Clustering Example

Problem: given observations X_i for $i = 1, \ldots, n$ group the observations into k populations.

Parallel to discriminant analysis but: no training data.

Here: just show some example analyses:

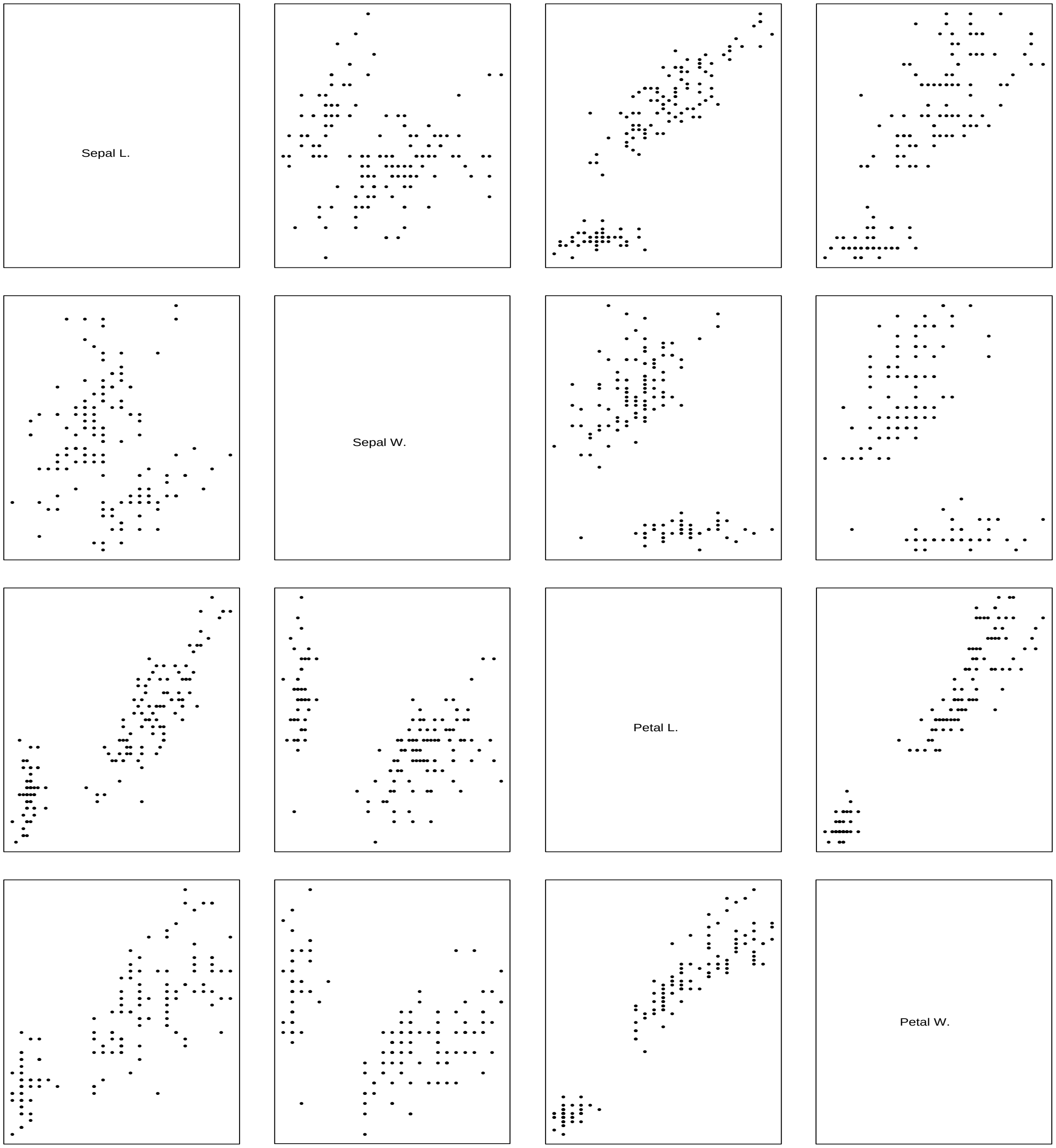
Cluster iris data: so $k = 3$ presumably.

Often: k not known.

Many possible SPlus functions including: `agnes`, `clara`, `pam`, `hclust`

Example: Cluster the iris data.

Put all 150 observations into 150×4 matrix. (Remove species labels.)


Sepal L.
Sepal W.
Petal L.
Petal W.

