

Figure 10.1. This graph shows the 63 training samples and the 25 test samples in the coordinates of the first two PCA basis. The training samples are represented by small filled symbols while the testing samples are the unfilled larger symbols. The data shows a nearly random pattern that illustrates the poor performance of this classification rule.

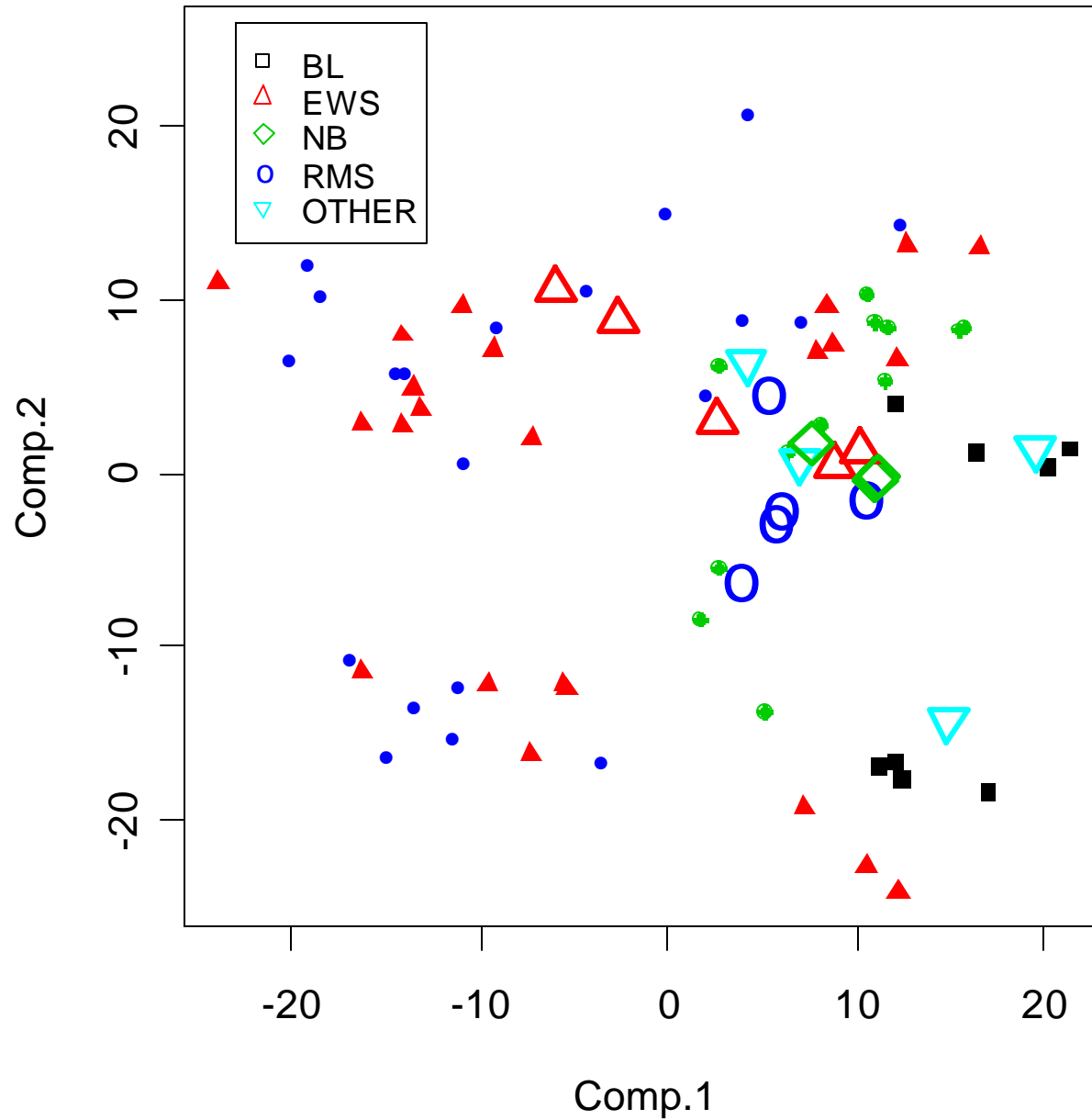


Figure 10.2. Principal Components for 450 significant genes. This graph shows the 63 training samples and the 25 test samples in the two first PCA basis. The data shows a strong clustering pattern that explains the excellent performance of the classification rules.

