SVM Classification

Using the iris data set

```
df <- iris[]
str(df)
```

```
## 'data.frame':    150 obs. of  5 variables:
##  $ Sepal.Length: num  5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.4 4.9 ...
##  $ Sepal.Width : num  3.5 3 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 ...
##  $ Petal.Length: num  1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 ...
##  $ Petal.Width : num  0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 ...
##  $ Species     : Factor w/ 3 levels "setosa","versicolor",..: 1 1 1 1 1 1 1 1 1 1 ...
```

train/test split

```
set.seed(1234)
i <- sample(1:nrow(df), 0.75*nrow(df), replace=FALSE)
train <- df[i,]
test <- df[-i,]
```

linear SVM

```
library(e1071)
svm1 <- svm(Species~., data=train, kernel="linear", cost=10, scale=TRUE)
summary(svm1)
```

```
##
## Call:
## svm(formula = Species ~ ., data = train, kernel = "linear", cost = 10,
##     scale = TRUE)
##
##
## Parameters:
##    SVM-Type:  C-classification
##  SVM-Kernel:  linear
##        cost:  10
##
## Number of Support Vectors:  15
##
##  ( 3 7 5 )
##
##
## Number of Classes:  3
##
## Levels:
##  setosa versicolor virginica
```

evaluate

```
pred <- predict(svm1, newdata=test)
table(pred, test$Species)
```

```
##
## pred         setosa versicolor virginica
##   setosa         15          0         0
##   versicolor      0         12         0
##   virginica       0          0        11
```

```
mean(pred==test$Species)
```

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

plot

```
# plot the support vectors
plot(svm1, test, Petal.Width ~ Petal.Length,
     slice = list(Sepal.Width = 3, Sepal.Length = 4))
```

SVM classification plot