

**BUSS4933 Advanced Machine Learning for**

**Business Insights**

**(2022S2)**

**Term Project**

Due date: Saturday 12 October 2022

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Predictors of COVID-19 Pneumonia

In December 2019, the Coronavirus Disease 2019 (COVID-19) began its rapid spread worldwide, becoming the fifth documented pandemic throughout history (Moore, 2021). Despite many skepticisms, its asymptomatic and contagious incubation period allowed it to spread effectively in a series of surges (Achenbach, Cha, & Sellers, 2021; Maragakis, 2021). By the end of 2020, there were almost 2 million COVID-19 deaths reported, with an estimate of at least 3 million excess mortalities (World Health Organization, 2021).

Being a significantly pro-inflammatory condition, one of the common mechanisms that COVID-19 kills is through instigating pneumonia as a lung complication (Galiatsatos, 2022). In 2022, about 15% of people with COVID-19 develop serious complications, with 75% being pneumonia (Wiersinga, Rhodes, Cheng, Peacock, & Prescott, 2020; Cleveland Clinic, 2022).

Pneumonia is a respiratory infection that causes the air sacs in one or both lungs to fill with pus and other liquids (Johns Hopkins, n.d.). Although most people respond well to pneumonia treatment, it has the potential to be life-threatening. In particular, for people with impaired immune systems such as elderlies, children, or patients with pre-existing conditions, pneumonia tends to lead to complications (Johns Hopkins, n.d.).

Unlike the standard pneumonia, pneumonia caused by COVID-19 are often severe which are often associated with very high mortality. This is because, it uses the individuals’ immune system to spread, allowing it to last longer and cause widespread damage in multiple areas of the body (Cleveland Clinic, 2022). It also often impairs both lungs, limiting one’s ability to take in oxygen causing agonizing symptoms, such as shortness of breath and coughing, alongside lasting lung injuries that persists months after its recovery (Galiatsatos, 2022).

Unfortunately, a significant proportion of COVID-19 pneumonia patients are presented with a lack of certain symptoms. For example, a significant proportion of COVID-19 patients do not exhibit dyspnoea, despite it being a common predictor of regular pneumonia. This insidious nature of COVID-19 pneumonia worsened prognosis by increasing the difficulty of disease diagnosis, resulting in a sudden increase in need for high-intensity care (Goyal, et al., 2021). This is a problem as a substantial increase in severe cases can overwhelm less prepared hospitals, which doubles the mortality rate of COVID-19 pneumonia from 20% to 40% (Cleveland Clinic, 2022). To exacerbate the issue is the fact that resource-constrained environments are now common due to sudden surges of cases and poor economics. All of these factors associate COVID-19 pneumonia with severe disease development and high mortality (Mahendra, Nuchin, Kumar, Shreedhar, & Mahesh, 2021).

To further complicate the issue, patients without dyspnoea may instead present with other symptoms of hypoxia, such as severe fatigue, exertional fatigue and/or altered mental status (Goyal, et al., 2021). Ultimately, the great difficulty of diagnosis identifies a necessity in discerning symptoms specific to COVID-19 pneumonia to help with diagnosis and reduce its mortality rate.

Logically, to help with diagnosis, we need to identify explainable risk factors associated with COVID-19 pneumonia, especially latent ones. By identifying risk factors, healthcare workers can better predict and prevent the development of pneumonia by employing early interventions. Doing so is more effective than treating severe COVID-19 pneumonia after it arises and is advantageous in conserving resources. Being aware of more risk factors can also further inform the general public on how to keep themselves safe through the understanding of to adopt and avoid. For example, smoking is a known risk factor because it damages the lungs which increases the risk of COVID-19 pneumonia, hence not smoking the risk of COVID-19 pneumonia decreases (Cleveland Clinic, 2022). Accordingly, the differing and deadly nature of COVID-19 pneumonia stresses the importance of exploring risk factors to increase its diagnosis and reduce its mortality rate.

**1 Exploratory Data Analysis (EDA)**

*1.1 Dataset*

The dataset used was from the ‘COVID-19 Case Surveillance Restricted Use Detailed Data’. It is a database of patient-level data recorded in the United States (US) and uploaded on a monthly basis from April of 2020 till the current date November 2022. Despite an incomplete download the entire database, 158 of the files were downloaded and unzipped. The downloaded files contained 1,433,415,248 observations in total. The dataset contained at most 33 features which can be found in Appendix A, with some of the earlier files missing one or two features.

The incompleteness of the dataset is due to the ‘Unknown’, ‘Missing’, and ‘NA’ values which varies by jurisdiction and time period. The value “Unknown” represents when jurisdictions specify that the value is unknown, the value “Missing” represents when jurisdictions do not provide a value, and the value “NA” represents when the value is suppressed as part of privacy protections. For the sake of simplicity, these three values are put under one class ‘Unknown’ for all predictors.

As ‘pna\_ya’ is the target variable, the ‘Unknown’, ‘Missing’ and ‘NA’ values in this feature are removed as they do not provide any useful information. Since there is an ample amount of data, it was assumed that dropping these observations would not lead to any significant impact. Accordingly, out of 1,433,415,248 observations, 1,337,516,466 observations were dropped, which leaves 95,898,782 (6.69% data remaining).

