Open Access
Full Length Article

ORIGINAL ARTICLE

COVID-19 Genomic Sequences Analysis using Google Variant Transformation

Haroon Zeb Khan[1], Muhammad Munwar Iqbal[2], Muhammad Salman Bashir[3]

[1, 2] Department of Computer Science, University of Engineering and Technology, Taxila
[3]Department of Computer Science and IT, Virtual University of Pakistan

ABSTRACT

Coronavirus genomics has been of various patterns since the pandemic began. The variants appear to differ in terms of both transmission and infection rates consistently. It analyzes genomic variants of coronaviruses to extract insights for research. This work employed the Variant Transform tool to process the Coronavirus variant caller format files with big-query for genomic variant analysis enveloped on the Google Cloud Platform. We opted for Google Cloud Platform (GCP), particularly Google Cloud Life Sciences Suite with Free-tier Track. We downloaded genome sequences of COVID–19 and then transformed them into raw variant caller format files (VCF). Then analyzing COVID–19 VCF files by Google Variant Transforms tool. We have converted 30 coronavirus genomic sequences into Variant Caller format files using bioinformatics tools, then attained a table of coronavirus variant sites as variant residues through a big query and displayed the results with Data studio. Another part is Deep Variant's genetic analysis of non-viral genomic data, and its corresponding supported four model implementation. Our main breakthrough was storing Coronavirus Variant caller format files into big-query for Coronavirus Genomic analysis.

Keywords: Big query, Coronavirus, Genomic sequences, Variant Transforms, Variant Caller Format

Author`s Contribution
[1,2] Data analysis, interpretation and manuscript writing, Active participation in data collection, [2] Conception, synthesis, planning of research, [3.] Interpretation and discussion

Address of Correspondence
Muhammad Munawar Iqbal
Email: munwar.iq@uettaxila.edu.pk

Article info.
Received: March 07, 2021
Accepted: June 17, 2021
Published: June 30, 2021

Cite this article: *Khan HZ, Iqbal MM, Bashir MS. COVID-19 Genomic Sequences Analysis using Google Variant Transformation. J. inf. commun. technol. robot. appl.2021; 12(1):28-35*

Funding Source: *Nil*
Conflict of Interest: *Nil*

INTRODUCTION

Coronavirus Disease (COVID) appeared in late December 2019, and people complained of shortness of breath and high-grade fever. At first, the most probable diagnosis, pneumonia, was the cause of illness that emerged rapidly in Wuhan, China [1]. At that stage, it was assumed that this was pneumonia or season cold and the infection of this contagious disease. World Health Organization (WHO) announced its first novel coronavirus-2019 [2, 3]. Coronavirus-2019 is the successor to its predecessors, for example, Severe Acute Respiratory Syndrome (SARS) and Middle Eastern Respiratory Syndrome (MERS). However, the infection of the virus is zoonotic, and humans act as a carrier for the virus to spread faster [4]. People with cardiovascular diseases, asthma, diabetes, and aged people are at higher risk than individuals, and children are passive

carriers of virus transmission [5]. The Coronavirus strain SARS-CoV-2 spread at an alarming rate throughout the globe, traveling recently by people amid Wuhan. Additionally, health workers and paramedic staff were infected rapidly, and some of them died [6].

There was no antecedent work in variants stored with a high-power computing cloud platform. The Variant Transforms tool is the solution to store billions of records of the VCF files into the big query to cope with this limitation. Genomic non-viral data was not previously analyzed to identify genetic variants [7]. Using neural networks in the deep learning setting with a gold-standard analysis pipeline produced more accurate results, better performance, and low computation time compared to other variant callers shown in Figure 1.

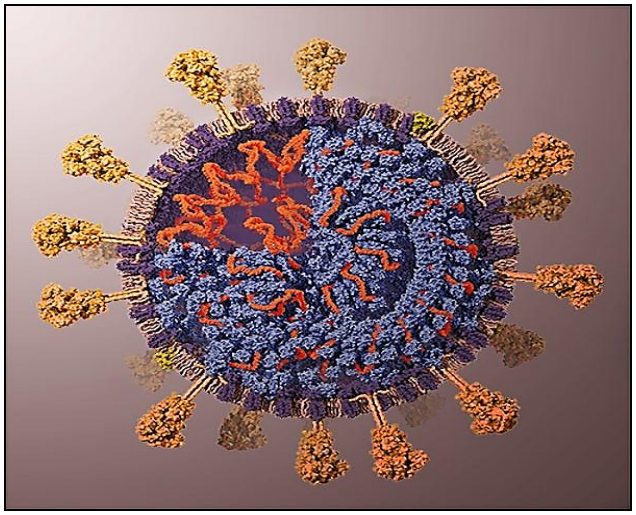


Figure 1: 3D Modelling of SARS-CoV–2 Molecular Structure [8]

