R Notebook

Code

This is an R Markdown (http://rmarkdown.rstudio.com) Notebook. When you execute code within the notebook, the results appear beneath the code.

Try executing this chunk by clicking the *Run* button within the chunk or by placing your cursor inside it and pressing *Cmd+Shift+Enter*.

—SVM classification—

Red dataset

Hide

```
library(kernlab)
library(e1071)
library(MASS)

set.seed(1)
red <- read.csv('winequality-red.csv', header = TRUE, sep=";")
red <- na.omit(red)
red.quality <- red$quality
red[,-12] <- scale(red[,-12])

# Red dataset
train_red_idx <- sample(nrow(red) * 0.8) # 80-20 train-test split
train.red <- red[train_red_idx,]
train.red$quality <- as.factor(train.red$quality)
train.red.quality <- train.red$quality

test.red <- red[-train_red_idx,]
test.red$quality <- as.factor(test.red$quality)
test.red.quality <- test.red$quality
# test.red <- test.red[,-12]

# # Backward model selection
# library(leaps)
# regfit.bwd=regsubsets(quality~.,data=train.red,nvmax=11,method="backward")
# summary(regfit.bwd)
#
# test.mat=model.matrix(quality~.,data=test.red) # create an X matrix of test data
# val.errors=rep(NA,19)
# for(i in 1:19){
#    coefi=coef(regfit.best,id=i)
#    pred=test.mat[,names(coefi)]%*%coefi
#    val.errors[i]=mean((Hitters$Salary[test]-pred)^2)
# }
# val.errors
# which.min(val.errors)
# coef(regfit.best,10)

set.seed(1)

gamma <- 2^seq(-15, 3, 1)
test_accuracy <- rep(0, length(gamma))
fit_time <- rep(0, length(gamma))
i = 1

start <- proc.time()

for(g in gamma){
  start_it <- proc.time()
  model = svm(quality~., data = train.red, gamma=g)
  fit_time[i] <- proc.time() - start_it
  test_accuracy[i] <- mean(test.red.quality == predict(model, test.red))
  i = i + 1
}
```

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t length
```

Hide

```
print(cv_time_red <- proc.time() - start) # total CV time
```

```
   user  system elapsed 
  3.955   0.095   4.214 
```

Hide

```
print(fit_time[which.max(test_accuracy)]) # fit time of best model
```

```
[1] 0.15
```

Hide

```
print(best_gamma_red <- 2^(which.max(test_accuracy) - 16)) # gamma yielding highest test accuracy
```

