MIMIC-III NLP

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AI in Healthcare

What Disease Did I Pick?

I selected disease codes related to 4010 – Malignant Essential Hypertension. Malignant essential hypertension is a severe and life-threatening form of high blood pressure that develops rapidly and can cause damage to multiple organs.

What About the Text Data?

The objective of this analysis is to extract medical entities using Named Entity Recognition (NER) with SpaCy, SciSpaCy, Word2Vec, and t-SNE plots.

Additionally, used bc5cdr, BlueBert, MedSpacy to perform a similar analysis.

GitHub and Google Colab Links:

https://colab.research.google.com/github/AnkitaSavaliya/AIH/blob/main/MIMIC_III_NLP.ipynb

https://github.com/AnkitaSavaliya/AIH/blob/main/MIMIC_III_NLP.ipynb

https://github.com/AnkitaSavaliya/AIH/blob/main/MIMIC-III_NLP.pptx

Data Preparation

```
from google.colab import auth
auth.authenticate user()
print('Authenticated')
!gcloud projects list
from google.cloud import bigguery
# Construct a BigQuery client object.
client = bigguery.Client(project='clinical-entity-extraction')
ICD codes related to Hypertension:
 4010 - Malignant essential hypertension
 4011 - Benign essential hypertension
 4019 - Unspecified essential hypertension
# Fetch notes only for ICD-9 code 4010(Malignant essential hypertension)
query = """
  SELECT SUBJECT ID, TEXT, CATEGORY
    FROM `physionet-data.mimiciii notes.noteevents`
    WHERE SUBJECT_ID IN (
        SELECT d.SUBJECT ID
        FROM `physionet-data.mimiciii_clinical.diagnoses_icd` d
        WHERE d.ICD9 CODE = '4010' -- Hypertension code
        AND d.SEQ NUM = 1 -- Assuming 1 indicates primary diagnosis
    AND CATEGORY LIKE 'Discharge summary';
# Run the query
query job = client.query(query)
# Print the results
noteevents df = query job.to dataframe()
len(noteevents_df)
```

- Fetched rows from noteevents only for ICD-9 CODE 4010 and category
 'Discharge Summary' using the BigQuery client. Here selected records have 4010 (Maligant Hypertension) as primary diagnosis.
- The query returned 162 rows.
- Prepared a DataFrame with the required columns.
- Saved the query result to a CSV/XLSX file to reduce queries to the database.

```
patients_dict = {"SUBJECT_ID":[],"CATEGORY":[],"TEXT":[]};
for i in range(0, len(noteevents_df)):
    patients_dict["SUBJECT_ID"].append(noteevents_df.loc[i, 'SUBJECT_ID'])
    patients_dict["CATEGORY"].append(noteevents_df.loc[i, 'CATEGORY'])
    patients_dict["TEXT"].append(noteevents_df.loc[i, 'TEXT'])

patients_df = pd.DataFrame(patients_dict)

patients_df.shape

(162, 3)

#print first few records
patients_df.head(2)

# Download the patients_df dataframe in .csv and excel format
patients_df.to_csv(r'Patient_Summary_4010.csv', index = False)
patients_df.to_excel("Patient_Summary_4010.xlsx")
```

Spacy

Extract and Visualize SpaCy Entities

```
# Function to clean and extract tokens
def extract_cleaned_text(text, nlp_model):
    doc = nlp_model(str(text))
    tokens = [token.text for token in doc if not token.is_punct and not token.is_space and not token.is_stop]
    return " ".join(tokens) # Return cleaned text as a string
```

```
#Load Patient Discharge summary
patients_df_scapy = pd.read_csv("/content/drive/MyDrive/Colab Notebooks/AIH/Patient_Summary_4010.csv")

# Load the spacy model
nlp_spacy = spacy.load('en_core_web_sm')

# Apply token extraction
patients_df_scapy["Processed_Text"] = patients_df_scapy["TEXT"].apply(lambda text: extract_cleaned_text(text, nlp_spacy))
```

```
for i in range(0, 3):
    doc = nlp_spacy( patients_df_scapy['Processed_Text'][i])
    displacy.render(doc, style="ent")
    print("***************")
```

- Created a common function to clean text for the given model.
- Processed the **Discharge Summary** TEXT column using the **spaCy** model.
- Displayed spaCy entities using displaCy.



Spacy Entities

Word2Vec and t-SNE Visualization Using SpaCy-Processed Data

```
def build corpus(df, model="en core web sm"):
    Extracts named entities from the specified text column in a DataFrame using a spaCy model,
    builds a corpus.
    Parameters:
    - df (pd.DataFrame): DataFrame containing text data.
    - text column (str): Column name containing processed text.
    - model (str): spaCy model to use (default: "en core web sm").
    Returns:
    - corpus (list of lists): Extracted entities per document.
    nlp = model
    corpus = []
    for , row in df.iterrows():
       tokens = [ent.text for ent in nlp(row["Processed Text"]).ents]
        corpus.append(tokens)
    # Calculate word counts
    word counts = [len(doc) for doc in corpus]
    return corpus
```

