# CS595 Intro to Web Science, Assignment #9

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Create a blog-term matrix. Start by grabbing 100 blogs; include:

- http://f-measure.blogspot.com/
- http://ws-dl.blogspot.com/

and grab 98 more as per the method shown in class.

Use the blog title as the identifier for each blog (and row of the matrix). Use the terms from every item/title (RSS) or entry/title (Atom) for the columns of the matrix. The values are the frequency of occurrence. Essentially you are replicating the format of the "blogdata.txt" file included with the PCI book code. Limit the number of terms to the most "popular" (i.e., frequent) 500 terms, this is **after** the criteria on p. 32 (slide 7) has been satisfied.

#### Answer to Question 1

For this question, I had to use three scripts (1) getFeedList.py, (2) generatefeedvector.py and (3) reduceTerms.py.

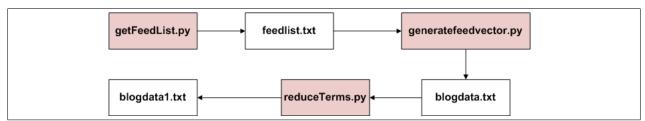


Figure 1: Creation of the Blog-Term Matrix

In Listing 4 (getFeedList.py), I "manually" added F-Measure and the WS-DL blogs, but creating the empty list feedlist and added those two blogs first. I then used the link for next blog http://www.blogger.com/next-blog?navBar=true&blogID=3471633091411211117 in a while loop to create a list of random blogs. I capture the atom feed uri using BeautifulSoup. I had to include the sleep function since my script stopped running before reaching even 10 blogs. I added the "?max-results=200" to each uri so that it would grab at most 200 entries. This script produced feedlist.txt as an output.

I used generatefeedvector.py (Listing 5) from the book [1]. I had to make minimal changes to it in order to handle an encoding error I had encountered. Some blog titles had special characters like the copyright symbol and there was one blog with a title written in Chinese. This script accepted feedlist.txt as an input and produced blogdata.txt as an output. My term output was approximately 3200 terms.

The final part of the problem was to take the 3200+ terms and reduce it to the 500 most frequent terms. In listing 6 (reduceTerms.py), I imported clusters.py in order to read in the blogdata.txt file. I then created an empty dictionary to store the sums of the term occurrences. I looped through the words which served as columns and summed the frequency. I then reverse sorted the dictionary and limited to the first 500 terms. Next I eliminate all the other terms from the matrix by only including terms that were found in the reverse sorted limited collection.

Create an ASCII and JPEG dendrogram that clusters (i.e., HAC) the most similar blogs (see slides 12 & 13). Include the JPEG in your report and upload the ASCII file to GitHub (it will be too unwieldy for inclusion in the report.)

#### Answer to Question 2

To answer this question, I relied on clusters.py and used the code samples from page 37 and page 40 of the book [1] and included them generateImages.py (Listing 1). The ASCII dendrogram is located in GitHub at https://github.com/vneblitt/cs595-f13/blob/master/assignment09/q02/blogclustascii.txt. The JPEG dendrogram using Python Imaging Library (PIL) is Figure 3.

Listing 1: generateImages.py

```
import sys
sys.path.insert(0, '/Users/vneblitt/Documents/cs595-f13/assignment09/library')
import clusters
# Create clusters
blognames, words, data=clusters.readfile('/Users/vneblitt/Documents/cs595-f13/assignment09/q01
    /blogdata1.txt')
clust=clusters.hcluster(data)
# Create ASCII dendrogram
clusters.printclust(clust,labels=blognames)
# Create Nicer dendrogram with PIL
clusters.drawdendrogram(clust,blognames,jpeg='blogclust.jpg')
```

It is quite difficult to see Figure 3, but a selected close-up (see Figure 2) shows that some of the clustering was moderately successful.

