

## Short Paper

# Limitations of the Cough Sound-Based COVID-19 Diagnosis Artificial Intelligence Model and its Future Direction: Longitudinal Observation Study

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## Abstract

**Background:** The outbreak of SARS-CoV-2 in 2019 has necessitated the rapid and accurate detection of COVID-19 to manage patients effectively and implement public health measures. Artificial intelligence (AI) models analyzing cough sounds have emerged as promising tools for large-scale screening and early identification of potential cases.

**Objective:** This study aimed to investigate the efficacy of using cough sounds as a diagnostic tool for COVID-19, considering the unique acoustic features that differentiate positive and negative cases. We investigated whether an AI model trained on cough sound recordings from specific periods, especially the early stages of the COVID-19 pandemic, were applicable to the ongoing situation with persistent variants.

**Methods:** We used cough sound recordings from 3 data sets (Cambridge, Coswara, and Virify) representing different stages of the pandemic and variants. Our AI model was trained using the Cambridge data set with subsequent evaluation against all data sets. The performance was analyzed based on the area under the receiver operating curve (AUC) across different data measurement periods and COVID-19 variants.

**Results:** The AI model demonstrated a high AUC when tested with the Cambridge data set, indicative of its initial effectiveness. However, the performance varied significantly with other data sets, particularly in detecting later variants such as Delta and Omicron, with a marked decline in AUC observed for the latter. These results highlight the challenges in maintaining the efficacy of AI models against the backdrop of an evolving virus.

**Conclusions:** While AI models analyzing cough sounds offer a promising noninvasive and rapid screening method for COVID-19, their effectiveness is challenged by the emergence of new virus variants. Ongoing research and adaptations in AI methodologies are crucial to address these limitations. The adaptability of AI models to evolve with the virus underscores their potential as a

foundational technology for not only the current pandemic but also future outbreaks, contributing to a more agile and resilient global health infrastructure.

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## KEYWORDS

COVID-19 variants; cough sound; artificial intelligence; diagnosis; human lifestyle; SARS-CoV-2; AI model; cough; sound-based; diagnosis; sounds app; development; COVID-19; AI

## Introduction

In 2019, the outbreak of SARS-CoV-2 set off a global pandemic, substantially impacting human lifestyles and posing an unprecedented challenge to health care systems worldwide [1]. Given its high infectivity, the urgent need for rapid and accurate COVID-19 detection has become paramount for effective patient management, timely isolation, and implementation of appropriate public health measures. Consequently, numerous studies have been undertaken to devise efficient methods for detecting infection status quickly and easily. Among these studies, artificial intelligence (AI) models that leverage prominent symptoms, such as coughing, have shown potential [2,3]. The ability to discern COVID-19 solely based on analyzing recorded cough sounds presents a straightforward and swift approach to screening individuals. These AI models offer hope for rapid, large-scale screening and early identification of potential cases. However, it is essential to acknowledge certain limitations in these research trends, particularly regarding variations in symptoms attributed to different SARS-CoV-2 variants [4]. The emergence of new variants has introduced complexities in symptom profiles, making it more challenging to rely solely on cough sounds for accurate COVID-19 detection. As the virus continues to evolve, ongoing research and adaptations in AI models will be crucial to address these challenges and improve the accuracy and effectiveness of diagnostic approaches. Particularly, patients with the Omicron variant have shown a decreased occurrence of characteristic symptoms such as loss of taste and smell, while cold-like symptoms such as sneezing and a blocked nose have increased [5]. In essence, the symptoms of COVID-19 have been increasingly resembling those of a common cold. This implies that the previous AI models designed to detect COVID-19 using cough sounds may not work as effectively or may not be as reliable both currently and in the future.