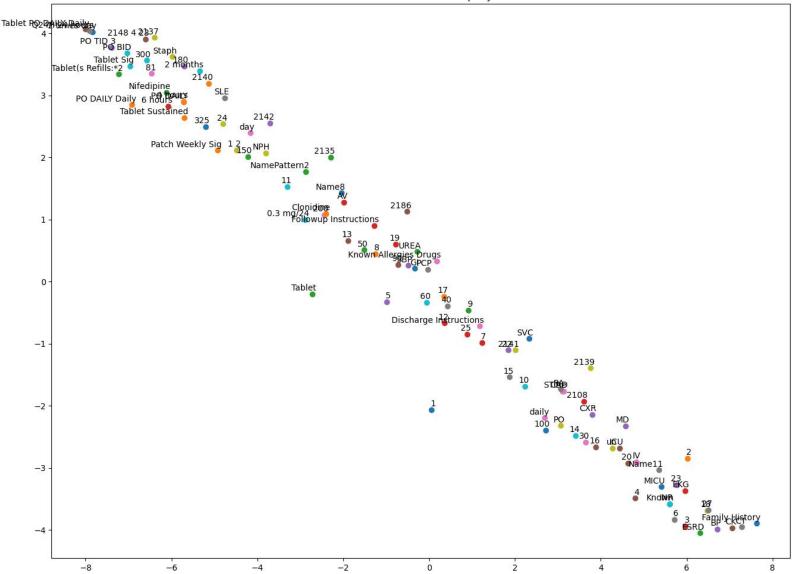
 Created common function to build corpus using given model SpaCy/SciSpaCy/other

```
#Build corpus for all the notes
corpus spacy = build corpus(patients df scapy, nlp spacy)
model word2vec spacy = Word2Vec(corpus spacy, min count=3)
model word2vec spacy.wv.similar by key("BP"), model word2vec spacy.wv.similar by key("Clonidine"
([('CT', 0.9998685121536255),
  ('MICU', 0.9998401403427124),
 ('IVC', 0.9998314380645752),
  ('EKG', 0.9998312592506409),
 ('RA', 0.9998170137405396),
 ('IV', 0.9998096227645874),
 ('CXR', 0.9998014569282532),
 ('Family History', 0.9997963309288025),
 ('Known', 0.9997953772544861),
 ('CK', 0.9997934699058533)],
[('3', 0.9996775388717651),
 ('25', 0.9996731281280518),
  ('100', 0.9996365308761597),
 ('PO', 0.999612033367157),
 ('30', 0.9995716214179993),
 ('50', 0.9995605945587158),
  ('200', 0.9995548725128174),
  ('6', 0.9995482563972473),
  ('7', 0.9995362758636475),
 ('10', 0.9995243549346924)])
```

- Defined common function for t-SNE plot.
- Call function using corpus built using Spacy processed text.

```
def tsne plot(model, words, words limit = None, model title="", preTrained=False):
   Creates and displays two t-SNE plots:
   1. Simple scatter plot with labels.
   2. Scatter plot with distance-based coloring.
   Parameters:
   - model: The Word2Vec model or pre-trained model.
   - words: List of words to visualize.
   - words limit : Limit the number of words to visualize.
   - model title: Title of the model.
   - preTrained: Boolean flag to choose between Word2Vec or pre-trained model.
   labels = []
   tokens = []
   # Apply t-SNE for dimensionality reduction
   tsne model = TSNE(perplexity=30, early exaggeration=12, n components=2, init='pca', max iter=1000, random state=23)
   # Prepare tokens and labels
   for word in words[:words limit]:
        if preTrained:
           tokens.append(model[word]) # Pre-trained word vectors
       else:
            tokens.append(model.wv[word]) # Word2Vec model vectors
       labels.append(word)
   tokens = np.array(tokens)
   new values = tsne model.fit transform(tokens)
```

t-SNE visualization of the top 100 words from Word2Vec (SpaCy), with a limited word count for better label clarity.



