Abstract—The Covid-19 pandemic has been one of the most devastating events in recent history, claiming the lives of more than 5 million people worldwide. Even with the worldwide distribution of vaccines, there is an apparent need for affordable, reliable, and accessible screening techniques to serve parts of the World that do not have access to Western medicine. Artificial Intelligence can provide a solution utilizing cough sounds as a primary screening mode for COVID-19 diagnosis. This paper presents multiple models that have achieved relatively respectable performance on the largest evaluation dataset currently presented in academic literature. Through investigation of a self-supervised learning model (Area under the ROC curve, AUC = 0.807) and a convolutional neural network (CNN) model (AUC = 0.802), we observe the possibility of model bias with limited datasets. Moreover, we observe that performance increases with training data size, showing the need for the worldwide collection of data to help combat the Covid-19 pandemic with non-traditional means.

Index Terms—COVID-19, Cough, Self-supervised Learning, Support Vector Machine, Convolutional Neural Networks.

I. INTRODUCTION

To date, COVID-19 has claimed the lives of over 800,000 individuals in the United States and 5 million Worldwide [1]. The highly infectious nature of COVID-19 has filled up hospital beds in record numbers, surpassing hospital capacity and causing immense strain on healthcare systems Worldwide. While global vaccination efforts are underway, distribution efforts have been impeded in low and middle-income countries. Additionally, the emergence of new viral variants like the Omicron has decreased the effectiveness of current vaccines in the prevention of COVID-19 spread [2].

One of the main contributors to the spread of COVID-19 is that a proportion of infected people show mild or moderate symptoms while infectious [4]. There is a high demand for frequent, rapid, and affordable testing. To this date, reverse transcription-polymerase chain reaction (RT-PCR) tests in nasopharyngeal swabs are the gold standard for detecting COVID-19 in clinical practice due to their high sensitivity and specificity [5]. However, despite the reliability of RT-PCR tests, some issues have arisen during mass application. One such example is that these tests require costly reagents and tools that have prevented equal access globally. Furthermore, administering and processing the test poses a risk of possible infection, and the test results take hours to days to return. An alternative is an antigen detection test for COVID-19 such as the COVID-19 Ag Respi-Strip, a rapid immunochromatographic test for detecting SARS-CoV-2 antigen. This test has the ability to deliver results in as little as 15 minutes, a factor that is helpful in hospital diagnosis for the safety of its patients. However, the antigen test has shown low sensitivity, with studies showing that its sensitivity was as low as 30.2% [6], and there is often limited test supply during COVID-19 surges. To date, a rapid, accessible, and affordable testing method has not been deployed yet.

Emerging Artificial Intelligence (AI) technologies have shown the ability to create fast, affordable, and accessible solutions. There is increasing evidence that machine learning and deep learning methods can analyze cough sounds of infected patients and predict COVID-19 [7]. Multiple research groups have been gathering sound recordings for COVID-19 patients of all ages, in various settings, symptomatic and asymptomatic, and at different periods relative to symptom onset. These allow the AI algorithms to learn audio characteristics of COVID-19 illness in patients with various demographic and medical conditions. A potential, purely digital COVID-19 detection method would allow for a smartphone-based rapid, equitable COVID-19 test with minimal infection risk, economic burden, and supply chain issues - all helpful factors to control COVID-19 spread. Given the importance, there is an urgent need to explore and develop machine learning-based digital COVID-19 tests.
Studies reveal that cough samples can be used for diagnosing respiratory syndromes such as pneumonia, pulmonary diseases, and asthma [8] [9] [10]. Recently, researchers have explored the possibility of screening COVID-19 using cough signals. In [11], the authors have demonstrated that a binary machine learning classifier is sufficient to identify COVID-19 cough and breath signals from healthy individuals or asthmatic patients. In [12], a framework for AI speech processing that pre-screens cough to identify COVID by leveraging acoustic bio-marker as features. In this study, 96 cough samples are collected from users with bronchitis and 136 with pertussis in addition to the COVID positive and healthy cough samples. Moreover, this study uses three independent, parallel classifiers, namely, a deep transfer learning-based multi-class classifier (DTL-MC), a classical machine learning-based multi-class classifier (CML-MC), and a deep transfer learning-based binary class classifier (DTL-BC). These three independent classifiers are used due to the insufficient data available for learning. Lastly, handcrafted features like spectral centroid (SC), spectral roll-off (SR), zero-crossing rate (ZCR), MFCC, delta-delta MFCC can be used to train long short-term memory (LSTM) network models as shown in [13]. Classification on voice samples demonstrated the least accuracy among other acoustic features like cough and breath.

