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# Study of Certain Corona Family Related Viruses based on Percentage Nucleotide Concentration and Golden Ratios and a Novel Sonic Attack Technique to Deactivate all Mutating Viruses

*Ethirajan Govindarajan*

## ABSTRACT

A set of 130 complete genome data of Corona type viruses are analyzed and classified based on their Percentage Concentrations of Nucleotides and Golden Ratios. The purpose of this study is to extract finer and hidden details about the evolutionary nature of Corona type viruses. It was found that all Corona type viruses evolve by random mutation but with their basic structural and functional genetic property maintained in the system biological sense. This has already been verified by extracting common digital spatial and spectral patterns during a study on "Pairwise Spatial Correlation of SARS-Corona Viruses" and on "Pairwise Spectral Correlation of SARS-Corona Viruses". The scope of this paper is limited to the study of a set of 130 virus metadata in terms of certain quantificational measures such as (i) Golden Ratios (GR) and (ii) Percentage Concentrations of Nucleotides (pA, pT, pG and pC), and classification of those viruses based on these measures.

**Keywords:** corona type viruses, golden ratios, percentage concentrations of nucleotides, artificial intelligence, sonic bursts.

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# Study of Certain Corona Family Related Viruses based on Percentage Nucleotide Concentration and Golden Ratios and a Novel Sonic Attack Technique to Deactivate all Mutating Viruses

Ethirajan Govindarajan

## CAUTION

*This is a theoretical investigation carried out on certain genome data of Corona type viruses archived in NCBI and results reported in this document are outcomes based on certain subjective definitions, notions and genome data analysis. Results presented here are to be deliberated and interpreted by Genetic Scientists, Agriculture Scientists, Biologists, Biotechnologists, Biochemists, Biophysicists and Microbiologists. This research report is meant for public use.*

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## ABSTRACT

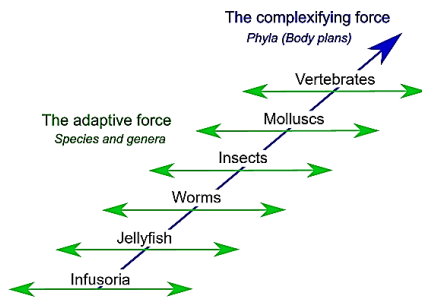
A set of 130 complete genome data of Corona type viruses are analyzed and classified based on their Percentage Concentrations of Nucleotides and Golden Ratios. The purpose of this study is to extract finer and hidden details about the evolutionary nature of Corona type viruses. It was found that all Corona type viruses evolve by random mutation but with their basic structural and functional genetic property maintained in the system biological sense. This has already been verified by extracting common digital spatial and spectral patterns during a study on “Pairwise Spatial Correlation of SARS-Corona Viruses” and on “Pairwise Spectral Correlation of SARS-Corona Viruses”. The scope of this paper is limited to the study of a set of 130 virus metadata in terms of certain quantificational measures such as (i) Golden Ratios (GR) and (ii) Percentage Concentrations of Nucleotides (pA, pT, pG and pC), and classification of those viruses based on these measures. Despite many drugs, vaccines and immunity boosters that move around the world with the idea of bringing down the pandemic state of affairs, the unpredictable ramification due to structural and genetic functional variations of Corona type viruses causes a serious concern, more specifically, a doubt/fear whether God has created these viruses or Man has created them. However, one should continue doing research in developing various diagnostic tools and therapeutic measures. Dismembering virus structures with ‘sonic’ frequencies that resonate with the natural frequencies of RNA forms and dismember them is one way of looking into solving this problem. This paper advocates a novel technique of generating pure tones as bursts and explores the possibilities of breaking the virus RNA sequences that are present inside the body or in the environment.

## Curtain Raiser

सूक्ष्मयोनीनि भूतानि तर्कं गम्यानि कानि चित  
पक्ष्मणो ऽपि निपातेन येषां सयात सकन्धपर्ययः

*There are many creatures that are so minute that their existence can only be inferred.  
With the falling of the eyelids alone, they are destroyed. (Mahabharata)*

RNAs and DNAs are the fundamental units used in this process of consumables and consumers interchanging their roles. Life Forms are constructs made up of these units. RNAs could be viewed as ‘Viruses’. They are constructive as well as destructive. Viruses play a constructive role in the forward process of evolution when the hosts can consume them, whereas, the same viruses play a destructive role in devolution, the reverse process of evolution when the hosts are unable to consume them.



“Lamarck's theory of evolution involved a complexifying force that progressively drives animal body plans towards higher levels, creating a ladder of phyla, as well as an adaptive force that causes animals with a given body plan to adapt to circumstances. The idea of progress in such theories permits the opposite idea of decay, seen in devolution”.

[https://en.wikipedia.org/wiki/Devolution\\_\(biology\)](https://en.wikipedia.org/wiki/Devolution_(biology))

At present, SARS-Corona type viruses act as destructive viruses and they do their job. It is up to humans to understand them, their role and try to delay the process of becoming consumables for them in the reverse process.

उद्यन्नादित्यः क्रिमीन्हन्तु निम्नोचन्हन्तु रश्मिभिः ।  
ये अन्तः क्रिमयो गवि ॥ १ ॥  
विश्वरूपं चतुरक्षं क्रिमिं सारङ्गमर्जुनम् ।  
शृणाम्यस्य पृष्टीरपि वृक्षामि यच्छिरः ॥ २ ॥  
अत्रिवद्धः क्रिमयो हन्मि कण्ववज्जमदग्निवत् ।  
अगस्त्यस्य ब्रह्मणा सं पिनष्यहं क्रिमीन् ॥ ३ ॥  
हतो राजा क्रिमीणामुतैषां स्थपतिर्हितः ।  
हतो हतमाता क्रिमिर्हतभ्राता हतस्वसा ॥ ४ ॥  
हतासो अस्य वेशसो हतासः परिवेशसः ।  
अथो ये क्षुल्लका इव सर्वे ते क्रिमयो हताः ॥ ५ ॥  
प्र ते शृणामि शृङ्गे याभ्यां वितुदायसि ।  
भिनसि ते कुषुम्भं यस्ते विषधानः ॥ ६ ॥

May the sun as he rises up kill the virus with his rays and also while setting let him kill the virus. Let these rays destroy the virus that lives within the beings. **I destroy the structure of the virus and demolish the virus in all of its forms.** Oh virus ! I will crush you in the same way as the Rishi Atri, Rishi Kanva and Rishi Jamadagni - the lords of cleanliness - crush you with a great grinder and with blazing fire. I crush you thoroughly with the knowledge of cleanliness. The king of the virus has been killed and their progenitor chieftain also is killed. The virus is killed along with his mother, his brothers and sisters. Neighbors of the virus are killed along with the virus' acquaintances. The subsidiary viruses and smaller viruses have been killed as well. I crush your antennas with which you torment others and I pierce your vicious pouch which is the store of your poison.

<https://bhawnayagya.org/atharva-veda-hymn-for-eradication-of-virus/>

This report is a result of intensive research carried out by devoted scientists who work with passion. The team acknowledges **Professor Jean-Claude Perez** for his suggestion to study partially deleted genomes like strains evolved in WA, Seattle, USA referenced in his research paper titled “COVID-19, SARS and Bats Coronaviruses Genomes Unexpected Exogeneous RNA Sequences”, (<https://osf.io/d9e5g/>). His timely advice and technical references in connection with Corona viruses is highly appreciated. The team also acknowledges “Edouard Aime, Alessandro Masciarelli, Alexandra HC, Alexandra Simplissima, Béatrice LOPEZ, birgitta.neher, Cerdan, Christian PELLEGRINI, Christian Perronne, Daniel Favre, Diego Lucio Rapoport,

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**Keywords:** corona type viruses, golden ratios, percentage concentrations of nucleotides, artificial intelligence, sonic bursts.

## I. DATA USED FOR ANALYSIS

More than 70,000 virus genome data have been listed in NCBI website. However, one hundred and thirty complete genomes of various categories of viruses are drawn from NCBI web site <https://www.ncbi.nlm.nih.gov/genbank/sars-cov-2-seqs/> for data analysis. The data given by NCBI is expected to be genuine.

### Arteriviridae

- S1. >NC\_001639.1 Lactate dehydrogenase-elevating virus, complete genome
- S2. >NC\_001961.1 Porcine respiratory and reproductive syndrome virus, complete genome
- S3. >NC\_002532.2 Equine arteritis virus, complete genome
- S4. >NC\_003092.2 Simian hemorrhagic fever virus, complete genome
- S5. >NC\_025112.1 Mikumi yellow baboon virus 1 isolate MYBV\_M58, complete genome
- S6. >NC\_025113.1 Southwest baboon virus 1 isolate SWBV\_16986\_11/4/2013, complete genome
- S7. >NC\_026439.1 Forest pouched giant rat arterivirus isolate PREDICT-06509, complete genome
- S8. >NC\_026509.1 DeBrazzas monkey arterivirus isolate PREDICT-06530, complete genome
- S9. >NC\_027124.1 Pebjah virus isolate I621, complete genome
- S10. >NC\_029053.1 Kafue Kinda chacma baboon virus isolate KKCBV-1, complete genome
- S11. >NC\_029992.1 UNVERIFIED: Free State vervet virus isolate VSAI1003, complete genome
- S12. >NC\_035127.1 Olivier's shrew virus 1 isolate Gkd-1, complete genome
- S13. >NC\_038291.1 Porcine reproductive and respiratory syndrome virus 2, complete genome
- S14. >NC\_038293.1 Simian hemorrhagic encephalitis virus isolate Sukhumi, complete genome
- S15. >NC\_043487.1 Lelystad virus, complete genome
- S16. >NC\_048209.1 Zambian malbrouck virus 1 isolate SHFVagmMal\_seqID\_01, partial genome

### Duplornaviricota

- S17. >NC\_003555.1 Giardia lamblia virus, complete genome
- S18. >NC\_005883.1 Chalaro elegans RNA Virus 1, complete genome
- S19. >NC\_007523.1 Coniothyrium minitans RNA virus, complete genome
- S20. >NC\_009224.1 Botryotinia fuckeliana totivirus 1, complete genome
- S21. >NC\_009890.1 Black raspberry virus F, complete genome
- S22. >NC\_014609.1 Armigeres subalbatus virus SaX06-AK20, complete genome
- S23. >NC\_024151.1 Beauveria bassiana victorivirus NZL/1980 isolate 6887, complete genome
- S24. >NC\_025214.1 Botryosphaeria dothidea victorivirus 1 isolate GY25, complete genome
- S25. >NC\_027212.1 Camponotus yamaokai virus genomic RNA, complete genome
- S26. >NC\_030295.1 Golden shiner totivirus isolate GSTV/US/MN/2014, partial genome
- S27. >NC\_030867.1 Fusarium poae victorivirus 1 genomic RNA, complete genome
- S28. >NC\_035674.1 Australian Anopheles totivirus isolate AATV 150840, complete genome
- S29. >NC\_038928.1 Aspergillus foetidus slow virus 1 CP gene and RdRp gene, genomic RNA
- S30. >NC\_038929.1 Beauveria bassiana victorivirus 1, complete genome
- S31. >NC\_040431.1 Diatom colony associated dsRNA virus 13 genomic RNA, complete genome
- S32. >NC\_040632.1 Gigaspora margarita giardia-like virus 1 isolate GmGIV1-BEG34, complete genome
- S33. >NC\_040653.1 Fusarium asiaticum victorivirus 1 isolate F16176, complete genome
- S34. >NC\_040659.1 Diatom colony associated dsRNA virus 10 genomic RNA, complete genome
- S35. >NC\_040660.1 Diatom colony associated dsRNA virus 11 genomic RNA, complete genome
- S36. >NC\_040775.1 Diatom colony associated dsRNA virus 12 genomic RNA, complete genome
- S37. >NC\_040793.1 Alternaria arborescens victorivirus 1 genomic RNA, complete genome

### Gresnaviridae

- S38. >NC\_046959.1 Guangdong greater green snake arterivirus strain LPSG2430 1ab protein, putative glycoprotein, and hypothetical protein genes, complete cds

### Kitrinoviricota

- S39. >NC\_000939.2 Pothos latent virus genes for replicase, capsid protein and movement protein
- S40. >NC\_001461.1 Bovine viral diarrhea virus 1, complete genome
- S41. >NC\_001512.1 O'nyong-nyong virus, complete genome
- S42. >NC\_001513.1 Ononis yellow mosaic virus, complete genome
- S43. >NC\_001564.2 Cell fusing agent virus strain Galveston, complete genome

- S44. >NC\_001642.1 Bamboo mosaic virus, complete genome  
 S45. >NC\_001728.1 Odontoglossum ringspot virus, complete genome  
 S46. >NC\_001948.1 Rupestris stem pitting associated virus-1, complete genome  
 S47. >NC\_002604.1 Botrytis virus F, complete genome  
 S48. >NC\_002729.1 Banana mild mosaic virus, complete genome  
 S49. >NC\_002795.1 Aconitum latent virus, complete genome  
 S50. >NC\_003557.1 Garlic latent virus, complete genome  
 S51. >NC\_003603.1 Groundnut rosette virus complete genome, strain MC1  
 S52. >NC\_003608.1 Hibiscus chlorotic ringspot virus, complete genome  
 S53. >NC\_003634.1 Physalis mottle virus, complete genome  
 S54. >NC\_003679.1 Border disease virus X818, complete genome  
 S55. >NC\_003852.1 Obuda pepper virus, complete genome  
 S56. >NC\_003900.1 Aura virus, complete genome  
 S57. >NC\_004724.1 Grapevine rootstock stem lesion associated virus, complete genome  
 S58. >NC\_005062.1 Omsk hemorrhagic fever virus, complete genome  
 S59. >NC\_005132.1 Botrytis virus X, complete genome  
 S60. >NC\_006939.1 Olive mild mosaic virus, complete genome  
 S61. >NC\_007733.2 Angelonia flower break virus, complete genome  
 S62. >NC\_009028.2 Ilheus virus, complete genome  
 S63. >NC\_009892.1 Peach chlorotic mottle virus, complete genome  
 S64. >NC\_011535.1 Grapevine Algerian latent virus, complete genome  
 S65. >NC\_011538.1 Nemesia ring necrosis virus, complete genome  
 S66. >NC\_011552.1 Peach mosaic virus, complete genome  
 S67. >NC\_011559.1 Anagyris vein yellowing virus, complete genome  
 S68. >NC\_012533.2 Kedougou virus strain DakAar D1470, complete genome  
 S69. >NC\_012534.1 Bagaza virus strain DakAr B209, complete genome  
 S70. >NC\_012812.1 Bovine viral diarrhea virus 3 Th/04\_KhonKaen, complete genome  
 S71. >NC\_013006.1 Kalanchoe latent virus, complete genome  
 S72. >NC\_015782.2 Grapevine Pinot gris virus complete genome, genomic RNA  
 S73. >NC\_016038.2 Brassica yellows virus isolate BrYV-ABJ, complete genome  
 S74. >NC\_016404.1 Actinidia virus B, complete genome  
 S75. >NC\_016440.1 Garlic common latent virus, complete genome  
 S76. >NC\_016959.1 Ndumu virus, complete genome  
 S77. >NC\_018713.1 Pestivirus strain Aydin/04-TR, complete genome  
 S78. >NC\_020470.1 Andean potato latent virus, complete genome  
 S79. >NC\_020471.1 Andean potato mild mosaic virus isolate Hu, complete genome  
 S80. >NC\_023439.1 Kama virus strain LEIV-20776Tat polyprotein gene, complete cds  
 S81. >NC\_023892.1 Gaillardia latent virus isolate 5/18-05-2010, complete genome  
 S82. >NC\_024458.1 Pitaya virus X isolate P37, complete genome  
 S83. >NC\_024887.1 Middelburg virus isolate ArB-8422, complete genome  
 S84. >NC\_026620.1 Jutiapa virus strain JG-128, complete genome  
 S85. >NC\_028793.2 Phasey bean mild yellows virus isolate NSWCP15, complete genome  
 S86. >NC\_030693.1 Grapevine Red Globe virus isolate Graciano-T101, complete genome  
 S87. >NC\_031327.1 Anopheles flavivirus variant 1, complete genome  
 S88. >NC\_040842.1 Potexvirus sp., complete genome  
 S89. >NC\_040837.1 Grapevine associated tympo-like virus, complete genome  
 S90. >NC\_040800.1 Actinidia seed-borne latent virus isolate 01227, complete genome  
 S91. >NC\_040788.1 Kampung Karu virus isolate SWK\_P44, complete genome  
 S92. >NC\_040776.1 Rocio virus strain SPH 34675, complete genome  
 S93. >NC\_039237.1 Bovine viral diarrhea virus 2 polyprotein gene, complete cds  
 S94. >NC\_039218.1 Kyasanur forest disease virus polyprotein gene, complete cds  
 S95. >NC\_039217.1 Phascolus vulgaris endornavirus 1 isolate PvEV-1\_Brazil polyprotein gene, complete cds  
 S96. >NC\_038966.1 Atractylodes mottle virus isolate SK, complete genome  
 S97. >NC\_036587.1 Babaco mosaic virus isolate Tandapi, complete genome  
 S98. >NC\_035462.1 Ocimum basilicum RNA virus 1 isolate DV1 RNA-dependent RNA polymerase and movement protein genes  
 S99. >NC\_035453.1 Actinidia virus 1 isolate K75, complete genome  
 S100. >NC\_035116.1 Lake Sinai Virus TO ORF1, RNA-dependent RNA polymerase, ORF3, and ORF4 genes, complete cds  
 S101. >NC\_035071.1 Apis flavivirus isolate RI-A polyprotein gene, complete cds  
 S102. >NC\_034833.1 Agave tequilana leaf virus isolate agave azul-Mex1, complete genome  
 S103. >NC\_034242.1 Ochlerotatus caspius flavivirus isolate 1608 polyprotein gene, complete cds  
 S104. >NC\_034216.1 Lagenaria siceraria endornavirus-Hubei isolate JZ, complete genome  
 S105. >NC\_034207.1 African eggplant yellowing virus isolate eMA4, complete genome  
 S106. >NC\_034205.1 Grapevine rupestris vein feathering virus isolate Mauzac, complete genome  
 S107. >NC\_033828.1 Peach virus D isolate SK, complete genome  
 S108. >NC\_033725.1 Bamaga virus isolate CY4270 polyprotein gene, complete cds  
 S109. >NC\_033724.1 Kadam virus from Uganda polyprotein gene, complete cds  
 S110. >NC\_033723.1 Gadgets Gully virus from Australia polyprotein gene, complete cds  
 S111. >NC\_033699.1 Jugra virus strain P-9-314 polyprotein gene, complete cds  
 S112. >NC\_033693.1 Boubou virus strain DAK AR B490 polyprotein gene, complete cds  
 S113. >NC\_032088.1 New Mapoon virus, complete cds  
 S114. >NC\_031752.1 Botrytis cinerea endornavirus 1 strain HBtom-372, complete genome  
 S115. >NC\_031463.1 Ceratobasidium endornavirus B isolate Murdoch-2 polyprotein and ORF2 genes, complete cds  
 S116. >NC\_031462.1 Ceratobasidium endornavirus A isolate Murdoch-1 polyprotein gene, complete cds  
 S117. >NC\_043110.1 Banzi virus strain SAH 336 polyprotein gene, complete cds

GTGCCACATC CTCTACCCGGC CTGGTTACAC CGTATGATGT GCACCTGGTG ACCTCCACAC CCCGCGGGCC GAGCTCTTTG GCTTCGGCTC CAGAAGGGAC CTACTTGGCC  
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 TGATCCGAGT AATTGGAGCA CGAGTAATGG CCGGCACCTA GTTCTCTGTT GGTACCATCT GCGGAGACTG TGGAGAAGCC TGTGAAGATG TGTGAAGACT CCAAGTGAAC  
 TCARAAGAAC AACCTCGCCG CCAAAAGCCG ACCCGACTGG GCAGTAAAGT GGTGCGCAAG CTCGAAATTTG ACGGAGTAAG TTACAAACAG GTCTGCGATA AGGCTAGGG  
 TGATGTAGCA TATGAAGCTT TCTGTGGTGT TCAAAACTCG AGACTCCGCA CCGTTGGCAC TTTGTTGGCC GTCCACAATT AAGAATCAT AGAATTAAT ATTTGGAGAC  
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Now, the numerical equivalent of the above genome S1: >NC\_001639.1 is given below.

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Study of Certain Corona Family Related Viruses Based on Percentage Nucleotide Concentration and Golden Ratios and a Novel Sonic Attack Technique to Deactivate all Mutating Viruses



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4221441243	4433432234	3433222233	2321241314	2332222434	4343321234	3311314231	4413242312	4413242312	1214131133	2142213133
1234412411	3221232411	4413123441	2441221233	4113332222	3331234222	3341412311	1122342144	1234223123	1232112141	4134232421
1232424121	2324241441	1332434313	1442333321	3332322244	4413133421	2233131141	2433143114	2411322323	2414124244	1141212134
1334223311	1333133432	3414121242	1123242433	4224443441	2241334434	2242341323	2121123211	4412411322	2134112311	1441213441
2413422233	1441241114	1412444241	4132134231	3414421233	4233232411	2341124224	2324222241	2423223413	4334122234	2223233122
3211232214	2343242144	4133242324	2223322244	2124412313	1433321131	4341442131	3223344421	1122241442	2123211312	3232334323
3223131122	4221221424	4414442222	2323231423	1231214223	2313313241	2442414132	1422331222	2314224444	3123123244	1322322324
4241121212	3341411243	4412411234	4423323224	3441214124	1132444124	3123222334	1123212413	4132422422	2132414112	2422232322
1211413414	4441323313	4141124131	1232114414	3244223344	1242223123	3231432331	1111233212	3232213132	1412243144	1424222241
2442332233	2422311232	4244214222	4241334342	4414234433	4432342141	4311334232	3132322222	1124121341	1412444122	1331123232
4234231234	1244441133	3232412122	1414121112	1133132231	4441232214	1412331243	3441133231	1333322331	1221122241	1421144433
2342331412	3114123223	4411422132	3144223342	3432342211	2141443432	2313421113	3111423312	2241244141	1222222112	3232423344
1222334432	2232121112	2221423132	1232313241	2122411112	1111442334	1231134222	3113422431	4433444142	2242224444	2132321323
1112333311	4332212114	4223322223	3441212212	2334112123	1112322231	1311122333	4132332233	1214412414	3322122344	1222232222
1222232122	2242424214	4311112344	2343443413	3411413424	1144113112	2231242141	1422114422	3232313423	1123231443	3322241141
1412224332	2143433213	1314122232	1122222441	3422231424	1422112224	4223112222	4221441443	4441422322	1312224222	2412233341
2232134233	1331334212	2334121114	1321232412	2134241121	2123411322	3234442242	4344224122	2242242342	3213134132	2133112232
1231342331	3121211323	4144131222	1411122223	2442231214	1111331111	3242144331	1443413244	3322423323	3134134123	3443132412
3421411334	4144411223	1332211314	4322323424	3123232321	1134432343	3342111144	3244423443	1111123331	3344213112	2223231241
1142244233	2124131214	2312234422	2132223142	2121444411	2234412421	4134422113	3222224323	3414222334	2332122321	1121222221
2222212111	2232232322	1322232322	1222312321	4412412242	3221441124	4132234342	3242424331	3423221223	4442432323	3334122214
1424223241	1312132111	4233123321	4241312344	3323234222	4421332131	1322141244	2134444144	4134414323	3141442423	1433143241
3134421144	1412432411	4114434422	2323322133	1134413321	3214442232	3114333413	2233244433	1422241113	1424323422	3333411311
1334432124	1111331343	3221144222	2311321232	4241111211	3113111134	3344131121	1133334111	4413411422	1124132231	2211234122
3422434112	3443314131	1211133111	3334131113	1131131134	1344411342	3414224442	1233433314	4124231242	4434441232	1231444421
1231332141	1123232131	2442412233	2114422322	4112411332	3323314132	3214422132	2314244331	3331241122	2414232413	2224123422
4411434123	4414232243	3421122112	3422423421	1224224234	2211313221	4112321132	4123241324	1312431343	1424134422	2232112211
2234312223	3423334433	1122								

**Important Note:**

The concepts and tools presented here in this paper have been tried on all 130 virus genomes. However, basic results pertaining to S1: >NC\_001639.1 Lactate dehydrogenase-elevating virus, complete genome only are provided here due to space constraints. So, let us consider this genome for further analysis. The major aim of this paper is to provide certain feasible computational techniques for classifying any given large set of genome sequences. The first technique is “Classification of 130 virus genomes based on **Four level Auto Correlation Measures (ACMs)**”. The second technique is “Classification of 130 virus genomes based on **Percentage Concentration of Nucleotides and Pairwise Correlation Coefficients**”. The third technique is “Classification of 130 virus genomes based on **JCP Golden Ratio (GR)** values of the sequences.

