| ■ You o | g package to cleanup the articles e.g, str.maketrans(", ", string. punctuation) r to convert text to lower case that way you get fewer n-grams $ams(x.split(), n)$ using ngrams from nltk on the content + title for computing n-grams, for this data $n = 2$ is suffcient |
|--|--|
| 3. Conve can do s | earn use n-gram at word level for this task ith different n-gram values can use ngrams from nltk for this can use ngrams into binary vector representation for each document. Some optimzations if the matrix is too big. (10 points) |
| For exampleSelectionYou refinalle(a) | ole, It top 10000 most frequent n-grams. May also try smaller values of n (like 2 or 3) which result in fewer n-grams. May, you can also try sparse matrix representation. Like csr_matrix from scipy.sparse. It works even with full vocabulary. Given a list of n-grams for each document, see how to builid a sparse matrix here |
| 4. We no number long as | eed hash function that maps integers 0, 1,, k – 1 to bucket s 0 through k – 1. It might be impossible to avoid collisions but as the collions are too many it won't matter much. (10 points) est would be using the builtin hash() function, it can be for example, hash(rownumber) % Numberofbuckets |
| • It can also 5. Compoints) | enerate several of these hash functions by xoring a random integer (hash(rownumber)^randint) % Numberofbuckets be a as simple as (rownumber * randint) % Numberofbuckets oute minhash following the faster algorithm from the lecture (10 |
| values in (10 poin Easiest was You should | signature bands into buckets. Find a way to combine all the signary a band and hash them into a number of buckets ususally very high ts) Bay is to add all the signature values in the bucket and use a similar hash function like before and use the same hash function for all bands. And all documents ending up in same bucket for at least one band are ad as candidate pairs. |
| • plot the p | parameters to make sure the threshold is appropriate. (10 points) brobability of two similar items falling in same bucket for different threshold values see the best parameters and get nearest neighbors of each articles |
| 9. Write | the nearest neibhors of each document to submissions.csv (compeded, first column is the current document followed by a list of nearest |
| neighbo | e a report + notebook + submission file in a zip file (5 points) for the assignment |
| <pre>import nu from nltk import st import re from scip import ra from coll import ma</pre> | ampy as np a import ngrams aring equests by.sparse import csr_matrix andom ections import Counter |
| import co | |
| data = da 2. Shingle | equests.get(json_url).json() ata[0:5000] # Only using 5000 artiles for performance e the documents, using all of the data s here, meaning we get pairs of words. |
| def getFr | <pre>requentNgrams(articles): .ngled_articles = [] : article in articles: article = article["Content"] n = 2 # K-shingling, using 2 for now as it says in the description</pre> |
| | <pre># To lower case article = article.lower() # Remove punctuation and parentheses translator=str.maketrans('','',string.punctuation) article = article.translate(translator) # Replace newline with a space article = article.replace("\n", " ")</pre> |
| | <pre># Split on the spaces, so that we can apply n-gram at word level word_list = article.split(" ") # Remove empty entries word_list = [word for word in word_list if word] # Create k-shingles for the list of words shingles = list(ngrams(word_list, n))</pre> |
| # Shingle | <pre># Add the SET(shingles) (no duplicates) to our list of all shingled articles</pre> |
| 3. Turn th f we were not documents co | e shingles into binary matrixes. For this I only use the 1000 most common shing using the 1000 most common, we could just gather a set of all possible shingles and loop over these when we check ntain the shingle or not. Had to reduce for performance |
| # Tak all_s for s a # Use count | <pre>c.naryMatrix(docs): de each set of shingles, make it into a list and add it to a list that we can use to COUNT when the shingles = [] shingles in docs: all_shingles += list(shingles) e counter to find the most only the most common shingles across articles der = Counter(all_shingles) common_shingles = counter.most_common(1000) # 1000 most common shingles</pre> |
