

# COVID Long Haulers

## Final Submission

### BMI 6016-001 Biomed Data Wrangling

Shad Morton, [shad.morton@utah.edu](mailto:shad.morton@utah.edu), u1328277  
Logan Greydanus, [u1324767@utah.edu](mailto:u1324767@utah.edu), u1324767  
John Arnn, [john.arnn@utah.edu](mailto:john.arnn@utah.edu), u1328576  
Kevin Yang, [kevin.yang@hsc.utah.edu](mailto:kevin.yang@hsc.utah.edu), u0630183

<https://github.com/jwarnn/BMI-6016-Group-Covid-Long-Haulers>

### The Wrangling Problem

The novelty of SARS-CoV-2 and the wide range of reported symptoms makes it difficult to predict the long-term complications that may follow the short-term effects. In the future it will be crucial to determine which patients are at risk of developing these complications and to understand the underlying mechanisms that trigger their development. This information will help identify at-risk populations, triaging patients and developing new care plans as variants are discovered. In this approach; population health, clinical and translational informaticians will need to work together to parse and apply these new data. Unfortunately the long-term complications and symptoms of SARS-CoV-2 are not well defined in the medical literature which makes identifying meaningful data from health records beyond the capabilities of this project. Instead we will use the medical records of patients who have had confirmed cases of SARS-CoV-2 to create a dataset to be used for a clustering analysis to explore what symptoms 14 days after that diagnosis are related to which demographics, previous diagnoses and medication use. We had to harmonize, integrate, and transform large datasets in order to accomplish our goal.

### **Data quality assessment (descriptive statistics) of the dataset(s). Use graphs were applicable**

The primary goal of the medications dataset was to create a binary array using the codes attached to the patient ids. So the assessment done on the medications dataset was to check for 'Unknown' values and NaN values:

```
df[df['code'].str.contains('Unknown')]
```

---

```
patient_id encounter_id code_system code start_date route brand strength derived_by_TriNetX
```

---

It appears there are no 'Unknown' code values.

```
print('any NaN values?', df.isnull().values.any())
```

```
any NaN values? True
```

There are NaN values that need to be dropped with df.dropna().

The patient csv contained seven rows of data for > 1.6 million unique patient ids.

```
In [7]: # read in the patient csv
df3 = pd.read_csv('patient.csv')
```

```
In [8]: # basic stats
df3.describe()
```

```
Out[8]:
```

	year_of_birth	age_at_death	postal_code
count	1.655079e+06	21412.000000	0.0
mean	1.974726e+03	66.624977	NaN
std	2.149369e+01	17.767804	NaN
min	1.929000e+03	0.000000	NaN
25%	1.957000e+03	58.000000	NaN
50%	1.974000e+03	69.000000	NaN
75%	1.991000e+03	80.000000	NaN
max	2.020000e+03	90.000000	NaN