Different types of testing for Coronavirus were performed, for instance, Reverse Transcription Polymerase Chain Reaction (RT-PCR), High-Resolution Computer Tomography (HRCT), Specific High Sensitivity Enzymatic Reporting Unlocking (SHERLOCK) one pot (SPOT).[9, 10]. The SHERLOCK test takes one hour and gives precise results. Our key contribution to this research was as follows:

1. The conceptual research design of the genomic idea includes SARS-CoV-2 genomes.
2. Extracting genomic variants led to 30 Variant Caller Format (VCF) files.
3. Setting code for Variant Transforms

This paper is organized into five sections. Section I introduces the Coronavirus, and Section II Contains related work. Section III presents the methodology. Section IV contains results and evaluation, and finally, Section V concludes the paper.

BACKGROUND

The related work section displays prominent research since the pandemic occurred. Nicholas O Grady et al. presented a cloud-based model, Patient Repository of Biomedical Entities (PROBE), in which data was analyzed, visualized, and shared within the context of a clinical trial based on breast cancer. The implementation of PROBE was for the prediction of biomarkers within the clinical investigation, providing access to Pan-Cancer Atlas and integration of pathological imaging datasets within the cloud infrastructure. However, the lack of risk stratification in diagnostics needs more improvisation [11]. Hirotaka Iwaki et al. presented accelerating medicines partnership Parkinson's Disease program developed a research platform for Parkinson Disease (PD), which can integrate with analysis, storage of sequencing data in whole-genome setting, RNA expression data, the clinical dataset to harmonize in multiple cohort case studies. They used the Variant Transforms Annotation feature as VEP [12].

Itay Bar-Or et al. used genomic surveillance for SARS-CoV–2 variants detection through Israel wastewater samples in nine locations [13]. The samples were taken from August 2020 to February 2021. The results showed a high concentration of the genome and mutations found that COVID–19 variant B.1.1.7 across Israel in the central and northern part in December 2020, and the pandemic spread in other parts of Israel in the first two months of 2021 [14]. Jennifer L. Guthrie et al. presented an analysis of SARS-CoV–2 genomes and sequencing data released from Public Health Ontario from September 6, 2020, to Oct10, 2020. The samples collected from patients in the eastern region in Ontario classified SARS-CoV–2 lineages were found, for example, pangolin (v2.08). A genomic surveillance strategy was applied in one patient that tells COVID–19 lineage B.1.177 of European origin previously found in Spain in the Summer of 2020 [15].

Chitra Pattabiraman et al. presented lineage division and analyzed sequences of 75 SARS-CoV–2 international travelers entering Southern India, Karnataka, from December 22, 2020, to January 31, 2021. The outcomes

of this study displayed SARS-CoV–2 34 lineages, 32.9%, 24/73 of B.1.1.7. However, the lineages B.1.36 and B.1 were designated as both imported lineages; B.1.136 lineage accounted for 27.04%, 20/73 while lineage B.1 showed 19.2%, 14/73, but other active lineages B.1.36 accounted for 43.7%, 45/103, B.1 lineage accounted for 25.2%, 26/103. It was noticed that lineage B.1.36 was responsible for the epidemic locally [14]. Katharina Jahn et al. conducted sequencing of genomes from 122 wastewater samples across Switzerland in three locations to analyze SARS-CoV–2 variants of concern, for example, B.1.1.7, B.1.351and P.1 variants, respectively. The authors developed a bioinformatics tool for analyzing multiple mutation signatures. The outcome of this study was that B.1.1.7 variant was found in two Swiss cities and observed in wastewater samples up to 1 week before its detection in the clinical data. The B.1.1.7 variant was found as highly prevalent in the alpine ski resort. When British tourists visited in December 2020, at a time when rare variants were present in Switzerland, other variants of concern COVID–19 variants, for instance, B.1.351 and P.1 lineage in this study, found no presence in the three Swiss locations [16].