Due to computational power and time, only 3 files with removed observations were used for modelling. The three files were:

1. COVID\_Cases\_Restricted\_Details\_03312021\_Part\_1.parquet
2. COVID\_Cases\_Restricted\_Details\_03312021\_Part\_2.parquet
3. COVID\_Cases\_Restricted\_Details\_03312021\_Part\_3.parquet

These three files represented the data collected during March of 2021. It is important to understand the context around this time in the US to better handle the dataset. For example, earlier in January 2021, vaccines were made available for first responders and individuals 65 and older (macmillan learning, 2022). This may indicate that whether the patient is a healthcare worker would not be a likely predictor of COVID-19 pneumonia as they are unlikely to get COVID-19 pneumonia due to being vaccinated.

These files were combined into one data frame containing 1515261. The dataset also contained all 33 features, however ‘race’ and ‘ethnicity’ was merged into ‘race\_ethnicity\_combined’ which resulted in 32 features. Further feature reduction was conducted by removing all 4 datetime data: ‘cdc\_report\_dt’, ‘cdc\_case\_earliest\_dt’, ‘onset\_dt’, and ‘pos\_spec\_dt’. This is because the features lack value as they only indicate the initial date, but not the duration.

A number of predictors was also removed due to target leakage, which included: hosp\_yn, death\_yn icu\_yn, mechvent\_yn. This is because the pattern within these predictors likely has a causal relationship with the target variable, however in the wrong direction. For this reason, these predictors do not provide healthcare worker with valuable information in predicting COVID-19 pneumonia.

*1.2 Pneumonia*

The target variable ('pna\_yn') is heavily imbalanced, with 'No' making up 93% of the training observations Figure 1. Accordingly, of 1,015,224 observations, only 6.7% of patients presented with pneumonia.

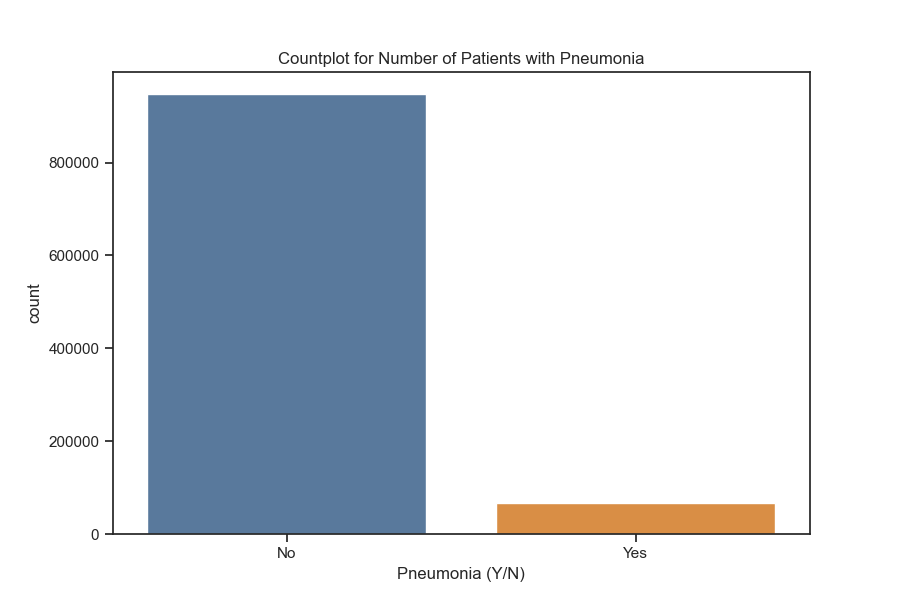


Figure : Pneumonia Countplot

The low proportion of patients with pneumonia was likely because the most prominent variant of COVID-19 in March 2021 was the Omicron. While Omicron was notoriously known to spread quickly by evading the immunity provided by prior infection and vaccination, they do not pose a greater risk of death and severe illness, such as pneumonia. Although it does not provide immunity, vaccinations are also known to reduce the risk of pneumonia (Kelly, 2022; Ito, Kitahara, Miwata, Okimoto, & Takafuta, 2022). Pneumonia was present in 78& unvaccinated patients but only 41% of fully vaccinated patients (Schiebler & Bluemke, 2022). Accordingly, since vaccinations became available to those most vulnerable, which are healthcare workers and elderlies, it makes sense that the rate of pneumonia was lower within the current dataset.

*1.3 Predictors*

Of the remaining 24 predictors, 19 was evaluated to be important based on exploratory data analysis (Appendix B). For each feature, a univariate and bivariate visualization was conducted, before a collective dependence measure was taken.

*1.4 Dependence measures (PhiK)*

To obtain an understanding of the degree of correlations between the variables, the correlation coefficient Phik was calculated. Similar to Cramer’s , the metric meant for two categorical variables and also based on Pearson’s chi-squared contingency test. It is able to capture non-linear dependencies and less sensitive to outliers compared to Cramer’s . The values of Phik are ranges between 0 and 1, where 0 denotes no correlation and 1 denotes a perfect correlation (Lewinson, 2021). Additionally, to validate the significance of the correlation, a measure of their statistical significance was taken using G-test with a p-value threshold of 0.05 (Baaka, Koopman, Snoek, & Klous, 2019).

