The Perceptron Learning Algorithm

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1 The Idea of a Perceptron

The perceptron learning algorithm is one of the most basic algorithms in machine learning, and it was originally created by Frank Rosenblatt in 1962. As a linear classifier, a perceptron belongs to the family of supervised machine learning algorithms. Although simple and basic, the perceptron algorithm is of tremendous importance because it can be applied to the design of other machine learning algorithms. For example, one of the ways in which the neural networks can be implemented is to build a multilayer perceptron. The goal of a perceptron is to find a separating hyperplane that successfully divides the data into two distinct groups based on given labels. Importantly, to make the algorithm work, we need assume that the given data are linearly separable. This assumption is called "linear separability."

$\mathbf{X} = [x_{ij}]_{m\times n} \quad (x_{ij} \in \mathbf{R}^m)$ and $\mathbf{Y} = [y_j]_{n\times 1} \quad (y_j \in (0,1))$, where $i = (1,2,3,...,m)$ and $j = (1,2,3,...,n)$. Denote each data point $(\mathbf{X}_j, y_j)$ where $j = (1,2,3,...,n)$ and $\mathbf{X}_j = [x_{1j}, x_{2j}, x_{2j}, \cdots, x_{mj}]_{m\times 1}$. Note that n is the input size and m is the number of features. Assume that there is a separating hyperplane $\beta_0 + \sum_{i=1}^{m} \beta_i x_i = 0$ (based on the assumption of linear separability) that separates $\{\mathbf{X}_j | y_j = 1\}$ and $\{\mathbf{X}_j | y_j = 0\}$. The hyperplane is k-1 dimensional. We can write a function to represent this idea:

$$f(\mathbf{X}_j) = y_j = \begin{cases} 1, & \text{if} \sum_{i=1}^{m} \beta_i x_{ij} \geq \beta_0 \\ 0, & \text{if} \sum_{i=1}^{m} \beta_i x_{ij} < \beta_0 \end{cases}$$

β_0 is simply a threshold. The logic behind this function is that we can dichotomize the data based on the hyperplane the $\beta_0 + \sum_{i=1}^{m} \beta_i x_{ij} = 0$ where β_0 is the threshold. Note that y_i is equal to 0 or 1. Thus we can rewrite the function into another simpler format:

$$\begin{aligned} f(\mathbf{X}_j) &= \text{sign}\left[\left(\sum_{i=1}^{m} \beta_i x_{ij}\right) - \beta_0\right] \\ &= \text{sign}\left[\left(\sum_{i=1}^{m} \beta_i x_{ij}\right) + \beta_0 \cdot (-1)\right] \\ &= \text{sign}\left(\sum_{i=0}^{m} \beta_i x_{ij}\right) \end{aligned}$$

Now the job of a perceptron is to perform $f(x_i)$ to correctly separate the data. In other words, by learning the data, a perceptron should be able to find a hyperplane $\widehat{\beta}_0 + \sum_{i=1}^{m} \widehat{\beta}_i x_{ij} = 0$. Therefore, we can write a

function that a perceptron is going to perform:

$$\begin{aligned}\widehat{f(\mathbf{X}_j)} = \widehat{y_j} &= \text{sign}\left(\sum_{i=0}^{m} \widehat{\beta}_i x_i\right) \\ &= \text{sign}\left(\mathbf{X}^T \cdot \widehat{\boldsymbol{\beta}}_{\text{PLA}}\right)\end{aligned}$$

In summary, a perceptron can find $\widehat{\boldsymbol{\beta}}_{\text{PLA}}$ so that $\widehat{y_j}$ is equal to y_j. In this sense, a perceptron is a technique of nonstatistical, nonparametric estimation. This is why a perceptron is a machine learning algorithm, although we use the language of statistics to present it.

