

Lab 6 Vaso

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28/2/2020

Question 1: Genetic algorithm

In this assignment, you will try to perform one-dimensional maximization with the help of a genetic algorithm.

1. Define the function

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

```
f <- function(x){  
  f= x^2/exp(x) - 2*exp(-(9*sin(x))/(x^2 + x + 1))  
  return(f)  
}
```

2. Define the function crossover(): for two scalars x and y it returns their “kid” as (x+y)/2.

```
crossover <- function(x,y){  
  kid = (x+y)/2  
  return(kid)  
}
```

3. Define the function mutate() that for a scalar x returns the result of the integer division x^2 mod 30. (Operation mod is denoted in R as %%).

```
mutate <- function(x){  
  res = x^2 %% 30  
  return(res)  
}
```

4. Write a function that depends on the parameters *maxiter* and *mutprob* and:

- (a) Plots function f in the range from 0 to 30. Do you see any maximum value?
- (b) Defines an initial population for the genetic algorithm as $X = (0,5,10,15,\dots,30)$.
- (c) Computes vector Values that contains the function values for each population point.

(d) Performs maxiter iterations where at each iteration

- i. Two indexes are randomly sampled from the current population, they are further used as parents (use sample()).
- ii. One index with the smallest objective function is selected from the current population, the point is referred to as victim (use order()).
- iii. Parents are used to produce a new kid by crossover. Mutate this kid with probability mutprob (use crossover(), mutate()).
- iv. The victim is replaced by the kid in the population and the vector Values is updated.
- v. The current maximal value of the objective function is saved.

(e) Add the final observations to the current plot in another colour.

```
## The max value of the initial population is
```

```
## [1] -1.951947
```

```
## $population
```

```
## [1] 0.00 13.75 7.50 15.00 20.00 25.00 27.50
```

```
##
```

```
## $values
```

```
## [1] -2.000000 -1.919668 -1.724415 -1.951947 -1.961344 -2.003663 -1.984025
```

```
##
```

```
## $max_value
```

```
## [1] -1.724415
```

```
## $population
```

```
## [1] 3.12500 15.00000 6.25000 15.00000 21.97266 13.12500 7.50000
```

```
##
```

```
## $values
```

```
## [1] -1.549543 -1.951947 -1.937529 -1.951947 -1.999342 -1.949121 -1.724415
```

```
##
```

```
## $max_value
```

```
## [1] -1.549543
```

```
## $population
```

```
## [1] 13.12500 14.06250 6.25000 15.00000 3.847656 6.253928 9.227600
```

```
##
```

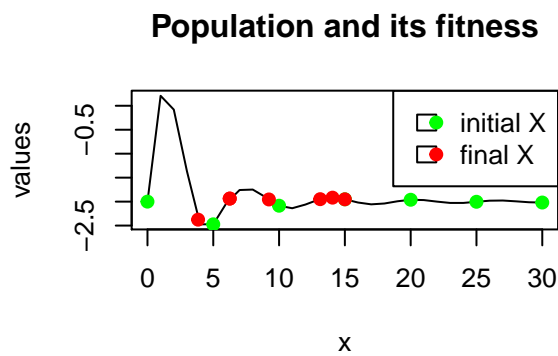
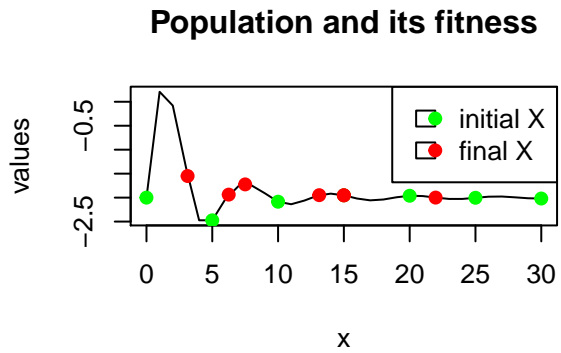
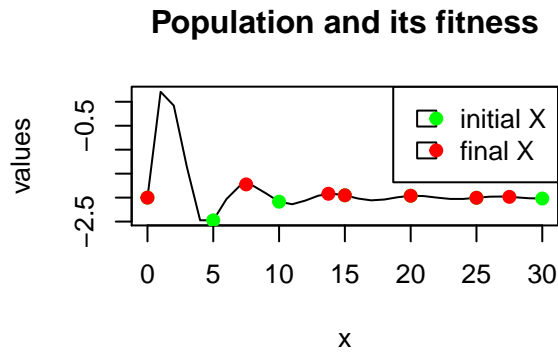
```
## $values
```

```
## [1] -1.949121 -1.917255 -1.937529 -1.951947 -2.376255 -1.936182 -1.954998
```

```
##
```

```
## $max_value
```