## Methods

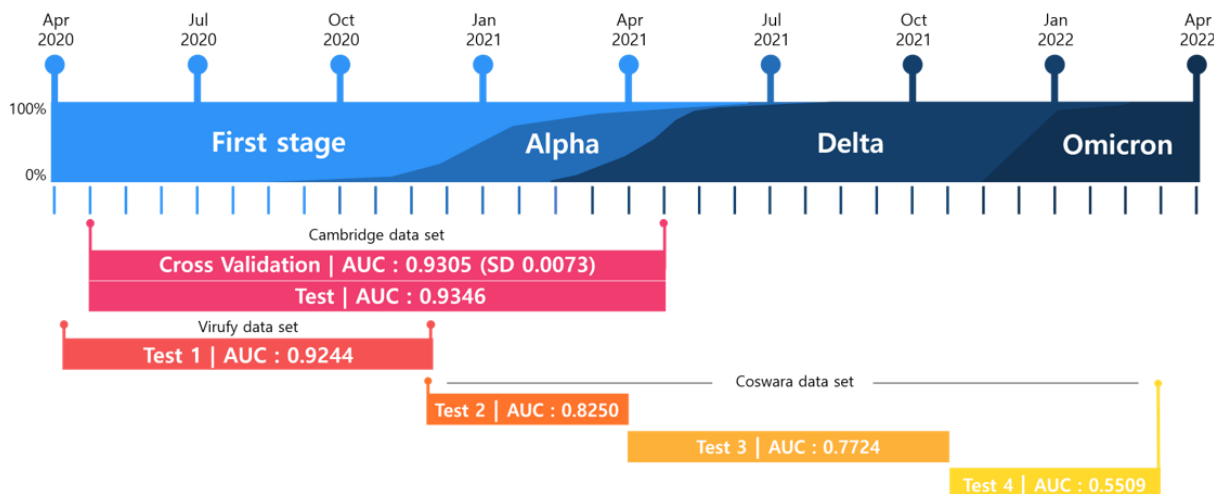
### Overview

In this study, we first used cough sounds as a diagnostic tool for COVID-19 stems from distinctive acoustic features that can differentiate between positive and negative cases. Building on prior research that used mel spectrograms to discern variance in cough sound spectra, our study adopts the variable frequency complex demodulation technique. Variable frequency complex demodulation offers a higher resolution than mel spectrograms, thus amplifying the discernibility of these patterns [6]. As depicted in Figure S1 in [Multimedia Appendix 1](#), the cough sound spectra of patients with COVID-19 exhibit a unique

irregular spectral intensity distribution, characterized by an initial decline followed by a subsequent rise over time. In contrast, the spectra from non-COVID-19 groups display a more uniform pattern, typically showing either a consistent distribution or a gradual decline in intensity. Furthermore, our analysis extends to the differentiation in audio signal features between the 2 patient groups. The examination of 5 selected audio signal features indicates clear distinctions, which are consistent across different data sets. Illustrated in [Figure S2 in Multimedia Appendix 1 \[6-9\]](#), we observe that the mean spectral roll-off for patients with SARS-CoV-2 positive trends toward lower values compared with that of negative individuals. Conversely, the mean spectral bandwidth is generally higher for those with COVID-19. Additional features, such as the SD of the spectral centroid, present lower values for positive cases, whereas the SD of spectral bandwidth is elevated, and the SD of the zero-crossing rate is reduced when compared with negative cases.

Furthermore, we aimed to demonstrate that an AI model trained on cough sound recordings from a specific period, especially the early stages of the COVID-19 pandemic, is not applicable to the ongoing situation with persistent variants. To illustrate these findings, we used 3 cough data sets named Cambridge, Coswara, and Virufy [5,10,11]. The Cambridge data set consists of audio recordings of variable-length cough audio collected through the COVID-19 Sounds App, developed by the University of Cambridge. The data measurement period encompasses the early stages of the wild type and Alpha variant occurrences (April 30, 2020, to April 26, 2021). We trained our AI model using the Cambridge data set. More specifically, we split the data into 8:2 for train and test data. Subsequently, for the train data, we performed 3-fold cross-validation and evaluated the model using the test data. The Virufy data set also includes crowdsourced cough sounds to identify patterns that signify respiratory diseases, such as COVID-19. The data measurement period primarily covers the early stages when the wild type was present (April 9, 2020, to November 26, 2020). We used the data set as additional test data. The Coswara data set also includes worldwide crowdsourced data collected through a website app, including cough, breath, and voice recordings for COVID-19 diagnosis. The data measurement period extended from the Alpha variant to the Omicron variant occurrences. We also used the data set as additional test data. To evaluate the performance of our AI model based on different variants, we categorized the data into 3 periods, each dominated by the Alpha, Delta, and Omicron variants, respectively. We summarized the data sets, along with the periods and COVID-19 variant status in which they were measured, in [Figure 1](#) and [Tables S1 and S2 in Multimedia Appendix 1 \[6-9\]](#).