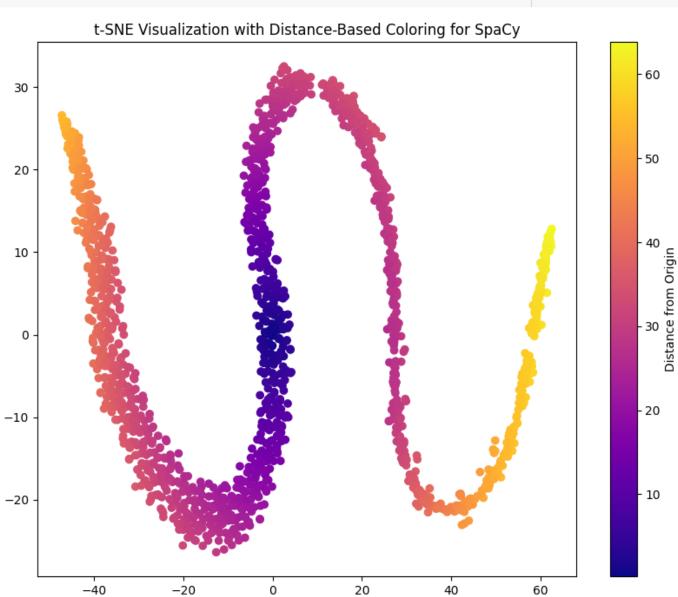
From Word2Vec similarity and above plot we can see that, the entity recognition using SpaCy was limited in extracting hypertension-related terms, likely because it focuses on general English entities rather than clinical ones.

```
def tsne plot no label(model, words, words limit=None, model title="", preTrained=False, reference word=None):
   Creates and displays a t-SNE plot without labels, using color mapping based on distance.
    Parameters:
    - model: The Word2Vec model or pre-trained model.
    - words: List of words to visualize.
    - words limit: Maximum number of words to visualize.
    - model title: Title of the model (used for plot labeling).
    - preTrained: Boolean flag indicating whether to use a pre-trained model.
    - reference word: (Unused in this function) Placeholder for potential relevance-based coloring.
    tokens = []
    # Apply t-SNE for dimensionality reduction
   tsne model = TSNE(perplexity=30, early exaggeration=12, n components=2, init='pca', max iter=1000, random state=23)
    # Extract word vectors
    for word in words[:words limit]:
        if preTrained:
            tokens.append(model[word]) # Use vectors from a pre-trained model
        else:
            tokens.append(model.wv[word]) # Use vectors from a Word2Vec model
    tokens = np.array(tokens)
    new values = tsne model.fit transform(tokens)
    # Create a scatter plot with color based on distance from the origin
    plt.figure(figsize=(10, 8))
   distances = np.sqrt(new_values[:, 0]**2 + new_values[:, 1]**2) # Compute Euclidean distance from origin
    plt.scatter(new_values[:, 0], new_values[:, 1], c=distances, cmap='plasma')
    plt.colorbar(label="Distance from Origin") # Add a color bar for reference
    plt.title(f"t-SNE Visualization with Distance-Based Coloring for {model title}")
    plt.show()
```

- Defined common function to generates a t-SNE scatter plot of word embeddings, coloring points based on their distance from the origin.
- Call function using corpus built using Spacy processed text.

t-SNE Visualization with Distance-Based Coloring Of All Words from Word2Vec (SpaCy)

 $tsne_plot_no_label(model_word2vec_spacy, np.array(list(model_word2vec_spacy.wv.key_to_index.keys())), \ None, \ 'SpaCy') \\$



