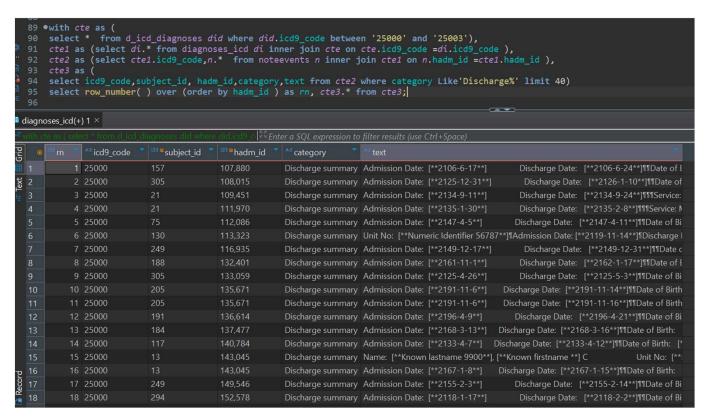


Tools and Dataset Used:

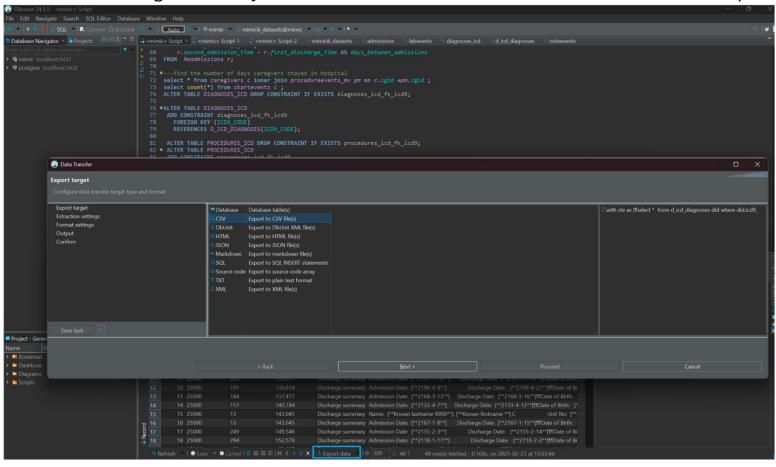
- Filename: https://github.com/dalwari/mimic-iii-clinical-database-demo-1.4/blob/main/mimic_nlp.ipynb
- Dataset Used: https://github.com/dalwari/mimic-iii-clinical-database-demo-1.4/blob/main/nlp_med_notes.csv
- Package Used: Spacy, Scispacy, BioClinicalBERT, Word2Vec, TSNE
- Application Used: Dbeaver, VSCode

Dataset Preparation:

- Write a sql query in Dbeaver
- Use the 'Export data' option in Dbeaver to extract the dataset result as CSV file into NLP workspace



- The disease of interest here is diabetes
- The icd9 code for diabetes is between '25000' and '25003'
- First we need to join d_icd_diagnoses and diagnoses_icd
- The result of previous step subquery is joined with noteevents on hospital admission id.
- The notes of 'Discharge Summary' needs to be filtered out limited to 40 records in order to process effectively.



Named Entity Recognition:

Import the Spacy, Scispacy, Word2Vec, TSNE libraries

```
import pandas as pd
pd.options.mode.chained_assignment = None
import numpy as np
import re
from gensim.models import Word2Vec
import gensim.downloader as api
from sklearn.manifold import TSNE
import matplotlib.pyplot as plt
from spacy import displacy
import spacy
spacy.require_gpu()
```

Load the spacy model

```
nlp = spacy.load('en_core_web_sm')
```

- Prepare utility functions like,
- clean_and_split_paragraph()
- extract_entities()
- fetch_entities()
- visualize_entities()
- extract_corpus()
- fetch_corpus()
- extract_passage_by_label()
- do_data_process()

