End-2-End COVID-19 Detection from Breath & Cough Audio

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SUMMARY BOX
Our main contributions are as follows:

• We demonstrate the first attempt to diagnose COVID-19 using end-to-end deep learning from a crowd-sourced dataset of audio samples, achieving ROC-AUC of 0.846

• Our model, the COVID-19 Identification ResNet, (CIDeR), has potential for rapid scalability, minimal cost, and improving performance as more data becomes available. This could enable regular COVID-19 testing at a population scale

• We introduce a novel modelling strategy using a custom deep neural network to diagnose COVID-19 from a joint breath and cough representation

• We release our four stratified folds for cross parameter optimisation and validation on a standard public corpus and details on the models for reproducibility and future reference

INTRODUCTION
The Coronavirus disease 2019 (COVID-19), caused by the severe-acute-respiratory-syndrome-coronavirus 2 (SARS-CoV-2), is the first global pandemic of the 21st century. Since its emergence in December 2019, it has led to over 75 million confirmed cases and more than 1.6 million deaths in over 200 countries (WHO)1 SARS-CoV-2 causes either asymptomatic infection or clinical disease, which ranges from mild to life-threatening 11. Developing a swift and accurate test, able to identify both symptomatic and asymptomatic cases, is therefore essential for pandemic control.

Vocal biomarkers of SARS-CoV-2 infection have been described, thought to relate to the clinical and subclinical effects of the virus on the lower respiratory tract, neuro-muscular function, senses of taste and smell and on proprioceptive feedback. Together, these produce a reduction in complexity of the co-ordination of respiratory and laryngeal motion in both symptomatic and asymptomatic individuals 2.

Recently, several audio applications have been released that capture the breath or cough of individuals. Examples include the ‘Coughvid’ 3, ‘Breath for Science’ 2, ‘Coswara’ 4, and ‘CoughAgainstCovid’ 5. With the release of these datasets, several studies have been published that leverage breath and/or cough signals alongside machine learning to detect the virus 6 7 8 9 10 11. However, these approaches try to compute representations of the breath and cough signals separately. In contrast, our approach computes a joint representation using a single model.

We postulate that end-to-end deep learning using convolutional neural networks (CNNs) could be successfully applied to this assessment task. This article describes a proof of concept study of automatic symptomatic and asymptomatic COVID-19 recognition using combined breathing and coughing information from audio recordings using an end-to-end CNN design. The code for our experiments and all details for reproduction of findings can be found at https://github.com/glam-imperial/cider.

METHODS
The objective is supervised learning binary classification for diagnosing COVID-19 as positive or negative using audio sig-
nals. Our implementation, displayed in Figure 1, has two distinct stages which are outlined below:

1. **Spectrogram extraction** As shown in Figure 1, each participant in the study carried out by the University of Cambridge [6] could submit waveform audio (WAV) files including a breath sample and a cough sample. We first compute the spectrogram of each of these WAV files to obtain a visual representation of the spectrum of audio frequencies against time. Next, we perform a log transformation, converting the spectrogram from an amplitude representation to a decibel representation. These transformations are implemented using the *librosa* [12] python package.

   Each WAV file lasts between one and forty-eight seconds with a mean of ten seconds. As uniform duration is required for CNN input, we chunk the whole WAV file into $s$-second segments, using right padding for files shorter than $s$-seconds. This creates an image of size \( \{F, W\} \), where \( F \propto \text{fft}_n \) and \( W \propto sr \times s \) and \( \text{fft}_n \) and \( sr \) are parameters used when computing the spectrogram. During model training, we only process one WAV segment (sampled uniformly). At inference time, we perform majority voting, whereby each chunk is processed in parallel, and the output label becomes the modal classification from each of the chunks.

2. **Convolutional Neural Network** CldeR is based on ResNets [13], a variant of the CNN architecture, which uses residual blocks. As shown in Figure 1, a residual block consists of two convolutions, batch normalisation [14], and a Rectified Linear Unit (ReLU) non-linearity. These blocks use “skip” connections which add the output from these operations to the input activations for this layer. This alleviates the vanishing gradient problem, facilitating deeper architectures with more layers, thereby permitting richer hierarchical learnt representations. The number of convolutional channels for each of CldeR’s nine layers are annotated in Figure 1.

   We concatenate the log spectrograms of the breath and cough samples depth-wise, creating an \( \{F, W, 2\} \) matrix as the model input. The CNN outputs a single logit which is then passed through a sigmoid layer to obtain a \((0, 1)\) score, representing the probability of a COVID-positive sample. A weighted binary-cross entropy loss function [15] is used during training to address the class imbalance in the dataset.

**Training strategy** Prior work [6] used “10-fold-like” cross validation during training (see the paper for details). In contrast, we implement a stratified 3-fold cross optimisation and additional validation partitioning using 2 / 1 (rotating development + train) / 1 (always held out fixed test) folds, respectively. This is to best optimise parameters independently of the test set with a small dataset while ensuring that the test set remains a) fixed for easier comparison with other work, and b) truly blind, eliminating the possibility of CldeR overfitting to the test set. Our stratified sampling methodology ensures that our folds represent disjoint sets of participants and each of the strata (next section) are approximately uniformly distributed across each fold. To enable reproducibility, the folds are fully released in the accompanying code.

