Clustering and classification with genomic applications

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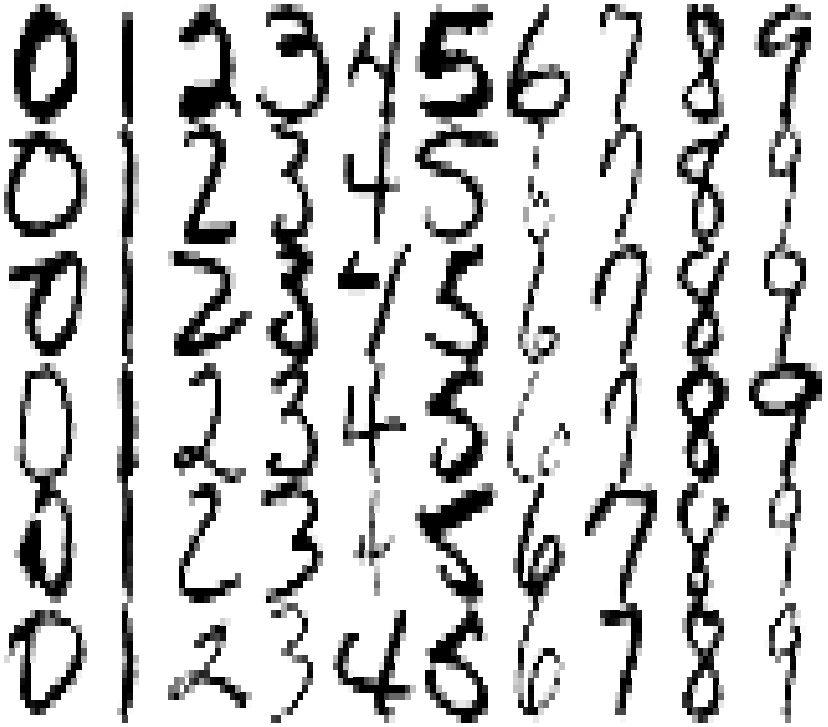
Slides by Gregoire Pau, EMBL, from last year's course, are liberally re-used

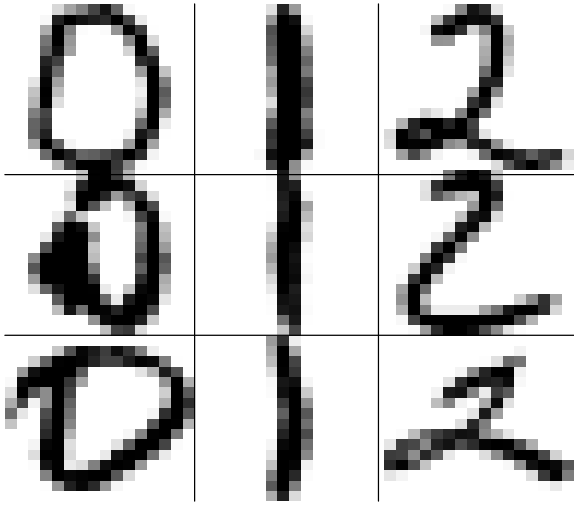
Road map

- artificial example on digit recognition: getting acquainted with features, cases, clustering and classification errors
- some broad principles
- clustering review
- classification review
- cross-validation, prediction error estimation, and software

```
> library(ElemStatLearn)
> example(zip.train)
```



Questions about these images that could be solved using statistical analysis or machine learning:

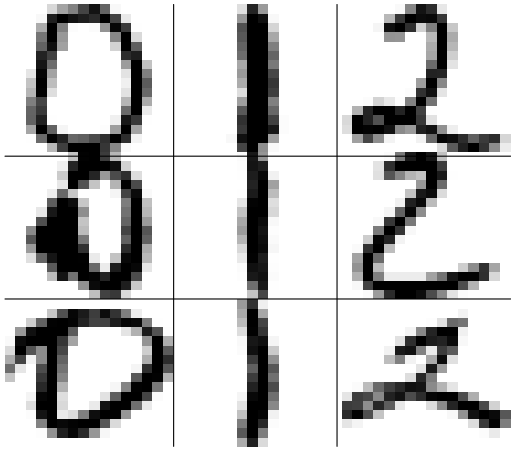


Given a handwriting sample:

- what digit was written?
- how can I most efficiently infer the digit written from the data provided?

