# Module4 HD vectors ngrams ToDo

September 29, 2021

```
[1]: ##Load modules and libraries
import numpy as np
import os.path
import string
import matplotlib
import matplotlib.pyplot as plt

# For my hw1 code
SEED = 1234
RNG = np.random.default_rng(SEED)
import time
```

# 1 Function to generate Item memory for symbols

```
[2]: def makeItemMemory(dimension):
    alphabet = list(string.ascii_lowercase+' ') # set of used symbols
    HDdic = {}
    for symb in alphabet:
        HDdic[symb] = 2*np.random.randint(low=0, high=2, size=dimension)-1 #

    →assign a random bipolar HD vector
    return HDdic
```

## 2 Parameters

```
[3]: langLabels = ['pol', 'ces', 'slk', 'slv', 'bul', 'ron', 'ita', 'por', ⊔

→'spa', 'fra', 'eng', 'deu', 'nld', 'dan', 'swe', 'fin', 'hun', 'est', □

→'lav', 'lit', 'ell'] # Names of training files for different languages

langFull = ['Polish', 'Czech', 'Slovak', 'Slovene', 'Bulgarian', 'Romanian', □

→'Italian', 'Portuguese', 'Spanish', 'French', 'English', 'German', □

→'Dutch', 'Danish', 'Swedish', 'Finnish', 'Hungarian', 'Estonian', 'Latvian', □

→'Lithuanian', 'Greek'] # Full names of languages

dimension = 1024 # Dimensionality for high-dimensional vectors

n=3 # size of n-gram
```

```
<code>dataSizeLimit=20000</code> # number symbols to consider for each language. If set to O_{\square} \hookrightarrow then take full dataset
```

# 3 Initialize profile vectors

```
[4]: def initProfiles(dimension: int = dimension, langLabels: list = langLabels):
    HDProfiles = {}
    for lang in langLabels:
        HDProfiles[lang] = np.zeros(dimension) # initialize profile vectors
    return HDProfiles
```

# 4 Function to form an HD vector for a given n-gram

```
#Function from my HW1
    #####################
    def bind(vector1: np.array, vector2: np.array) -> np.array:
        bound_vector = vector1 * vector2
        return bound vector
    def permutation(vector1: np.array) -> np.array:
        #Using roll for consistent permutation
        permuted_vector = np.roll(vector1, 1)
        return permuted_vector
    def makengramHD(seq: str, HDdic: dict, dimension: int = dimension) -> np.array:
        HDgram=np.ones(dimension) # initialize n-gram's HD vector to all ones
        #ToDo use binding and permutation operations to create n-gram's HD vector
        for letter in seq:
            letter_embedding = HDdic[letter]
            HDgram = bind(
                            letter embedding,
                            permutation(
                                           HDgram
                                       )
                        )
        return HDgram
```

5 Construct HD vectors representing n-gram statistics for each language

```
[6]: def construct_hdvec(dimension: int = dimension, n: int = n, langLabels: list = 1
      →langLabels) -> dict:
         HDdic=makeItemMemory(dimension) # make item memory for the set of used_
      →symbols (26 letters + space)
         HDProfiles=initProfiles(dimension, langLabels) # initialize profile HD_
      \rightarrow vectors
         #For each language
         for lang in langLabels:
             #print (lang)
             data_file_name=os.path.abspath(os.path.join('training_texts', lang +'.
      →txt')) # get training data
             with open(data_file_name, 'r') as f:
                 langdData = f.read() # read file
             f.close()
             # if training data should be trimmed
             if dataSizeLimit>0 and len(langdData)>dataSizeLimit:
                 langdData=langdData[0:dataSizeLimit]
             #Construct profile HD vectors
             start = time.time()
             for i in range(0,len(langdData)-n+1):
                 seq=langdData[i:i+n] # pick the current n-gram
                 HDgram=makengramHD(seq, HDdic, dimension) # get n-gram's HD vector
                 HDProfiles[lang] += HDgram # update profile HD vector
               print(f"Language {lang} took {time.time()- start} sec")
         return HDProfiles
```

# 6 Compute cosine similarities between profile HD vectors

```
[7]: from typing import Tuple

def get_cossim(HDProfiles: dict, langLabels: list = langLabels, langFull: list

⇒= langFull) → Tuple[np.array, list]:

Languages=[] # full names of the lanuages in the right order

keys=list(HDProfiles.keys()) # order of lanuages in the dictionary

for key in keys:

ind=langLabels.index(key)

Languages.append(langFull[ind])
```

```
# Get profiles HD vector into an array

profiles=np.array(list(HDProfiles.values()))

#ToDo calculate cosine similarity between HD vectors in "profiles"

from sklearn.metrics.pairwise import cosine_similarity #Using because its_□

probably faster, have my code in comments in case this is not allowed

cos_sim = cosine_similarity(profiles)

# rows = profiles.shape[0]

# cos_sim = np.zeros((rows,rows))

# for i in range(rows):

# for j in range(rows):

# cos_sim[i][j] = np.dot(rows[i], rows[i]) / (np.linalg.

norm(rows[i]) * np.linalg.norm(rows[j]))

return cos_sim, Languages
```

## 7 Visualize cosine similarities

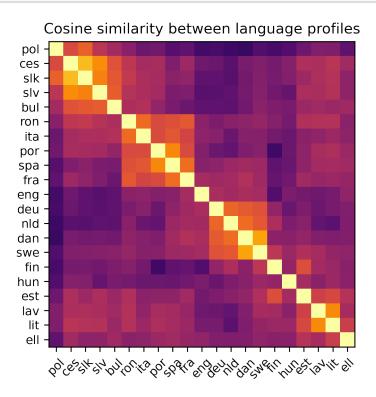
## 7.1 Question 1

Visualize the cosine similarities between languages' profile HD vectors (for example, by showing a heatmap of pairwise similarities). Are your results qualitatively similar to Figure 1 in "Language Geometry Using Random Indexing"?