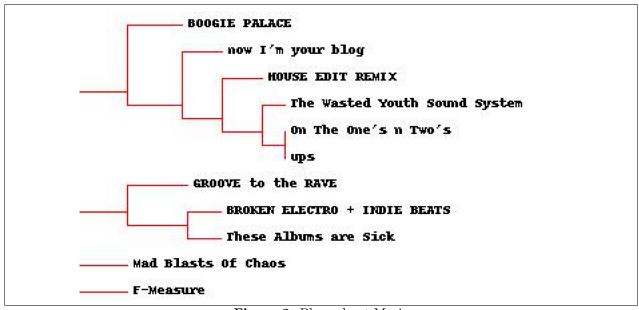


Figure 2: Blogs about Music

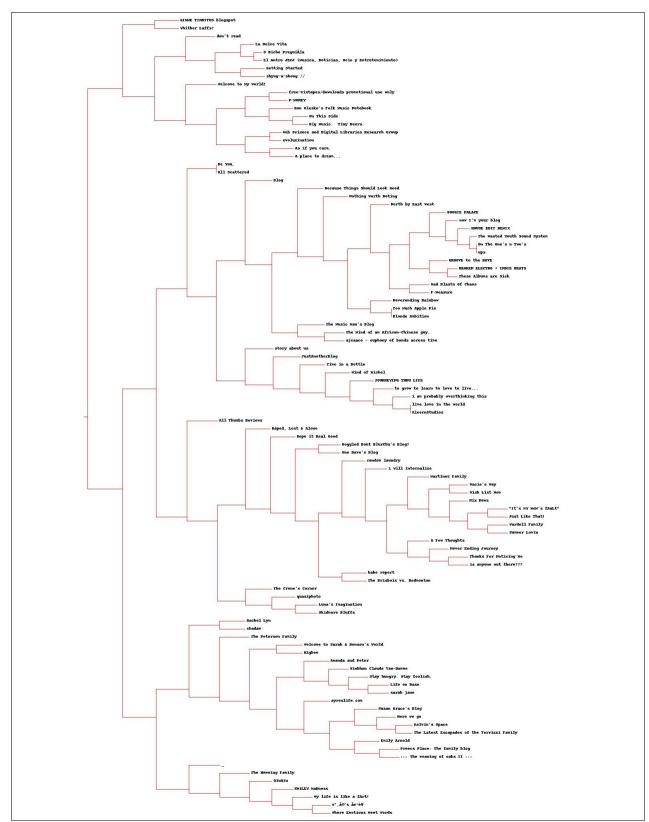


Figure 3: JPEG Dendrogram

Cluster the blogs using K-Means, using k=5, 10, 20 (see slide 18). How many iterations were required for each value of k?

### Answer to Question 3

To answer this question, I again relied on clusters.py and used the code samples from page 44 of the book [1] and included them getKMeans.py (Listing 2). I ran this a few times and got different results each time. Segaran explains this in Chapter 3, "Because this function uses random centroids to start with, the order of the results retired will almost always be different. It's also possible for the contents of the clusters to be different depending on the initial locations of the centroids." [1] Listing 8 shows the actual output of the script and Table 1 shows the summary data.

Listing 2: getKMeans.py

No. of Iterations
6
7
100

Table 1: K-Means Iterations

Use MDS to create a JPG of the blogs similar to slide 29. How many iterations were required?

#### Answer to Question 4

I had to reduce the MDS image down to 20% in order to include it in this report, but that makes it too hard to read (see Figure ??). The full one is located in GitHub at https://github.com/vneblitt/cs595-f13/blob/master/assignment09/q04/blogs2d.jpg.

When I first ran the code, I encounter a divide-by-zero error that would not allow the code to fully execute. I had to remove the following four blogs from the blog-term matrix since their entire row in the matrix contained zeros.

- Blonde Ambition
- ups
- Alcorn Studios
- All Scattered

I ran into this problem earlier when I had only managed to get 60 terms from Q1 and I thought I would not encounter this problem since I included the summaries and descriptions had achieved 3200+ terms and then reduced the terms down to the 500 most frequent.

Listing 3: getMDS.py

```
import sys
sys.path.insert(0, '/Users/vneblitt/Documents/cs595-f13/assignment09/library')
import clusters
blognames, words, data=clusters.readfile('blogdata1.txt')
coords=clusters.scaledown(data)
clusters.draw2d(coords, blognames, jpeg='blogs2d.jpg')
```

I examined blogs listed near F-Measure in the close-up (Figure 4) and saw some of the same ones in the JPEG dendrogram, but I also saw a few that were not included.