Mouawad et al. utilize various statistical measures to detect COVID-19 from cough and the sustained vowel sound ‘ah’ [14]. Best recurrence structures were extracted using variable Markov Oracle as a pre-processing stage. The DiCOVA challenge was initiated to encourage researchers in COVID-19 diagnosis using acoustics [15]. Among the two datasets used in the DiCOVA challenge, one focuses only on cough sounds, and the other contains a collection of audio recordings, including counting numbers, phonation of sustained vowels, and breath. 11 most common symptoms combined with an established feature set of 384 features, obtained by applying 12 functions on the 16 frame-level descriptors and the respective delta coefficients, are classified using support vector machine (SVM) with a linear kernel in [16]. In the first experiment, feature level fusion is implemented by concatenating the audio and the symptom features into a single matrix. In the second experiment, decision level fusion is explored by finding the maximum probability among two models trained independently, which is reported to yield superior performance.

In this section of our study, we explain the resource we acquired along with a description of the steps taken to extract information from the cough samples before they were handled by our model development team. Afterward, we explore the techniques that were used to train each model.

A. Dataset

Multiple publicly available datasets were combined and utilized to ensure minimal bias during model training. Among the crowdsourced data that were utilized were COUGHVID [21] and Coswara [22] datasets. As a publicly-available dataset of global cough audio recordings, COUGHVID is one of the largest COVID-19 related cough datasets. COUGHVID includes a total of 20,072 cough recordings labeled as positive COVID-19, symptomatic COVID-19 negative, and asymptomatic COVID-19 negative, along with other clinical information and metadata [21]. The dataset contains samples from a wide array of ages, genders, pre-existing respiratory conditions, and geographic locations - all of which are useful data to consider when training an unbiased deep learning model. Similarly, the publicly available Coswara dataset was crowdsourced from participants around the globe utilizing a smartphone-based data collection platform [22]. Virufy processed the Coswara dataset and labeled over 2000 coughs resulting in the diverse demographics of samples, with 1839 samples as COVID-19 negative (“healthy”) and 411 samples as COVID-19 positive (“infected”). Furthermore, to increase the usefulness of AI systems like ours in hospital settings, we sought to train our model on clinically gathered datasets. Subsequently, we utilized the IATOS dataset, which is a publicly available dataset gathered by the city government of Buenos Aires, Argentina, using WhatsApp chatbots. This validated dataset includes 2196 positive and 2199 negative patients in 11 hospital facilities where RT-PCR studies were carried out on patients suspected of COVID and 14 out-of-hospital isolation units for patients with confirmed COVID mild cases [23].
## Dataset and Performance of State-of-the-art Algorithms

| Reference | Model | No. of Samples | Metric Reported | Dataset Availability |
|-----------|-------|----------------|-----------------|----------------------|
| [11]      | PCA reduced handcrafted & VG-Gish features with binary classifier | 141/298 | AUC: 80 | On-request |
| [12]      | MFCC with one Poisson biomarker layer and 3 pre-trained ResNet50 in parallel | 2660/2660 | Sensitivity: 98.5, Specificity: 94.2, AUC: 97 | Public |
| [13]      | Handcrafted features like SC, SR, ZCR, MFCC and delta-delta are classified using LSTM | 60/180 | F1-score: 97.9, AUC: 97.4, Accuracy: 97 | Private |
| [14]      | MFCC with repetition structure classified using XGBoost | 32/1895 | Accuracy: 97, AUC: 84 | Private |
| [15]      | MFCC, Delta and Delta-delta coefficients were used as features to train LR, MLP and Random Forest (RF) classifiers | 62/380 | LR-AUC: 66.95, MLP-AUC: 68.54, RF-AUC: 70.69 | Public |
| [16]      | 11 Covid related symptoms with 384 features obtained from the voice samples are classified using SVM and decision-level fusion | 326/502 | Sensitivity: 68, Specificity: 82, AUC: 79, Accuracy: 79 | Private |
| [17]      | MFCC, MFCC velocity and acceleration along with log frame energies, ZCR and kurtosis are used as features with ResNet50 | 110/1105 | AUC: 98, Accuracy: 95.33, Specificity: 98, Sensitivity: 93 | Public |
| [18]      | Intrinsic mode functions using EMD together with DWT features, ReliefF feature selection and SVM | 595/592 | Specificity: 97.3, Accuracy: 98.4, F1-score: 98.6 | Public (Virufy) |
| [19]      | Wavelet scattering features with Boosting classifier | 84/1019 | Accuracy: 88.52, Sensitivity: 87.19, Specificity: 89.82 | Private |
| [20]      | YAMNet with TFR analysis | 346/346 | Accuracy: 83.67, AUC: 93.56, Sensitivity: 89.58, Specificity: 71.58 | Public |