**Figure 1.** Area under the receiver operating curve (AUC) values for each data set and measurement period.



**Ethical Considerations**

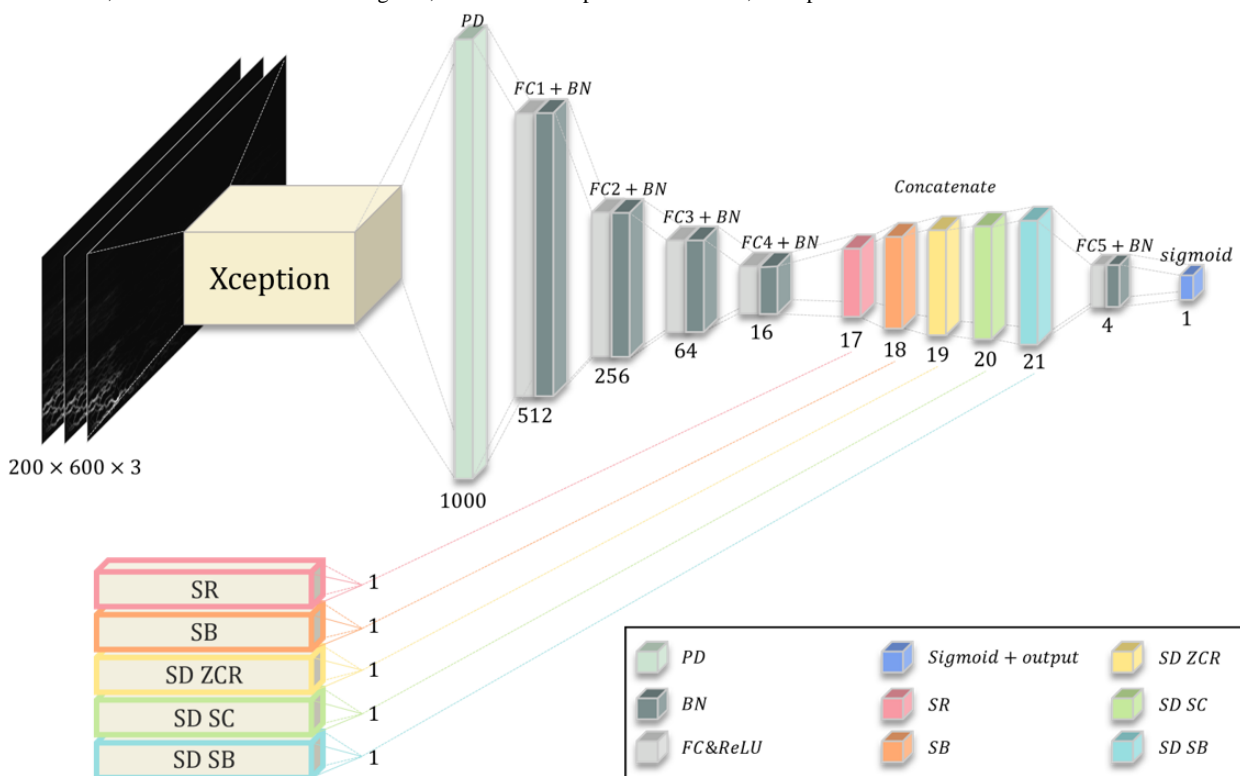
The protocol of this study was approved by the institutional review board of Kyung Hee University Hospital (KHUH 2022-06-042).

**Results**

After the cough sound preprocessing, we developed an AI model to detect COVID-19 from extracted features and time-frequency spectrum using variable frequency complex demodulation (Multimedia Appendix 1 [6-9]). Table S2 in Multimedia Appendix 1 [6-9] summarizes the performance of our proposed

AI model according to each data set and data measurement period. The results show that the cross-validation and test results from the Cambridge data set overlap, with an area under the receiver operating curve (AUC) of 0.93. Furthermore, the Virufy data set, which was measured around a similar period as the Cambridge data set, also demonstrated a similar performance: the AUC was 0.92. On the other hand, in the case of the Coswara data set, divided into 3 groups based on the variants, it was observed that the AUC for Alpha was 0.83; for Delta, 0.77; and for Omicron, 0.55; this indicates a decline in performance as the variants progressed. Figures 1 and 2 summarize the overall performance for each data set and measurement period.

**Figure 2.** Our proposed model architecture. BN: batch normalization; FC: fully connected; PD: prediction; SB: spectral bandwidth; SD SC: SD of spectral centroid; SD ZCR: SD of zero crossing rate; SD SB: SD of spectral bandwidth; SR: spectral rolloff.



## Discussion

The fight against COVID-19 has been marked by the deployment of various traditional diagnostic methods, each serving as a critical pillar in our response to the pandemic. Central among these is the reverse transcription-polymerase chain reaction test, widely regarded as the gold standard for its high specificity and sensitivity [12,13]. Rapid antigen tests and serological assays have also been instrumental, offering quick screening and insight into past infections, respectively. Despite their strengths, these methods have limitations, including resource dependency, time constraints, and varying degrees of accuracy. In this context, AI has emerged as a powerful aid, augmenting traditional diagnostic methods and addressing their shortcomings. By facilitating enhanced data analysis and interpretation, AI algorithms have the potential to streamline reverse transcription-polymerase chain reaction workflows, improve the reliability of antigen tests, and provide a more nuanced understanding of serological data. The integration of AI extends further to the analysis of medical imaging, where it

aids in identifying patterns indicative of COVID-19, thus offering a valuable complement to molecular testing [14-16].