```
[1] 0.25
```

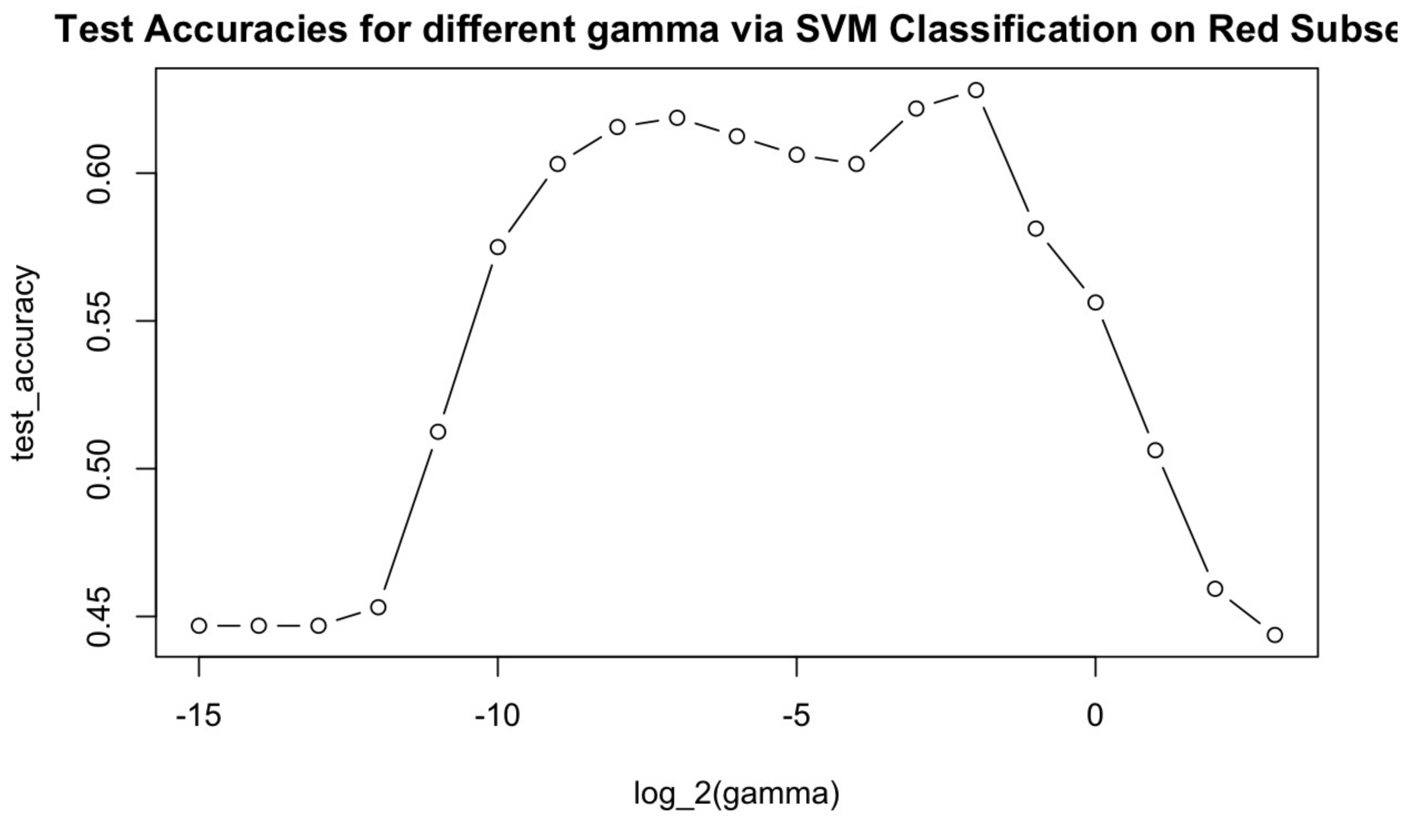
Hide

```
print(test_acc_red <- max(test_accuracy)) # test accuracy
```

```
[1] 0.628125
```

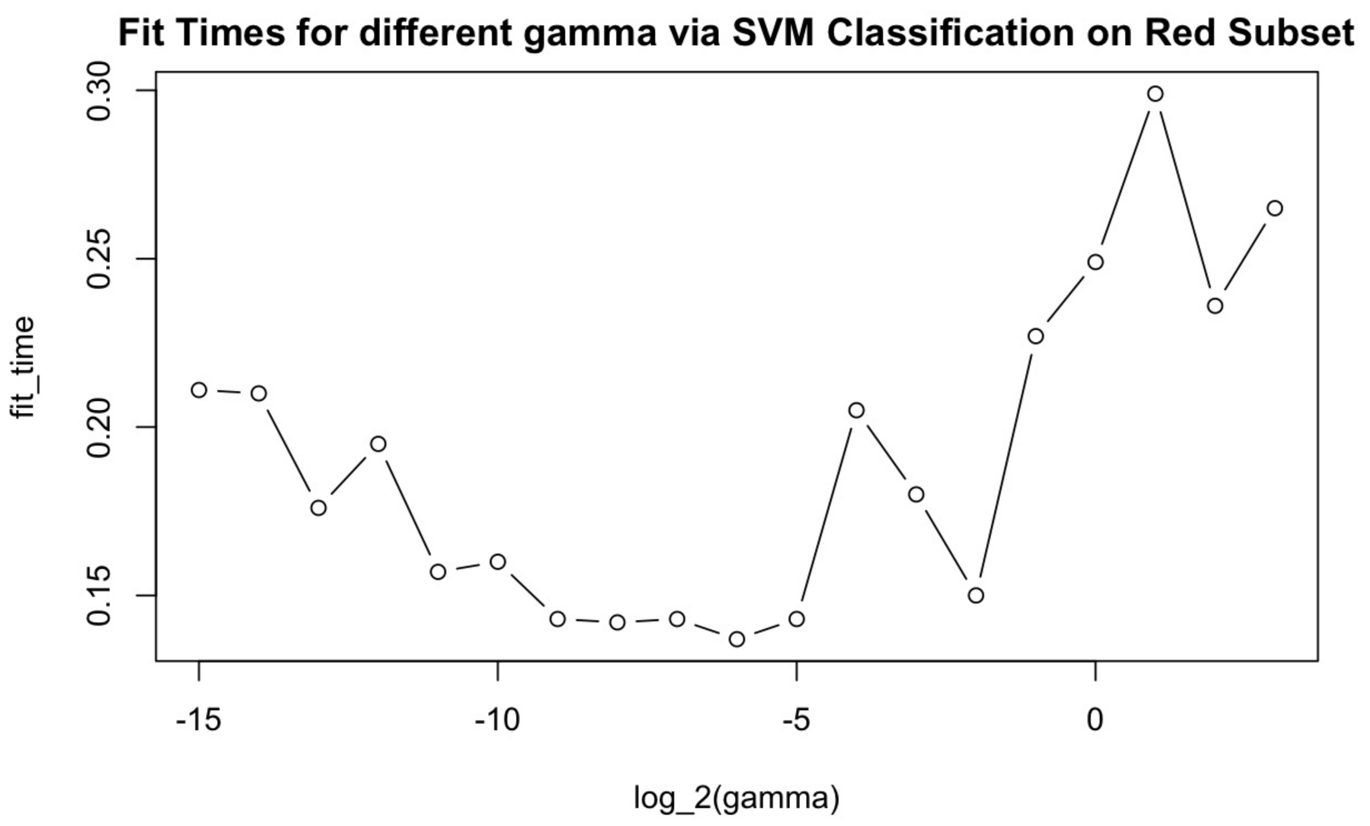
Hide

```
plot(log2(gamma), test_accuracy, type='b', xlab = 'log_2(gamma)', main='Test Accuracies for different gamma via S
VM Classification on Red Subset')
```



Hide

```
plot(log2(gamma), fit_time, type='b', xlab = 'log_2(gamma)', main='Fit Times for different gamma via SVM Classifi
cation on Red Subset')
```



Hide