In addition to the aforementioned datasets, we also gathered and utilized our own crowdsourced and clinical datasets. Virufy’s crowdsourced dataset was collected using our study app (https://virufy.org/study) which requests users to input demographic information, such as age, gender, and comorbidities, along with their PCR test results. This app is publicly advertised on our website and as well as through press releases via Forbes, Yahoo, and various media outlets in South America and India. Additionally, we took sufficient measures to protect patient’s privacy with our informed consent forms and privacy policy (https://virufy.org/privacy_policy/). For Virufy’s clinical dataset, in recognizing that the majority of identified COVID-19 positive patients present at clinics for testing, we developed a protocol for data collection at clinics. After extensive ethical review and scientific oversight, we achieved IRB approval for our data collection method. In this method, patients presenting for COVID tests are first requested to input demographic information, such as age, gender, and comorbidities, into our app (https://virufy.org/study). After doing so, they are requested to wear a surgical or cloth mask and cough intentionally into the smartphone. Finally, when test results are available, they are reported in the app and linked to the patient’s cough. This protocol increases the likelihood that our data quality is high and clinically valid due to oversight by hospital staff and the IRB committee. This oversight also helps to establish acceptance for use in scientific research and clinical validation studies. Figure 1 shows the labeled data size for training, validation, and test sets as well as the unlabeled data size that is used during unsupervised learning.

### B. Audio Preprocessing

To provide readily usable data for model development, the cough audio data goes through two main stages: standardization and preprocessing. Data standardization repackages the raw data including, the data labels, naming conventions, and file types according to Virufy’s internal Common Data Format (CDF). The preprocessing stage takes the standardized data to filter and prepare usable samples by detecting background...
noise and removing any inadequate data, such as samples with no coughs detected from it. The initial standardization and preprocessing scripts were in Colab notebooks and were run manually and separately tested for each dataset source. To make this more streamlined, we moved most of the code to one centralized GitHub repository (https://github.com/virufy). We automated much of the data processing pipeline and its corresponding testing, in addition to making improvements to cough detection and computation time.

1) Standardization: The dataset standardization was originally performed through individual Colab notebooks by data source; for example, FluSense data was processed separately from Coughvid data. Colab notebooks may require someone to manually run the preprocessing notebook, authenticate access to AWS S3 to upload the standardized data and check that the program finished running. This placed a significant burden on model developers, and the underlying structure made it difficult to keep track of what changes were made to which notebook. To provide a uniform, centralized infrastructure for standardization, we moved many of the notebooks to one Github repository and wrote Python scripts that automated the standardization including the authentication and upload. The repository provided an organized structure that allows us to make any additional changes transparently.

2) Preprocessing: Given that audio files from different datasets can have different numbers of audio channels and sampling rates, the audio files are first converted to mono and resampled at a 16 kHz sampling rate. A series of checks are applied to the standardized audio to remove low-quality audio files. The following checks are conducted:

a) Volume Detection: The volume of the audio file needs to be sufficient as it would be difficult to extract meaningful data even if amplification is used. The maximum amplitude of the audio file is calculated to detect the volume of the audio file.

b) Clipping Detection: Clipping indicates that some samples in the audio file are missing as the amplitude of the samples was truncated. The ratio of clipping in the audio file is calculated by analyzing peaks and their flatness.

c) Cough Detection: A pre-trained CNN model based on ResNet-18 architecture provided in [24] is used to determine if the audio file contains a cough. The CNN model outputs a probability of whether a cough was detected in the audio file.

