4_medication_analysis

August 1, 2023

[1]:
```
import json
import os
from sklearn.feature_extraction.text import CountVectorizer
import pandas as pd
import numpy as np
from drug_named_entity_recognition import find_drugs
import json5
import sys

parent_dir = os.path.abspath("..")
if parent_dir not in sys.path:
    sys.path.append(parent_dir)
from path import DATA_PROCESSED_DOCUMENTS_DIR
```

[2]:
```
chief_complaint = "shortness-of-breath"
folder_location = os.path.join(
    DATA_PROCESSED_DOCUMENTS_DIR / chief_complaint / "black-or-african-american"
)
b_docs = []
w_docs = []
for filename in os.listdir(folder_location):
    file_location = os.path.join(folder_location, filename)
    if os.path.isfile(file_location):
        with open(file_location) as d:
            try:
                file_contents = d.read()
                content = json.loads(file_contents)
                b_docs.append(content)
            except Exception as e:
                try:
                    # pull of first and last line, gpt sometimes response with␣
 ↪a leading ```json and ends with ```
                    tmp = file_contents.splitlines(True)
                    while "{" not in tmp[0]:
                        tmp = tmp[1:]
                    while "}" not in tmp[-1]:
                        tmp = tmp[:-1]
```

```
                    tmp = "".join(tmp)
                    content = json5.loads(tmp)
                    b_docs.append(content)
                except Exception as e:
                    # print(f"{file_location} Error: {e}")
                    pass

folder_location = os.path.join(
    DATA_PROCESSED_DOCUMENTS_DIR / chief_complaint / "white-or-caucasian"
)
for filename in os.listdir(folder_location):
    file_location = os.path.join(folder_location, filename)
    if os.path.isfile(file_location):
        with open(file_location) as d:
            try:
                file_contents = d.read()
                content = json.loads(file_contents)
                w_docs.append(content)
            except Exception as e:
                try:
                    # pull of first and last line, gpt sometimes response with␣
 ↪a leading ```json and ends with ```
                    tmp = file_contents.splitlines(True)
                    while "{" not in tmp[0]:
                        tmp = tmp[1:]
                    while "}" not in tmp[-1]:
                        tmp = tmp[:-1]
                    tmp = "".join(tmp)
                    content = json5.loads(tmp)
                    w_docs.append(content)
                except Exception as e:
                    # print(f"{file_location} Error: {e}")
                    pass
```

[3]:
```
print(len(b_docs))
print(len(w_docs))
```

```
4933
4935
```

[4]:
```
b_normalized_medications = []
for doc in b_docs:
    if doc.get("medications") is not None:
        res = []
        res = doc.get("medications").split(" ")
        try:
            res.remove("other")
```

```
        except ValueError:
            pass
        res = find_drugs(res, is_ignore_case=True)
        b_normalized_medications.append(res)
len(b_normalized_medications)
```

[4]: 4917

[5]:
```
b_normalized_medications[:2]
```

[5]:
```
[[({'name': 'Lisinopril',
    'synonyms': {'Lisinopril',
     'Lisinoprilum',
     'Lysinopril',
     'Prinivil',
     'Zestril'},
    'medline_plus_id': 'a692051',
    'nhs_url': 'https://www.nhs.uk/medicines/lisinopril',
    'wikipedia_url': 'https://en.wikipedia.org/wiki/Lisinopril',
    'mesh_id': 'D002316',
    'drugbank_id': 'DB00722'},
   4,
   4),
  ({'name': 'Atorvastatin',
    'synonyms': {'Atorvastatin',
     'Lipitor',
     'Liptonorm',
     'Sortis',
     'atorvastatina',
     'atorvastatine',
     'atorvastatinum'},
    'medline_plus_id': 'a600045',
    'nhs_url': 'https://www.nhs.uk/medicines/atorvastatin',
    'wikipedia_url': 'https://en.wikipedia.org/wiki/Atorvastatin',
    'mesh_id': 'D019161',
    'drugbank_id': 'DB01076'},
   9,
   9)],
 [({'name': 'Lisinopril',
    'synonyms': {'Lisinopril',
     'Lisinoprilum',
     'Lysinopril',
     'Prinivil',
     'Zestril'},
    'medline_plus_id': 'a692051',
    'nhs_url': 'https://www.nhs.uk/medicines/lisinopril',
    'wikipedia_url': 'https://en.wikipedia.org/wiki/Lisinopril',
```

```
    'mesh_id': 'D002316',
    'drugbank_id': 'DB00722'},
   0,
   0),
  ({'name': 'Atorvastatin',
    'synonyms': {'Atorvastatin',
     'Lipitor',
     'Liptonorm',
     'Sortis',
     'atorvastatina',
     'atorvastatine',
     'atorvastatinum'},
    'medline_plus_id': 'a600045',
    'nhs_url': 'https://www.nhs.uk/medicines/atorvastatin',
    'wikipedia_url': 'https://en.wikipedia.org/wiki/Atorvastatin',
    'mesh_id': 'D019161',
    'drugbank_id': 'DB01076'},
   4,
   4)]]
```