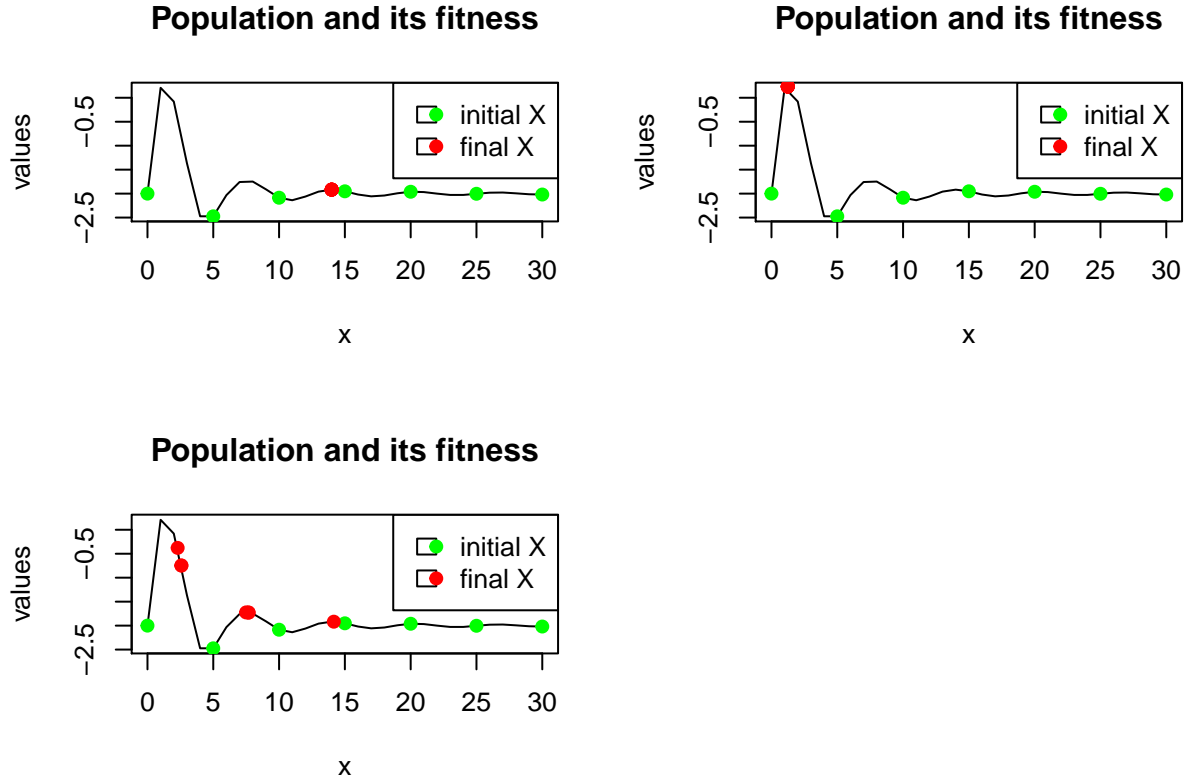
```
## [1] -1.917255
```



```
## $population
## [1] 13.99895 13.99895 13.99895 13.99895 13.99895 13.99895 13.99895
##
## $values
## [1] -1.917091 -1.917091 -1.917091 -1.917091 -1.917091 -1.917091 -1.917091
##
## $max_value
## [1] -1.917091

## $population
## [1] 1.239183 1.239153 1.239198 1.239123 1.239213 1.239243 1.239198
##
## $values
## [1] 0.234853 0.234853 0.234853 0.234853 0.234853 0.234853 0.234853
##
## $max_value
## [1] 0.234853

## $population
## [1] 7.494428 2.578678 2.294006 7.684867 14.160156 7.684867 2.578678
##
## $values
## [1] -1.7244482 -0.7460108 -0.3782303 -1.7273524 -1.9181358 -1.7273524 -0.7460108
##
## $max_value
## [1] -0.3782303
```