d) Cough Segmentation: The regions that contain coughs in the audio file are determined through the segmentation process described in [25]. Unlike the other checks that are conducted, the cough segmentation algorithm uses audio files that are converted to mono and resampled at 44.1 kHz as inputs. The segmentation algorithm first removes background noise through a combination of low pass and high pass filters and resamples the filtered audio with a 4.41 kHz sampling rate.

e) Background Noise Detection: Loud background noise can obscure the audio characteristics of the signal in interest. To evaluate the loudness of the background noise in the audio file, the ratio of the max power of cough segments and non-cough segments is calculated. The cough segments and non-cough segments are determined in the cough segmentation check.

The outputs from the aforementioned checks are used as thresholds to determine low-quality audio files. Audio files that do not meet the thresholds are removed and are not used in subsequent steps, such as feature extraction, model training, and inference.

C. Support Vector Machine

One of the effective supervised learning methods in machine learning is support vector machine (SVM) [26]. The classes are separated from each other by a hyperplane passing through the closer elements. SVMs perform well when the data is linearly separable. However, kernel functions can be used to non-linearly separate the data when it is not linearly separable. In our experiments, we have utilized the radial basis function for the SVM kernel. To map the SVM outputs to probabilities within the [0, 1] range, the SVM outputs are fed into logistic regression. Platt Scaling is used to transform the SVM output to probability values [27].

Short-time fourier transform (STFT) and mel-frequency cepstral coefficients (MFCC) [28] have been used by several researchers for classifying the Covid-19 cough or voice samples [12] [13] [14]. The handcrafted features such as spectral centroid, spectral roll-off, root mean square, Mel-frequency cepstral coefficients (MFCC), delta-MFCC, and double delta MFCC are used for classification using the support vector machine (SVM). Mean, standard deviation, maximum and minimum of the above-mentioned features are computed with time and are then normalized before being used by the SVM.

1) Spectral Centroid: Spectral centroid (SC) measures the change in frequency and phase content over time and it defines the shape of the magnitude spectrogram of STFT by determining its center of gravity from the normalized frame [29].

2) Spectral Roll-off: Spectral roll-off (SR) measures the skewness of the spectrogram by determining the central frequency of the spectrogram bin at which 25% and 75% of the magnitude are concentrated [30].

3) Root Mean Square of the Spectrogram: The loudness of the signal can be determined using the root mean square (RMS) of the spectrogram. Lower RMS values are a result of high signal energy in a block of the spectrogram [31].
4) **Mel-frequency Cepstral Coefficients:** The fast Fourier transform (FFT) bins from the log-amplitude of the magnitude spectrum are grouped and smoothed according to the Mel-scale. Finally, discrete cosine transform is applied to decorrelate the feature vector. It is found that 13 MFCCs are sufficient to represent speech, voice, or cough samples \[^{32}\]. MFCCs are given by

\[
C(m) = \sum_{n=1}^{N} \log Y(n) \cos \left( \frac{n\pi}{M} \left( m - \frac{1}{2} \right) \right)
\]

when \( m \) denotes the index of the MFCC and \( Y(n) \) denotes the output of the \( n \)-channel of the filter bank.

5) **\( \Delta \) and \( \Delta^2 \) MFCC:** The first-order derivative of MFCC is given by \[^{33}\]

\[
D[n] = C[n + r] - C[n - r]
\]

where \( r \) generally takes 2 or 3 as a value. \( \Delta^2 \) MFCC is obtained by determining the derivative of the subsequent delta cepstral features.

### D. Self-Supervised Learning with Transformers

In our work, we also used the Self Supervised Learning (SSL) method with the unlabeled data to pre-train the network and we added labeled data to the pretraining dataset to learn better representations. In addition, we utilized an auxiliary task of predicting masked input while reducing the reconstruction loss. To the best of our knowledge, the work that is closest to our approach is that of Xue et al. \[^{34}\]. In contrast, \[^{34}\] used masking to prevent overfitting and used contrastive loss. Both approaches employ popular transformer architectures, but we used the spectrogram image as input to the transformer network and masked the input spectrogram both in the time and frequency domain. In contrast, Xue et al. \[^{34}\] used MFCC and applied masking in the time domain only. Our work used the s3prl \[^{35}\] library for pretraining the upstream network and training the downstream network. More specifically, we have adapted upstream TERA \[^{36}\] and modified downstream Speaker Classification parts of the library for our Covid-19 classification task from audio samples. We did not employ any pre-trained network weights. Both upstream and downstream models are trained from scratch by using the training set described in Figure \[^{1}\].

