5_pmh_analysis

August 1, 2023

[1]:

```python
import json
import os
from sklearn.feature_extraction.text import CountVectorizer
import pandas as pd
import numpy as np
import json5
import spacy
import medspacy
import random
from medspacy.ner import TargetMatcher, TargetRule
from medspacy.visualization import visualize_ent, visualize_dep
from spacy.tokens import Span
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]:

```python
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]:

```
# Grab the text from each document's past medical history section
b_pmh = []
```

```
for doc in b_docs:
    if doc.get("past_medical_history") is not None:
        b_pmh.append(doc.get("past_medical_history"))

w_pmh = []
for doc in w_docs:
    if doc.get("past_medical_history") is not None:
        w_pmh.append(doc.get("past_medical_history"))
```

[5]:

```
# We want to see if each patient has a history of any of the following␣
 ↪conditions
nlp = medspacy.load()
print(nlp.pipe_names)

try:
    Span.set_extension("icd10_code", default="")
except:
    pass

# Add rules for target concept extraction
target_matcher = nlp.get_pipe("medspacy_target_matcher")
target_rules = [
    TargetRule("hypertension", category="CONDITION", attributes={"icd10_code":␣
 ↪"I10"}),
    TargetRule(
        "hyperlipidemia", category="CONDITION", attributes={"icd10_code": "E78.
 ↪5"}
    ),
    TargetRule(
        "osteoarthritis", category="CONDITION", attributes={"icd10_code": "M19.
 ↪90"}
    ),
    TargetRule(
        "osteoporosis", category="CONDITION", attributes={"icd10_code": "M81.0"}
    ),
    TargetRule(
        "dyslipidemia", category="CONDITION", attributes={"icd10_code": "E78.5"}
    ),
    TargetRule(
        literal="Type II Diabetes Mellitus",
        category="CONDITION",
        attributes={"icd10_code": "E11.9"},
    ),
    TargetRule(
        literal="diabetes mellitus type 2",
        category="CONDITION",
        pattern=[
            {"LOWER": "diabetes"},
            {"LOWER": "mellitus"},
            {"LOWER": "type"},
            {"LOWER": {"IN": ["two", "ii", "2"]}},
        ],
        attributes={"icd10_code": "E11.9"},
    ),
    TargetRule(
        literal="gerd",
        category="CONDITION",
        pattern=[
            {"LOWER": "gastroesophageal"},
            {"LOWER": "reflux"},
            {"LOWER": "disease"},
        ],
        attributes={"icd10_code": "K21.9"},
    ),
    TargetRule(
        literal="GERD", category="CONDITION", attributes={"icd10_code": "K21.9"}
    ),
    TargetRule(
        literal="Type II Diabetes Mellitus",
        category="CONDITION",
        pattern=[
            {"LOWER": "type"},
            {"LOWER": {"IN": ["two", "ii", "2"]}},
            {
                "LOWER": {
                    "IN": [
                        "dm",
                        "diabetes mellitus",
                        "diabetes",
                    ]
                }
            },
        ],
        attributes={"icd10_code": "E11.9"},
    ),
    TargetRule("asthma", category="CONDITION", attributes={"icd10_code": "J45"}),
    TargetRule(
        "atrial fibrillation",
        category="CONDITION",
        attributes={"icd10_code": "I48.91"},
    ),
    TargetRule(
        "hypercholesterolemia",
        category="CONDITION",
        attributes={"icd10_code": "E78.00"},
    ),
    TargetRule(
        "high cholesterol",
        category="CONDITION",
        pattern=[{"LOWER": {"IN": ["high", "elevated"]}}, {"LOWER": "cholesterol"}],
        attributes={"icd10_code": "E78.00"},
    ),
    TargetRule(