```
NA
NA
```

White dataset

Hide

```
library(kernlab)
library(e1071)
```

```
package ‘e1071’ was built under R version 3.6.2
```

Hide

```r
library(MASS)

white <- read.csv('winequality-white.csv', header = TRUE, sep=";")
white <- na.omit(white)
white.quality <- white$quality
white[,-12] <- scale(white[,-12])

set.seed(1)
train_white_idx <- sample(nrow(white) * 0.8) # 80-20 train-test split
train.white <- white[train_white_idx,]
train.white$quality <- as.factor(train.white$quality)
train.white.quality <- train.white$quality

test.white <- white[-train_white_idx,]
test.white$quality <- as.factor(test.white$quality)
test.white.quality <- test.white$quality
# test.white <- test.white[,-12]

# # Backward model selection
# library(leaps)
# regfit.bwd=regsubsets(quality~.,data=train.white,nvmax=11,method="backward")
# summary(regfit.bwd)
#
# test.mat=model.matrix(quality~.,data=test.white) # create an X matrix of test data
# val.errors=rep(NA,19)
# for(i in 1:19){
#    coefi=coef(regfit.best,id=i)
#    pred=test.mat[,names(coefi)]%*%coefi
#    val.errors[i]=mean((Hitters$Salary[test]-pred)^2)
# }
# val.errors
# which.min(val.errors)
# coef(regfit.best,10)

set.seed(1)

gamma <- 2^seq(-15, 3, 1)
test_accuracy <- rep(0, length(gamma))
fit_time <- rep(0, length(gamma))
i = 1

start <- proc.time()

for(g in gamma){
  start_it <- proc.time()
  model = svm(quality~., data = train.white, gamma=g)
  fit_time[i] <- proc.time() - start_it
  test_accuracy[i] <- mean(as.character(test.white.quality) == as.character(predict(model, test.white)))
  i = i + 1
}
```

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t length
```

Hide

```r
print(cv_time_white <- proc.time() - start) # total CV time
```

```
   user  system elapsed 
 36.059   0.505  37.336 
```

Hide

```r
print(fit_time[which.max(test_accuracy)]) # fit time of best model
```

```
[1] 1.668
```

Hide

```
print(best_gamma_white <- 2^(which.max(test_accuracy) - 16)) # gamma yielding highest test accuracy
```

```
[1] 0.015625
```

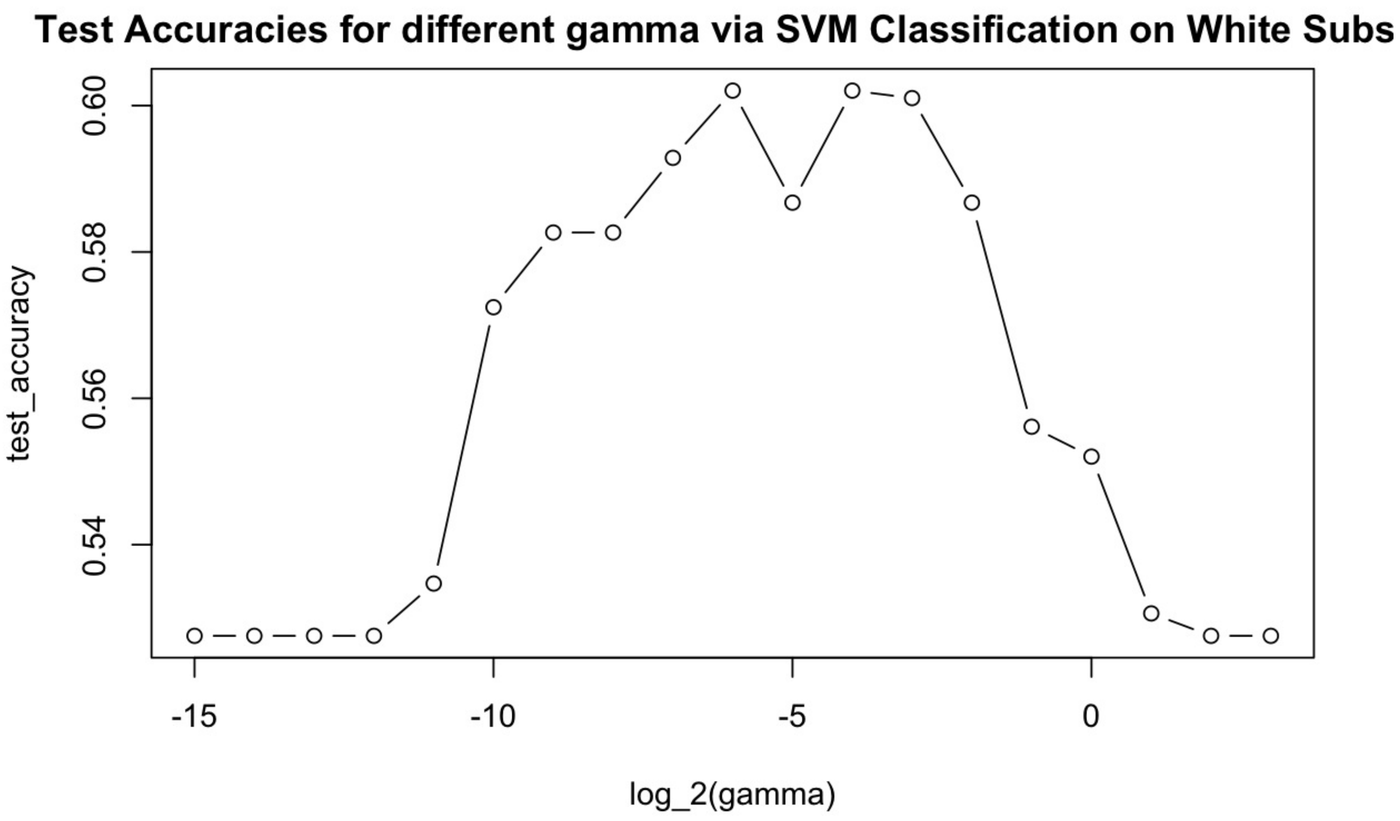
Hide

```
print(test_acc_white <- max(test_accuracy)) # test accuracy
```

```
[1] 0.6020408
```