Building a learning procedure for handwritten digits

- formalize what is to be learned – what is the underlying process, and what aspects of it are to be clarified through the planned analysis?
- formalize the data representation
  - *cases* arise in an identical fashion from the process of interest
  - *features* are measured on cases in a uniform way
  - departures from these uniformity conditions are recorded in experimental metadata, and may be useful as features or for stratification
- *look at the data* and assess its agreement with your expectations



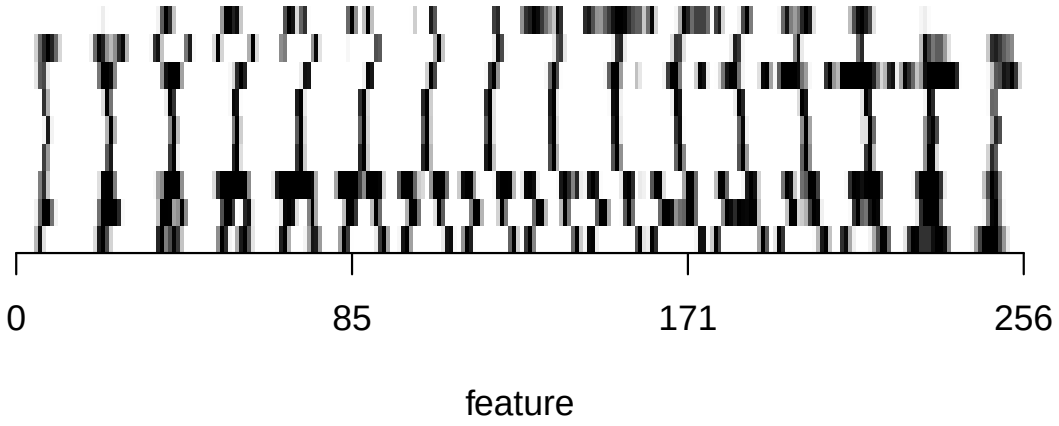
Fact: each digit you see is a 16 x 16 digitization of a scan

- What are the *cases* for the data seen here? How many cases?
- What are the *features* for the data seen here? How many features?

Fact: num3 is a 9 x 256 matrix, first three rows are digitizations of '0', ... last three rows are digitizations of '2'

There is no privileged representation of features for algorithmic analysis – a different view of 9 scans follows