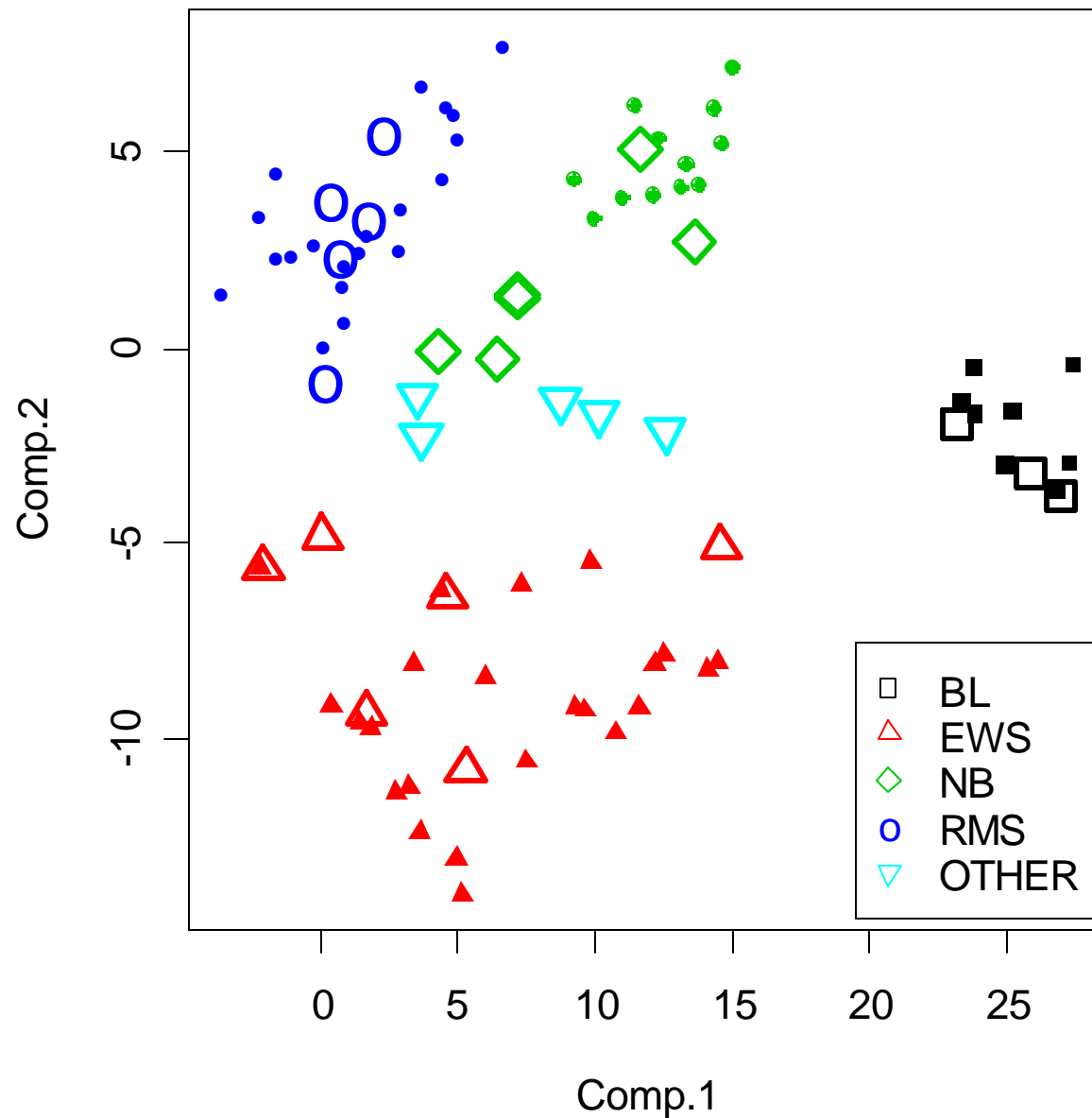


Figure 10.3. Two cluster means of 50 significant genes. This graph shows the 63 training samples and the 25 test samples in the two first PCA basis. The data shows a strong clustering pattern that explains the excellent performance of the classification rules.