For the current dataset, the calculated pair-wise Phik coefficients are shown in Figure 2, which were all determined to be statistically significant (p-value>0.05) as found in Appendix .

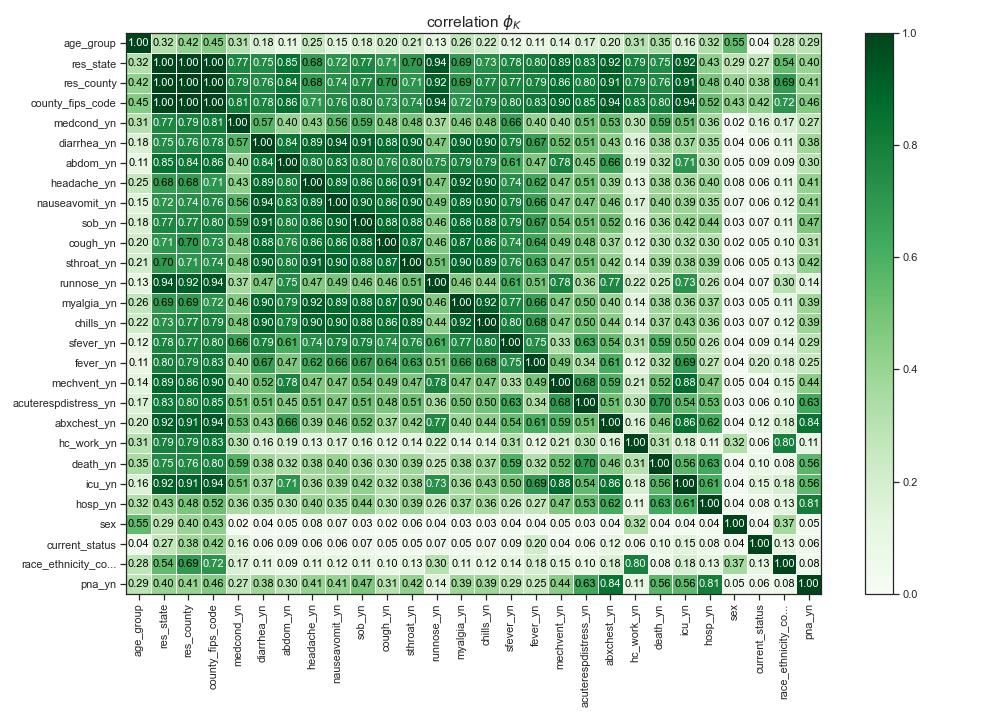


Figure : Heatmap of Phik pair-wise correlation matrix

There is a perfect correlation between ‘county\_fips\_code’, ‘res\_county’, and ‘res\_state’. Not only do they have a correlation of 1 with each other, but the exhibit very similar relationship with other features. Since county\_fips\_code exhibit very high cardinality (46309 classes) compared to res\_county (901 classes) and res\_state (56 classes), ‘county\_fips\_code’ was dropped to prevent multicollinearity and conserve computational time. On the other hand, ‘res\_state’ was dropped as it exhibit perfect collinearity with ‘res\_county’, however ‘res\_county’ was able to provide more refined geographical information. A more refined information provides greater predictive value and information of the ‘res\_state’ may be derived from ‘res\_county’, but not the other way around.

Although PhiK matrix demonstrates that there are a number of other features which exhibits low correlation with pna\_ya, they will be kept. These variables include ‘current\_status’, ‘sex’, ‘race\_ethnicity\_combined’, ‘runnose\_yn’, and ‘hc\_work\_yn’. This is in case they provide latent information and so will be removed later on depending on feature importance analysis.

**2 Feature engineering**

*2.1 ‘Unknown’ class*

To deal with all three variants of missing values, an ‘unknown’ class was created to denote missingness. This is because the ‘missingness’ can provide valuable information, if the values are not missing by random. Due to time constraint, it was assumed that all ‘Unknown’, ‘Missing’, and ‘NA’ values were missing not at random. Then they were merged into one big ‘Unknown’ class by replacing all 'Missing' and ‘NA’ values with ‘Unknown’.

*2.2 Categorical encoding*

The majority of features which exhibits the classes 'yes', 'no' and 'unknown’ were label encoded. The 'res\_county' feature was target encoded because it had a high number of classes. The 'age\_group' feature was manually encoded by taking the mean of each bins, with the exception of the '80+' bin which was converted into '85' for the sake of uniformity. Encoding methods such as one-hot encoding was avoided due to the high number of features, which will lead to a very large dataset. Target encoding was avoided so as to avoid overfitting. A summary of the encoding method used can be found in Appendix C.

*2.3 Feature scaling*

Feature scaling is important for the two models implemented logistic regression (LR) and Linear Support Vector Classifier (SVC). Since LR uses Gradient Descent during optimization, feature scaling is important because it speed up the convergence process. Additionally, the logistic regression algorithm tends to assume that features with greater magnitude are more relevant. Thus, scaling these features into the same range allows the model to truly evaluate the best features based on their predictive value, regardless of their relevance (Bhor, 2022).

