

HMC-COVID-19: Hidden Markov Chains Model for COVID-19 Diagnosis

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Abstract—Markov chains are probabilistic models that are useful in different image processing tasks. This paper presents an approach based on Hidden Markov Chain (HMCs) to diagnose COVID-19, that we named HMC-COVID-19. To assess the performance of the proposed solution, we use a public dataset of chest X-RAY images. Our solution has been evaluated using the accuracy of prediction. The preliminary results are promising and can be further enhanced.

Index Terms—Hidden Markov Chains (HMC), COVID-19 diagnosis, HMC-COVID-19, Image classification

I. INTRODUCTION

On March 12, 2020, the World Health Organization (WHO) designated the COVID-19 virus to be pandemic. Around the world, 768 237 788 confirmed cases of COVID-19, with 6 951 677 fatalities, were officially reported to WHO on July 19, 2023. A total of 13 474 267 147 doses of vaccination have been given as of July 11, 2023 [1]. There have been 266,356 cases of contamination and 6,875 deaths linked to the coronavirus recorded in Algeria since the start of the epidemic [2]. There are several types of tests to diagnose the COVID-19 virus such as RT-PCR test, Antigen test, and scanner. These tests' degree of accuracy differs. A negative test result does not guarantee that you are free of the COVID-19 virus.

As we all know, image classification plays a crucial role in medical diagnostics, especially in the current pandemic situation. Accurate and efficient identification of COVID-19 symptoms in medical images is of utmost importance for timely diagnosis and treatment. In this regard, the use of advanced models such as deep learning and Markov models has gained considerable attention.

In terms of performance, deep learning models have demonstrated superior accuracy rates compared to traditional machine learning algorithms and Markov models. Their ability to automatically extract relevant features from medical images, combined with extensive training on large datasets, enables deep learning models to achieve state-of-the-art performance in image classification tasks, including COVID-19 diagnosis. However, it is worth mentioning that deep learning models

often require substantial computational resources and large amounts of annotated data to train effectively.

On the other hand, Markov models offer a different approach [3], [4], [5], [6], and [7]. These models are based on the principle of probabilistic transitions between states. By analyzing the statistical dependencies among different image features, Markov models can effectively capture the sequential relationships in image data. Although they may not possess the same level of complexity as deep learning models, Markov models can still provide valuable insights for image classification tasks related to COVID-19.

The Markov models can excel in situations where data scarcity and computational limitations pose challenges for deep learning models. Markov models can efficiently capture the dependencies between image features and provide a compact representation of the data. While they may not achieve the same accuracy as deep learning models, their computational efficiency and ability to handle small datasets make them valuable alternatives, especially in resource-constrained environments.

Both deep learning models and Markov models have their strengths and weaknesses when it comes to image classification for COVID-19. Deep learning models offer superior accuracy but require significant computational resources and extensive training data. Markov models, while less accurate, can still provide valuable insights, particularly in scenarios with limited resources. Ultimately, the choice of model depends on the specific requirements, available resources, and the importance placed on accuracy versus efficiency. In this paper, we use the Hidden Markov Chain (HMC) model for COVID-19 diagnosis using X-Ray images. We named the proposed solution HMC-COVID-19. The results are promising and can be further enhanced.

The remainder of this paper is organized as follows: In Section II, we describe our motivation. Section III describes our solution. In Section IV, we give the details of the used dataset. Preliminary results are shown in Section V; finally, Section VI concludes the paper.