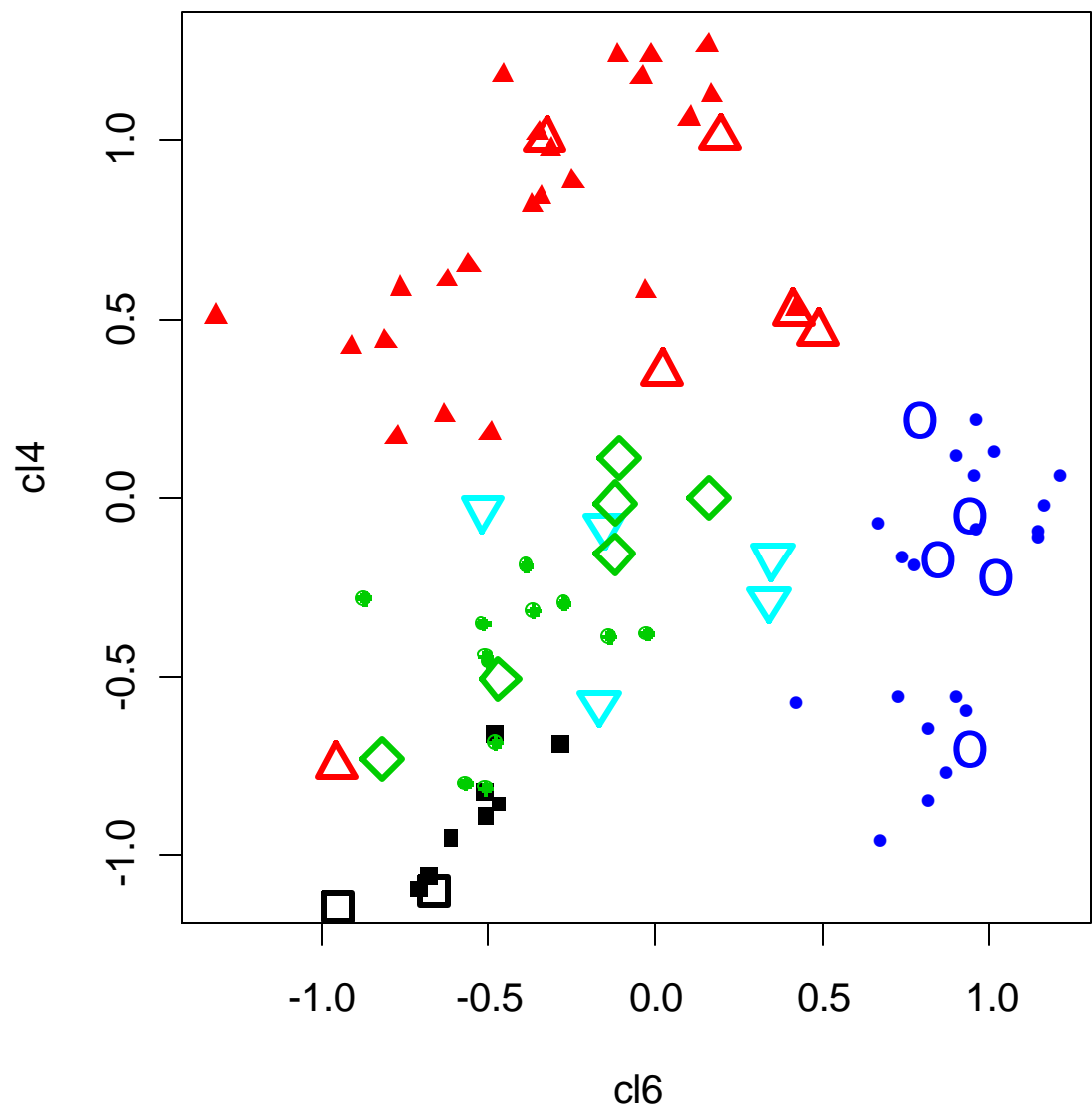


Figure 10.4. The first two Principal Components for the means of 10 clusters obtained from a subset of the top 50 significant genes. This graph shows the 63 training samples and the 25 test samples in the two first PCA basis. The graph shows that for the EWS tumors two observations in the testing and one in the training are in the boundary with the group of NB tumors.