SciSpacy

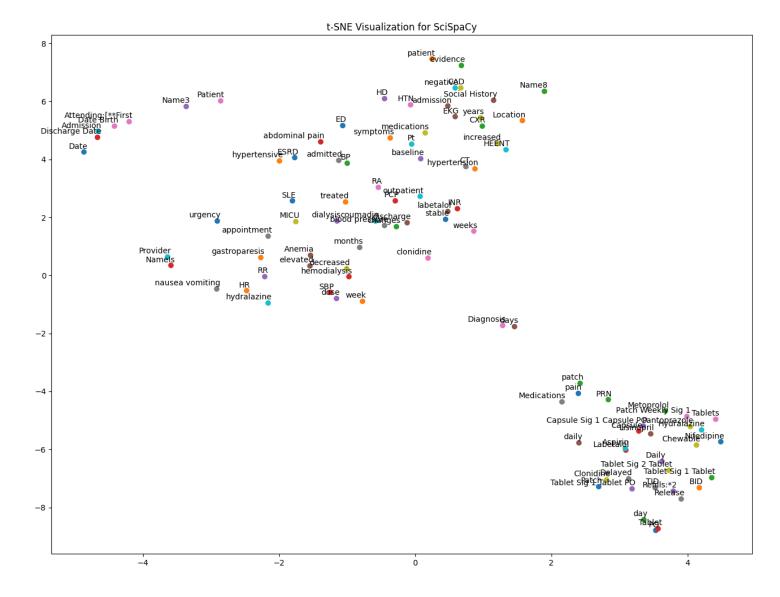
Extract and Visualize SciSpaCy Entities

```
#Load Patient Discharge summary
      patients df SciSpaCy = pd.read csv("/content/drive/MyDrive/Colab Notebooks/AIH/Patient Summary 4010.csv")
      nlp SciSpaCy = spacy.load('en core sci md') # Load the specified NLP model
      # Apply token extraction
      patients df SciSpaCy["Processed Text"] = patients df SciSpaCy["TEXT"].apply(lambda text: extract cleaned text(text, nlp SciSpaCy))
      for i in range(0, 3):
               doc = nlp_SciSpaCy( patients_df_SciSpaCy['Processed_Text'][i])
               displacy.render(doc, style="ent", jupyter=True)
 Admission entity Date 2140 1 19 Discharge Date entity 2140 1 21 Date Birth entity 2117 8 7 Sex F Service entity MEDICINE Allergies Penicillins entity Attending: [**First entity Name3 entity LF 2297 Chief Complaint headache entity Major Surgical Invasive
                                                                 Ms. Known lastname entity 22 year old female entity SLE entity lupus nephritis entity ESRD entity HD entity malignant entity HTN entity h/o TTP entity
                                                 Awoke entity a.m. 8/10 left sided frontal HA sure d/t entity flare uveitis entity started Monday entity d/t HTN entity Decided skip entity
numbness weakness entity change gait chest entity pain SOB entity + Diarrhea entity x 1 day entity ED entity patient entity 217/140 elevated entity 254/152 > received labetolol entity IV 30 mg x 1 MSO4 entity 4 mg pressures entity
         SBPs entity 208 HA entity improved Repeat labetolol entity 50 mg x 1 repeated dose entity morphine entity dropped pressures 193/134 > labetolol entity gtt entity started as a given HA entity resolved Head CT entity negative entity
                                                                                                              diet ENTITY Past Medical History 1 Lupus 2134 ENTITY Diagnosed ENTITY began swolen fingers rash painful joints 2 ENTITY
                                    3 months entity 2 years began dialysis entity 3 times week entity 2137 TTh Sat Awaiting entity living donor transplant entity mother 3 HTN entity 2137 Normal BPs entity run 180's/120 1 hypertensive crisis entity
                           seizures entity past 4 Uveitis entity secondary entity SLE entity 4.15.5 HOCM entity Echo entity 2.137.6 Vaginal bleeding entity 2.139.9.20.7 Mulitple episodes dialysis reactions entity 8 Anemia entity 9 Coag neg entity
                                 HD line infection entity 615 10 H/O UE ENTITY clot ENTITY couradin entity longer Social History entity Lives Location entity 669 mother entity 16 year entity old brother entity Graduated Name2 NI School entity go
                                                              school Denies entity T/E/D. Family History entity -No history entity -
                     Physical Exam Vitals entity 98.0 173/51 86 15 100 RA ENTITY HEENT ENTITY Leve injected w/periorbital edema R eye reactive w/ EOMI anicteric entity sclera entity MMM entity OP entity clear
                                         + S4 III/VI ENTITY systolic ejection murmur LUSB ENTITY radiating apex axilla ENTITY intensifies w/ Valsalva rub ENTITY Lungs CTAB ENTITY
rebound guarding entity GU entity CVAT entity Ext warm 2 entity + DP entity pulses entity L femoral dialysis catheter entity Neuro AOx3 CN II-XII entity intact strength/sensation entity grossly intact Pertinent Results UA entity
                                                                                               CXR ENTITY acute CP ENTITY abnormality ENTITY EKG ENTITY NSR ENTITY nml ENTITY axis nml intervals borderline LAE LVH J point elevation V2, V3 TWI ENTITY aVL V5 V6 change
                                                                                                Brief Hospital ENTITY Course A/P ENTITY
                                                                                                                                                        Patient ENTITY 22 year old female ENTITY SLE ENTITY lupus nephritis ENTITY
                                                                                                                                                                                                                                                                    ESRD ENTITY HD ENTITY presents hypertensive ENTITY
         Hypertensive entity urgency Unclear precipitant entity Possibly secondary pain entity worsening entity uveitis entity Compliant entity
ENTITY drip ED ENTITY good BP response ENTITY subsequently transitioned PO ENTITY anti-hypertensives ICU ENTITY stable SBPs ENTITY 150s-170s baseline ENTITY 170s-190s nephrologist ENTITY recommendations home lisinopril ENTITY
increased entity 40 mg po bid entity 40 mg po qd better baseline entity BP entity control clinical evidence entity end organ damage UA entity difficult ro interpret setting CRF entity CE entity x 1 negative entity
```

Word2Vec and t-SNE Visualization Using SciSpaCy-Processed Data

```
corpus scispacy = build corpus(patients df SciSpaCy, nlp SciSpaCy)
model word2vec scispacy = Word2Vec(corpus scispacy, min count=3)
model word2vec scispacy.wv.similar by key("BP"), model word2vec scispacy.wv.similar by key("Clonidine")
([('HR', 0.9993711709976196),
  ('admitted', 0.9993606805801392),
  ('MICU', 0.9992586374282837),
  ('RR', 0.9992402791976929),
  ('gastroparesis', 0.9992167353630066),
  ('patient', 0.9991229176521301),
  ('ED', 0.9990416169166565),
  ('symptoms', 0.9990056753158569),
  ('HTN', 0.998991072177887),
  ('HD', 0.9989602565765381)],
 [('Patch', 0.9993199706077576),
  ('Lisinopril', 0.998427152633667),
  ('Patch Weekly Sig 1', 0.9981398582458496),
  ('Prednisone', 0.997868537902832),
  ('Transdermal QWED', 0.9976481795310974),
  ('Labetalol', 0.9975727200508118),
  ('Aspirin', 0.9974137544631958),
  ('Amlodipine', 0.9971833229064941),
  ('Metoclopramide', 0.9970840811729431),
  ('Refills:*0', 0.99689781665802)])
len(model word2vec scispacy.wv.key to index.keys())
3276
tsne plot(model word2vec scispacy, np.array(list(model word2vec scispacy.wv.key to index.keys())), 100, 'SciSpaCy')
```