## II. CLASSIFICATION OF 130 VIRUS GENOMES BASED ON AUTO CORRELATION MEASURES

Consider the virus genome sequence S1: >NC\_001639.1. The graphical inverse S1<sup>-1</sup> of S1 is given below.

TTAAGGCCGG	GTCGGTTTAC	CGTTAAATTA	TGTTTTCCGA	CTCAGCGCAG	TAGACTGATG	GTAAGTGAAT	TAACTATTGAG	AATTCGTCCT	TTAATCGCT	TTCGTAAAT
ATTCGGCTGT	CACCGTACCG	AACCTTCGTA	CTTTGACTGT	CACCTTAACT	AGGGAGGCCF	CAGTGTGATC	CATGTGTGAC	FTGGTGGAA	CCTTGTGTC	CAATGGTTAC
TCCTAGATGT	GTAACATATG	AGTAATCCCC	AGTAGTGTAC	CGCCTCTAGT	CTACCAGGGC	GGTATCCCTT	CACGTCGAAC	CCGACGAAGA	AGAAAAGAC	GGGAAAGGA
AATAAGACAG	GCCGTAAACG	TTCCGTTACG	AATTAAGTTA	CTAATTAAC	GACCAAAACG	GGAATAAAGA	CCGGCGAAA	GAAAGATAAA	ACTCTGTATG	AAGTTTTCCA
ATTGGCCGAG	AAAATATATC	CGGAAGAACG	GGGCTTCGTG	CTCAGAAACT	FTGGAGCCGT	CAAGTGTCC	CATGATGGAC	GAAGGATG	GTTGTTCCCG	GTTGTTCCCG
CAACAATCTC	TACACCAATC	CGAGACTGCA	GGCAGTCTCC	ACAGGTGCAC	CGACCAACCC	CGATCTACA	TTGAAGATGG	ATCCCTCGTG	TTGGCCGTAG	ACTCATGGTA
GGTCAATGA	TAGAATGTTT	CTCACATTTA	CGGGGTGTCC	TCCCGTATT	GTCAGAGCTC	TCTGTGCTG	TGACACAAC	ATTGCTTAC	TACCATGTAG	TTTATGTGTT
TTGATTGTGT	TGTTAAATAT	TTTTATTTTT	ATAAATGTTA	TGGTCGGTTT	CACGGTGCCT	TTTGGAAATC	CGACATCTAC	CGTTAAACCC	ATATTCAGTT	TGATTTCCGT
TAGTCATAGA	CTATGGTCTC	TCAAACTAGT	GTTTTAAGAT	CCGGAGGGTG	AAAAGCCGCT	CGCTCCAAA	TCGGCCGTGC	CGAAAGTGTG	GTAGCTCGTG	TTCGCCAAT
GAGGATTAAC	CAACCGGAAC	ATCGTACTGA	CGCCGTACGA	CGAGGTGGTA	TTGGCTGTAC	CCTGAAGCCA	TCTGAAGATG	AAACCATATG	CAAGGATG	GTTGTTCCCG
CCACGTGAAT	ATAGAGTTCG	AGTATGTATA	GGATTGACGA	GATGTCGCTC	TCTTTACTT	CGCTCTTCC	CGTGTGAAC	GATATATACT	CGATTACTGT	ATGACAATA
CGGTTATTCG	AGGAGTTCGA	TGTTACGGGT	TACTTTCTTT	TAGATTGTC	ACCCGCCACC	ATTCCTTTAA	GTTCTTTAA	TTCACTCAGT	TTCGACCTTT	TTAATGTTTA
CAGAGATGCC	CAATTGGCCT	TACAACAAC	TTGGCCGAGT	GTAAGTCGAG	TGTGTCCAA	AGTTTAAAGA	CCAACCTGAC	AACCGGACCC	CGCTCCGATA	CCGTCGGTAA
AAGCCATCTC	TCTTTATATG	TTTATTTTGT	TTTACCGTTA	TTGGCACCAC	CATAGGTTGG	TGACGGGTTA	AAGAAGTTTG	AAAAGTATA	CGGTTATAT	ACCGGTTTGT
GTTCCAATAT	TTGCCAAGGG	TAAAGTGATG	TGATCCCTTT	TCTTTACACC	GGCCAGCTTC	GAAAGTTTCA	AGTACGGTCC	AAATAAAGC	TTATCTAGT	GCTATGAGTC
ATTTTAAATA	TGTTTGGCCG	TTTACCGGTC	TGTGTAATTT	TTTAAACCTT	ACTTTAGGTC	AAAGGAAATC	GAGTTGGCCG	ACATAATTCG	TGCGTCGGTT	CCAGTGATTC
AACCGTTGTA	CAAGTACAGG	CGTGGCCACC	ATCAACTTTA	ATTAAGTTTG	GGGAAGTGG	ACCGGCTAGG	TACACATTTG	ACCCAGTGG	GGAAAAATA	CACATATAC
TGTGGGAACC	CATACGTAGT	TGCTGTGATA	GGGATTACCC	TACAACGATA	CTAATTTTTG	TGAGTGTCCG	AAGCACATCG	TGCCCGGCT	CACCTCCGGC	ACTTCTTCAT
CCTCTGTAG	TTCTGGTTGG	TCCATCTTTT	CTCACAGCT	TACATGATG	TGTGTATGTT	AAAAGGTGTC	AGTGGTAGTT	TCTACCGGTT	CCTGCACCAA	TGTAAGACTA
ACACGAGGTC	ACCCACAGAC	AATATTGTGT	TTCTTAAAC	TGATTTCTTC	TGACGACTAT	GTAACGGTTT	GTAGTACCC	TGAACTACAT	ACCCGTTGTC	GTTCCCGTAA
TACCGCTAAC	ACCGTATATA	ACTCCTGTTG	TTGACCTGTA	GTAGCCCTTC	CAGTTTTAGG	TTCATGTAC	CTCTACTGAG	GAGTGTTCAT	AGTATCAGT	GTTGTTTTCC
CACCCCTCAT	ATPCTTAAAG	FTGGTGGCGG	TGTGTAGAA	GATATCCACT	TTAAATCCCG	TGTGAGATCC	ACGCAAGATG	GGCAGGATC	CTATCCCTTT	GTTCTGCTGT
GGACCATCTG	GGGTCATCTG	AATGTTAGTT	GTTCTGGTTA	CGGGGAGCTT	FTACTACTTT	CGTCTTCTA	AGTCACTGT	GCTCGGATTC	CACCGATCGA	TGACACTTCC
TACAACAAC	ACCAGGTTTC	GACTACCGAT	ACCAAGTAA	CGATTTGAAC	TACCAATGTA	ATATGTGAGC	TCTTCGCGG	ACTTACCGCC	CTTCGGCTCT	GTAATCTATA
CACGTCGGGA	GGGAAAGGTT	CGGACGATAG	ACAACCTTCA	CAGTGTGTTG	AACTACAAGA	GTTTACAAGA	GGTTACGGA	CCCAACTCAT	TGGGATGGG	TCCAGAGGCC
TGGAAACACT	CTGTATATCT	CGGTAATCTG	TGACACATA	CTGTAGTAGT	CGTACAGTGC	TTAAAAGTAC	ACGGTTTCGT	AGGCTTTTTG	GAACGGTATT	ACCTACCGTA
GACCAACTGT	ATTGAACACT	CGTAGAGATT	TCATGGAAGA	CATACAGTCT	GACCACTGAC	AAAGCTGAGC	GTCGCTATG	GGCGCTTAT	TGGTCAGACT	ATGTTGGTTG
GTCGTCGGTC	GGCCGCTACC	ATTCGCGTTT	TTCTTACGGG	TTCTTTAGTT	CTTATAGTCT	CTACTTCTGT	TACTCGACT	ATTTACGTTG	AAGTTATCCG	AACAATAATT
CTCAACGTTG	TAATGGGTAA	TGAACCCCTT	GTACATGGGT	GACGGAAATG	TCGGTTGCC	ATGACGTCAT	AGAAAATGTT	CCCGCCGTTT	TAATGAACAC	CATATCCACC
TACCGGCTGC	AAAATTTTAC	ATACGTAAT	CGCACGCTG	TAGTTCCGGG	CGCTCGGTTA	TCCGAGAAGC	TTTGTCTGCA	AGTATCAGTC	CACCTCGAAG	TGAACACTCG
CAGTAACTGT	CCCTGCTAAG	CTAGTCTTTG	ACTACTCGTG	AGTGAATCCA	TTAAACCTGT	TAAACCTGTT	GGAACTGTAA	CAACTGTGTA	AGTAGGTTTA	GTTTCTCTG
CGGAGGGGAA	AGTCTTGAA	AATCTTCCG	TCTGTACCGA	AGGTACCCG	CATACGGGAG	CACCTTTATG	CTCATCGTA	GAAAGGTTG	GTATTCGAAC	TGCCAGACT
TTAGTTGGTC	ATCCAACATT	AGGTACGAGA	AACTTCCCCC	CACCTCCACT	CTTAGGTTAA	GACCACTCAT	CTGTAGTAC	TGTCATGTGT	CGGGAAAACG	CCGGAAAAGGA
CCTGTTGACT	CGGTTGGGAA	ATGTTGACTC	GGTCCGTTGT	AGTACCCCCC	ATCCCTGGAT	TCCCAATGAT	CTACTGTAGG	TGGTTGTAG	GAAGGAAACT	GAAACGGTTA
CTTCCGCACT	CCCGTAAAGA	CAAGTTTAA	TTAAGTAA	AGTAAAGTTA	TAAAGCTGAT	TAAAGCTGAT	TAGGAGGGTC	AACTGTACTA	CCTTAGTCCG	TCCCTATGTT
AGAGGGGAAA	ATTTATAAAC	CAGTTTATA	TTCTATGGTG	GGTCCCTGTA	GGTCTTTAT	ATGAGCCCGG	ATGATATTATG	GGCCGCTGTT	TGCTGCGCCG	ACTTAAATA
AGGTAATAA	AGTACGGCGT	GTGGTCGGTA	AGCCCGGTGA	GTCAGATAA	GACCCGGCAA	TGCTGCCCGG	TTACAATATG	GTTAAGACCC	CCATAAAAAC	GTTTGACTTA
GTTTAGTCCC	CTTATTATCT	TTGGGTTTAA	TACTGGTTGA	ACCCGTTTGC	CTCTTCTGCA	CCGGAGGTCG	GGGTAGTCCA	CGACGTTAA	ATTTAGTCAA	CAGGACGCTA
CAGCACGGTC	GACAAAAGTGT	TGTGGTGGTT	GTTTAGTAAA	ACCAACTAGC	GCTGTGGTTT	TCCGGGTCG	AGTACAGGA	AGTACAAGT	TTTGAACAT	TATAACGCG





## 2.1 Dyadic intersection of a sequence and its inverse

The following proposition holds for any type of alphanumerical sequence.

### Proposition 2.1.1

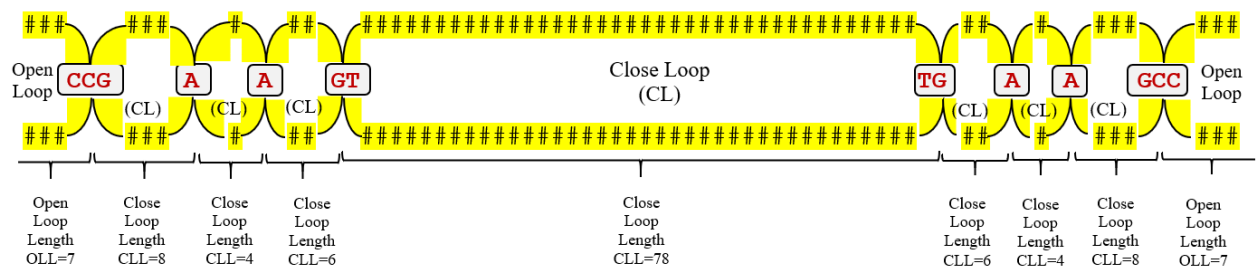
“Given any arbitrary numerical or alphanumerical sequence  $x_1$  of length  $N$ , one may obtain its inverse as  $x_1^{-1}$  of length  $N$ . The sequence  $x_1$  and its inverse  $x_1^{-1}$  are pairwise intersected and all matching symbols are identified. Two matched symbols are fused as one. The sequence of all fused matched symbols forms a palindrome sequence”.

#### Example 2.1.1

Comparison of the first 70 nucleotides  $s_1$  of the virus genome S1 and its inverse  $s_1^{-1}$

$s_1$	ATT <b>CCG</b> AAAA <b>GATTGT</b> GTGA ACCCGT <b>GCGG</b> TAACCGTCTA TTTCAAGGAG CCA <b>CTGGGAC</b> <b>AGTGCCCGC</b>
$s_1^{-1}$	CG <b>CCGGTGA</b> <b>CAGGGT</b> CACC GAGGAACTTT ATCTGCCAAT GGCGTGCCCA AGT <b>TGTTAG</b> <b>AAAAGCC</b> TTA

The pairwise intersection of  $s_1$  and  $s_1^{-1}$  denoted as  $s_1 \cap s_1^{-1}$  is **CCGAAGTTGAAGCC**. This sequence **CCGAAGTTGAAGCC** is a palindrome sequence. The unmatched symbols are denoted by the don't care symbol #. Now, the resulting pair of sequences is represented as:



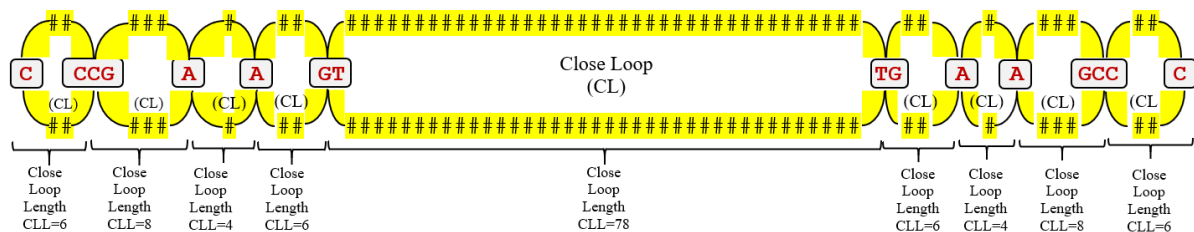
where # refers to don't care symbol, OLL refers to 'Open Loop Length', and CLL refers to 'Closed Loop Length'. The value of an OLL is calculated as  $2n+1$ , where 'n' is the number of don't care symbols present in the pair of sequences. The value of a CLL is calculated as  $2n+2$ , where 'n' is the number of don't care symbols present in a single strand. The OLL and CLL values calculated for the above example pair  $s_1 \cap s_1^{-1}$  is given as  $\{OLL=7, CLL=8, CLL=4, CLL=6, CLL=78, CLL=6, CLL=4, CLL=8, OLL=7\}$  or simply written as  $\{7, 8, 4, 6, 78, 6, 4, 8, 7\}$ . Note that the value of an OLL is always an odd number and the value of a CLL is always an even number. **Note that the sequence pair  $s_1 \cap s_1^{-1}$  is an open-ended pair.** Now the graphical inverse of the sequence  $s_1 \cap s_1^{-1}$  denoted as  $(s_1 \cap s_1^{-1})^{-1}$  is **CCGAAGTTGAAGCC**. It is observed that  $s_1 \cap s_1^{-1} \stackrel{\oplus}{=} (s_1 \cap s_1^{-1})^{-1}$ , where the symbol  $\oplus$  denotes the binary relation 'graphical equivalence', meaning the sequence is a palindrome. Moreover, the sequence of loop values also exhibits palindrome property. In this case, the maximum CLL value is 78 and the minimum CLL value is 4.

#### Example 2.1.2

Consider the sequence  $s_2$  given below and its inverse  $s_2^{-1}$

$s_2$	CTT <b>CCG</b> AAAA <b>GATTGT</b> GTGA ACCCGT <b>GCGG</b> TAACCGTCTA TTTCAAGGAG CCA <b>CTGGGAC</b> <b>AGTGCCCGC</b>
$s_2^{-1}$	CG <b>CCGGTGA</b> <b>CAGGGT</b> CACC GAGGAACTTT ATCTGCCAAT GGCGTGCCCA AGT <b>TGTTAG</b> <b>AAAAGCC</b> TT <b>C</b>

The pairwise intersection of  $s_2$  and  $s_2^{-1}$  denoted as  $s_2 \cap s_2^{-1}$  is **CCCGAAGTTGAAGCCC**. Now the graphical inverse of the sequence  $s_2 \cap s_2^{-1}$  denoted as  $(s_2 \cap s_2^{-1})^{-1}$  is **CCCGAAGTTGAAGCCC**. It is observed that  $s_2 \cap s_2^{-1} \stackrel{\oplus}{=} (s_2 \cap s_2^{-1})^{-1}$ , where the symbol  $\oplus$  denotes the binary relation 'graphical equivalence'. The sequence **CCCGAAGTTGAAGCCC** is a palindrome sequence. If the unmatched symbols are replaced by the symbol #, then then the resulting pair of sequences is represented as:



where # denotes don't care symbol and CLL refers to 'Closed Loop Length'. The value of a CLL is calculated as  $2n+2$ , where 'n' is the number of don't care symbols present in the pair of sequences. The CLL values calculated for the above example pair  $s_2 \cap s_2^{-1}$  is given as  $\{CLL=6, CLL=8, CLL=4, CLL=6, CLL=78, CLL=6, CLL=4, CLL=8, CLL=8, CLL=6\}$  or simply written as  $\{6, 8, 4, 6, 78, 6, 4, 8, 8, 6\}$ . **Note that the sequence pair  $s_2 \cap s_2^{-1}$  is a close-ended pair.** In this case also, the maximum CLL value is 78 and the minimum CLL value is 4.

**On the notion of ‘Self Similarity Index (SSI)’**

Let us consider the sequence  $x_1 = 1, 2, 3, 4, 5, 6, 7, 8, 9, 10$ . Now  $x_1^{-1} = 10, 9, 8, 7, 6, 5, 4, 3, 2, 1$ .

Both the sequences are compared. It is observed that not even a single match is found. The number of elements in the sequence is 10. One finds the ratio of ‘0’ to ‘10’ to be ‘0’. For convenience, one would call this ratio as ‘Self Similarity Index (SSI)’.

$$\begin{matrix} x_1 = & 1, & 2, & 3, & 4, & 5, & 6, & 7, & 8, & 9, & 10 \\ x_1^{-1} = & 10, & 9, & 8, & 7, & 6, & 5, & 4, & 3, & 2, & 1 \end{matrix}$$

So, SSI of  $x_1 = 0$ . Let us consider another sequence  $x_2 = 10, 10, 10, 10, 10, 10, 10, 10, 10, 10$ . Now, graphical inverse of  $x_2$  is  $x_2^{-1} = 10, 10, 10, 10, 10, 10, 10, 10, 10, 10$ . So,  $x_2 = x_2^{-1}$ . All elements of  $x_2$  match with all elements of  $x_2^{-1}$ . In this case, SSI of  $x_2$  is 1. This means that the SSI values range from 0 to 1 for all sequences. Therefore, one could attribute a real number SSI value to any sequence, from the cantor set [0.1]. Now the parameter SSI is formally expressed as  $SSI = (n/N)$ , where n is the number of matches found and N is the number of elements present in the sequence.

*Proposition 2.1.2*

**One can interpret a discrete Hilbert space  $I_N: (N \rightarrow \infty)$ , which is a sequence space, as a disjoint union of potentially denumerable subspaces, each having a unique SSI value.**

This proposition is a self evidential truth.

*Proposition 2.1.3*

**Every SSI based subspace of the discrete Hilbert space  $I_N: (N \rightarrow \infty)$  is potentially denumerable.**

This proposition is a self evidential truth.

*2.2 Dyadic pairing of nucleotides in a sequence and its inverse*

The following proposition holds for any type of virus genome sequence.

*Proposition 2.2.1*

Given any arbitrary nucleotides sequence  $x_1$  of length N, one may obtain its inverse as  $x_1^{-1}$  of length N. The sequence  $x_1$  and its inverse  $x_1^{-1}$  are compared and all of the natural pairing of nucleotides are identified. The sequence of all such natural pairs of nucleotides  $\langle A, T \rangle, \langle T, A \rangle, \langle G, C \rangle$  and  $\langle C, G \rangle$  forms a palindrome sequence.

*Example 2.2.1*

Natural Pairing of  $s_1$  and  $s_1^{-1}$

$s_1$	ATTCCGAAA GATTGTGTGA ACCCGTGCGG TAACCGTCTA TTTCAAGGAG CCACTGGGAC AGTGGCCCGC
$s_1^{-1}$	CGCCCGGTGA CAGGGTCACC GAGGAACTTT ATCTGCCAAT GGCCTGCCCA AGTGTGTTAG AAAAGCCTTA

The sequence of natural pairs of nucleotides along with don't care symbols is given below.

##### $\langle A, T \rangle$ ##### $\langle G, C \rangle$  $\langle T, A \rangle$  $\langle G, C \rangle$ ### $\langle C, G \rangle$  $\langle C, G \rangle$  $\langle T, A \rangle$  $\langle G, C \rangle$ ### $\langle T, A \rangle$  $\langle A, T \rangle$ ### $\langle C, G \rangle$  $\langle G, C \rangle$ ### $\langle T, A \rangle$  $\langle A, T \rangle$ ### $\langle C, G \rangle$  $\langle A, T \rangle$  $\langle G, C \rangle$ ### $\langle G, C \rangle$  $\langle G, C \rangle$ ### $\langle C, G \rangle$  $\langle A, T \rangle$  $\langle C, G \rangle$ ##### $\langle T, A \rangle$ #####

The sequence of natural pairs of nucleotides along with loop lengths is given below, and this is a palindrome sequence.

15 $\langle A, T \rangle$ 18 $\langle G, C \rangle$ 18 $\langle T, A \rangle$ 8 $\langle C, G \rangle$ 8 $\langle C, G \rangle$ 4 $\langle T, A \rangle$ 4 $\langle G, C \rangle$ 8 $\langle T, A \rangle$ 4 $\langle A, T \rangle$ 6 $\langle C, G \rangle$ 6 $\langle G, C \rangle$ 6 $\langle T, A \rangle$ 8 $\langle G, C \rangle$ 4 $\langle G, C \rangle$ 8 $\langle C, G \rangle$ 8 $\langle C, G \rangle$ 4 $\langle A, T \rangle$ 18 $\langle T, A \rangle$ 15

*Proposition 2.2.2*

Given any arbitrary nucleotides sequence  $x_1$  of length N, one may obtain its inverse as  $x_1^{-1}$  of length N. The sequence  $x_1$  and its inverse  $x_1^{-1}$  are compared and all of the unnatural pairing of nucleotides are identified. The sequence of all such unnatural pairs of nucleotides  $\langle A, C \rangle, \langle C, A \rangle, \langle T, G \rangle$  and  $\langle G, T \rangle$  forms a palindrome sequence.