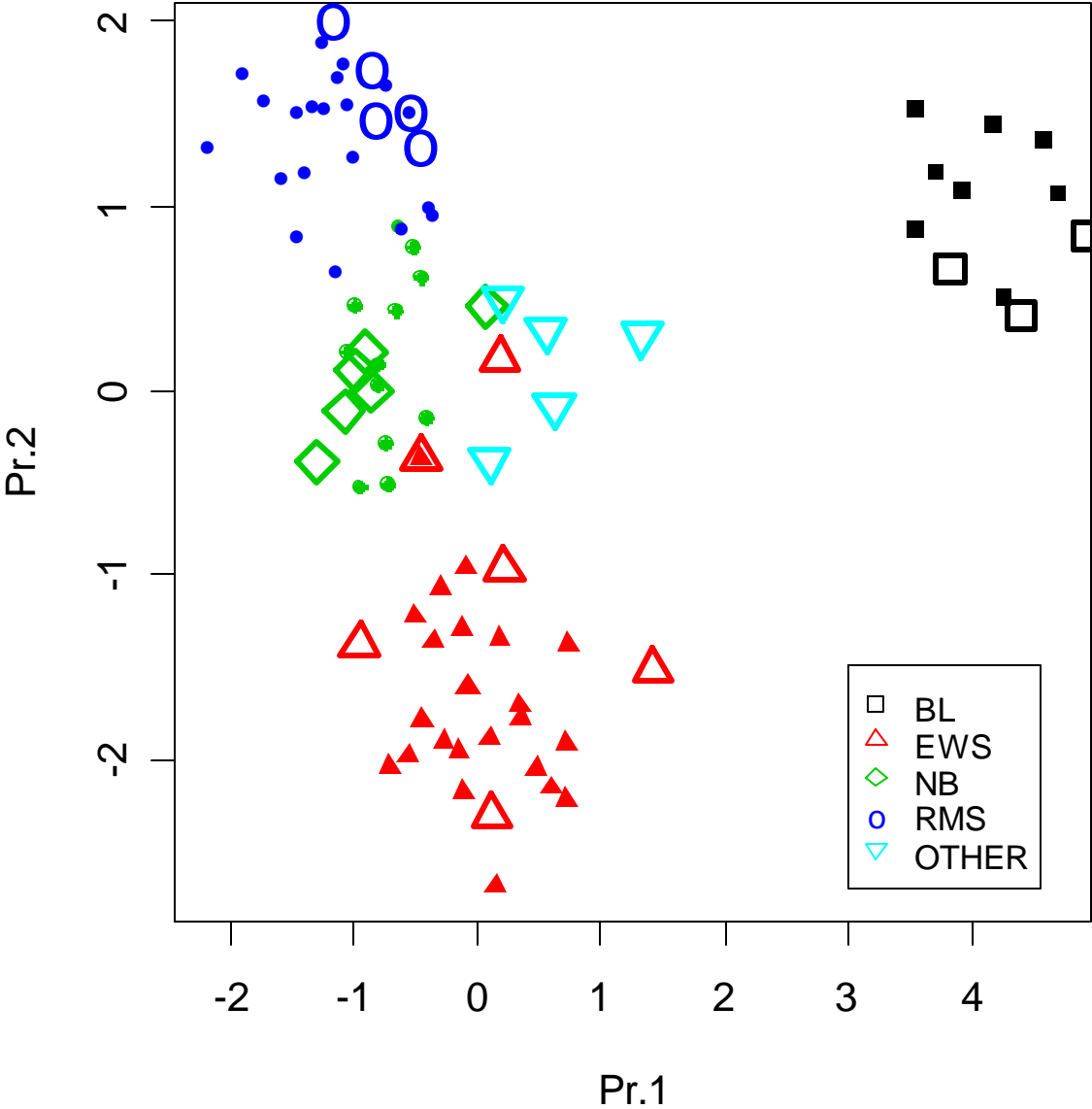


Figure 10.5. Principal Components for the top 30 significant genes. This graph shows the 63 training samples and the 25 test samples in the two first PCA basis. The data shows a strong clustering pattern that explains the excellent performance of the classification rules.