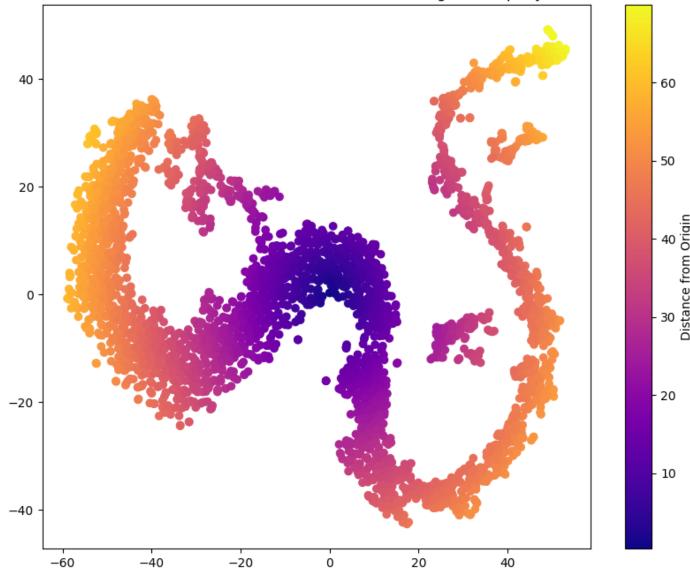
t-SNE visualization of the top 100 words from Word2Vec (SciSpaCy), with a limited word count for better label clarity.



From Word2Vec similarity and above plot, SciSpaCy primarily recognized medication names and formulations, such as Clonidine and Labetalol, but it did not specifically highlight key hypertension-related entities beyond drug mentions.

t-SNE Visualization with Distance-Based Coloring Of All Words from Word2Vec (SciSpaCy) tsne_plot_no_label(model_word2vec_scispacy, np.array(list(model_word2vec_scispacy.wv.key_to_index.keys())), None, 'SciSpaCy')





BC5CDR (BioCreative V Chemical-Disease Relation)

BC5CDR Entity Visualization Using SciSpaCy-Processed Data

en_ner_bc5cdr_md is a Named Entity Recognition (NER) model from SciSpaCy that specializes in identifying **diseases** and **chemicals** in text

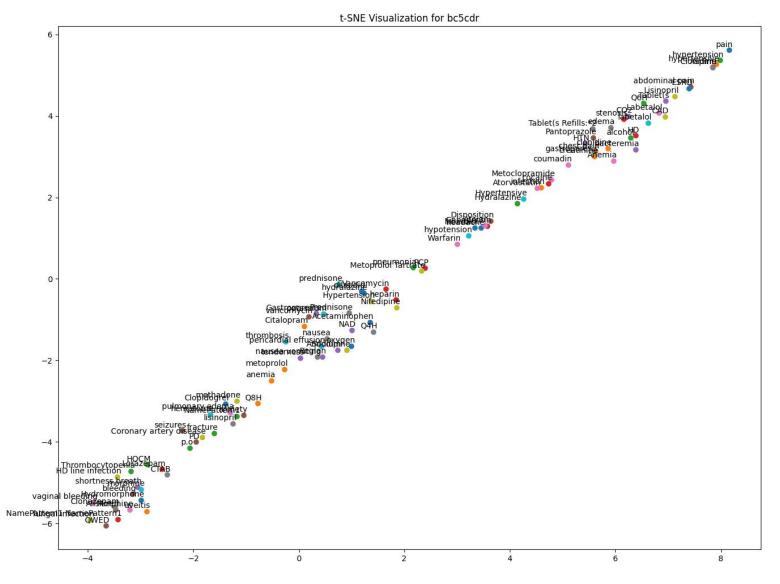


Word2Vec and t-SNE Visualization For BC5CDR

```
corpus_bc5cdr = build_corpus(patients_df_SciSpaCy, nlp_bc5cdr)
model word2vec bc5cdr = Word2Vec (corpus bc5cdr, min count=3, window=2, vector size=100)
model_word2vec_bc5cdr.wv.similar_by_word("BP"), model_word2vec_bc5cdr.wv.similar_by_word("Clonidine")
([('qid', 0.7542693614959717),
 ('Lactate', 0.7493560910224915),
 ('CP', 0.7465789914131165),
 ('papilledema', 0.745745837688446),
 ('atrial fibrillation', 0.7431225180625916),
 ('reglan', 0.7429000735282898),
 ('pleural effusions', 0.7415630221366882),
  ('Carvedilol', 0.740106999874115),
 ('fentanyl', 0.7399438619613647),
 ('coronary artery disease', 0.7399159073829651)],
 [('hypertension', 0.9987433552742004),
 ('pain', 0.9987409114837646),
 ('Aspirin', 0.998708963394165),
  ('Labetalol', 0.9986240267753601),
 ('hypertensive', 0.9985849857330322),
 ('abdominal pain', 0.9985615611076355),
 ('Lisinopril', 0.9985013604164124),
 ('chest pain', 0.9984785914421082),
  ('HTN', 0.9983934760093689),
 ('ESRD', 0.9983604550361633)])
len(model_word2vec_bc5cdr.wv.key_to_index.keys())
885
```

