4_medication_analysis

July 31, 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 = "abdominal-pain"
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))
```

```
4945
4951
```

[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]:
```
4935
```

[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'},
   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'},
   3,
   3)]]
```

[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]: 4941

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

[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	b.frequency_pct	\
6	metformin	201	326	0.040622	0.065912	
10	salbutamol	44	62	0.008892	0.012535	
11	albuterol	44	62	0.008892	0.012535	
8	metoprolol	87	100	0.017583	0.020218	
2	amlodipine	343	351	0.069321	0.070966	
9	losartan	50	57	0.010105	0.011524	
13	levothyroxine	31	37	0.006265	0.007481	
4	acetaminophen	286	291	0.057801	0.058835	
7	omeprazole	89	93	0.017987	0.018803	
15	naproxen	13	17	0.002627	0.003437	

	frequency_pct_diff	frequency_pct_diff_abs
6	0.025289	0.025289
10	0.003643	0.003643
11	0.003643	0.003643
8	0.002635	0.002635
2	0.001645	0.001645
9	0.001419	0.001419
13	0.001216	0.001216
4	0.001034	0.001034
7	0.000816	0.000816
15	0.000810	0.000810

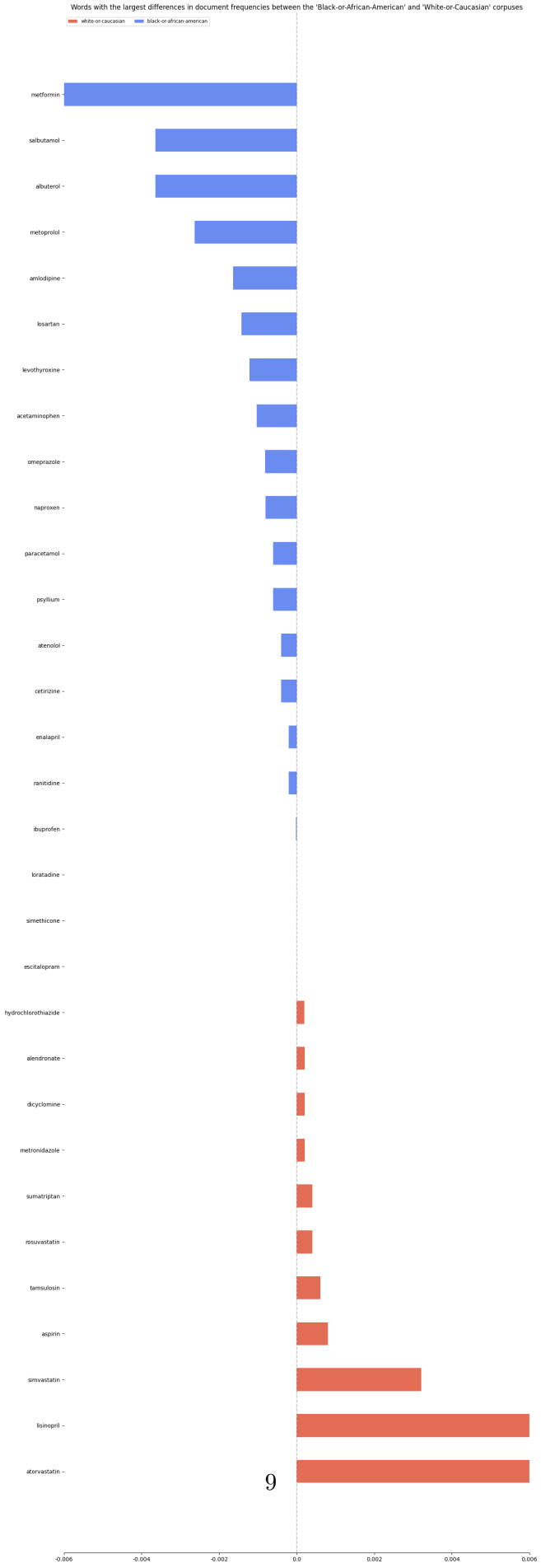
[12]:
```
# First order frequencies by magnature of difference (absolute value), take the␣
 ↪top 200 words with the greatest difference,
# then re-sort by actual difference so when we plot the values will be␣
 ↪sequential from smallest to largest bars
most = (
    wf_df.sort_values(by="frequency_pct_diff_abs", 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_xlim(-0.006, 0.006)
    # 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
salbutamol
albuterol
metoprolol
amlodipine
losartan
levothyroxine
acetaminophen
omeprazole
naproxen
paracetamol
psyllium
atenolol
cetirizine
enalapril
ranitidine
ibuprofen
loratadine
simethicone
escitalopram
hydrochlorothiazide
alendronate
dicyclomine
metronidazole
sumatriptan
rosuvastatin
tamsulosin
aspirin
simvastatin
lisinopril
atorvastatin
-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': 1974,
         'atorvastatin': 921,
         'amlodipine': 351,
         'metformin': 326,
         'ibuprofen': 301,
         'acetaminophen': 291,
         'simvastatin': 236,
         'metoprolol': 100,
         'omeprazole': 93,
         'salbutamol': 62,
         'albuterol': 62,
         'losartan': 57,
         'hydrochlorothiazide': 39,
         'levothyroxine': 37,
         'loratadine': 19,
         'naproxen': 17,
         'paracetamol': 9,
         'sumatriptan': 8,
         'aspirin': 8,
         'atenolol': 7,
         'alendronate': 6,
         'cetirizine': 5,
         'psyllium': 4,
```

```
             'tamsulosin': 3,
             'pantoprazole': 2,
             'simethicone': 2,
             'celecoxib': 2,
             'glipizide': 2,
             'ranitidine': 2,
             'timolol': 2,
             'enalapril': 2,
             'gabapentin': 1,
             'serotonin': 1,
             'metronidazole': 1,
             'ciprofloxacin': 1,
             'montelukast': 1,
             'rosuvastatin': 1,
             'calcitriol': 1,
             'escitalopram': 1,
             'acenocoumarol': 1,
             'ursodiol': 1,
             'lorazepam': 1,
             'dicyclomine': 1,
             'amitriptyline': 1,
             'bisacodyl': 1})
```