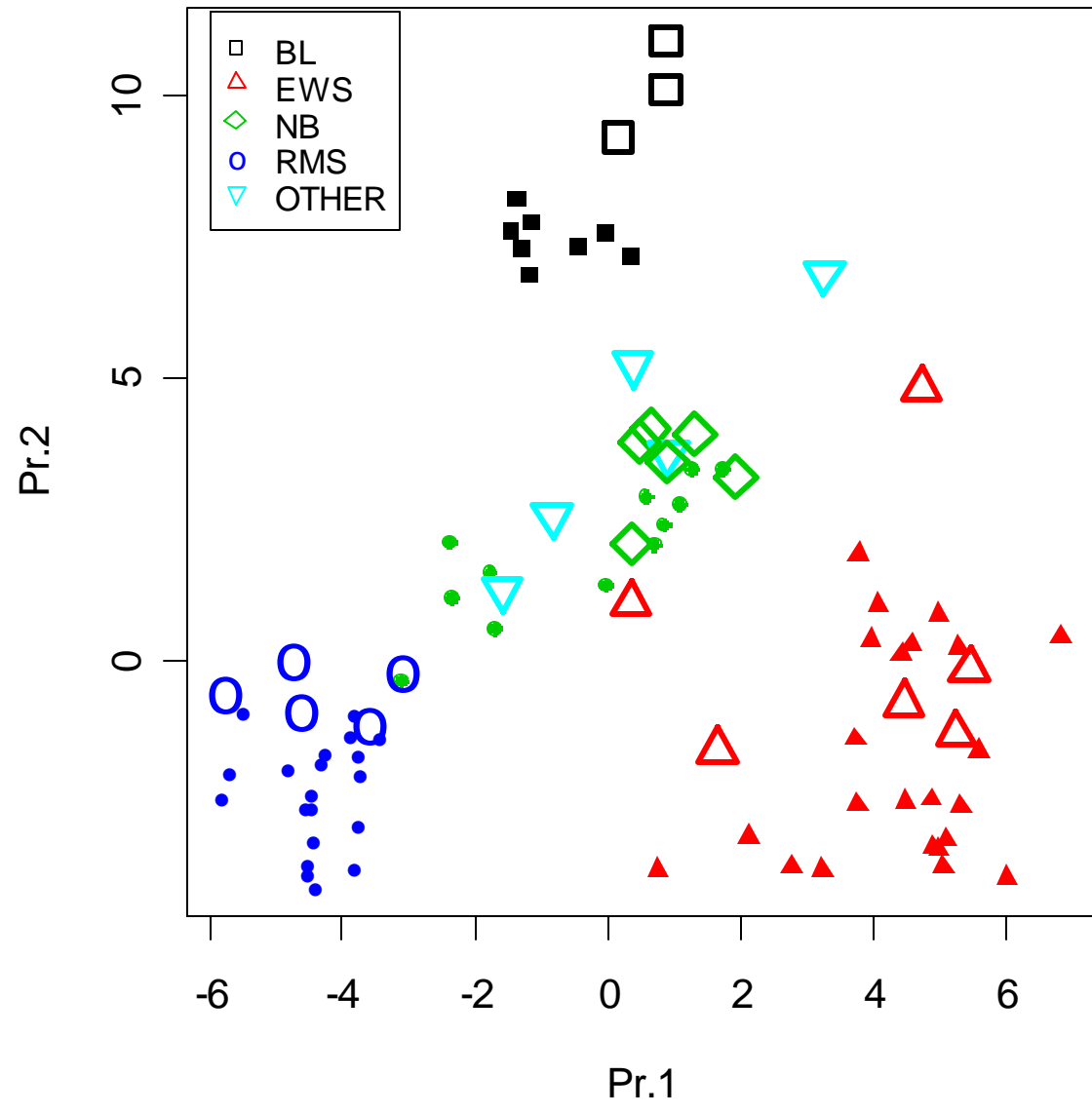


Figure 10.6. Classification tree for a function $f(X,Y)$.

