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CoV-Seq, a New Tool for SARS-CoV-2 Genome Analysis and Visualization: Development and Usability Study

Abstract

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COVID-19 was quickly declared a global pandemic after its discovery in late 2019. SARS-CoV-2 genomes are being sequenced and shared on public repositories at a rapid rate. Scientists must periodically refresh data sets in order to keep up with these changes, which is a time-consuming and labor-intensive process. Furthermore, scientists with little bioinformatics or programming experience may struggle. To fix these issues, we created CoV-Seq, an interactive web server that allows researchers to analyze SARS-CoV-2 genomes quickly and easily. In Python and JavaScript, CoV-Seq is implemented. This article includes the URLs for the web server and source code. We created CoV-Seq, a web-based tool for analyzing custom SARS-CoV-2 sequences quickly and easily. The web server includes an interactive module for personalized sequence analysis and a weekly modified index of genetic variations for all publicly available SARS-CoV-2 sequences. We think CoV-Seq would aid in our knowledge of COVID-19's genetic underpinnings.

Introduction

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The novel coronavirus SARS-CoV-2 has sparked an epidemic of viral pneumonia and has turned into a global pandemic since its discovery in late 2019. While attempts to curb its spread, SARS-CoV-2 had infected nearly 33 million patients and killed nearly 1 million people worldwide as of late September 2020 . Scientists sequenced the SARS-CoV-2 genome to learn more about its evolution and genetics. To fix these issues, we created the CoV-Seq framework. A data processing system that takes FASTA sequences and produces variant callers in variant call format (VCF) and open reading frame (ORF) predictions is part of CoV-Seq. The pipeline detects and annotates gene mutations while filtering reduced sequences, removing duplicates, aligning sequences, and identifying and filtering low-quality sequences. We have a web server that allows non-programmers to quickly analyze custom sequences. An integrated genome visualizer and tabulated views of genetic variations and ORF projections are included in the web interface Both of the findings are available for download for further review. We also have a present predominantly for increased processing in settings. We compiled SARS-CoV-2 molecules from the Global Initiative on Exchanging Bird Flu Sample, the Bio technology Information, the European Nucleic acid Database, and China National GeneBank to make data sharing easier.

Related Works

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