SVC uses the distance between data to create a decision boundary. Accordingly, it is important to scale the features so that the mapping of the values are within the same range. This allows for the SVC to improve the classifer performance significantly (Tokuç, 2022).

Two main methods of feature scaling are standardization and normalization; however, standardization was chosen for the current task. Standardization shifts the distribution of each feature so that they have a mean of 0 and standard deviation of 1. Standardization was chosen because compared to normalization, it centers the data and tends to train more generalizable models. To scale the features, the transformation in Equation 1 was applied, where denotes an observation, is the mean, and is the standard deviation of the feature values (Tokuç, 2022).

*2.4 Train Test Split*

The dataset was split into a training set with the test set making up 33% of the entire dataset. There was no split for validation set as cross-validation (cv) was used for hyperparameter tuning.

**3 Methodology**

Two main algorithms were selected for the current dataset: Logistic Regression (LR) and Linear Support Vector Classifier (LinearSVC). These models were hyperparameter tuned and variants of these models were created based on further feature selection. The models were evaluated based on their f1-score.

*3.1 Evaluation metric*

The f1-score was chosen because…

*3.2 Logistic regression*

3.2.1 Definition

# 

A logistic regression is a supervised learning algorithm used in binary classification. It models the relationship between features to predict the probability the input belongs to the default output class (Brownlee, 2020).

Given the columns and rows in a set of training data , the relationships between features are modelled by Equation 2.

where represents the intercept and is the coefficients of features .

The output is transformed into a probability using the logistic (aka sigmoid) function in Equation …, where denotes the probability that the input belongs to the default class, 0.

To classify the output value of the sigmoid function, a probability threshold is set. Given a probability threshold of 0.5, if is greater than 0.5, the input will be classified as 0, otherwise 1.

Given, the it models a relationship to obtain the probability

Probability threshold

Using a measure of error, the model is optimized

<https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression>

3.2.2 Hyperparameter tuning

To enhance the performance of the logistic model, two hyperparameters model were tuned. The ‘penalty’ which determines its regularization method and its ‘solver’ which determines how the algorithm optimizes the problem. The two parameters were tuned using a randomized search method and stratified k-fold cross-validation where . Notably, a stratified k-fold cross validation was implemented due to the imbalanced nature of the dataset. This is so that the training and validation set exhibits the same imbalanced as the test data so that the validation f1-score returned will be similar to the test f1 score.

Given the two penalty options {‘l1’ and ‘elasticnet’} and two solver options {‘sag’ and ‘saga’}, ‘l1’ and ‘saga’ was evaluated to be the best hyperparameters. An ‘l1’ penalty means that a penalty term equal to the absolute value of the magnitude will be added, allowing it to limit the size of its coefficient. With the ‘l1’ penalty, the algorithm is also known as the lasso regression (Glen, n.d.). Whereas a ‘saga’ solver means that the model uses utilizes a variant of the stochastic average gradient method which is able to support the ‘l1’ penalty (Yahya, 2018). Accordingly, a hyperparameter tuning found that the best logistic regression for the current dataset implements a lasso penalty term and utilizes a variant of the stochastic gradient method for the problem optimization.

3.2.3 Models

Firstly, a benchmark LR model was created by training the model using the entire dataset with the best hyperparameters - this model is denoted as LR (all). Since this model exhibits target leakage a following LR model was trained using the reduced 19 features and denoted as LR (eda). To analyze the model its feature importance was plotted and its regularization path was graphed.

The importance of each feature was derived from its coefficient which can be found in Figure 3. This is because the magnitude of the coefficient demonstrates its contribution towards predicting the probabilistic output. By this logic, features with low coefficients may be removed as they do not contribute in predicting the final output.

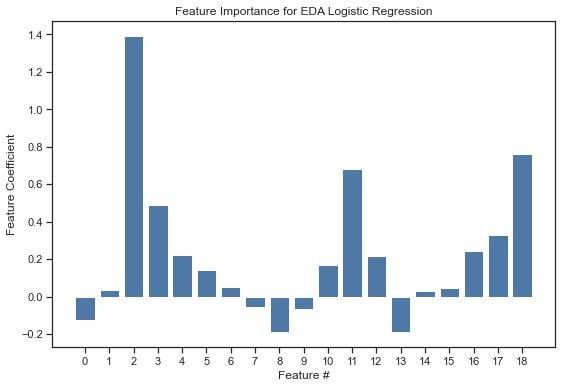
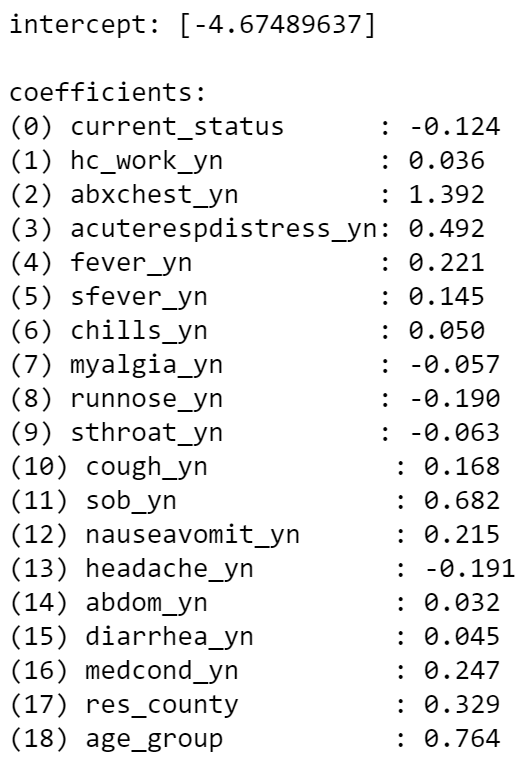
 