2 The Algorithm

An algorithm implementing the idea of perceptron is a trial-and-error approach. This means that the perceptron learning algorithm makes mistakes until it finds a separating hyperplane. Assume

$$\mathbf{X}^T_{(n+1)\times(m+1)} = \begin{bmatrix} x_{00} & x_{01} & x_{02} & \cdots & x_{0m} \\ x_{10} & x_{11} & x_{12} & \cdots & x_{1m} \\ x_{20} & x_{21} & x_{32} & \cdots & x_{2m} \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ x_{n0} & x_{n1} & x_{n2} & \cdots & x_{nm} \end{bmatrix}, \widehat{\boldsymbol{\beta}}_{(m+1)\times 1} = \begin{bmatrix} \widehat{\beta}_0 \\ \widehat{\beta}_1 \\ \widehat{\beta}_2 \\ \vdots \\ \widehat{\beta}_m \end{bmatrix}, \mathbf{Y}_{(n+1)\times 1} = \begin{bmatrix} y_0 \\ y_1 \\ y_2 \\ \vdots \\ y_n \end{bmatrix}$$

Suppose a perceptron learning algorithm will run t times until $\widehat{\boldsymbol{\beta}}_{\text{PLA}}$ is obtained. Denote $\mathbf{X}_{(t)}$ the t-th input of the data: $[x_{0(t)}, x_{1(t)}, x_{2(t)}, \cdots, x_{k(t)}]$, and the size of the training set is n. So $0 \leq t \leq n$. Let $\widehat{\boldsymbol{\beta}}_{(\boldsymbol{t})} = [\beta_{0(t)}, \beta_{1(t)}, \beta_{2(t)}, \cdots, \beta_{k(t)}]^T$ and $\mathbf{Y}_{(t)} = \text{y}_t$. Let $x_{i(t)} = 1$. The initial value of $\beta_{0(0)}$ is set to be 0. We specify a perceptron learning algorithm as follows:

Data: X, Y
Result: $\widehat{\boldsymbol{\beta}}$
initialization;
while $t \leq n$ **do**
  if $\left[sign\left(\mathbf{X}_{(t)}\widehat{\boldsymbol{\beta}}_{(t)}\right) \cdot \mathbf{Y}_{(t)}\right] > 0$ **then**
    $\widehat{\boldsymbol{\beta}}_{(t+1)} = \widehat{\boldsymbol{\beta}}_{(t)}$;
  else
    $\widehat{\boldsymbol{\beta}}_{(t+1)} = \widehat{\boldsymbol{\beta}}_{(t)} + \left(\mathbf{Y}_{(t)} \cdot \mathbf{X}_{(t)}\right)$;
  end
end
return $\widehat{\boldsymbol{\beta}}_{\text{PLA}} = \widehat{\boldsymbol{\beta}}_{(t+1)}$

3 An Implementation in R

The implementation of the perceptron algorithm is simple in R. As we can see the algorithm above, the code will be very straightforward.

```
> perceptron <- function(df,X,Y){
+   y <- Y
+   len_X <- length(X)
+   len_df <- nrow(df)
+   V_X <- c(rep(1,len_df))
+
+   ##---- To make the vector of X: V_X ----##
+   for (i in 1:len_X)
+   {
+     x_current <- X[i]
+     V_X <- c(V_X, eval(parse(text=paste("df$",x_current,sep=""))))
+   }
+
+   ##---- To make the matrix of X: M_X -----##
+   M_X <- matrix(V_X,ncol=(length(X)+1), byrow=FALSE)
+
+   ##---- To make the initial matrix of coefficients: B -----##
+   B <- matrix(c(0,rep(0,len_X)),ncol=1, byrow=FALSE)
+
+   do_not_match <- 1
+   while(do_not_match == 1)
+   {
+     do_not_match <- 0
+     for (i in 1:nrow(df))
+     {
+       do_not_match <- 0
+       if ( ((M_X[i,] %*% B) * (eval(parse(text=paste("df$",y,sep="")))[i]) ) <= 0 )
+       {
+         B <- B + ( M_X[i,]*(eval(parse(text=paste("df$",y,sep="")))[i]) )
+         do_not_match <- 1
+       }
+     }
+   }
+   return(B)
+ }
>
```

The parameter of "df" is the data that we would like to train, "X" is a list of the features we include, and "Y" is a vector of the labels corresponding to each data point. The function will return a vector "B," of which the first component is $\widehat{\boldsymbol{\beta}}_0$ and the rest are $\widehat{\boldsymbol{\beta}}_i$ where $i = (1, 2, 3, ..., m)$.