*Example 2.2.2*

Unnatural Pairing of  $s_1$  and  $s_1^{-1}$

$s_1$	ATTCCGAAA GATTGTGTGA ACCCGTGCGG TAACCGTCTA TTTCAAGGAG CCACTGGGAC AGTGGCCCGC
$s_1^{-1}$	CGCCCGGTGA CAGGGTCACC GAGGAACTTT ATCTGCCAAT GGCCTGCCCA AGTGTGTTAG AAAAGCCTTA

The sequence of unnatural pairs of nucleotides along with don't care symbols is given below.

$\langle A, C \rangle$  $\langle T, G \rangle$ ##### $\langle T, G \rangle$  $\langle T, G \rangle$ ##### $\langle A, C \rangle$ ### $\langle C, A \rangle$ ##### $\langle G, T \rangle$  $\langle G, T \rangle$ ### $\langle A, C \rangle$ ##### $\langle C, A \rangle$ ### $\langle T, G \rangle$  $\langle T, G \rangle$ ### $\langle A, C \rangle$ ### $\langle C, A \rangle$ ##### $\langle G, T \rangle$  $\langle G, T \rangle$ ##### $\langle G, T \rangle$  $\langle C, A \rangle$

The sequence of unnatural pairs of nucleotides along with loop lengths is given below, and this is a palindrome sequence.

$\langle A, C \rangle$  $\langle T, G \rangle$ 22 $\langle T, G \rangle$ 22 $\langle T, G \rangle$ 12 $\langle A, C \rangle$ 4 $\langle C, A \rangle$ 14 $\langle G, T \rangle$ 6 $\langle G, T \rangle$ 6 $\langle A, C \rangle$ 10 $\langle C, A \rangle$ 6 $\langle T, G \rangle$ 14 $\langle A, C \rangle$ 4 $\langle C, A \rangle$ 12 $\langle G, T \rangle$ 4 $\langle G, T \rangle$ 22 $\langle G, T \rangle$ 4 $\langle C, A \rangle$

This computational tool of dyadic intersection of a sequence and its inverse is applied to the actual virus genome sequence S1: >NC\_001639.1. The ‘single-strand sequence’ obtained after point-wise intersection of S1 and its graphical inverse  $S1^{-1}$  is given below. The don't care symbol # represents those characters which are not matched.





6C18G8T10C	4TG4T18CT4	A4T8C10CC2	0G14G24G4G	8TCC10AG6C	22A4T4C4CC	4C08A6A4A4	G10A6CG10C	4A6CC12GT6	G8T24C4CT6	A4G4T10AA4
4A4T14C8T	4D2T8T12A1	C10C6T4KCC	6A10G8G6A4	CA4GT2J2C1	0P4T44AG8A	6P4F16G22A	4F4C18G6T6T	4T20C12G2A	4T20C4CT6T	4G4G8T3C8A
8A30T20C8A	4C14G10T14	C4G4TGC16A	10GTC4T14C	12A20A12GT	12A20CA4GG	8AG6G16T1A	2A4C8A18GG	A8G8A6T4G4	CAA10GT6C8	G8GCG6G18A
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 GCGCCCAAGG TTGGTATTCT TTTTAAAGTT TACGGAGGAG TGAGTAAAG CDTTGGCGT TCCGTTGGCG GTTATATTG GGAACCTACG GTGGATGGGA ATATAAGAAC  
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 GATCTTTTCA AGTATTTTAA GAAGATTACG CTAGTCTTCA GAGCCTGTGG AAATGACCTT TGTTCAAGTAG TGTTTAAAAA TTGACCGCTC TGTACCTGTC GGGGCGCTT  
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 GTTTCCGAGT GGTATGGATT ATGTCTCGGG AAAGCTAATA GGCTATGCA GGTACTCTCT CCGTGCACCTT CGCGTGGGCT CCGCCTCGG CCCCCTCGG GTCCGCGTGC  
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 TGTCAAGATG AACCTTCTCG TTTAACGAGG CTTGTTGGCT TTGCGGTTTT TCGGTTGATT GCGGTTCTCT CCGGTTCTCT GTCTTTTCTG CTTGTTGACTA  
 TGTATCGAT ACATACTTTG TCCGAGTGGG TGAAGTAGGG GCGAAGTGGT GACTCTGTTG TGATGTTACA TTGGTAGCCC TACACGGGAA CTCTGGTCTCT GCGCACCTG  
 CGTTTGGGCT TGTGATTCAG TCGACTGGGG TAGTGTGGGT GCTGTGTTT TCGCGGACGT TAGCGCCCGG GTTTTGCATC AGCCTTAGTA CGTTCAGCCA CBTGTTACC  
 CTATTTCTTT CGTTGTCTCT TTGCATTAC ATCCGGTTGT GCAATGTGAC GCCATAGCAT TACTCCCCAA GGTGGTATT CTTTTTTAAG TTTACGGAGG AGTGAGTGAA  
 AGCCTTGGCT GTTCGGTTGG CBTGTTATTT TAGGAACCTAC GGGTGGATGG GAATATAAGA ATCCACCCGA AAAGAGATGA CGCTGGCTTG AGTTTGGATG CATGCTGAT  
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 GGTACTCTTT TTTGACCTTA ACCTAAGATG TTGCTTTTCTT CTTTTGCGGG TTGTTGTGGG TGTGTTGGG TGTATGCAATT GTCCAGGAGG CTTAAGAAAC GTTCGGCGGG  
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 AGGGTACTTT GGGT

### 2.3 Classification of 130 virus genomes based on loop lengths due to autocorrelation

Out of 130 virus genome sequences, one hundred and two have been identified as open-ended sequences such as S1, S2, S3, S4, S5, S7, S8, S9, S11, S13, S14, S19, S20, S21, S22, S23, S24, S25, S26, S28, S30, S31, S32, S33, S34, S35, S36, S37, S38, S39, S41, S42, S43, S44, S45, S46, S47, S49, S50, S51, S52, S53, S54, S55, S56, S57, S58, S59, S60, S61, S62, S63, S64, S65, S66, S67, S68, S69, S70, S71, S72, S73, S74, S77, S78, S79, S81, S83, S84, S85, S86, S88, S89, S90, S91, S92, S93, S95, S97, S98, S100, S101, S102, S103, S104, S106, S107, S108, S109, S110, S111, S112, S114, S115, S116, S118, S122, S123, S125, S126, S127, S130 and twenty eight have been identified as close-ended sequences such as S6, S10, S12, S15, S16, S17, S18, S27, S29, S40, S48, S75, S76, S80, S82, S87, S94, S96, S99, S105, S113, S117, S119, S120, S121, S124, S128, S129. The MLL values of 102 open-ended sequences is viewed as a sequence of MLL values and presented as a graph. The maximum and the minimum MLL values in the graph are identified and the difference between the maximum and minimum values is treated as a band. This band is divided into four equal level sub bands. Now all the 102 virus genomes are classified under the four level sub bands. The same procedure is followed to classify 28 close-ended sequences. Table 1 presents values of maximum and minimum loop lengths for all open and close-ended sequences and the respective four sub bands.

Table 1: Maximum and minimum values of loop lengths of open ended and close ended virus genomes

Sl. No.	Open Ended Sequences	Maximum Values of Loop Lengths	Minimum Values of Loop Lengths	Sl. No.	Close Ended Sequences	Maximum Values of Loop Lengths	Minimum Values of Loop Lengths
1	S1	58	3	1	S6	88	4
2	S2	54	4	2	S10	56	4
3	S3	46	3	3	S12	50	4
4	S4	50	3	4	S15	58	4
5	S5	70	3	5	S16	66	4
6	S7	66	4	6	S17	52	4
7	S8	52	4	7	S18	58	4



8	S9	48	4
9	S11	66	4
10	S13	54	3
11	S14	58	3
12	S19	44	4
13	S20	50	4
14	S21	48	4
15	S22	64	4
16	S23	44	4
17	S24	44	4
18	S25	32	4
19	S26	46	4
20	S28	40	4
21	S30	52	4
22	S31	40	4
23	S32	42	4
24	S33	62	4
25	S34	52	4
26	S35	46	4
27	S36	54	4
28	S37	52	4
29	S38	82	4
30	S39	32	4
31	S41	48	3
32	S42	82	4
33	S43	50	4
34	S44	44	4
35	S45	54	4
36	S46	50	4
37	S47	46	4
38	S49	56	4
39	S50	50	3
40	S51	38	4
41	S52	46	4
42	S53	44	4
43	S54	54	4
44	S55	46	4
45	S56	80	3
46	S57	52	4
47	S58	62	4
48	S59	44	3
49	S60	68	4
50	S61	40	4
51	S62	56	4
52	S63	58	4
53	S64	48	4
54	S65	54	4
55	S66	48	4
56	S67	44	4
57	S68	50	3
58	S69	48	4
59	S70	40	4
60	S71	50	4
61	S72	56	4
62	S73	48	4
63	S74	58	3
64	S77	46	4
65	S78	56	4
66	S79	44	4
67	S81	40	4
68	S83	58	4
69	S84	50	4
70	S85	44	4
71	S86	46	4
72	S88	42	4
73	S89	46	4
74	S90	50	4

8	S27	52	4
9	S29	44	4
10	S40	64	4
11	S48	70	4
12	S75	42	4
13	S76	48	4
14	S80	46	4
15	S82	46	4
16	S87	52	4
17	S94	44	4
18	S96	72	4
19	S99	62	4
20	S105	54	4
21	S113	42	4
22	S117	62	4
23	S119	60	4
24	S120	60	4
25	S121	56	4
26	S124	56	4
27	S128	58	4
28	S129	56	4

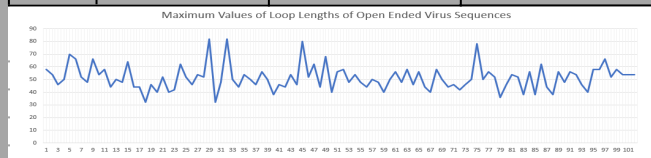


Fig. 1: Maximum Values of Loop Lengths of Open-Ended Sequences

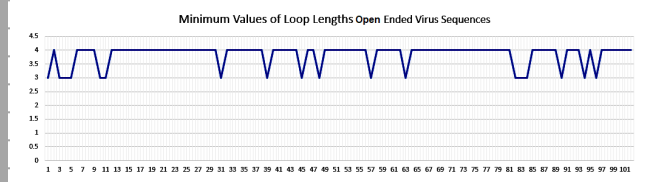


Fig. 2: Minimum Values of Loop Lengths of Open-Ended Sequences

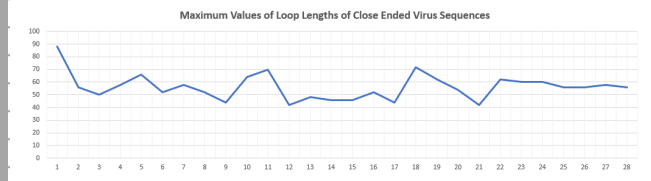


Fig. 3: Maximum Values of Loop Lengths of Close-Ended Sequences

Minimum Values of Loop Lengths of Close-Ended Sequences remains as 4 for all open-ended sequences. ‘Maximum Loop Length (MLL)’ value has been found to be a reliable quantificational measure of a virus genome, be it open ended or close ended. More the value of MLL of a sequence, less its SSI value. Every virus genome sequence would have a unique SSI value and MLL value. Given a finite set of virus genome sequences, one can find out the MLL value for every virus genome. In the case of 130 virus genome sequences, 102 MLL values have been found for open-ended sequences and 28 MLL values found for close-ended sequences. Fig. 4 shows the graph displaying 102 MLL values of open-ended genomes with four levels.

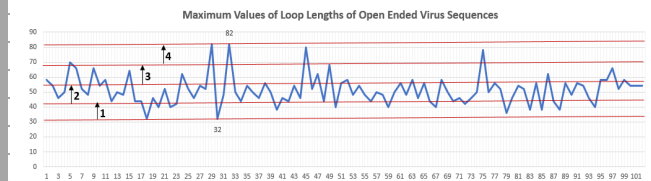


Fig. 4: MLL values of open-ended virus genomes with four levels

The genomes S29 and S32 are found to have maximum MLL value 82. Genome S30 is found to have minimum MLL value 32. The band of values from 32 to 82 is further divided into sub bands (i) 32-44, (ii)

75	S91	78	4
76	S92	50	4
77	S93	56	4
78	S95	52	4
79	S97	36	4
80	S98	46	4
81	S100	54	4
82	S101	52	3
83	S102	38	3
84	S103	56	3
85	S104	38	4
86	S106	62	4
87	S107	44	4
88	S108	38	4
89	S109	56	4
90	S110	48	3
91	S111	56	4
92	S112	54	4
93	S114	46	4
94	S115	40	3
95	S116	58	4
96	S118	58	3
97	S122	66	4
98	S123	52	4
99	S125	58	4
100	S126	54	4
101	S127	54	4
102	S130	54	4

45-57, (iii) 58-69 and (iv) 70-82. Fig. 5 shows the four sub bands and virus genomes belonging to those sub bands.

Table 2: Four sub bands and classified open-ended virus genomes

Open-Ended Virus Sequences		
Bands	MLL Ranges	Virus Sequences
1	32-44	S19, S23, S24, S25, S28, S31, S32, S39, S44, S51, S53, S59, S61, S67, S70, S79, S81, S85, S88, S97, S102, S104, S107, S108, S115
2	45-57	S2, S3, S4, S8, S9, S13, S20, S21, S26, S30, S34, S35, S36, S37, S41, S43, S45, S46, S47, S49, S50, S52, S54, S55, S57, S62, S64, S65, S66, S68, S69, S71, S72, S73, S77, S78, S84, S86, S89, S90, S92, S93, S95, S98, S100, S101, S103, S109, S110, S111, S112, S114, S123, S126, S127, S130
3	58-69	S1, S7, S11, S14, S22, S33, S58, S60, S63, S74, S83, S106, S116, S118, S122, S125,
4	70-82	S5, S38, S42, S91

Fig. 5: Shows graph displaying 28 MLL values of close-ended genomes with four levels

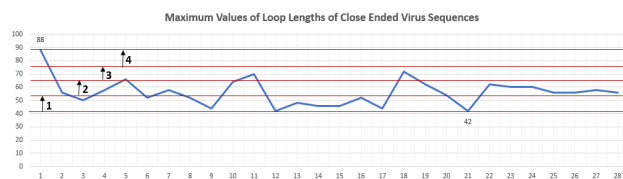


Fig. 5: MLL values of close-ended virus genomes with four levels

The band of values from 32 to 82 is further divided into sub bands (i) 42-53, (ii) 54-65, (iii) 66-76 and (iv) 77-88. Fig. 7 shows the four sub bands and virus genomes belonging to those sub bands.

Table 3: Four sub bands and classified close-ended virus genomes

Close-Ended Virus Sequences		
Bands	MLL Ranges	Virus Sequences
1	42-53	S12, S17, S27, S29, S75, S76, S80, S82, S87, S94, S113
2	54-65	S10, S15, S18, S99, S105, S117, S119, S120, S121, S124, S128, S129
3	66-76	S16, S48, S96,
4	77-88	S6

**Observations**

1. Auto Correlation Measures (ACMs) of virus sequences in band #1 are HIGH, meaning probability of they being susceptible for mutation or structural transformation is more.
2. The open-ended virus genomes S19, S23, S24, S25, S28, S31, S32, S39, S44, S51, S53, S59, S61, S67, S70, S79, S81, S85, S88, S97, S102, S104, S107, S108, S115 fall under band 1 and the are likely to undergo structural transformation.
3. The close-ended virus sequences S12, S17, S27, S29, S75, S76, S80, S82, S87, S94, S113 fall under band 1 and the are likely to undergo structural transformation.
4. The open-ended virus genomes S5, S38, S42, S91 fall under band 4 and they are likely to be stable virus genomes without undergoing any structural transformation.
5. The close-ended virus genome S6 falls under band 4 and it is likely to be a stable virus genome without undergoing any structural transformation.

**III. CLASSIFICATION OF 130 VIRUS GENOMES BASED ON CORRELATION COEFFICIENTS AND DIFFERENTIAL ERRORS**

The percentage concentration values of all four nucleotides in 130 virus genomes are calculated and subsequently the values of correlation coefficients and differential errors.

**3.1 Calculation of Percentage Concentration of Nucleotides of Viral Genome Sequences**

Analogous to the notion of pH value of a solution, the values of pA, pT, pG and pC of a genome sequence and possibly composition of these values like the proportion pA:pT:pG:pC seems to pave a way to classify and characterize genome sets. The definition of “Percentage Nucleotide Concentration” of a genome sequence is as follows. “Given a genome sequence, the number of a particular nucleotide, say A, present in that genome sequence is counted and the sum is divided by the total number of nucleotides in that genome sequence. The fraction when multiplied by 100 yields the Percentage Concentration of Adenine pA”. Similarly, one can evaluate pT, pG and pC.



### 3.1.1 Percentage Concentrations of 130 sequences

One hundred and thirty complete genomes of various categories of viruses are drawn from NCBI web site <https://www.ncbi.nlm.nih.gov/genbank/sars-cov-2-seqs/> for data analysis. The data given by NCBI is expected to be genuine. Now, pA, pT, pG and pC were calculated for all 130 virus genome data and values presented in table 4.

Table 4: Percentage Nucleotide Concentration Data of 130 Virus Genomes

Sl. No.	Seq. No.	Species	Accession ID	Total length	A	pA	T	pT	G	pG	C	pC
1	S1	Lactate dehydrogenase-elevating virus	NC_001639.1	14104	3244	23.00	3888	27.57	3646	25.85	3326	23.58
2	S2	Porcine respiratory and reproductive syndrome virus	NC_001961.1	15428	3353	21.73	3903	25.30	4047	26.23	4125	26.74
3	S3	Equine arteritis virus	NC_002532.2	12704	2692	21.19	3449	27.15	3305	26.02	3258	25.65
4	S4	Simian hemorrhagic fever virus	NC_003092.2	15717	3534	22.49	4307	27.40	3556	22.63	4314	27.45
5	S5	Mikumi yellow baboon virus	NC_025112.1	14927	3476	23.29	3853	25.81	3404	22.80	4194	28.10
6	S6	Southwest baboon virus	NC_025113.1	14851	3456	23.27	3909	26.32	3398	22.88	4088	27.53
7	S7	Forest pouched giant rat arterivirus	NC_026439.1	14953	3238	21.65	3920	26.22	3944	26.38	3851	25.75
8	S8	DeBrazzas monkey arterivirus	NC_026509.1	15684	3364	21.45	3816	24.33	3688	23.51	4816	30.71
9	S9	Pebjah virus	NC_027124.1	15478	3291	21.26	4077	26.34	3623	23.41	4487	28.99
10	S10	Kafue Kinda chacma baboon virus	NC_029053.1	14924	3311	22.19	4025	26.97	3333	22.33	4255	28.51
11	S11	Free State vervet virus	NC_029992.1	15247	3450	22.63	3929	25.77	3457	22.67	4411	28.93
12	S12	Oliver's shrew virus 1	NC_035127.1	13766	2948	21.42	3675	26.70	3438	24.97	3705	26.91
13	S13	Porcine reproductive and respiratory syndrome virus 2	NC_038291.1	15411	3345	21.71	3923	25.46	4036	26.19	4107	26.65
14	S14	Simian hemorrhagic encephalitis virus	NC_038293.1	15370	3406	22.16	3979	25.89	3502	22.78	4481	29.15
15	S15	Lelystad virus	NC_043487.1	15111	3247	21.49	3912	25.89	3815	25.25	4137	27.38
16	S16	Zambian malbrouck virus	NC_048209.1	15307	3454	22.56	4008	26.18	3431	22.41	4414	28.84
17	S17	Giardia lamblia virus	NC_003555.1	6277	1606	25.59	1530	24.37	1565	24.93	1576	25.11
18	S18	Chalara elegans RNA Virus 1	NC_005883.1	5310	1076	20.26	1441	27.14	1465	27.59	1328	25.01
19	S19	Coniothyrium minitans RNA virus	NC_007523.1	4975	1008	20.26	1024	20.58	1416	28.46	1527	30.69
20	S20	Botryotinia fuckeliana totivirus 1	NC_009224.1	5261	1232	23.42	1151	21.88	1392	26.46	1486	28.25
21	S21	Black raspberry virus F	NC_009890.1	5077	1516	29.86	1252	24.66	1336	26.31	973	19.16
22	S22	Armigeres subalbatus virus	NC_014609.1	7510	2239	29.81	1784	23.75	1672	22.26	1815	24.17
23	S23	Beauveria bassiana victorivirus	NC_024151.1	5327	961	18.04	1251	23.48	1375	25.81	1740	32.66
24	S24	Botryosphaeria dothidea victorivirus 1	NC_025214.1	5322	1145	21.51	1111	20.88	1519	28.54	1547	29.07
25	S25	Camponotus yamaokai virus	NC_027212.1	5704	1811	31.75	1359	23.83	1414	24.79	1120	19.64
26	S26	<b>Golden shiner totivirus</b>	<b>NC_030295.1</b>	7788	2902	<b>37.26</b>	2249	28.88	1436	18.44	1201	<b>15.42</b>
27	S27	Fusarium poae victorivirus 1	NC_030867.1	5124	1022	19.95	1058	20.65	1419	27.69	1625	31.71
28	S28	Australian Anopheles totivirus	NC_035674.1	6203	1570	25.31	1551	25.00	1730	27.89	1352	21.80
29	S29	Aspergillus foetidus slow virus 1	NC_038928.1	5194	1016	19.56	1172	22.56	1441	27.74	1563	30.09
30	S30	Beauveria bassiana victorivirus 1	NC_038929.1	5228	1065	20.37	1271	24.31	1418	27.12	1474	28.19
31	S31	Diatom colony associated dsRNA virus	NC_040431.1	4671	1147	24.56	1129	24.17	1401	29.99	994	21.28
32	S32	<b>Gigaspora margarita giardia-like virus</b>	<b>NC_040632.1</b>	4947	1772	<b>35.82</b>	1606	32.46	947	19.14	622	<b>12.57</b>
33	S33	Fusarium asiaticum victorivirus 1	NC_040653.1	5281	929	17.59	959	18.16	1560	29.54	1833	34.71
34	S34	Diatom colony associated dsRNA virus 13 genomic RNA	NC_040659.1	5082	1211	23.83	1188	23.38	1610	31.68	1073	21.11
35	S35	Diatom colony associated dsRNA virus 11 genomic RNA	NC_040660.1	5160	1270	24.61	1282	24.84	1587	30.76	1021	19.79
36	S36	Diatom colony associated dsRNA virus 12 genomic RNA	NC_040775.1	5941	1784	30.03	1389	23.38	1583	26.65	1185	19.95
37	S37	Alternaria arborescens victorivirus	NC_040793.1	5206	1154	22.17	1029	19.77	1486	28.54	1537	29.52
38	S38	Guangdong greater green snake arterivirus	NC_046959.1	18410	4712	25.59	5381	29.23	3886	21.11	4431	24.07
39	S39	Pothos latent virus	NC_000939.2	4415	1129	25.57	1206	27.32	1143	25.89	937	21.22
40	S40	Bovine viral diarrhea virus	NC_001461.1	12573	4049	32.20	2767	22.01	3233	25.71	2524	20.07
41	S41	O'nyong-nyong virus	NC_001512.1	11835	3676	31.06	2440	20.62	2859	24.16	2860	24.17
42	S42	Ononis yellow mosaic virus	NC_001513.1	6211	1330	21.41	1748	28.14	973	15.67	2160	34.78
43	S43	Cell fusing agent virus	NC_001564.2	10682	2618	24.51	2614	24.47	2919	27.33	2531	23.69
44	S44	Bamboo mosaic virus	NC_001642.1	6366	1925	30.24	1218	19.13	1339	21.03	1884	29.59
45	S45	Odontoglossum ringspot virus	NC_001728.1	6618	1990	30.07	2013	30.42	1441	21.77	1174	17.74
46	S46	Rupestris stem pitting associated virus	NC_001948.1	8744	2430	27.79	2560	29.28	2075	23.73	1678	19.19
47	S47	Botrytis virus F	NC_002604.1	6827	1689	24.74	1494	21.88	1405	20.58	2239	32.80
48	S48	Banana mild mosaic virus	NC_002729.1	7352	2511	34.15	2096	28.51	1571	21.37	1174	15.97
49	S49	Aconitum latent virus	NC_002795.1	8657	2306	26.64	2278	26.31	2149	24.82	1924	22.22
50	S50	Garlic latent virus	NC_003557.1	8363	2282	27.29	2413	28.85	1943	23.23	1725	20.63