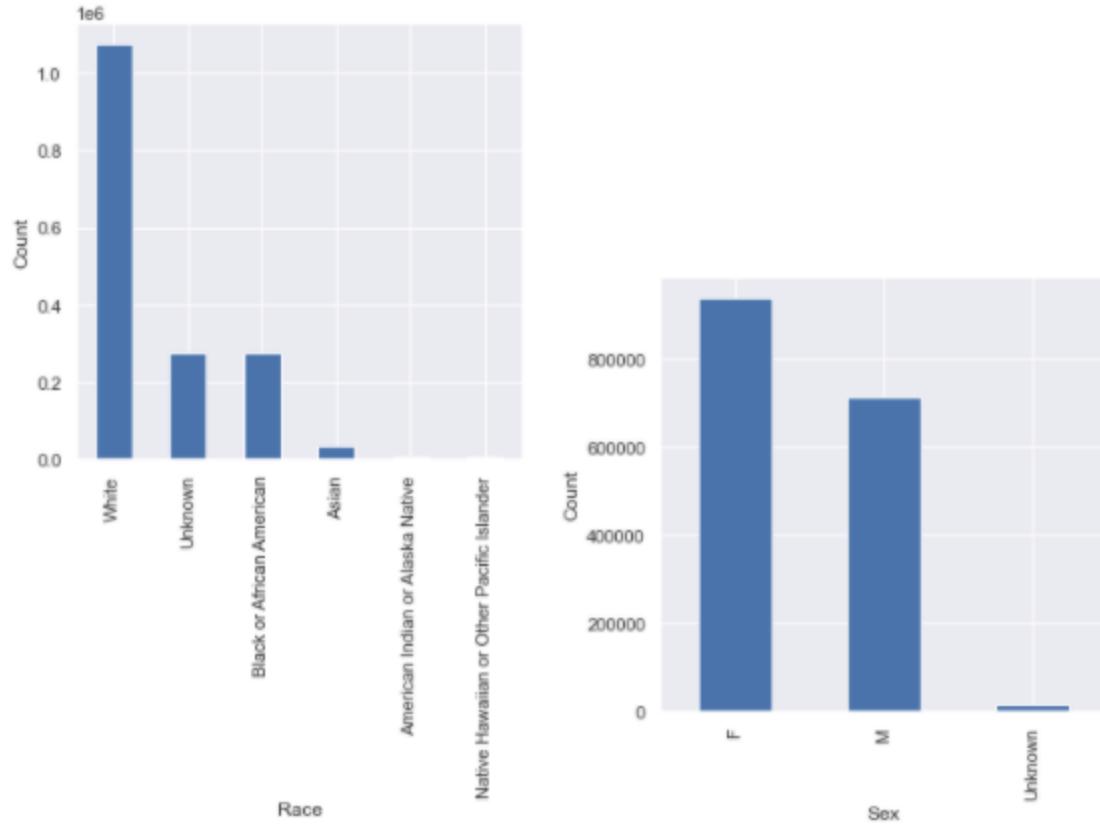
We see that we have over 1.6 million patients!

The mean age is (2021 - 1974 =) 47, with a standard deviation of 21 years.

The people who died, usually did at 66, but we have patients who have died as early as 58 or as late as 90.

Unfortunately, the postal code column is empty, so we wont be able to do any regional analysis :(

After dropping postal code, we had six rows of demographic information: id, sex, race, ethnicity, year of birth and age at death. Of these columns, only id is complete (no "unknown").



The diagnosis csv had 324,179,748 rows and six columns of data. Two of those columns, 'encounter\_id' and 'derived\_by\_TriNetX', did not provide any relevant information for the aims of the project and were dropped from the dataset. 'Patient\_id', 'code\_system', 'code' and 'date' are what remained. To access the data quality a few elements were explored including the agreement of between datasets common data elements like patient ids, and codes. These were in perfect agreement between one another. We also made sure the range of 'date' was logical for the dataset. 'Code\_system' had only two unique values, 'ICD-10-CM' and 'ICD-9-CM'; which could be found in the 'terminology.csv'. Next the presence of null values in the data set was performed with only two rows being found. These were dropped because the column 'code' was the missing value representing the most critical information in the dataset. Finally duplicate rows were dropped from this dataset using the pandas duplicate function where nearly 10% of the rows were dropped. Because this was a significant number a manual check of about ten of these rows was conducted which found they were duplicates across all columns. With these steps taken we found that the diagnosis per patient had a mean of 163.78, median of 41, minimum of 1, and a maximum of 69,238. We were also able to produce a list of the most common codes:

```

Out[54]: {'E78.5': ['Hyperlipidemia, unspecified'],
'E11.9': ['Type 2 diabetes mellitus without complications'],
'K21.9': ['Gastro-esophageal reflux disease without esophagitis'],
'F32.9': ['Major depressive disorder, single episode, unspecified'],
'Z79.899': ['Other long term (current) drug therapy'],
'I25.10': ['Atherosclerotic heart disease of native coronary artery without angina pectoris'],
'E03.9': ['Hypothyroidism, unspecified'],
'F41.9': ['Anxiety disorder, unspecified'],
'250.00': ['Diabetes mellitus without mention of complication, type II or unspecified type, not stated as uncontrolled'],
'G89.29': ['Other chronic pain'],
'Z00.00': ['Encounter for general adult medical examination without abnormal findings'],
'R05': ['Cough'],
'M54.5': ['Low back pain'],
'G47.33': ['Obstructive sleep apnea (adult) (pediatric)'],
'J45.909': ['Unspecified asthma, uncomplicated'],
'E66.9': ['Obesity, unspecified'],
'D64.9': ['Anemia, unspecified'],
'I48.91': ['Unspecified atrial fibrillation'],
'R07.9': ['Chest pain, unspecified'],
}

