PubH 7475/8475 Homework 1 (Spring 2021)
Due on Feb 3, 2021

1. Consider a breast cancer data set available in $R$. In $R$, use the following commands to learn and download the data:
```
> library("MASS")
> ?biopsy
> data(biopsy)
> biopsy[1:5,]
    ID V1 V2 V3 V4 V5 V6 V7 V8 V9 class
\begin{tabular}{llllllllllll}
1 & 1000025 & 5 & 1 & 1 & 1 & 2 & 1 & 3 & 1 & benign
\end{tabular}
\(21002945 \quad 5 \quad 4 \quad 4 \quad 5 \quad 7 \quad 10 \quad 3 \quad 2 \quad 1\) benign
3 1015425 3
4 1016277 6
5 1017023 4 4 1 1 1 3 2 2 1 3 3 1 1 benign
```

Because there are some missing values for V6, you can use the following to delete the observations with missing values:

```
biopsy2<-biopsy[!is.na(biopsy$V6),]
```

Alternatively, you can download the data from UC-Irvine Machine Learning Databases.
(a) Randomly split the data into a training set and a test set containing about $2 / 3$ and $1 / 3$ of total observations respectively.
(1) Apply a linear regssion model to obtain its training, test and LOOCV (based on only the training set) error rates;
(2) Apply kNN and for a set of the values of k , show their training, test and LOOCV error rates;
(3) Apply a logistic regression model to obtain its training, test and LOOCV (based on only the training set) error rates;

Which of the training error rate and LOOCV error rate approximates the test error rate better? ( 30 pts )
(b) Randomly split the data into a training set and a test set containing about $1 / 3$ and $2 / 3$ of total observations respectively. Repeat (1)-(3) in 1. How the performance depends on the size of the training dataset? (15 pts)

In (1) and (3), you can either use all the 9 predictors directly, or even better, use a variable selection scheme to select a model.
2. Read Guha et al (2012) about the main idea of "divide and recombine" (DR) (downloadable from the course web page). Suppose we have data $D=\left\{X_{1}, X_{2}, \ldots, X_{n}\right\}$, $n$ identically and independently distributed (iid) (scalar) observations from a normal distribution $N\left(\mu, \sigma^{2}\right)$.
(a) Show that, based on all $n$ observations in $D$, the maximum likelihood estimates $\mu$ and $\sigma^{2}$ are $\hat{\mu}(D)=\sum_{i=1}^{n} X_{i} / n$ and $\hat{\sigma}^{2}(D)=\sum_{i=1}^{n}\left[X_{i}-\hat{\mu}(D)\right]^{2} / n$. (10 pts)
(b) Now suppose that $n$ is an even number; we divide the sample into two equally sized subsamples $D_{1}=\left\{X_{1}, X_{2}, \ldots, X_{n / 2}\right\}$ and $D_{2}=\left\{X_{n / 2+1}, X_{n / 2+2}, \ldots, X_{n}\right\}$. If we apply the MLEs to the two subsamples, then combine them to obtains the DR estimate for $\mu$ as the following

$$
\tilde{\mu}(D)=\left[\hat{\mu}\left(D_{1}\right)+\hat{\mu}\left(D_{2}\right)\right] / 2 .
$$

How is the DR estimate compared to the original MLE $\hat{\mu}(D)$ (i.e. the same, worse or better)? why? (10 pts)
(c) (8000) If we apply the MLEs to the two subsamples, then combine them to obtains the DR estimate for $\sigma^{2}$ as the following

$$
\tilde{\sigma}^{2}(D)=\left[\hat{\sigma}^{2}\left(D_{1}\right)+\hat{\sigma}^{2}\left(D_{2}\right)\right] / 2 .
$$

How is the DR estimate compared to the original MLE $\hat{\sigma}^{2}(D)$ (i.e. the same, worse or better)? why? (20 pts)
3. (8000) Read Breiman (2001), Hand (2006) and Donoho (2015) (downloadable from the course web page); summarize the main points of each paper and briefly explain your view(s). (30 pts)

Please attach your computer program and relevant output.