4 Training Data

Now we can start to "train" our perceptron by calling the function with any data. To do so, I will use a well-known data set introduced by Ronald Fisher: Iris flower data set, as an example. Since it is a built-in data set in R, it is very straighforward to import the Iris data:

```
> data(iris)
> df<-iris
```

Then we take a partial look at the data:

```
> head(df)
```

```
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species
1          5.1         3.5          1.4         0.2  setosa
2          4.9         3.0          1.4         0.2  setosa
3          4.7         3.2          1.3         0.2  setosa
4          4.6         3.1          1.5         0.2  setosa
5          5.0         3.6          1.4         0.2  setosa
6          5.4         3.9          1.7         0.4  setosa
```

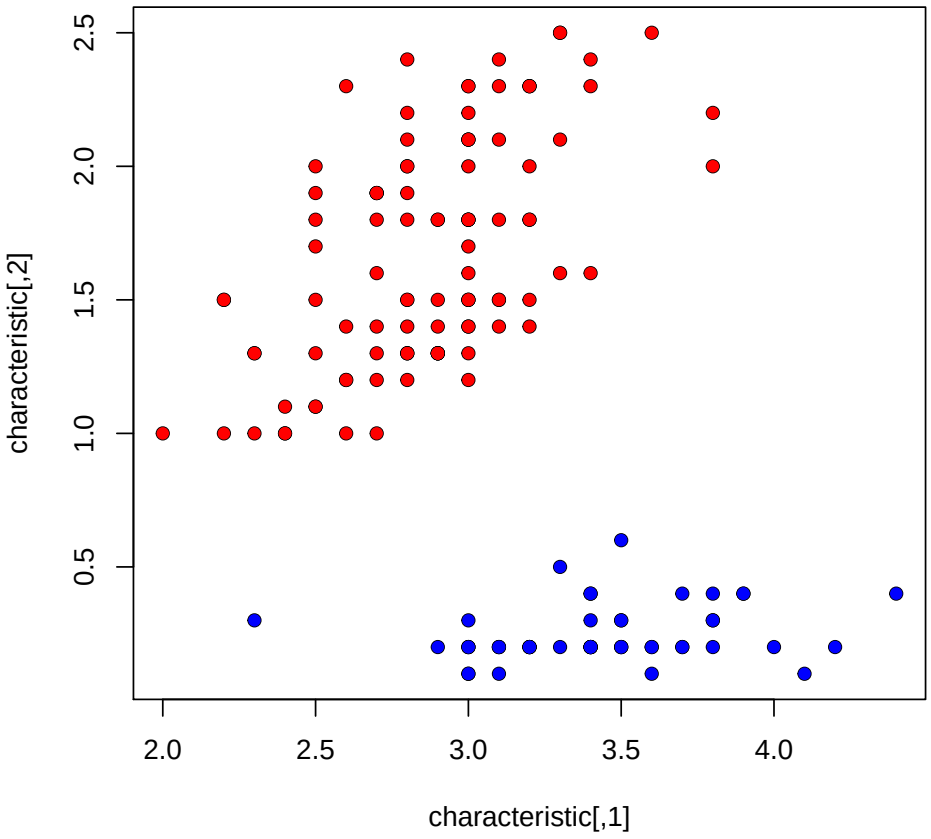
Columns 1 to 4 are flowers' characteristics. The last column, "Species," is a categorical variable:

```
> summary(df$Species)
```

```
    setosa versicolor  virginica
        50         50         50
```

This data set has been extensively explored, so I will skip the steps taken to find what are linearly separable. According to Wikipedia's artcile on Iris data, two groups are linearly separable based on variables "Sepal.width" and "Petal.width." The two groups are (1) versicolor and virginica and (2) setosa. Therefore, let's plot these two groups in terms of their petal width and sepal width:

```
> characteristic <- cbind(df$Sepal.Width,df$Petal.Width)
> plot(characteristic)
> points(subset(characteristic,df$Species=="setosa"),col="blue",pch=16)
> points(subset(characteristic,df$Species!="setosa"),col="red",pch=16)
```