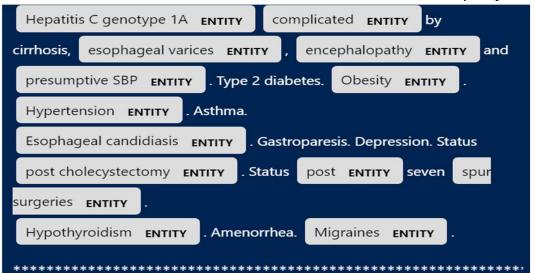
Utility Helper Functions:

- clean_and_split_paragraph() is used to perform data cleaning by removing the extra spaces and redundant lines.
- fetch_entities() and extract_entities() are used to print entities fetched using NER models.
- fetch_corpus() and extract_corpus() are used to print corpus recognized from the dataset.
- do_data_process() and extract_passage_by_label() are used to extract subparagraph from medical notes passage.
- visualize_entities() is used to identitfy the different types of entities provided by different Spacy and SciSpacy models
- For instance, History of Present Illness, Past Medical History, Brief Hospital Course, REVIEW OF SYSTEMS are the subparagraph labels

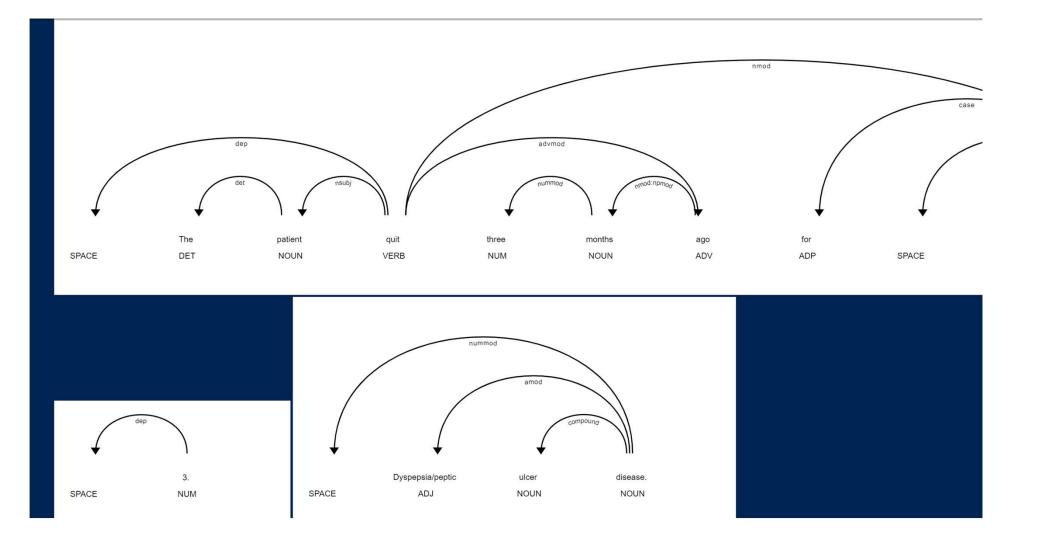
Load and clean the 'nlp_med_notes.csv' dataset

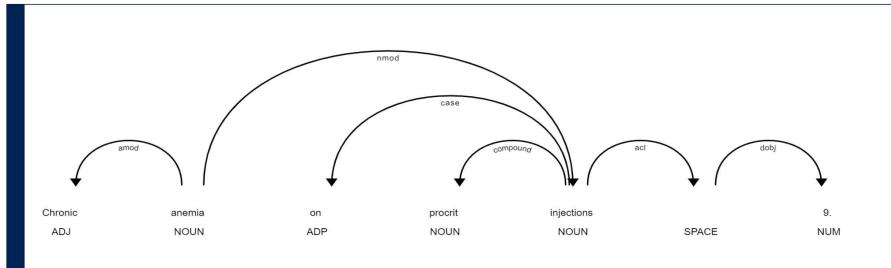
```
notes_df = pd.read_csv("nlp_med_notes.csv")['text']
notes=[]
for notes_data in notes_df:
    notes.append(clean_and_split_paragraph(notes_data))
```