51	S51	Groundnut rosette virus	NC_003603.1	4019	970	24.14	812	20.20	1176	29.26	1061	26.40
52	S52	Hibiscus chlorotic ringspot virus	NC_003608.1	3911	975	24.93	1012	25.88	1007	25.75	917	23.45
53	S53	<b>Physalis mottle virus</b>	<b>NC_003634.1</b>	6673	1503	22.52	1588	23.80	874	13.10	2708	40.58
54	S54	Border disease virus	NC_003679.1	12333	4007	32.49	2715	22.01	3203	25.97	2408	19.52
55	S55	Obuda pepper virus	NC_003852.1	6507	1949	29.95	1867	28.69	1520	23.36	1171	18.00
56	S56	Aura virus	NC_003900.1	1824	3462	29.28	2628	22.23	2828	23.92	2906	24.58
57	S57	Grapevine rootstock stem lesion associated virus	NC_004724.1	16527	4250	25.72	4624	27.98	4224	25.56	3429	20.75
58	S58	Omsk hemorrhagic fever virus	NC_005062.1	10787	2772	25.70	2229	20.66	3361	31.16	2425	22.48
59	S59	Botrytis virus X	NC_005132.1	6966	1813	26.03	1348	19.35	1288	18.49	2517	36.13
60	S60	Olive mild mosaic virus	NC_006939.1	3683	1041	28.27	868	23.57	900	24.44	874	23.73
61	S61	Angelonia flower break virus	NC_007733.2	3962	1054	26.60	937	23.65	990	24.99	981	24.76
62	S62	Ilheus virus	NC_009028.2	10755	2903	26.99	2229	20.73	3004	27.93	2619	24.35
63	S63	Peach chlorotic mottle virus	NC_009892.1	9005	2392	26.56	2669	29.64	2042	22.68	1902	21.12
64	S64	Grapevine Algerian latent virus	NC_011535.1	4731	1243	26.27	1167	24.67	1319	27.88	1002	21.18
65	S65	Nemosa ring necrosis virus	NC_011538.1	6285	1223	19.46	1467	23.34	1210	19.25	2385	37.95
66	S66	Peach mosaic virus	NC_011552.1	7988	2439	30.53	2249	28.15	1908	23.89	1392	17.43
67	S67	Anagryis vein yellowing virus	NC_011559.1	6151	1437	23.36	1585	25.77	1154	18.76	1975	32.11
68	S68	Kedougou virus strain DakAar D1470	NC_012533.1	10723	2922	27.25	2143	19.99	3219	30.02	2439	22.75
69	S69	Bagaza virus strain DakAr B209	NC_012534.1	10941	3190	29.16	2330	21.30	3088	28.22	2333	21.32
70	S70	Bovine viral diarrhoea virus 3	NC_012812.1	12337	3945	31.98	2694	21.84	3266	26.47	2426	19.66
71	S71	Kalanchoe latent virus	NC_013006.1	8517	2381	27.96	2215	26.01	2060	24.19	1857	21.80
72	S72	Grapevine Pinot gris virus	NC_015782.2	7259	2181	30.05	2230	30.72	1582	21.79	1266	17.44
73	S73	Brassica yellows virus	NC_016038.2	5666	1625	28.68	1300	22.94	1330	23.47	1411	24.90
74	S74	Actinidia virus B	NC_016404.1	7488	2449	32.71	1558	20.81	1897	25.33	1584	21.15
75	S75	Garlic common latent virus	NC_016440.1	8638	2313	26.78	2473	28.63	2136	24.73	1716	19.87
76	S76	Ndumu virus	NC_016959.1	1724	3259	27.80	2588	22.07	3210	27.38	2632	22.45
77	S77	Pestivirus strain	NC_018713.1	12292	3933	32.00	2728	22.19	3173	25.81	2458	20.00
78	S78	Andean potato latent virus	NC_020470.1	6337	1425	22.49	1742	27.49	892	14.08	2278	35.95
79	S79	Andean potato mild mosaic virus	NC_020471.1	6226	1344	21.59	1756	28.20	970	15.58	2154	34.60
80	S80	Kama virus	NC_023439.1	10688	2449	22.91	2280	21.33	3620	33.87	2339	21.88
81	S81	Gaillardia latent virus	NC_023892.1	8659	2457	28.38	2086	24.09	2286	26.40	1829	21.12
82	S82	Pitaya virus X	NC_024458.1	6677	1800	26.96	1465	21.94	1518	22.73	1894	28.37
83	S83	Middelburg virus	NC_024887.1	11550	3125	27.06	2313	20.03	3118	27.00	2994	25.92
84	S84	Jutiapa virus	NC_026620.1	10125	2916	28.80	2599	25.67	2752	27.18	1858	18.35
85	S85	Phasey bean mild yellows virus	NC_028793.2	5851	1510	25.81	1427	24.39	1460	24.95	1413	24.15
86	S86	Grapevine Red Globe virus	NC_030693.1	6863	1277	18.61	1476	21.51	1202	17.51	2908	42.37
87	S87	Anopheles flavivirus	NC_031327.1	10588	2729	25.77	2629	24.83	2889	27.29	2341	22.11
88	S88	Potexvirus	NC_040842.1	5839	1554	26.61	1260	21.58	1257	21.53	1768	30.28
89	S89	Grapevine associated tymo-like virus	NC_040837.1	6060	1699	28.04	1942	32.05	1503	24.80	916	15.12
90	S90	Actinidia seed-borne latent virus	NC_040800.1	8192	2847	34.75	2187	26.70	1884	23.00	1274	15.55
91	S91	Kampung Karu virus	NC_040788.1	10311	2885	27.98	2271	22.03	3053	29.61	2102	20.39
92	S92	Rocio virus	NC_040776.1	10794	2976	27.57	2169	20.09	3066	28.40	2583	23.93
93	S93	Bovine viral diarrhoea virus	NC_039237.1	12513	4045	32.33	2783	22.24	3186	25.46	2499	19.97
94	S94	Kyasaur forest disease virus	NC_039218.1	10376	2509	24.18	2139	20.61	3314	31.94	2414	23.27
95	S95	Phaseolus vulgaris endornavirus	NC_039217.1	14072	4836	34.37	3986	28.33	2783	19.78	2467	17.53
96	S96	Atractylodes mottle virus	NC_038966.1	8881	2426	27.32	2429	27.35	2180	24.55	1846	20.79
97	S97	Babaco mosaic virus	NC_036587.1	6692	2080	31.08	1479	22.10	1452	21.70	1681	25.12
98	S98	Ocimum basilicum RNA virus	NC_035462.1	6930	2255	32.54	2046	29.52	1554	22.42	1075	15.51
99	S99	Actinidia virus	NC_035453.1	18848	5414	28.72	5495	29.15	4453	23.63	3486	18.50
100	S100	Lake Sinai Virus	NC_035116.1	5877	1129	19.21	1730	29.44	1417	24.11	1601	27.24
101	S101	Apis flavivirus	NC_035071.1	20414	6142	30.09	4537	22.22	4813	23.58	4922	24.11
102	S102	Agave tequilana leaf virus	NC_034833.1	6958	2140	30.76	1572	22.59	1766	25.38	1480	21.27
103	S103	Ochlerotatus caspius flavivirus	NC_034242.1	10370	2787	26.88	2704	26.08	2748	26.50	2131	20.55
104	S104	Lagenaria siceraria endornavirus	NC_034216.1	15098	5582	36.97	3901	25.84	3120	20.66	2495	16.53
105	S105	African eggplant yellowing virus	NC_034207.1	5953	1588	26.68	1380	23.18	1517	25.48	1468	24.66
106	S106	Grapevine rupestris vein feathering virus	NC_034205.1	6730	1205	17.90	1598	23.74	1424	21.16	2498	37.12
107	S107	Peach virus	NC_033828.1	6612	1287	19.46	1277	19.31	1398	21.14	2650	40.08
108	S108	Bamaga virus	NC_033725.1	10203	2866	28.09	2441	23.92	2878	28.21	2018	19.78
109	S109	Kadam virus	NC_033724.1	10215	2601	25.46	2229	21.82	3177	31.10	2208	21.62
110	S110	Gadgets Gully virus	NC_033723.1	10251	2701	26.35	2209	21.55	3207	31.28	2134	20.82
111	S111	Jugra virus	NC_033699.1	10173	2948	28.98	2319	22.80	2751	27.04	2155	21.18
112	S112	Boubou virus	NC_033693.1	10173	2940	28.90	2338	22.98	2744	26.97	2151	21.14
113	S113	New Mapoon virus	NC_032088.1	10864	2872	26.44	2395	22.05	2947	27.13	2650	24.39
114	S114	Botrytis cinerea endornavirus	NC_031752.1	11557	4006	34.66	3151	27.26	2231	19.30	2169	18.77
115	S115	Ceratobasidium endornavirus	NC_031463.1	23635	9624	40.72	6181	26.15	4217	17.84	3613	15.29
116	S116	Ceratobasidium endorna virus	NC_031462.1	15207	4392	28.88	3640	23.94	3787	24.90	3388	22.28
117	S117	Banzi virus	NC_043110.1	10182	2778	27.28	2274	22.33	2867	28.16	2263	22.23

118	S118	White bream virus	NC 008516.1	26660	8975	33.66	6143	23.04	3758	14.10	7784	29.20
119	S119	Chinook salmon bafinivirus	NC 026812.1	27004	8268	30.62	6892	25.52	3909	14.48	7929	29.36
120	S120	Fathead minnow nidovirus	NC 038295.1	27318	9234	33.80	6954	25.46	4110	15.05	7020	25.70
121	S121	Bovine nidovirus	NC 027199.1	20261	5947	29.35	6839	33.75	5208	25.70	2266	11.18
122	S122	Ball python nidovirus	NC 024709.1	33452	11117	33.23	6932	20.72	6663	19.92	8740	26.13
123	S123	Xinzhou toro-like virus	NC 033700.1	30353	9555	31.48	9194	30.29	4934	16.26	6670	21.97
124	S124	Morelia viridis nidovirus	NC 035465.1	32399	10710	33.06	7139	22.03	6186	19.09	8364	25.82
125	S125	Breda virus	NC 007447.1	28475	7690	27.01	9959	34.97	6104	21.44	4718	16.57
126	S126	Porcine torovirus	NC 022787.1	28301	8124	28.71	10267	36.28	5579	19.71	4331	15.30
127	S127	Goat torovirus	NC 034976.1	28487	7686	26.98	10072	35.36	6083	21.35	4646	16.31
128	S128	Belling River virus	NC 046956.1	30742	10484	34.10	5273	17.15	5238	17.04	9747	31.71
129	S129	Hainan hebius popei torovirus	NC_046962.1	29409	8759	29.78	1760	39.99	6561	22.31	2328	7.92
130	S130	Guangdong red-banded snake torovirus	NC_046963.1	30859	9285	30.09	8097	26.24	5722	18.54	7755	25.13

The values of pA, pT, pG and pC are studied independently as well as pairwise. Figs. 6 to 9 respectively show graphs of pA, pT, pG and pC values of all 130 virus genome sequences.

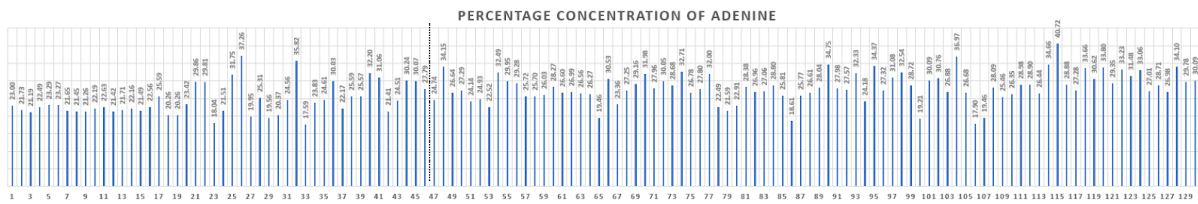


Fig. 6: pA values of all 130 virus genome sequences

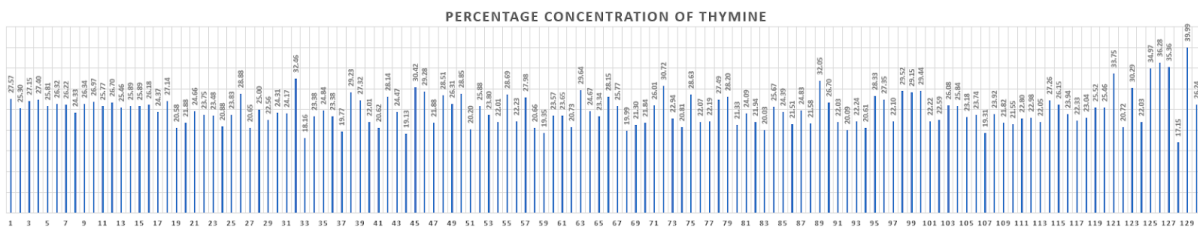


Fig. 7: pT values of all 130 virus genome sequences

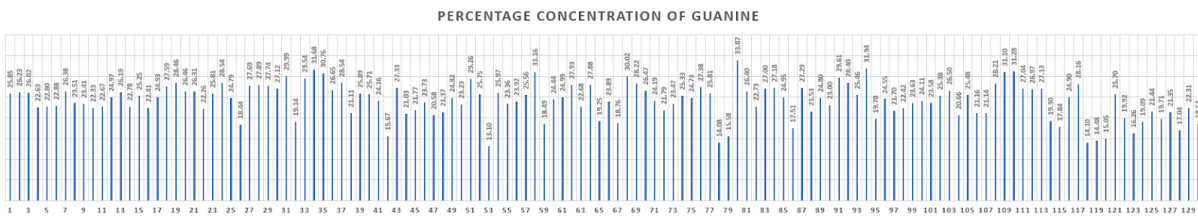


Fig. 8: pG values of all 130 virus genome sequences

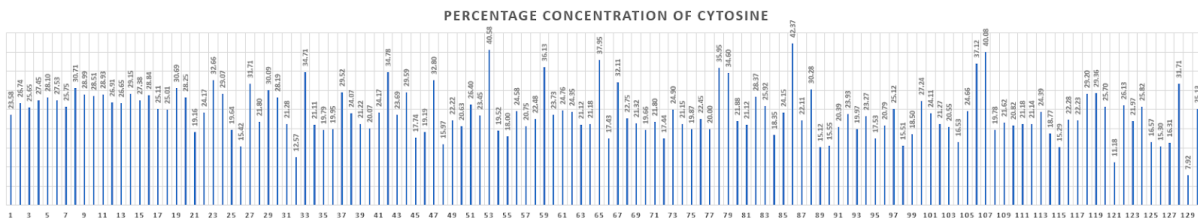


Fig. 9: pC values of all 130 virus genome sequences

Figs. 10 to 16 respectively show graphs of pA, pT, pG and pC values together, pA and pT values together, pA and pG values together, pA and pC values together, pT and pG values together, pT and pC values together, pG and pC values together of all 130 virus genomes.

Figs. 10 to shows Percentage Concentrations of Adenine, Thymine, Guanine and Cytosine

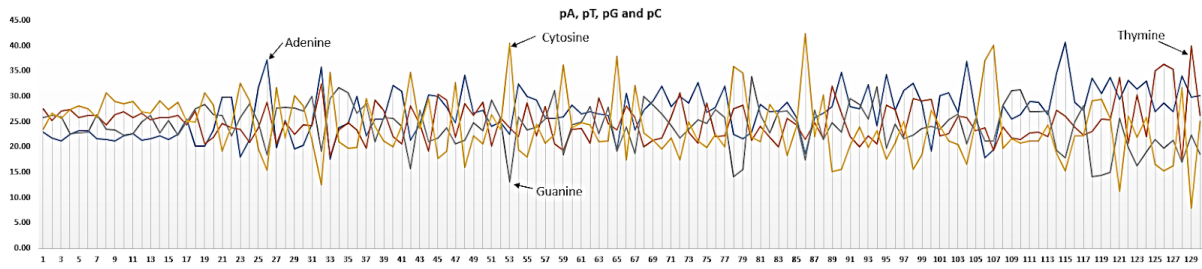


Fig. 10: pA, pT, pG and pC values of all 130 virus genome sequences

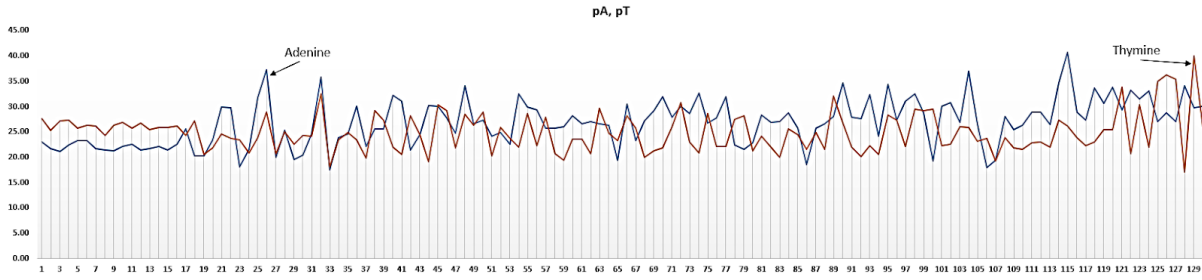


Fig. 11: pA and pT values of all 130 virus genome sequences

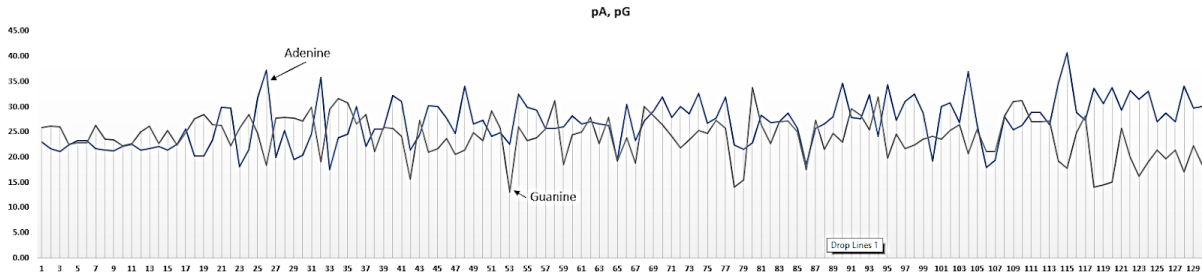


Fig. 12: pA and pG values of all 130 virus genome sequences

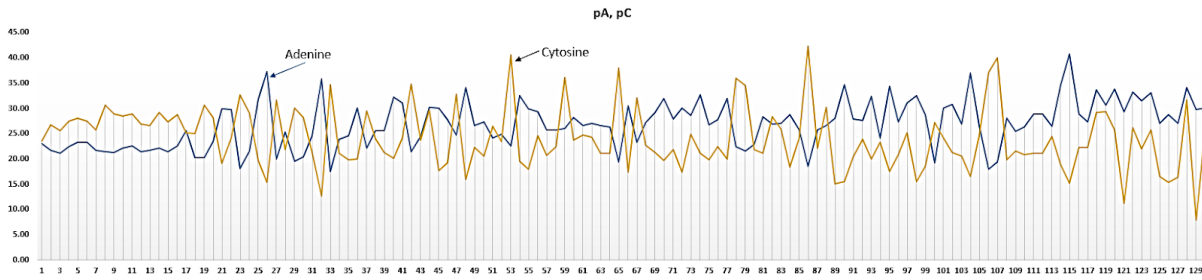


Fig. 13: pA and pC values of all 130 virus genome sequences

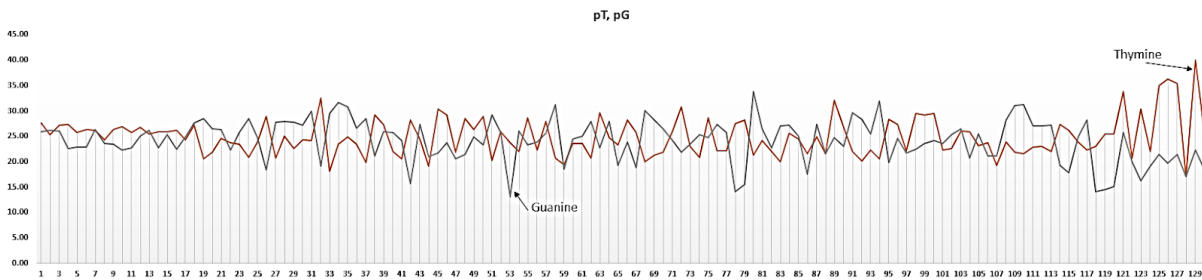


Fig. 14: pT and pG values of all 130 virus genome sequences



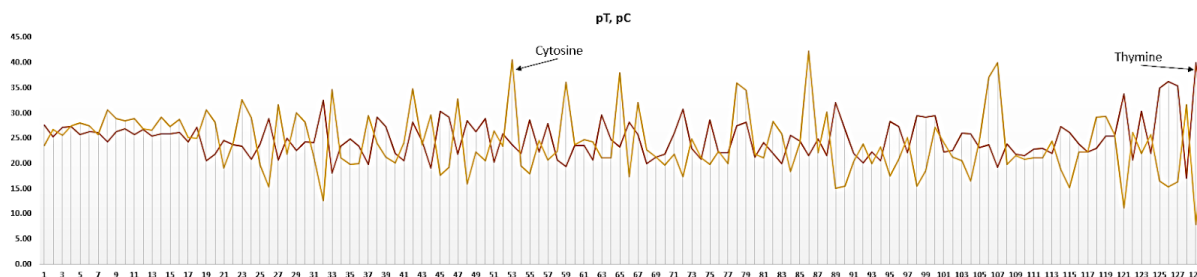


Fig. 15: pT and pC values of all 130 virus genome sequences

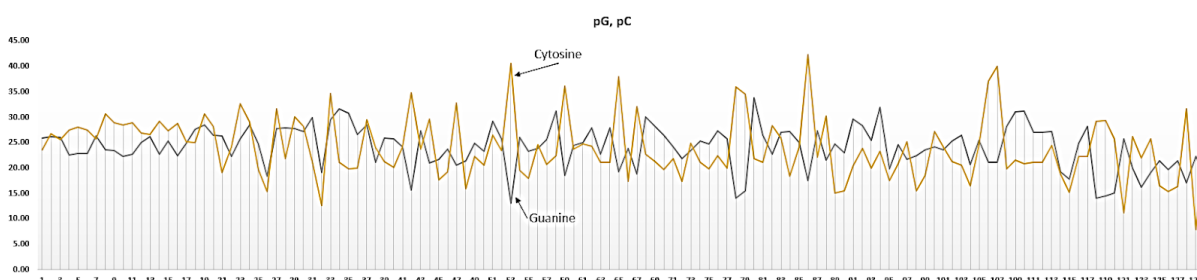


Fig. 16: pG and pC values of all 130 virus genome sequences

### 3.2 Correlation Coefficients of Pairs of Nucleotides

Now, the values of pA-pT, pA-pG, pA-pC, pT-pG, pT-pC and pG-pC are calculated and results shown in table 5. Resulting values are termed as 'errors' for convenience.

