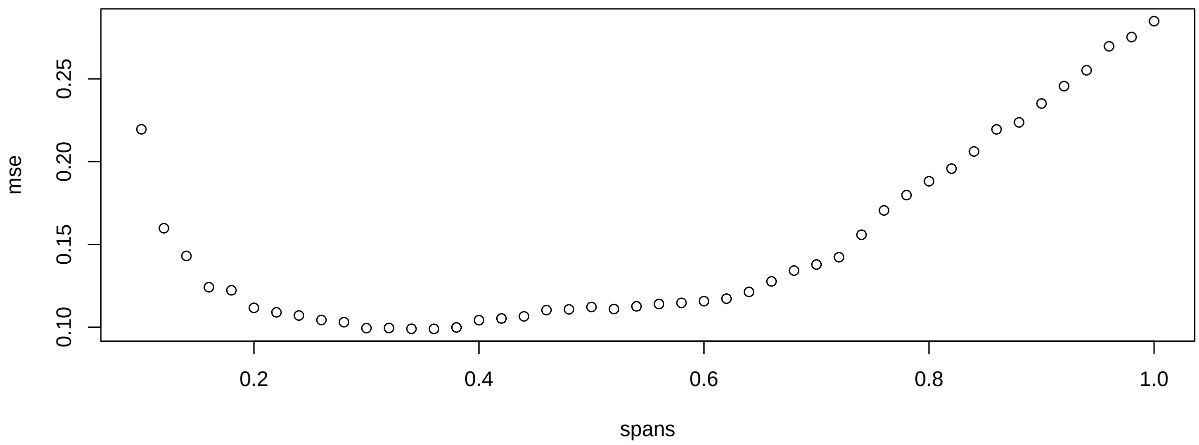
```
#> Warning: package 'caret' was built under R version 3.5.3
```

A3)

a)

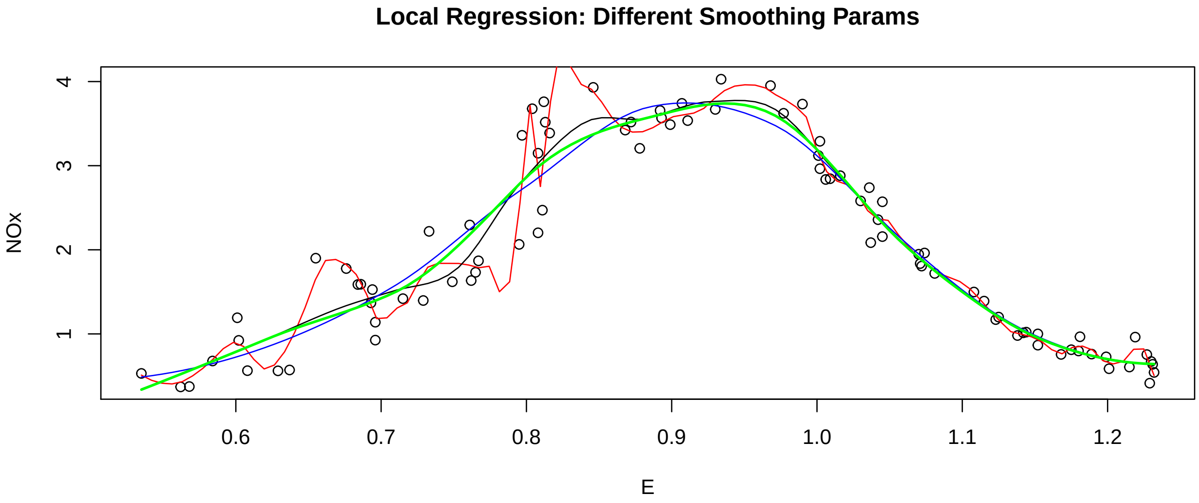
```r
set.seed(1337)
data(ethanol)

loessMod10 <- loess(NOx ~ E, data=ethanol, span=0.1) # 10% smoothing span
loessMod30 <- loess(NOx ~ E, data=ethanol, span=0.3) # 25% smoothing span
loessMod50 <- loess(NOx ~ E, data=ethanol, span=0.5)

spans = seq(0.1, 1, 0.02)

#Randomly shuffle the data
data <- ethanol[sample(nrow(ethanol)),]
#Create 10 equally size folds
folds <- cut(seq(1,nrow(data)),breaks=5,labels=FALSE)
#Perform 10 fold cross validation
test <- matrix(NA, ncol=2, nrow = length(spans))
mse1 <- c()
for (span in spans){
  mse <- c()
  for(j in 1:5){
    #Segement your data by fold using the which() function
    testIndexes <- which(folds==j,arr.ind=TRUE)
    testData <- data[testIndexes, ]
    trainData <- data[-testIndexes, ]
    #Use the test and train data partitions however you desire...

    fit <- loess(NOx ~ E, data=trainData, span=span, control = loess.control(surface="direct"))

    y.pred <- predict(fit, newdata = testData$E)
    y.true = testData$NOx

    mse <- append(mse, mean((y.pred-y.true)^2))

  }
  mse1 <- append(mse1, mean(mse))
}

test <- NULL
test$spans <- spans
test$mse <- mse1
test <- as.data.frame(test)

plot(test)
```



```
opt_spans <- test$spans[test$mse == min(test[,"mse"])]
opt_spans
#> [1] 0.36
loessMod_opt <- loess(NOx ~ E, data=ethanol, span=opt_spans)
```