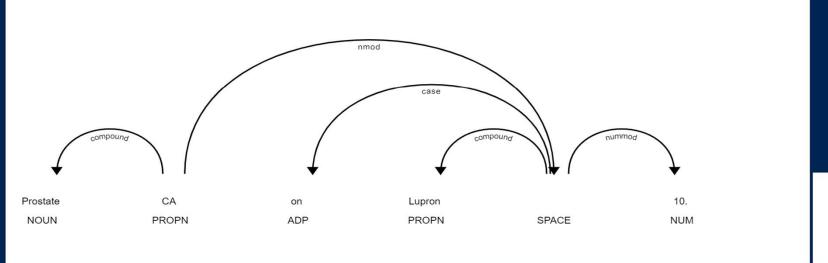
- For each record extract the 'PAST MEDICAL HISTORY' subparagraph from text (i.e medical notes) field.
- Visualize the extracted label_df to view the entities of spacy model.



- Create a dependency tree using displacy from spacy model to show the relationship between words in a sentence.
- A meaningful sentence can be extracted from 'REVIEW OF SYSTEMS' sub paragraph.





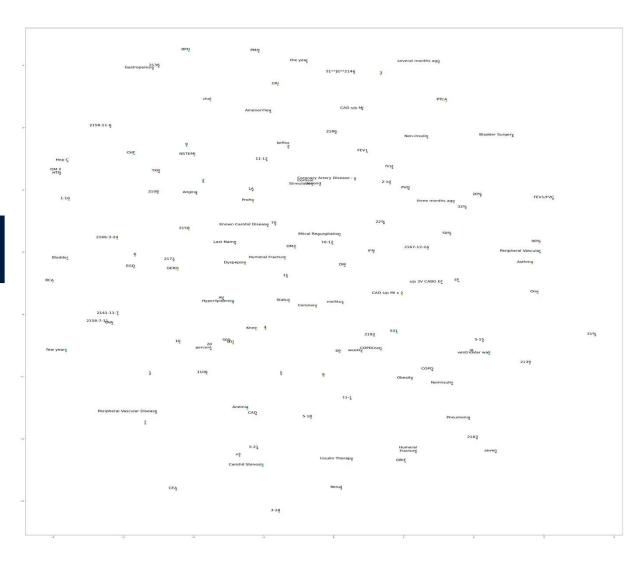


Gout NOUN

Spacy TSNE visualization: For Medication in medical notes

https://github.com/dalwari/mimic-iiiclinical-database-demo-1.4/blob/main/spacy_tsne_plot_diag.png

df =pd.read_csv("nlp_med_notes.csv")['text']
label_df=do_data_process(df,'MEDICATIONS')

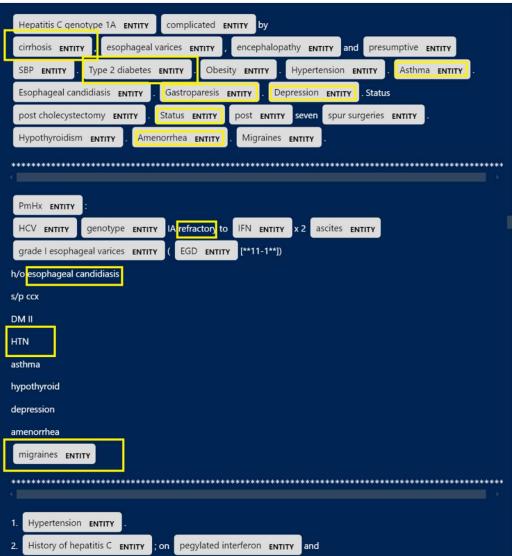


SciSpacy Usage:

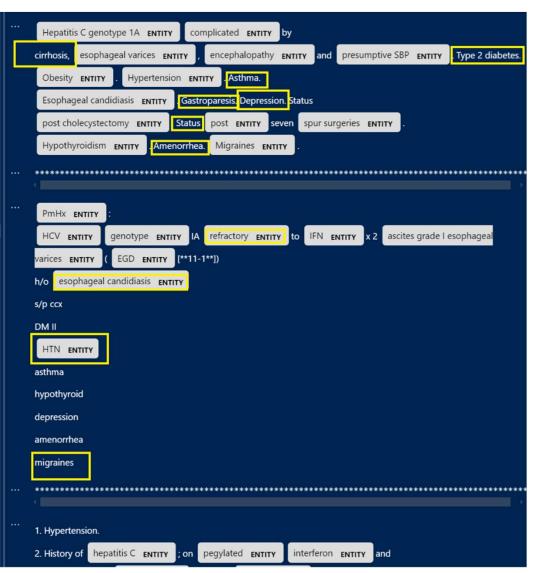
- SciSpacy models:
- en_core_sci_md
- en_core_sci_lg
- en_ner_craft_md
- en_ner_jnlpba_md
- en_ner_bionlp13cg_md
- en_ner_bc5cdr_md
- Load the model and visualize the corpus.

```
import en_ner_craft_md
nlp = en_ner_craft_md.load()
visualize_entities(label_df)
```

Sciscpacy: en_core_sci_lg



Spacy:



Scipacy: en_ner_craft_md

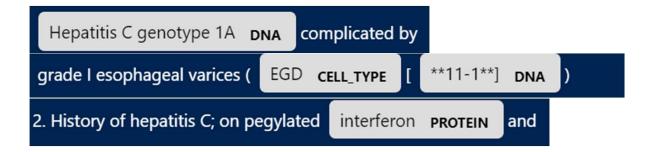


Spacy:

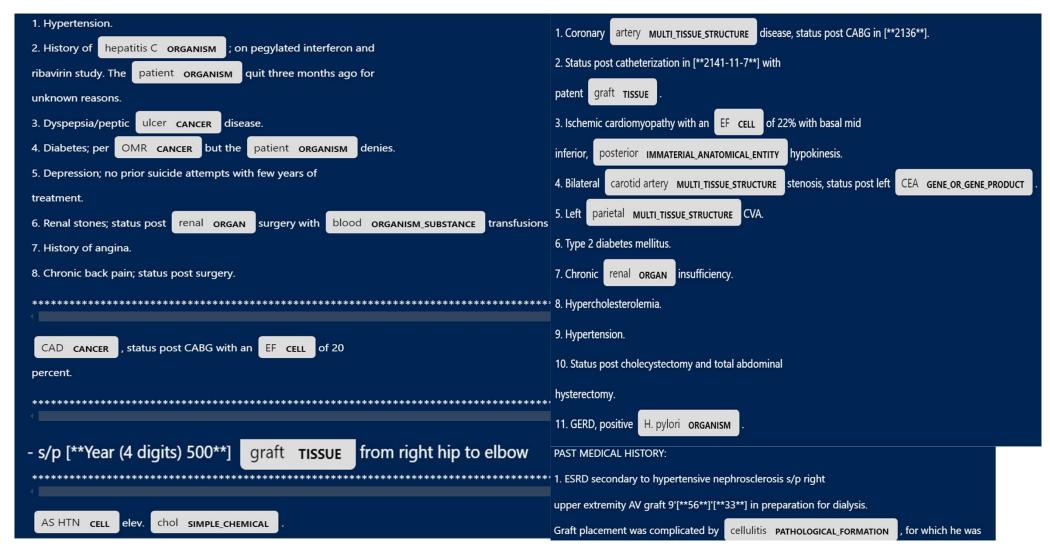
Scipacy: en_ner_craft_md

- SO stands for Sequence Ontology
- CL stands for Cell Ontology
- CHEBI stands for Chemical Entities of Biological Interest
- TAXON stands for Taxonomy
- GCP stands for Gene Ontology Cellular Component

Scipacy: en_ner_jnlpba_md



Scipacy: en_ner_bionlp13cg_md



Scipacy: en_ner_bc5cdr_md



Conclusion:

With the help of different spacy models we are able to extract different kinds of NERs.