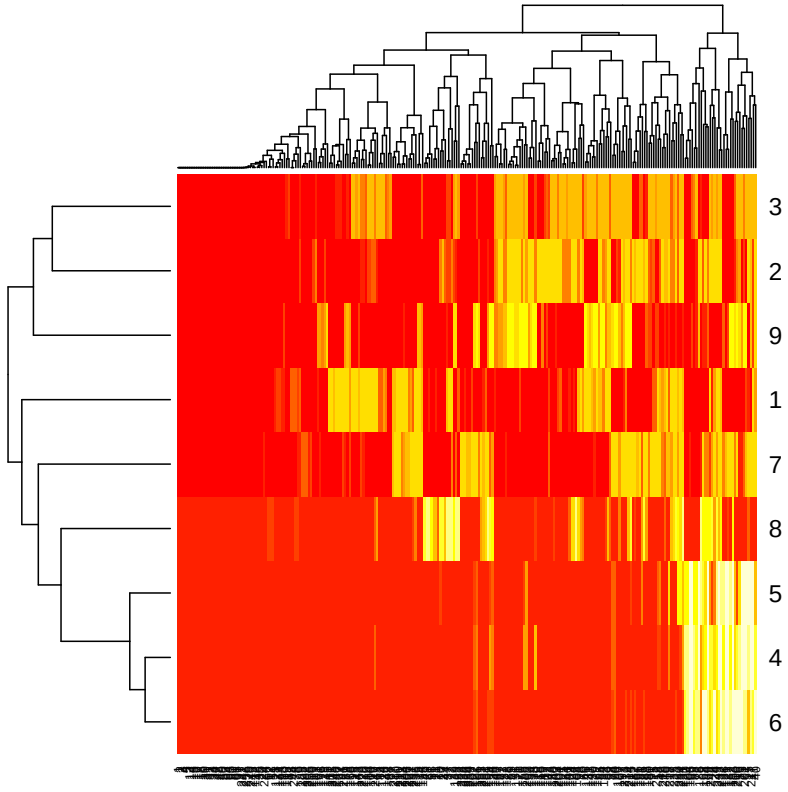
```
> par(mfrow=c(2,1))
> image(t(num3), col=gray((256:0)/256),axes=FALSE, xlab="feature")
> axis(1,at=seq(0,1,len=4),labels=round(seq(0,1,len=4)*256,0))
> par(mfrow=c(1,1))
```


0
85
171
256
feature

Another more familiar re-presentation

What do we learn about features? What about cases?

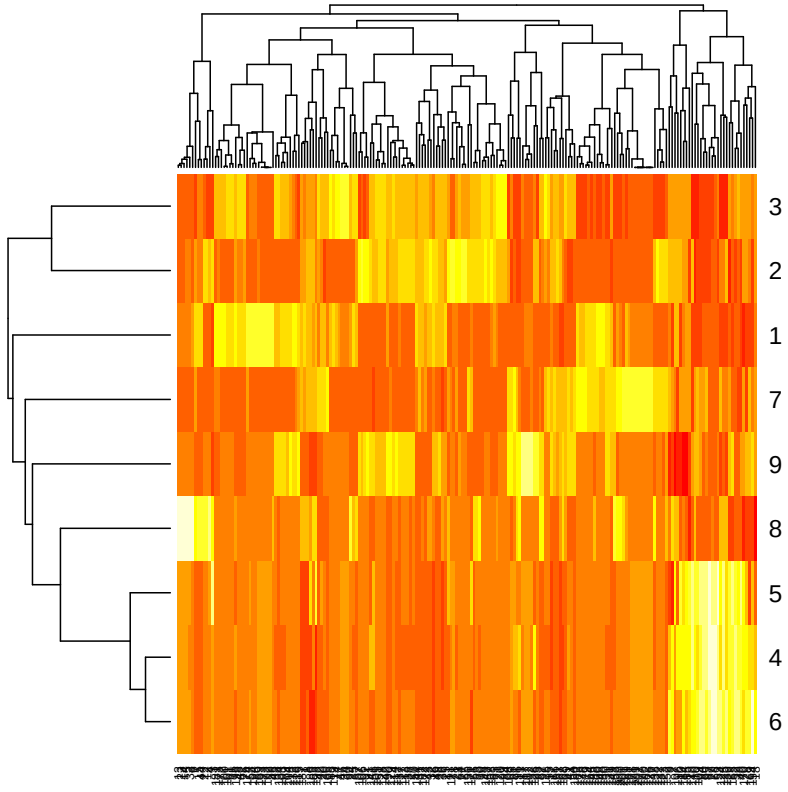
```
> heatmap(num3)
```



The failure of case clustering to recover the natural groups may be rectifiable by standardizing features to have comparable variability. Explain and evaluate:

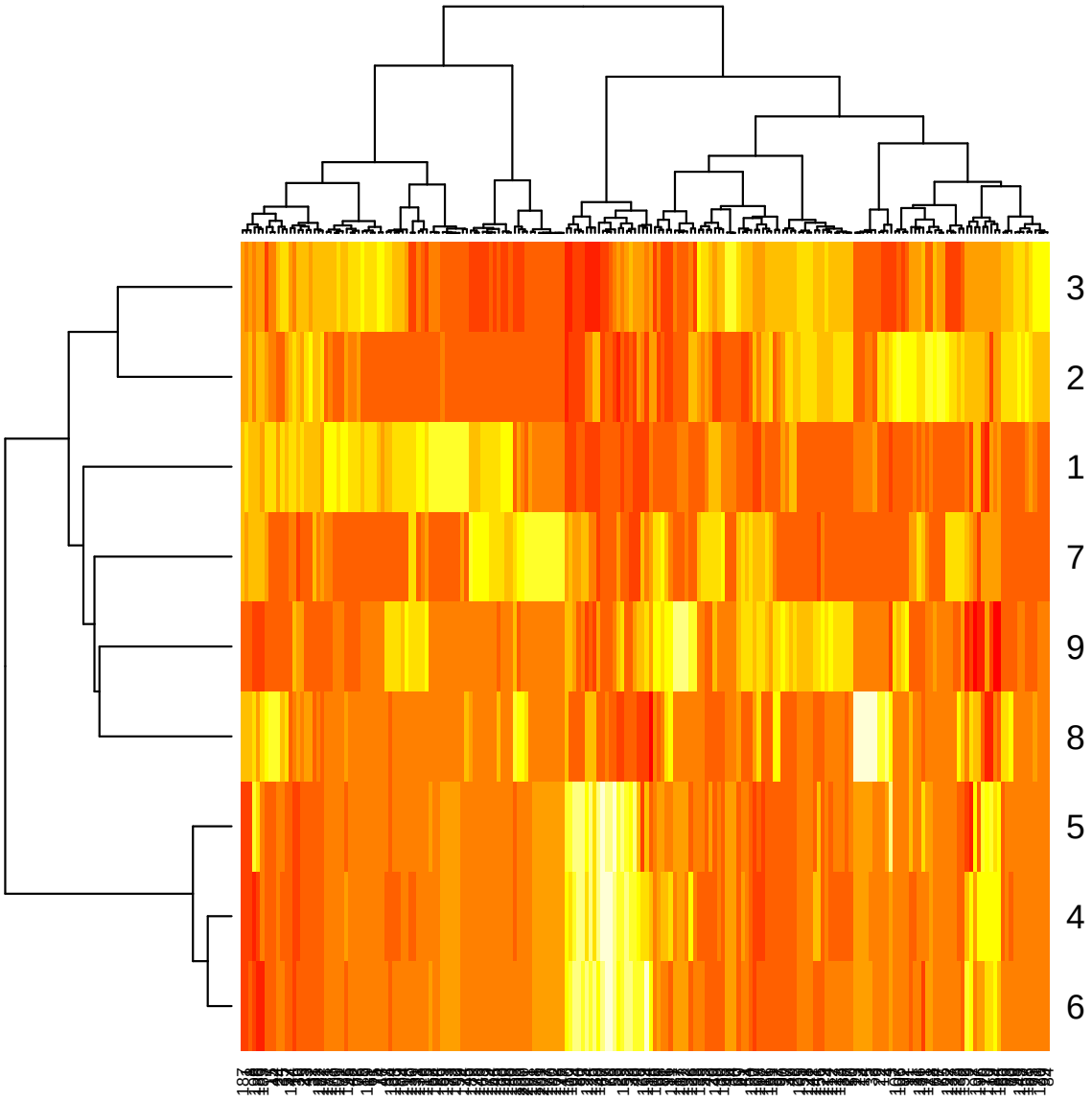
```
> heatmap(scale(num3))
Error in hclustfun(distfun(if (symm) x else t(x))) :
  NA/NaN/Inf in foreign function call (arg 11)
```

```
> drop = which(apply(num3,2,sd) < .2)
> heatmap(scale(num3[,-drop]))
```