[6]:
```
w_normalized_medications = []
for doc in w_docs:
    if doc.get("medications") is not None:
        res = []
        res = doc.get("medications").split(" ")
        try:
            res.remove("other")
        except ValueError:
            pass
        res = find_drugs(res, is_ignore_case=True)
        w_normalized_medications.append(res)
len(w_normalized_medications)
```

[6]: 4923

[7]:
```
# For each patient, parse out the medications and normalize them. De-dup them␣
 ↪so each patient has each medication listed only once.
b_just_names = list(
    map(
        lambda n: set(list(map(lambda m: m[0].get("name"), n))),
        b_normalized_medications,
    )
)
b_normalized_medications_names = [
    element for sublist in b_just_names for element in sublist
]
w_just_names = list(
```

```
    map(
        lambda n: set(list(map(lambda m: m[0].get("name"), n))),
        w_normalized_medications,
    )
)
w_normalized_medications_names = [
    element for sublist in w_just_names for element in sublist
]
b_just_names[:5]
# print(len(b_normalized_medications_names))
# print(len(w_normalized_medications_names))
```

[7]:
```
[{'Atorvastatin', 'Lisinopril'},
 {'Atorvastatin', 'Lisinopril'},
 {'Lisinopril'},
 set(),
 {'Metoprolol'}]
```

[8]:
```
b_cv = CountVectorizer(analyzer="word")
b_cv_fit = b_cv.fit_transform(b_normalized_medications_names)
b_word_list = b_cv.get_feature_names_out()
b_count_list = b_cv_fit.toarray().sum(axis=0)

b_word_freq = dict(zip(b_word_list, b_count_list))


w_cv = CountVectorizer(analyzer="word")
w_cv_fit = w_cv.fit_transform(w_normalized_medications_names)
w_word_list = w_cv.get_feature_names_out()
w_count_list = w_cv_fit.toarray().sum(axis=0)

w_word_freq = dict(zip(w_word_list, w_count_list))
```

[9]:
```
b_word_freq_df = pd.DataFrame(
    b_word_freq.items(), columns=["word", "b.frequency"]
).sort_values(by="b.frequency", ascending=False)
w_word_freq_df = pd.DataFrame(
    w_word_freq.items(), columns=["word", "w.frequency"]
).sort_values(by="w.frequency", ascending=False)
```

[10]:
```
wf_df = w_word_freq_df.merge(b_word_freq_df, how="inner", on="word")
```

[11]:
```
wf_df["w.frequency_pct"] = wf_df["w.frequency"] / wf_df["w.frequency"].sum()
wf_df["b.frequency_pct"] = wf_df["b.frequency"] / wf_df["b.frequency"].sum()
wf_df["frequency_pct_diff"] = wf_df["b.frequency_pct"] - wf_df["w.
 ↪frequency_pct"]
wf_df["frequency_pct_diff_abs"] = wf_df["frequency_pct_diff"].abs()
```

```
# Sort by largest values in absolue difference
wf_df.sort_values(by="frequency_pct_diff", ascending=False).head(10)
```

