

```

> 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_lda <- train(x, y, method = "lda", preProcess = "center")
> fit_lda
Linear Discriminant Analysis

```

```

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

```

```

Pre-processing: centered (10)
Resampling: Bootstrapped (25 reps)
Summary of sample sizes: 69, 69, 69, 69, 69, 69, ...
Resampling results:

```

```

Accuracy   Kappa
0.8707879  0.7358585

```

```

> t(fit_lda$finalModel$means) %>% data.frame() %>%
+ mutate(predictor_name = rownames(.)) %>%
+ ggplot(aes(cerebellum, hippocampus, label = predictor_name)) +
+ geom_point() +
+ geom_text() +
+ geom_abline()
>
> d <- apply(fit_lda$finalModel$means, 2, diff)
> ind <- order(abs(d), decreasing = TRUE)[1:2]
> plot(x[, ind], col = y)
>
>
>

```

```

> library(dslabs)
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> data("tissue_gene_expression")
> set.seed(1993, sample.kind="Rounding")

```

```

Warning message:
In set.seed(1993, sample.kind = "Rounding") :
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```

```

> y <- tissue_gene_expression$y
> x <- tissue_gene_expression$x
> x <- x[, sample(ncol(x), 10)]
> fit_lda <- train(x, y, method='lda')
> fit_lda
Linear Discriminant Analysis

```

```

189 samples
10 predictor
7 classes: 'cerebellum', 'colon', 'endometrium', 'hippocampus', 'kidney', 'liver', 'placenta'

```

```

No pre-processing
Resampling: Bootstrapped (25 reps)
Summary of sample sizes: 189, 189, 189, 189, 189, 189, ...
Resampling results:

```

```

Accuracy   Kappa
0.8194837  0.7816682

```