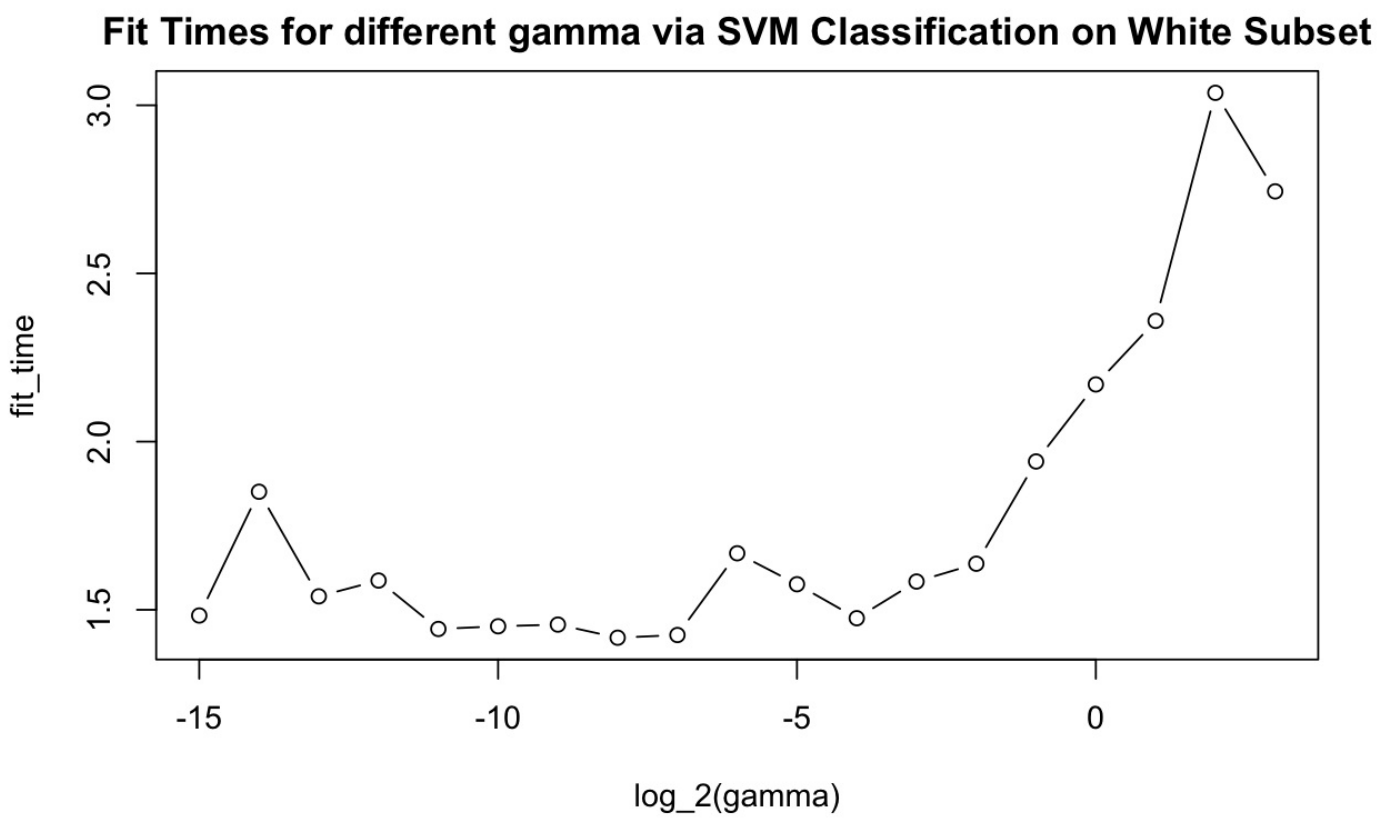
Hide

```
plot(log2(gamma), test_accuracy, type='b', xlab = 'log_2(gamma)', main='Test Accuracies for different gamma via S
VM Classification on White Subset')
```



Hide

```
plot(log2(gamma), fit_time, type='b', xlab = 'log_2(gamma)', main='Fit Times for different gamma via SVM Classifi
cation on White Subset')
```