Word2Vec and TSNE plot usage:

Apply **fetch_corpus()** to retrieve the list of corpus from the medical note.

```
corpus=[]
       for data in label_df:
           corpus.append(fetch_corpus(data))
       print(list(corpus))
·· ['diabetes mellitus', 'Hypertension', 'Chronic cervical spine disease', 'Congestive heart failure']
       [['cirrhosis', 'esophageal varices', 'encephalopathy', 'diabetes', 'Obesity',
       Hypertension', 'Esophageal candidiasis', 'Gastroparesis', 'Depression', 'Hypothyroidism',
       'Amenorrhea', 'Migraines'], ['PmHx:\nHCV genotype IA refractory', 'IFN', 'esophageal
       varices', 'esophageal candidiasis', 'ccx\nDM II\n', 'hypothyroid', 'depression',
       'amenorrhea', 'migraines'], ['Hypertension', 'hepatitis C', 'pegylated interferon
       and\nribavirin', 'ulcer disease', 'Diabetes', 'Depression', 'Renal stones', 'angina',
       'Chronic back pain'], ['CAD'], ['Hypertension'], ['chol', 'NIDDM', 'diverticulosis', 'hiatal
       hernia', 'obesity', 'appy'], ['Coronary artery disease', 'artery stenosis', 'CVA', 'diabetes
       mellitus', 'Chronic renal insufficiency', 'Hypercholesterolemia', 'Hypertension', 'GERD'],
       ['Coronary artery disease', 'diabetes mellitus', 'Hypertension', 'Arthritis'], ['ESRD',
       'hypertensive nephrosclerosis', 'cellulitis', 'keflex', 'DM', 'glyburide', 'glipizide',
       'HTN', 'clonidine', 'lisinopril', 'nifedipine', 'PVD', 'CVA', 'Secondary
       hyperparathyroidism', 'anemia', 'procrit', 'Prostate', 'Lupron', 'Gout'], ['ESRD',
       'hypertensive nephrosclerosis', 'cellulitis', 'keflex', 'DM', 'glyburide', 'glipizide',
       'HTN', 'clonidine', 'lisinopril', 'nifedipine', 'PVD', 'CVA', 'Secondary
       hyperparathyroidism', 'anemia', 'procrit', 'Prostate', 'Lupron', 'Gout'], ['GERD'], ['CAD',
       'COPD', 'hyperlipidemia', 'claustrophobia', 'diabetes\nmellitus type 2'], ['DM2', '^chol',
       'hypothyroid', 'arthritis'], ['Coronary artery disease', 'Persantine', 'septal/inferior',
       'left ventricular hypokinesis', 'Congestive heart failure', 'depressed', 'diabetes
       mellitus', 'Hypertension', 'Hyperlipidemia', 'Onychomycosis', 'Anemia', 'leukocytosis',
       'Chronic obstructive pulmonary disease', 'obstructive/restrictive deficit'], ['CAD', 'AICD',
       'hypothyroid', 'DM', 'varicose vein removal'], ['CAD', 'atrial fibrillation', 'htn', 'GERD',
       'Anemia'], ['artery disease', 'Atrial fibrillation', 'Hypertension', 'Hyperlipidemia',
       'Anemia'], ['artery disease', 'Atrial fibrillation', 'Hypertension', 'Hyperlipidemia',
       'Anemia'], ['Oligodendroglioma', 'oligoastrocytoma', 'infertility', 'temozolomide',
       'seizures', 'temozolomide', 'dexamethasone', 'sepsis', 'encephalopathy', 'tumor',
       'weakness', 'steroid myopathy', 'Hyperglycemia', 'steroid'], ['UTIs', 'NIDDM',
       'Hypercholesterolemia', 'Autoimmune Hepatitis'], ['cirrhosis', 'HCC', 'cirrhosis',
       'Ascites', 'encephalopathy', 'HD', 'MWF'], ['cirrhosis and hepatocellular carcinoma',
       'liver\nfailure', 'ascites', 'encephalopathy', 'Type II DM\n- Adrenal Insufficiency:
       [**2158-11-6**].', 'Cortisol', 'Urolithiasis'], ['Hypertension'], ['cirrhosis and
       hepatocellular carcinoma'], ['Diabetes', 'Dyslipidemia', 'Hypertension', 'prostatic
       hypertrophy', 'Arthritis', 'Gout', 'Bladder stone'], ['dilated cardiomyopathy', 'mitral
       regurgitation', 'diabetes', 'steroids', 'Pneumonia', 'ceftriaxone', 'azithromycin'],
       ['Hypertension', 'DM II', 'CAD', 'steroids', 'duodenal ulcer', 'CHF', 'dementia'],
```

