```
# load data
library(mlbench)
```

Warning: package 'mlbench' was built under R version 4.4.1

```
data(BreastCancer)
BreastCancer$Id <- NULL
BreastCancer$Marg.adhesion <- NULL
BreastCancer <- na.omit(BreastCancer)
summary(BreastCancer)
```

```
##   Cl.thickness   Cell.size      Cell.shape    Epith.c.size   Bare.nuclei
## 1      :139    1      :373    1      :346    2      :376    1      :402
## 5      :128    10     : 67    2      : 58    3      : 71    10     :132
## 3      :104    3      : 52    10     : 58    4      : 48    2      : 30
## 4      : 79    2      : 45    3      : 53    1      : 44    5      : 30
## 10     : 69    4      : 38    4      : 43    6      : 40    3      : 28
## 2      : 50    5      : 30    5      : 32    5      : 39    8      : 21
## (Other):114    (Other): 78    (Other): 93    (Other): 65    (Other): 40
##   Bl.cromatin   Normal.nucleoli    Mitoses          Class
## 3      :161    1      :432    1      :563    benign   :444
## 2      :160    10     : 60    2      : 35    malignant:239
## 1      :150    3      : 42    3      : 33
## 7      : 71    2      : 36    10     : 14
## 4      : 39    8      : 23    4      : 12
## 5      : 34    6      : 22    7      :  9
## (Other): 68    (Other): 68    (Other): 17
```

```
library(boot)

set.seed(123)

# build a logistic regression model using all variables
glm.fit <- glm(Class ~ ., data = BreastCancer, family = binomial)
```

Warning: glm.fit: algorithm did not converge

Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

```
cv.error <- cv.glm(BreastCancer, glm.fit, K=5)
```

Warning: glm.fit: algorithm did not converge
Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

Warning: glm.fit: algorithm did not converge

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```
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: algorithm did not converge

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: algorithm did not converge

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
```

```r
cv.error$delta[1]
```

```
## [1] 0.06111194
```

Another Method

```r
set.seed(234)

k <- 5
n <- nrow(BreastCancer)

folds <- sample(rep(1:k, length.out= n))

cv.error <- numeric(k)

for (i in 1:k) {
  train_data <- BreastCancer[folds != i, ]
  test_data <- BreastCancer[folds == i, ]

  fit.glm <- glm(Class ~ ., data = train_data, family = binomial)

  prob <- predict(fit.glm, newdata=test_data, type = "response")

  pred_class <- ifelse(prob > 0.5, "malignant", "benign")

  cv.error[i] <- mean(pred_class != test_data$Class)
}
```

```
## Warning: glm.fit: algorithm did not converge

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: algorithm did not converge

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```

Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

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Warning: glm.fit: algorithm did not converge

Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

cv.error

[1] 0.04379562 0.06569343 0.09489051 0.06617647 0.05147059