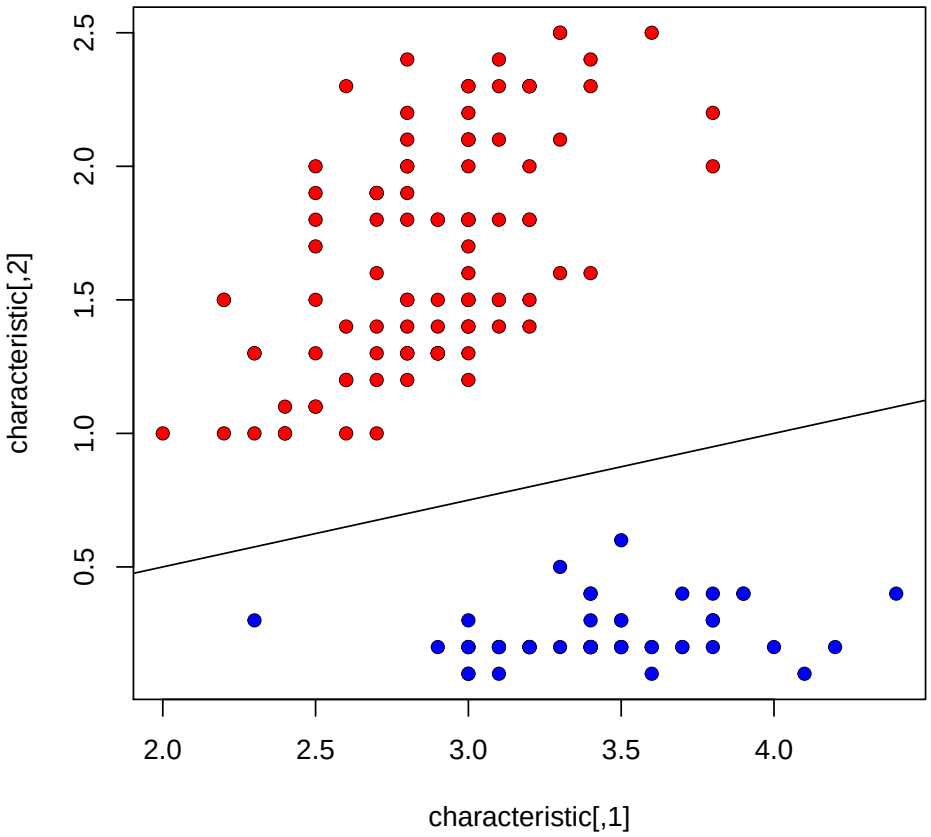
In the above plot, the x-axis is Sepal.width and y-axis Petal.width. Blue circles are the species of setosa (group 2), and red circles are the species of both versicolor and virginica (group 1). The plot clearly shows that the two groups can be separated. Next, the goal is to obtain a hyperplane by running the perceptron function I built previously. Prior to calling the function, we need to make $\mathbf{X}$ and $\mathbf{Y}$:

```
> X<-c("Sepal.Width","Petal.Width")
> Y<-"Species"
```

```
> perecptron(df,X,Y)
```

After running the perceptron function, we get a matrix where $\widehat{\beta}_0 = 0.0$, $\widehat{\beta}_1 = -0.3$, and $\widehat{\beta}_2 = -1.2$. Thus we obtain a separating hyperplane: $-0.3x_1 - 1.2x_2 = 0$

```
> plot(characteristic)
> points(subset(characteristic,df$Species=="setosa"),col="blue",pch=16)
> points(subset(characteristic,df$Species!="setosa"),col="red",pch=16)
> abline(0.0/-1.2,-0.3/-1.2,col="black")
```


characteristic[,2]
0.5
1.0
1.5
2.0
2.5
2.0
2.5
3.0
3.5
4.0
characteristic[,1]