Code Snippet:

The resultant presents the similarity logits for the word 'encephalopathy'

```
model1 = Word2Vec(corpus, min_count=1)
   model1.wv['encephalopathy']
✓ 0.0s
array([-8.7531786e-03, 2.1741530e-03, -8.6094369e-04, -9.3106795e-03,
      -9.4064260e-03, -1.4538610e-03, 4.4581434e-03, 3.7536507e-03,
      -6.5508662e-03, -6.8758638e-03, -5.0241956e-03, -2.3389754e-03,
      -7.2221956e-03, -9.5775630e-03, -2.7493779e-03, -8.3579253e-03,
      -6.0137236e-03, -5.7307631e-03, -2.3647691e-03, -1.7745970e-03,
      -8.9362776e-03, -6.9540367e-04, 8.1498129e-03, 7.6987552e-03,
      -7.2270953e-03, -3.6619261e-03, 3.0702241e-03, -9.5547633e-03,
       1.4801961e-03, 6.5093059e-03, 5.7971054e-03, -8.7778289e-03,
      -4.5126704e-03, -8.1743700e-03, 3.6444104e-05, 9.3236137e-03,
       5.9737498e-03, 5.0418158e-03, 5.0477851e-03, -3.3005176e-03,
       9.5378207e-03, -7.3622023e-03, -7.3122410e-03, -2.2796686e-03,
      -7.5115956e-04, -3.1877523e-03, -6.4017362e-04, 7.4983523e-03,
      -6.7837693e-04, -1.5929459e-03, 2.7603914e-03, -8.3850855e-03,
       7.8556603e-03, 8.5417535e-03, -9.6132429e-03, 2.4651806e-03,
       9.9031590e-03, -7.6433863e-03, -6.9885631e-03, -7.6803914e-03,
       8.3996654e-03, -6.9426361e-04, 9.1576520e-03, -8.1540635e-03,
       3.7199876e-03, 2.6663735e-03, 7.5992203e-04, 2.3442844e-03,
      -7.5090886e-03, -9.2971604e-03, 2.3168572e-03, 6.1675226e-03,
       8.0000097e-03, 5.6976336e-03, -7.6059706e-04, 8.2836589e-03,
      -9.3513643e-03, 3.3959236e-03, 2.5762038e-04, 3.8506044e-03,
       7.3216450e-03, -6.7115389e-03, 5.5358177e-03, -9.4783595e-03,
      -8.4873615e-04, -8.6890254e-03, -5.0572841e-03, 9.3041677e-03,
      -1.8036201e-03, 2.8908700e-03, 9.0945661e-03, 8.9400755e-03,
      -8.2035558e-03, -3.0187166e-03, 9.9292845e-03, 5.0835693e-03,
      -1.5810047e-03, -8.7010888e-03, 2.9685348e-03, -6.6635790e-03],
     dtype=float32)
```

The code snippet shows the similar words that the model contains within it.

```
model1.wv.similar_by_word('encephalopathy')

> 0.0s

[('diverticulosis', 0.30835863947868347),
    ('Renal stones', 0.2804599106311798),
    ('esophageal candidiasis', 0.2360624074935913),
    ('Hyperglycemia', 0.20393291115760803),
    ('Fracture', 0.2022656798362732),
    ('Persantine', 0.19107292592525482),
    ('Gastroparesis', 0.17959770560264587),
    ('Hypercholesterolemia', 0.168697327375412),
    ('Secondary hyperparathyroidism', 0.16342854499816895),
    ('Peripheral Vascular Disease', 0.14657379686832428)]
```