| for s # Non # rows | <pre>de_shingles = [] shingle in most_common_shingles: unique_shingles.append(shingle[0]) w, unique shingles holds the 1000 MOST COMMON shingles across articles # Loop over these shingles, and check if they are in each article</pre> |
| for r | <pre>cy_matrix = csr_matrix((rows, cols), dtype=np.int8).toarray() cow, shingle in enumerate(unique_shingles): cor col, article in enumerate(docs): if shingle in article: binary_matrix[row][col] = 1 else: binary_matrix[row][col] = 0</pre> |
| # Binary binmatrix | matrix = getBinaryMatrix(shingles) hashfunctions using a simple random number to create a big hash |
| def getHa # Eac hashF | oly just permutations of a list. The value of their number does not matter as much, similar documents will get the same which is the point. AshFunctionValues (numrows, numhashfunctions): AshFunction is Tunctions = [] In range (numhashfunctions): AshFunction = [] # Store the hash function permutations Tandom number = random.random() # Creates a random number between 0 and 1 |
| f h | |
| numHashFu hashmatri | nction matrix Inctions = 100 # 100 is a clean number Inctions = getHashFunctionValues(len(binmatrix), numHashFunctions) Inature Matrixes using the optimal algorithm from the slides, using the tions I previously created. |
| mentions of the signature will with the signature will with the signature with the signature of the signatur | oping over and replacing the current value, if the hash value is smaller than what is already there. There has been no me case if we do NOT find a match though (given that we use common shingles and not ALL shingles), but in this case be left with a number in the columns that is +1 the total rows, meaning it should not make sense really. Sented based on the optimized algorithm Chash SignatureMatrix (binary_matrix, hash_val_matrix): Seture matrix = csr matrix((len(hash val matrix), len(binary matrix[0])), dtype=np.int64).toan |
| signa # pri for r | <pre>inture_matrix[:] = len(binary_matrix)+1 # Did not see any measures to account for this, slide int("Cap: " + str(len(binary_matrix)+1)) # Perhaps not compare CAPS in the future? row, docs in enumerate(binary_matrix): for col, num in enumerate(docs): if num == 1: for idx, hashfunction in enumerate(hash_val_matrix):</pre> |
| # Signatu signmatri | signature_matrix are matrix x = getMinHashSignatureMatrix(binmatrix, hashmatrix) ne signatures into LSH buckets, where we store their document id, such that sin |
| Bands and Rovare comparing | ts are placed together. ws plays a role here by; If we use fewer rows, like 1, we will probably have more matches, but they might not be similar documents to each other based on a SINGLE shingle. If we set rows to be 2, we now need a PAIR of shingle in the base means fewer matches, but documents are probably more similar. etc. SH (signature_matrix, num_bands, num_buckets): |
| num_r # Fir bands for i | <pre>crows from num_bands cows = math.floor(len(signature_matrix) / num_bands) cst, seperate the signature matrix in to bands cs = [] in range(0, len(signature_matrix), num_rows): cands.append(signature_matrix[i:i+num_rows]) condly, take each band, hash the columns towards a bucket(unique per band), store the DOCUMEN</pre> |
| bucke for b b | # This way, we can see which documents we should compare, as we found similarities ets = [] # Store all bucket dictionaries for all bands and in bands: bucket = {} # Using dictionary instead of list, since not all indexes are used perhaps columnValues = band.transpose() for docIndex, column in enumerate(columnValues): # Using the same hash function as before, but since str() gives it a BIG number, the rand |
| ř | <pre>hashValue = (hash(str(column)) % num_buckets) # Using string() convertion to be able to if hashValue in bucket.keys(): bucket[hashValue].append(docIndex) else: bucket[hashValue] = [] bucket[hashValue].append(docIndex)</pre> |
| # We try num_bands num_bucke | with 10 bands $s = 10$ ets = 1000 ets = getLSH(signmatrix, num bands, num buckets) |
| plt.f | <pre>range(len(b)): figure() Probability(s, b[i], r[i])</pre> |
| for i in plt.f | Figure() Probability(s, b[i], r[i]) |
| for i in plt.f plotF | Figure() Probability(s, b[i], r[i]) |
| for i in plt.f plotF plt.show() 10 - 0.8 - 1.0 - 0.0 - 0.0 | rows=1, band=100 rows=1, band=100 0.2 0.4 0.6 0.8 10 Similarity Threshold |
| for i in plt.f plots plt.show() 10 - 0.8 - 4,11111111111111111111111111111111111 | rows=1, band=100 rows=1, band=100 0.2 0.4 0.6 0.8 10 Similarity Threshold |
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