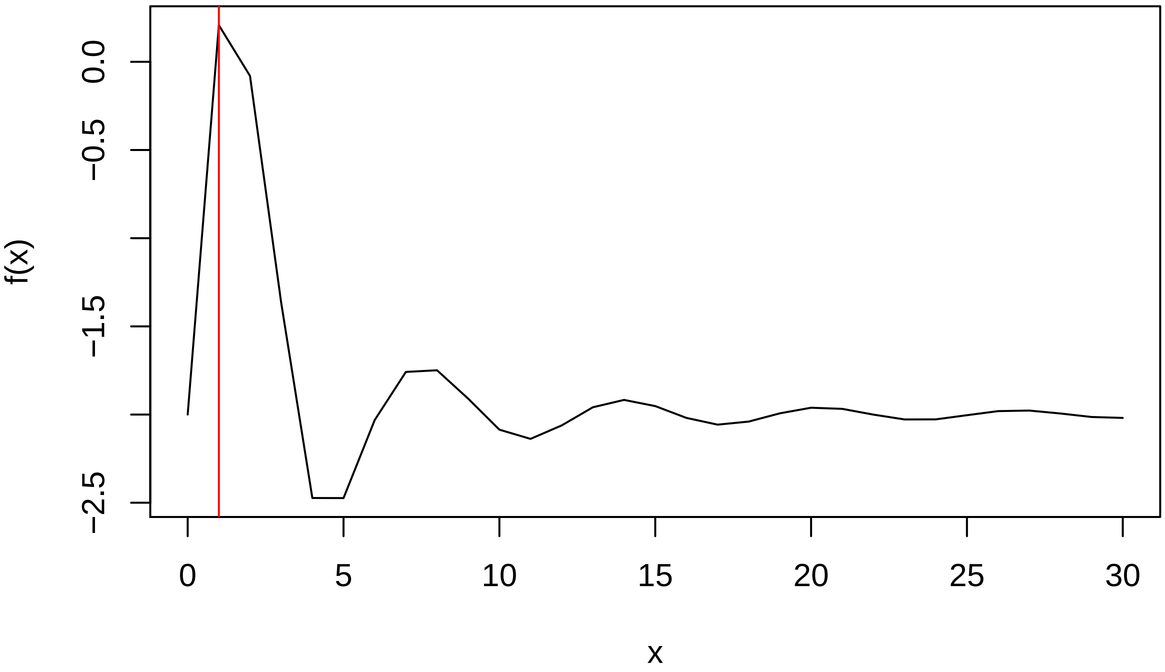
(c). A vector called `Values` are computed, containing the function values for each population point.

(d). The `genetic()` function performs `maxiter` iterations. For each iteration…

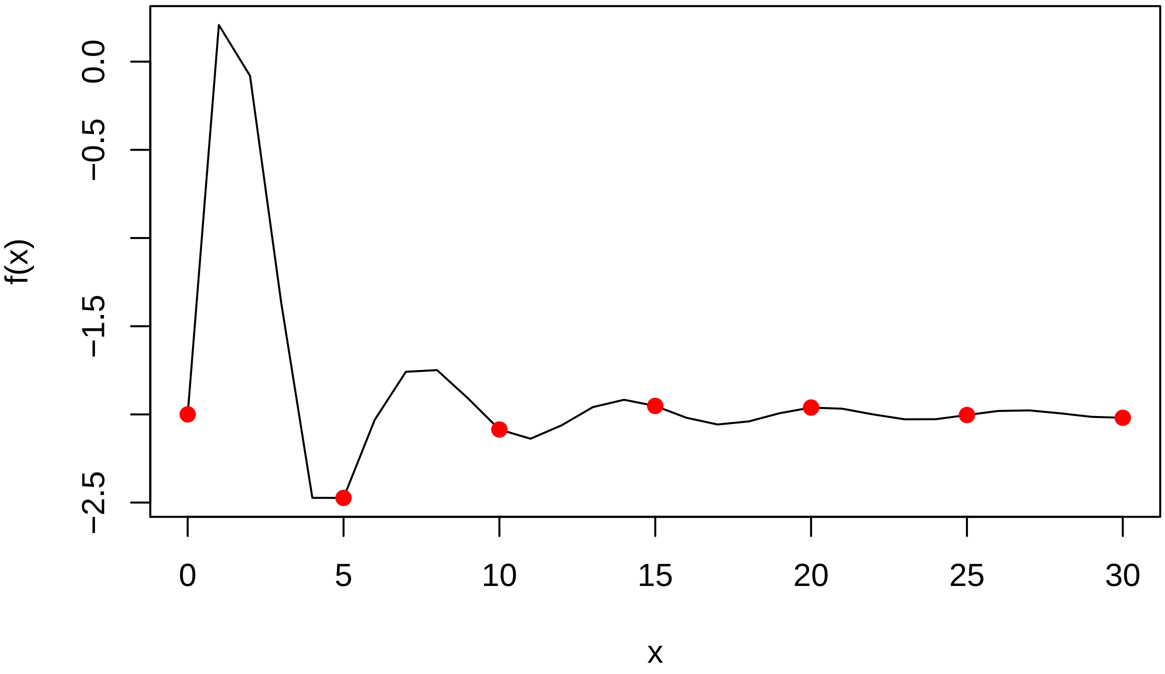
(e).

5.

By using the defined functions from previous tasks (1.1-1.4), we are going to observe the initial population and final population. This is done by running the code with different combinations of `maxiter`$= 10, 100$ and `mutprob`$= 0.1, 0.5, 0.9$.



```
## [1]  0  5 10 15 20 25 30
## [1] -2.000000 -2.473573 -2.085654 -1.951947 -1.961344 -2.003663 -2.019194
```



Question 2: EM algorithm

1.

2.

3.

4.

Appendix

```
knitr::opts_chunk$set(echo = FALSE)
# R version
RNGversion('3.5.1')
#1.1
f <- function(x){
  return(x^2/exp(x) - 2*exp(-1*(9*sin(x)) / (x^2 + x + 1)))
}

#1.2
crossover <- function(x,y){
  return((x+y) / 2)
}

#1.3
mutate <- function(x){
  return(x^2 %% 30)
}
#4
#4
genetic <- function(maxiter, mutprob){
  #a
  plot(x = seq(0,30), y = f(seq(0,30)), type = "l", xlab = "x", ylab = "f(x)")
  abline(v=seq(0,30)[which.max(f(seq(0,30)))], col="red" )

  #b
  X = seq(0,30,5)

  #c
  Values = f(X)

  #d
  #set seed
  set.seed(1234567890)
  for (i in 1:maxiter) {
    #i
    parents = match(sample(X, 2),X)
    #ii
    victim = order(Values)[1]

    #iii
    kid = round(crossover(parents[1],parents[2]))
    p = runif(1)
    if (p < mutprob) {
      kid = mutate(kid)
    }

    #iv
    X[victim] = kid
    Values = f(X)

    #v
    max = max(Values)
  }

  #e
  print(X)
  print(Values)
  plot(x = seq(0,30), y = f(seq(0,30)), type = "l", xlab = "x", ylab = "f(x)")
  points(x = X, y = Values, col = "red", pch = 19)
}


# Just testing no change, i.e. initial population
genetic(1,0)
# R version
RNGversion('3.5.1')
# Packages
```