        "hypertriglyceridemia", category="CONDITION", attributes={"icd10_code": "E78.1"}
    ),
    TargetRule(
        "myocardial infarction",
        category="CONDITION",
        pattern=[
            {"LOWER": "myocardial"},
            {"LOWER": "infarction"},
        ],
        attributes={"icd10_code": "I21.9"},
    ),
    TargetRule(
        "coronary artery disease",
        category="CONDITION",
        attributes={"icd10_code": "I25.10"},
    ),
    TargetRule(
        "Irritable Bowel Syndrome",
        category="CONDITION",
        pattern=[
            {"LOWER": "irritable"},
            {"LOWER": "bowel"},
            {"LOWER": "syndrome"},
        ],
        attributes={"icd10_code": "K58"},
    ),
    TargetRule(
        "IBS",
        category="CONDITION",
        pattern=[
            {"LOWER": "ibs"},
        ],
        attributes={"icd10_code": "K58"},
    ),
    TargetRule(
        "Nephrolithiasis",
        category="CONDITION",
        pattern=[
            {"LOWER": "nephrolithiasis"},
        ],
        attributes={"icd10_code": "N20.0"},
    ),
    TargetRule(
        "Kidney Stones",
        category="CONDITION",
        pattern=[
            {"LOWER": "kidney"},
            {
                "LOWER": {
                    "IN": [
                        "stones",
                        "stone",
                    ]
                },
            },
        ],
        attributes={"icd10_code": "N20.0"},
    ),
    TargetRule(
        "Gallstones",
        category="CONDITION",
        pattern=[
            {"LOWER": "gallstones"},
        ],
        attributes={"icd10_code": "K80"},
    ),
    TargetRule(
        "Cholelithiasis",
        category="CONDITION",
        pattern=[
            {"LOWER": "cholelithiasis"},
        ],
        attributes={"icd10_code": "K80"},
    ),
    TargetRule(
        "Diverticulosis",
        category="CONDITION",
        pattern=[
            {"LOWER": "diverticulosis"},
        ],
        attributes={"icd10_code": "K57.9"},
    ),
    TargetRule(
        "Endometriosis",
        category="CONDITION",
        pattern=[
            {"LOWER": "endometriosis"},
        ],
        attributes={"icd10_code": "N80.9"},
    ),
    TargetRule(
        "Appendicitis",
        category="CONDITION",
        pattern=[
            {"LOWER": "appendicitis"},
        ],
        attributes={"icd10_code": "K35.80"},
    ),
    TargetRule(
        "Migraine",
        category="CONDITION",
        pattern=[
            {"LOWER": "migraine"},
            {"LOWER": "migraines"},
        ],
        attributes={"icd10_code": "G43.909"},
    ),
    TargetRule(
        "Pancreatitis",
        category="CONDITION",
        pattern=[
            {"LOWER": "pancreatitis"},
        ],
        attributes={"icd10_code": "K85.9"},
    ),
    TargetRule(
        "Cholecystitis",
        category="CONDITION",
        pattern=[
            {"LOWER": "cholecystitis"},
        ],
        attributes={"icd10_code": "K81"},
    ),
    TargetRule(
        "Diverticulitis",
        category="CONDITION",
        pattern=[
            {"LOWER": "diverticulitis"},
        ],
        attributes={"icd10_code": "K57.92"},
    ),
    TargetRule(
        "Gastritis",
        category="CONDITION",
        pattern=[
            {"LOWER": "gastritis"},
        ],
        attributes={"icd10_code": "K29"},
    ),
    TargetRule(
        "Gastric Ulcers",
        category="CONDITION",
        pattern=[
            {"LOWER": "gastric"},
            {"LOWER": {"IN": ["ulcers", "ulcer"]}},
        ],
        attributes={"icd10_code": "K25.9"},