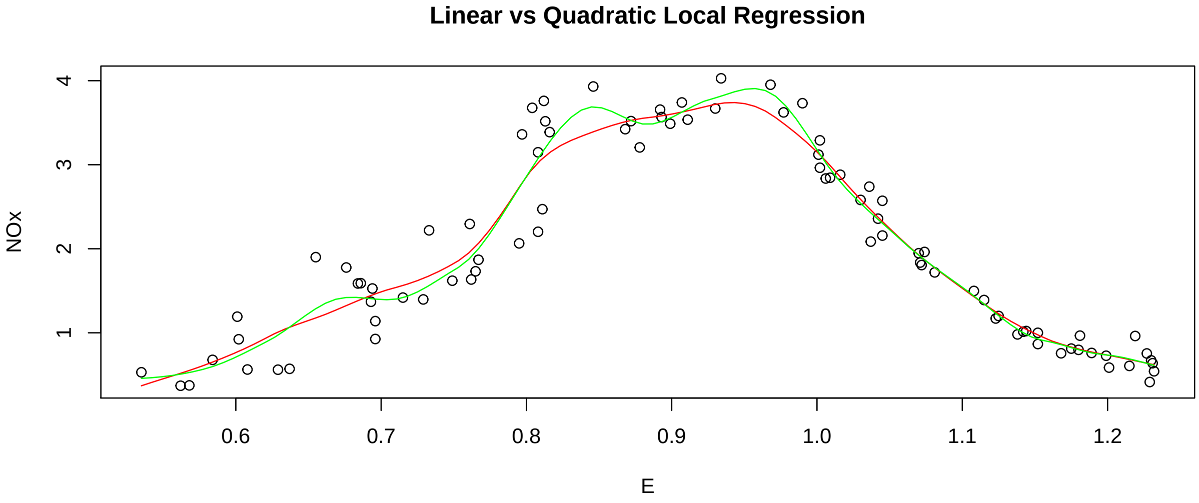
b)

```
tricube_10 <- locfit(NOx~lp(E,nn=0.1), data=ethanol)
tricube_30 <- locfit(NOx~lp(E,nn=0.3), data=ethanol)
tricube_50 <- locfit(NOx~lp(E,nn=0.5), data=ethanol)
tricube_opt <- locfit(NOx~lp(E,nn=opt_spans), data=ethanol)

plot(ethanol$NOx, x=ethanol$E, main="Local Regression: Different Smoothing Params", xlab="E", ylab="NOx
lines(tricube_10, col="red")
lines(tricube_30, col="black")
lines(tricube_50, col="blue")
lines(tricube_opt, col="green", lw=2)
```



c)