Table 5: Values of pA-pT, pA-pG, pA-pC, pT-pG, pT-pC and pG-pC

Seq. No.	pA	pT	pG	pC	pA-pT	pA-pG	pA-pC	pT-pG	pT-pC	pG-pC
S1	23.00	27.57	25.85	23.58	-4.57	-2.85	-0.58	1.72	3.98	2.27
S2	21.73	25.30	26.23	26.74	-3.56	-4.50	-5.00	-0.93	-1.44	-0.51
S3	21.19	27.15	26.02	25.65	-5.96	-4.83	-4.46	1.13	1.50	0.37
S4	22.49	27.40	22.63	27.45	-4.92	-0.14	-4.96	4.78	-0.04	-4.82
S5	23.29	25.81	22.80	28.10	-2.53	0.48	-4.81	3.01	-2.28	-5.29
S6	23.27	26.32	22.88	27.53	-3.05	0.39	-4.26	3.44	-1.21	-4.65
S7	21.65	26.22	26.38	25.75	-4.56	-4.72	-4.10	-0.16	0.46	0.62
S8	21.45	24.33	23.51	30.71	-2.88	-2.07	-9.26	0.82	-6.38	-7.19
S9	21.26	26.34	23.41	28.99	-5.08	-2.14	-7.73	2.93	-2.65	-5.58
S10	22.19	26.97	22.33	28.51	-4.78	-0.15	-6.33	4.64	-1.54	-6.18
S11	22.63	25.77	22.67	28.93	-3.14	-0.05	-6.30	3.10	-3.16	-6.26
S12	21.42	26.70	24.97	26.91	-5.28	-3.56	-5.50	1.72	-0.22	-1.94
S13	21.71	25.46	26.19	26.65	-3.75	-4.48	-4.94	-0.73	-1.19	-0.46
S14	22.16	25.89	22.78	29.15	-3.73	-0.62	-6.99	3.10	-3.27	-6.37
S15	21.49	25.89	25.25	27.38	-4.40	-3.76	-5.89	0.64	-1.49	-2.13
S16	22.56	26.18	22.41	28.84	-3.62	0.15	-6.27	3.77	-2.65	-6.42
S17	25.59	24.37	24.93	25.11	1.21	0.65	0.48	-0.56	-0.73	-0.18
S18	20.26	27.14	27.59	25.01	-6.87	-7.33	-4.75	-0.45	2.13	2.58
S19	20.26	20.58	28.46	30.69	-0.32	-8.20	-10.43	-7.88	-10.11	-2.23
S20	23.42	21.88	26.46	28.25	1.54	-3.04	-4.83	-4.58	-6.37	-1.79
S21	29.86	24.66	26.31	19.16	5.20	3.55	10.70	-1.65	5.50	7.15
S22	29.81	23.75	22.26	24.17	6.06	7.55	5.65	1.49	-0.41	-1.90
S23	18.04	23.48	25.81	32.66	-5.44	-7.77	-14.62	-2.33	-9.18	-6.85
S24	21.51	20.88	28.54	29.07	0.64	-7.03	-7.55	-7.67	-8.19	-0.53
S25	31.75	23.83	24.79	19.64	7.92	6.96	12.11	-0.96	4.19	5.15
S26	37.26	28.88	18.44	15.42	8.38	18.82	21.84	10.44	13.46	3.02
S27	19.95	20.65	27.69	31.71	-0.70	-7.75	-11.77	-7.05	-11.07	-4.02
S28	25.31	25.00	27.89	21.80	0.31	-2.58	3.51	-2.89	3.21	6.09

S29	19.56	22.56	27.74	30.09	-3.00	-8.18	-10.53	-5.18	-7.53	-2.35
S30	20.37	24.31	27.12	28.19	-3.94	-6.75	-7.82	-2.81	-3.88	-1.07
S31	24.56	24.17	29.99	21.28	0.39	-5.44	3.28	-5.82	2.89	8.71
S32	35.82	32.46	19.14	12.57	3.36	16.68	<b>23.25</b>	13.32	19.89	6.57
S33	17.59	18.16	29.54	34.71	-0.57	-11.95	-17.12	-11.38	-16.55	-5.17
S34	23.83	23.38	31.68	21.11	0.45	-7.85	2.72	-8.30	2.26	10.57
S35	24.61	24.84	30.76	19.79	-0.23	-6.14	4.83	-5.91	5.06	10.97
S36	30.03	23.38	26.65	19.95	6.65	3.38	10.08	-3.27	3.43	6.70
S37	22.17	19.77	28.54	29.52	2.40	-6.38	-7.36	-8.78	-9.76	-0.98
S38	25.59	29.23	21.11	24.07	-3.63	4.49	1.53	8.12	5.16	-2.96
S39	25.57	27.32	25.89	21.22	-1.74	-0.32	4.35	1.43	6.09	4.67
S40	32.20	22.01	25.71	20.07	10.20	6.49	12.13	-3.71	1.93	5.64
S41	31.06	20.62	24.16	24.17	10.44	6.90	6.89	-3.54	-3.55	-0.01
S42	21.41	28.14	15.67	34.78	-6.73	5.75	-13.36	12.48	-6.63	-19.11
S43	24.51	24.47	27.33	23.69	0.04	-2.82	0.81	-2.86	0.78	3.63
S44	30.24	19.13	21.03	29.59	11.11	9.21	0.64	-1.90	-10.46	-8.56
S45	30.07	30.42	21.77	17.74	-0.35	8.30	12.33	8.64	12.68	4.03
S46	27.79	29.28	23.73	19.19	-1.49	4.06	8.60	5.55	10.09	4.54
S47	24.74	21.88	20.58	32.80	2.86	4.16	-8.06	1.30	-10.91	-12.22
S48	34.15	28.51	21.37	15.97	5.64	12.79	18.19	7.14	12.54	5.40
S49	26.64	26.31	24.82	22.22	0.32	1.81	4.41	1.49	4.09	2.60
S50	27.29	28.85	23.23	20.63	-1.57	4.05	6.66	5.62	8.23	2.61
S51	24.14	20.20	29.26	26.40	3.93	-5.13	-2.26	-9.06	-6.20	2.86
S52	24.93	25.88	25.75	23.45	-0.95	-0.82	1.48	0.13	2.43	2.30
S53	22.52	23.80	13.10	40.58	-1.27	9.43	-18.06	10.70	-16.78	<b>-27.48</b>
S54	32.49	22.01	25.97	19.52	10.48	6.52	12.97	-3.96	2.49	6.45
S55	29.95	28.69	23.36	18.00	1.26	6.59	11.96	5.33	10.70	5.36
S56	29.28	22.23	23.92	24.58	7.05	5.36	4.70	-1.69	-2.35	-0.66
S57	25.72	27.98	25.56	20.75	-2.26	0.16	4.97	2.42	7.23	4.81
S58	25.70	20.66	31.16	22.48	5.03	-5.46	3.22	-10.49	-1.82	8.68
S59	26.03	19.35	18.49	36.13	6.68	7.54	-10.11	0.86	-16.78	-17.64
S60	28.27	23.57	24.44	23.73	4.70	3.83	4.53	-0.87	-0.16	0.71
S61	26.60	23.65	24.99	24.76	2.95	1.62	1.84	-1.34	-1.11	0.23
S62	26.99	20.73	27.93	24.35	6.27	-0.94	2.64	-7.21	-3.63	3.58
S63	26.56	29.64	22.68	21.12	-3.08	3.89	5.44	6.96	8.52	1.55
S64	26.27	24.67	27.88	21.18	1.61	-1.61	5.09	-3.21	3.49	6.70
S65	19.46	23.34	19.25	37.95	-3.88	0.21	-18.49	4.09	-14.61	-18.70
S66	30.53	28.15	23.89	17.43	2.38	6.65	13.11	4.27	10.73	6.46
S67	23.36	25.77	18.76	32.11	-2.41	4.60	-8.75	7.01	-6.34	-13.35
S68	27.25	19.99	30.02	22.75	7.26	-2.77	4.50	-10.03	-2.76	7.27
S69	29.16	21.30	28.22	21.32	7.86	0.93	7.83	-6.93	-0.03	6.90
S70	31.98	21.84	26.47	19.66	10.14	5.50	12.31	-4.64	2.17	6.81
S71	27.96	26.01	24.19	21.80	1.95	3.77	6.15	1.82	4.20	2.38
S72	30.05	30.72	21.79	17.44	-0.68	8.25	12.61	8.93	13.28	4.35
S73	28.68	22.94	23.47	24.90	5.74	5.21	3.78	-0.53	-1.96	-1.43
S74	32.71	20.81	25.33	21.15	11.90	7.37	11.55	-4.53	-0.35	4.18
S75	26.78	28.63	24.73	19.87	-1.85	2.05	6.91	3.90	8.76	4.86
S76	27.80	22.07	27.38	22.45	5.72	0.42	5.35	-5.31	-0.38	4.93
S77	32.00	22.19	25.81	20.00	9.80	6.18	12.00	-3.62	2.20	5.82
S78	22.49	27.49	14.08	35.95	-5.00	8.41	-13.46	13.41	-8.46	-21.87
S79	21.59	28.20	15.58	34.60	-6.62	6.01	-13.01	12.62	-6.39	-19.02
S80	22.91	21.33	33.87	21.88	1.58	<b>-10.96</b>	1.03	<b>-12.54</b>	-0.55	11.99
S81	28.38	24.09	26.40	21.12	4.28	1.97	7.25	-2.31	2.97	5.28
S82	26.96	21.94	22.73	28.37	5.02	4.22	-1.41	-0.79	-6.43	-5.63
S83	27.06	20.03	27.00	25.92	7.03	0.06	1.13	-6.97	-5.90	1.07
S84	28.80	25.67	27.18	18.35	3.13	1.62	10.45	-1.51	7.32	8.83
S85	25.81	24.39	24.95	24.15	1.42	0.85	1.66	-0.56	0.24	0.80
S86	18.61	21.51	17.51	42.37	-2.90	1.09	<b>-23.77</b>	3.99	<b>-20.87</b>	-24.86
S87	25.77	24.83	27.29	22.11	0.94	-1.51	3.66	-2.46	2.72	5.18
S88	26.61	21.58	21.53	30.28	5.04	5.09	-3.67	0.05	-8.70	-8.75
S89	28.04	32.05	24.80	15.12	-4.01	3.23	12.92	7.24	16.93	9.69
S90	34.75	26.70	23.00	15.55	8.06	11.76	19.20	3.70	11.15	7.45

S91	27.98	22.03	29.61	20.39	5.95	-1.63	7.59	-7.58	1.64	9.22
S92	27.57	20.09	28.40	23.93	7.48	-0.83	3.64	-8.31	-3.84	4.47
S93	32.33	22.24	25.46	19.97	10.09	6.86	12.36	-3.22	2.27	5.49
S94	24.18	20.61	31.94	23.27	3.57	-7.76	0.92	-11.32	-2.65	8.67
S95	34.37	28.33	19.78	17.53	6.04	14.59	16.83	8.55	10.79	2.25
S96	27.32	27.35	24.55	20.79	-0.03	2.77	6.53	2.80	6.56	3.76
S97	31.08	22.10	21.70	25.12	8.98	9.38	5.96	0.40	-3.02	-3.42
S98	32.54	29.52	22.42	15.51	3.02	10.12	17.03	7.10	14.01	6.91
S99	28.72	29.15	23.63	18.50	-0.43	5.10	10.23	5.53	10.66	5.13
S100	19.21	29.44	24.11	27.24	-10.23	-4.90	-8.03	5.33	2.19	-3.13
S101	30.09	22.22	23.58	24.11	7.86	6.51	5.98	-1.35	-1.89	-0.53
S102	30.76	22.59	25.38	21.27	8.16	5.38	9.49	-2.79	1.32	4.11
S103	26.88	26.08	26.50	20.55	0.80	0.38	6.33	-0.42	5.53	5.95
S104	36.97	25.84	20.66	16.53	11.13	16.31	20.45	5.17	9.31	4.14
S105	26.68	23.18	25.48	24.66	3.49	1.19	2.02	-2.30	-1.48	0.82
S106	17.90	23.74	21.16	37.12	-5.84	-3.25	-19.21	2.59	-13.37	-15.96
S107	19.46	19.31	21.14	40.08	0.15	-1.68	-20.61	-1.83	-20.77	-18.94
S108	28.09	23.92	28.21	19.78	4.17	-0.12	8.31	-4.28	4.15	8.43
S109	25.46	21.82	31.10	21.62	3.64	-5.64	3.85	-9.28	0.21	9.49
S110	26.35	21.55	31.28	20.82	4.80	-4.94	5.53	-9.74	0.73	10.47
S111	28.98	22.80	27.04	21.18	6.18	1.94	7.80	-4.25	1.61	5.86
S112	28.90	22.98	26.97	21.14	5.92	1.93	7.76	-3.99	1.84	5.83
S113	26.44	22.05	27.13	24.39	4.39	-0.69	2.04	-5.08	-2.35	2.73
S114	34.66	27.26	19.30	18.77	7.40	15.36	15.90	7.96	8.50	0.54
S115	40.72	26.15	17.84	15.29	14.57	<b>22.88</b>	<b>25.43</b>	8.31	10.87	2.56
S116	28.88	23.94	24.90	22.28	4.95	3.98	6.60	-0.97	1.66	2.62
S117	27.28	22.33	28.16	22.23	4.95	-0.87	5.06	-5.82	0.11	5.93
S118	33.66	23.04	14.10	29.20	10.62	19.57	4.47	8.95	-6.16	-15.10
S119	30.62	25.52	14.48	29.36	5.10	16.14	1.26	11.05	-3.84	-14.89
S120	33.80	25.46	15.05	25.70	8.35	18.76	8.10	10.41	-0.24	-10.65
S121	29.35	33.75	25.70	11.18	-4.40	3.65	18.17	8.05	22.57	<b>14.52</b>
S122	33.23	20.72	19.92	26.13	12.51	13.31	7.11	0.80	-5.40	-6.21
S123	31.48	30.29	16.26	21.97	1.19	15.22	9.50	14.03	8.32	-5.72
S124	33.06	22.03	19.09	25.82	11.02	13.96	7.24	2.94	-3.78	-6.72
S125	27.01	34.97	21.44	16.57	-7.97	5.57	10.44	13.54	18.41	4.87
S126	28.71	36.28	19.71	15.30	-7.57	8.99	13.40	16.56	20.97	4.41
S127	26.98	35.36	21.35	16.31	-8.38	5.63	10.67	14.00	19.05	5.04
S128	34.10	17.15	17.04	31.71	<b>16.95</b>	17.06	2.40	0.11	-14.55	-14.67
S129	29.78	39.99	22.31	7.92	<b>-10.20</b>	7.47	21.87	<b>17.68</b>	<b>32.07</b>	14.39
S130	30.09	26.24	18.54	25.13	3.85	11.55	4.96	7.70	1.11	-6.59

Figs. 17 to 22 respectively show graphs of pA-pT error values, pA-pG error values, pA-pC error values, pT-pG error values, pT-pC error values and pG-pC error values.

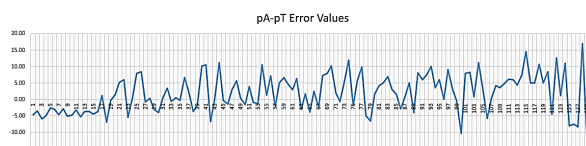


Fig. 17: Graph of pA-pT error values

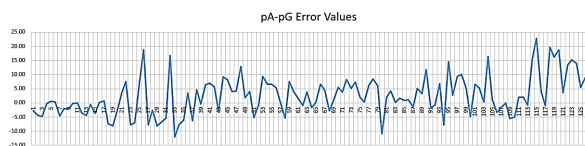


Fig. 18: Graph of pA-pG error values

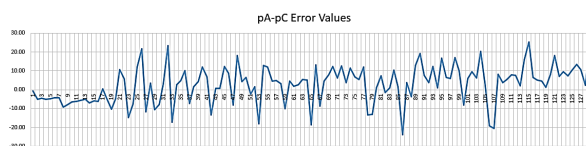


Fig. 19: Graph of pA-pC error values

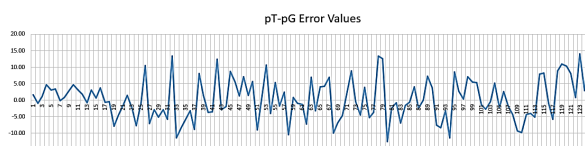


Fig. 20: Graph of pT-pG error values

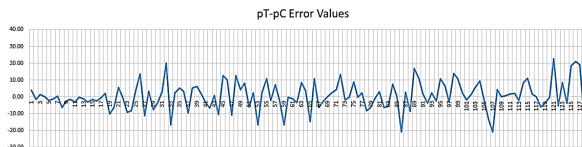


Fig. 21: Graph of pT-pC error values

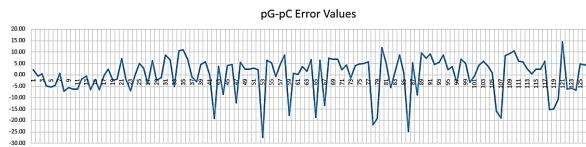


Fig. 22: Graph of pG-pC error values

### 3.2.1 Measure of Correlation Coefficients of Pairs of Nucleotides

Given a finite number of genome sequences (in this case 130), the values of pA, pT, pG and pC are evaluated. Then, the values of pA-pT, pA-pG, pA-pC, pT-pG, pT-pC and pG-pC are evaluated. Now, the Correlation Coefficient  $\tau$  of A and T, for instance, is defined as  $\tau(A,T) = \text{Max}(pA-pT) - \text{Min}(pA-pT)$ . Less the error, more the correlation coefficient  $\tau$  of A and T. This could be generalized to all other nucleotide combinations. Correlation Coefficient  $\tau$  of each of the ordered pair is calculated as

1.  $\tau(A,T) = \text{Max}(pA-pT) - \text{Min}(pA-pT) = 16.95 + 10.20 = 27.15$
2.  $\tau(A,G) = \text{Max}(pA-pG) - \text{Min}(pA-pG) = 22.88 + 10.96 = 33.84$
3.  $\tau(A,C) = \text{Max}(pA-pC) - \text{Min}(pA-pC) = 25.43 + 23.77 = 49.20$
4.  $\tau(T,G) = \text{Max}(pT-pG) - \text{Min}(pT-pG) = 17.68 + 12.54 = 30.22$
5.  $\tau(T,C) = \text{Max}(pT-pC) - \text{Min}(pT-pC) = 32.07 + 20.87 = 52.94$
6.  $\tau(G,C) = \text{Max}(pG-pC) - \text{Min}(pG-pC) = 14.52 + 27.48 = 42$

The correlation coefficients  $\tau$  of all possible pairs of nucleotides are shown in Fig. 23

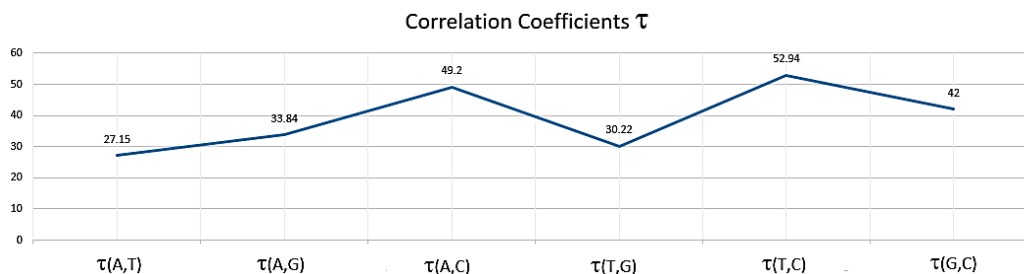


Fig. 23: Correlation coefficients of all possible pairs of nucleotides

#### Observations

1. Pairwise Correlation Coefficient  $\tau(A,T) = 27.15$
2. Pairwise Correlation Coefficient  $\tau(A,G) = 33.84$
3. Pairwise Correlation Coefficient  $\tau(A,C) = 49.2$
4. Pairwise Correlation Coefficient  $\tau(T,G) = 30.22$
5. Pairwise Correlation Coefficient  $\tau(T,C) = 52.94$
6. Pairwise Correlation Coefficient  $\tau(G,C) = 42$
7. Less the value of  $\tau$ , more the ordered couple of nucleotides is correlated.
8.  $\langle A,T \rangle$  form natural pair and highly correlated.
9.  $\langle A,G \rangle$  form unnatural pair and correlated to a certain extent.
10.  $\langle A,C \rangle$  form unnatural pair and moderately uncorrelated.
11.  $\langle T,G \rangle$  form unnatural pair and correlated to a great extent.
12.  $\langle T,C \rangle$  form unnatural pair and highly uncorrelated.
13.  $\langle G,C \rangle$  form natural pair and uncorrelated.
14. **One can select natural pairing of  $\langle A,T \rangle$  and  $\langle G,C \rangle$ . Note that the pair  $\langle A,T \rangle$  is correlated and the pair  $\langle G,C \rangle$  uncorrelated.**
15. **One can select unnatural pairing of  $\langle T,G \rangle$  and  $\langle A,C \rangle$ . Note that the pair  $\langle T,G \rangle$  is correlated and the pair  $\langle A,C \rangle$  is uncorrelated – a significant observation**

To summarize, a total of 130 virus sequences related to Corona virus family was tested in terms of percentage concentrations of nucleotides. The significant observation made after analyzing all 130 sequences, the natural pair of nucleotides Adenine and Thymine are highly correlated, whereas the natural pair of Guanine and Cytosine are uncorrelated. Similarly, the unnatural pair of Thymine and Guanine are correlated and the unnatural pair of Adenine and Cytosine are uncorrelated.

#### Inference

**This phenomenon seems to be a natural occurrence in all genome sequences.**

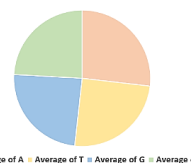
### 3.3 Differential Errors of percentage concentrations of nucleotides with respect to their averages

From entries in Table 6, one would observe that the average percentage concentrations of all nucleotides are almost same. This amounts to saying that all four nucleotides are almost equally distributed in any genome sequence. Details are given below.



**Table 6:** Percentage Concentration Averages of Nucleotides

Percentage Concentration Averages of Nucleotides	
Average of pA	26.84
Average of pT	24.92
Average of pG	24.12
Average of pC	24.11



The percentage concentration of nucleotides in all 130 virus sequences have been evaluated and the average values found as pA = 26.84, pT = 24.92, pG = 24.12 and pC = 24.11. Table 7 presents the percentage concentration values of each nucleotide subtracted from the respective average values.