```

## Steps taken to wrangle (and integrate) the data.

The lab results csv was very large (over 630 million rows) and difficult to wrangle. The file was over 80 GB and contained eight rows; id, encounter id, code\_system, code, date, the number value of a lab result (if applicable) and a text value of a lab result (if applicable). It was not feasible to load it in as a pandas dataframe on my computer to run a complete data assessment, so it was chunked into a smaller dataframe containing only “positive” text results in the text value row. After that dataframe was made, it was filtered for 17 COVID specific LOINC codes to make the final dataset with 181,950 positive COVID test results.

A similar strategy was used to wrangle the diagnosis csv. This csv, containing over 300 million rows was chunked into a smaller dataframe by first filtering for five COVID specific diagnoses. After filtering, this dataframe had 340,563 COVID diagnoses. This dataframe was then appended to the filtered lab results dataframe and sorted by date (descending). The tail end of the dataset had some older dates, so we decided to drop all the entries with a COVID diagnosis or positive lab result before 2019.

	<b>patient_id</b>	<b>encounter_id</b>	<b>code_system</b>	<b>code</b>	<b>date</b>
<b>211377</b>	b3990d354fb8caf63d269d33978152cd6a456991	526ccc470b713bb98558beb1303724137e36edc0	ICD-10-CM	U07.1	20040331
<b>211392</b>	b3990d354fb8caf63d269d33978152cd6a456991	526ccc470b713bb98558beb1303724137e36edc0	ICD-10-CM	U07.1	20040331
<b>211375</b>	b3990d354fb8caf63d269d33978152cd6a456991	526ccc470b713bb98558beb1303724137e36edc0	ICD-10-CM	U07.1	20040331
<b>211395</b>	b3990d354fb8caf63d269d33978152cd6a456991	526ccc470b713bb98558beb1303724137e36edc0	ICD-10-CM	U07.1	20040331
<b>211391</b>	b3990d354fb8caf63d269d33978152cd6a456991	526ccc470b713bb98558beb1303724137e36edc0	ICD-10-CM	U07.1	20040331