Figure : Feature importance of LR (eda)

Based on Figure 3, the feature importance of the model may be distinguished. Since the current report aims to identify crucial predictors to aid health-worker identify COVID-19 pneumonia, it is important to have a limited but robust number of features for health-care workers to remember. For this reason, a threshold of 0.100 was selected as the cutoff point for feature reduction based on feature importance. In the order of importance, the 5 most influential features include: ‘abxchest\_yn’, ‘age\_group’, ‘sob\_yn’, ‘acuterespdistress\_yn’, and ‘res\_county’. All 5 features have a coefficient greater than 0.300. The next following features are ‘medcond\_yn’, ‘fever\_yn’, ‘nauseavomit\_yn’, ‘cough\_yn’, ‘sfever\_yn’, and ‘chills\_yn’. In an attempt to reduce features, further exploration will be conducted by training a model using these 10 identified predictors.

The regularization path is a visualization of how the the lasso regularization term of the logistic regression behaves. Found in Figure 4, the 19 coefficients are plotted against the weight vector of the regularization term . is a sklearn hyperparameter that denotes the strength of the penalty term. For example, will lead to a sparser solution than , therefore a will result in less coefficients. Accordingly, from the left-hand side to right-hand side of the x-axis, the models are ordered from strongest regularized to least regularized (Gramfort, n.d.).

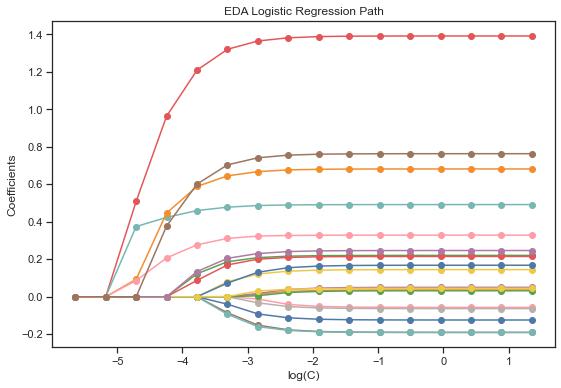


Figure : Regression path for LR (EDA)

Based on Figure 4, when is too small, the LR (eda) could not fit the coefficients to any features. However, when C is too high, too many unnecessary coefficients were fit into the model. Interestingly, at approximately before and after , the

Based on the regularization path of the LR (eda) model, there was a notable change in the number of predictors at approximately before and after . When , the highest number of features was 5, but the next growth in feature when resulted in the addition of 3 features simultaneously but at a relatively small magnitude. With relatively low coefficient it was determined that these features do not pose great importance. The following features added had even lower coefficient, emphasizing their lack of predictive value. To achieve the balance in the trade-off between complexity and interpretability, a was manually chosen. As further exploration, a model will also be created with 5 features chosen based on feature importance.

3.2.4 Further feature reduction

A further feature reduction was explored to obtain the most defining identifier for COVID-19 Pneumonia. Two models were explored based on conservative and non-conservative manual and naïve feature selection. For the non-conservative feature selection, 5 features were retained as per the regression path analysis. This model was denoted as LR (non-conservative). Its feature importance graph and coefficient may be found in Figure 5.

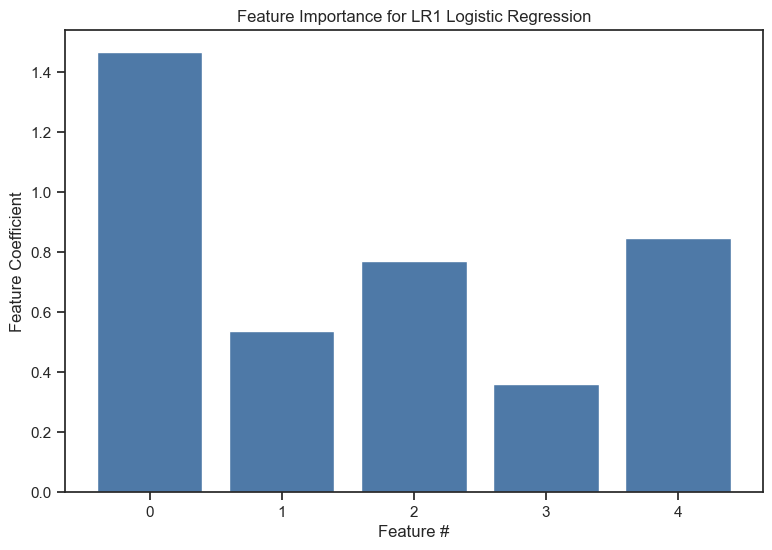
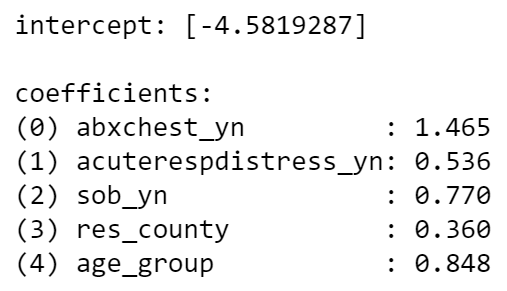
 

Figure : Feature importance and coefficients of LR (non-conservative) model

For the conservative feature selection, 10 features were retained. This is by setting a minimum threshold of 0.1 for coefficients. Accordingly, a feature was kept if its associated coefficient was greater than 0.1 ), otherwise it was removed. This model was denoted as LR (conservative). Its feature importance and coefficient may be found in Figure 6.