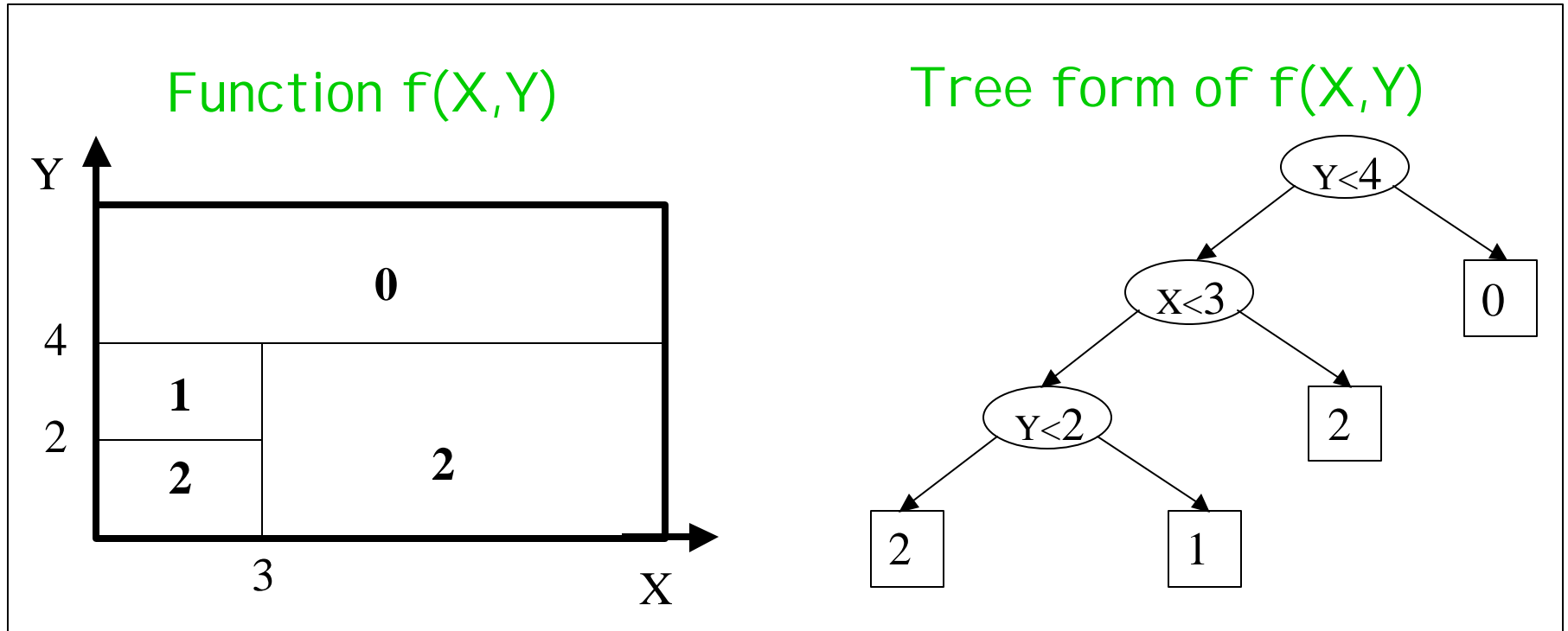


Figure 10.7. Classification tree for the cancer groups using 10 principal components of the top 100 cancer genes. The classification rule produces zero mistakes in the training set and five mistakes in the testing set.

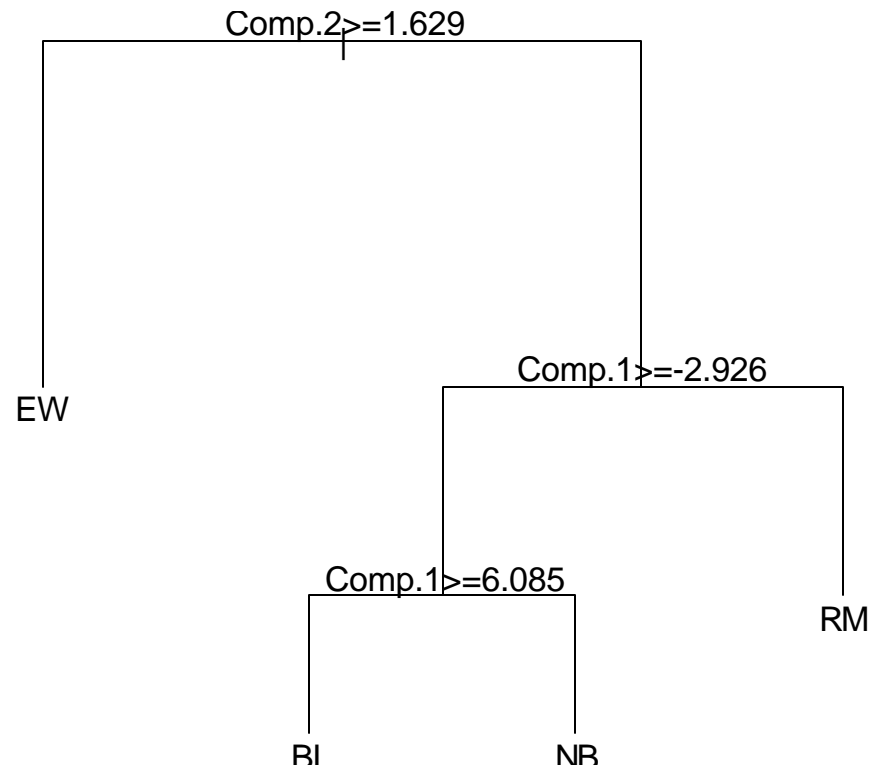


Figure 10.8. Graph of an ANN with one hidden layer.