**Baseline** Our approach is not directly comparable with the study from [6] as they do not explicitly provide their folds and discard some audio samples. To this purpose, to create a performance reference for CldeR, we implement a linear kernel Support Vector Machine (SVM) [16] baseline. We extract openSMILE features [17] for each wavfile following the Interspeech 2016 ComParE challenge format [18] and perform Principal Component Analysis (PCA) [19], selecting the top 100 components by highest explained variance. We follow the cross optimisation procedure outlined above, using the develop-
opment set to optimise the complexity parameter\(^5\) and reporting final results using the held-out test set.

**DATASET**
The dataset used in this work consists of 517 crowdsourced coughing and breathing audio recordings from 355 participants, of which 62 participants had tested positive for COVID-19 within 14 days of the recording\(^6\). The samples were collected via android and web apps developed by [6] and can be found at [https://www.covid-19-sounds.org](https://www.covid-19-sounds.org). To be classified as COVID-negative, participants had to meet a number of stringent criteria described in [6]. These participants were then divided into 3 categories: those with no cough (healthy-no-symptoms), those with a cough (healthy-with-cough) and those who had asthma (asthma-with-cough). The COVID-positive class is constituted of the 62 COVID-positive participants and is further divided into the sub classes COVID-no-cough, and COVID-cough representing 39 COVID positive participants without a cough and 23 participants with a cough, respectively.

**EXPERIMENTS & RESULTS**
As indicated above, we perform a 3-fold cross optimisation using the rotating development plus train folds. Recall that the test set is fixed and always held out during optimisation. For evaluation metrics, we utilise the Area Under Curve of the Receiver Operating Characteristics curve (AUC-ROC), and Unweighted Average Recall (UAR), both of which are robust to imbalanced datasets. AUC-ROC maps the relationship between sensitivity and the false positive rate as the classification threshold is varied, and UAR computes the mean recall per class. The models’ performance is sensitive to initialisation parameters, so we report the mean and standard deviation from three training runs. Table 1 details our hyperparameter search and optimal values used for the final model.

Our model performs the three tasks described in the dataset publication [6], and an additional fourth task. Tasks 1-4 are as follows:

**Task 1** Distinguishing between COVID-positive and the strata healthy-no-symptoms (62 vs 245 participants).

**Task 2** Distinguishing between COVID-positive participants with a cough (COVID-cough) and the strata healthy-with-cough (23 vs 30 participants).

**Task 3** Distinguishing between COVID-positive participants with a cough (COVID-cough) and the strata asthma-with-cough (23 vs 19 participants).

**Task 4** Distinguishing between COVID-positive and COVID-negative (62 vs 293 participants).

Note that the number of participants deviates from [6], as we also use those audio clips shorter than two seconds resulting in partially more participants considered.

Results obtained for each task are shown in Table 2 alongside the baseline. CIdeR outperforms on all tasks bar task 2 with high margin on both metrics. The results for tasks 1, 3, and 4 are statistically significant with a level of significance of 0.01 in a two-sided two sample t-test for difference in sample means.

**DISCUSSION**
The results in Table 2 demonstrate two key points: 1) it is possible to diagnose COVID-19 using a CNN-based model trained on crowdsourced data; 2) CIdeR obtains a high AUC-ROC of 0.846 on task 4, the task which uses the entire sample, and so represents the most pertinent task. These suggest that jointly processing breath and cough audio signals using a CNN-based classifier could act as an effective and scalable method for COVID-19 diagnosis.

The only task where CIdeR fails to outperform the baseline in our experiments is task 2. We posit this is jointly due to the small number of samples and the similarity of audio patterns of healthy participants with a cough and those with COVID-19, creating a challenging task. We leave further analysis for future work.

A key limitation of this study is the size and demographics of the publicly available dataset [6]. We are limited to 62 COVID-positive participants, limiting the breadth of any

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\(^5\)Values between 1e\(^-5\) and 1 on a logarithmic scale.

\(^6\)The dataset used in this study is a small subset of the full dataset that has been collected by the University of Cambridge, which has yet to be made fully public. As of July 2020 the full dataset totalled 10,000 samples from roughly 7,000 participants.

| Parameter                  | Min.    | Max.    | Step | Optimal |
|----------------------------|---------|---------|------|---------|
| Learning rate              | 5e\(^-5\) | 5e\(^-4\) | 5e\(^-5\) | 1e\(^-4\) |
| Batch size                 | 8       | 32      | 2\(^e\) | 16      |
| Audio segment length [s]   | 1       | 8       | 2\(^e\) | 8       |
| Spectral bands (f_{M}#]    | 512     | 2,048   | 2\(^e\) | 1,024   |
| Sample rate sr [kHz]       | 24      | 48      | 2\(^e\) | 24      |

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Table 1 Overview of the hyperparameter search detailing the interval, step size, and optimal parameters (used to obtain the reported figures in this article – for details cf. the above named GitHub repository). Hyperparameters were optimised for task 4, and subsequently used on all tasks. *Interval constructed using a logarithmic scale. Adam [20] was used for optimisation.
CIdeR’s diagnostic capabilities would significantly increase. In spite of the small dataset, it seems likely that further improvements in diagnostic performance would result if more samples were available. The potential of end-to-end deep learning to jointly learn representation and classification is evident from the results. Applying this technology to respiratory sound monitoring of population spread, and therefore holds great potential.

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