1) **Architecture:** Our model uses the transformer encoder architecture to extract representations from cough audio signals. The transformer encoder network has three layers, each with a hidden layer size of 768, 12 attention heads, and a feed-forward network of 3072. Transformer encoder layers learn representation by masked signal prediction task as shown in Figure \[^{2}\]. The masked signal prediction task could be described as follows. The input cough audio is transformed to a spectrogram image and then randomly masked in frequency and time domain as described in \[^{11}\]–\[^{12}\]. This masked spectrogram image is fed into the transformer encoder layers. Transformer encoder layers learn representations while the prediction network following the transformer encoder layers tries to reconstruct the original spectrogram of the cough audio. The prediction network consists of 2 feed-forward layers with a hidden size of 768. The reconstruction loss is backpropagated through the prediction network and transformer encoder layers. This process is also called upstream training. Once upstream training is complete, the prediction network is removed, the upstream model is frozen, and representations from the transformer encoder are fed into the downstream model. The upstream model is based on the TERA \[^{36}\] implementation of the s3prl \[^{35}\] library.

The downstream model consists of three linear layers followed by normalization and non-linear activation layers, a mean pooling layer, and a classification layer. The first linear layer converts the hidden size 768 of encoder output to 512. The following two linear layers both have size 512. Next, the mean pooling layer calculates the mean of the representation across the time axis, ending up with a 512-dimensional vector. Finally, the classification layer uses a 512-dimensional vector to classify cough audio as either COVID or not COVID. The downstream model training is done by backpropagating the classification error through the downstream model. The downstream model is adapted and modified from the Speaker Classification task of the s3prl \[^{35}\] library.

2) **Input:** Virify preprocessing library detects cough boundaries, and cough boundary metadata is given to the model alongside the input audio. The audio signal is then converted to cough-only audio by removing the silent parts in the audio signal. The cough-only audio signal is then converted into a spectrogram image using librosa \[^{37}\]. Short-Time Fourier Transform (STFT) function with \( n_{freq}=2048 \), \( \text{win}_\text{length}=640 \), and \( \text{hop}_\text{length}=320 \) at 16KHz audio sample rate. The logarithm of the spectrogram is finally taken. With these values of STFT function, each 40 ms of the audio signal is converted into 1025 frequency bins with a shift of 20 ms along the time axis. The spectrogram time axis varies depending on the input audio length. This variation is handled by first padding the audio signal with zeros for batch processing and then masking the input for later stages of input processing.

During upstream training, the log spectrogram is masked both in time and frequency bands before sending it to the transformer encoder. The amount of mask in the time domain is set as 0.15, while the maximum amount of masked frequency bands is 0.20. Additionally, 0.10 of time, a Gaussian noise of mean 0 and variance 0.2 is added to the spectrogram image.

Masking is not applied to log spectrogram during downstream training. The log spectrogram is input to the frozen upstream model, and the transformer encoder outputs the input representation. This representation is fed into the downstream model.

3) **Upstream Training:** During upstream training, an auxiliary task of spectrogram prediction from masked input spectrogram is used to learn the representation of the input. This task enables self-supervised learning using the unlabeled data in addition to labeled data. As a result, the transformer encoder can learn better representations for cough audio by using more data.
We trained the upstream model using ≈13K unlabeled and ≈10K labeled cough audio samples (see Figure 1) using a batch size of 64, with a maximum learning rate of 1.e-4 over 400K steps. The learning rate warms up from zero to a maximum value over the first 28K steps and decays linearly to zero afterward. We used MSE as a loss function during reconstruction and the AdamW optimizer [38] to update the upstream model parameters.