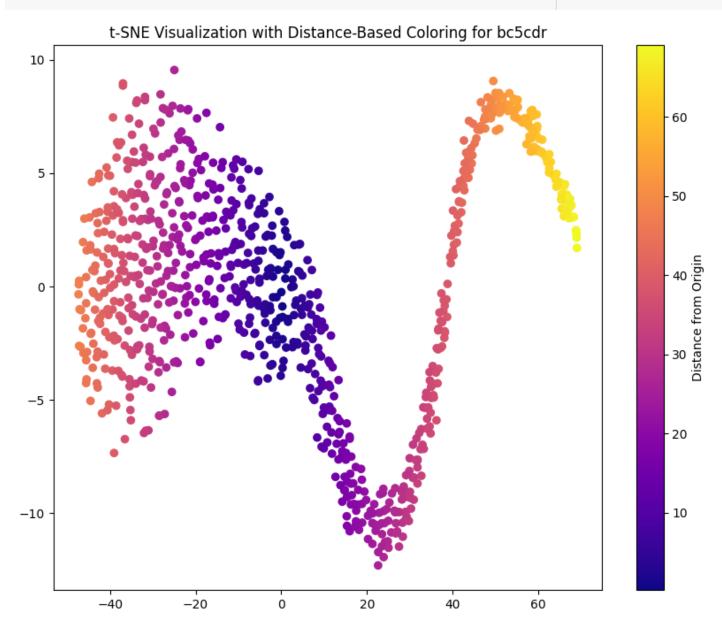
tsne_plot(model_word2vec_bc5cdr,np.array(list(model_word2vec_bc5cdr.wv.key_to_index.keys())), 100, 'bc5cdr')

t-SNE visualization of the top 100 words from Word2Vec (bc5cdr), with a limited word count for better label clarity.



Based on Word2Vec similarity and the above plot, BC5CDR appears to capture disease and medication entities well, with a good emphasis on hypertension-related terms (e.g., "hypertension," "hypertensive," "lisinopril", "metoprolol").

t-SNE Visualization with Distance-Based Coloring Of All Words from Word2Vec (bc5cdr) tsne_plot_no_label(model_word2vec_bc5cdr,np.array(list(model_word2vec_bc5cdr.wv.key_to_index.keys())), None, 'bc5cdr')



MedSpacy

Custom Rule-Based Entity Extraction with MedspaCy NLP Pipeline

```
# Load MedspaCy NLP pipeline
nlp_medspacy = medspacy.load()
# Add rules for target concept extraction
target_matcher = nlp_medspacy.get_pipe("medspacy_target_matcher")
# Define custom rules for better entity detection
target rules = [
   TargetRule("hyperlipidemia", "DISEASE"),
   TargetRule("02", "SUBSTANCE"),
   TargetRule("Fi02", "SUBSTANCE"),
   TargetRule("hypertension", "DISEASE"),
   TargetRule("obesity", "CONDITION"),
   TargetRule("cardiac", "CONDITION"),
   TargetRule("SLE", "DISEASE"), # Systemic Lupus Erythematosus
   TargetRule("lupus nephritis", "DISEASE"),
   TargetRule("ESRD", "DISEASE"), # End-Stage Renal Disease
   TargetRule("dialysis", "TREATMENT"), # Hemodialysis is also treatment
   TargetRule("hemodialysis", "TREATMENT"),
   TargetRule("SBP", "MEASUREMENT"), # Systolic Blood Pressure
   TargetRule("HR", "MEASUREMENT"), # Heart Rate
   TargetRule("TPN", "TREATMENT"),
   TargetRule("Prednisone", "MEDICATION"),
   TargetRule("Lisinopril", "MEDICATION"),
   TargetRule("Labetalol", "MEDICATION"),
   TargetRule("Clonidine", "MEDICATION"),
   TargetRule("Valsartan", "MEDICATION"),
   TargetRule("Sevelamer", "MEDICATION"),
   TargetRule("Atropine", "MEDICATION"),
   TargetRule("Morphine sulfate", "MEDICATION"),
   TargetRule("Diarrhea", "SYMPTOM"),
   TargetRule("Headache", "SYMPTOM"),
   TargetRule("nausea", "SYMPTOM"),
   TargetRule("vomiting", "SYMPTOM"),
   TargetRule("shortness of breath", "SYMPTOM"),
   TargetRule("fever", "SYMPTOM"),
   TargetRule("chills", "SYMPTOM")
target matcher.add(target rules)
```

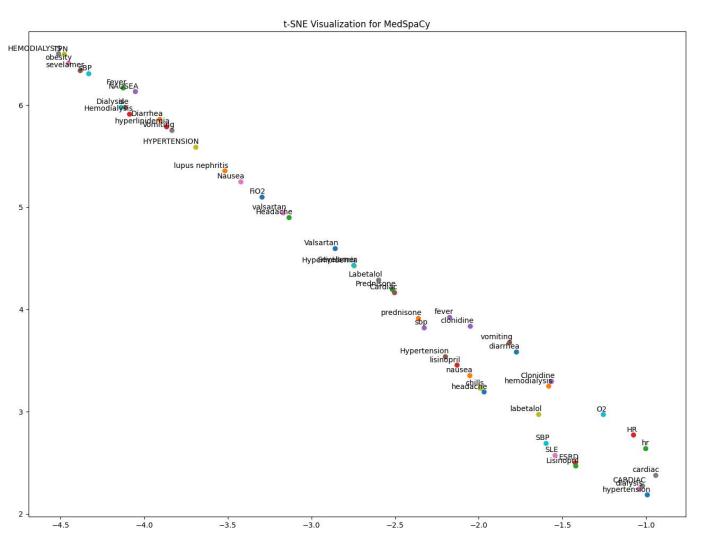
- MedSpaCy is a library designed for processing clinical and biomedical text.
- In this code, MedSpaCy is being enhanced by adding custom target rules to better detect specific medical entities such as diseases, treatments, symptoms, and medications in clinical notes.
- Loaded the MedspaCy NLP pipeline. Used the medspacy_target_matcher to add custom rules for extracting medical concepts.
- Defined specific target rules to identify entities like diseases (e.g., hypertension), treatments (e.g., hemodialysis), medications (e.g., Lisinopril), symptoms (e.g., headache), and measurements (e.g., SBP).
- Applied these rules to clinical text for improved entity detection.