Cluster into 2, 3 ,4 groups using `pam`:

```
pamiris2 <- pam(x,2)
pamiris3 <- pam(x,3)
pamiris4 <- pam(x,4)
```

Output for two clusters:

```
> pam(x,2)
Call: pam(x = x, k = 2)
Medoids:
     Sepal L. Sepal W. Petal L. Petal W.
[1,]      5.0      3.4      1.5      0.2
[2,]      6.2      2.8      4.8      1.8
Clustering vector:
  [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
 [38] 1 1 1 1 1 1 1 1 1 1 1 1 1 2 2 2 2 2
      2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
 [75] 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
      2 2 2 2 2 1 2 2 2 2 2 2 2 2 2 2 2 2
[112] 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
      2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
[149] 2 2
```

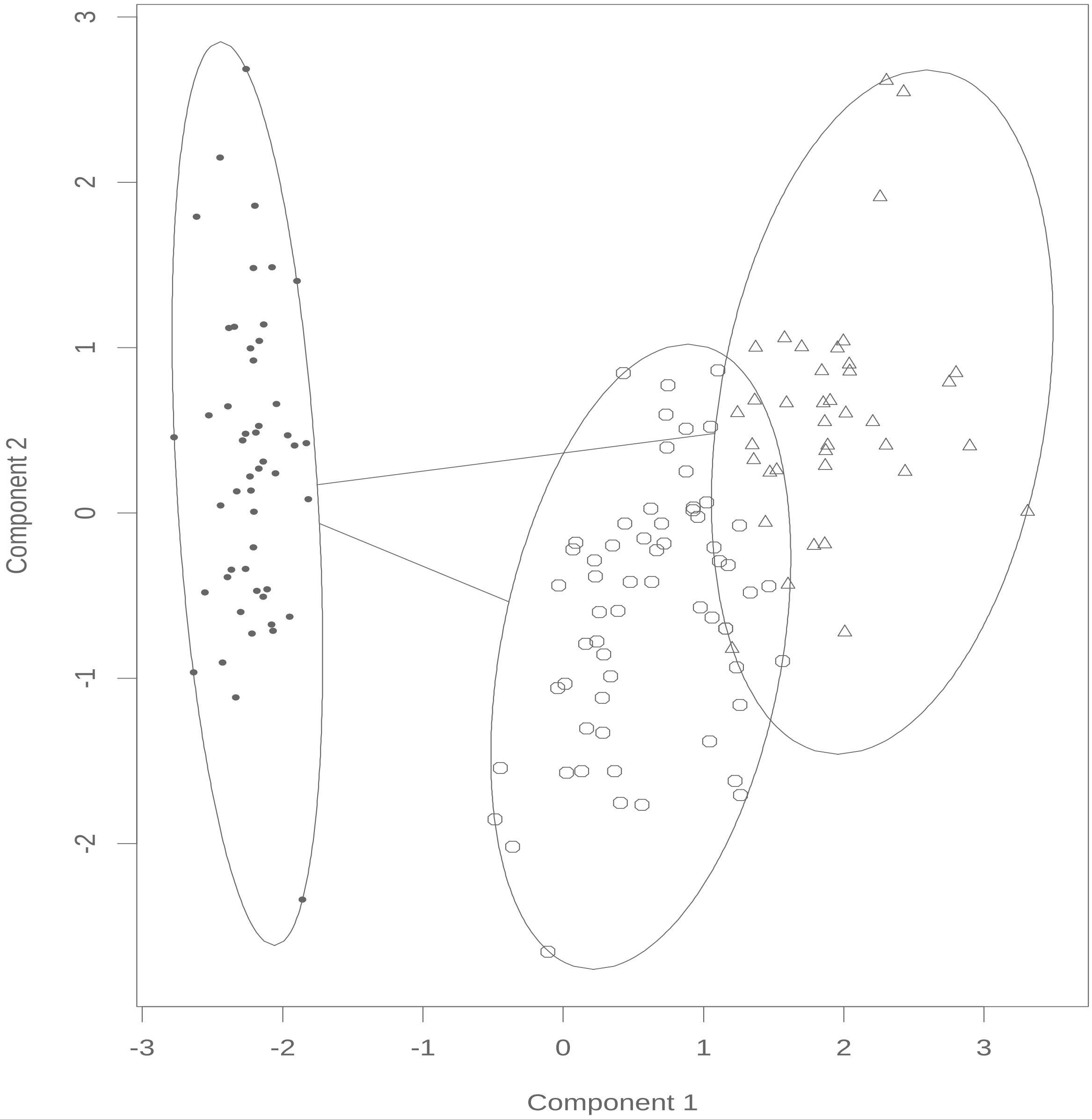
Notice that the algorithm correctly groups together the first 50 observations. The other two species are then lumped together.

```
> pam(x,3)
Call:
pam(x = x, k = 3)
Medoids:
     Sepal L. Sepal W. Petal L. Petal W.
[1,]      5.0      3.4      1.5      0.2
[2,]      6.0      2.9      4.5      1.5
[3,]      6.8      3.0      5.5      2.1
Clustering vector:
  [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
 [38] 1 1 1 1 1 1 1 1 1 1 1 1 1 2 2 3 2 2
      2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
 [75] 2 2 2 3 2 2 2 2 2 2 2 2 2 2 2 2 2 2
      2 2 2 2 2 2 2 2 3 2 3 3 3 3 2 3 3 3 3
[112] 3 3 2 2 3 3 3 3 2 3 2 3 2 3 3 2 2 3
      3 3 3 3 2 3 3 3 3 2 3 3 3 2 3 3 3 2 3
[149] 3 2
```