**Table 7:** Values of pA, pT, pG and pC subtracted from their average values

Sequences	pA	pT	pG	pC	Avg-pA	Avg-pT	Avg-pG	Avg-pC
S1	23.00	27.57	25.85	23.58	3.84	-2.65	-1.73	0.53
S2	21.73	25.30	26.23	26.74	5.10	-0.38	-2.11	-2.62
S3	21.19	27.15	26.02	25.65	5.65	-2.23	-1.90	-1.53
S4	22.49	27.40	22.63	27.45	4.35	-2.48	1.49	-3.33
S5	23.29	25.81	22.80	28.10	3.55	-0.89	1.31	-3.98
S6	23.27	26.32	22.88	27.53	3.57	-1.40	1.24	-3.41
S7	21.65	26.22	26.38	25.75	5.18	-1.30	-2.26	-1.64
S8	21.45	24.33	23.51	30.71	5.39	0.59	0.60	-6.59
S9	21.26	26.34	23.41	28.99	5.58	-1.42	0.71	-4.88
S10	22.19	26.97	22.33	28.51	4.65	-2.05	1.78	-4.40
S11	22.63	25.77	22.67	28.93	4.21	-0.85	1.44	-4.82
S12	21.42	26.70	24.97	26.91	5.42	-1.78	-0.86	-2.80
S13	21.71	25.46	26.19	26.65	5.13	-0.54	-2.07	-2.54
S14	22.16	25.89	22.78	29.15	4.68	-0.97	1.33	-5.04
S15	21.49	25.89	25.25	27.38	5.35	-0.97	-1.13	-3.26
S16	22.56	26.18	22.41	28.84	4.27	-1.26	1.70	-4.72
S17	25.59	24.37	24.93	25.11	1.25	0.55	-0.82	-0.99
S18	20.26	27.14	27.59	25.01	6.57	-2.22	-3.47	-0.90
S19	20.26	20.58	28.46	30.69	6.58	4.34	-4.35	-6.58
S20	23.42	21.88	26.46	28.25	3.42	3.04	-2.34	-4.13
S21	29.86	24.66	26.31	19.16	-3.02	0.26	-2.20	4.95
S22	29.81	23.75	22.26	24.17	-2.98	1.17	1.85	-0.05
S23	18.04	23.48	25.81	32.66	8.80	1.44	-1.69	-8.55
S24	21.51	20.88	28.54	29.07	5.32	4.04	-4.42	-4.95
S25	31.75	23.83	24.79	19.64	-4.91	1.10	-0.67	4.48
S26	37.26	28.88	18.44	15.42	-10.42	-3.96	5.68	8.69
S27	19.95	20.65	27.69	31.71	6.89	4.27	-3.58	-7.60
S28	25.31	25.00	27.89	21.80	1.53	-0.08	-3.77	2.32
S29	19.56	22.56	27.74	30.09	7.28	2.36	-3.63	-5.98
S30	20.37	24.31	27.12	28.19	6.47	0.61	-3.01	-4.08
S31	24.56	24.17	29.99	21.28	2.28	0.75	-5.88	2.83
S32	35.82	32.46	19.14	12.57	-8.98	-7.54	4.97	11.54
S33	17.59	18.16	29.54	34.71	9.25	6.76	-5.42	-10.59
S34	23.83	23.38	31.68	21.11	3.01	1.54	-7.56	3.00
S35	24.61	24.84	30.76	19.79	2.23	0.08	-6.64	4.33
S36	30.03	23.38	26.65	19.95	-3.19	1.54	-2.53	4.17
S37	22.17	19.77	28.54	29.52	4.67	5.15	-4.43	-5.41
S38	25.59	29.23	21.11	24.07	1.24	-4.31	3.01	0.05
S39	25.57	27.32	25.89	21.22	1.27	-2.40	-1.77	2.89
S40	32.20	22.01	25.71	20.07	-5.37	2.91	-1.60	4.04
S41	31.06	20.62	24.16	24.17	-4.22	4.30	-0.04	-0.05
S42	21.41	28.14	15.67	34.78	5.42	-3.22	8.45	-10.66
S43	24.51	24.47	27.33	23.69	2.33	0.45	-3.21	0.42
S44	30.24	19.13	21.03	29.59	-3.40	5.79	3.08	-5.48
S45	30.07	30.42	21.77	17.74	-3.23	-5.50	2.34	6.37
S46	27.79	29.28	23.73	19.19	-0.95	-4.36	0.39	4.92
S47	24.74	21.88	20.58	32.80	2.10	3.04	3.54	-8.68
S48	34.15	28.51	21.37	15.97	-7.32	-3.59	2.75	8.15
S49	26.64	26.31	24.82	22.22	0.20	-1.39	-0.71	1.89

S50	27.29	28.85	23.23	20.63	-0.45	-3.93	0.88	3.49
S51	24.14	20.20	29.26	26.40	2.70	4.72	-5.14	-2.29
S52	24.93	25.88	25.75	23.45	1.91	-0.96	-1.63	0.67
S53	22.52	23.80	13.10	40.58	4.31	1.12	11.02	-16.47
S54	32.49	22.01	25.97	19.52	-5.65	2.91	-1.85	4.59
S55	29.95	28.69	23.36	18.00	-3.11	-3.77	0.76	6.12
S56	29.28	22.23	23.92	24.58	-2.44	2.69	0.20	-0.46
S57	25.72	27.98	25.56	20.75	1.12	-3.06	-1.44	3.37
S58	25.70	20.66	31.16	22.48	1.14	4.26	-7.04	1.63
S59	26.03	19.35	18.49	36.13	0.81	5.57	5.63	-12.02
S60	28.27	23.57	24.44	23.73	-1.43	1.35	-0.32	0.38
S61	26.60	23.65	24.99	24.76	0.23	1.27	-0.87	-0.65
S62	26.99	20.73	27.93	24.35	-0.15	4.20	-3.81	-0.24
S63	26.56	29.64	22.68	21.12	0.27	-4.72	1.44	2.99
S64	26.27	24.67	27.88	21.18	0.56	0.25	-3.76	2.93
S65	19.46	23.34	19.25	37.95	7.38	1.58	4.86	-13.83
S66	30.53	28.15	23.89	17.43	-3.70	-3.23	0.23	6.69
S67	23.36	25.77	18.76	32.11	3.48	-0.85	5.36	-7.99
S68	27.25	19.99	30.02	22.75	-0.41	4.94	-5.90	1.37
S69	29.16	21.30	28.22	21.32	-2.32	3.62	-4.11	2.79
S70	31.98	21.84	26.47	19.66	-5.14	3.08	-2.36	4.45
S71	27.96	26.01	24.19	21.80	-1.12	-1.09	-0.07	2.31
S72	30.05	30.72	21.79	17.44	-3.21	-5.80	2.32	6.67
S73	28.68	22.94	23.47	24.90	-1.84	1.98	0.64	-0.79
S74	32.71	20.81	25.33	21.15	-5.87	4.11	-1.22	2.96
S75	26.78	28.63	24.73	19.87	0.06	-3.71	-0.61	4.25
S76	27.80	22.07	27.38	22.45	-0.96	2.85	-3.26	1.66
S77	32.00	22.19	25.81	20.00	-5.16	2.73	-1.70	4.12
S78	22.49	27.49	14.08	35.95	4.35	-2.57	10.04	-11.83
S79	21.59	28.20	15.58	34.60	5.25	-3.28	8.54	-10.48
S80	22.91	21.33	33.87	21.88	3.92	3.59	-9.75	2.23
S81	28.38	24.09	26.40	21.12	-1.54	0.83	-2.28	2.99
S82	26.96	21.94	22.73	28.37	-0.12	2.98	1.38	-4.25
S83	27.06	20.03	27.00	25.92	-0.22	4.89	-2.88	-1.81
S84	28.80	25.67	27.18	18.35	-1.96	-0.75	-3.06	5.76
S85	25.81	24.39	24.95	24.15	1.03	0.53	-0.84	-0.04
S86	18.61	21.51	17.51	42.37	8.23	3.41	6.60	-18.26
S87	25.77	24.83	27.29	22.11	1.06	0.09	-3.17	2.00
S88	26.61	21.58	21.53	30.28	0.22	3.34	2.59	-6.16
S89	28.04	32.05	24.80	15.12	-1.20	-7.13	-0.68	9.00
S90	34.75	26.70	23.00	15.55	-7.92	-1.78	1.12	8.56
S91	27.98	22.03	29.61	20.39	-1.14	2.90	-5.49	3.73
S92	27.57	20.09	28.40	23.93	-0.73	4.83	-4.29	0.18
S93	32.33	22.24	25.46	19.97	-5.49	2.68	-1.34	4.14
S94	24.18	20.61	31.94	23.27	2.66	4.31	-7.82	0.85
S95	34.37	28.33	19.78	17.53	-7.53	-3.41	4.34	6.58
S96	27.32	27.35	24.55	20.79	-0.48	-2.43	-0.43	3.33
S97	31.08	22.10	21.70	25.12	-4.24	2.82	2.42	-1.01
S98	32.54	29.52	22.42	15.51	-5.70	-4.60	1.69	8.60
S99	28.72	29.15	23.63	18.50	-1.89	-4.23	0.49	5.62
S100	19.21	29.44	24.11	27.24	7.63	-4.52	0.01	-3.13
S101	30.09	22.22	23.58	24.11	-3.25	2.70	0.54	0.00
S102	30.76	22.59	25.38	21.27	-3.92	2.33	-1.26	2.84
S103	26.88	26.08	26.50	20.55	-0.04	-1.15	-2.38	3.56
S104	36.97	25.84	20.66	16.53	-10.13	-0.92	3.45	7.59
S105	26.68	23.18	25.48	24.66	0.16	1.74	-1.37	-0.55
S106	17.90	23.74	21.16	37.12	8.93	1.18	2.96	-13.00
S107	19.46	19.31	21.14	40.08	7.37	5.61	2.97	-15.96
S108	28.09	23.92	28.21	19.78	-1.25	1.00	-4.09	4.34
S109	25.46	21.82	31.10	21.62	1.38	3.10	-6.98	2.50
S110	26.35	21.55	31.28	20.82	0.49	3.37	-7.17	3.30

S111	28.98	22.80	27.04	21.18	-2.14	2.12	-2.93	2.93
S112	28.90	22.98	26.97	21.14	-2.06	1.94	-2.86	2.97
S113	26.44	22.05	27.13	24.39	0.40	2.88	-3.01	-0.28
S114	34.66	27.26	19.30	18.77	-7.83	-2.34	4.81	5.35
S115	40.72	26.15	17.84	15.29	-13.88	-1.23	6.27	8.83
S116	28.88	23.94	24.90	22.28	-2.04	0.98	-0.79	1.84
S117	27.28	22.33	28.16	22.23	-0.45	2.59	-4.04	1.89
S118	33.66	23.04	14.10	29.20	-6.83	1.88	10.02	-5.08
S119	30.62	25.52	14.48	29.36	-3.78	-0.60	9.64	-5.25
S120	33.80	25.46	15.05	25.70	-6.96	-0.54	9.07	-1.58
S121	29.35	33.75	25.70	11.18	-2.51	-8.83	-1.59	12.93
S122	33.23	20.72	19.92	26.13	-6.40	4.20	4.20	-2.01
S123	31.48	30.29	16.26	21.97	-4.64	-5.37	7.86	2.14
S124	33.06	22.03	19.09	25.82	-6.22	2.89	5.02	-1.70
S125	27.01	34.97	21.44	16.57	-0.17	-10.05	2.68	7.55
S126	28.71	36.28	19.71	15.30	-1.87	-11.36	4.40	8.81
S127	26.98	35.36	21.35	16.31	-0.14	-10.44	2.76	7.81
S128	34.10	17.15	17.04	31.71	-7.27	7.77	7.08	-7.59
S129	29.78	39.99	22.31	7.92	-2.95	-15.07	1.81	16.20
S130	30.09	26.24	18.54	25.13	-3.25	-1.32	5.57	-1.02

Figs. 24 to 27 respectively show the graphs of differential errors of percentage concentration values with respect to average values.



Fig. 24: Differential errors of pA values with respect to its average value

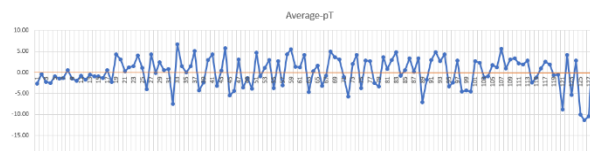


Fig. 25: Differential errors of pT values with respect to its average value

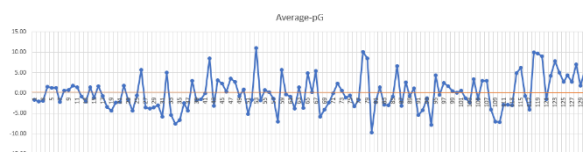


Fig. 26: Differential errors of pG values with respect to its average value

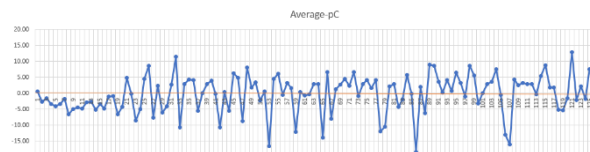


Fig. 27: Differential errors of pC values with respect to its average value

Tables 8 to 11 respectively present both positive and negative differential error values of all four nucleotides.

Table 8: Positive and negative differential error values of pA

Positive Values					Negative Values			
Sl. No.	Seq. No	pA	Avg-pA		Sl. No.	Seq. No	pA	Avg-pA
1	S1	23.00	3.84		1	S21	29.86	-3.02
2	S2	21.73	5.10		2	S22	29.81	-2.98
3	S3	21.19	5.65		3	S25	31.75	-4.91
4	S4	22.49	4.35		4	S26	37.26	-10.42
5	S5	23.29	3.55		5	S32	35.82	-8.98
6	S6	23.27	3.57		6	S36	30.03	-3.19
7	S7	21.65	5.18		7	S40	32.20	-5.37
8	S8	21.45	5.39		8	S41	31.06	-4.22
9	S9	21.26	5.58		9	S44	30.24	-3.40
10	S10	22.19	4.65		10	S45	30.07	-3.23
11	S11	22.63	4.21		11	S46	27.79	-0.95
12	S12	21.42	5.42		12	S48	34.15	-7.32
13	S13	21.71	5.13		13	S50	27.29	-0.45
14	S14	22.16	4.68		14	S54	32.49	-5.65
15	S15	21.49	5.35		15	S55	29.95	-3.11
16	S16	22.56	4.27		16	S56	29.28	-2.44
17	S17	25.59	1.25		17	S60	28.27	-1.43

18	S18	20.26	6.57		18	S62	26.99	-0.15
19	S19	20.26	6.58		19	S66	30.53	-3.70
20	S20	23.42	3.42		20	S68	27.25	-0.41
21	S23	18.04	8.80		21	S69	29.16	-2.32
22	S24	21.51	5.32		22	S70	31.98	-5.14
23	S27	19.95	6.89		23	S71	27.96	-1.12
24	S28	25.31	1.53		24	S72	30.05	-3.21
25	S29	19.56	7.28		25	S73	28.68	-1.84
26	S30	20.37	6.47		26	S74	32.71	-5.87
27	S31	24.56	2.28		27	S76	27.80	-0.96
28	S33	17.59	9.25		28	S77	32.00	-5.16
29	S34	23.83	3.01		29	S81	28.38	-1.54
30	S35	24.61	2.23		30	S82	26.96	-0.12
31	S37	22.17	4.67		31	S83	27.06	-0.22
32	S38	25.59	1.24		32	S84	28.80	-1.96
33	S39	25.57	1.27		33	S89	28.04	-1.20
34	S42	21.41	5.42		34	S90	34.75	-7.92
35	S43	24.51	2.33		35	S91	27.98	-1.14
36	S47	24.74	2.10		36	S92	27.57	-0.73
37	S49	26.64	0.20		37	S93	32.33	-5.49
38	S51	24.14	2.70		38	S95	34.37	-7.53
39	S52	24.93	1.91		39	S96	27.32	-0.48
40	S53	22.52	4.31		40	S97	31.08	-4.24
41	S57	25.72	1.12		41	S98	32.54	-5.70
42	S58	25.70	1.14		42	S99	28.72	-1.89
43	S59	26.03	0.81		43	S101	30.09	-3.25
44	S61	26.60	0.23		44	S102	30.76	-3.92
45	S63	26.56	0.27		45	S103	26.88	-0.04
46	S64	26.27	0.56		46	S104	36.97	-10.13
47	S65	19.46	7.38		47	S108	28.09	-1.25
48	S67	23.36	3.48		48	S111	28.98	-2.14
49	S75	26.78	0.06		49	S112	28.90	-2.06
50	S78	22.49	4.35		50	S114	34.66	-7.83
51	S79	21.59	5.25		51	S115	40.72	-13.88
52	S80	22.91	3.92		52	S116	28.88	-2.04
53	S85	25.81	1.03		53	S117	27.28	-0.45
54	S86	18.61	8.23		54	S118	33.66	-6.83
55	S87	25.77	1.06		55	S119	30.62	-3.78
56	S88	26.61	0.22		56	S120	33.80	-6.96
57	S94	24.18	2.66		57	S121	29.35	-2.51
58	S100	19.21	7.63		58	S122	33.23	-6.40
59	S105	26.68	0.16		59	S123	31.48	-4.64
60	S106	17.90	8.93		60	S124	33.06	-6.22
61	S107	19.46	7.37		61	S125	27.01	-0.17
62	S109	25.46	1.38		62	S126	28.71	-1.87
63	S110	26.35	0.49		63	S127	26.98	-0.14
64	S113	26.44	0.40		64	S128	34.10	-7.27
					65	S129	29.78	-2.95
					66	S130	30.09	-3.25

Table 9: Positive and negative differential error values of pT

Positive Values				Negative Values			
Sl. No.	Seq. No	pT	Avg-pT	Sl. No.	Seq. No	pT	Avg-pT
1	S8	24.33	0.59	1	S1	27.57	-2.65
2	S17	24.37	0.55	2	S2	25.30	-0.38
3	S19	20.58	4.34	3	S3	27.15	-2.23
4	S20	21.88	3.04	4	S4	27.40	-2.48
5	S21	24.66	0.26	5	S5	25.81	-0.89
6	S22	23.75	1.17	6	S6	26.32	-1.40
7	S23	23.48	1.44	7	S7	26.22	-1.30
8	S24	20.88	4.04	8	S9	26.34	-1.42
9	S25	23.83	1.10	9	S10	26.97	-2.05

10	S27	20.65	4.27		10	S11	25.77	-0.85
11	S29	22.56	2.36		11	S12	26.70	-1.78
12	S30	24.31	0.61		12	S13	25.46	-0.54
13	S31	24.17	0.75		13	S14	25.89	-0.97
14	S33	18.16	6.76		14	S15	25.89	-0.97
15	S34	23.38	1.54		15	S16	26.18	-1.26
16	S35	24.84	0.08		16	S18	27.14	-2.22
17	S36	23.38	1.54		17	S26	28.88	-3.96
18	S37	19.77	5.15		18	S28	25.00	-0.08
19	S40	22.01	2.91		19	S32	32.46	-7.54
20	S41	20.62	4.30		20	S38	29.23	-4.31
21	S43	24.47	0.45		21	S39	27.32	-2.40
22	S44	19.13	5.79		22	S42	28.14	-3.22
23	S47	21.88	3.04		23	S45	30.42	-5.50
24	S51	20.20	4.72		24	S46	29.28	-4.36
25	S53	23.80	1.12		25	S48	28.51	-3.59
26	S54	22.01	2.91		26	S49	26.31	-1.39
27	S56	22.23	2.69		27	S50	28.85	-3.93
28	S58	20.66	4.26		28	S52	25.88	-0.96
29	S59	19.35	5.57		29	S55	28.69	-3.77
30	S60	23.57	1.35		30	S57	27.98	-3.06
31	S61	23.65	1.27		31	S63	29.64	-4.72
32	S62	20.73	4.20		32	S66	28.15	-3.23
33	S64	24.67	0.25		33	S67	25.77	-0.85
34	S65	23.34	1.58		34	S71	26.01	-1.09
35	S68	19.99	4.94		35	S72	30.72	-5.80
36	S69	21.30	3.62		36	S75	28.63	-3.71
37	S70	21.84	3.08		37	S78	27.49	-2.57
38	S73	22.94	1.98		38	S79	28.20	-3.28
39	S74	20.81	4.11		39	S84	25.67	-0.75
40	S76	22.07	2.85		40	S89	32.05	-7.13
41	S77	22.19	2.73		41	S90	26.70	-1.78
42	S80	21.33	3.59		42	S95	28.33	-3.41
43	S81	24.09	0.83		43	S96	27.35	-2.43
44	S82	21.94	2.98		44	S98	29.52	-4.60
45	S83	20.03	4.89		45	S99	29.15	-4.23
46	S85	24.39	0.53		46	S100	29.44	-4.52
47	S86	21.51	3.41		47	S103	26.08	-1.15
48	S87	24.83	0.09		48	S104	25.84	-0.92
49	S88	21.58	3.34		49	S114	27.26	-2.34
50	S91	22.03	2.90		50	S115	26.15	-1.23
51	S92	20.09	4.83		51	S119	25.52	-0.60
52	S93	22.24	2.68		52	S120	25.46	-0.54
53	S94	20.61	4.31		53	S121	33.75	-8.83
54	S97	22.10	2.82		54	S123	30.29	-5.37
55	S101	22.22	2.70		55	S125	34.97	-10.05
56	S102	22.59	2.33		56	S126	36.28	-11.36
57	S105	23.18	1.74		57	S127	35.36	-10.44
58	S106	23.74	1.18		58	S129	39.99	-15.07
59	S107	19.31	5.61		59	S130	26.24	-1.32
60	S108	23.92	1.00					
61	S109	21.82	3.10					
62	S110	21.55	3.37					
63	S111	22.80	2.12					
64	S112	22.98	1.94					
65	S113	22.05	2.88					
66	S116	23.94	0.98					
67	S117	22.33	2.59					
68	S118	23.04	1.88					
69	S122	20.72	4.20					
70	S124	22.03	2.89					
71	S128	17.15	7.77					

Table 10: Positive and negative differential error values of pG

Positive Values					Negative Values			
Sl. No.	Seq. No	pG	Avg-pG		Sl. No.	Seq. No	pG	Avg-pG
1	S4	22.63	1.49		1	S1	25.85	-1.73
2	S5	22.80	1.31		2	S2	26.23	-2.11
3	S6	22.88	1.24		3	S3	26.02	-1.90
4	S8	23.51	0.60		4	S7	26.38	-2.26
5	S9	23.41	0.71		5	S12	24.97	-0.86
6	S10	22.33	1.78		6	S13	26.19	-2.07
7	S11	22.67	1.44		7	S15	25.25	-1.13
8	S14	22.78	1.33		8	S17	24.93	-0.82
9	S16	22.41	1.70		9	S18	27.59	-3.47
10	S22	22.26	1.85		10	S19	28.46	-4.35
11	S26	18.44	5.68		11	S20	26.46	-2.34
12	S32	19.14	4.97		12	S21	26.31	-2.20
13	S38	21.11	3.01		13	S23	25.81	-1.69
14	S42	15.67	8.45		14	S24	28.54	-4.42
15	S44	21.03	3.08		15	S25	24.79	-0.67
16	S45	21.77	2.34		16	S27	27.69	-3.58
17	S46	23.73	0.39		17	S28	27.89	-3.77
18	S47	20.58	3.54		18	S29	27.74	-3.63
19	S48	21.37	2.75		19	S30	27.12	-3.01
20	S50	23.23	0.88		20	S31	29.99	-5.88
21	S53	13.10	11.02		21	S33	29.54	-5.42
22	S55	23.36	0.76		22	S34	31.68	-7.56
23	S56	23.92	0.20		23	S35	30.76	-6.64
24	S59	18.49	5.63		24	S36	26.65	-2.53
25	S63	22.68	1.44		25	S37	28.54	-4.43
26	S65	19.25	4.86		26	S39	25.89	-1.77
27	S66	23.89	0.23		27	S40	25.71	-1.60
28	S67	18.76	5.36		28	S41	24.16	-0.04
29	S72	21.79	2.32		29	S43	27.33	-3.21
30	S73	23.47	0.64		30	S49	24.82	-0.71
31	S78	14.08	10.04		31	S51	29.26	-5.14
32	S79	15.58	8.54		32	S52	25.75	-1.63
33	S82	22.73	1.38		33	S54	25.97	-1.85
34	S86	17.51	6.60		34	S57	25.56	-1.44
35	S88	21.53	2.59		35	S58	31.16	-7.04
36	S90	23.00	1.12		36	S60	24.44	-0.32
37	S95	19.78	4.34		37	S61	24.99	-0.87
38	S97	21.70	2.42		38	S62	27.93	-3.81
39	S98	22.42	1.69		39	S64	27.88	-3.76
40	S99	23.63	0.49		40	S68	30.02	-5.90
41	S100	24.11	0.01		41	S69	28.22	-4.11
42	S101	23.58	0.54		42	S70	26.47	-2.36
43	S104	20.66	3.45		43	S71	24.19	-0.07
44	S106	21.16	2.96		44	S74	25.33	-1.22
45	S107	21.14	2.97		45	S75	24.73	-0.61
46	S114	19.30	4.81		46	S76	27.38	-3.26
47	S115	17.84	6.27		47	S77	25.81	-1.70
48	S118	14.10	10.02		48	S80	33.87	-9.75
49	S119	14.48	9.64		49	S81	26.40	-2.28
50	S120	15.05	9.07		50	S83	27.00	-2.88
51	S122	19.92	4.20		51	S84	27.18	-3.06
52	S123	16.26	7.86		52	S85	24.95	-0.84
53	S124	19.09	5.02		53	S87	27.29	-3.17
54	S125	21.44	2.68		54	S89	24.80	-0.68
55	S126	19.71	4.40		55	S91	29.61	-5.49
56	S127	21.35	2.76		56	S92	28.40	-4.29
57	S128	17.04	7.08		57	S93	25.46	-1.34
58	S129	22.31	1.81		58	S94	31.94	-7.82