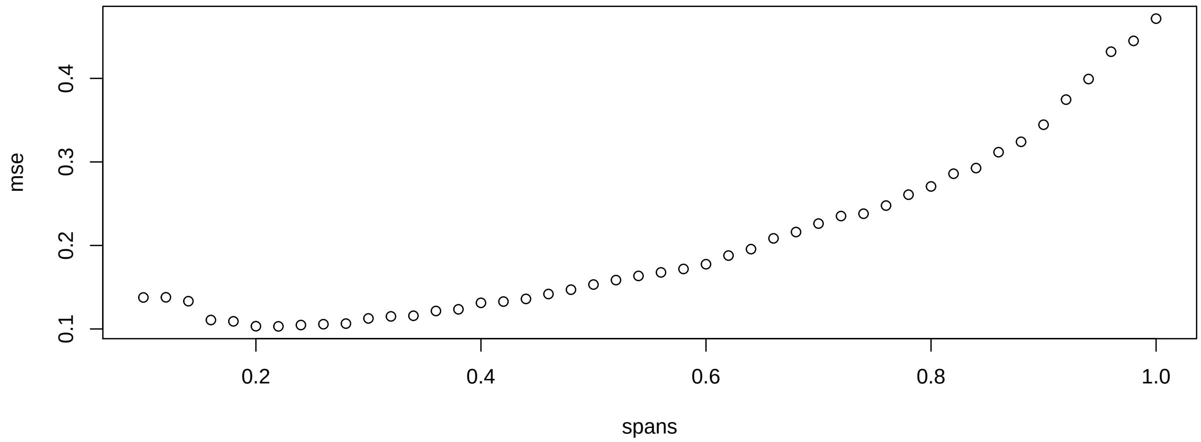
```
lin <- locfit(NOx ~ E, data=ethanol, alpha = 0.2, deg=1)
quad <- locfit(NOx ~ E, data=ethanol, alpha = 0.2, deg=2)

plot(ethanol$NOx, x=ethanol$E, main="Linear vs Quadratic Local Regression", xlab="E", ylab="NOx")
lines(lin, col="red")
lines(quad, col="green")
```



```
lin_pred <- cbind(predict(lin, newdata = c(0.65)), predict(lin, newdata = c(9)))
quad_pred <- cbind(predict(quad, newdata = c(0.65)), predict(quad, newdata = c(9)))

preds <- as.data.frame(rbind(lin_pred, quad_pred), row.names = c("lin","quad"))
colnames(preds) <- c("0.65", "9")
preds
#>          0.65          9
#> lin  1.146328   -27.68762
#> quad 1.229701 -1686.31546
```

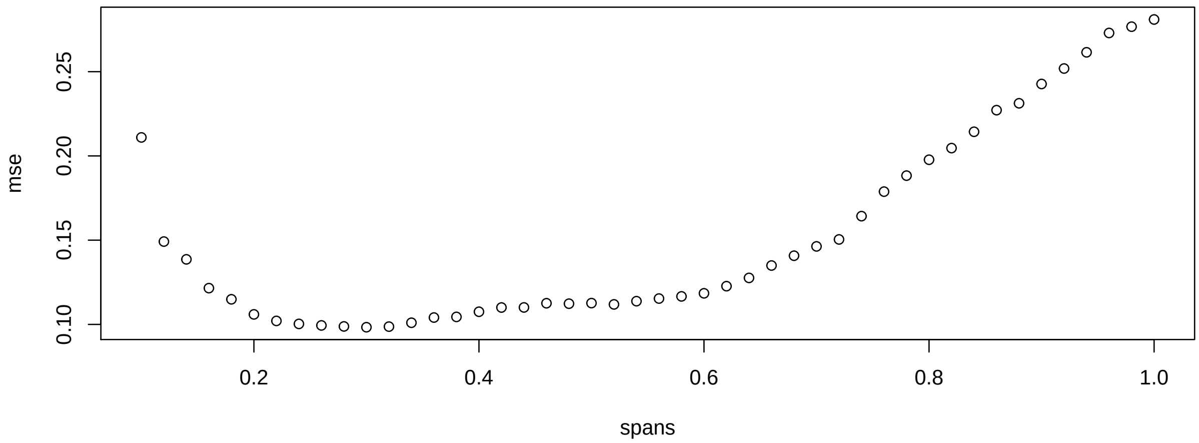
d)

```
set.seed(1337)

mse1 <- c()
for (span in spans){
  mse <- c()
  for(j in 1:5){
    #Segement your data by fold using the which() function
    testIndexes <- which(folds==j,arr.ind=TRUE)
    testData <- data[testIndexes, ]
    trainData <- data[-testIndexes, ]
    #Use the test and train data partitions however you desire...

    fit <- locfit(NOx ~ E, data=trainData, alpha = span, deg=1)

    y.pred <- predict(fit, newdata = testData$E)
    y.true = testData$NOx

    mse <- append(mse, mean((y.pred-y.true)^2))

  }
  mse1 <- append(mse1, mean(mse))
}

lin_cv <- NULL
lin_cv$spans <- spans
lin_cv$mse <- mse1
lin_cv <- as.data.frame(lin_cv)

plot(lin_cv)
```