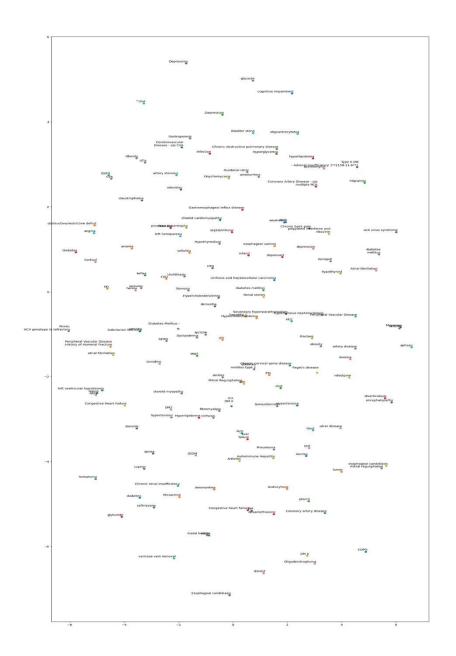
TSNE plot:

```
vocabs = model1.wv.key_to_index.keys()
new_v = list(vocabs)
tsne_plot(model1, new_v)
```

The corpus are plotted in tsne word embedding as per their logits.

SciSpacy TSNE plot:

https://github.com/dalwari/mimic-iii-clinical-database-demo-1.4/blob/main/tsne_plot_diag.png



Clinical BERT:

Import transformers and classification package.

```
from transformers import AutoTokenizer,
AutoModelForTokenClassification
from transformers import pipeline
```

• Initialize model.

```
tokenizer = AutoTokenizer.from_pretrained("emilyalsentzer/Bio_ClinicalBERT")
model = AutoModelForTokenClassification.from_pretrained("emilyalsentzer/Bio_ClinicalBERT")
nlp = pipeline("ner", model=model, tokenizer=tokenizer)
```

• Load dataset and examine 'PHYSICAL EXAMINATION' sub passage.

- The output displays label and score for each word in a sentence.
- The label is categorized by ClinicalBERT into LABEL_0 and LABEL_1
- The score is given to each word in that label category.

```
result=[]
for data in label_df:
    value=nlp(data)
    print(value)

    0.4s

[{'entity': 'LABEL_0', 'score': 0.6019393, 'index': 1, 'word': 'the', 'start': 0, 'end': 3}, {
[{'entity': 'LABEL_0', 'score': 0.5833172, 'index': 1, 'word': 'the', 'start': 0, 'end': 3}, {
[{'entity': 'LABEL_1', 'score': 0.524752, 'index': 1, 'word': 'vital', 'start': 0, 'end': 5},
[{'entity': 'LABEL_1', 'score': 0.59145355, 'index': 1, 'word': 'vs', 'start': 0, 'end': 2}, {
[{'entity': 'LABEL_1', 'score': 0.60578763, 'index': 1, 'word': 'height', 'start': 0, 'end': 6}, {'entity': 'LABEL_0', 'score': 0.5948016, 'index': 1, 'word': '-', 'start': 0, 'end': 1}, {'entity': 'LABEL_1', 'score': 0.52503663, 'index': 1, 'word': 'vital', 'start': 0, 'end': 5},
[{'entity': 'LABEL_1', 'score': 0.5799533, 'index': 1, 'word': 'vital', 'start': 0, 'end': 5},
```

- For tokenization use import ntlk package
- nltk.tokenize is used to split each text in list into individual words

```
from nltk.tokenize import word_tokenize
import nltk
nltk.download('punkt')
```

ClinicalBert can be visualized on 'PHYSICAL EXAM' label extracted subpassage from medical notes.

```
df =pd.read_csv("nlp_med_notes.csv")['text']
label_df=do_data_process(df,'Physical Exam')
```

Tokenized notes presents the tokens extracted from the 'PHYSICAL EXAM' label_df

```
tokenized_notes tokenized_notes = [word_tokenize(text.lower()) for text in label_df] tokenized_notes

'outline of the content of the content
```

Word Vector is created by substituting the tokenized_notes.

```
model = Word2Vec(sentences=tokenized_notes, vector_size=100, window=5, min_count=2,
workers=4)
```

ClinicalBERT TSNE visualization: For Medication in medical notes

https://github.com/dalwari/mimic-iiiclinical-database-demo-1.4/blob/main/clinical_bert_tsne_plot.png