    ),
    TargetRule(
        "Constipation",
        category="CONDITION",
        pattern=[
            {"LOWER": "constipation"},
        ],
        attributes={"icd10_code": "K59.00"},
    ),
    TargetRule(
        "COPD",
        category="CONDITION",
        pattern=[
            {"LOWER": "copd"},
        ],
        attributes={"icd10_code": "J44.9"},
    ),
    TargetRule(
        "Chronic Obstructive Pulmonary Disease",
        category="CONDITION",
        pattern=[
            {"LOWER": "chronic"},
            {"LOWER": "obstructive"},
            {"LOWER": "pulmonary"},
            {"LOWER": "disease"},
        ],
        attributes={"icd10_code": "J44.9"},
    ),
    TargetRule(
        "Other Seasonal Allergic Rhinitis",
        category="CONDITION",
        attributes={"icd10_code": "J30.2"},
    ),
    TargetRule(
        "Seasonal Allergies",
        category="CONDITION",
                pattern=[
            {"LOWER": "seasonal"},
            {"LOWER": {"IN": ["allergies", "allergy"]}},
        ],
        attributes={"icd10_code": "J30.2"},
    ),
    TargetRule(
        "Congestive Heart Failure",
        category="CONDITION",
        pattern=[
            {"LOWER": "congestive"},
            {"LOWER": "heart"},
            {"LOWER": "failure"},
        ],
        attributes={"icd10_code": "I50.9"},
    ),
    TargetRule(
        "CHF",
        category="CONDITION",
        pattern=[
            {"LOWER": "chf"},
        ],
        attributes={"icd10_code": "I50.9"},
    ),
    TargetRule(
        "Hypothyroidism",
        category="CONDITION",
        pattern=[
            {"LOWER": "hypothyroidism"},
        ],
        attributes={"icd10_code": "E03.9"},
    ),
    TargetRule(
        "Hypothyroid",
        category="CONDITION",
        pattern=[
            {"LOWER": "hypothyroid"},
        ],
        attributes={"icd10_code": "E03.9"},
    ),
    TargetRule(
        "Hyperthyroidism",
        category="CONDITION",
        pattern=[
            {"LOWER": "hyperthyroidism"},
        ],

        attributes={"icd10_code": "E05"},
    ),
    TargetRule(
        "Hyperthyroid",
        category="CONDITION",
        pattern=[
            {"LOWER": "hyperthyroid"},
        ],
        attributes={"icd10_code": "E05"},
    ),
    TargetRule(
        "High Blood Pressure",
        category="CONDITION",
        pattern=[
            {"LOWER": "high"},
            {"LOWER": "blood"},
            {"LOWER": "pressure"},
        ],
        attributes={"icd10_code": "I10"},
    ),
]

ICD_TO_TEXT_MAP = {
    "I10": "hypertension",
    "E78.5": "hyperlipidemia",
    "M19.90": "osteoarthritis",
    "E11.9": "type ii diabetes mellitus",
    "E78.00": "hypercholesterolemia",
    "J45": "asthma",
    "I48.91": "atrial fibrillation",
    "M81.0": "osteoporosis",
    "K21.9": "gastroesophageal reflux disease ",
    "I21.9": "myocardial infarction",
    "I25.10": "coronary artery disease",
    "K85.9": "pancreatitis",
    "G43.909": "migraine",
    "K35.80": "appendicitis",
    "N80.9": "endometriosis",
    "K57.9": "diverticulosis",
    "K80": "cholelithiasis",
    "N20.0": "nephrolithiasis",
    "K58": "ibs",
    "K81": "cholecystitis",
    "K57.92": "diverticulitis",
    "K29": "gastritis",
    "K25.9": "gastric ulcers",
    "K59.00": "constipation",
    "J44.9": "copd",
    "J30.2": "other seasonal allergic rhinitis",
    "I50.9": "congestive heart failure",
    "E03.9": "hypothyroidism",
    "E05": "hyperthyroidism",
}

target_matcher.add(target_rules)
```

```
['medspacy_pyrush', 'medspacy_target_matcher', 'medspacy_context']
```

