Exercises04-Revised

February 21, 2015

Latent Semantic Analysis (LSA) is a method for reducing the dimnesionality of documents treated as a bag of words. It is used for document classification, clustering and retrieval. For example, LSA can be used to search for prior art given a new patent application. In this homework, we will implement a small library for simple latent semantic analysis as a practical example of the application of SVD. The ideas are very similar to PCA.

We will implement a toy example of LSA to get familiar with the ideas. If you want to use LSA or similar methods for statiscal language analyis, the most efficient Python library is probably gensim - this also provides an online algorithm - i.e. the training information can be continuously updated. Other useful functions for processing natural language can be found in the Natural Language Toolkit.

Note: The SVD from scipy.linalg performs a full decomposition, which is inefficient since we only need to decompose until we get the first k singluar values. If the SVD from scipy.linalg is too slow, please use the sparsesvd function from the sparsesvd package to perform SVD instead. You can install in the usual way with

```
!pip install sparsesvd
    Then import the following
from sparsesvd import sparsesvd
from scipy.sparse import csc_matrix
    and use as follows
sparsesvd(csc_matrix(M), k=10)
```

Exercise 1 (10 points). Calculating pairwise distance matrices.

Suppose we want to construct a distance matrix between the rows of a matrix. For example, given the matrix

```
M = np.array([[1,2,3],[4,5,6]])
```

the distance matrix using Euclidean distance as the measure would be

```
[[ 0.000 1.414 2.828]
[ 1.414 0.000 1.414]
[ 2.828 1.414 0.000]]
```

if M was a collection of column vectors.

Write a function to calculate the pairwise-distance matrix given the matrix M and some arbitrary distance function. Your functions should have the following signature:

```
def func_name(M, distance_func):
    pass
```

- 0. Write a distance function for the Euclidean, squared Euclidean and cosine measures.
- 1. Write the function using looping for M as a collection of row vectors.
- 2. Write the function using looping for M as a collection of column vectors.
- 3. Write the function using broadcasting for M as a collection of row vectors.
- 4. Write the function using broadcasting for M as a collection of column vectors.

For 3 and 4, try to avoid using transposition (but if you get stuck, there will be no penalty for using transpoition). Check that all four functions give the same result when applied to the given matrix M.

```
In [5]: # Your code here
```

Exercise 2 (10 points). Write 3 functions to calculate the term frequency (tf), the inverse document frequency (idf) and the product (tf-idf). Each function should take a single argument docs, which is a dictionary of (key=identifier, value=dcoument text) pairs, and return an appropriately sized array. Convert '-' to '' (space), remove punctuation, convert text to lowercase and split on whitespace to generate a collection of terms from the dcoument text.

- tf = the number of occurrences of term i in document j
- idf = $\log \frac{n}{1+df_i}$ where n is the total number of documents and df_i is the number of documents in which term i occurs.

Print the table of tf-idf values for the following document collection

```
s1 = "The quick brown fox"
s2 = "Brown fox jumps over the jumps jumps jumps"
s3 = "The the the lazy dog elephant."
s4 = "The the the the dog peacock lion tiger elephant"
docs = {'s1': s1, 's2': s2, 's3': s3, 's4': s4}
```

Note: You can use either a numpy array or pandas dataframe to store the matrix. However, we suggest using a Pnadas dataframe since that will allow you to keep track of the row (term) and column (document) names in a single object. Of course, you could also maintain a numpy matrix, a list of terms, and a list of documents separately if you prefer.

```
In []: # Your code here

# Suggeste function signatures
def tf(doc):
    """Returns the number of times each term occurs in a dcoument.
    We preprocess the document to strip punctuation and convert to lowercase.
    Terms are found by splitting on whitespace."""
```

```
pass

def tfs(docs):
    """Create a term frequency dataframe from a dictionary of documents."""
    pass

def idf(docs):
    """Find inverse document frequency series from a dictionry of doucmnets."""
    pass

def tf_idf(docs):
    """Return the product of the term-frequency and inverse document frequency."""
    pass
```

Exercise 3 (10 points).

- 1. Write a function that takes a matrix M and an integer k as arguments, and reconstructs a reduced matrix using only the k largest singular values. Use the scipy.linagl.svd function to perform the decomposition. This is the least squares approximation to the matrix M in k dimensions.
- 2. Apply the function you just wrote to the following term-frequency matrix for a set of 9 documents using k=2 and print the reconstructed matrix M'.

3. Calculate the pairwise correlation matrix for the original matrix M and the reconstructed matrix using k=2 singular values (you may use scipy.stats.spearmanr to do the calculations). Consider the fist 5 sets of documents as one group G1 and the last 4 as another group G2 (i.e. first 5 and last 4 columns). What is the average within group correlation for G1, G2 and the average cross-group correlation for G1-G2 using either M or M'. (Do not include self-correlation in the within-group calculations.).

```
In [6]: # Your code here
```

Exercise 4 (20 points). Clustering with LSA

- 1. Begin by loading a pubmed database of selected article titles using 'cPickle'. With the following: import cPickle docs = cPickle.load(open('pubmed.pic'))
 - Create a tf-idf matrix for every term that appears at least once in any of the documents. What is the shape of the tf-idf matrix?
- 2. Perform SVD on the tf-idf matrix to obtain $U\Sigma V^T$ (often written as $T\Sigma D^T$ in this context with T representing the terms and D representing the documents). If we set all but the top k singular values to 0, the reconstructed matrix is essentially $U_k\Sigma_kV_k^T$, where U_k is $m\times k$, Σ_k is $k\times k$ and V_k^T is $k\times n$. Terms in this reduced space are represented by $U_k\Sigma_k$ and documents by $\Sigma_kV_k^T$. Reconstruct the matrix using the first k=10 singular values.

- 3. Use agglomerative hierarchical clustering with complete linkage to plot a dendrogram and comment on the likely number of document clusters with k = 100. Use the dendrogram function from SciPy.
- 4. Determine how similar each of the original documents is to the new document mystery.txt. Since $A = U\Sigma V^T$, we also have $V = A^TUS^{-1}$ using orthogonality and the rule for transposing matrix products. This suggests that in order to map the new document to the same concept space, first find the tf-idf vector v for the new document this must contain all (and only) the terms present in the existing tf-idx matrix. Then the query vector q is given by $v^TU_k\Sigma_k^{-1}$. Find the 10 documents most similar to the new document and the 10 most dissimilar.
- 5. Many documents often have some boilerplate material such as organization information, Copyright, etc. at the front or back of the document. Does it matter that the front and back matter of each document is essentially identical for either LSA-based clustering (part 3) or information retrieval (part 4)? Why or why not?

In [7]: # your code here

0.1 Notes on the Pubmed articles

These were downloaded with the following script.

```
from Bio import Entrez, Medline
Entrez.email = "YOUR EMAIL HERE"
import cPickle
try:
   docs = cPickle.load(open('pubmed.pic'))
except Exception, e:
   print e
   docs = \{\}
    for term in ['plasmodium', 'diabetes', 'asthma', 'cytometry']:
        handle = Entrez.esearch(db="pubmed", term=term, retmax=50)
        result = Entrez.read(handle)
       handle.close()
        idlist = result["IdList"]
       handle2 = Entrez.efetch(db="pubmed", id=idlist, rettype="medline", retmode="text")
       result2 = Medline.parse(handle2)
        for record in result2:
            title = record.get("TI", None)
            abstract = record.get("AB", None)
            if title is None or abstract is None:
            docs[title] = '\n'.join([title, abstract])
            print title
        handle2.close()
    cPickle.dump(docs, open('pubmed.pic', 'w'))
docs.values()
```