In the literature, we have identified that the research gap in computing genomic variance is the complement between a genetic sample and a reference genome. The pavement of diagnosing patient disease and devising innovative treatment methods is the key to attaining the therapeutic objective. Every variant corresponding sample is retained as a particular file format, which is a variant file format (VCF). In contrast, the files are regarded for data science and machine learning on such genomic data. Data, particularly variants such as mutations in Coronavirus, can be identified and retracted to extract meaningful insights to analyze variants and unravel the genesis of the disease. Secondly, genomic variance computation and processing demand a state-of-the-art technology such as Google Cloud Platform (GCP) because it has a specific suite for genomic analysis, for instance, the Cloud life sciences suite. Additionally, to the best of our knowledge, there was no processing platform of a high standard for the genomic variants that could handle gigantic variants data and process in no time. For example, Variant Transforms has flourished on Mayo Clinic's genomic data platform and sparked many VCF files by Google Variant Transforms.

RESEARCH METHODOLOGY

This section includes the research methodology in which we performed various steps. First, we downloaded SARS-CoV-2 genome sequences through NCBI Sequence Read Archive (SRA) study SRP266465 involves COVID–19 patients of Massachusetts General Hospital data given by Broad Institute of Harvard and MIT to NCBI from which we used 30 accessions [17]. For 30 SRA accessions, we generate 30 VCF files. We opted for the Google Cloud Platform GCP Cloud Life sciences suite for our work. These 30 VCF files were uploaded to Google Cloud Storage Bucket created genomevt-v-1, in the multi-region as location type, we had used Variant Transforms for the processing of 30 VCF files. The step-by-step approach for the Variant Transforms as shown in Figure 2

.

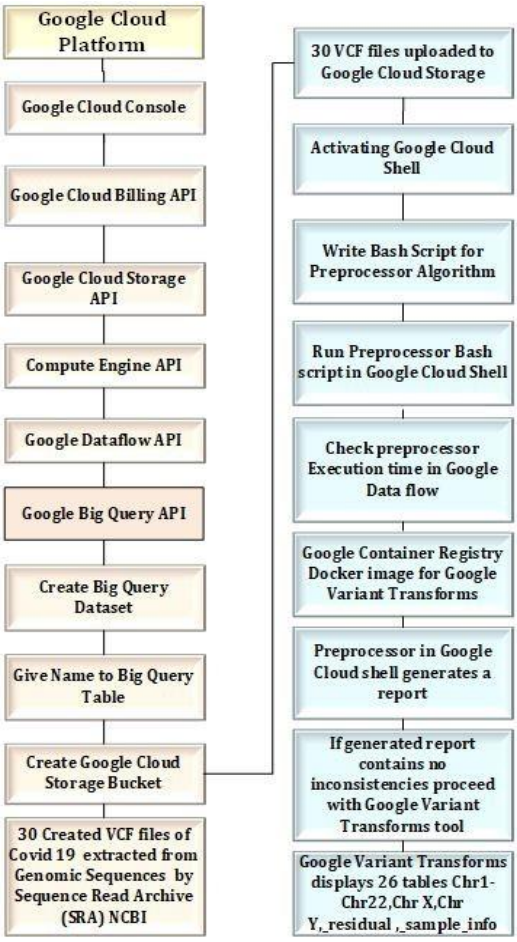


Figure 1: Research Methodology of Variant Transforms

It comprises first uploading VCF files into the cloud storage and then running bash script using wild card approach for all the 30 VCF files at once through Variant Transforms Preprocessor in Google Cloud Shell, which could check for any inconsistency in the subjected VCF files. Dataflow computes the Variant transforms job VCF-to-big-query-process lasts for approximately 10 minutes. The preprocess prints a report about the VCF files in tab-separated values (TSV) format as "VCF-report. tsv" and resolved headers of all 30 VCF files in the VCF format resolved-headers.VCF is shown in Figure 3.