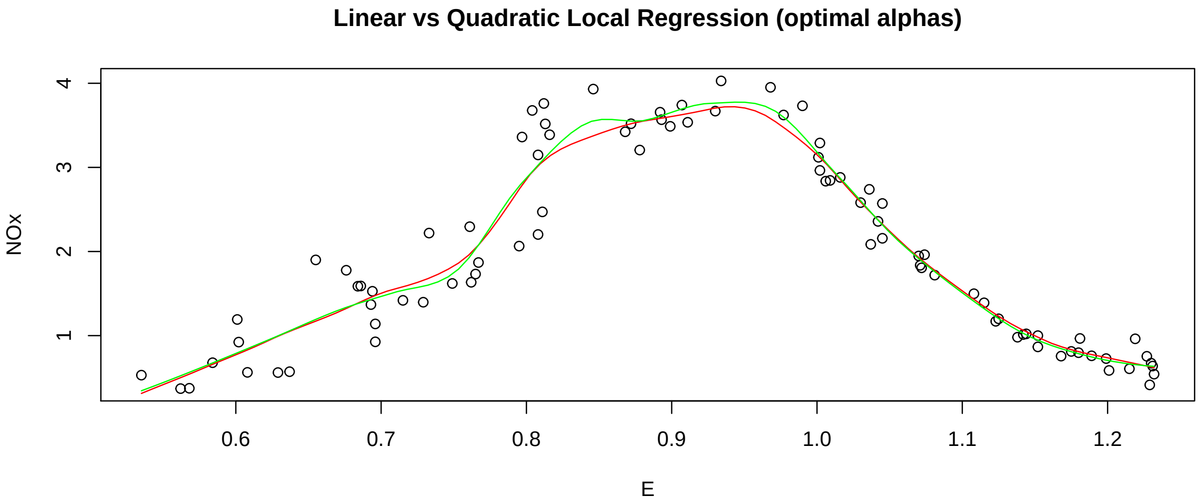
```
opt_lin <- lin_cv$spans[lin_cv$mse == min(lin_cv[,"mse"])]
opt_lin
#> [1] 0.22
```

```
mse1 <- c()
for (span in spans){
  mse <- c()
  for(j in 1:5){
    #Segement your data by fold using the which() function
    testIndexes <- which(folds==j,arr.ind=TRUE)
    testData <- data[testIndexes, ]
    trainData <- data[-testIndexes, ]
    #Use the test and train data partitions however you desire...

    fit <- locfit(NOx ~ E, data=trainData, alpha = span, deg=2)

    y.pred <- predict(fit, newdata = testData$E)
    y.true = testData$NOx

    mse <- append(mse, mean((y.pred-y.true)^2))

  }
  mse1 <- append(mse1, mean(mse))
}

quad_cv <- NULL
quad_cv$spans <- spans
quad_cv$mse <- mse1
quad_cv <- as.data.frame(quad_cv)

plot(quad_cv)
```



```
opt_quad <- quad_cv$spans[quad_cv$mse == min(quad_cv[,"mse"])]
opt_quad
#> [1] 0.3

lin_opt <- locfit(NOx ~ E, data=ethanol, alpha = opt_lin, deg=1)
quad_opt <- locfit(NOx ~ E, data=ethanol, alpha = opt_quad, deg=2)
```

```
plot(ethanol$NOx, x=ethanol$E, main="Linear vs Quadratic Local Regression (optimal alphas)", xlab="E", y
lines(lin_opt, col="red")
lines(quad_opt, col="green")
```



f)

```
sum(residuals(loessMod10)^2)
#> [1] 3.382258
sum(residuals(loessMod30)^2)
#> [1] 7.18373
sum(residuals(loessMod50)^2)
#> [1] 9.168455
sum(residuals(loessMod_opt)^2)
#> [1] 7.443603

sum(residuals(tricube_10)^2)
#> [1] 3.442665
sum(residuals(tricube_30)^2)
#> [1] 7.093455
sum(residuals(tricube_50)^2)
#> [1] 9.067521
sum(residuals(tricube_opt)^2)
#> [1] 7.976709

sum(residuals(lin_opt)^2)
#> [1] 7.481113
sum(residuals(quad_opt)^2)
#> [1] 7.093455
```