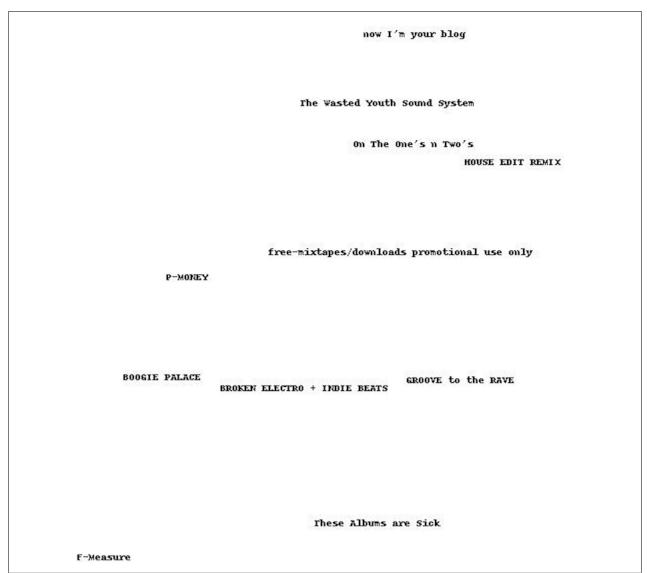


Figure 4: Music Blogs with MDS

## Question 5 - Extra Credit (5 points)

Re-run Q2, but this time with proper TFIDF calculations instead of the hack discussed on slide 7 (p. 32). Use the same 500 words, but this time replace their frequency count with TFIDF scores as computed in assignment #3. Document the code, techniques, methods, etc. used to generate these TFIDF values. Upload the new file to GitHub.

Compare and contrast the resulting dendrogram with the dendrogram from Q2.

Note: Ideally you would not reuse the same 500 terms and instead come up with TFIDF scores for all the terms and choose the top 500 from that list, but I am trying to limit the amount of work necessary.

#### Answer to Question 5

Not attempted.

### A Full Version of getFeedList.py

Listing 4: getFeedList.py

```
from bs4 import BeautifulSoup
from urllib2 import HTTPError
import urllib2
import time
f = open('feedlist.txt', 'w')
# These two are automatically in the list
firstfeed = 'http://f-measure.blogspot.com/feeds/posts/default'
secondfeed = 'http://ws-dl.blogspot.com/feeds/posts/default
feedlist = []
feedlist.append(firstfeed)
feedlist.append(secondfeed)
while len(feedlist) <= 100:
    try:
        nextblog = 'http://www.blogger.com/next-blog?navBar=true&blogID=3471633091411211117'
        html = urllib2.urlopen(nextblog).read()
        soup = BeautifulSoup(html)
        atomfeedurl = soup.find_all('link', attrs = {'type': 'application/atom+xml'})[0].
            attrs['href']
    except HTTPError as h:
        pass
    except IndexError as i:
        pass
    if atomfeedurl:
        if atomfeedurl not in feedlist:
            print atomfeedurl
            feedlist.append(atomfeedurl)
    time.sleep(1)
for item in feedlist:
    f.write(item + '?max-results=200' + '\n')
f.close()
```

## B Full Version of generatefeedvector.py

Listing 5: generatefeedvector.py

```
import feedparser
import re

# Returns title and dictionary of word counts for an RSS feed
def getwordcounts(url):
    # Parse the feed
d=feedparser.parse(url)
wc={}
```

```
# Loop over all the entries
  for e in d.entries:
      if 'summary' in e: summary=e.summary
      else: summary=e.description
    # Extract a list of words
      words=getwords(e.title+' '+summary)
      for word in words:
        wc.setdefault(word,0)
        wc[word]+=1
  return d.feed.title,wc
def getwords(html):
 # Remove all the HTML tags
  txt=re.compile(r'<[^>]+>').sub('',html)
 # Split words by all non-alpha characters
  words=re.compile(r'[^A-Z^a-z]+').split(txt)
  # Convert to lowercase
  return [word.lower() for word in words if word!='']
apcount={}
wordcounts={}
feedlist = [line for line in file ('feedlist.txt')]
for feedurl in feedlist:
  try:
    title , wc=getwordcounts (feedurl)
    wordcounts [title]=wc
    for word, count in wc.items():
      apcount.setdefault (word,0)
      if count > 1:
        apcount [word]+=1
  except:
    print 'Failed to parse feed %s' % feedurl
wordlist = []
for w, bc in apcount.items():
  frac=float (bc)/len (feedlist)
  if frac > 0.1 and frac < 0.5:
    wordlist.append(w)
out=file ('blogdata.txt', 'w')
out.write('Blog')
for word in wordlist: out.write('\t%s' % word)
out.write('\n')
for blog, wc in wordcounts.items():
  print blog
  blog = blog.encode('UTF-8')
  out.write(blog)
  for word in wordlist:
    if word in wc: out.write('\t%d' % wc[word])
    else: out.write('\t0')
  out.write('\n')
```

