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A Genomic Signal Processing-Based Coronavirus Classification Model Using Deep Learning with Web-Based Console

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Abstract

Various strains of Coronavirus have led to numerous deaths worldwide with CoViD-19 being the most recent. Hence, the need for various research studies to determine and develop technologies that would reduce the spread of this virus as well as aid in the early diagnosis of the disease. The Severe Acute Respiratory Syndrome CoV (SARS-CoV), which emerged in 2003, Middle East Respiratory Syndrome CoV (MERS-CoV) in 2012 and Severe Acute Respiratory

Syndrome CoV 2 (SARS-CoV-2) which is generally regarded as CoViD-19, in 2019 have very similar symptoms and genetics. Without proper diagnosis of these strains, they may be mistaken for one another. Therefore, there is a need to distinguish CoViD-19 from the other two Coronaviruses to enhance prompt and specific treatment. In this study, we developed a deep learning model with a web console for the classification of genomic sequences of the three Coronavirus strains using genomic signal processing. The DNA sequences harvested from the Virus Pathogen Database and Analysis Resource (ViPR) was used as dataset and these sequences were transformed to RGB images using Voss and Z-curve encodings. A convolutional neural network (CNN) model was consequently used for classification and incorporated in a web application platform developed with the Django framework. The results of the transformation of the images highlights the similarities of the three coronaviruses in terms of visual and genetic characteristics with the CNN model distinctly classifying SARS-CoV-2, SARS-CoV and MERS-CoV with a training and validation accuracies of 95.58% and 85% respectively which compares favourably with other results in the literature.

Keywords

- **MERS-CoV**
- **SARS-CoV**
- **SARS-CoV-2**
- **Genomic Signal Processing**
- **Deep Convolutional Neural Network (DCNN)**

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