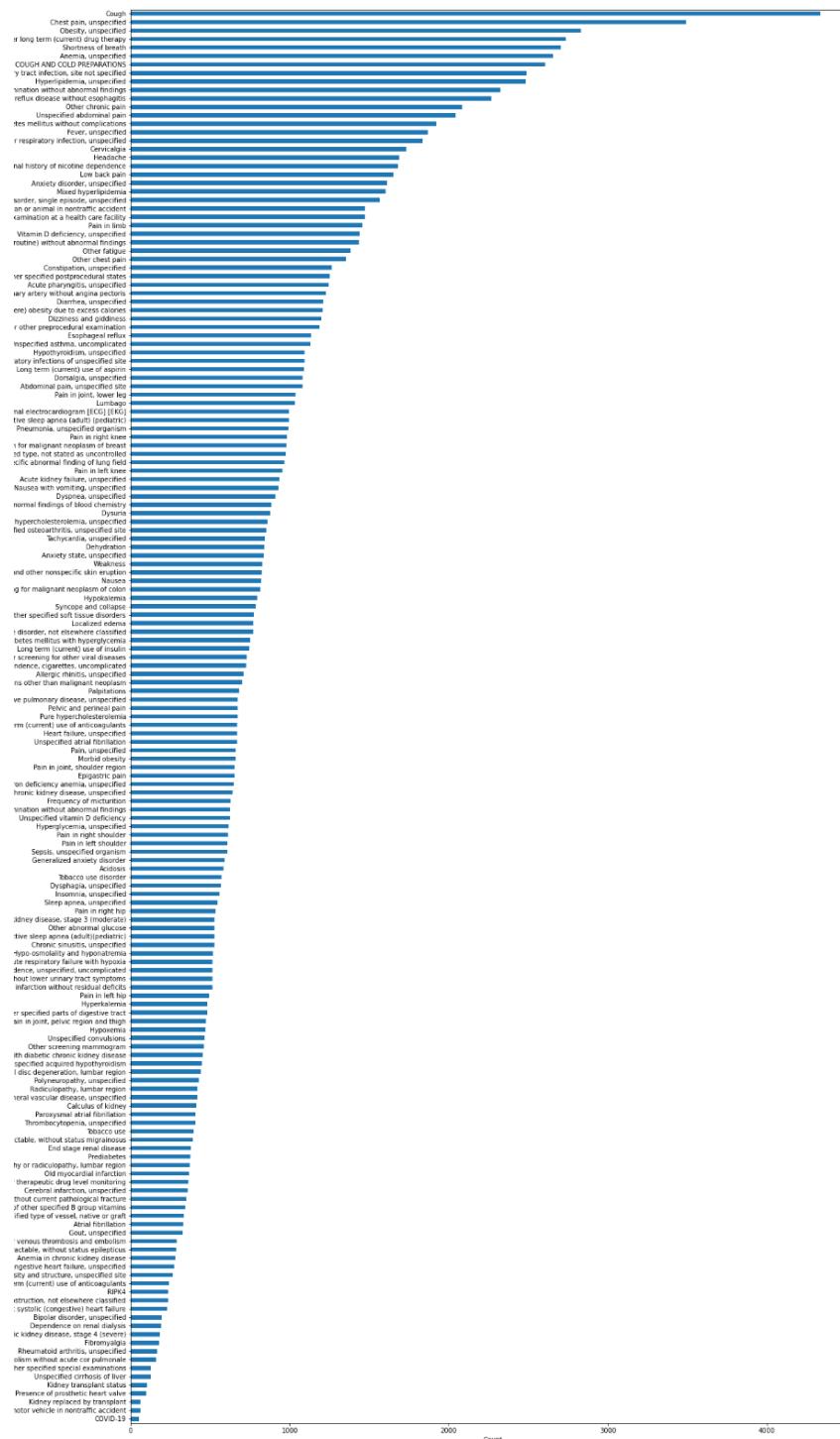
After these entries were dropped, we dropped duplicate patient ids keeping the only the first entry. This gave us a dataset with 189,205 patients with COVID which was merged to the patient csv to make the master file.