[11]:

	word	w.frequency	b.frequency	w.frequency_pct	\
8	metformin	98	133	0.016263	
4	amlodipine	326	351	0.054099	
12	furosemide	43	64	0.007136	
0	lisinopril	1382	1375	0.229340	
13	loratadine	42	54	0.006970	
15	losartan	30	39	0.004978	
16	hydrochlorothiazide	30	38	0.004978	
17	aspirin	20	28	0.003319	
6	metoprolol	122	126	0.020246	
14	ipratropium	32	35	0.005310	

	b.frequency_pct	frequency_pct_diff	frequency_pct_diff_abs
8	0.022535	0.006272	0.006272
4	0.059471	0.005372	0.005372
12	0.010844	0.003708	0.003708
0	0.232972	0.003632	0.003632
13	0.009149	0.002180	0.002180
15	0.006608	0.001630	0.001630
16	0.006438	0.001460	0.001460
17	0.004744	0.001425	0.001425
6	0.021349	0.001103	0.001103
14	0.005930	0.000620	0.000620

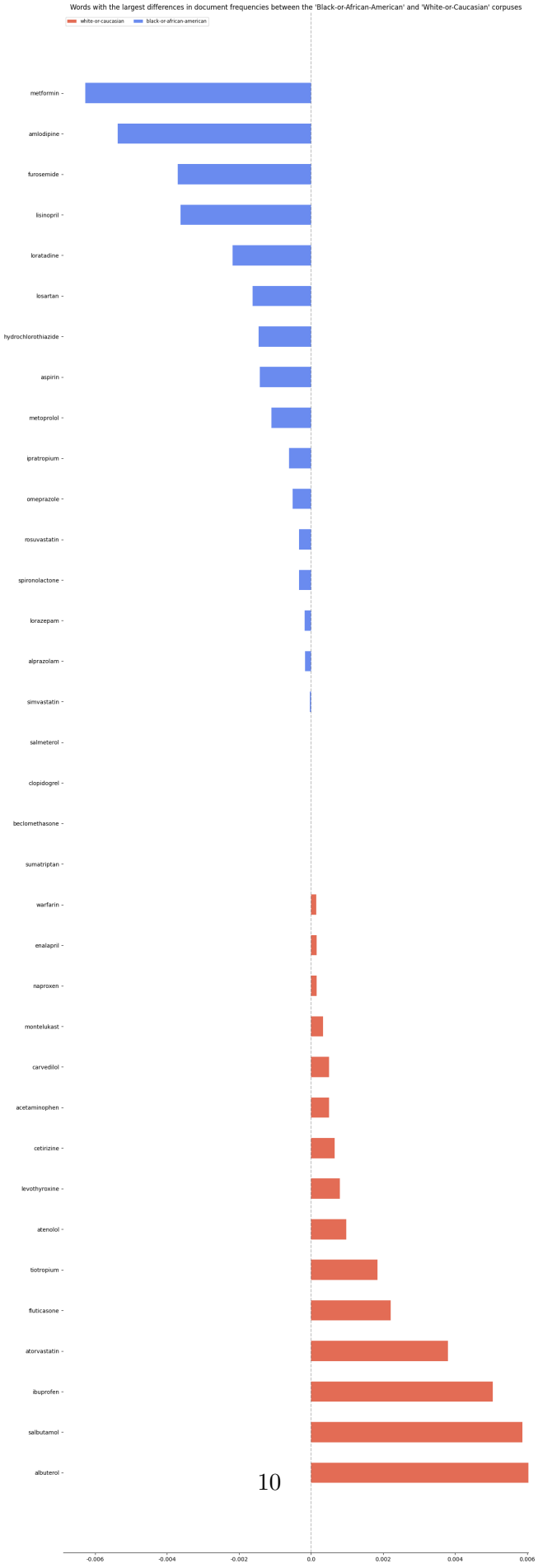
[12]:
```
# First order frequencies by magnature of difference (absolute value), take the␣
 ↪top 200 words with the greatest difference,
# then re-sort by actual difference so when we plot the values will be␣
 ↪sequential from smallest to largest bars
most = (
    wf_df.sort_values(by="frequency_pct_diff_abs", ascending=False)
    .head(200)
    .sort_values(by="frequency_pct_diff", ascending=False)
)

chart_data = {}

# Create a map with the word as the frequency, and the magnitude vector as the␣
 ↪value\
# a vector of [0, n] will plot a blue bar
# a vector of [n, 0] will plot an orange bar
# a vector with a negative n [-n, 0] will plot a bar on the left
# a vector with a positive n [n, 0] will plot a bar on the right
# {"word": [-1, 0]} will plot an orange bar for "word" on the left of 0 with␣
 ↪length 1
```

```
# {"word": [0, 0.5]} will plot a blue bar for "word" on the right of 0 with␣
 ↪length 0.5
# in order to generate a good Positive Negative bar chart, we assign b freq to␣
 ↪the left side (negative)
# and w freq to the right side (positive)
for row in most.iterrows():
    if row[1]["w.frequency_pct"] > row[1]["b.frequency_pct"]:
        # orange bars
        chart_data[row[1]["word"]] = [
            row[1]["w.frequency_pct"] - row[1]["b.frequency_pct"],
            0,
        ]
    else:
        # blue bars
        chart_data[row[1]["word"]] = [
            0,
            -(row[1]["b.frequency_pct"] - row[1]["w.frequency_pct"]),
        ]
```