MedSpacy Visualization Using SciSpaCy-Processed Data

```
# Visualize named entities using displacy for first few notes
for i in range(0, 3):
    # Process the shift note
    doc = nlp_medspacy(patients_df_SciSpaCy['Processed_Text'][i])
    # visulize
    visualize_ent(doc)
    print("*******************")
```

Admission Date 2140 1 19 Discharge Date 2140 1 21 Date Birth 2117 8 7 Sex F Service MEDICINE Allergies Penicillins Attending; **First Name3 LF 2297 Chief Complaint headache symptom Major Surgical Invasive Procedure Hemodialysis TREATMENT History Present Illness Ms. Known upus nephritis disease transplant list Patient received hemodialysis treatment house 500 ml ultrafiltrate complications dry weight 45 kg patient Began Sevalamer 800 TID transdermal QW Prednisone Medication 40 mg PO QD Atropine Medication 1 Hospital Prednisolone Acetate 1 Q1H Moxifloxacin eve drops gid Lorazepam 1 mg PO Q4 6H PRN Discharge Medications 1 Labetalol Medications 200 mg Tablet Sig 3 Tablet PO TID 3 times day Tablet(s 2

t-SNE visualization of the top 100 words from Word2Vec (MedSpaCy), with a limited word count for better label clarity.



```
#Build corpus
corpus_medspacy = build_corpus(patients_df_SciSpaCy, nlp_medspacy)

from gensim.models import Word2Vec
model_word2vec_medspacy = Word2Vec(corpus_medspacy, min_count=3)

len(model_word2vec_medspacy.wv.key_to_index.keys())

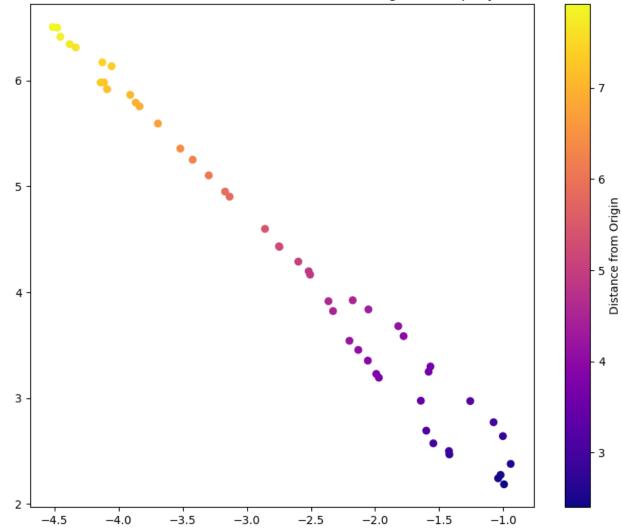
50

tsne_plot(model_word2vec_medspacy,np.array(list(model_word2vec_medspacy.wv.key_to_index.keys())), None, 'MedSpaCy')
```

Based on the plot, MedSpaCy effectively identifies and clusters terms associated with hypertension (e.g., Hypertension, Lisinopril, Labetalol, SBP, Clonidine, Headache, and Nausea). This suggests that the model is successfully recognizing and extracting a diverse range of hypertension-related entities, including medications, symptoms, and conditions, from the clinical text.

t-SNE Visualization with Distance-Based Coloring Of All Words from Word2Vec (MedSpaCy) tsne_plot_no_label(model_word2vec_medspacy,np.array(list(model_word2vec_medspacy|.wv.key_to_index.keys())), None, 'MedSpaCy')





BlueBert

t-SNE Visualization For BlueBert

```
# Visualization of notes filtered with SciSpacy using ClinicalBert
import numpy as np
import torch
from sklearn.manifold import TSNE
import string
import matplotlib.pyplot as plt
from transformers import AutoModel, AutoTokenizer, BertModel
# Load the BERT model and tokenizer
model name = "bionlp/bluebert pubmed mimic uncased L-12 H-768 A-12"
tokenizer = AutoTokenizer.from pretrained(model name)
blue bert model = BertModel.from pretrained('bionlp/bluebert pubmed mimic uncased L-12 H-768 A-12')
blue bert model.eval()
# Set first note as text
doc = nlp_SciSpaCy(patients_df_SciSpaCy['Processed_Text'][0])
corpus=
for ent in doc.ents:
    corpus.append(ent.text)
input_text = ' '.join(corpus)
input_tokens = input_text.split()
word embs = []
for token in input tokens:
    # Check if the token is a valid word
    if token not in string.punctuation:
        # Encode the token using the BERT model
       inputs = tokenizer(token, return tensors="pt")
       with torch.no grad():
            outputs = blue bert model(**inputs)
        token emb = outputs.last hidden state.mean(dim=1).squeeze().numpy()
        word embs.append(token emb)
```

- This script utilizes BlueBERT
 (bionlp/bluebert_pubmed_mimic_uncased_L-12_H-768_A-12) to extract word embeddings from clinical notes processed with SciSpaCy.
- Named entities are identified and tokenized, then their embeddings are computed using BlueBERT.
- Only one note was used here because processing all notes with BlueBERT for embedding extraction requires significant time and memory.
- The embeddings are visualized in a 2D space using t-SNE, highlighting relationships among clinical terms.