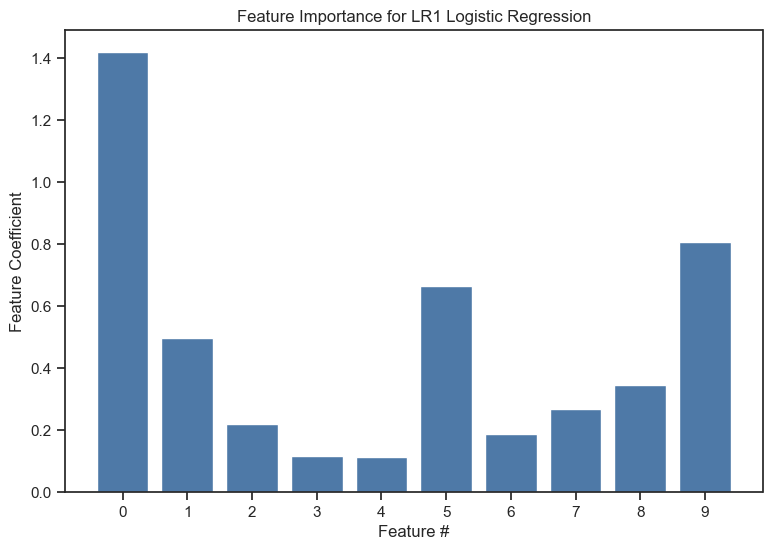
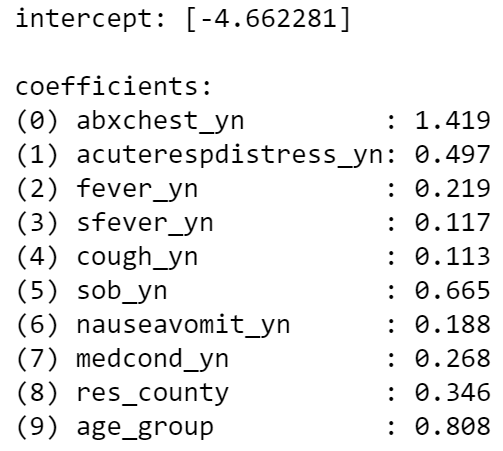
 

Figure : Feature importance and coefficients of LR (conservative) model

Model

*3.3 Linear Support Vector Classifier (SVC)*

3.3.1 Definition

3.3.2 Hyperparameter tuning

To obtain the best performing SVC model, the ‘penalty’ hyperparameter was tuned. Between ‘l1’ and ‘l2’ regularization, a grid search stratified 5-fold cross-validation found that an ‘l1’ penalty term provided a better f1-score. The use of ‘l1’ penalty term leads to sparse vector, meaning that it will indirectly conduct feature selection.

3.3.3 Model

3.3.4 Further feature reduction

**4 Results**

*4.1 Experiments*

|  |  |  |
| --- | --- | --- |
| **Model** | **F1 valid** | **F1 test** |
| LR (all) | 0.747 | 0.751 |
| LR (eda) | 0.711 | 0.716 |
| LR (non-conservative) | 0.770 | 0.704 |
| LR (conservative) | 0.709 | 0.713 |
| SVC (all) | 0.742 | 0.747 |
| SVC (eda) | 0.699 | 0.703 |
| SVC (model) | 0.698 | 0.702 |

Figure : Table of f1-scores of the different models

Evidently, models that were trained based on all features (all) resulted in better predictive performance. However, these models are not useful as they utilize predictors which will cause target leakage. Of the two models based on features selection derived from domain knowledge, visualization, and statistical parameters (eda), the LR was able to predict whether patients have COVID-19 pneumonia.

For both LR and SVC, a further feature reduction was conducted based on feature importance. For LR a non-conservative LR (non-conservative) and conservative approach was taken LR (conservative). While the non-conservative approach found a decrease in predictive power, the conservative approach returned relatively similar results as LR (eda). Due to the high cost in inaccurate predictions, it was determined that the LR (conservative) was better than the LR (non-conservative) model.

The further reduction based on feature importance (model) was conducted for the SVC model. After further feature reduction, the predictive performance of the SVC model did not change. Accordingly, between SVC (eda) and SVC (model), SVC (model) was determined to be better due to exhibiting a more conservative support vector as well as being more time efficient.

The best model was determined to be the LR (model2). This is because both model with all features exhibited target leakage and are not useful for the current aim. Between the two SVC, the SVC (model) was determined to be better due to its smaller pool of features and lower computational time. However, between LR (eda) and SVC (model), LR (eda) was determined to be better as it has greater predictive power which is important in the health setting. Accordingly, The best model was determined to be LR (eda).