[13]:
```
# Positive Negative Bar Chart to better visualize where word frequencies␣
 ↪diverge between data sets
# Based on https://stackoverflow.com/a/69976552/11407943
import numpy as np
import matplotlib.pyplot as plt


category_names = ["white-or-caucasian", "black-or-african-american"]
results = chart_data


def survey(results, category_names):
    """
    Parameters
    ----------
    results : dict
        A mapping from question labels to a list of answers per category.
        It is assumed all lists contain the same number of entries and that
        it matches the length of *category_names*. The order is assumed
        to be from 'Strongly disagree' to 'Strongly aisagree'
    category_names : list of str
        The category labels.
    """

    labels = list(results.keys())
    data = np.array(list(results.values()))
    data_cum = data.cumsum(axis=1)
    middle_index = data.shape[1] // 2
```

```
    offsets = 0  # data[:, range(middle_index)].sum(axis=1) # + data[:,␣
↪middle_index]/2

    # Color Mapping
    category_colors = plt.get_cmap("coolwarm_r")(np.linspace(0.15, 0.85, data.
↪shape[1]))

    fig, ax = plt.subplots(figsize=(15, 50))

    # Plot Bars
    for i, (colname, color) in enumerate(zip(category_names, category_colors)):
        widths = data[:, i]
        starts = data_cum[:, i] - widths - offsets
        rects = ax.barh(
            labels, widths, left=starts, height=0.5, label=colname, color=color
        )

    # Add Zero Reference Line
    ax.axvline(0, linestyle="--", color="black", alpha=0.25)

    # X Axis
    # ax.set_xticks(np.arange(-0.0035, 0.0035, 0.003))
    ax.xaxis.set_major_formatter(lambda x, pos: str(x))

    # Y Axis
    ax.invert_yaxis()

    # Remove spines
    ax.spines["right"].set_visible(False)
    ax.spines["top"].set_visible(False)
    ax.spines["left"].set_visible(False)

    # Ledgend
    ax.legend(
        ncol=len(category_names),
        bbox_to_anchor=(0, 0.99),
        loc="lower left",
        fontsize="small",
    )

    # Set Background Color
    fig.set_facecolor("#FFFFFF")

    return fig, ax


fig, ax = survey(results, category_names)
```

```
plt.title(
    "Words with the largest differences in document frequencies between the␣
 ↪'Black-or-African-American' and 'White-or-Caucasian' corpuses"
)
plt.show()
```