Our research has focused on the novel application of AI in analyzing cough sounds, a symptom-based method with promise for noninvasive, rapid screening. We demonstrated that AI models, when trained on cough sounds, could provide a swift approach to preliminary screening, though their performance varied with the emergence of new variants. Despite the performance variability, the inherent adaptability of AI models ensures their lasting relevance. These models can be reconfigured as pretrained frameworks ready to be fine-tuned against emerging viral strains. Such adaptability allows for the rapid deployment of AI tools in response to evolving pathogens, showcasing the potential of AI to serve not only the current pandemic but also as a foundational technology for future outbreaks. The capacity of these AI models to evolve in step with the virus paves the way for an agile diagnostic ecosystem that can quickly adapt to new threats, ultimately contributing to a more resilient global health infrastructure.

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## Data Availability

The data sets generated or analyzed during this study are available from the corresponding author on reasonable request.

## Authors' Contributions

JL had full access to all of the data in the study and took responsibility for the integrity of the AI model and performance analysis. All authors approved the final version before submission. The study's concept and design were devised by DKY and JL. The acquisition was led by JK and JL. Model development was spearheaded by JK. Analysis and interpretation involved DKY and JL. Validation was performed by YSC, YJL, SGY, and KWK. Drafting of the manuscript was done by JK, DKY, and JL. Critical revision of the manuscript for important intellectual content was a collective effort of all authors. Study supervision was undertaken by DKY and JL. JL and DKY supervised the study and are guarantors for this study. JL and DKY contributed equally as corresponding authors. The corresponding authors attest that all listed authors meet authorship criteria and that no others meeting the criteria have been omitted.

## Conflicts of Interest

None declared.

## Multimedia Appendix 1

Supplemental tables and figures.

[PDF File (Adobe PDF File), 589 KB-Multimedia Appendix 1]

## References

1. Cha Y, Jung W, Seo M, Rahmati M. The emerging pandemic recent: SARS-CoV-2. *Life Cycle*. 2023;3:e2. [FREE Full text] [doi: [10.54724/lc.2023.e2](https://doi.org/10.54724/lc.2023.e2)]
2. Laguarda J, Hueto F, Subirana B. COVID-19 artificial intelligence diagnosis using only cough recordings. *IEEE Open J Eng Med Biol*. 2020;1:275-281. [FREE Full text] [doi: [10.1109/OJEMB.2020.3026928](https://doi.org/10.1109/OJEMB.2020.3026928)] [Medline: [34812418](https://pubmed.ncbi.nlm.nih.gov/34812418/)]
3. Andreu-Perez J, Perez-Espinosa H, Timonet E, Kiani M, Giron-Perez MI, Benitez-Trinidad AB, et al. A generic deep learning based cough analysis system from clinically validated samples for point-of-need Covid-19 test and severity levels. *IEEE Trans Serv Comput*. 2022;15(3):1220-1232. [FREE Full text] [doi: [10.1109/TSC.2021.3061402](https://doi.org/10.1109/TSC.2021.3061402)] [Medline: [35936760](https://pubmed.ncbi.nlm.nih.gov/35936760/)]