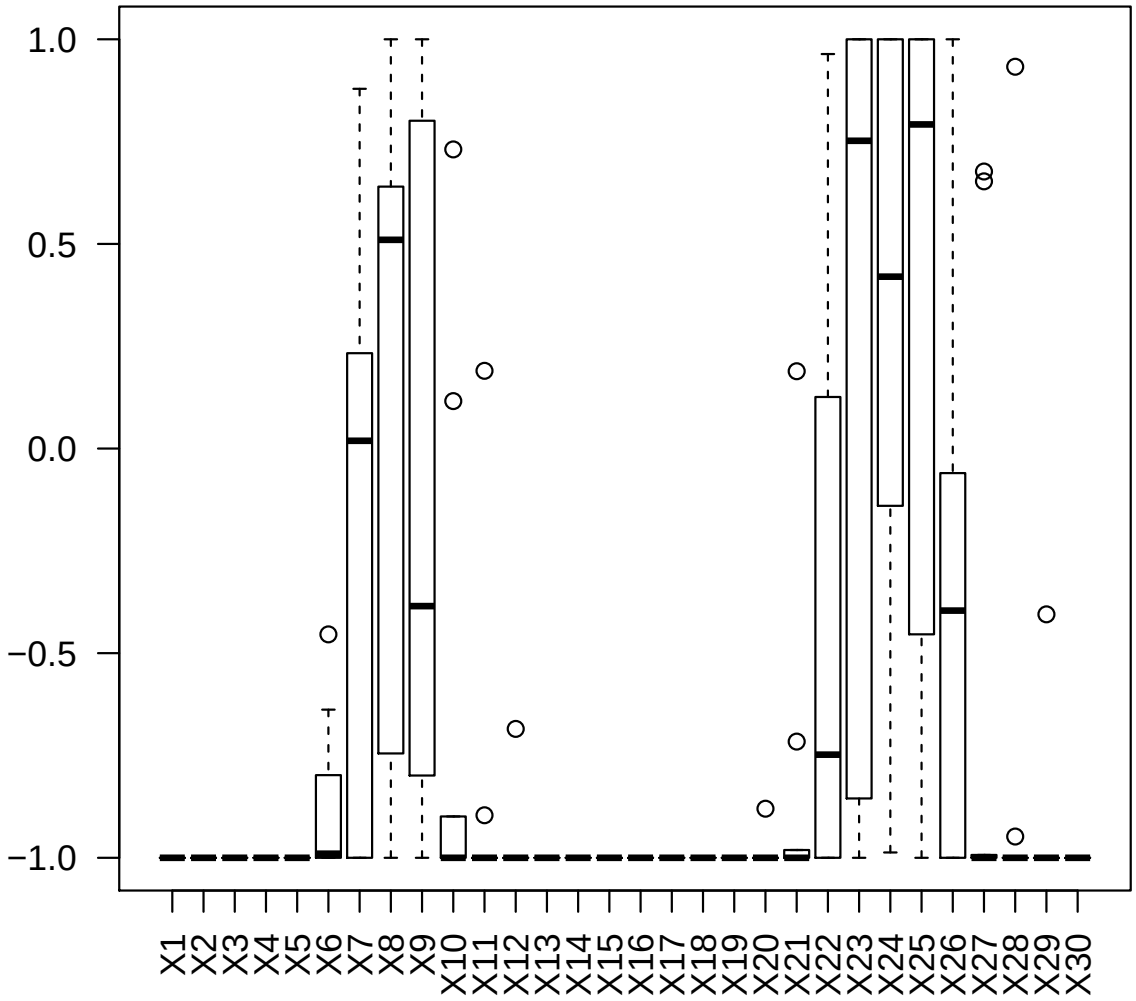
Getting around the defaults of `heatmap`

```
> wclust = function(...) hclust(...,method="ward")
> heatmap(scale(num3[,-drop]), hclustfun=wclust)
```