Words with the largest differences in document frequencies between the 'Black-or-African-American' and 'White-or-Caucasian' corpuses
white-or-caucasian
black-or-african-american
metformin
amlodipine
furosemide
lisinopril
loratadine
losartan
hydrochlorothiazide
aspirin
metoprolol
ipratropium
omeprazole
rosuvastatin
spironolactone
lorazepam
alprazolam
simvastatin
salmeterol
clopidogrel
beclomethasone
sumatriptan
warfarin
enalapril
naproxen
montelukast
carvedilol
acetaminophen
cetirizine
levothyroxine
atenolol
tiotropium
fluticasone
atorvastatin
ibuprofen
salbutamol
albuterol
-0.006
-0.004
-0.002
0.0
0.002
0.004
0.006

[14]:
```
import scipy
from sklearn.feature_extraction import text
from collections import Counter
```

[15]:
```
b_just_names_lower = [list(map(lambda x: x.lower(), arr)) for arr in␣
 ↪b_just_names]
b_list_of_doc_counter = list(map(Counter, b_just_names_lower))
# element for sublist in w_just_names for element in sublist
w_just_names_lower = [list(map(lambda x: x.lower(), arr)) for arr in␣
 ↪w_just_names]
w_list_of_doc_counter = list(map(Counter, w_just_names_lower))
b_just_names_lower
b_medications_names_counter = Counter(
    [element for sublist in b_just_names_lower for element in sublist]
)
w_medications_names_counter = Counter(
    [element for sublist in w_just_names_lower for element in sublist]
)
```

[16]:
```
b_medications_names_counter
```

[16]:
```
Counter({'lisinopril': 1375,
         'salbutamol': 1125,
         'albuterol': 1125,
         'atorvastatin': 958,
         'amlodipine': 351,
         'simvastatin': 202,
         'metformin': 133,
         'metoprolol': 126,
         'acetaminophen': 94,
         'furosemide': 64,
         'loratadine': 54,
         'tiotropium': 42,
         'losartan': 39,
         'hydrochlorothiazide': 38,
         'ipratropium': 35,
         'fluticasone': 33,
         'ibuprofen': 29,
         'aspirin': 28,
         'levothyroxine': 9,
         'warfarin': 6,
         'atenolol': 5,
         'omeprazole': 4,
         'sertraline': 3,
```

```
             'rosuvastatin': 3,
             'enalapril': 3,
             'naproxen': 3,
             'cetirizine': 3,
             'lorazepam': 3,
             'spironolactone': 3,
             'salmeterol': 2,
             'alprazolam': 2,
             'lovastatin': 1,
             'escitalopram': 1,
             'budesonide': 1,
             'donepezil': 1,
             'montelukast': 1,
             'beclomethasone': 1,
             'prednisone': 1,
             'clopidogrel': 1,
             'carvedilol': 1,
             'paracetamol': 1,
             'sumatriptan': 1})
```

[17]:
```
w_medications_names_counter
```

[17]:
```
Counter({'lisinopril': 1382,
         'albuterol': 1185,
         'salbutamol': 1184,
         'atorvastatin': 1001,
         'amlodipine': 326,
         'simvastatin': 206,
         'metoprolol': 122,
         'acetaminophen': 99,
         'metformin': 98,
         'ibuprofen': 60,
         'tiotropium': 54,
         'fluticasone': 47,
         'furosemide': 43,
         'loratadine': 42,
         'ipratropium': 32,
         'hydrochlorothiazide': 30,
         'losartan': 30,
         'aspirin': 20,
         'levothyroxine': 14,
         'atenolol': 11,
         'cetirizine': 7,
         'warfarin': 7,
         'enalapril': 4,
         'carvedilol': 4,
         'naproxen': 4,
```

```
 'montelukast': 3,
 'lorazepam': 2,
 'salmeterol': 2,
 'rosuvastatin': 1,
 'beclomethasone': 1,
 'alprazolam': 1,
 'clopidogrel': 1,
 'sumatriptan': 1,
 'spironolactone': 1,
 'omeprazole': 1})
```