59	S130	18.54	5.57		59	S96	24.55	-0.43
					60	S102	25.38	-1.26
					61	S103	26.50	-2.38
					62	S105	25.48	-1.37
					63	S108	28.21	-4.09
					64	S109	31.10	-6.98
					65	S110	31.28	-7.17
					66	S111	27.04	-2.93
					67	S112	26.97	-2.86
					68	S113	27.13	-3.01
					69	S116	24.90	-0.79
					70	S117	28.16	-4.04
					71	S121	25.70	-1.59

Table 11: Positive and negative differential error values of pC

Positive Values				Negative Values			
Sl. No.	Seq. No	pC	Avg-pC	Sl. No.	Seq. No	pC	Avg-pC
1	S1	23.58	0.53	1	S2	26.74	-2.62
2	S21	19.16	4.95	2	S3	25.65	-1.53
3	S25	19.64	4.48	3	S4	27.45	-3.33
4	S26	15.42	8.69	4	S5	28.10	-3.98
5	S28	21.80	2.32	5	S6	27.53	-3.41
6	S31	21.28	2.83	6	S7	25.75	-1.64
7	S32	12.57	11.54	7	S8	30.71	-6.59
8	S34	21.11	3.00	8	S9	28.99	-4.88
9	S35	19.79	4.33	9	S10	28.51	-4.40
10	S36	19.95	4.17	10	S11	28.93	-4.82
11	S38	24.07	0.05	11	S12	26.91	-2.80
12	S39	21.22	2.89	12	S13	26.65	-2.54
13	S40	20.07	4.04	13	S14	29.15	-5.04
14	S43	23.69	0.42	14	S15	27.38	-3.26
15	S45	17.74	6.37	15	S16	28.84	-4.72
16	S46	19.19	4.92	16	S17	25.11	-0.99
17	S48	15.97	8.15	17	S18	25.01	-0.90
18	S49	22.22	1.89	18	S19	30.69	-6.58
19	S50	20.63	3.49	19	S20	28.25	-4.13
20	S52	23.45	0.67	20	S22	24.17	-0.05
21	S54	19.52	4.59	21	S23	32.66	-8.55
22	S55	18.00	6.12	22	S24	29.07	-4.95
23	S57	20.75	3.37	23	S27	31.71	-7.60
24	S58	22.48	1.63	24	S29	30.09	-5.98
25	S60	23.73	0.38	25	S30	28.19	-4.08
26	S63	21.12	2.99	26	S33	34.71	-10.59
27	S64	21.18	2.93	27	S37	29.52	-5.41
28	S66	17.43	6.69	28	S41	24.17	-0.05
29	S68	22.75	1.37	29	S42	34.78	-10.66
30	S69	21.32	2.79	30	S44	29.59	-5.48
31	S70	19.66	4.45	31	S47	32.80	-8.68
32	S71	21.80	2.31	32	S51	26.40	-2.29
33	S72	17.44	6.67	33	S53	40.58	-16.47
34	S74	21.15	2.96	34	S56	24.58	-0.46
35	S75	19.87	4.25	35	S59	36.13	-12.02
36	S76	22.45	1.66	36	S61	24.76	-0.65
37	S77	20.00	4.12	37	S62	24.35	-0.24
38	S80	21.88	2.23	38	S65	37.95	-13.83
39	S81	21.12	2.99	39	S67	32.11	-7.99
40	S84	18.35	5.76	40	S73	24.90	-0.79
41	S87	22.11	2.00	41	S78	35.95	-11.83
42	S89	15.12	9.00	42	S79	34.60	-10.48
43	S90	15.55	8.56	43	S82	28.37	-4.25
44	S91	20.39	3.73	44	S83	25.92	-1.81



45	S92	23.93	0.18		45	S85	24.15	-0.04
46	S93	19.97	4.14		46	S86	42.37	-18.26
47	S94	23.27	0.85		47	S88	30.28	-6.16
48	S95	17.53	6.58		48	S97	25.12	-1.01
49	S96	20.79	3.33		49	S100	27.24	-3.13
50	S98	15.51	8.60		50	S105	24.66	-0.55
51	S99	18.50	5.62		51	S106	37.12	-13.00
52	S101	24.11	0.00		52	S107	40.08	-15.96
53	S102	21.27	2.84		53	S113	24.39	-0.28
54	S103	20.55	3.56		54	S118	29.20	-5.08
55	S104	16.53	7.59		55	S119	29.36	-5.25
56	S108	19.78	4.34		56	S120	25.70	-1.58
57	S109	21.62	2.50		57	S122	26.13	-2.01
58	S110	20.82	3.30		58	S124	25.82	-1.70
59	S111	21.18	2.93		59	S128	31.71	-7.59
60	S112	21.14	2.97		60	S130	25.13	-1.02
61	S114	18.77	5.35					
62	S115	15.29	8.83					
63	S116	22.28	1.84					
64	S117	22.23	1.89					
65	S121	11.18	12.93					
66	S123	21.97	2.14					
67	S125	16.57	7.55					
68	S126	15.30	8.81					
69	S127	16.31	7.81					
70	S129	7.92	16.20					

**Observations**

Number of Positive Values of Avg-pA = 64 Number of Negative Values of Avg-pA = 66	Positive and negative values of Avg-pT are distributed in the ratio <b>64:66</b> (almost equally distributed). This property has been observed in all 130 sequences.
Number of Positive Values of Avg-pT = 71 Number of Negative Values of Avg-pT = 59	Positive and negative values of Avg-pT are distributed in the ratio <b>71:59</b> . This property has been observed in all 130 sequences.
Number of Positive Values of Avg-pG = 59 Number of Negative Values of Avg-pG = 71	Positive and negative values of Avg-pG are distributed in the ratio <b>59:71</b> . This property has been observed in all 130 sequences.
Number of Positive Values of Avg-pC = 70 Number of Negative Values of Avg-pC = 60	Positive and negative values of Avg-pC are distributed in the ratio <b>70:60</b> . This property has been observed in all 130 sequences.

From tables 7 to 10, it is clear that there is a pattern of distribution of nucleotides in all 130 virus sequences. This observation paves a new avenue for further research in bio-informatics.

**3.4 Virus Genomes with Dominant Nucleotides**

From the given set of 130 virus genome sequences, the subset of sequences consisting of maximum number of Adenines are separated, which are called A-Dominant sequences. Similarly, T-Dominant sequences, G-Dominant sequences and C-Dominant sequences are separated. There are 52 A-Dominant sequences, 21 T-Dominant sequences, 22 G-Dominant sequences and 35 C-Dominant sequences in the set of 130 virus genomes. They are given in tables 12 to 15.

*Table 12: A-Dominant Virus Sequences (52)*

Sl. No.	Seq. No.	Species	Accession ID	Total length	A	pA	T	pT	G	pG	C	pC
1	S17	Giardia lamblia virus	NC_003555.1	6277	1606	25.59	1530	24.37	1565	24.93	1576	25.11
2	S21	Black raspberry virus F	NC_009890.1	5077	1516	29.86	1252	24.66	1336	26.31	973	19.16
3	S22	Armigeres subalbatus virus	NC_014609.1	7510	2239	29.81	1784	23.75	1672	22.26	1815	24.17
4	S25	Camponotus yamaokai virus	NC_027212.1	5704	1811	31.75	1359	23.83	1414	24.79	1120	19.64
5	S26	Golden shiner totivirus	NC_030295.1	7788	2902	37.26	2249	28.88	1436	18.44	1201	15.42
6	S32	Gigaspora margarita giardia-like virus	NC_040632.1	4947	1772	35.82	1606	32.46	947	19.14	622	12.57
7	S36	Diatom colony associated dsRNA virus 12 genomic RNA	NC_040775.1	5941	1784	30.03	1389	23.38	1583	26.65	1185	19.95
8	S40	Bovine viral diarrhea virus	NC_001461.1	12573	4049	32.20	2767	22.01	3233	25.71	2524	20.07
9	S41	O'nyong-nyong virus	NC_001512.1	11835	3676	31.06	2440	20.62	2859	24.16	2860	24.17
10	S44	Bamboo mosaic virus,	NC_001642.1	6366	1925	30.24	1218	19.13	1339	21.03	1884	29.59
11	S48	Banana mild mosaic virus	NC_002729.1	7352	2511	34.15	2096	28.51	1571	21.37	1174	15.97
12	S49	Aconitum latent virus	NC_002795.1	8657	2306	26.64	2278	26.31	2149	24.82	1924	22.22



13	S54	Border disease virus	NC_003679.1	12333	4007	32.49	2715	22.01	3203	25.97	2408	19.52
14	S55	Obuda pepper virus	NC_003852.1	6507	1949	29.95	1867	28.69	1520	23.36	1171	18.00
15	S56	Aura virus	NC_003900.1	11824	3462	29.28	2628	22.23	2828	23.92	2906	24.58
16	S60	Olive mild mosaic virus	NC_006939.1	3683	1041	28.27	868	23.57	900	24.44	874	23.73
17	S61	Angelonia flower break virus	NC_007733.2	3962	1054	26.60	937	23.65	990	24.99	981	24.76
18	S66	Peach mosaic virus	NC_011552.1	7988	2439	30.53	2249	28.15	1908	23.89	1392	17.43
19	S69	Bagaza virus strain DakAr B209	NC_012534.1	10941	3190	29.16	2330	21.30	3088	28.22	2333	21.32
20	S70	Bovine viral diarrhea virus 3	NC_012812.1	12337	3945	31.98	2694	21.84	3266	26.47	2426	19.66
21	S71	Kalanchoe latent virus	NC_013006.1	8517	2381	27.96	2215	26.01	2060	24.19	1857	21.80
22	S73	Brassica yellows virus	NC_016038.2	5666	1625	28.68	1300	22.94	1330	23.47	1411	24.90
23	S74	Actinidia virus B	NC_016404.1	7488	2449	32.71	1558	20.81	1897	25.33	1584	21.15
24	S76	Ndumu virus	NC_016959.1	11724	3259	27.80	2588	22.07	3210	27.38	2632	22.45
25	S77	Pestivirus strain	NC_018713.1	12292	3933	32.00	2728	22.19	3173	25.81	2458	20.00
26	S81	Gaillardia latent virus	NC_023892.1	8659	2457	28.38	2086	24.09	2286	26.40	1829	21.12
27	S83	Middelburg virus	NC_024887.1	11550	3125	27.06	2313	20.03	3118	27.00	2994	25.92
28	S84	Jutiapa virus	NC_026620.1	10125	2916	28.80	2599	25.67	2752	27.18	1858	18.35
29	S85	Phasey bean mild yellows virus	NC_028793.2	5851	1510	25.81	1427	24.39	1460	24.95	1413	24.15
30	S90	Actinidia seed-borne latent virus	NC_040800.1	8192	2847	34.75	2187	26.70	1884	23.00	1274	15.55
31	S93	Bovine viral diarrhea virus	NC_039237.1	12513	4045	32.33	2783	22.24	3186	25.46	2499	19.97
32	S95	Phaseolus vulgaris endornavirus	NC_039217.1	14072	4836	34.37	3986	28.33	2783	19.78	2467	17.53
33	S97	Babaco mosaic virus	NC_036587.1	6692	2080	31.08	1479	22.10	1452	21.70	1681	25.12
34	S98	Ocimum basilicum RNA virus	NC_035462.1	6930	2255	32.54	2046	29.52	1554	22.42	1075	15.51
35	S101	Apis flavivirus	NC_035071.1	20414	6142	30.09	4537	22.22	4813	23.58	4922	24.11
36	S102	Agave tequilana leaf virus	NC_034833.1	6958	2140	30.76	1572	22.59	1766	25.38	1480	21.27
37	S103	Ochlerotatus caspius flavivirus	NC_034242.1	10370	2787	26.88	2704	26.08	2748	26.50	2131	20.55
38	S104	Lagenaria siceraria endornavirus	NC_034216.1	15098	5582	36.97	3901	25.84	3120	20.66	2495	16.53
39	S105	African eggplant yellowing virus	NC_034207.1	5953	1588	26.68	1380	23.18	1517	25.48	1468	24.66
40	S111	Jugra virus	NC_033699.1	10173	2948	28.98	2319	22.80	2751	27.04	2155	21.18
41	S112	Bouboui virus	NC_033693.1	10173	2940	28.90	2338	22.98	2744	26.97	2151	21.14
42	S114	Botrytis cinerea endornavirus	NC_031752.1	11557	4006	34.66	3151	27.26	2231	19.30	2169	18.77
43	S115	Ceratobasidium endornavirus	NC_031463.1	23635	9624	40.72	6181	26.15	4217	17.84	3613	15.29
44	S116	Ceratobasidium endorna virus	NC_031462.1	15207	4392	28.88	3640	23.94	3787	24.90	3388	22.28
45	S118	White bream virus	NC_008516.1	26660	8975	33.66	6143	23.04	3758	14.10	7784	29.20
46	S119	Chinook salmon bafinivirus	NC_026812.1	27004	8268	30.62	6892	25.52	3909	14.48	7929	29.36
47	S120	Fathead minnow nidovirus	NC_038295.1	27318	9234	33.80	6954	25.46	4110	15.05	7020	25.70
48	S122	Ball python nidovirus	NC_024709.1	33452	11117	33.23	6932	20.72	6663	19.92	8740	26.13
49	S123	Xinzhou toro-like virus	NC_033700.1	30353	9555	31.48	9194	30.29	4934	16.26	6670	21.97
50	S124	Morelia viridis nidovirus	NC_035465.1	32399	10710	33.06	7139	22.03	6186	19.09	8364	25.82
51	S128	Bellinger River virus	NC_046956.1	30742	10484	34.10	5273	17.15	5238	17.04	9747	31.71
52	S130	Guangdong red-banded snake torovirus	NC_046963.1	30859	9285	30.09	8097	26.24	5722	18.54	7755	25.13

Fig. 28 shows graph of Percentage Concentrations in virus sequences of dominant adenines and other nucleotides

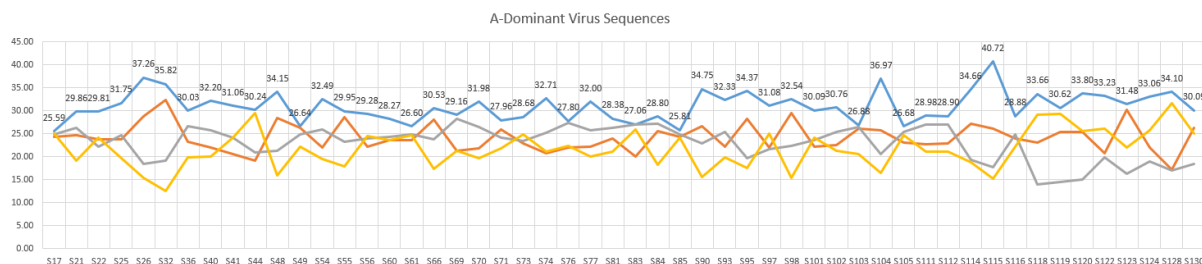


Fig. 28: Percentage Concentrations in virus sequences of dominant adenines and other nucleotides

13	S80	Kama virus	NC_023439.1	10688	2449	22.91	2280	21.33	3620	33.87	2339	21.88
14	S87	Anopheles flavivirus	NC_031327.1	10588	2729	25.77	2629	24.83	2889	27.29	2341	22.11
15	S91	Kampung Karu virus	NC_040788.1	10311	2885	27.98	2271	22.03	3053	29.61	2102	20.39
16	S92	Rocio virus	NC_040776.1	10794	2976	27.57	2169	20.09	3066	28.40	2583	23.93
17	S94	Kyasanur forest disease virus	NC_039218.1	10376	2509	24.18	2139	20.61	3314	31.94	2414	23.27
18	S108	Bamaga virus	NC_033725.1	10203	2866	28.09	2441	23.92	2878	28.21	2018	19.78
19	S109	Kadam virus	NC_033724.1	10215	2601	25.46	2229	21.82	3177	31.10	2208	21.62
20	S110	Gadgets Gully virus	NC_033723.1	10251	2701	26.35	2209	21.55	3207	31.28	2134	20.82
21	S113	New Mapoon virus	NC_032088.1	10864	2872	26.44	2395	22.05	2947	27.13	2650	24.39
22	S117	Banzi virus	NC_043110.1	10182	2778	27.28	2274	22.33	2867	28.16	2263	22.23

Table 13: T-Dominant Virus Sequences (21)

Sl. No.	Seq. No.	Species	Accession ID	Total length	A	pA	T	pT	G	pG	C	pC
1	S1	Lactate dehydrogenase-elevating virus	NC_001639.1	14104	3244	23.00	3888	27.57	3646	25.85	3326	23.58
2	S3	Equine arteritis virus	NC_002532.2	12704	2692	21.19	3449	27.15	3305	26.02	3258	25.65
3	S38	Guangdong greater green snake arterivirus	NC_046959.1	18410	4712	25.59	5381	29.23	3886	21.11	4431	24.07
4	S39	Pothos latent virus	NC_000939.2	4415	1129	25.57	1206	27.32	1143	25.89	937	21.22
5	S45	Odontoglossum ringspot virus,	NC_001728.1	6618	1990	30.07	2013	30.42	1441	21.77	1174	17.74
6	S46	Rupestris stem pitting associated virus	NC_001948.1	8744	2430	27.79	2560	29.28	2075	23.73	1678	19.19
7	S50	Garlic latent virus	NC_003557.1	8363	2282	27.29	2413	28.85	1943	23.23	1725	20.63
8	S52	Hibiscus chlorotic ringspot virus	NC_003608.1	3911	975	24.93	1012	25.88	1007	25.75	917	23.45
9	S57	Grapevine rootstock stem lesion associated virus	NC_004724.1	16527	4250	25.72	4624	27.98	4224	25.56	3429	20.75
10	S63	Peach chlorotic mottle virus	NC_009892.1	9005	2392	26.56	2669	29.64	2042	22.68	1902	21.12
11	S72	Grapevine Pinot gris virus	NC_015782.2	7259	2181	30.05	2230	30.72	1582	21.79	1266	17.44
12	S75	Garlic common latent virus	NC_016440.1	8638	2313	26.78	2473	28.63	2136	24.73	1716	19.87
13	S89	Grapevine associated tymo-like virus	NC_040837.1	6060	1699	28.04	1942	32.05	1503	24.80	916	15.12
14	S96	Atractyodes mottle virus	NC_038966.1	8881	2426	27.32	2429	27.35	2180	24.55	1846	20.79
15	S99	Actinidia virus	NC_035453.1	18848	5414	28.72	5495	29.15	4453	23.63	3486	18.50
16	S100	Lake Sinai Virus	NC_035116.1	5877	1129	19.21	1730	29.44	1417	24.11	1601	27.24
17	S121	Bovine nidovirus	NC_027199.1	20261	5947	29.35	6839	33.75	5208	25.70	2266	11.18
18	S125	Breda virus	NC_007447.1	28475	7690	27.01	9959	34.97	6104	21.44	4718	16.57
19	S126	Porcine torovirus	NC_022787.1	28301	8124	28.71	10267	36.28	5579	19.71	4331	15.30
20	S127	Goat torovirus	NC_034976.1	28487	7686	26.98	10072	35.36	6083	21.35	4646	16.31
21	S129	Hainan hebivirus popei torovirus	NC_046962.1	29409	8759	29.78	11760	39.99	6561	22.31	2328	7.92

Fig. 29 shows graph of Percentage Concentrations in virus sequences of dominant thymines and other nucleotides

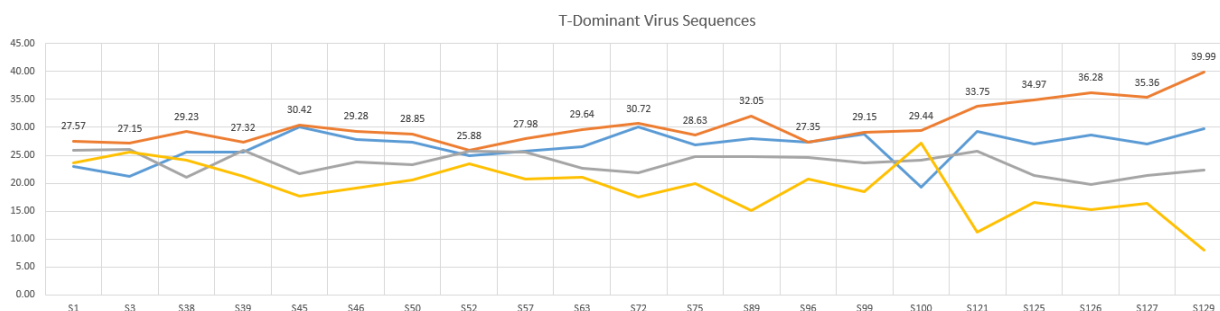


Fig. 29: Percentage Concentrations in virus sequences of dominant thymines and other nucleotides

Table 14: G-Dominant Virus Sequences (22)

Sl. No.	Seq. No.	Species	Accession ID	Total length	A	pA	T	pT	G	pG	C	pC
1	S7	Forest pouched giant rat arterivirus	NC_026439.1	14953	3238	21.65	3920	26.22	3944	26.38	3851	25.75
2	S18	Chalara elegans RNA Virus 1	NC_005883.1	5310	1076	20.26	1441	27.14	1465	27.59	1328	25.01
3	S28	Australian Anopheles totivirus	NC_035674.1	6203	1570	25.31	1551	25.00	1730	27.89	1352	21.80

4	S31	Diatom colony associated dsRNA virus	NC_040431.1	4671	1147	24.56	1129	24.17	1401	29.99	994	21.28
5	S34	Diatom colony associated dsRNA virus 13 genomic RNA	NC_040659.1	5082	1211	23.83	1188	23.38	1610	31.68	1073	21.11
6	S35	Diatom colony associated dsRNA virus 11 genomic RNA	NC_040660.1	5160	1270	24.61	1282	24.84	1587	30.76	1021	19.79
7	S43	Cell fusing agent virus	NC_001564.2	10682	2618	24.51	2614	24.47	2919	27.33	2531	23.69
8	S51	Groundnut rosette virus	NC_003603.1	4019	970	24.14	812	20.20	1176	29.26	1061	26.40
9	S58	Omsk hemorrhagic fever virus	NC_005062.1	10787	2772	25.70	2229	20.66	3361	31.16	2425	22.48
10	S62	Ilheus virus	NC_009028.2	10755	2903	26.99	2229	20.73	3004	27.93	2619	24.35
11	S64	Grapevine Algerian latent virus	NC_011535.1	4731	1243	26.27	1167	24.67	1319	27.88	1002	21.18
12	S68	Kedougou virus strain DakAar D1470	NC_012533.1	10723	2922	27.25	2143	19.99	3219	30.02	2439	22.75
13	S80	Kama virus	NC_023439.1	10688	2449	22.91	2280	21.33	3620	33.87	2339	21.88
14	S87	Anopheles flavivirus	NC_031327.1	10588	2729	25.77	2629	24.83	2889	27.29	2341	22.11
15	S91	Kampung Karu virus	NC_040788.1	10311	2885	27.98	2271	22.03	3053	29.61	2102	20.39
16	S92	Rocio virus	NC_040776.1	10794	2976	27.57	2169	20.09	3066	28.40	2583	23.93
17	S94	Kyasanur forest disease virus	NC_039218.1	10376	2509	24.18	2139	20.61	3314	31.94	2414	23.27
18	S108	Bamaga virus	NC_033725.1	10203	2866	28.09	2441	23.92	2878	28.21	2018	19.78
19	S109	Kadam virus	NC_033724.1	10215	2601	25.46	2229	21.82	3177	31.10	2208	21.62
20	S110	Gadgets Gully virus	NC_033723.1	10251	2701	26.35	2209	21.55	3207	31.28	2134	20.82
21	S113	New Mapoon virus	NC_032088.1	10864	2872	26.44	2395	22.05	2947	27.13	2650	24.39
22	S117	Banzi virus	NC_043110.1	10182	2778	27.28	2274	22.33	2867	28.16	2263	22.23

Fig. 30 shows graph of Percentage Concentrations in virus sequences of dominant guanines and other nucleotides