[6]:

```
# Extract conditions from PMH
b_nlp_pmh = []
for doc in b_pmh:
    doc = nlp(doc)
    b_nlp_pmh.append(doc)
```

[7]:

```
w_nlp_pmh = []
for doc in w_pmh:
    doc = nlp(doc)
    w_nlp_pmh.append(doc)
```

[8]:

```
# Quick test to make sure negation detection works
# negation test
test = "The patient has a history of hypertension which is well-controlled with␣
 ↪medication. She also has a history of gallstones but has not had  any␣
 ↪previous episodes of cholecystitis or pancreatitis ."
doc = nlp(test)
visualize_ent(doc)
for ent in doc.ents:
    print(ent._.is_negated)
```

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```

```
False
False
True
True
```

[9]:

```
# Quick visualization of entity extraction
for doc in w_nlp_pmh[:1000]:
    visualize_ent(doc)
```

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[10]:

```
for doc in b_nlp_pmh[:10]:
    visualize_ent(doc)
```

```
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```

[11]:

```
# Test entity extraction, making sure to ignore negated entities
test = b_nlp_pmh[0:2]
test.append(
    nlp(
        "patient admits to type 2 diabetes but denies any hypertension. he␣
 ↪takes metformin for his type 2 diabetes."
    )
)
print(list(map(lambda x: [y for y in list(x.ents) if y._.is_negated == False],␣
 ↪test)))
print(
    list(
        map(
            lambda x: [y._.icd10_code for y in list(x.ents) if y._.is_negated␣
 ↪== False],
            test,
        )
    )
)
# De-dup
print(
    list(
        map(
            lambda x: set(
                [y._.icd10_code for y in list(x.ents) if y._.is_negated ==␣
  ↪False]
            ),
            test,
        )
    )
)
```

```
[[hypertension, hyperlipidemia, coronary artery disease], [Hypertension,
hyperlipidemia], [type 2 diabetes, type 2 diabetes]]
[['I10', 'E78.5', 'I25.10'], ['I10', 'E78.5'], ['E11.9', 'E11.9']]
[{'I10', 'E78.5', 'I25.10'}, {'I10', 'E78.5'}, {'E11.9'}]
```

[12]:

```
# Do entity extraction on the PMH section of the notes, skipping negated␣
  ↪entities. Make sure to de-duplicate the entities.
b_just_names = list(
    map(
        lambda x: set(
            [y._.icd10_code for y in list(x.ents) if y._.is_negated == False]
        ),
        b_nlp_pmh,
    )
)

b_normalized_conditions_names = [
    element for sublist in b_just_names for element in sublist
]
w_just_names = list(
    map(
        lambda x: set(
            [y._.icd10_code for y in list(x.ents) if y._.is_negated == False]
        ),
        w_nlp_pmh,
    )
)
w_normalized_conditions_names = [
    element for sublist in w_just_names for element in sublist
]
print(len(b_normalized_conditions_names))
print(len(w_normalized_conditions_names))
```

```
6179
6223
```

[13]:

```
# Count the instances of each word in the black and white conditions.␣
 ↪Conditions are de-duped, so if a condition appears multiple times in a␣
 ↪single participant's data, it is only counted once.
# We fix this later before doing statistical analysis.
from collections import Counter

b_word_freq = Counter(b_normalized_conditions_names)
w_word_freq = Counter(w_normalized_conditions_names)
```

[14]:

```
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)
```

[15]:

```
wf_df = w_word_freq_df.merge(b_word_freq_df, how="inner", on="word")
wf_df
```

[15]:

```
      word  w.frequency  b.frequency
0      I10         2438         2514
1    E78.5         1499         1444
2      J45         1011          994
3    J44.9          487          409
4   M19.90          278          231
5    J30.2          201          204
6    I50.9           97          117
7    E11.9           82          124
8   I25.10           44           49
9   E78.00           21           23
10   M81.0           18           11
11   I21.9           16           27
12   E03.9           15           12
13  I48.91           13           14
14   K21.9            2            5
```

[16]:

```
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(25)
```

```
[16]:       word  w.frequency  b.frequency  w.frequency_pct  b.frequency_pct  \
      0      I10         2438         2514         0.391835         0.406928
      7    E11.9           82          124         0.013179         0.020071
      6    I50.9           97          117         0.015590         0.018938
      11   I21.9           16           27         0.002572         0.004370
      8   I25.10           44           49         0.007072         0.007931
      5    J30.2          201          204         0.032305         0.033020
      14   K21.9            2            5         0.000321         0.000809
      9   E78.00           21           23         0.003375         0.003723
      13  I48.91           13           14         0.002089         0.002266
      12   E03.9           15           12         0.002411         0.001942
      10   M81.0           18           11         0.002893         0.001781
      2      J45         1011          994         0.162488         0.160893
      1    E78.5         1499         1444         0.240919         0.233733
      4   M19.90          278          231         0.044680         0.037391
      3    J44.9          487          409         0.078271         0.066203