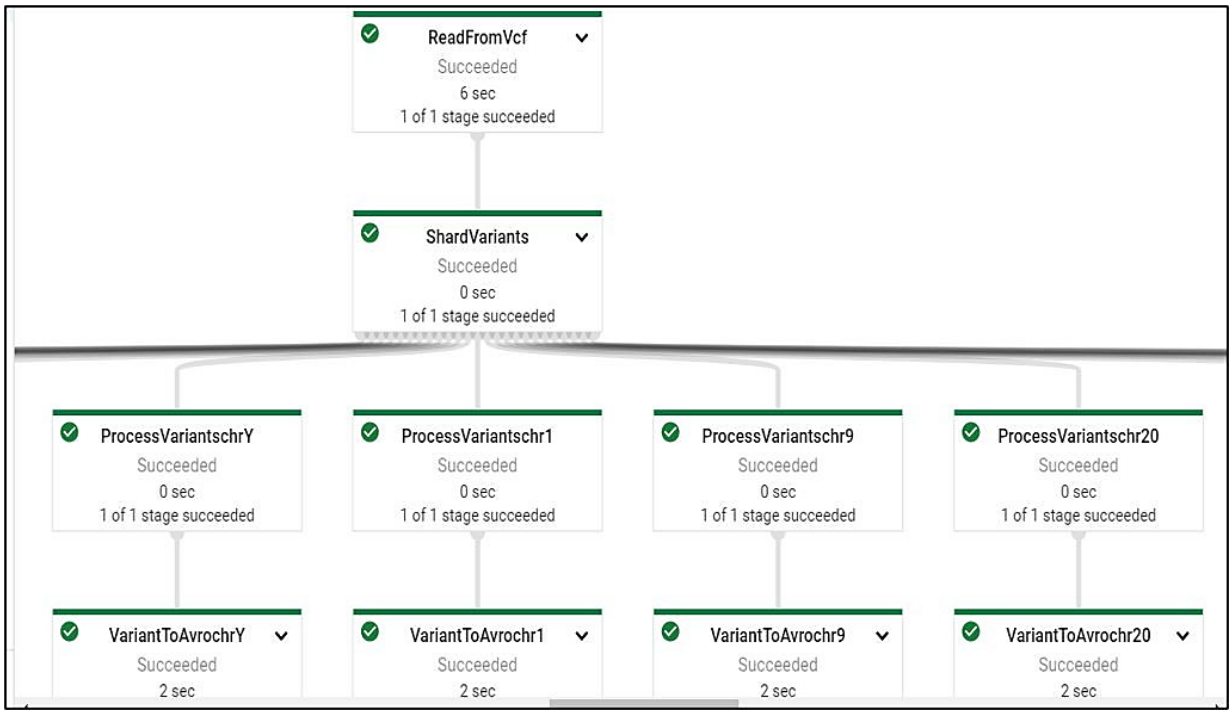


Figure 2: Variant Transforms Algorithm

RESULT AND EVALUATION

This section describes the results obtained in this work as in the methodology section. We used the wild card approach for the 30 VCF files present in the Google Cloud Storage Bucket named genomevt-v-1. In addition, we used Big Query. First, we created a Big Query dataset named gencovt in the United States (US) data as geographic location. We named our table for our VCF files result as cvariant-covid19. We run a variant transforms bash script in Cloud Shell, Dataflow. Computed the job VCF-to-big query, which lasted for approximately 15 minutes. After completion of the Variant transforms job in the big query, it generated a total of 26 tables for variants of SARS-CoV-2, which can be listed here (from Chr1-Chr22) are autosomal chromosomes, whereas cvariant-covid19- ChrX, cvaraint-covid19-ChrY, are (pair of Sex Chromosomes), cvaraint-covid19-residual, (SARS- CoV-2 Variants table) cvariant-covid19-sample-info (listed 30 VCF files as Sample Table) respectively.

In these 26 tables created by the Variant Transforms tool in the big query, only two tables, cvariant-covid19-residual and cvariant-covid19-sample-info, were non-empty while the rest of the tables were empty, which describes that the dataset was based on viral genome of Coronavirus, as viruses do not possess chromosomes. However, living organisms retain chromosomes. The sample-info table contains information about the sample id, sample name, file path, and ingestion time, while the residual table comprises all relevant information describing the variants, as shown in table 2. Depending on the extraction of information, the big query uses SQL query to display results in the tabular form. We presented the dataflow computation job graph for the variant

transform algorithm as shown in figure 2. We show the Variant transforms data flow job graph different from the preprocessor graph as shown in figure 3. The algorithm of this job graph by data flow starts from reading VCF files and then shards all variants from all subjected VCF files. Afterward, it processes variants first autosomal chromosomes and sex chromosomes. Finally, it processed variants transformed to Avro chromosomes, where Avro is a file format for storing processed variants data. The big query generated two non-empty tables. One describes the 30 VCF files sample details as shown in table 2, and the other table consists of variants information as shown in table 1. However, Table 2 is fixed, whereas table 2 is presented here as one of the data science scenarios obtained from the Master table of a big query containing 2924 rows corresponding to 2924 records. We created table 2, which has reference names, reference bases, and alternate bases. alt, start-position, end-position, Mann-Whitney U Test values which comprise Read position bias (RPB), Base quality Bias (BQB), Mapping quality bias (MQB), and Mapping quality vs. Strand bias (MQSB), and the final field Variant Distance Bias (VDB), which checks for a random collection of variant bases in the region where mapped reads are present.