[18]:
```
total_keys = list(
    set(
        list(w_medications_names_counter.keys())
        + list(b_medications_names_counter.keys())
    )
)
new_counts = {}
aa = []
ca = []
for k in total_keys:
    # [aa,ca]
    new_counts[k] = [
        b_medications_names_counter.get(k, 0),
        w_medications_names_counter.get(k, 0),
    ]
    aa.append(b_medications_names_counter.get(k, 0))
    ca.append(w_medications_names_counter.get(k, 0))

c_table = pd.DataFrame.from_dict(new_counts)
c_table.rename(index={0: "b.freq"}, inplace=True)
c_table.rename(index={1: "w.freq"}, inplace=True)
c_table
```

[18]:

	clopidogrel	donepezil	omeprazole	naproxen	simvastatin	cetirizine	\
b.freq	1	1	4	3	202	3	
w.freq	1	0	1	4	206	7	

	metoprolol	albuterol	montelukast	atenolol	…	atorvastatin	\
b.freq	126	1125	1	5	…	958	
w.freq	122	1185	3	11	…	1001	

	loratadine	salbutamol	fluticasone	aspirin	escitalopram	\
b.freq	54	1125	33	28	1	
w.freq	42	1184	47	20	0	

	paracetamol	carvedilol	acetaminophen	levothyroxine

```
b.freq            1           1             94              9
w.freq            0           4             99             14

[2 rows x 42 columns]
```

[19]:
```python
class bcolors:
    HEADER = "\033[95m"
    OKBLUE = "\033[94m"
    OKCYAN = "\033[96m"
    OKGREEN = "\033[92m"
    WARNING = "\033[93m"
    FAIL = "\033[91m"
    ENDC = "\033[0m"
    BOLD = "\033[1m"
    UNDERLINE = "\033[4m"
```

[20]:
```python
sig_results = []
# Chi square independence test
# https://www.dir.uniupo.it/pluginfile.php/138296/mod_resource/content/0/
 ↪22-colloc-bw.pdf
for k in list(set(total_keys)):
    # For AA [Number of instances of current word, Number of instances of all␣
 ↪other words]
    x1 = [c_table[k].iloc[0], c_table.iloc[0].sum() - c_table[k].iloc[0]]
    # For CA [Number of instances of current word, Number of instances of all␣
 ↪other words]
    y1 = [c_table[k].iloc[1], c_table.iloc[1].sum() - c_table[k].iloc[1]]
    test = scipy.stats.chi2_contingency([x1, y1])
    word = c_table[k].name
    if test.pvalue < 0.05:
        sig_results.append(word)
        print(f"{bcolors.OKGREEN}{bcolors.BOLD}Medication: {k}{bcolors.ENDC}")
        print(f"AA: {x1}")
        print(f"CA: {y1}")
        print(
            f'There {bcolors.OKGREEN}is a significant difference{bcolors.ENDC}␣
 ↪in the use of medication "{word}" between the groups with a p-value of␣
 ↪{bcolors.OKGREEN +"{:0.3f}".format(test.pvalue) + bcolors.ENDC}'
        )
        print(f"")
    # else:
    #     print(f"{bcolors.FAIL}{bcolors.BOLD}Medication: {k}{bcolors.ENDC}")
    #     print(f"AA: {x1}")
    #     print(f"CA: {y1}")
    #     print(
```

```
    #         f'There {bcolors.FAIL}is no significant difference{bcolors.ENDC}␣
 ↪in the use of medication "{word}" between the groups with a p-value of␣
 ↪{bcolors.FAIL +"{:0.3f}".format(test.pvalue) + bcolors.ENDC}'
    #     )
    #     print(f"")
if len(sig_results) == 0:
    print(
        f"{bcolors.BOLD}{bcolors.FAIL}No significant differences in any␣
 ↪conditions between groups found{bcolors.ENDC}"
    )
```

```
Medication: furosemide
AA: [64, 5847]
CA: [43, 5983]
There is a significant difference in the use of medication "furosemide"
between the groups with a p-value of 0.041

Medication: ibuprofen
AA: [29, 5882]
CA: [60, 5966]
There is a significant difference in the use of medication "ibuprofen"
between the groups with a p-value of 0.002

Medication: metformin
AA: [133, 5778]
CA: [98, 5928]
There is a significant difference in the use of medication "metformin"
between the groups with a p-value of 0.016
```