Genetic algorithm is widely used for optimization problems. This algorithm is inspired by the evolutionary theory and the ideas of natural selection. So, based on this idea, we start with an initial population and based on an objective function that evaluates the fitness of each point in the population we keep every time those candidates that have the best fitness values and then those candidates reproduce and give the offsprings. This is done using the successor functions, which are *crossover()* and *mutation()* and then comes selection. *Crossover* is used to combine two parents and produce a child and *mutation* takes a candidate and returns a slightly different candidate. Mutation is very important for the genetic algorithm because sometimes some important genes might be missing from the population and thus, mutation allows as to search as much as possible in the search space and avoid getting stuck in local maxima(or minima).

At first we are asked to plot function f in the range from 0 to 30 and see if there's a maximum value. So, in this graph we can observe the global maximum value is approximately 0.20 and is given when x is around 2.

The first three plots represent the results of the algorithm run with **maxiter**=10 and **mutprob**=0.1,0.5 and 0.9 respectively.

The last three plots represent the results of the algorithm run with **maxiter**=100 and **mutprob**=0.1,0.5 and 0.9 respectively.

For **maxiter**=10 we can see that the algorithm does not converge to the global maximum for none of the three probabilities. When *mutprob*=0.5 the max value is -1.549543 which is the biggest compared to the other two max values obtained with mutation probabilities 0.1 and 0.9 but still it's quite far from the global maximum. We would say that probably 10 iterations were not enough for the algorithm to converge and the algorithm gets stuck to local maxima.

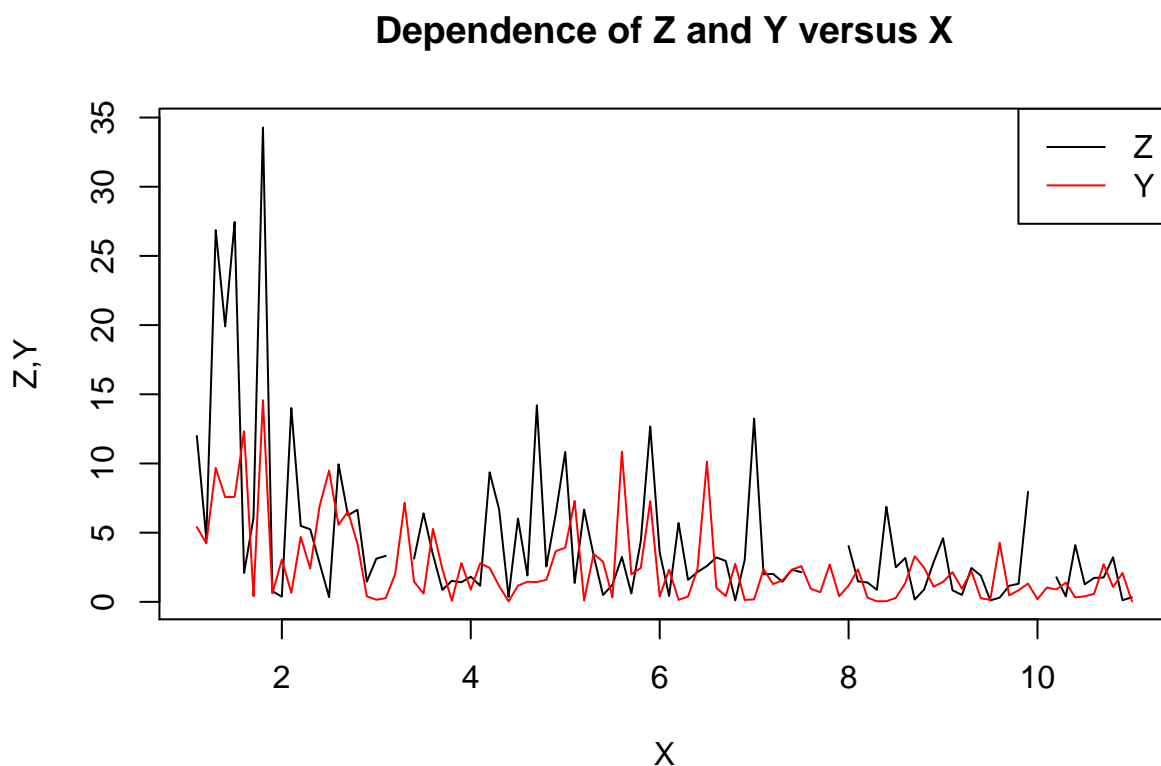
On the other hand, when **maxiter**=100 we see that the algorithm converged with *mutprob*=0.5 and the maximum value obtained is 0.234853. For *mutprob*=0.9 the maximum value found was -0.3782303 which was close to the global but still not converged and the maximum value obtained with *mutprob*=0.1 was even further from the optimal one.