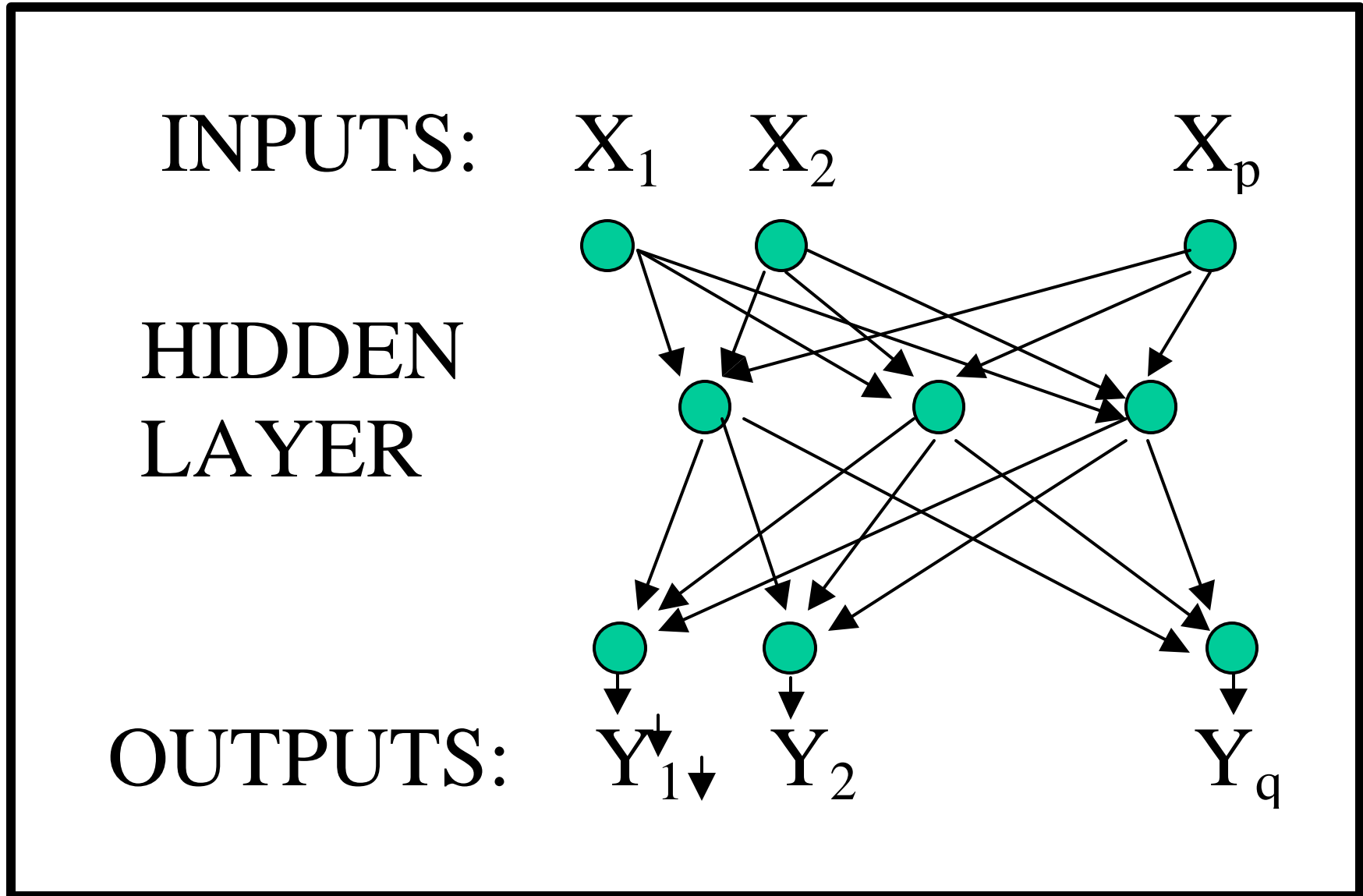


Figure 10.9. SVM example with two groups of points. The shaded area represents the separation region. The arrows indicate the location of the support vectors.