Table 1: Variant Site Residue Table

S.No	Start Position	End Position	Reference Name	Reference Bases	MQB	MQSB	BQB	PV4	RPB	SGB	VBD	Record count
1	18484	19872	NC 045512.2	C	1	1	0.909091	1	0.818182	-0.453602	0.6	4
2	28360	28360	NC 045512.2	T	0.999953	0.995664	0.975468	1	0.233929	-0.693147	0.130402	3
3	2416	2416	NC 045512.2	C	1	0.999987	1	1	1	-0.693147	0.997474	3
4	28337	28337	NC 045512.2	G	1	0.999138	1	1	1	-0.693147	0.991373	3
5	28883	28883	NC 045512.2	G	0.990479	0.868433	0.0578885	1	0.231979	-0.693147	8.62216e-7	3
6	16875	16883	NC 045512.2	TACAAC AAC	null	0.95494	null	1	null	-0.453602	0.505913	3
7	25843	25843	NC 045512.2	A	1	1	0.825177	1	0.00006248	-0.651104	0.000019721	3
8	25843	25843	NC 045512.2	A	1	1	0.887746	1	0.109217	-0.616816	0.000481013	3
9	26233	26233	NC 045512.2	G	1	1	1	1	1	-0.693147	0.000041484	3
10	23403	23403	NC 045512.2	A	1	0.994879	1	1	1	-0.693147	0.143395	3
11	14408	14408	NC 045512.2	C	0.999265	0.027975	0.0822216	1	0.0979562	-0.693147	0.0350496	3
12	3037	3037	NC 045512.2	C	1	0.984749	1	1	1	-0.693147	0.00192569	3
13	25563	25563	NC 045512.2	G	1	0.999986	1	1	1	-0.693147	1.66242e-7	3
14	18848	18848	NC 045512.2	C	1	1	0.948064	1	0.0265162	-0.556411	0.0162466	3
15	19872	19872	NC 045512.2	G	1	1	0.366897	1	0.960687	-0.590765	0.00187095	3

