

```

> library(dslabs)
> library(caret)
> data("tissue_gene_expression")
> set.seed(1993, sample.kind="Rounding")
Warning message:
In set.seed(1993, sample.kind = "Rounding") :
  non-uniform 'Rounding' sampler used
> ind <- which(tissue_gene_expression$y %in% c("cerebellum", "hippocampus"))
> y <- droplevels(tissue_gene_expression$y[ind])
> x <- tissue_gene_expression$x[ind, ]
> x <- x[, sample(ncol(x), 10)]
>
>
> fit_qda <- train(x, y, method='qda')
> fit_qda
Quadratic Discriminant Analysis

69 samples
10 predictors
2 classes: 'cerebellum', 'hippocampus'

No pre-processing
Resampling: Bootstrapped (25 reps)
Summary of sample sizes: 69, 69, 69, 69, 69, ...
Resampling results:

Accuracy   Kappa
0.8147954  0.6339053

>
>
> fit_qda$finalModel
Call:
qda(x, grouping = y)

Prior probabilities of groups:
cerebellum hippocampus
0.5507246  0.4492754

Group means:
      SAPCD1  HEMK1  PLCB1  SPI1  RAB1B  MSH4  IL18R1
cerebellum 6.986817 7.438612 5.040267 6.048843 10.26148 5.325845 5.421491
hippocampus 7.027106 7.350232 5.023790 6.490261 10.24046 5.247354 5.539534
      OAZ2  FOXE3  C21orf62
cerebellum 10.00821 6.022749 5.911605
hippocampus 9.65903 6.062418 5.721539
> t(fit_qda$finalModel$means) %>% data.frame() %>% mutate(predictor_name = rownames(.))
  cerebellum hippocampus predictor_name
1    6.986817    7.027106      SAPCD1
2    7.438612    7.350232      HEMK1
3    5.040267    5.023790      PLCB1
4    6.048843    6.490261      SPI1
5   10.261483   10.240458      RAB1B
6    5.325845    5.247354      MSH4
7    5.421491    5.539534      IL18R1
8   10.008207    9.659030      OAZ2
9    6.022749    6.062418      FOXE3
10   5.911605    5.721539     C21orf62
> t(fit_qda$finalModel$means) %>% data.frame() %>% mutate(predictor_name = rownames(.)) %>%
+ ggplot(aes(cerebellum, hippocampus, label = predictor_name)) +
+ geom_point() +
+ geom_text() +
+ geom_abline()
>

```