To conclude, the algorithm found the optimal maximum value(0.234853) for **maxiter**=100 and *mutprob*=0.5.

Question 2: EM algorithm

The data file `physical.csv` describes a behavior of two related physical processes $Y=Y(X)$ and $Z=Z(X)$.

1. Make a time series plot describing dependence of Z and Y versus X. Does it seem that two processes are related to each other? What can you say about the variation of the response values with respect to X?



First thing we observe when looking at this time series plot is that there are some blank points in Z, which means that some data are missing. Z has quite a few peaks, with the highest ones being observed for small values of X. Y also has a quite similar pattern to Z, with peaks that are more intense at the beginning, but generally smaller values than Z. As we said, the variation of both response values compared to X is higher for small values of X and smaller for bigger values of X.

2. Note that there are some missing values of Z in the data which implies problems in estimating models by maximum likelihood. Use the following model $Y_i \sim \exp(X_i/\lambda)$, $Z_i \sim \exp(X_i/2\lambda)$ where λ is some unknown parameter. The goal is to derive an EM algorithm that estimates λ .

With optimal value λ , loglikelihood will be maximized. However, due to several missing values of Z, expected value of loglikelihood will be maximized instead. Through this task, we will try to estimate the optimal value

λ that could return the maximum expected value of loglikelihood. Furthermore, the number of iterations performed to obtain optimal λ will be found.

The process of obtaining above mentioned two is based on the following mathematics:

1. Assume that Y and Z are independent.
2. Calculate likelihood function of λ

$$L(\lambda|Y, Z) = \frac{\prod_{i=1}^n x_i^2}{(2\lambda^2)^n} e^{-\frac{\sum_{i=1}^n x_i y_i}{\lambda} - \frac{\sum_{i=1}^n x_i z_i}{2\lambda}}$$

3. Calculate loglikelihood function of λ

$$l(\lambda|Y, Z) = -2n\log(\lambda) - \frac{\sum_{i=1}^n x_i y_i}{\lambda} - \frac{\sum_{i=1}^n x_i z_i}{2\lambda} + C$$

The terms that does not contain λ do not affect loglikelihood value, because those values are fixed. Therefore, on above mathematical expression, such terms are written as a constant, C .

4. Find expected loglikelihood

$$E[l(\lambda|Y, Z)] = E\left[-2n\log(\lambda) - \frac{\sum_{i=1}^n x_i y_i}{\lambda} - \frac{\sum_{i \in \text{observed}} x_i z_i}{2\lambda} - \frac{\sum_{j \in \text{unobserved}} x_j z_j}{2\lambda} + C\right]$$

All terms except $\frac{\sum_{j \in \text{unobserved}} x_j z_j}{2\lambda}$ are from observed data. Expected value of a constant number is a constant number. So there is only one term that involves uncertainty. Since Z follows exponential distribution with parameter $\frac{x_j}{2\lambda_{t-1}}$, unobserved Z_i 's expected value will be $\frac{2\lambda_{t-1}}{x_j}$, such that λ_{t-1} represents λ value obtained in previous iteration.

$$E\left[\frac{\sum_{j \in \text{unobserved}} x_j z_j}{2\lambda}\right] = \sum_{j \in \text{unobserved}} \frac{x_j}{2\lambda} \frac{2\lambda_{t-1}}{x_j} = \sum_{j \in \text{unobserved}} \frac{\lambda_{t-1}}{\lambda} = U \frac{\lambda_{t-1}}{\lambda}, \text{ U is a number of unobserved Z.}$$

5. Take a derivative of the expected loglikelihood with respect to λ

$$\frac{\partial l(\lambda)}{\partial \lambda} = \frac{-2n}{\lambda} + \frac{\sum_{i=1}^n x_i y_i}{\lambda^2} + \frac{\sum_{i \in \text{observed}} x_i z_i}{2\lambda^2} + U \frac{\lambda_{t-1}}{\lambda^2}$$