## C Full Version of reduceTerms.py

Listing 6: reduceTerms.py

```
import sys
sys.path.insert(0, '/Users/vneblitt/Documents/cs595-f13/assignment09/library')
```

```
import clusters
blognames, words, data=clusters.readfile('blogdata.txt')
# print 'blog name: ' + blognames[0]
# column
# print 'term: ' + words[3]
# junction
# print 'value: ' + str(data[0][3])
# print 'number of blogs: ' + str(len(blognames))
# print 'number of words: ' + str(len(words))
wordsums = \{\}
for j in range(len(words)):
        sum = 0
        for i in range (len(blognames)):
        sum = sum + data[i][j]
# print words[j] + ' ' + str(sum)
        wordsums[j] = int(sum)
# print wordsums
a = sorted (wordsums, key=wordsums.get, reverse=True) [0:500]
# print (len(a))
# print a
print 'Blog',
for m in range (len (words)):
        if m in a:
                 print \ '\ t' + words[m],
print
for i in range (len (blognames)):
        print blognames [i],
        for j in range(len(words)):
                 if j in a:
                          print '\t' + str(int(data[i][j])),
        print
```

## D Full Version of clusters.py

This code is used for Q2, Q3, and Q4.

Listing 7: clusters.py

```
from PIL import Image,ImageDraw

def readfile(filename):
    lines=[line for line in file(filename)]

# First line is the column titles
    colnames=lines[0].strip().split('\t')[1:]
    rownames=[]
    data=[]
    for line in lines[1:]:
        p=line.strip().split('\t')
```

```
# First column in each row is the rowname
    rownames.append(p[0])
    # The data for this row is the remainder of the row
    data.append([float(x) for x in p[1:]])
  return rownames, colnames, data
from math import sgrt
def pearson(v1,v2):
  # Simple sums
  sum1=sum(v1)
  sum2=sum(v2)
  # Sums of the squares
  sum1Sq=sum([pow(v,2) for v in v1])
  sum 2Sq = sum ([pow(v,2) \text{ for } v \text{ in } v2])
  # Sum of the products
  pSum=sum([v1[i]*v2[i] for i in range(len(v1))])
  # Calculate r (Pearson score)
  num=pSum-(sum1*sum2/len(v1))
  den = sqrt((sum1Sq-pow(sum1,2)/len(v1))*(sum2Sq-pow(sum2,2)/len(v1)))
  if den==0: return 0
  return 1.0-num/den
class bicluster:
  def __init__ (self, vec, left=None, right=None, distance=0.0,id=None):
    self.left=left
    self.right=right
    self.vec=vec
    self.id=id
    self.distance=distance
def hcluster (rows, distance=pearson):
  distances={}
  currentclustid=-1
  # Clusters are initially just the rows
  clust = [bicluster(rows[i], id=i) for i in range(len(rows))]
  while len(clust) > 1:
    lowestpair = (0,1)
    closest=distance(clust[0].vec, clust[1].vec)
    # loop through every pair looking for the smallest distance
    for i in range(len(clust)):
      for j in range(i+1,len(clust)):
        # distances is the cache of distance calculations
        if (clust[i].id, clust[j].id) not in distances:
          distances [(clust [i].id, clust [j].id)] = distance (clust [i].vec, clust [j].vec)
        d=distances [(clust[i].id,clust[j].id)]
        if d<closest:
          c losest=d
          lowestpair=(i,j)
    # calculate the average of the two clusters
    mergevec=[
    (clust [lowestpair [0]]. vec [i]+clust [lowestpair [1]]. vec [i]) /2.0
    for i in range(len(clust[0].vec))]
    # create the new cluster
    newcluster=bicluster (mergevec, left=clust [lowestpair [0]],
                          right=clust [lowestpair [1]],
```

```
distance=closest, id=currentclustid)
   # cluster ids that weren't in the original set are negative
    currentclustid -=1
    del clust [lowestpair [1]]
