

```

> library(dslabs)
> library(caret)
> library(tidyverse)
> set.seed(1, sample.kind = "Rounding")
Warning message:
In set.seed(1, sample.kind = "Rounding") :
  non-uniform 'Rounding' sampler used
> data(tissue_gene_expression)
> class(tissue_gene_expression)
[1] "list"
> names(tissue_gene_expression)
[1] "x" "y"
> class(tissue_gene_expression$x)
[1] "matrix"
> class(tissue_gene_expression$y)
[1] "factor"
> dim(tissue_gene_expression$x)
[1] 189 500
> dim(as.matrix(tissue_gene_expression$y))
[1] 189 1
> y <- tissue_gene_expression$y
> x <- tissue_gene_expression$x
> y[1:10]
[1] cerebellum cerebellum cerebellum cerebellum cerebellum cerebellum
[7] cerebellum cerebellum cerebellum cerebellum
Levels: cerebellum colon endometrium hippocampus kidney liver placenta
> x[1:10, 1:10]
      MAML1      LHPP      SEPT10      B3GNT4      ZNF280D      SOX12      C21orf62
cerebellum_1  9.825680  8.327163  5.499382  8.692371  5.642305  6.254751  5.840938
cerebellum_2  9.631247  8.542827  5.644292  8.833679  5.685083  6.289460  6.065646
cerebellum_3  9.690548  8.476486  5.717187  8.498623  5.958232  6.215924  5.771117
cerebellum_4  9.991592  8.506430  5.789430  8.421143  5.736563  6.512055  5.851617
cerebellum_5  9.578130  8.371783  5.779698  8.818455  5.630886  6.201556  5.965732
cerebellum_6  9.860121  8.278559  5.718611  8.728139  5.708949  6.367384  5.769961
cerebellum_7  9.773119  8.429068  5.833339  8.641901  6.316711  6.251236  5.904653
cerebellum_8  9.683163  8.544539  5.635356  8.810830  5.867560  6.368056  5.925835
cerebellum_9  9.989940  9.350519  6.873389  8.846305  5.749636  6.326722  5.828319
cerebellum_10 10.375016  8.893877  5.920607  8.707563  5.525131  6.616960  5.733619
      PER3      HOXA10      HOXC5
cerebellum_1  8.330565  5.520803  7.660495
cerebellum_2  8.263576  5.528077  7.569041
cerebellum_3  9.102294  5.599405  7.418460
cerebellum_4  9.210058  5.561197  7.332254
cerebellum_5  8.502172  5.601099  7.535668
cerebellum_6  8.766777  5.681404  7.535398
cerebellum_7  9.347572  5.554998  7.377026
cerebellum_8  8.303106  5.702986  7.468757
cerebellum_9  8.735844  5.532744  7.337115
cerebellum_10 7.236387  5.958967  7.314246
> test_index <- createDataPartition(y, list = FALSE)
> train_set <- x[-test_index, ]
> test_set <- x[test_index, ]
> delta <- c(1, 3, 5, 7, 9, 11)
>
> accuracy <- sapply(delta, function(x) {
+   fit <- knn3(train_set, y[-test_index], k = x)
+   y_hat <- predict(fit, newdata = test_set, type = "class")
+   mean(y_hat == y[test_index])
+ })
> accuracy
[1] 0.9895833 0.9687500 0.9479167 0.9166667 0.9166667 0.9062500
>

```