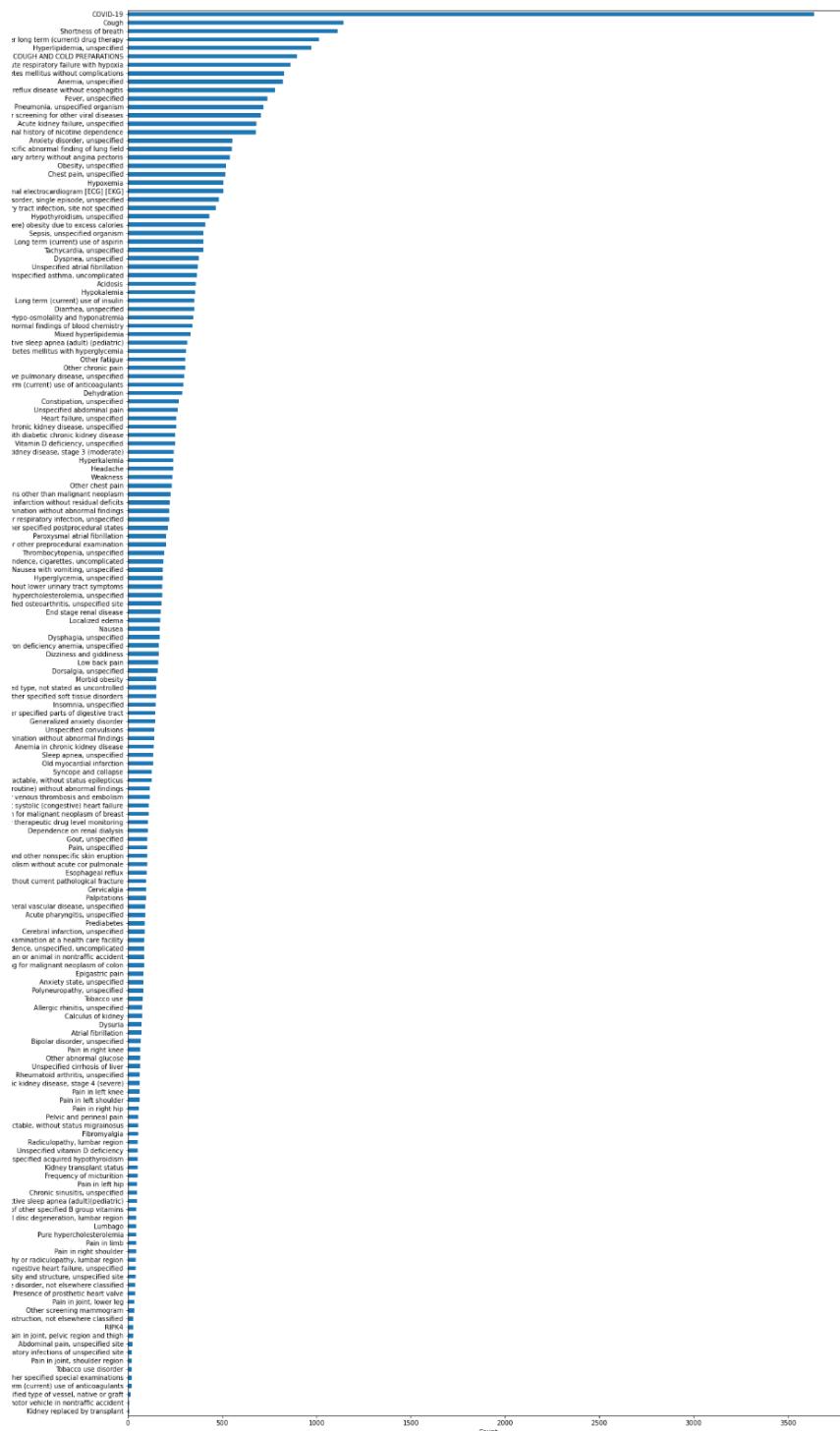
With the master file in hand, we were able to split the diagnosis and medication datasets by pre-COVID and (14 day) post-COVID datasets. For pre-COVID datasets we filtered on “date” according to a patient\_id, date tuple and then the top 200 diagnoses

codes. For the post-COVID datasets, we converted the integer date field to a date type using pandas, added 14 days, then reconverted to integer in concordance with the other data files. Again we filtered based on a patient\_id, 14\_date tuple and then the top 200 diagnoses. These are the dataframes that we turned into boolean array.