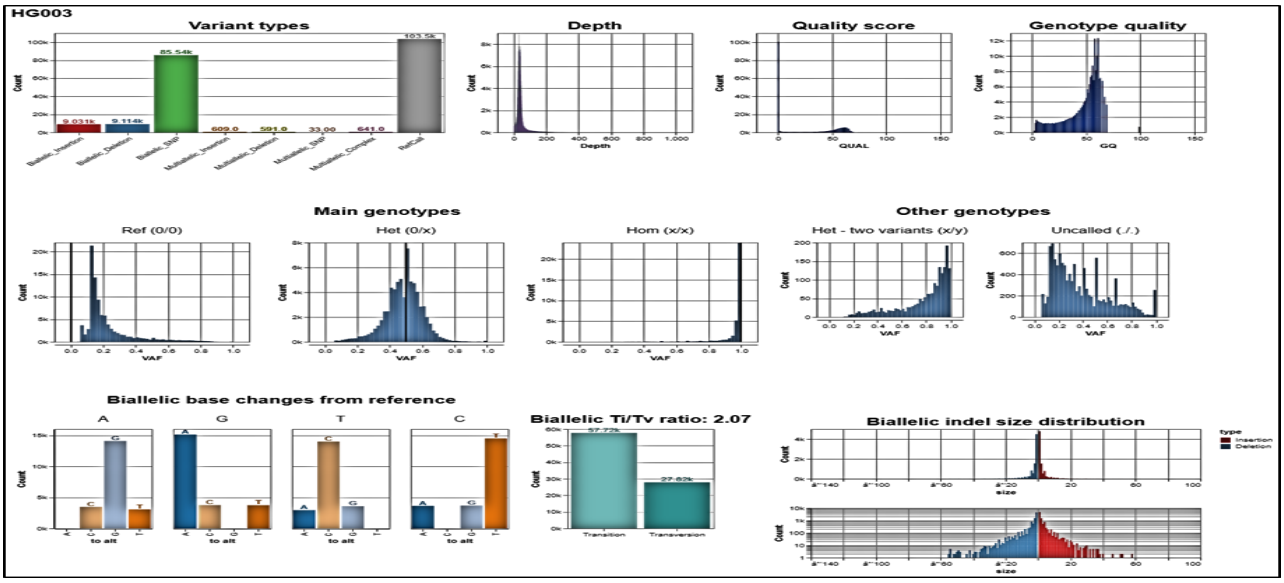
Table 2: Sample_info Table 30 VCF files

S. No	Sample id	Sample name	File path	Ingestion date	Record count
1.	3216550734874377043	SRR11953670.sort.bam	gs://genomevt v-1/vcf/SRR11953670.var-final.vcf	2021-03-09 13:04:00 UTC	1
2.	352489629759615578	SRR11953671.sort.bam	gs://genomevt v-1/vcf/SRR11953671.var-final.vcf	2021-03-09 13:04:00 UTC	1
3.	8227663251833541077	SRR11953672.sort.bam	gs://genomevt v-1/vcf/SRR11953672.var-final.vcf	2021-03-09 13:04:00 UTC	1
4.	8357062031852223960	SRR11953673.sort.bam	gs://genomevt v-1/vcf/SRR11953673.var-final.vcf	2021-03-09 13:04:00 UTC	1
5.	2806340148173514704	SRR11953674.sort.bam	gs://genomevt v-1/vcf/SRR11953674.var-final.vcf	2021-03-09 13:04:00 UTC	1
6.	2582873836293763020	SRR11953675.sort.bam	gs://genomevt v-1/vcf/SRR11953675.var-final.vcf	2021-03-09 13:04:00 UTC	1
7.	979035968381476808	SRR11953676sort.bam	gs://genomevt v-1/vcf/SRR11953676.var-final.vcf	2021-03-09 13:04:00 UTC	1
8.	5277621863161793105	SRR11953677.sort.bam	gs://genomevt v-1/vcf/SRR11953677.var-final.vcf	2021-03-09 13:04:00 UTC	1
9.	566504859183568350	SRR11953678sort.bam	gs://genomevt v-1/vcf/SRR11953678var-final.vcf	2021-03-09 13:04:00 UTC	1
10.	3833680178983260965	SRR11953679.sort.bam	gs://genomevt v-1/vcf/SRR11953679.var-final.vcf	2021-03-09 13:04:00 UTC	1
11.	8533412563562316116	SRR11953680sort.bam	gs://genomevt v-1/vcf/SRR11953680.var-final.vcf	2021-03-09 13:04:00 UTC	1
12.	3519872865606448254	SRR11953681.sort.bam	gs://genomevt v-1/vcf/SRR11953681.var-final.vcf	2021-03-09 13:04:00 UTC	1
13.	3662038835489796241	SRR11953683.sort.bam	gs://genomevt v-1/vcf/SRR11953683.var-final.vcf	2021-03-09 13:04:00 UTC	1
14.	5890621020233963195	SRR11953684.sort.bam	gs://genomevt v-1/vcf/SRR11953684.var-final.vcf	2021-03-09 13:04:00 UTC	1
15.	5316490262417333523	SRR11953685.sort.bam	gs://genomevt v-1/vcf/SRR11953685.var-final.vcf	2021-03-09 13:04:00 UTC	1
16.	150785628643285227	SRR11953686.sort.bam	gs://genomevt v-1/vcf/SRR11953686.var-final.vcf	2021-03-09 13:04:00 UTC	1

17.	7413376885039050630	SRR11953687.sort.bam	gs://genomevt v-1/vcf/SRR11953687.var-final.vcf	2021-03-09 13:04:00 UTC	1
18.	668647478787251403	SRR11953688.sort.bam	gs://genomevt v-1/vcf/SRR11953688.var-final.vcf	2021-03-09 13:04:00 UTC	1
19.	2040752609674665819	SRR11953689.sort.bam	gs://genomevt v-1/vcf/SRR11953689.var-final.vcf	2021-03-09 13:04:00 UTC	1
20.	3189181725568227223	SRR11953690.sort.bam	gs://genomevt v-1/vcf/SRR11953690.var-final.vcf	2021-03-09 13:04:00 UTC	1
21.	7689594917302935664	SRR11953691sort.bam	gs://genomevt v-1/vcf/SRR11953691.var-final.vcf	2021-03-09 13:04:00 UTC	1
22.	3349372544095480697	SRR11953692.sort.bam	gs://genomevt v-1/vcf/SRR11953692.var-final.vcf	2021-03-09 13:04:00 UTC	1
23.	7351685286731755226	SRR11953693.sort.bam	gs://genomevt v-1/vcf/SRR11953693.var-final.vcf	2021-03-09 13:04:00 UTC	1
24.	8127585703603632648	SRR11953694.sort.bam	gs://genomevt v-1/vcf/SRR11953694.var-final.vcf	2021-03-09 13:04:00 UTC	1
25.	2543651269845840959	SRR11953695.sort.bam	gs://genomevt v-1/vcf/SRR11953695.var-final.vcf	2021-03-09 13:04:00 UTC	1
26.	1311637592895431099	SRR11953696.sort.bam	gs://genomevt v-1/vcf/SRR11953696var-final.vcf	2021-03-09 13:04:00 UTC	1
27.	1542741616589133359	SRR11953697.sort.bam	gs://genomevt v-1/vcf/SRR11953697.var-final.vcf	2021-03-09 13:04:00 UTC	1
28.	5909100411738514128	SRR11953698.sort.bam	gs://genomevt v-1/vcf/SRR11953698.var-final.vcf	2021-03-09 13:04:00 UTC	1
29.	3344475419929969819	SRR11953699.sort.bam	gs://genomevt v-1/vcf/SRR11953699.var-final.vcf	2021-03-09 13:04:00 UTC	1
30.	5297186131858853415	SRR11953700.sort.bam	gs://genomevt v-1/vcf/SRR11953700.var-final.vcf	2021-03-09 13:04:00 UTC	1

