Tutorial 10

1. Both linear regression model and separating hyperplane in classification (in e.g. SVM) are looking for a linear combination of covariates. Explain their difference in the estimation and the rules in prediction.

2. we can use support vector machine learning for function estimation. Consider the motorcycle data. plot the fitted curve. discuss the role of *gamma* in SVM.

3. For the leukemia gene expression data ((**training points)**. Use sample 11—33 as training set and the others as validation set, compare SVM and FDA.

4. For data set

$$\begin{array}{cc} X & Y(classes) \\ X_1 = (x_{11}, ..., x_{1p}) & (A_1, B_1) = (0, 1) \\ X_2 = (x_{21}, ..., x_{2p}) & (A_2, B_2) = (0, 1) \\ ... & \\ X_n = (x_{n1}, ..., x_{np}) & (A_n, B_n) = (1, 0) \end{array}$$

consider the following classification scheme: for a new sample $x_{new} = (x_1, ..., x_p)$, choose h and calculate

$$\hat{A}(x_{new}) = \frac{\sum_{i=1}^{n} K(||X_i - x_{new}||/h) A_i}{\sum_{i=1}^{n} K(||X_i - x_{new}||/h)}$$

and

$$\hat{B}(x_{new}) = \frac{\sum_{i=1}^{n} K(||X_i - x_{new}||/h) B_i}{\sum_{i=1}^{n} K(||X_i - x_{new}||/h)}$$

Define the probability that $x_{new} \in A$ and B respectively as

$$p_A(x_{new}) = \frac{\exp(\hat{A}(x_{new}))}{\exp(\hat{A}(x_{new})) + \exp(\hat{B}(x_{new}))}, \quad p_B(x_{new}) = \frac{\exp(\hat{B}(x_{new}))}{\exp(\hat{A}(x_{new})) + \exp(\hat{B}(x_{new}))}$$

We classify $x_{new} \in A$ if $p_A(x_{new}) > p_B(x_{new})$, and $x_{new} \in B$ otherwise.

Consider the banknotes data with (**training set** and (**validation set**, with h = 1 what is the classification error? try different h.