## **Repeat data quality assessment of the wrangled data**

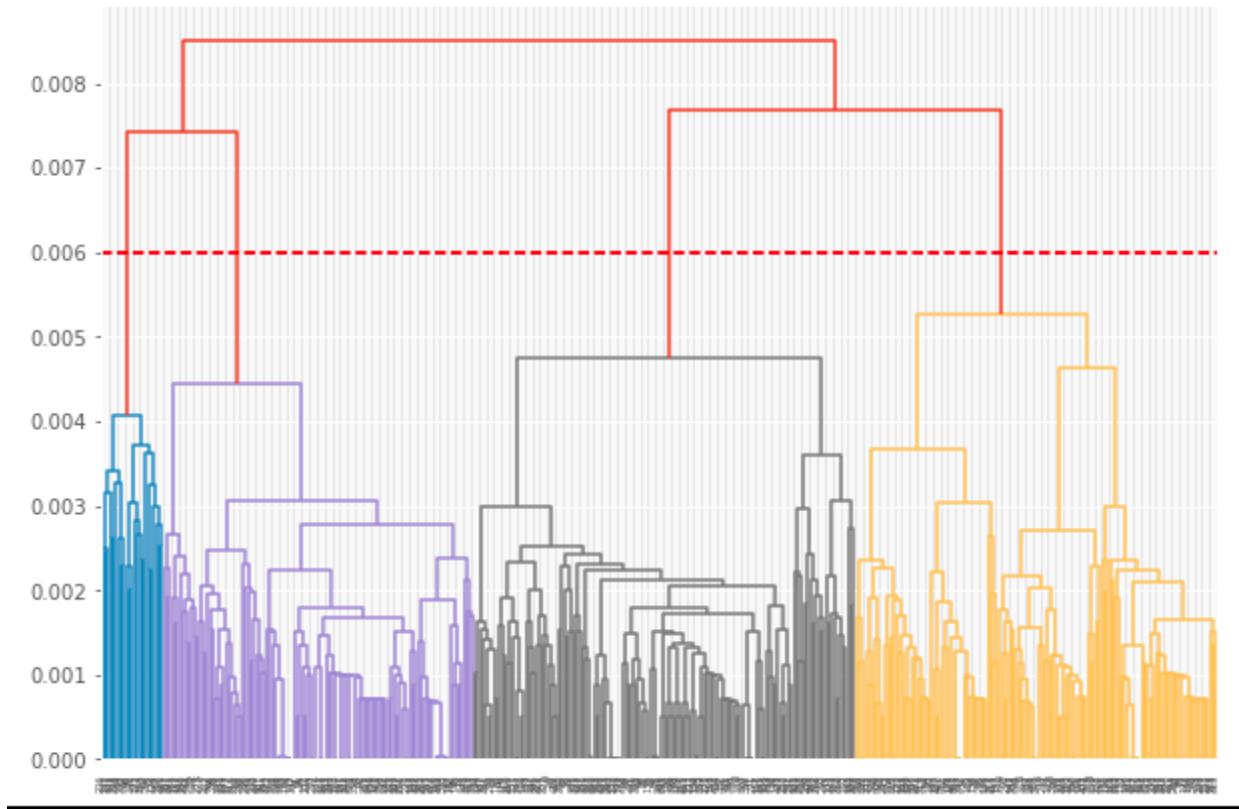
To assess the quality of the wrangled data, before we converted the diagnosis dataset into a boolean array we needed to discover if the post-COVID dataframe was different from the pre-COVID dataframe and whether or not it contained “long-haul COVID” diagnoses. To this end we were supplied a paper by a group of researchers in Sweden who conducted a study of long-haul COVID in groups of health care workers with mild cases of COVID-19. In their study, they reported; anosmia, ageusia, fatigue and dyspnea as the most common effects<sup>3</sup>. In our dataset we discovered fatigue and dyspnea in our post-COVID data set as well as many other interesting long-haul candidates.





## **Any evidence to show that the wrangled data is usable such early clustering results, values for surgical measures or descriptive statistics of pre and post covid diagnoses/medication**

In order to see if a clustering analysis was possible on the data set, a dendrogram plot was created in order to visualize clusters within the dataset. To begin, the csv file containing the boolean array for diagnosis codes along with patient demographics was read into a pandas dataframe. Certain categorical data columns were dropped and dummy data (i.e. columns with 0 or 1) were created for the “sex” and “race” columns. The data was normalized using the sklearn preprocessing library function “normalize”. The dendrogram was created using the “dendrogram” function from the scipy.cluster.hierarchy library.



The results of creating the dendrogram can be seen above. This shows that using the diagnosis codes and demographic data the patients can be separated into many groups. The largest vertical distance is often used in dendrograms to represent the largest amount of difference present between clusters. Using this method here, the patients would be separated into four clusters.

## Lessons Learned

The major challenge with this project was learning how to handle large datasets, these were anywhere from 50-128gb in size! We handled this by chunking our datasets into smaller files. For example, the medications dataset was chunked into 88 smaller files with each having  $10^7$  rows at most. For this project, python in the jupyter notebook was the primary tool but with how long it would take to filter a pandas dataframe, we tried to use a select statement in SQLite. However it ended up being roughly 10% slower. A major lesson we all learned was time and task management. This is the first time all of us had to manage large datasets before so even simpler tasks would take a while to run. And if we were to get too greedy, it would take hours to see the wrong results, so with task management, the code should be tested on the smallest amount possible (chunk of chunks).

## References

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