The tables were created by google big query and produced results by data studio. The retrospective literature we presented did not have this research that we exploited using Coronavirus genomic variants enveloped on the Google Cloud platform: Variant Transforms, Big query, Dataflow, so this research is incomparable.

The first Deep Variant model in this genomic research is Whole-genome sequencing (WGS). We presented the result of this model. The HG003 is the data set sample. We showed the variant types. In the Whole-genome sequencing (WGS) case study, we showed that variant types, including Biallelic_SNP, were the dominant variant type with 85.54k and the RefCall was 103.5k, while both Biallelic insertion and deletion reached 9k. The Biallelic bases transform from reference bases. For instance, AGTC becomes GACT, and the Biallelic Transition to Transversion ratio was recorded at 2.07, where Transition was 57.72k, and Transversion was 27.02k. The depth was sky-rocketed increased, it gained a peak above 8k, then it showed an as dramatic decrease, and it reaches 200 as shown in figure 5.4, the quality score QUAL increased rapidly to 100k then, it dramatically decreases to 55, the quality of genotype showed a steady increase from 1500 to above 12k then it showed a downward trend and reached 55 as GQ. Afterward, three main genotypes were presented. For example, homozygous, heterozygous, and reference setting for the Variant Allele Fraction (VAF) was computed. The Ref setting (0/0), for VAF, first it showed a dramatic increase reaches 20k, then it drops at 0.02 then it gained peak at above 20k then it showed a dramatic decrease at 0.9, and it is levelled off. In the heterozygous scenario (0/x), it showed a slight increase at 0.1, and it gained a peek at 8k, then it gained a sudden drop and reached to1.0, and it is plateaued. The homozygous setting (x/x) showed a steady increase at 0.5 and reached the highest point of 1.0, shown in Figure 4



However, the other genotypes, consisting of VAF for heterozygous two variants (x/y) and uncalled (/) for heterozygous it, showed a slight increase and it gained a peak at 1.0, and the uncalled (/) it gained a slight increase at 0.1, and it reaches the peak at 600 and then it showed slight fluctuation in between in 0.4, 0.5, 0.6, 0.8 and it reaches 1.0. The Biallelic insertion and deletion distribution were shown in whole-genome sequencing. It increased steadily, then it gained a peak, and then it decreased.

CONCLUSION

This study used Google Cloud Platform Cloud Life sciences Suite. There will be more variants in the essence of our work summates as time progresses. The importance of variants will be paramount, leading to drug or vaccine discovery for the Coronavirus. This work created 30 variant caller format files from Coronavirus genome sequences using its reference genome. When we first executed the Variant Transforms tool Preprocessor algorithm for the 30 VCF files, then, after successful execution, it generated a report which found no inconsistency. Which was a bottleneck for further analysis of variants using Variant transforms running bash script. First, it is good practice to run VCF files through the Variant transforms preprocessor tool. Moreover, out of 26 tables, two tables were reserved for residual and sample information. The processing time calculated by the Google data flow for the preprocessing phase was minimized by 10 minutes, and for the non-Preprocess phase, it was minimized up to 15 minutes. Google Deep Variant only identifies genetic variants, not viral variants. In the future, it is a promising challenge for the upcoming researchers in the Coronavirus era. Genomics.

