

Biostat 830 Assignment 1

Due: Tuesday, Feb 6, in class

You don't *have to* work on all the problems: 1 to 3 are mandatory, you can select one of the 4 and 5 to work on.

1. Lecture Note 2, Exercise 1.
2. Lecture Note 2, Exercise 4. Compare the weights used by knn prediction algorithm
3. Implement a bootstrap method to estimate the EPE of the linear classifier that we used in the class and compare it to the K -fold cross-validation results for $K = 2, 5$ and 10.
4. For linear prediction function, generalized cross-validation (GCV) provides a convenient approximation to leave-one-out cross-validation. Consider a linear smoothing function,

$$\hat{\mathbf{f}} = \mathbf{H}\mathbf{y},$$

i.e., each fitted value is a linear combination of observed outcomes in the training data. An example of this is the least square fit. The matrix \mathbf{H} is used to construct a prediction function subsequently. Here we focus on the cross-validation problem with the training data.

- (a) Show that if \mathbf{H} is obtained from least squares algorithm,

$$y_i - \hat{f}^{-i}(x_i) = \frac{y_i - \hat{f}(x_i)}{1 - H_{ii}},$$

where H_{ii} denotes the i -th diagonal element of \mathbf{H} .

- (b) Use above result to show that

$$|y_i - \hat{f}^{-i}(x_i)| \geq |y_i - \hat{f}(x_i)|.$$

- (c) Show that the generalized cross-validation result, using a squared error loss, can be approximated by

$$\text{GCV}(\hat{f}) = \frac{1}{N} \sum_{i=1}^N \left[\frac{y_i - \hat{f}(x_i)}{1 - \text{trace}(\mathbf{H})/N} \right]^2$$

- (d) Conduct a numerical study to compare the results of GCV and leave-one-out cross-validation for a linear prediction function of your choice.

5. For the knn classifier that we discussed in the class
- (a) Implement a method of your choice to select the tuning parameter k , i.e., the “optimal” number of nearest neighbors.
 - (b) Estimate the EPE for your optimal k using the training data
 - (c) Simulate new data according to the true generative model and re-estimate the EPE for the estimated optimal k .