    del clust [lowestpair [0]]
    clust.append(newcluster)
  return clust [0]
def printclust (clust, labels=None, n=0):
 # indent to make a hierarchy layout
  for i in range(n): print '',
  if clust.id < 0:
   # negative id means that this is branch
   print '-'
  else:
   # positive id means that this is an endpoint
    if labels—None: print clust.id
    else: print labels[clust.id]
 # now print the right and left branches
  if clust.left!=None: printclust(clust.left,labels=labels,n=n+1)
  if clust.right!=None: printclust(clust.right, labels=labels, n=n+1)
def getheight (clust):
 # Is this an endpoint? Then the height is just 1
  if clust.left=None and clust.right=None: return 1
 # Otherwise the height is the same of the heights of
 # each branch
 return getheight(clust.left)+getheight(clust.right)
def getdepth(clust):
 # The distance of an endpoint is 0.0
   if \ clust.left =\!\!\!=\!\! None \ and \ clust.right =\!\!\!=\!\! None \colon \ return \ 0 
 # The distance of a branch is the greater of its two sides
 # plus its own distance
  return max(getdepth(clust.left),getdepth(clust.right))+clust.distance
def drawdendrogram (clust, labels, jpeg='clusters.jpg'):
 # height and width
 h=getheight(clust)*20
 w = 1200
  depth=getdepth(clust)
 # width is fixed, so scale distances accordingly
  scaling=float(w-150)/depth
 # Create a new image with a white background
  img=Image.new('RGB',(w,h),(255,255,255))
  draw=ImageDraw.Draw(img)
  draw.line((0,h/2,10,h/2),fill=(255,0,0))
 # Draw the first node
  drawnode (draw, clust, 10, (h/2), scaling, labels)
  img.save(jpeg,'JPEG')
def drawnode (draw, clust, x, y, scaling, labels):
  if clust.id < 0:
    h1=getheight (clust.left) *20
    h2=getheight (clust.right) *20
    top=y-(h1+h2)/2
    bottom=y+(h1+h2)/2
    # Line length
```

```
ll=clust.distance*scaling
    # Vertical line from this cluster to children
    draw.line((x, top+h1/2, x, bottom-h2/2), fill=(255, 0, 0))
    # Horizontal line to left item
    draw.line((x, top+h1/2, x+ll, top+h1/2), fill = (255, 0, 0))
   # Horizontal line to right item
    draw.line((x,bottom-h2/2,x+l1,bottom-h2/2),fill=(255,0,0))
    # Call the function to draw the left and right nodes
    drawnode(draw, clust.left, x+ll, top+h1/2, scaling, labels)
    drawnode (draw, clust.right, x+ll, bottom-h2/2, scaling, labels)
    # If this is an endpoint, draw the item label
    draw.text((x+5,y-7), labels[clust.id],(0,0,0))
def rotatematrix (data):
  newdata=[]
  for i in range(len(data[0])):
    newrow=[data[j][i] for j in range(len(data))]
    newdata.append(newrow)
  return newdata
import random
def kcluster (rows, distance=pearson, k=4):
 # Determine the minimum and maximum values for each point
  ranges = [(min([row[i] for row in rows]), max([row[i] for row in rows]))
  for i in range(len(rows[0]))]
 # Create k randomly placed centroids
  clusters = [[random.random()*(ranges[i][1] - ranges[i][0]) + ranges[i][0]
  for i in range(len(rows[0]))] for j in range(k)]
  lastmatches=None
  for t in range (100):
    print 'Iteration %d' % t
    bestmatches = [[] for i in range(k)]
    # Find which centroid is the closest for each row
    for j in range(len(rows)):
      row=rows[j]
      bestmatch=0
      for i in range(k):
        d=distance(clusters[i],row)
        if d<distance(clusters[bestmatch],row): bestmatch=i
      bestmatches [bestmatch].append(j)
    # If the results are the same as last time, this is complete
    if bestmatches==lastmatches: break
    lastmatches=bestmatches
    # Move the centroids to the average of their members