4) Downstream Training: Once upstream model training is complete, we freeze the upstream model parameters at the end of the 400K steps and start with downstream model training. During downstream training, we only use labeled data. We use the same ≈10K labeled data used during upstream training. We set batch size as 8, learning rate as 1.e-4, and used AdamW optimizer. Due to the imbalance in positive and negative classes, we used an upsampling strategy for positive classes with a ratio of 5:1. Compared to upstream, downstream training takes much fewer steps to train. We set the steps as 6K with an initial 1K step of warming up. After every 300 training steps, we evaluated the network with ≈2600 validation samples. We picked the downstream parameters that give the maximum AUC. We observed that downstream training converges after 3-4 epochs.

E. Convolution Neural Network

This model is a continuation of the work presented by Rasmussen et al (2021) at the Applied Machine Learning and Data Analytics conference at the end of 2021. This manuscript is currently in preparation for submission to a peer-reviewed journal [39]. This model was inspired by modern convolutional networks with a few key differences. First, there are no Batch Normalization (BN) layers. Generally, BN is used in residual networks (ResNets) for object classification and detection from RGB images. We have not found BN effective when we are working with monochrome sonographs. The second difference is that this architecture does not use skip connections. Traditional ResNets use skip connections due to extreme depth, and skip connections help to alleviate the vanishing gradient problem. This architecture does not use skip connections since it is shallow compared to modern ResNets. Minor modifications have been made to the model compared to what will be published in the conference paper. The differences are how the sonographs have been created and the extension of the CNN’s repeated layers, along with a global average pooling layer instead of flattening the features before being passed to the dense layers.

1) Balancing the Dataset: Before creating the sonographs, a direct 4:1 ratio of up-sampling of all positives from each training dataset is performed. This up-sampling allowed the combination of the datasets to be approximately balanced regarding the ratio of positives to negatives. After up-sampling all positives from each dataset, all samples, including the negatives, were randomly augmented using the library “Audiomentions” [40]. The augments that were performed include shifting the audio time-wise and adding a Gaussian single-to-noise ratio. The values used for the “Shift” function were: a min fraction of -.5, a max fraction of .5, and a p-value of 1. These values ensured that all of the new samples
created were shifted randomly time-wise and guaranteed all of the new samples were augmented. The values used for the “AddGaussianNoise” function were: a min_SNR of .25, a max_SNR of .9, and a p-value of .5. This step increased the likelihood that approximately half of all the new samples created had a Gaussian signal-to-noise ratio added to them in between the specified interval. These steps created a resulting training set that had one set of normal negatives, one set of augmented negatives, four sets of normal positives, and four sets of augmented positives.

2) Feature Extraction: For the creation of each sonograph from the samples described above, the library Librosa was used [41]. Once the audio was loaded with the library, the audio was condensed using the cough segments that were extracted by the pre-processing step described in Section 3.1 of this paper. Afterward, regardless of how many seconds of audio was extracted by the cough segmenter, all samples were fit into an approximate 4 second window. If there were less than 4-seconds of audio extracted per sample, zeros were padded at the end of the audio. If more than 4 seconds were extracted per sample, the audio was cut off. This previous step allowed all sonographs created to have a standard size and prevented the need to resize the sonographs, which dilates it and negatively affects the data quality. Once all samples were put into a standardized data array, augmentations described above were performed and Librosa extracted the MFCC features of the audio. Sixty-four MFCCs were used, along with a hop length of 256 and an n_fft window size of 512. These values were used as opposed to the default values because they allowed us to “zoom in” on the temporal features of the audio as opposed to concentrating on the frequency resolution of the sonograph. The resulting sonograph was a 64 by 256-pixel MFCC representation of the four-second condensed audio.

3) Architecture: Our study initially passed the input described above to a convolution layer with a stride value of 1 by 1, 32 filters, and a dimension of 7 by 7 to look for the most general features. Next, this output was passed to another convolution layer with a stride value of 1 by 1, 64 filters, and 5 \times 5 dimension, to look for slightly less general features with roughly 32-fold the number of nodes. Afterward, the previous layer’s output was passed to a 2 by 2 max-pooling layer with a stride of 2 by 2 to halve the spatial data vertically and horizontally for the next layer. This layer is followed by another sequence of convolution and pooling layers. In this case, the convolution layer consisted of a stride value of 1 by 1, 256 filters, and the dimension of 3 \times 3, and the max-pooling layer was the same as the previous. These previous two layers were repeated twice and helped derive more specific features from the previous layers. These repeated layers were followed by a final convolution layer with a stride value of 1 by 1, 512 filters, and dimension of 3 \times 3, which helps find only the smallest features from the previous layers with the largest amount of nodes in the network. The final output of the last convolutional layer was then passed to a Global Average Pooling layer which condenses the output to the 256-dimensional dense layer. The output from this dense layer was routed to the final output layer, classifying the image as a zero or one. All layers use a ReLU activation function and a dropout rate of 0.2, while the final layer uses a sigmoid activation with no dropout for the final output. Table II has been provided below to show the above layout of the proposed CNN architecture.