4. Choi YJ, Acharya KP. How serious is the Omicron variant? transmissibility, genomics, and responses to COVID-19 vaccines, and 'Stealth' Omicron variants. *Life Cycle*. 2022;2:e7. [FREE Full text] [doi: [10.54724/lc.2022.e7](https://doi.org/10.54724/lc.2022.e7)]
5. Whitaker M, Elliott J, Bodinier B, Barclay W, Ward H, Cooke G, et al. Variant-specific symptoms of COVID-19 in a study of 1,542,510 adults in England. *Nat Commun*. 2022;13(1):6856. [FREE Full text] [doi: [10.1038/s41467-022-34244-2](https://doi.org/10.1038/s41467-022-34244-2)] [Medline: [36369151](https://pubmed.ncbi.nlm.nih.gov/36369151/)]
6. Wang H, Siu K, Ju K, Chon KH. A high resolution approach to estimating time-frequency spectra and their amplitudes. *Ann Biomed Eng*. 2006;34(2):326-338. [doi: [10.1007/s10439-005-9035-y](https://doi.org/10.1007/s10439-005-9035-y)] [Medline: [16463086](https://pubmed.ncbi.nlm.nih.gov/16463086/)]
7. Sharma G, Umapathy K, Krishnan S. Trends in audio signal feature extraction methods. *Applied Acoustics*. Jan 2020;158:107020. [doi: [10.1016/j.apacoust.2019.107020](https://doi.org/10.1016/j.apacoust.2019.107020)]
8. Chang AB. The physiology of cough. *Paediatr Respir Rev*. Mar 2006;7(1):2-8. [doi: [10.1016/j.prrv.2005.11.009](https://doi.org/10.1016/j.prrv.2005.11.009)] [Medline: [16473809](https://pubmed.ncbi.nlm.nih.gov/16473809/)]
9. Chollet F. Xception: deep learning with depthwise separable convolutions. Presented at: 2017 IEEE Conference on Computer Vision and Pattern Recognition (CVPR); 2017, 2017;1800-1807; Honolulu, HI. [doi: [10.1109/CVPR.2017.195](https://doi.org/10.1109/CVPR.2017.195)]
10. Orlandic L, Teijeiro T, Aienza D. The COUGHVID crowdsourcing dataset, a corpus for the study of large-scale cough analysis algorithms. *Sci Data*. 2021;8(1):156. [FREE Full text] [doi: [10.1038/s41597-021-00937-4](https://doi.org/10.1038/s41597-021-00937-4)] [Medline: [34162883](https://pubmed.ncbi.nlm.nih.gov/34162883/)]
11. Bhattacharya D, Sharma NK, Dutta D, Chetupalli SR, Mote P, Ganapathy S, et al. Coswara: a respiratory sounds and symptoms dataset for remote screening of SARS-CoV-2 infection. *Sci Data*. 2023;10(1):397. [FREE Full text] [doi: [10.1038/s41597-023-02266-0](https://doi.org/10.1038/s41597-023-02266-0)] [Medline: [37349364](https://pubmed.ncbi.nlm.nih.gov/37349364/)]
12. Park M, Won J, Choi BY, Lee CJ. Optimization of primer sets and detection protocols for SARS-CoV-2 of coronavirus disease 2019 (COVID-19) using PCR and real-time PCR. *Exp Mol Med*. 2020;52(6):963-977. [FREE Full text] [doi: [10.1038/s12276-020-0452-7](https://doi.org/10.1038/s12276-020-0452-7)] [Medline: [32546849](https://pubmed.ncbi.nlm.nih.gov/32546849/)]
13. Tombuloglu H, Sabit H, Al-Khallaf H, Kabanja JH, Alsaeed M, Al-Saleh N, et al. Multiplex real-time RT-PCR method for the diagnosis of SARS-CoV-2 by targeting viral N, RdRP and human RP genes. *Sci Rep*. 2022;12(1):2853. [FREE Full text] [doi: [10.1038/s41598-022-06977-z](https://doi.org/10.1038/s41598-022-06977-z)] [Medline: [35181721](https://pubmed.ncbi.nlm.nih.gov/35181721/)]
14. Chung H, Ko H, Lee H, Yon DK, Lee WH, Kim TS, et al. Development and validation of a deep learning model to diagnose COVID-19 using time-series heart rate values before the onset of symptoms. *J Med Virol*. 2023;95(2):e28462. [doi: [10.1002/jmv.28462](https://doi.org/10.1002/jmv.28462)] [Medline: [36602055](https://pubmed.ncbi.nlm.nih.gov/36602055/)]
15. Chung H, Ko H, Kang WS, Kim KW, Lee H, Park C, et al. Prediction and feature importance analysis for severity of COVID-19 in South Korea using artificial intelligence: model development and validation. *J Med Internet Res*. 2021;23(4):e27060. [FREE Full text] [doi: [10.2196/27060](https://doi.org/10.2196/27060)] [Medline: [33764883](https://pubmed.ncbi.nlm.nih.gov/33764883/)]
16. Ko H, Chung H, Kang WS, Park C, Kim DW, Kim SE, et al. An artificial intelligence model to predict the mortality of COVID-19 patients at hospital admission time using routine blood samples: development and validation of an ensemble model. *J Med Internet Res*. 2020;22(12):e25442. [FREE Full text] [doi: [10.2196/25442](https://doi.org/10.2196/25442)] [Medline: [33301414](https://pubmed.ncbi.nlm.nih.gov/33301414/)]

## Abbreviations

**AI:** artificial intelligence

**AUC:** area under the receiver operating curve

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