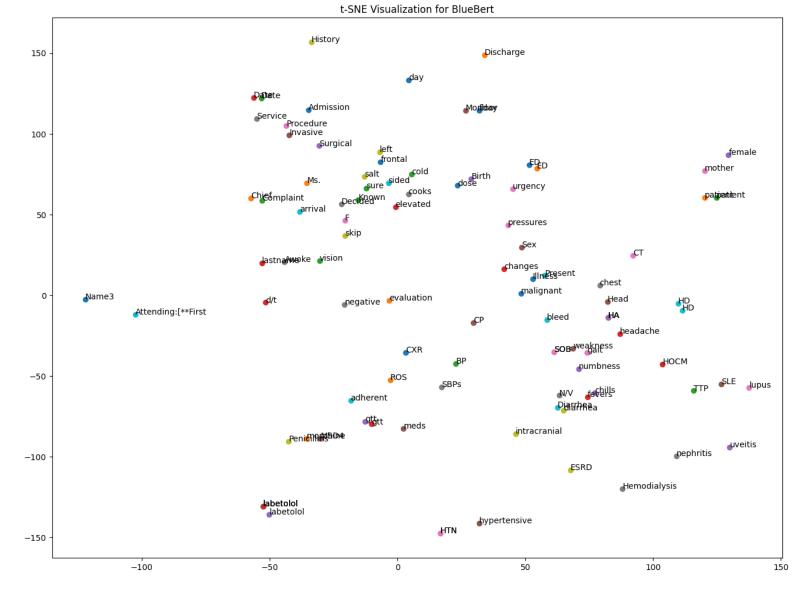
```
# Perform t-SNE dimensionality reduction
tsne_model = TSNE(n_components=2, perplexity=10, random_state=42)
word_embs_2d = tsne_model.fit_transform(np.array(word_embs))
print(len(word_embs_2d))
# Create a scatter plot of the word embeddings in 2D space
plt.figure(figsize=(16,12))
for i in range(100):
    plt.scatter(word_embs_2d[i, 0], word_embs_2d[i, 1])
    plt.annotate(input_tokens[i], (word_embs_2d[i, 0], word_embs_2d[i, 1]))

plt.title(f"t-SNE Visualization for BlueBert")
plt.show()
```

t-SNE visualization of the top 100 words from Word2Vec (BlueBert), with a limited word

count for better label

clarity.

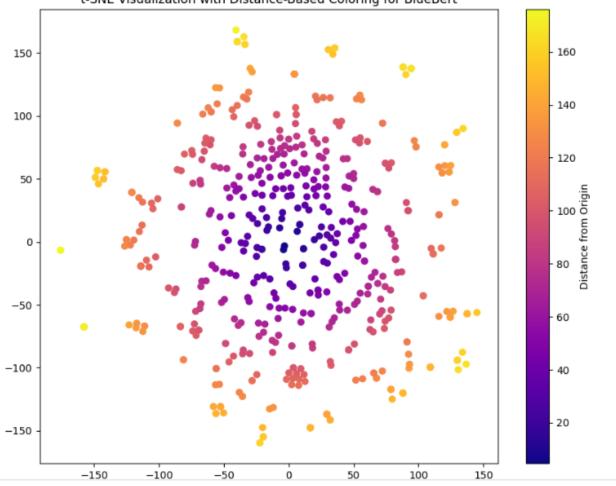


Based on Word2Vec similarity and the plot, BlueBert effectively captures key medical terms related to hypertension, such as **Labetalol**, **hypertension**, and **hemodialysis**. It groups related terms like **HTN**, **hypertensive**, **BP**, **SBPs**, and medications like **Labetalol**, indicating its ability to identify and understand hypertension-related concepts.

t-SNE Visualization with Distance-Based Coloring Of All Words from Word2Vec (BlueBert)

```
plt.figure(figsize=(10, 8))
distances = np.sqrt(word_embs_2d[:, 0]**2 + word_embs_2d[:, 1]**2)
plt.scatter(word_embs_2d[:, 0], word_embs_2d[:, 1], c=distances, cmap='plasma')
plt.colorbar(label="Distance from Origin")
plt.title(f"t-SNE Visualization with Distance-Based Coloring for BlueBert")
plt.show()
```

t-SNE Visualization with Distance-Based Coloring for BlueBert



Conclusion

The MIMIC data, especially the free-text notes, contains a lot of shorthand, misspellings, and extra details like dates and measurements that aren't useful for Named Entity Recognition (NER). Pre-trained models like BlueBERT, BC5CDR, and MedSpaCy, tailored for the medical field and charting terminology, tend to extract more relevant and accurate entities in NER than models like SpaCy and SciSpaCy.