4) Training Hyper-parameters: The model was trained with a learning rate of .0001 for 100 epochs and a batch size consisting of 16. Model checkpoints were used based on the best AUC achieved on the validation set to prevent overfitting. A binary cross entropy-based loss function was used along with the Adamax optimizer. The details of the number of generated parameters for the different layers are presented in Table III.

IV. Results

In this section of our study, we provide a comparative analysis of the models presented in our work. We explain the validation results, along with the AUC for our test set. Future work is planned to further modify and improve our models, along with collecting more data.

A. Validation Results

To compare our deep learning models to a simple baseline architecture, we used our shallow learning SVM model. SVM model achieved a specificity of 0.96, a sensitivity of 0.14, and an AUC of 0.75. These numbers are heavily skewed toward specificity, and could be alleviated by modifying the output thresholds, however that would most likely come at a cost to other metrics to improve the sensitivity. The self supervised learning model achieved much more balanced results with a specificity of 0.51, a sensitivity of 0.89, and an AUC of 0.807 on the validation data. Also, the CNN performed comparably with a specificity of 0.74, a sensitivity of 0.77, and an AUC of 0.802. Note that sensitivity, specificity, and AUC values are reported at an output threshold of 0.5. Table III has been provided later in the paper to compare all performance metrics collected.

B. Different Samples Sizes

To provide analysis on how the amount of data can affect a model’s performance, we show the self supervised and CNN model performance with different dataset sizes. To do this, we have provided the results on the same validation set while decreasing the number of samples used for training by a factor of .8, .6, .4, and .2 using random sampling of the dataset. Although there is only a slight performance degradation, we can see there is a general downward trend of performance as the sample sizes decrease, also the performance metrics of the models are more variable, with some of the metrics skewed towards specificity or sensitivity. Table III will compile these results as well.

C. Test Results

For the test results, we have under reported the performance metrics of both the self supervised learning and CNN models to limit any bias in our model for future work. Currently, we
are planning on modifying all the models currently being researched at Virufy, adding more samples to the many datasets we have already collected, and publishing a new paper with more complete performance metrics on the enlarged dataset. As such, we have decided to only report the AUC for the test data. The self-supervised learning model achieved an AUC of 0.791. Also, the CNN performed comparably with an AUC of 0.775. These performance metrics are also tuned to the output threshold of .5 to delineate positives and negatives and have been compiled in table III.

| Layer         | Strides | Window Size | Filters | Parameters    | Output         |
|---------------|---------|-------------|---------|---------------|----------------|
| Convolution 1 | 1 x 1   | 7 x 7       | 32      | 1,600         | (64x256x32)    |
| Convolution 2 | 1 x 1   | 5 x 5       | 64      | 51,264        | (64x256x64)    |
| Max Pooling   | 2 x 2   | 2 x 2       | N/A     | N/A           | (32x128x64)    |
| Convolution 3 | 1 x 1   | 3 x 3       | 256     | 147,712       | (32x128x256)   |
| Max Pooling   | 2 x 2   | 2 x 2       | N/A     | N/A           | (16x64x256)    |
| Convolution 4 | 1 x 1   | 3 x 3       | 256     | 590,080       | (16x64x256)    |
| Max Pooling   | 2 x 2   | 2 x 2       | N/A     | N/A           | (8x32x256)     |
| Convolution 5 | 1 x 1   | 3 x 3       | 512     | 590,080       | (8x32x256)     |
| Max Pooling   | 2 x 2   | 2 x 2       | N/A     | N/A           | (4x16x256)     |
| Convolution 6 | 1 x 1   | 3 x 3       | 512     | 1,180,160     | (4x16x512)     |
| Global Average Pool | N/A | N/A       | N/A     | N/A           | (512)          |
| Dense 1       | N/A     | N/A         | 256     | 131,328       | (256)          |
| Dense 2       | N/A     | N/A         | 1       | 257           | 0 or 1         |

