

# PAPER RESEARCH

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***Paper Name:** COVID SEQUENCE, a New Tool for SARS-CoV-2 Genome Analysis and Visualization: Development and Usability Study.*

## Introduction:

What is a coronavirus?

**Coronavirus** are a large family of viruses that are known to cause illness ranging from the common cold to more severe diseases such as Middle East Respiratory syndrome and severe acute respiratory syndrome “SARS”, coronavirus can be transmitted from person to person and to understand its evolution and genetics scientists have sequenced SARS COVID-19 from patients and make statistics from groups of people with different ages and genders so now we have a huge data set to take genomic sequences to keep up with the latest updates. Scientists need to frequently download and clean new data sets, **COVID -19 SEQ** consists of different components: a data analysis that takes **FASTA** sequences and generates variant call sets in **VCF** “variant call format” also known as **processed files**: includes a genomic data

and **ORF** “*open reading frames*” is the part of reading frame that has the ability to be translated , the pipeline automatically filters low –quality sequences and remove duplicate sequences , performs sequence alignment and identifies ,annotates genetic variant , we use a web server to enable the rapid analysis of sequences without using programming web interface includes an interactive genome visualizer and tabulated displays of genetic variants and ORF predictions further we use command-line interface to facilitate data sharing .

## Abstract:

The genomes of SARS **COVID-19** rapidly sequenced and to keep up with updates and evolution scientists want to refresh and re-clean data sets but scientists have limited with Bioinformatics tools and programming to analyse the sequences so to handle these problems they developed **COVID -19** SEQ by using “web server “which facilitate analysing the sequence implemented in python and JavaScript using web server the results when we have a new sequence **COVID -19** SEQ predicts Gene Boundaries ,the locations of genes ,identifies genetic variations ,identifying elements on the genome ,a process called gene prediction and attaching biological information to these elements by using **A command- line interface** is available for high throughput processing so the conclusions scientists have developed the SARS-COV-2 sequences and they handled web service for fast and easy analysis so the web server provides an interactive module for analysis and annotations the genome they thought that understanding the genome will help to know a whole sequences an predict any variations in the sequences .

## Related work:

**Comparison With Prior Works** the existing software packages VAPID **Reference** : “Shean RC, Makhsous N, Stoddard GD, Lin MJ, Greninger AL. VAPiD: a lightweight cross-platform viral annotation pipeline and identification tool to facilitate virus genome submissions to NCBI GenBank. BMC Bioinformatics 2019 Jan 23;20(1):48 [FREE Full text] [CrossRef] [Medline]” , and viral Genome ORF reader(VIGOR) **Reference:** ” Wang S, Sundaram JP, Spiro D. VIGOR, an annotation program for small viral genomes. BMC Bioinformatics 2010 Sep 07;11:451 [FREE Full text] [CrossRef] [Medline] “ , focus on **gene annotations** to our knowledge a software package that identifies, annotates, and visualizes genetic variants of SARS-CoV-2 has not previously been created

,they developed the **cov-seq web server** for fast and easy analysis of **SARS-CoV-2** sequences, they hope **COV-SEQ** will help improve our understanding of the genetics of **COVID-19**,in the future,they plan to expand the scope of COV-SEQ to include other viruses but **now CoV-Seq is currently limited to SARS-CoV-2 sequences**,The web server does not allow custom reference sequences other than **SARS-CoV-2**. We chose to focus on this virus because it has constituted the majority of processing requests during the **COVID-19 pandemic**. We plan to provide additional functionality to accept custom reference sequences in a future release.