segmenting images to data

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flower image

How images are described in R

- Grayscale
- matrix of pixel intensities from 0 (black) to 1 (white) "Intensity matrices"
- 8bits/pixel (bpp) means 256 color levels
- decimals between 0 and 1 as matrix values indicate darkness
- number of columns indicates width (in pixels), number of rows indicates length
- clusters choose ranges of decimals to group matrix
- input to clustering algorithm is the matrix described above, but reorganized
- each column will represent a decimal value/shade (ex. .2 or .1)
 - done with as.vector() function
- Distance matrix:
- Distance between elements of intensity vector.
- Calculate "pairwise distance" between each elements and the other elements
- Do this for each element in the cluster
- (will be done $n^*(n-1)/2$ times) because of a to b is b to a

Inputting data to matrix/vector/distance:

```
flower <- read.csv("flower.csv", header = FALSE)
#remember, default is header = TRUE
str(flower)</pre>
```

```
'data.frame':
                    50 obs. of 50 variables:
   $ V1 : num 0.0991 0.0991 0.1034 0.1034 0.1034 ...
   $ V2 : num 0.112 0.108 0.112 0.116 0.108 ...
   $ V3 : num 0.134 0.116 0.121 0.116 0.112 ...
   $ V4 : num 0.138 0.138 0.121 0.121 0.112 ...
##
   $ V5 : num  0.138  0.134  0.125  0.116  0.112 ...
##
   $ V6 : num 0.138 0.129 0.121 0.108 0.112 ...
##
   $ V7 : num 0.129 0.116 0.103 0.108 0.112 ...
   $ V8 : num 0.116 0.103 0.103 0.103 0.116 ...
##
   $ V9 : num  0.1121  0.0991  0.1078  0.1121  0.1164 ...
   $ V10: num 0.121 0.108 0.112 0.116 0.125 ...
   $ V11: num 0.134 0.125 0.129 0.134 0.129 ...
   $ V12: num 0.147 0.134 0.138 0.129 0.138 ...
               0.000862 0.146552 0.142241 0.142241 0.133621 ...
##
   $ V13: num
               0.000862 0.000862 0.142241 0.133621 0.12931 ...
##
   $ V14: num
##
   $ V15: num 0.142 0.142 0.134 0.121 0.116 ...
   $ V16: num 0.125 0.125 0.116 0.108 0.108 ...
   $ V17: num 0.1121 0.1164 0.1078 0.0991 0.0991
##
   $ V18: num 0.108 0.112 0.108 0.108 0.108 ...
   $ V19: num 0.121 0.129 0.125 0.116 0.116 ...
   $ V20: num 0.138 0.129 0.125 0.116 0.116 ...
   $ V21: num 0.138 0.134 0.121 0.125 0.125 ...
```

```
## $ V22: num 0.134 0.129 0.125 0.121 0.103 ...
## $ V23: num 0.125 0.1207 0.1164 0.1164 0.0819 ...
## $ V24: num 0.1034 0.1034 0.0991 0.0991 0.1034 ...
## $ V25: num 0.0948 0.0905 0.0905 0.1034 0.125 ...
## $ V26: num 0.0862 0.0862 0.0991 0.125 0.1422 ...
## $ V27: num 0.086207 0.086207 0.103448 0.12931 0.000862 ...
## $ V28: num 0.0991 0.1078 0.1164 0.1293 0.1466 ...
## $ V29: num 0.116 0.134 0.134 0.121 0.142 ...
   $ V30: num 0.121 0.138 0.142 0.129 0.138 ...
## $ V31: num 0.121 0.134 0.142 0.134 0.129 ...
## $ V32: num 0.116 0.134 0.129 0.116 0.112 ...
## $ V33: num 0.108 0.112 0.116 0.108 0.108 ...
## $ V34: num 0.1078 0.1078 0.1034 0.0991 0.1034 ...
## $ V35: num 0.1078 0.1034 0.0991 0.0991 0.0991 ...
## $ V36: num 0.1078 0.1034 0.1034 0.0905 0.0862 ...
## $ V37: num 0.1078 0.1078 0.1034 0.0819 0.0733 ...
## $ V38: num 0.0948 0.0991 0.0776 0.069 0.0733 ...
## $ V39: num 0.0733 0.056 0.0474 0.0474 0.056 ...
## $ V40: num 0.0474 0.0388 0.0431 0.0474 0.0603 ...
## $ V41: num 0.0345 0.0345 0.0388 0.0474 0.0647 ...
## $ V42: num 0.0259 0.0259 0.0345 0.0431 0.056 ...
## $ V43: num 0.0259 0.0259 0.0388 0.0517 0.0603 ...
## $ V44: num 0.0302 0.0302 0.0345 0.0517 0.0603 ...
   $ V45: num 0.0259 0.0259 0.0259 0.0388 0.0474 ...
## $ V46: num 0.0259 0.0172 0.0172 0.0259 0.0345 ...
## $ V47: num 0.01724 0.01724 0.00862 0.02155 0.02586 ...
## $ V48: num 0.0216 0.0129 0.0129 0.0172 0.0302 ...
   $ V49: num 0.0216 0.0216 0.0216 0.0345 0.0603 ...
## $ V50: num 0.0302 0.0345 0.0388 0.0603 0.0776 ...
#r doesn't read this like it represents a distance matrix. just reg vars and obs
flowermatrix <- as.matrix(flower)</pre>
#turned into matrix
flowervector = as.vector(flowermatrix)
str(flowervector)
## num [1:2500] 0.0991 0.0991 0.1034 0.1034 0.1034 ...
#turned into vector, dataframe with as.vector() command will return dataframe, not individual vectors
#distance matrix:
distance = dist(flowervector, method = "euclidean")
str(distance)
   'dist' num [1:3123750] 0 0.00431 0.00431 0.00431 0.01293 ...
## - attr(*, "Size")= int 2500
## - attr(*, "Diag")= logi FALSE
## - attr(*, "Upper")= logi FALSE
## - attr(*, "method")= chr "euclidean"
## - attr(*, "call")= language dist(x = flowervector, method = "euclidean")
Heigharachial clustering:
```

```
clusterintensity = hclust(distance, method = "ward")

## The "ward" method has been renamed to "ward.D"; note new "ward.D2"

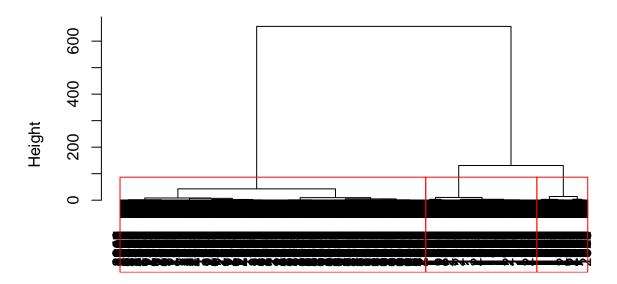
#"ward" method minimizes variance within and distance between each clusterplot

#make dendrogram

plot(clusterintensity)

#3clusters on dentrogram represented with rectangular area
rect.hclust(clusterintensity, k = 3, border = "red")
```