Weighted Test Accuracy

Hide

```
(nrow(test.red) * test_acc_red + nrow(test.white) * test_acc_white) / (nrow(test.red) + nrow(test.white))
```

```
[1] 0.6084615
```

— SVM regression (epsilon-insensitive loss) —

Red dataset

Hide

```
set.seed(1)
red <- read.csv('winequality-red.csv', header = TRUE, sep=";")
red <- na.omit(red)
red.quality <- red$quality
red[,-12] <- scale(red[,-12])

# Red dataset
train_red_idx <- sample(nrow(red) * 0.8) # 80-20 train-test split
train.red <- red[train_red_idx,]
# train.red$quality <- as.factor(train.red$quality)
train.red.quality <- train.red$quality

test.red <- red[-train_red_idx,]
# test.red$quality <- as.factor(test.red$quality)
test.red.quality <- test.red$quality
# test.red <- test.red[,-12]

# # Backward model selection
# library(leaps)
# regfit.bwd=regsubsets(quality~.,data=train.red,nvmax=11,method="backward")
# summary(regfit.bwd)
#
# test.mat=model.matrix(quality~.,data=test.red) # create an X matrix of test data
# val.errors=rep(NA,19)
# for(i in 1:19){
#    coefi=coef(regfit.best,id=i)
#    pred=test.mat[,names(coefi)]%*%coefi
#    val.errors[i]=mean((Hitters$Salary[test]-pred)^2)
# }
# val.errors
# which.min(val.errors)
# coef(regfit.best,10)

set.seed(1)

gamma <- 2^seq(-15, 3, 1)
test_accuracy <- rep(0, length(gamma))
fit_time <- rep(0, length(gamma))
i = 1

start <- proc.time()

for(g in gamma){
  start_it <- proc.time()
  model = svm(quality~., data = train.red, gamma=g, type='eps-regression')
  fit_time[i] <- proc.time() - start_it
  test_accuracy[i] <- mean(abs(test.red.quality - predict(model, test.red)) <= 0.5)
  i = i + 1
}
```

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t length
```

Hide

```
print(cv_time_red <- proc.time() - start) # total CV time
```

```
   user  system elapsed 
  3.205   0.057   3.267 
```

Hide

```
print(fit_time[which.max(test_accuracy)]) # fit time of best model
```

```
[1] 0.128
```

Hide

```
print(best_gamma_red <- 2^(which.max(test_accuracy) - 16)) # gamma yielding highest test accuracy
```