          frequency_pct_diff  frequency_pct_diff_abs
      0             0.015092                0.015092
      7             0.006892                0.006892
      6             0.003348                0.003348
      11            0.001799                0.001799
      8             0.000860                0.000860
      5             0.000716                0.000716
      14            0.000488                0.000488
      9             0.000348                0.000348
      13            0.000177                0.000177
      12           -0.000468                0.000468
      10           -0.001112                0.001112
      2            -0.001594                0.001594
      1            -0.007187                0.007187
      4            -0.007289                0.007289
      3            -0.012068                0.012068
```

```
[17]: # First order frequencies by magnitude 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"]),
        ]
```

[18]:

```
# 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(map(lambda i: ICD_TO_TEXT_MAP.get(i), 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)

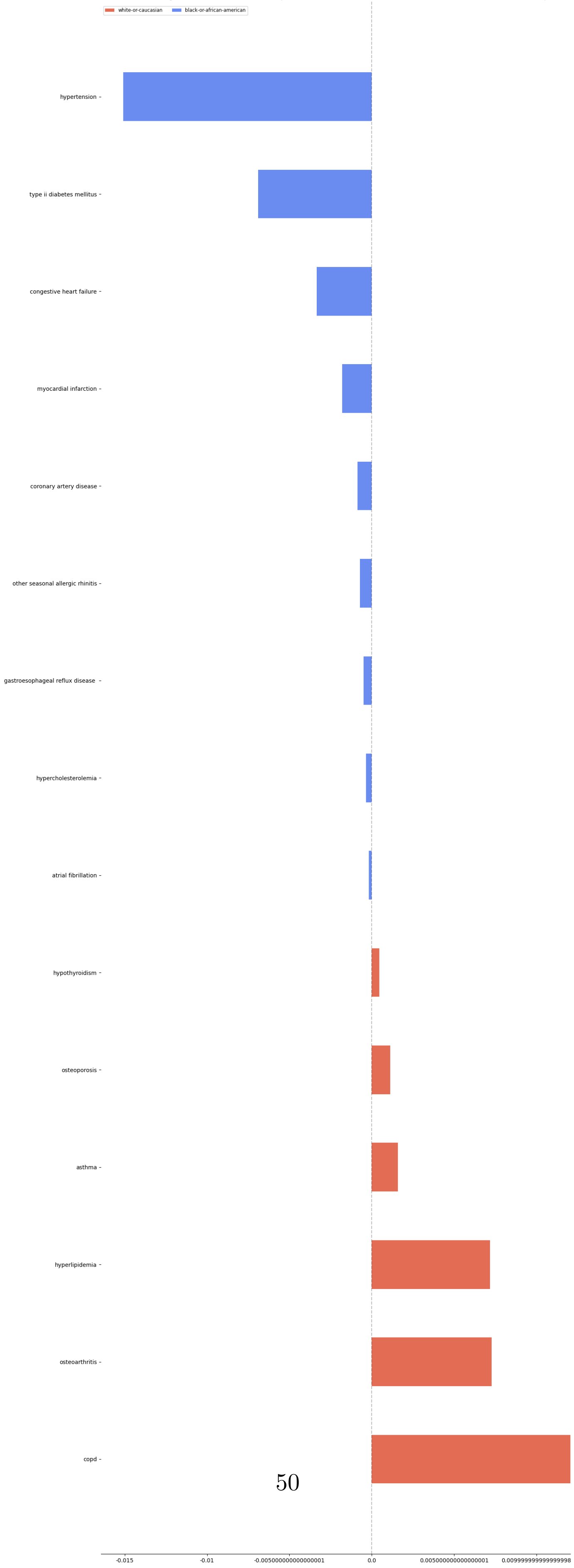
    # Ledgend
    ax.legend(
        ncol=len(category_names),
        bbox_to_anchor=(0, 0.99),
        loc="lower left",
        fontsize="small",
    )