*4.2 Best model*

*4.3 Further application*

Although, the non-conservative model did not return the best score, it is able to provide valuable information. With relatively similar predictive power, it was able to model the probability of COVID-19 pneumonia with a scarce number of features. Hence, healthcare workers can utilize these features on a daily basis to notice the onset of COVID-19 Pneumonia. These predictors include ‘res\_county’, ‘acuterespdistress\_yn’, ‘sob\_yn’, ‘age\_group’, and ‘abxchest\_yn’. Accordingly, notable predictors of COVID-19 pneumonia include: the patient’s county, whether they have acute respiratory distress syndrome, whether they have shortness of breath, the patient’s age, and whether they have an abnormal chest x-ray.

**5 Evaluation & Future work**

As mentioned, in the field of medicine, an inaccurate prediction has drastic consequences. For this reason, it is integral to further improve the performance of the model. There are a number of improvements possible for future work which includes feature transformation, treating missing values and outliers, and also using more training data (Ray, 2020).

The majority of predictors within the dataset are heavily imbalanced. However, the current project did not apply any techniques to create a more balanced dataset. For example, under-sampling of the abundant class or over-sampling of the minority class can be used to balance a new dataset. Accordingly, further feature engineering can be implemented to improve the model performance.

Similarly, further feature engineering can take place by handling the missing values. Due to the missing values, only approximately 7% of the dataset was used. This loss of data may have been unavoidable as these observation in particular were missing for the target feature. However, imputing missing values for the predictors may improve the performance of the model. For the current dataset in particular, ‘Unknown’ and ‘Missing’ may be imputed, it may be useful to keep the ‘NA’ values as a class as they represent classified information. This is because the ‘Unknown’ and ‘Missing’ values were missing at random and therefore calls for deletion or imputation, whilst ‘NA’ are not missing at random and so can be kept as an ‘NA’ class. Possible methods of handling categorical missing values include imputing it with the most frequent value – a crude method but timely method; otherwise by developing a model to predict missing values and imputing its prediction – a extensive but rewarding method. Hence, to improve model performance, it is recommended that future work attempts to impute ‘Unknown’ and ‘Missing’ values, whist maintaining the ‘NA’ class.

The current project takes on a very small proportion of this database, therefore it is possible to add more data in an attempt to increase the model’s predictive power. As previously mentioned, the ‘COVID-19 Case Surveillance Restricted Use Detailed Data’ database contains observations from April 2020 and continues to grow. That said, as the current world is recovering from COVID-19 both from vaccines and weaker variants existing, valuable information is more likely to be derived from data that was uploaded early on. This may also explain the moderate level of predictive power in the current model as the majority of patients by March 2021 no longer catches the more severe variants of COVID-19 which causes pneumonia. Hence, it is recommended that future work within the current field explore the data before January 2021, which is before the vaccines were rolled out.

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# Appendix A

## Features and their details

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Variable** | **Description** | **Source** | **Values** | **Type** |
| current\_status | Current status of the persons’ COVID-19 tests? | Case Report Form | Laboratory-confirmed case Probable case | String |
| cdc\_report\_dt | Date case was first reported to the CDC | Calculated | YYYY-MM-DD | Date |
| cdc\_case\_earliest\_dt | Date related to illness/ Date received by CDC | Calculated | YYYY-MM-DD | Date |
| sex | Sex | Case Report Form | Male Female Unknown Other Missing | String |
| age\_group | Age group | Calculated | 0 - 9 Years 10 - 19 Years 20 - 39 Years 40 - 49 Years 50 - 59 Years 60 - 69 Years 70 - 79 Years 80 + Years Missing NA | String |
| race | Race | Calculated | American Indian/Alaska Native Asian Black Multiple/Other Native Hawaiian/Other Pacific Islander White Unknown Missing NA | String |
| ethnicity | Ethnicity | Case Report Form | Hispanic Non-Hispanic Unknown Missing NA | String |
| county\_fips\_code | County FIPS Code | Calculated | NA if suppressed null if could not be matched | String |
| res\_county | County of residence | Case Report Form | NA if suppressed Missing if not available | String |
| res\_state | State of residence | Case Report Form | NA if suppressed Missing if not available | String |
| onset\_dt | Date of symptom onset | Case Report Form | YYYY-MM-DD | Date |
| pos\_spec\_dt | Date of first positive specimen collection | Case Report Form | YYYY-MM-DD | Date |
| hosp\_yn | Was the patient hospitalized? | Case Report Form | Yes No Unknown Missing | String |
| icu\_yn | Was the patient admitted to an intensive care unit (ICU)? | Case Report Form | Yes No Unknown Missing | String |
| death\_yn | Did the patient die as a result of this illness? | Case Report Form | Yes No Unknown Missing | String |
| hc\_work\_yn | Is the patient a health care worker in the United States? | Case Report Form | Yes No Unknown Missing | String |
| pna\_yn | Did the patient develop pneumonia? | Case Report Form | Yes No Unknown Missing | String |
| abxchest\_yn | Did the patient have an abnormal chest X-ray? | Case Report Form | Yes No Unknown Missing | String |
| acuterespdistress\_yn | Did the patient have acute respiratory distress syndrome? | Case Report Form | Yes No Unknown Missing | String |
| mechvent\_yn | Did the patient receive mechanical ventilation (MV)/intubation? | Case Report Form | Yes No Unknown Missing | String |
| fever\_yn | Fever >100.4F (38C) | Case Report Form | Yes No Unknown Missing | String |
| sfever\_yn | Subjective fever (felt feverish) | Case Report Form | Yes No Unknown Missing | String |
| chills\_yn | Chills | Case Report Form | Yes No Unknown Missing | String |
| myalgia\_yn | Muscle aches (myalgia) | Case Report Form | Yes No Unknown Missing | String |
| runnose\_yn | Runny nose (rhinorrhea) | Case Report Form | Yes No Unknown Missing | String |
| sthroat\_yn | Sore throat | Case Report Form | Yes No Unknown Missing | String |
| cough\_yn | Cough (new onset or worsening of chronic cough) | Case Report Form | Yes No Unknown Missing | String |
| sob\_yn | Shortness of breath (dyspnea) | Case Report Form | Yes No Unknown Missing | String |
| nauseavomit\_yn | Nausea or Vomiting | Case Report Form | Yes No Unknown Missing | String |
| headache\_yn | Headache | Case Report Form | Yes No Unknown Missing | String |
| abdom\_yn | Abdominal pain | Case Report Form | Yes No Unknown Missing | String |
| diarrhea\_yn | Diarrhea (≥3 loose/looser than normal stools/24hr period) | Case Report Form | Yes No Unknown Missing | String |
| medcond\_yn | Pre-existing medical conditions? | Case Report Form | Yes No Unknown Missing | String |