6. Set above equal to 0, find λ and update its value

$$\lambda = \frac{(\sum_{i=1}^n x_i y_i) + (\frac{\sum_{i \in \text{observed}} x_i z_i}{2}) + (U \lambda_{t-1})}{2n}$$

3. Implement this algorithm in R, use $\lambda_0 = 100$ and convergence criterion “stop if the change in λ is less than 0.001”. What is the optimal λ and how many iterations were required to compute it?

```
set.seed(12345)

n= nrow(data)
Zobs= Z[!is.na(Z)]
Zmiss= Z[is.na(Z)]
```

```

M= length(Zmiss)

lambda <- vector()
lambda[1] = 100

i=2
repeat{
  lambda[i] = (sum(X*Y) + 0.5*sum(X[which(!is.na(Z))]*Zobs) + M*lambda[i-1]) / (2*n)

  if (abs(lambda[i]- lambda[i-1]) < 0.001){
    break()
  }
  i = i+1
}

num_iter = length(lambda)
optimal = lambda[num_iter]

cat("The optimal lambda is:", "\n")

```

```
## The optimal lambda is:
```

```
optimal
```

```
## [1] 10.69566
```

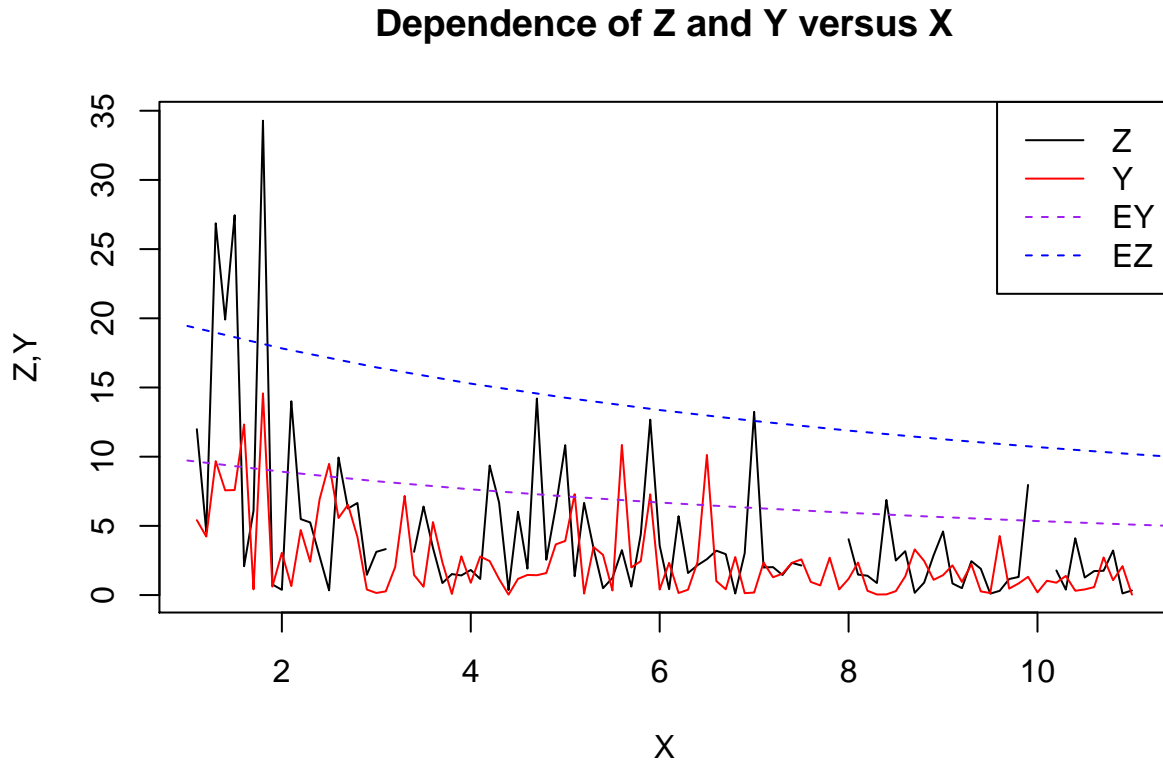
```
cat("and the number of iterations required is:", "\n")
```

```
## and the number of iterations required is:
```

```
num_iter
```

```
## [1] 6
```

4. Plot $E[Y]$ and $E[Z]$ versus X in the same plot as Y and Z versus X . Comment whether the computed λ seems to be reasonable.