REFERENCES

1. Andersen, K., and Rambaut, A.: 'A, Lipkin WL, Holmes EC, Garry RF', The proximal origin of SARS-CoV-2. Nat Med, 2020, 26, pp. 450-452
2. Steens, A., De Blasio, B.F., Veneti, L., Gimma, A., Edmunds, W.J., Van Zandvoort, K., Jarvis, C.I., Forland, F., and Robberstad, B.: 'Poor self-reported adherence to COVID-19-related quarantine/isolation requests, Norway, April to July 2020', Eurosurveillance, 2020, 25, (37), pp. 2001607
3. Mousavizadeh, L., and Ghasemi, S.: 'Genotype and phenotype of COVID-19: Their roles in pathogenesis', Journal of Microbiology, Immunology and Infection, 2021, 54, (2), pp. 159-163
4. Lee, P.-I., and Hsueh, P.-R.: 'Emerging threats from zoonotic coronaviruses-from SARS and MERS to 2019-nCoV', Journal of microbiology, immunology, and infection, 2020, 53, (3), pp. 365
5. Mueller, A.L., McNamara, M.S., and Sinclair, D.A.: 'Why does COVID-19 disproportionately affect older people?', Aging (albany NY), 2020, 12, (10), pp. 9959
6. Mehdi, M., Waseem, M., Rehm, M.H., Aziz, N., Anjum, S., and Javid, M.A.: 'Depression and Anxiety in Health Care Workers during COVID-19', Biomedica, 2020, 36
7. Newhouse, C.N., Saleh, T., Fuller, T., Kerin, T., Cambou, M.C., Swayze, E.J., Le, C., Seo, W., Trejo, M., and Garner, O.B.: 'Predictors of SARS-CoV-2 Infection in Youth at a Large, Urban Healthcare Center in California, March–September 2020', Frontiers in pediatrics, 2021, 9
8. Challener, D.W., Challener, G.J., Gow-Lee, V.J., Fida, M., Shah, A.S., and O'Horo, J.C.: 'Screening for COVID-19: Patient factors predicting positive PCR test', Infection Control & Hospital Epidemiology, 2020, 41, (8), pp. 968-969
9. Tahamtan, A., and Ardebili, A.: 'Real-time RT-PCR in COVID-19 detection: issues affecting the results', Expert review of molecular diagnostics, 2020, 20, (5), pp. 453-454
10. Lins, M., Vandevenne, J., Thillai, M., Lavon, B.R., Lanclus, M., Bonte, S., Godon, R., Kendall, I., De Backer, J., and De Backer, W.: 'Assessment of small pulmonary blood vessels in COVID-19 patients using HRCT', Academic radiology, 2020, 27, (10), pp. 1449-1455
11. Mahas, A., Wang, Q., Marsic, T., and Mahfouz, M.M.: 'A Novel Miniature CRISPR-Cas13 System for SARS-CoV-2 Diagnostics', ACS synthetic biology, 2021, 10, (10), pp. 2541-2551
12. O'Grady, N., Gibbs, D.L., Abdilleh, K., Asare, A., Asare, S., Venters, S., Brown-Swigart, L., Hirst, G.L., Wolf, D., and Yau, C.: 'PRoBE the cloud toolkit: finding the best biomarkers of drug response within a breast cancer clinical trial', JAMIA open, 2021, 4, (2), pp. ooab038
13. Bar-Or, I., Weil, M., Indenbaum, V., Bucris, E., Bar-Ilan, D., Elul, M., Levi, N., Aguvaev, I., Cohen, Z., and Shirazi, R.: 'Detection of SARS-CoV-2 variants by genomic analysis of wastewater samples in Israel', Science of The Total Environment, 2021, 789, pp. 148002
14. Capoluongo, E., Nardelli, C., Esposito, M.V., Buonomo, A.R., Gelzo, M., Pinchera, B., Zappulo, E., Viceconte, G., Portella, G., and Setaro, M.: 'Case Report: Discovery a Novel SARS-CoV-2 Variant in a Six-Months Long-Term Swab Positive Female Suffering From Non-Hodgkin Lymphoma', Frontiers in Oncology, 2021, pp. 2880
15. Bakshi, R., Kaur, S., Kaur, K., Kaur, R., Boparai, J.K., Ghai, R., Kaur, T., Kaur, A., Kaur, J., and Verma, K.: 'Molecular Analysis and Genome Sequencing of SARS-CoV-2 during Second Wave 2021 Revealed Variant Diversity in India', Journal of Pure and Applied Microbiology, 2021, 15, (4), pp. 1864-1873
16. Jahn, K., Dreifuss, D., Topolsky, I., Kull, A., Ganesanandamoorthy, P., Fernandez-Cassi, X., Bänziger, C., Devaux, A.J., Stachler, E., and Caduff, L.: 'Detection and surveillance of SARS-CoV-2 genomic variants in wastewater', medRxiv, 2021
17. Lai, C.-C., Shih, T.-P., Ko, W.-C., Tang, H.-J., and Hsueh, P.-R.: 'Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and coronavirus disease-2019 (COVID-19): The epidemic and the challenges', International journal of antimicrobial agents, 2020, 55, (3), pp. 105924.