[17]:
```
w_medications_names_counter
```

[17]:
```
Counter({'lisinopril': 2031,
         'atorvastatin': 1055,
         'amlodipine': 343,
         'ibuprofen': 301,
         'acetaminophen': 286,
         'simvastatin': 252,
         'metformin': 201,
         'omeprazole': 89,
         'metoprolol': 87,
         'losartan': 50,
         'salbutamol': 44,
         'albuterol': 44,
         'hydrochlorothiazide': 40,
         'levothyroxine': 31,
         'loratadine': 19,
         'naproxen': 13,
         'aspirin': 12,
         'sumatriptan': 10,
         'alendronate': 7,
         'paracetamol': 6,
         'tamsulosin': 6,
         'sertraline': 5,
```

```
 'atenolol': 5,
 'cetirizine': 3,
 'rosuvastatin': 3,
 'simethicone': 2,
 'oxycodone': 2,
 'famotidine': 2,
 'metronidazole': 2,
 'docusate': 2,
 'dicyclomine': 2,
 'meloxicam': 1,
 'ranitidine': 1,
 'benazepril': 1,
 'furosemide': 1,
 'escitalopram': 1,
 'enalapril': 1,
 'methimazole': 1,
 'esomeprazole': 1,
 'lansoprazole': 1,
 'fluoxetine': 1,
 'psyllium': 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]:

	aspirin	serotonin	furosemide	ursodiol	famotidine	metoprolol	\
b.freq	8	1	0	1	0	100	
w.freq	12	0	1	0	2	87	

```
        docusate  acenocoumarol  acetaminophen  sertraline  …  timolol  \
b.freq         0              1            291           0  …        2
w.freq         2              0            286           5  …        0

        alendronate  atorvastatin  calcitriol  sumatriptan  fluoxetine  \
b.freq            6           921           1            8           0
w.freq            7          1055           0           10           1

        atenolol  metformin  oxycodone  omeprazole
b.freq         7        326          0          93
w.freq         5        201          2          89

[2 rows x 56 columns]
```

[19]:
```
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]:
```
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 frequency of the word {word} with a p-value of {bcolors.OKGREEN +"{: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: atorvastatin
AA: [921, 4043]
CA: [1055, 3911]
There is a significant difference in the frequency of the word
atorvastatin with a p-value of 0.001

Medication: metformin
AA: [326, 4638]
CA: [201, 4765]
There is a significant difference in the frequency of the word
metformin with a p-value of 0.000
```