    # 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



[19]:

```
import scipy
from sklearn.feature_extraction import text
from collections import Counter
```

[20]:

```
b_just_names_lower = [
    list(map(lambda x: ICD_TO_TEXT_MAP.get(x), 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: ICD_TO_TEXT_MAP.get(x), arr)) for arr in w_just_names
]
w_list_of_doc_counter = list(map(Counter, w_just_names_lower))
b_conditions_names_counter = Counter(
    [element for sublist in b_just_names_lower for element in sublist]
)
w_conditions_names_counter = Counter(
    [element for sublist in w_just_names_lower for element in sublist]
)
```

[21]:

```
b_conditions_names_counter
```

[21]:

```
Counter({'hypertension': 2514,
         'hyperlipidemia': 1444,
         'asthma': 994,
         'copd': 409,
         'osteoarthritis': 231,
         'other seasonal allergic rhinitis': 204,
         'type ii diabetes mellitus': 124,
         'congestive heart failure': 117,
         'coronary artery disease': 49,
         'myocardial infarction': 27,
         'hypercholesterolemia': 23,
         'atrial fibrillation': 14,
         'hypothyroidism': 12,
         'osteoporosis': 11,
         'gastroesophageal reflux disease ': 5,
         'constipation': 1})
```

[22]:

```
w_conditions_names_counter
```

[22]:

```
Counter({'hypertension': 2438,
         'hyperlipidemia': 1499,
         'asthma': 1011,
         'copd': 487,
         'osteoarthritis': 278,
         'other seasonal allergic rhinitis': 201,
         'congestive heart failure': 97,
         'type ii diabetes mellitus': 82,
         'coronary artery disease': 44,
         'hypercholesterolemia': 21,
         'osteoporosis': 18,
         'myocardial infarction': 16,
         'hypothyroidism': 15,
         'atrial fibrillation': 13,
         'gastroesophageal reflux disease ': 2,
         'cholelithiasis': 1})
```

[23]:

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

[23]:

```
        asthma  atrial fibrillation  osteoarthritis  myocardial infarction  \
b.freq     994                   14             231                     27   
w.freq    1011                   13             278                     16   

        hypercholesterolemia  congestive heart failure  copd  hypothyroidism  \
b.freq                    23                       117   409              12   
w.freq                    21                        97   487              15   

        other seasonal allergic rhinitis  constipation  osteoporosis  \
b.freq                               204             1            11   
w.freq                               201             0            18   
```

```
        type ii diabetes mellitus  hyperlipidemia  hypertension  \
b.freq                        124            1444          2514
w.freq                         82            1499          2438

        coronary artery disease  gastroesophageal reflux disease   \
b.freq                       49                                5
w.freq                       44                                2

        cholelithiasis
b.freq               0
w.freq               1
```

[24]:

```
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"
```

[25]:

```
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.BOLD}Condition: {k}{bcolors.ENDC}")
        print(f"    W   ^W")
        print(f"AA: {x1}")
        print(f"CA: {y1}")
        print(
            f'There {bcolors.OKGREEN}is a significant difference{bcolors.ENDC}␣
 ↪in the prevalence of the condition "{word}" between the groups with a␣
 ↪p-value of {bcolors.OKGREEN +"{:0.3f}".format(test.pvalue) + bcolors.ENDC}'
```

```python
        )
        print(f"")
if len(sig_results) == 0:
    print(
        f"{bcolors.BOLD}{bcolors.FAIL}No significant differences in any conditions between groups found{bcolors.ENDC}"
    )
```

```
Condition: osteoarthritis
    W   ^W
AA: [231, 5948]
CA: [278, 5945]
There is a significant difference in the prevalence of the condition
"osteoarthritis" between the groups with a p-value of 0.045

Condition: copd
    W   ^W
AA: [409, 5770]
CA: [487, 5736]
There is a significant difference in the prevalence of the condition
"copd" between the groups with a p-value of 0.010

Condition: type ii diabetes mellitus
    W   ^W
AA: [124, 6055]
CA: [82, 6141]
There is a significant difference in the prevalence of the condition
"type ii diabetes mellitus" between the groups with a p-value of 0.003
```