3
2
1
7
9
8
5
4
6

Explain the interest of:

```
> sum(apply(num3,2,mad) == 0)
[1] 184
> par(las=2)
> boxplot(data.frame(num3[,1:30]))
```

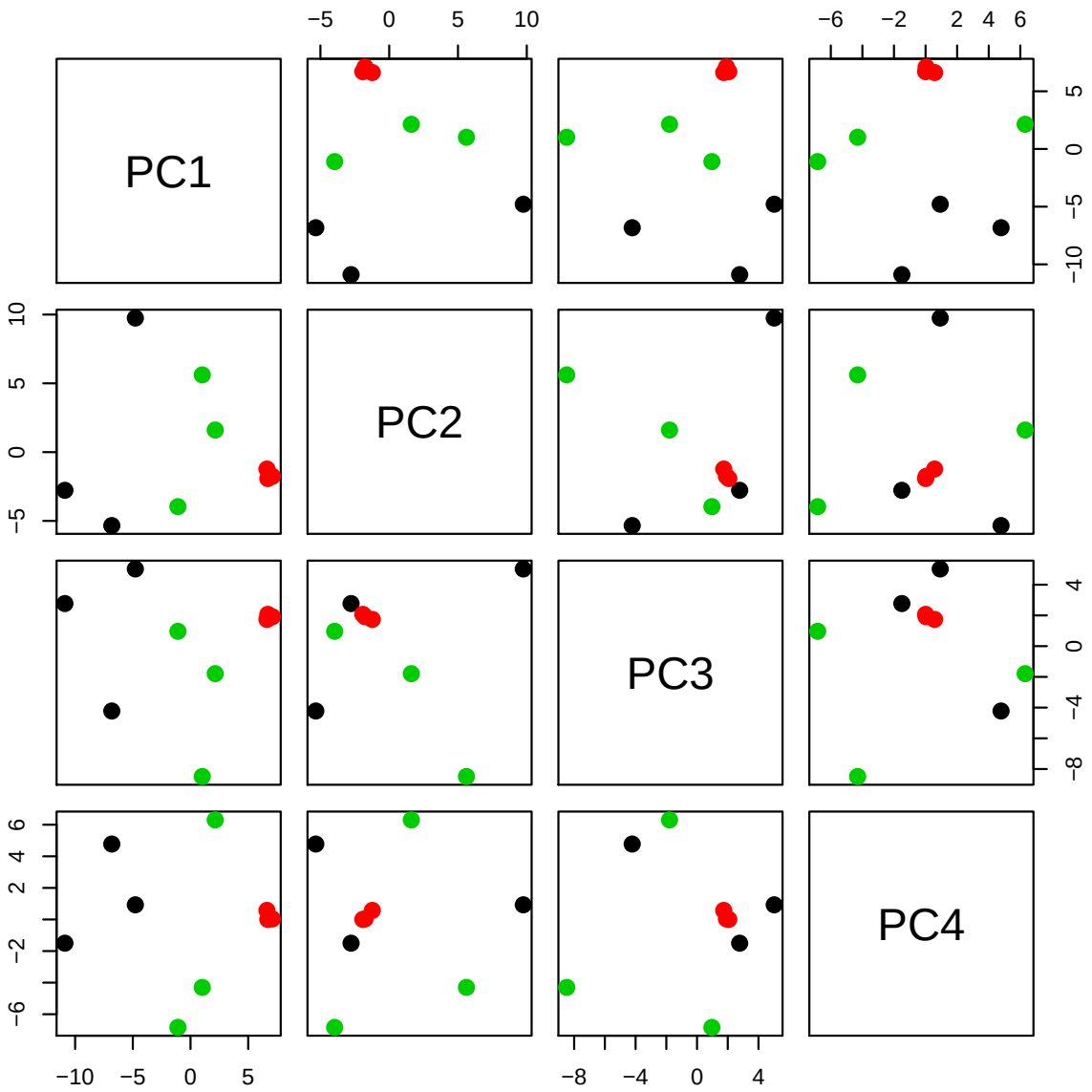

1.0
0.5
0.0
−0.5
−1.0
X1
X2
X3
X4
X5
X6
X7
X8
X9
X10
X11
X12
X13
X14
X15
X16
X17
X18
X19
X20
X21
X22
X23
X24
X25
X26
X27
X28
X29
X30