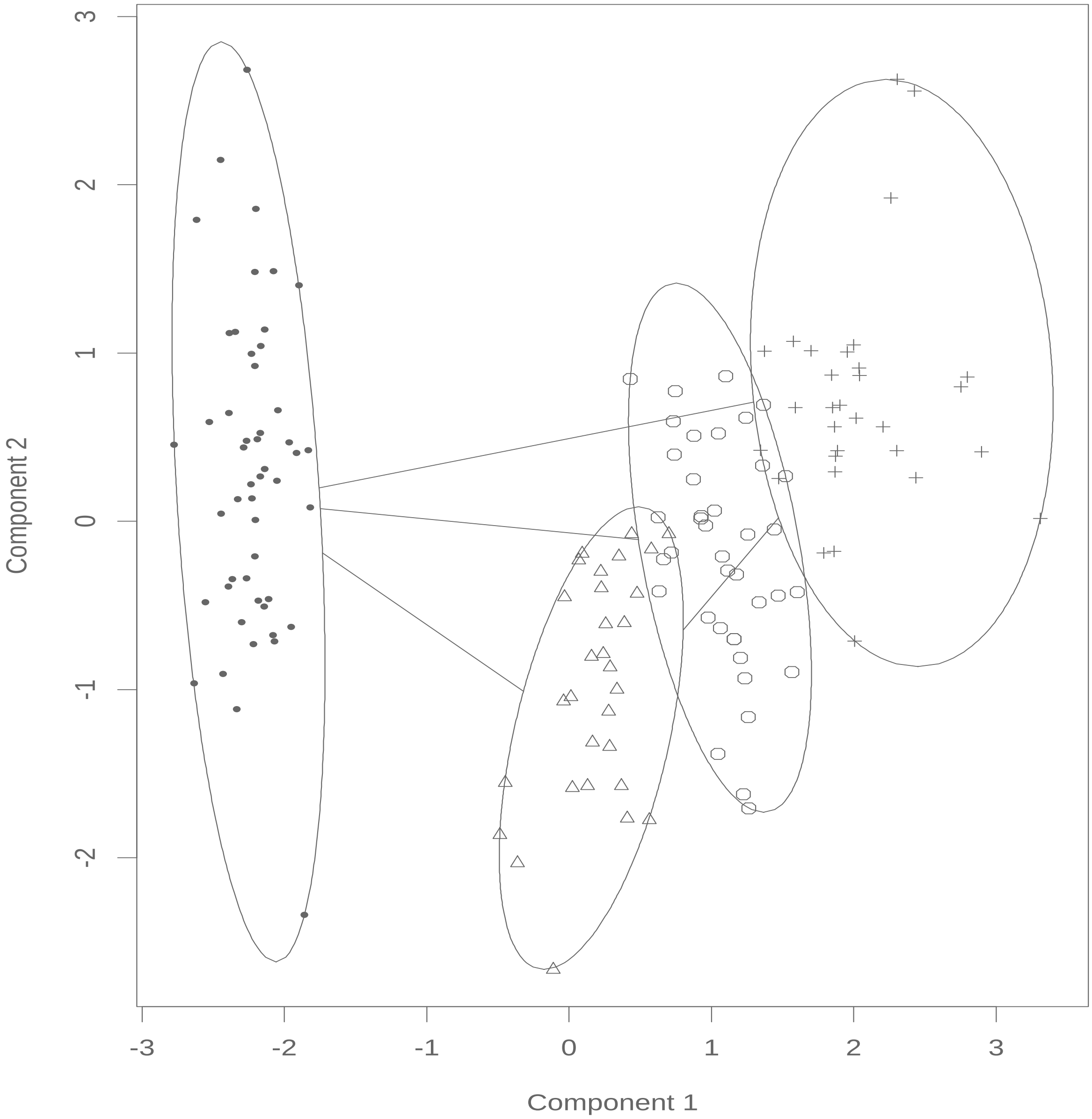
Notice difficulty with 2 versus 3. Total of two from group 2 clustered into group 3; total of 14 from group 3 clustered into group 2.