Since $Y_i \sim \exp(X_i/\lambda)$, $Z_i \sim \exp(X_i/2\lambda)$ the expected value of Y will be $E(Y) = \lambda/X$ and the expected value of Z will be $E(Z) = \lambda/2X$.

Both lines that represent the expected values seen in the plot seem to be reasonable for representing the mean as they have more or less the same pattern as the data so it seems that the mean is following. Also, $E(Y)$ is higher in the plot and this is actually reasonable as Z has generally a bit higher values compared to Y and also the mean of Z is two times the mean of Y.

Appendix

```
f <- function(x){
  f= x^2/exp(x) - 2*exp(-(9*sin(x))/(x^2 + x + 1))
  return(f)
}
crossover <- function(x,y){
  kid = (x+y)/2
  return(kid)
}
mutate <- function(x){
  res = x^2 %% 30
  return(res)
}
set.seed(12345)
GA <- function(maxiter,mutprob){

  X <- seq(0,30,5)
  v <- c(0:30)
  initialplot <- plot(v,f(v),main="Population and its fitness",xlab="x",ylab = "values",type="l")
  points(X,f(X),col="green",type = "p",pch=19) #plot also the initial population for comparison

  parent <- vector(length = 2)
  kid <- vector(length = 2)
  victim <- 0
  max_value <- 0

  X <- seq(0,30,5) #initialize population
  values <- f(X)

  i=1
  while (i <= maxiter){

    parent <- sample(X,2)

    victim <- order(values)[1] #index of the smallest obj func value

    kid <- crossover(parent[1],parent[2])

    #Use runif to see if new kid needs to be mutated
    prop_mutat = runif(1,0,1)

    if (prop_mutat < mutprob){
      new_kid = mutate(kid)
    } else {
      new_kid = kid
    }

    #replace victim by new kid and update values
    X[victim] = new_kid
    values = f(X) #update values
  }
}
```

```

    max_value = max(values) #current maximal value of the objective function
    i=i+1

}
initialplot
points(X,values,col="red",type = "p",pch=19)
legend("topright",-1, -0.5, legend=c("initial X", "final X"),
      col=c("green", "red"), pch=19)
return(list("population"=X,"values"=values,"max_value"=max_value))
}

X <- seq(0,30,5)
cat("The max value of the initial population is","\n")
max(f(X))

par(mfrow=c(2,2))
GA(10,0.1)
GA(10,0.5)
GA(10,0.9)

par(mfrow=c(2,2))
GA(100,0.1)
GA(100,0.5)
GA(100,0.9)

data <- read.csv("~/Computational Stat/732A90_VT2020_Materials/physical1.csv")
X <- data$X
Y <- data$Y
Z <- data$Z
plot(X,Z,main="Dependence of Z and Y versus X",type="l",ylab="Z,Y")
lines(X,Y,col="red")
legend("topright",legend=c("Z", "Y"),lty =1,
      col=c("black", "red"))
set.seed(12345)

n= nrow(data)
Zobs= Z[!is.na(Z)]
Zmiss= Z[is.na(Z)]

M= length(Zmiss)

lambda <- vector()
lambda[1] = 100

i=2
repeat{
  lambda[i] = (sum(X*Y) + 0.5*sum(X[which(!is.na(Z))]*Zobs) + M*lambda[i-1]) / (2*n)

  if (abs(lambda[i]- lambda[i-1]) < 0.001){
    break()
  }
  i = i+1
}

```

```

}

num_iter = length(lambda)
optimal = lambda[num_iter]

cat("The optimal lambda is:","\n")
optimal

cat("and the number of iterations required is:","\n")
num_iter

EY <- optimal/X
EZ <- (2*optimal)/X
plot(X,Z,main="Dependence of Z and Y versus X",type="l",ylab="Z,Y")
lines(X,Y,col="red")
lines(EY,col="purple",lty=2)
lines(EZ,col="blue",lty=2)

legend("topright",legend=c("Z", "Y", "EY", "EZ"),lty =c(1,1,2,2),
      col=c("black", "red", "purple", "blue"))

```