```
[1] 0.001953125
```

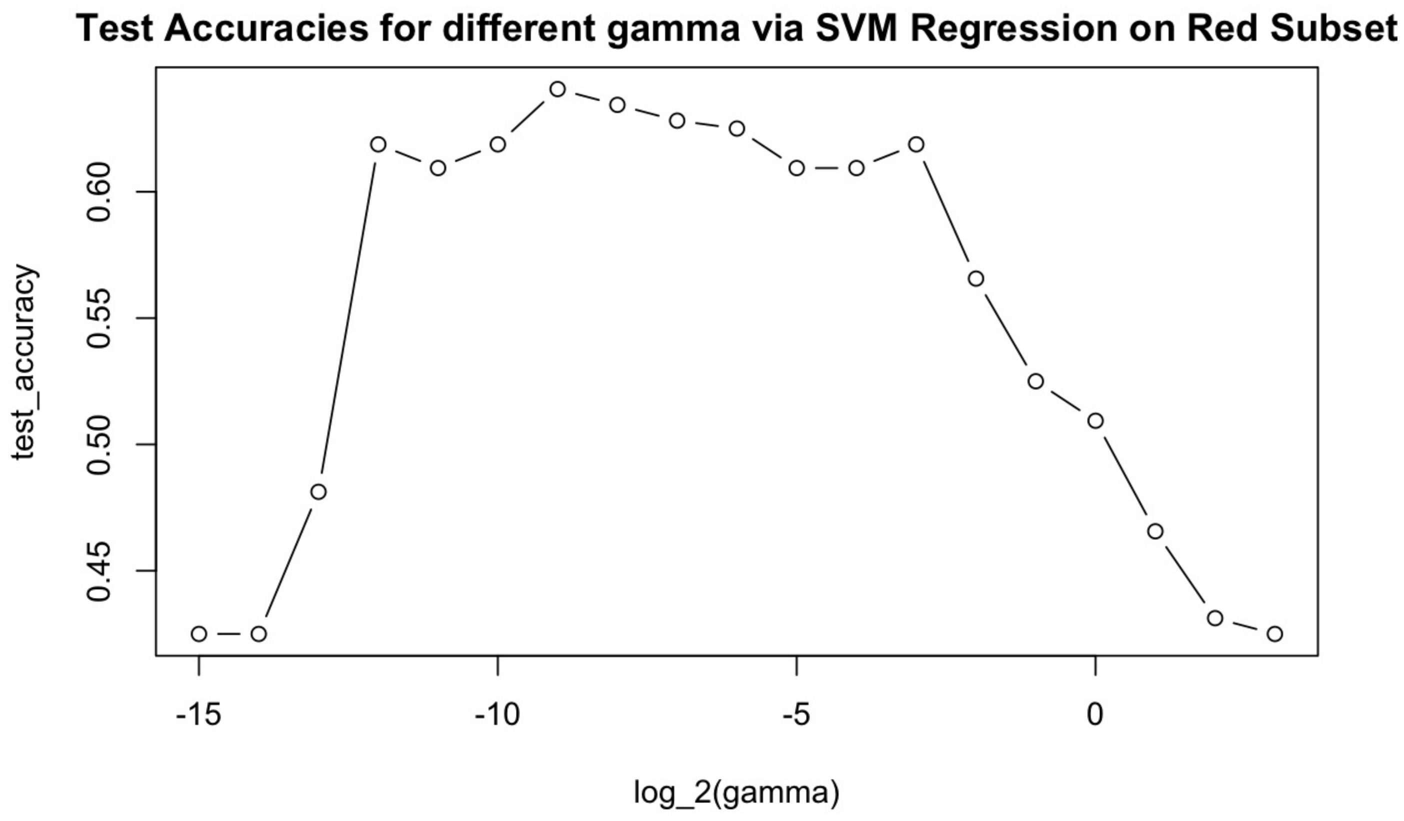
Hide

```
print(test_acc_red <- max(test_accuracy)) # test accuracy
```

```
[1] 0.640625
```

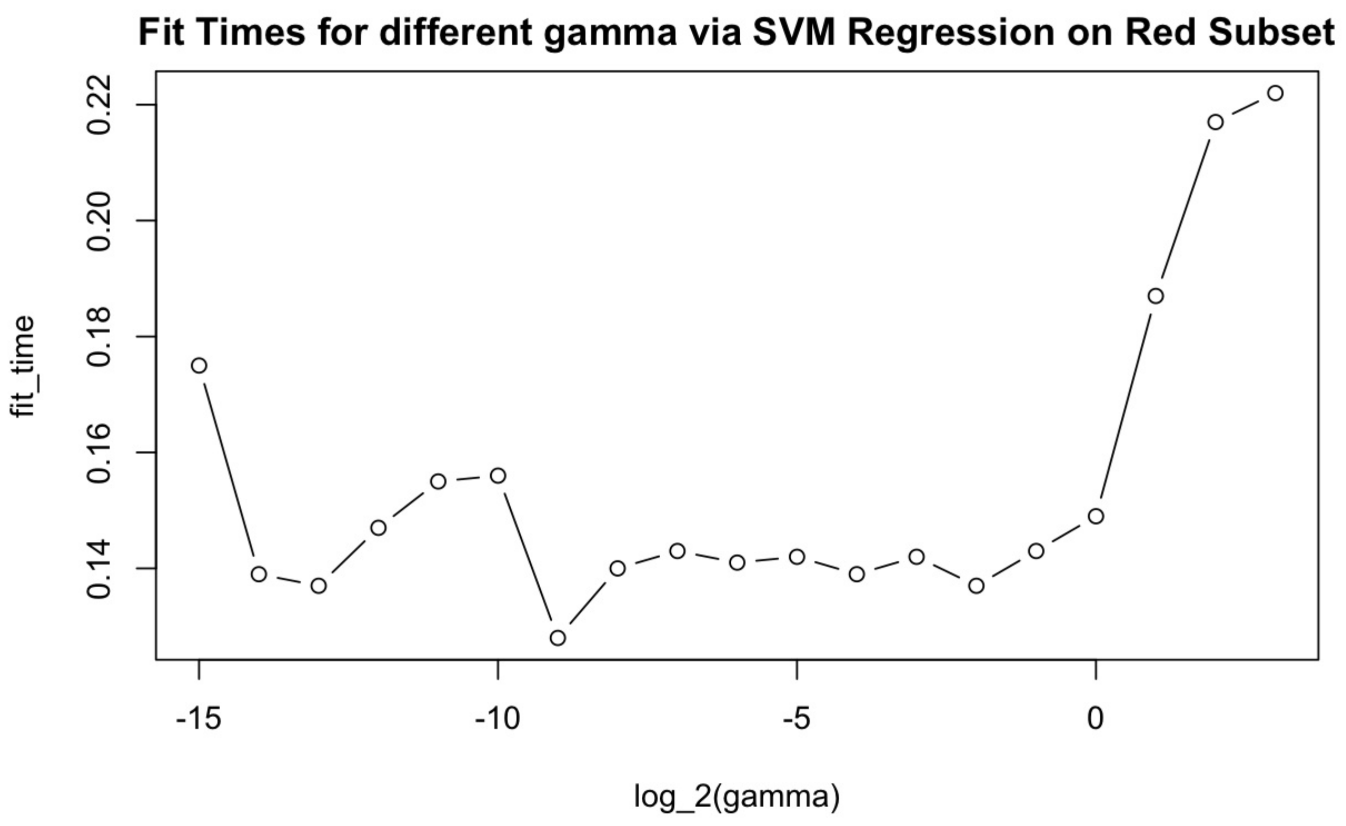
Hide

```
plot(log2(gamma), test_accuracy, type='b', xlab = 'log_2(gamma)', main='Test Accuracies for different gamma via S
VM Regression on Red Subset')
```



Hide

```
plot(log2(gamma), fit_time, type='b', xlab = 'log_2(gamma)', main='Fit Times for different gamma via SVM Regressi
on on Red Subset')
```



White dataset

Hide