Table II


V. DISCUSSION

In this study, we compile a dataset of approximately 30,000 high-quality coughs including around 16,000 labeled coughs and about 3,400 COVID-19 positive coughs from globally crowdsourced and clinical sources. We also show that the self-supervised, CNN, and SVM approaches achieve an AUC of 0.807, 0.802, and 0.75 on the validation set respectively, and that the self-supervised and CNN approaches achieve an AUC of 0.791 and 0.775 on the test set respectively.

Our best performing network, the SSL approach, had a sensitivity of 0.87 at a specificity of 0.49. Although the metrics are lower when compared to the rapid antigen (sensitivity > 80%, specificity > 97%; [42]) and the rt-PCR tests, our approach has the advantage of being easily repeatable. Multiple testing can increase the accuracy of the results. Furthermore, a cough-based approach has the advantage of being readily accessible on mobile phones and requiring less time and cost for results than any other form of testing.

This effort builds on previous works showing the experimental efficacy of detecting COVID-19 from coughs [7]. One of the main issues preventing wider adoption of cough-based COVID tests has been the persistent doubt about bias and generalizability [43], [44]. Our study advances prior work in the field by applying deep learning techniques to the largest aggregate evaluation dataset of rt-PCR tested, high-quality, COVID-19 positive coughs paired with COVID-19 negative coughs collected in similar settings. Furthermore, our datasets includes crowdsourced coughs (Virufy, COUGHVID, Coswara) and PCR-verified clinical ones (Virufy-India, IATOS). By using datasets from multiple sources, we hope to ameliorate dataset-inherent bias. Additionally, our results on varying the sample size show a trend of increasing performance with increasing sample size, identifying the need to continue collecting coughs to improve model performance.

In this study, we compare the performance of a self-supervised learning (SSL) and CNN approach to a baseline SVM model. As expected, we find that the SVM, a simpler model, is not able to differentiate the cough signals as well as the SSL and CNN models. We also compare the SSL approach that takes advantage of unlabeled coughs with the more traditional fully-supervised CNN approach. There is a small difference between the models’ AUCs, with the SSL approach having a 0.016 higher AUC on the test set, however the SSL model is slightly skewed toward sensitivity. Currently, it is unclear which model is better. There can be multiple improvements made to both models with different types of upsampling techniques, hyperparameter tuning, output threshold tuning, and over-fitting prevention techniques. There can also be improvements to the pre-processing and feature extraction steps such as separating the cough segments into individual samples and concatenating them for a final prediction on a single audio file. Also, the type of data collected by the Virufy team, and other teams around the world, can affect model performance. Another possible next step is to experiment with a fusion model incorporating predictions from the SSL-transformer, CNN, SVM, and other approaches to improve prediction performance.
There are several limitations that should be noted. Previous studies have demonstrated a higher AUC and other metrics than the ones that we show in our study. However, our study’s performance is likely closer to the real-world performance of such a test due to our larger and more diverse training dataset. Furthermore, most academic papers regarding COVID-19 classification with AI suffer from reproducibility issues, along with the fact that a lot of papers have only a small validation set, and no test set, which increases the possibility of biased models. Another limitation is that the labels from our crowdsourced training data (72.6% of labeled dataset) are unverified. This unverified data has incorporated error into our models and will affect the performance in real world environments. Future work should be done to invest resources in collecting more PCR-verified coughs. Lastly, the crowdsourced audio data is prone to noise that may lead to algorithmic prediction bias. We try to account for this issue by only including high-quality data from all sources using an internally developed cough screening tool. Furthermore, our inclusion of multiple data sources should reduce the effect of background noise specific to datasets.

VI. CONCLUSION

This study is a step forward toward an accurate, reliable, and accessible audio-based COVID-19 diagnostic test, showing adequate performance on a large and diverse dataset. In addition to improving model performance, future work should focus on collecting high-volumes of PCR-verified samples and assessing the model generalizability to new datasets. Decision-making errors should be closely studied to understand how prediction performance is affected by audio recording conditions, patient symptoms, and the time point during the course of COVID-19 infection.

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