    for i in range(k):
      avgs = [0.0] * len(rows[0])
      if len(bestmatches[i])>0:
        for rowid in bestmatches[i]:
          for m in range(len(rows[rowid])):
            avgs [m]+=rows [rowid][m]
        for j in range(len(avgs)):
          avgs [j]/=len (bestmatches [i])
        clusters [i]=avgs
  return bestmatches
def tanamoto(v1, v2):
 c1, c2, shr = 0, 0, 0
```

```
for i in range(len(v1)):
    if v1[i]!=0: c1+=1 \# in v1
    if v2[i]!=0: c2+=1 \# in v2
    if v1[i]!=0 and v2[i]!=0: shr+=1 \# in both
  return 1.0 - (float(shr)/(c1+c2-shr))
def scaledown (data, distance=pearson, rate=0.01):
  n=len(data)
  # The real distances between every pair of items
  realdist = [[distance(data[i], data[j]) for j in range(n)]
               for i in range (0,n)
  # Randomly initialize the starting points of the locations in 2D
  loc = [[random.random(), random.random()] for i in range(n)]
  fakedist = [[0.0 \text{ for } j \text{ in } range(n)] \text{ for } i \text{ in } range(n)]
  lasterror=None
  for m in range (0,1000):
    # Find projected distances
    for i in range(n):
       for j in range(n):
         fakedist[i][j]=sqrt(sum([pow(loc[i][x]-loc[j][x],2)
                                       for x in range(len(loc[i]))])
    # Move points
    grad = [[0.0, 0.0] \text{ for i in } range(n)]
    totalerror=0
    for k in range(n):
       for j in range(n):
         if j==k: continue
         # The error is percent difference between the distances
         errorterm = (fakedist[j][k] - realdist[j][k]) / realdist[j][k]
         # Each point needs to be moved away from or towards the other
         # point in proportion to how much error it has
         \operatorname{grad}[k][0] + = ((\operatorname{loc}[k][0] - \operatorname{loc}[j][0]) / \operatorname{fakedist}[j][k]) * \operatorname{errorterm}
         \operatorname{grad}[k][1] + = ((\operatorname{loc}[k][1] - \operatorname{loc}[j][1]) / \operatorname{fakedist}[j][k]) * \operatorname{errorterm}
         # Keep track of the total error
         totalerror+=abs(errorterm)
    print totalerror
    # If the answer got worse by moving the points, we are done
    if lasterror and lasterror < totalerror: break
    lasterror=totalerror
    # Move each of the points by the learning rate times the gradient
    for k in range(n):
       loc[k][0] -= rate*grad[k][0]
       loc[k][1] -= rate * grad[k][1]
  return loc
def draw2d(data,labels,jpeg='mds2d.jpg'):
  img=Image.new('RGB',(2000,2000),(255,255,255))
  draw=ImageDraw.Draw(img)
  for i in range(len(data)):
    x = (data[i][0] + 0.5) *1000
    y = (data[i][1] + 0.5) *1000
    draw.text((x,y), labels[i],(0,0,0))
  img.save(jpeg,'JPEG')
```

# E Output from getKMeans.py

Listing 8: kmeansoutput.txt

Listing 6: kineansoutput.txt				
k=5				
Iteration 0				
Iteration 1				
Iteration 2				
Iteration 3				
Iteration 4				
Iteration 5				
k=10				
Iteration 0				
Iteration 1				
Iteration 2				
Iteration 3				
Iteration 4				
Iteration 5				
Iteration 6				
k=20				
Iteration 0				
Iteration 1				
Iteration 2				
Iteration 3				
Iteration 4				
Iteration 5				
Iteration 6				
Iteration 7				
Iteration 8				
Iteration 9				
Iteration 10				
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Iteration 87
Iteration 88
Iteration 89
Iteration 90
Iteration 91
Iteration 92
Iteration 93
Iteration 94
Iteration 95
Iteration 96
Iteration 97
Iteration 98
Iteration 99
```

## References

[1] SEGARAN, T. Programming Collective Intelligence: Building Smart Web 2.0 Applications. O'Reilly, 2007.