```
white <- read.csv('winequality-white.csv', header = TRUE, sep=";")
white <- na.omit(white)
white.quality <- white$quality
white[,-12] <- scale(white[,-12])

set.seed(1)
train_white_idx <- sample(nrow(white) * 0.8) # 80-20 train-test split
train.white <- white[train_white_idx,]
# train.white$quality <- as.factor(train.white$quality)
train.white.quality <- train.white$quality

test.white <- white[-train_white_idx,]
# test.white$quality <- as.factor(test.white$quality)
test.white.quality <- test.white$quality
# test.white <- test.white[,-12]

# # Backward model selection
# library(leaps)
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# summary(regfit.bwd)
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# val.errors=rep(NA,19)
# for(i in 1:19){
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#    pred=test.mat[,names(coefi)]%*%coefi
#    val.errors[i]=mean((Hitters$Salary[test]-pred)^2)
# }
# val.errors
# which.min(val.errors)
# coef(regfit.best,10)

set.seed(1)

gamma <- 2^seq(-15, 3, 1)
test_accuracy <- rep(0, length(gamma))
fit_time <- rep(0, length(gamma))
i = 1

start <- proc.time()

for(g in gamma){
  start_it <- proc.time()
  model = svm(quality~., data = train.white, gamma=g, type='eps-regression')
  fit_time[i] <- proc.time() - start_it
  test_accuracy[i] <- mean(abs(test.white.quality - predict(model, test.white)) <= 0.5)
  i = i + 1
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t length
```

Hide

```
print(cv_time_white <- proc.time() - start) # total CV time
```

```
   user  system elapsed 
 27.852   0.369  28.544 
```

Hide

```
print(fit_time[which.max(test_accuracy)]) # fit time of best model
```

```
[1] 1.276
```

Hide

```
print(best_gamma_white <- 2^(which.max(test_accuracy) - 16)) # gamma yielding highest test accuracy
```