#### **7.1.1** Answer

Yes, we can see the clustering between the Slavic languages, Romanic languages, Uralic languages.

# [10]: run\_experiment()



## 7.2 Question 2

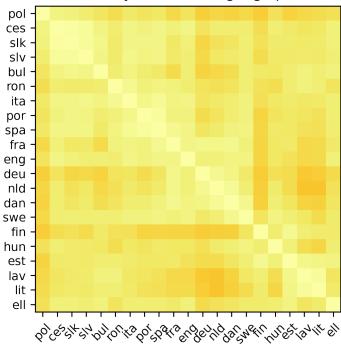
By default, the size of n-grams is set to 3. How does your visualization change if you change the value of n? What value of n seems to be optimal? What happens to cosine similarities when n is either too small or too large?

### **7.2.1** Answer

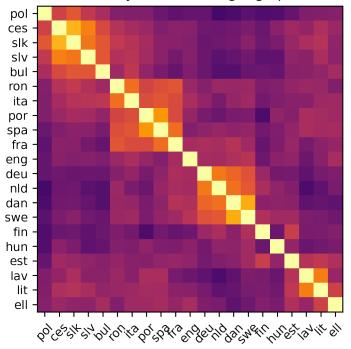
N of 3 seems optimal. If n is too small, every language is very similar to each other. This is because we are simply adding random vectors (there are no permutations applied, which are needed to create the notion of a sequence) to create our language embedding. While random vectors are orthogonal, this means that there non-zero bits (in the simple binary setting) are in non-overlapping regions. Thus, we essentially create vectors of 1s (in the binary case) when doing letter-grams. This idea

extends to the case of bipolar vectors (following Pentti's paper from lec1). If n is too big, the cos similarity matrix becomes too sparse. I think is because we are comparing frequencies of larger substrings which occur less in our text corpus (especially given my data limit of 20k).

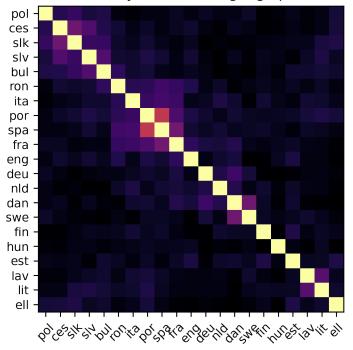




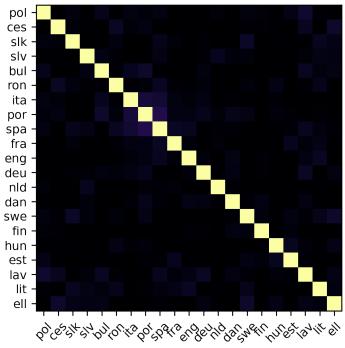




# Cosine similarity between language profiles n=5







## 7.3 Question 3

By default, the dimensionality of HD vectors is set to 1,024. Is this dimensionality enough to visualize the similarity between languages' n-gram statistics? What happens if the dimensionality of HD vectors is reduced dramatically?

### **7.3.1** Answer

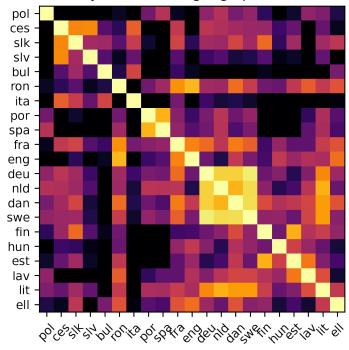
Yes, this dimensionality is enough. When reducing the dimensionality dramatically, we see the clustering gets worse as the matrix gets more sparse. However, some high level patterns such as similarity in Urlic languages are still seen.

```
[12]: for dim in [10, 64, 128]:

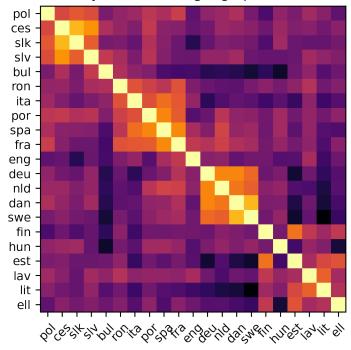
run_experiment(dimension=dim, title=f"Cosine similarity between language

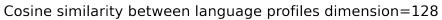
→profiles dimension={dim}")
```

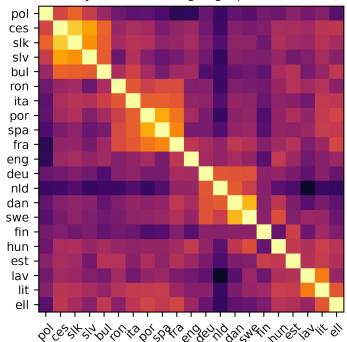
Cosine similarity between language profiles dimension=10



Cosine similarity between language profiles dimension=64







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