# Appendix B

## Feature Selection

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Features** | **ALL** | **EDA** | **SVC** | **LR non-con** | **LR con** |
| current\_status | keep | keep | drop | drop | drop |
| cdc\_report\_dt | drop | drop | drop | drop | drop |
| cdc\_case\_earliest\_dt | drop | drop | drop | drop | drop |
| sex | keep | drop | drop | drop | drop |
| age\_group | keep | keep | keep | keep | keep |
| race | keep | drop | drop | drop | drop |
| ethnicity | keep | drop | drop | drop | drop |
| county\_fips\_code | keep | drop | drop | drop | drop |
| res\_county | keep | keep | keep | keep | keep |
| res\_state | keep | drop | drop | drop | drop |
| onset\_dt | drop | drop | drop | drop | drop |
| pos\_spec\_dt | drop | drop | drop | drop | drop |
| hosp\_yn | drop | drop | drop | drop | drop |
| icu\_yn | drop | drop | drop | drop | drop |
| death\_yn | drop | drop | drop | drop | drop |
| hc\_work\_yn | keep | keep | drop | drop | drop |
| pna\_yn | target | target | target | target | target |
| abxchest\_yn | keep | keep | keep | keep | keep |
| acuterespdistress\_yn | keep | keep | keep | keep | keep |
| mechvent\_yn | drop | drop | drop | drop | drop |
| fever\_yn | keep | keep | keep | drop | keep |
| sfever\_yn | keep | keep | keep | drop | keep |
| chills\_yn | keep | keep | drop | drop | drop |
| myalgia\_yn | keep | keep | keep | drop | drop |
| runnose\_yn | keep | keep | keep | drop | drop |
| sthroat\_yn | keep | keep | keep | drop | drop |
| cough\_yn | keep | keep | keep | drop | keep |
| sob\_yn | keep | keep | keep | keep | keep |
| nauseavomit\_yn | keep | keep | keep | drop | keep |
| headache\_yn | keep | keep | keep | drop | drop |
| abdom\_yn | keep | keep | drop | drop | drop |
| diarrhea\_yn | keep | keep | drop | drop | drop |
| medcond\_yn | keep | keep | keep | drop | keep |
| **Number of features** | 24 | 19 | 14 | 5 | 10 |

# Appendix C

## Encoding Method

|  |  |
| --- | --- |
| **Predictors** | **Encoding Method** |
| pna\_ya | Binary encoding |
| current\_status | Label encoding |
| sex | Label encoding |
| age\_group | Manually binned |
| race\_ethnicity\_combined | Target encoding |
| county\_fips\_code | Target encoding |
| res\_county | Target encoding |
| res\_state | Target encoding |
| hosp\_yn | Label encoding |
| icu\_yn | Label encoding |
| death\_yn | Label encoding |
| hc\_work\_yn | Label encoding |
| abxchest\_yn | Label encoding |
| acuterespdistress\_yn | Label encoding |
| fever\_yn | Label encoding |
| sfever\_yn | Label encoding |
| chills\_yn | Label encoding |
| myalgia\_yn | Label encoding |
| runnose\_yn | Label encoding |
| sthroat\_yn | Label encoding |
| cough\_yn | Label encoding |
| sob\_yn | Label encoding |
| nauseavomit\_yn | Label encoding |
| headache\_yn | Label encoding |
| abdom\_yn | Label encoding |
| diarrhea\_yn | Label encoding |
| medcond\_yn | Label encoding |

# Appendix D

## Statistical Significance of Phik