```
[1] 0.125
```

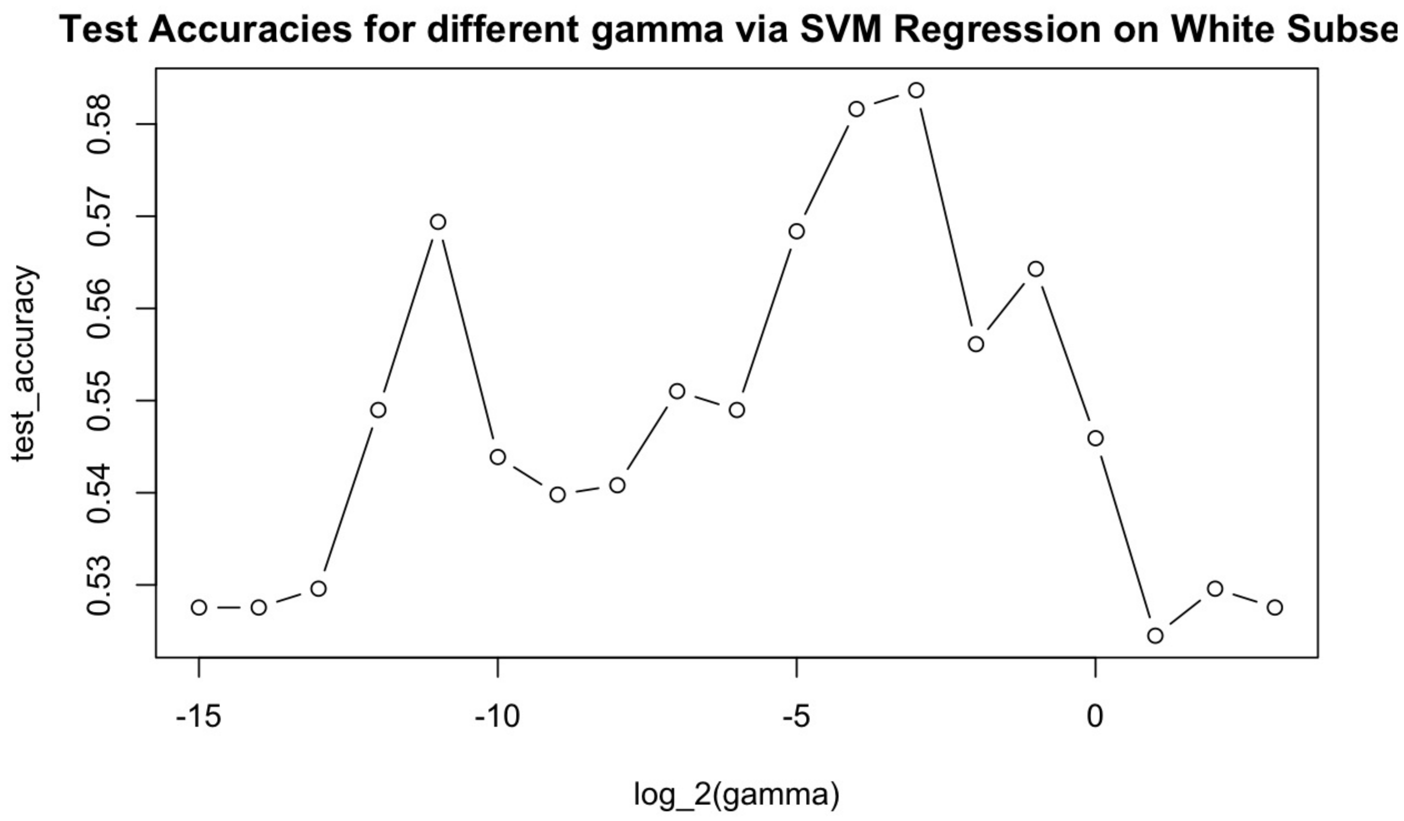
Hide

```
print(test_acc_white <- max(test_accuracy)) # test accuracy
```

```
[1] 0.5836735
```

Hide

```
plot(log2(gamma), test_accuracy, type='b', xlab = 'log_2(gamma)', main='Test Accuracies for different gamma via S
VM Regression on White Subset')
```



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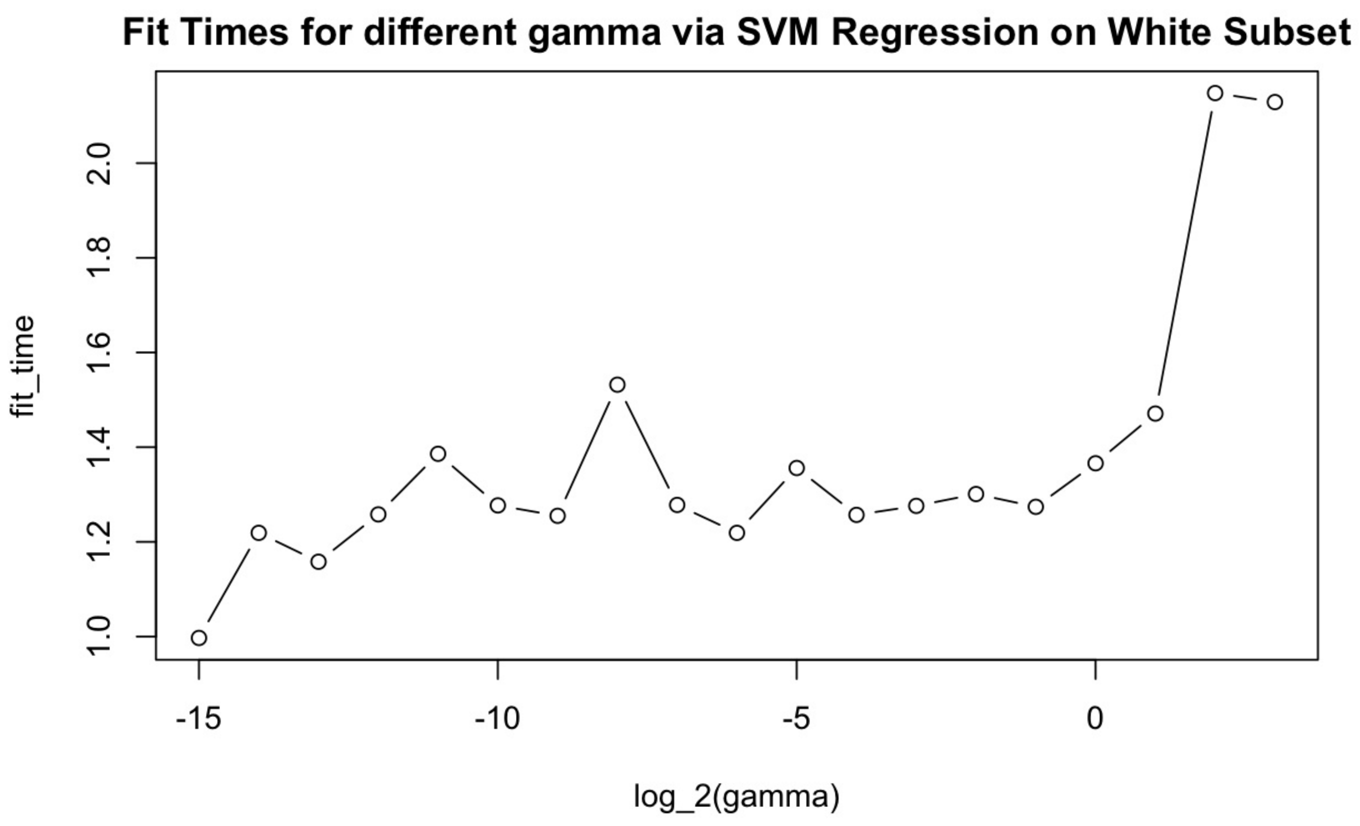
```
plot(log2(gamma), fit_time, type='b', xlab = 'log_2(gamma)', main='Fit Times for different gamma via SVM Regressi
on on White Subset')
```



Weighted Test Accuracy

```
(nrow(test.red) * test_acc_red + nrow(test.white) * test_acc_white) / (nrow(test.red) + nrow(test.white))
```

```
[1] 0.5976923
```

When you save the notebook, an HTML file containing the code and output will be saved alongside it (click the *Preview* button or press *Cmd+Shift+K* to preview the HTML file).

The preview shows you a rendered HTML copy of the contents of the editor. Consequently, unlike *Knit*, *Preview* does not run any R code chunks. Instead, the output of the chunk when it was last run in the editor is displayed.

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