Cluster Dendrogram



distance hclust (*, "ward.D")

#reminders: all observations are on the bottom row; vertical lengths represent distances between each c #suggestion: make cutoff/choose number of clusters where the distance between different numbers of clus

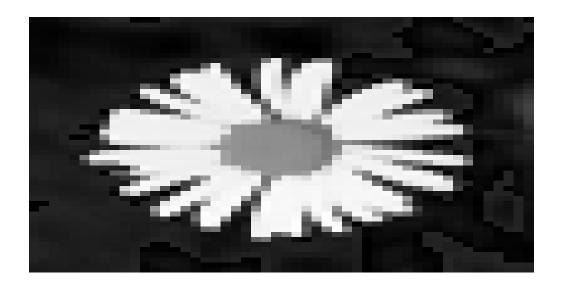
#creates clusters via segmentation #see new matrix with same dimensions but with new values determined by cluster number: flowerclusters = cutree(clusterintensity, k = 3) flowerclusters

0.08574315 0.50826255 0.93147713

#creates image as input by rewriting dimensions of vector into a matrix with original dimensions (50 x dim(flowerclusters) = c(50, 50) image(flowerclusters, axes = FALSE)



#review what initial greyscale image looks like
image(flowermatrix, axes = FALSE, col = grey(seq(0, 1, length = 256)))



BrainScans