Visualization after dimension reduction, with labels

```
> m1 = prcomp(num3)
> dim(m1$x)
```

```
[1] 9 9
```

```
> m1 = prcomp(num3)
> pairs(m1$x[,1:4], col=rep(1:3,each=3), pch=19, cex=1.5)
```


PC1
PC2
PC3
PC4
−5 0 5 10
−6 −2 2 4 6
10 5 0 −5
5 0 −5 −10
−5 0 5 10
4 0 −4 −8
6 4 2 −2 −6
−10 −5 0 5
−8 −4 0 4

Using the ExpressionSet container to represent the features and labels

```
> NN = zip.train[zip.train[,1] %in% c(0,1,2),]
> NNMAT = t(NN[1:25,-1])
> NNFAC = factor(NN[1:25,1])
> num25 = new("ExpressionSet", exprs=NNMAT)
> num25$lab = NNFAC

> num25

ExpressionSet (storageMode: lockedEnvironment)
assayData: 256 features, 25 samples
  element names: exprs
protocolData: none
phenoData
  sampleNames: 1 2 ... 25 (25 total)
  varLabels: lab
  varMetadata: labelDescription
featureData: none
experimentData: use 'experimentData(object)'
Annotation:
```

It isn't from an array, but it is a nice unified representation....

Using MLInterfaces to compare learning procedures (and some timings)

First, diagonal LDA

```
> g4spec = xvalSpec("LOG", 4, balKfold.xvspec(4))
> dldaSca = unix.time(
+    dlda1 <- MLearn(lab~., num25, dldaI, g4spec)
+ )
> print(dldaSca)

   user  system elapsed
  0.961   0.071   1.039

> confuMat(dlda1)

     predicted
given 0 1 2
    0 7 0 2
    1 0 9 0
    2 1 0 6
```

Second, feed-forward neural network

```
> nnutSca = unix.time(
+   nnet1 <- MLearn(lab~., num25, nnetI, g4spec,
+         size=8, decay=0.01, MaxNWts=2500, maxit=200)
+ )

> print(nnutSca)

   user  system elapsed
 38.806   0.306  41.379

> confuMat(nnet1)

     predicted
given 0 1 2
    0 7 0 2
    1 0 9 0
    2 0 3 4
```

With two-core system

```
> library(multicore)
> g4spec = xvalSpec("LOG", 4, balKfold.xvspec(4))
> dldaMT = unix.time(dlda2 <- MLearn(lab~., num25, dldaI, g4spec))
> print(dldaMT)

   user  system elapsed
  0.061   0.017   0.802

> confuMat(dlda2)

     predicted
given 0 1 2
    0 7 0 2
    1 0 9 0
    2 1 0 6

> nnutMT = unix.time(nnet2 <- MLearn(lab~., num25, nnetI, g4spec,
+    size=8, decay=0.01, MaxNWts=2500, maxit=200))

> print(nnutMT)

   user  system elapsed
 24.372   0.903  27.285

> confuMat(nnet2)

     predicted
given 0 1 2
    0 7 0 2
    1 0 9 0
    2 0 3 4
```

Summary of introduction

- Multivariate data arise through digitization of images
- Joint distribution of features may be very complex
- Interactive statistical analysis can be used to reduce feature complexity
- When case labels are available, assessment of discriminative capacity of features using PCA can be straightforward
- `MLearn` can be used to exercise celebrated methods against the data fairly simply
  - tuning parameters must be supplied manually
  - various species of cross-validation and feature elimination are supported