Now a method which does not require specification of number of classes but doesn't estimate number of classes either. Hierarchical clustering.

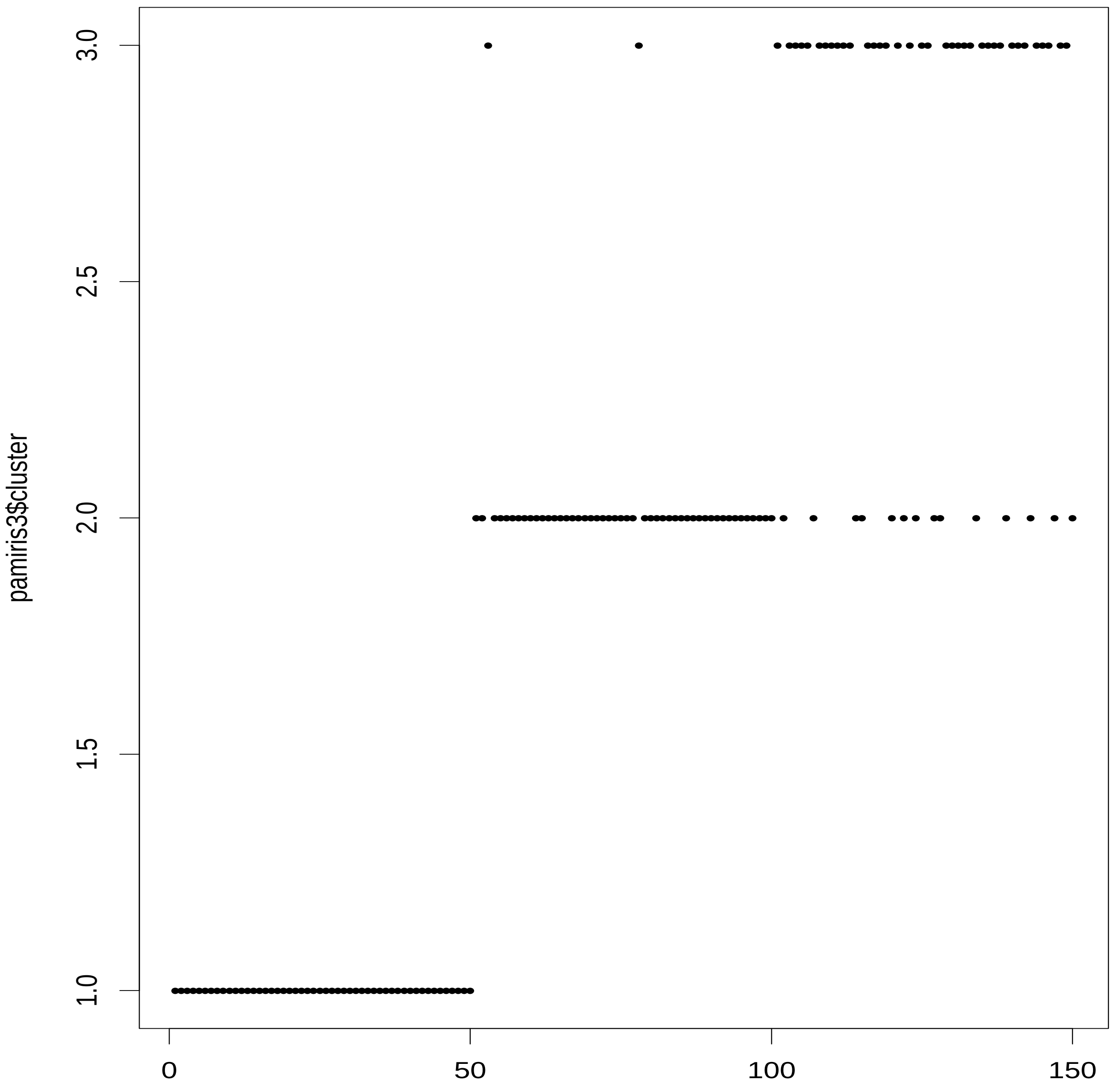
```
> agnesiris <- agnes(x)
> cutree(agnesiris,k=2)
  [1] 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
      2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
 [38] 2 2 2 2 2 2 2 2 2 2 2 2 2 1 1 1 1 1 1
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
 [75] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
[112] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
[149] 1 1
attr(, "height"):
[1] 0.8964852 0.2645751
> plot(cutree(agnesiris,k=2))
> plot(cutree(agnesiris,k=3))
> plot(cutree(agnesiris,k=4))
```



These two components explain 95.81 % of the point variability.



These two components explain 95.81 % of the point variability.


pamiris3$cluster
1.0
1.5
2.0
2.5
3.0
0
50
100
150