Genetic Algorithm

Define the function

Below is the objective function:

$$f(x) := \frac{x^2}{e^x} - 2e^{\left(-\left(\frac{9\sin x}{x^2 + x + 1}\right)\right)}$$

```
#objective function . This is used to check the fitness of the population
funcs <- function(x){
   frst_trm = x^2/exp(x)
   scnd_trm = 2*exp(-(9*sin(x))/((x^2)+x+1))

   y <- frst_trm - scnd_trm
   return(y)
}</pre>
```

Define the function crossover

```
#Produce new kid
crossover <- function(x,y){
    return((x+y)/2)
}</pre>
```

Define function mutate

```
#Mutate the kid
mutate <- function(x) {
    return((x^2)%%30)
}</pre>
```

Function for genetic algorithm

```
x <- replace(x,victim,kid)

new_val <- funcs(kid) #calculate objective function with respect to the new kid
    Values <-replace(Values,victim,new_val) #Update the resultant objective function
}

return(list(x,Values))
}

gene_algo1 <- genetic_algorithm(10100,0.1)
gene_algo2 <- genetic_algorithm(10100,0.5)
gene_algo3 <- genetic_algorithm(10100,0.9)

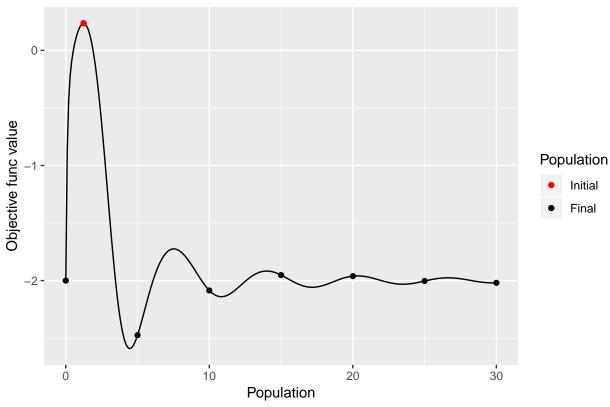
x <- seq(0,30,by=0.1)
val <- funcs(x)

data_pt <- cbind(x=x,val=val)
data_pt <- as.data.frame(data_pt)

x_ini=seq(0,30,by=5)
y_ini=funcs(x_ini)</pre>
```

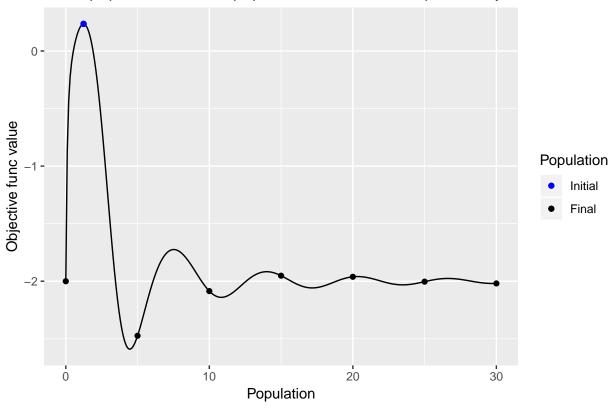
With mutation probability 0.1, not all the 5 points might reach maximum because the probability is very low. But it might happen due to random chance that the points might reach maxima since we are doing many iterations.

Initial population vs final population with mutation probability 0.1



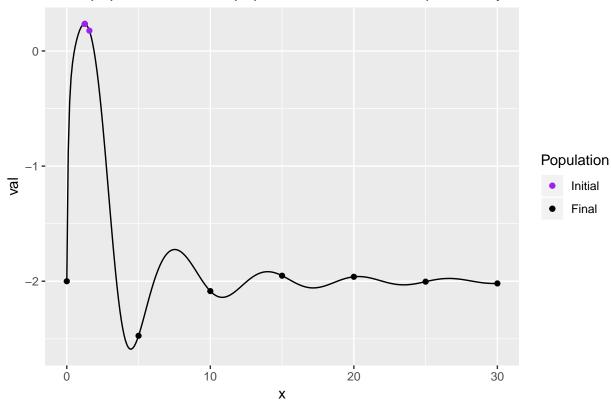
With mutation probability 0.5, the probability for the initial population to mutate is more than the previous one. Here we can see all the 5 points has converged to one.

Initial population vs final population with mutation probability 0.5



With mutation probability 0.9, the probability to mutate further increases than the previous one. So most of the points lies on the peak.

Initial population vs final population with mutation probability 0.9



Analysis

Here we choose victim based on the objective function. Basically we can cosnider the victim as the weakest in the population. So we tend to replace the weakest with the strong one with each iteration. With many iteration, all the the points in the population converges to maximum. With mutation probability 0.1, the tendency to mutate is very less. But with many iterations, the mutation keeps happens although at slow rate. The mutation further increases with probability 0.5 and 0.9