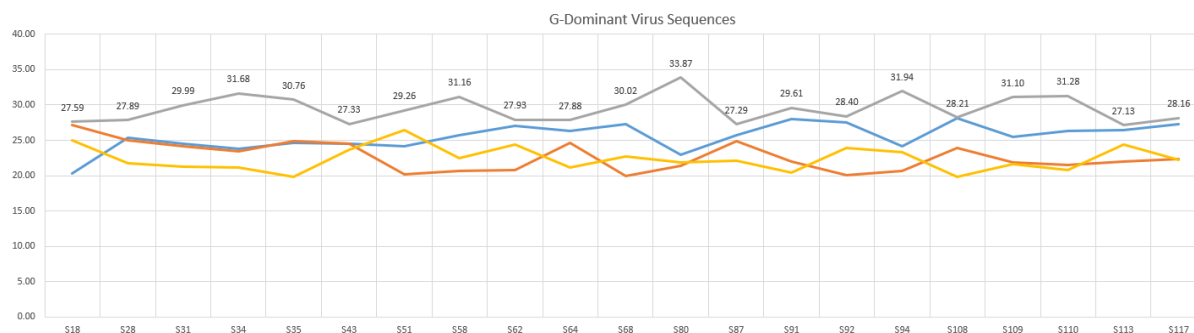


Fig. 30: Percentage Concentrations in virus sequences of dominant guanines and other nucleotides

Table 15: C-Dominant Virus Sequences (35)

Sl. No.	Seq. No.	Species	Accession ID	Total length	A	pA	T	pT	G	pG	C	pC
1	S2	Porcine respiratory and reproductive syndrome virus	NC_001961.1	15428	3353	21.73	3903	25.30	4047	26.23	4125	26.74
2	S4	Simian hemorrhagic fever virus	NC_003092.2	15717	3534	22.49	4307	27.40	3556	22.63	4314	27.45
3	S5	Mikumi yellow baboon virus	NC_025112.1	14927	3476	23.29	3853	25.81	3404	22.80	4194	28.10
4	S6	Southwest baboon virus	NC_025113.1	14851	3456	23.27	3909	26.32	3398	22.88	4088	27.53
5	S8	DeBrazzas monkey arterivirus	NC_026509.1	15684	3364	21.45	3816	24.33	3688	23.51	4816	30.71
6	S9	Pebjah virus	NC_027124.1	15478	3291	21.26	4077	26.34	3623	23.41	4487	28.99
7	S10	Kafue Kinda chacma baboon virus	NC_029053.1	14924	3311	22.19	4025	26.97	3333	22.33	4255	28.51
8	S11	Free State vervet virus	NC_029992.1	15247	3450	22.63	3929	25.77	3457	22.67	4411	28.93
9	S12	Olivier's shrew virus 1	NC_035127.1	13766	2948	21.42	3675	26.70	3438	24.97	3705	26.91
10	S13	Porcine reproductive and respiratory syndrome virus 2	NC_038291.1	15411	3345	21.71	3923	25.46	4036	26.19	4107	26.65
11	S14	Simian hemorrhagic encephalitis virus	NC_038293.1	15370	3406	22.16	3979	25.89	3502	22.78	4481	29.15
12	S15	Lelystad virus	NC_043487.1	15111	3247	21.49	3912	25.89	3815	25.25	4137	27.38
13	S16	Zambian malbrouck virus	NC_048209.1	15307	3454	22.56	4008	26.18	3431	22.41	4414	28.84
14	S19	Coniothyrium minitans RNA virus	NC_007523.1	4975	1008	20.26	1024	20.58	1416	28.46	1527	30.69
15	S20	Botryotinia fuckeliana totivirus 1	NC_009224.1	5261	1232	23.42	1151	21.88	1392	26.46	1486	28.25
16	S23	Beauveria bassiana victorivirus	NC_024151.1	5327	961	18.04	1251	23.48	1375	25.81	1740	32.66
17	S24	Botryosphaeria dothidea victorivirus 1	NC_025214.1	5322	1145	21.51	1111	20.88	1519	28.54	1547	29.07
18	S27	Fusarium poae victorivirus 1	NC_030867.1	5124	1022	19.95	1058	20.65	1419	27.69	1625	31.71

19	S29	Aspergillus foetidus slow virus I	NC_038928.1	5194	1016	19.56	1172	22.56	1441	27.74	1563	30.09
20	S30	Beauveria bassiana victorivirus I	NC_038929.1	5228	1065	20.37	1271	24.31	1418	27.12	1474	28.19
21	S33	Fusarium asiaticum victorivirus I	NC_040653.1	5281	929	17.59	959	18.16	1560	29.54	1833	34.71
22	S37	Alternaria arborescens victorivirus	NC_040793.1	5206	1154	22.17	1029	19.77	1486	28.54	1537	29.52
23	S42	Ononis yellow mosaic virus	NC_001513.1	6211	1330	21.41	1748	28.14	973	15.67	2160	34.78
24	S47	Botrytis virus F	NC_002604.1	6827	1689	24.74	1494	21.88	1405	20.58	2239	32.80
25	S53	Physalis mottle virus	NC_003634.1	6673	1503	22.52	1588	23.80	874	13.10	2708	40.58
26	S59	Botrytis virus X	NC_005132.1	6966	1813	26.03	1348	19.35	1288	18.49	2517	36.13
27	S65	Nemesia ring necrosis virus	NC_011538.1	6285	1223	19.46	1467	23.34	1210	19.25	2385	37.95
28	S67	Anagryis vein yellowing virus	NC_011559.1	6151	1437	23.36	1585	25.77	1154	18.76	1975	32.11
29	S78	Andean potato latent virus	NC_020470.1	6337	1425	22.49	1742	27.49	892	14.08	2278	35.95
30	S79	Andean potato mild mosaic virus	NC_020471.1	6226	1344	21.59	1756	28.20	970	15.58	2154	34.60
31	S82	Pitaya virus X	NC_024458.1	6677	1800	26.96	1465	21.94	1518	22.73	1894	28.37
32	S86	Grapevine Red Globe virus	NC_030693.1	6863	1277	18.61	1476	21.51	1202	17.51	2908	42.37
33	S88	Potexvirus	NC_040842.1	5839	1554	26.61	1260	21.58	1257	21.53	1768	30.28
34	S106	Grapevine rupestris vein feathering virus	NC_034205.1	6730	1205	17.90	1598	23.74	1424	21.16	2498	37.12
35	S107	Peach virus	NC_033828.1	6612	1287	19.46	1277	19.31	1398	21.14	2650	40.08

Fig. 31 shows graph of Percentage Concentrations in virus sequences of dominant cytosines and other nucleotides

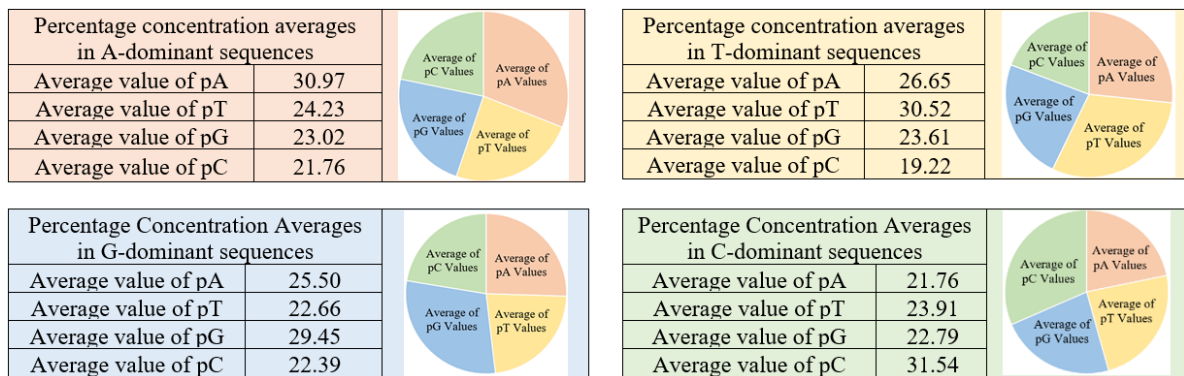
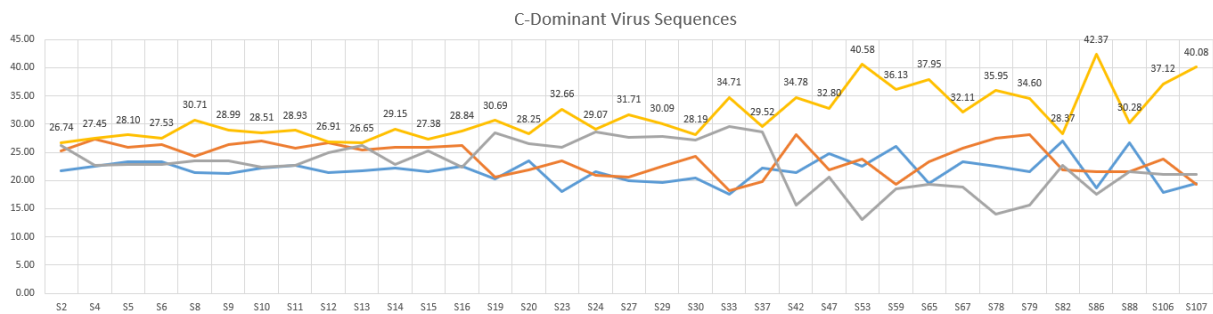


Fig. 32: Percentage concentration averages of all dominant sequences

Thus, classification of all 130 virus genomes have been carried out based on correlation coefficients and differential errors.

The next quantificational measure used to classify 130 genome sequences is based on the fundamental notion of 'Golden Ratio' defined for certain geometric figures and numerical sequences.

#### IV. CLASSIFICATION OF 130 VIRUS GENOMES BASED ON JCP GOLDEN RATIO VALUES

The term 'Golden Ratio (GR)' refers to a number mostly observed while taking ratios of distances in simple geometric figures such as pentagon, pentagram, decagon and dodecahedron. It is usually denoted by the symbol  $\phi$ .

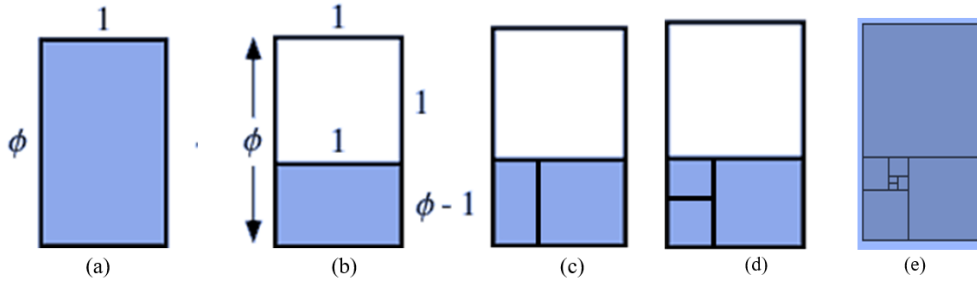


Fig. 33: Rectangle that exhibits Golden Ratio Property (GRP)

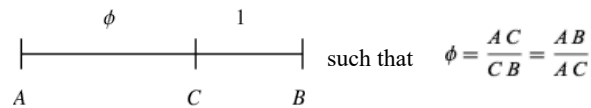
Fig. 33(a) shows a rectangle having sides in the ratio  $1: x$ . Now, for a unique value of  $x$ , which is denoted as  $\phi$ , partitioning the given rectangle as a square and a small rectangle as shown in Fig. 33(b), the smaller rectangle will have its sides in the same ratio  $1: x$ . One can further partition the small rectangle into a square and a smaller rectangle. This kind of partitioning could be carried out indefinitely. One can observe smaller rectangles have their sides in the ratio  $1: x$  in every partitioning. Now the rectangle shown in Fig. 33(a) is called a 'Golden Rectangle'. Such a rectangle and successive points dividing a golden rectangle into squares lie on a logarithmic spiral, giving a figure known as a whirling square. This property of rectangles having sides in the ratio  $1: x$  is called Golden Ratio Property (GRP). The unique number is  $x = \phi = 1.618$ .

Based on this definition one would obtain the equation:

$$\frac{\phi}{1} = \frac{1}{\phi - 1}, \quad \phi^2 - \phi - 1 = 0.$$

#### Euclid's Definition

Consider a line segment AB divided as AC and CB in the ratio  $\phi:1$ .



$$\frac{\phi + 1}{\phi} = \phi, \text{ and now one obtains } \phi^2 - \phi - 1 = 0,$$

Solving this quadratic equation, one obtains

$$\phi = \frac{1}{2}(1 + \sqrt{5})$$

1.618033988749894848204586834365638117720 ...

#### Fibonacci Series

Another fascinating connection with the Fibonacci numbers is given by the series

$$\phi = 1 + \sum_{n=1}^{\infty} \frac{(-1)^{n+1}}{F_n F_{n+1}}.$$

One can represent the series as a nested radical such as

$$\phi = \sqrt{1 + \sqrt{1 + \sqrt{1 + \sqrt{1 + \dots}}}}$$

This is equivalent to the recurrence equation  $a_n^2 = a_{n-1} + 1$ , with  $a_1 = 1$ , giving  $\lim_{n \rightarrow \infty} a_n = \phi$ .  $\phi$  is the "worst" real number for rational approximation because its continued fraction representation  $\phi = [1, 1, 1, 1, \dots]$

$$1 + \frac{1}{1 + \frac{1}{1 + \dots}}$$



Let  $x_n = p_n/q_n$  converge according to the recurrence relation  $x_n = 1 + \frac{1}{x_{n-1}}$  with  $x_1 = 1$

Now, this has the solution  $x_n = \frac{F_{n+1}}{F_n}$ , where  $F_n$  is the  $n^{\text{th}}$  Fibonacci number

Let  $x_n = p_n/q_n$  converge according to the recurrence relation with  $x_1 = 1$

As a result, one obtains the equation:

$$\phi = \lim_{n \rightarrow \infty} x_n = \lim_{n \rightarrow \infty} \frac{F_n}{F_{n-1}}$$

Golden Ratio is also obtained using the recurrence relation  $\phi^n = \phi^{n-1} + \phi^{n-2}$ .

The question that arises here is whether it is possible to attribute or extend the notion of ‘Golden Ratio’ to arbitrary geometrical figures and arbitrary sequences and arrays. Mainly, the objective of this paper is to classify virus genome sequences based on a quantificational measure ‘Golden Ratio’.

### Golden Ratios of Virus Genome Sequences due to Jean Claude Perez

Jean Claude Perez proposed a method of attributing a quantificational measure on the lines of ‘Golden Ratio’. Golden Ratio (GR) of a viral sequence may be treated as the solution of rational polynomial  $(x1A + x2T) / (x3G + x4C)$ , where  $x1$ ,  $x2$ ,  $x3$  and  $x4$  denote certain coefficients; A denotes the number of Adenines in the sequence; T denotes the number of Thymines in the sequence; G denotes the number of Guanines in the sequence; C denotes the number of Cytosines in the sequence. In order to honor Jean Claude Perez, we denote this Golden Ratio as ‘JCP Golden Ratio’.

#### 4.1 JCP Golden Ratio (GR) Calculations

Since life began on earth, four types of bases A, G, C, and T/U form two sets of natural base pairs  $A \leftrightarrow T$  and  $G \leftrightarrow C$  that have remained unchanged as the components of nucleic acids that replicate and transfer genetic information. Throughout evolution, except for the U to T modification, the four base structures have not changed. Recently, researchers have developed new artificial pairs of nucleobases (unnatural base pairs) that function alongside the natural base pairs. Some unnatural base pairs in duplex DNA can be efficiently and faithfully amplified in a polymerase chain reaction (PCR) using thermostable DNA polymerases. The addition of unnatural base pair systems could expand the genetic alphabet of DNA, thus providing a new mechanism for the generation novel biopolymers by the site-specific incorporation of functional components into nucleic acids and proteins. Moreover, the process of unnatural base pair development might provide clues to the origin of the natural base pairs in a primordial soup on the early Earth. In this Account, we describe the development of four representative types of unnatural base pairs that function as pairs of nucleobases in PCR and reconsider the origin of the natural nucleic acids. They are  $A \leftrightarrow C$ ,  $T \leftrightarrow G$ ,  $A \leftrightarrow G$  and  $T \leftrightarrow C$ . This section of the paper proposes classification of a set of 130 virus genomes based on the extended notion of ‘Goldent Ratios’. Two types of pairing are considered here: (i) natural pairing  $A \leftrightarrow T$  and  $G \leftrightarrow C$  and unnatural pairing  $A \leftrightarrow C$ ,  $T \leftrightarrow G$ . The rational polynomial used for calculating Golden Ratio of sequences obeying natural pairing is  $(x1A + x2T) / (x3G + x4C)$  and (ii) the rational polynomial used for calculating Golden Ratio of sequences obeying natural pairing is  $(x1A + x2C) / (x3T + x4G)$ . Now, Golden Ratios (GRs) of all 130 virus genome sequences are calculated for all eight assignments A1 to A8 in the context of ‘Natural Pairing’. Eight assignments of values, for instance, 1, 2, 3 and 4 to coefficients are considered here such that A1:  $x1=1$ ,  $x2=2$ ,  $x3=3$  and  $x4=4$ . One can cyclically permute the sequence of assigned values 1,2,3,4 as 4,1,2,3 and further permute as 3,4,1,2, and 2,3,4,1. One may have the graphical inverse of A1=1,2,3,4 as A5=4,3,2,1 and permute it as A6=1,4,3,2, A7=2,1,4,3 and A8=3,2,1,4. Golden Ratios are obtained for all the eight assignments and results studied. One can repeat this for sequences obeying unnatural pairing also.

<p><b>Golden Ratio (GR)</b> of Viral Sequence obeying <b>Natural Pairing</b> may be treated as the solution of rational polynomial <math>(x1A + x2T) / (x3G + x4C)</math>, where <math>x1</math>, <math>x2</math>, <math>x3</math> and <math>x4</math> denote the coefficients; A denotes the number of Adenines in the sequence; T denotes the number of Thymines in the sequence; G denotes the number of Guanines in the sequence; C denotes the number of Cytosines in the sequence. The term ‘<b>Natural Pairing</b>’ refers to pairing of (i) Adenine and Thymine and (ii) Guanine and Cytosine. The first assignment A1 refers to the numerical values of the coefficients in the rational polynomial <math>x1=1</math>; <math>x2=2</math>; <math>x3=3</math> and <math>x4=4</math>. Assignments A2, A3 and A4 refer to the cyclically permuted values. Assignments A5, A6, A7 and A8 refer to the graphical inverse and their cyclic permutations.</p>		x	x	x	x
		1	2	3	4
	A1	1	2	3	4
	A2	4	1	2	3
	A3	3	4	1	2
	A4	2	3	4	1
	A5	4	3	2	1
	A6	1	4	3	2
	A7	2	1	4	3
A8	3	2	1	4	

The results are given below in tables 16 to 28 along with bar graphs.

Table 16: Golden Ra of Virus Genomes S1 to S10 (Natural pairing)

Seq. No.	Accession ID	Total length	A	T	G	C	Golden Ratios for Natural Pairing							
							A1	A2	A3	A4	A5	A6	A7	A8
S1	NC_001639.1	14104	3244	3888	3646	3326	0.454	0.976	2.455	1.013	2.32	1.068	0.422	1.032
S2	NC_001961.1	15428	3353	3903	4047	4125	0.389	0.845	2.087	0.906	2.055	0.93	0.371	0.869
S3	NC_002532.2	12704	2692	3449	3305	3258	0.417	0.867	2.227	0.954	2.139	1.003	0.384	0.916
S4	NC_003092.2	15717	3534	4307	3556	4314	0.435	0.919	2.284	1.078	2.368	1.075	0.418	0.923
S5	NC_025112.1	14927	3476	3853	3404	4194	0.414	0.915	2.191	1.039	2.314	1.015	0.412	0.898
S6	NC_025113.1	14851	3456	3909	3398	4088	0.424	0.93	2.246	1.054	2.347	1.039	0.418	0.92
S7	NC_026439.1	14953	3238	3920	3944	3851	0.406	0.867	2.18	0.929	2.105	0.968	0.38	0.907
S8	NC_026509.1	15684	3364	3816	3688	4816	0.362	0.791	1.903	0.928	2.042	0.9	0.361	0.772
S9	NC_027124.1	15478	3291	4077	3623	4487	0.397	0.832	2.078	0.991	2.164	0.987	0.381	0.835
S10	NC_029053.1	14924	3311	4025	3333	4255	0.42	0.888	2.198	1.063	2.318	1.048	0.407	0.883

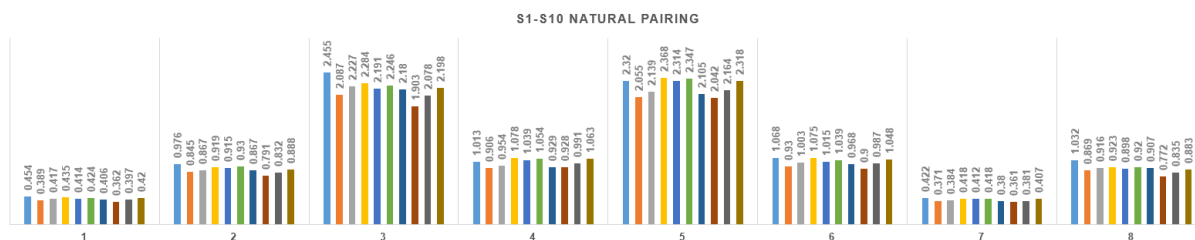


Table 17: Golden Ratios of Virus Genomes S11 to S20 (Natural pairing)

Seq. No.	Accession ID	Total length	A	T	G	C	Golden Ratios for Natural Pairing							
							A1	A2	A3	A4	A5	A6	A7	A8
S11	NC_029992.1	15247	3450	3929	3457	4411	0.403	0.879	2.122	1.024	2.259	0.998	0.4	0.862
S12	NC_035127.1	13766	2948	3675	3438	3705	0.409	0.859	2.17	0.969	2.156	0.995	0.384	0.886
S13	NC_038291.1	15411	3345	3923	4036	4107	0.392	0.848	2.1	0.911	2.064	0.936	0.372	0.873
S14	NC_038293.1	15370	3406	3979	3502	4481	0.399	0.86	2.096	1.014	2.225	0.992	0.393	0.848
S15	NC_043487.1	15111	3247	3912	3815	4137	0.395	0.843	2.1	0.939	2.101	0.958	0.376	0.862
S16	NC_048209.1	15307	3454	4008	3431	4414	0.41	0.886	2.153	1.043	2.291	1.019	0.404	0.871
S17	NC_003555.1	6277	1606	1530	1565	1576	0.424	1.012	2.318	0.995	2.34	0.984	0.431	1.001
S18	NC_005883.1	5310	1076	1441	1465	1328	0.407	0.83	2.181	0.9	2.026	0.97	0.364	0.901
S19	NC_007523.1	4975	1008	1024	1416	1527	0.295	0.682	1.592	0.707	1.629	0.698	0.296	0.674
S20	NC_009224.1	5261	1232	1151	1392	1486	0.349	0.839	1.901	0.838	1.962	0.816	0.36	0.817

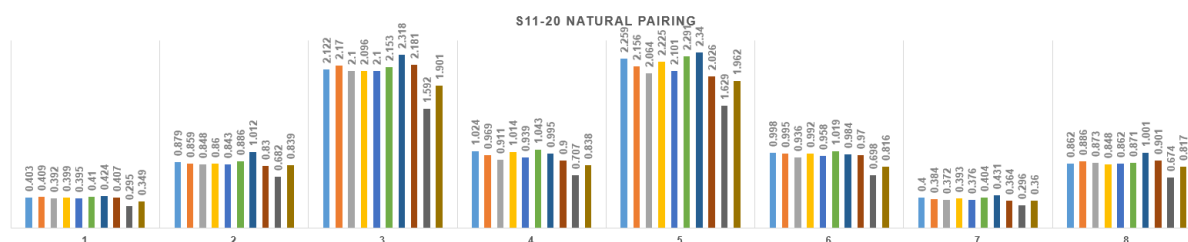
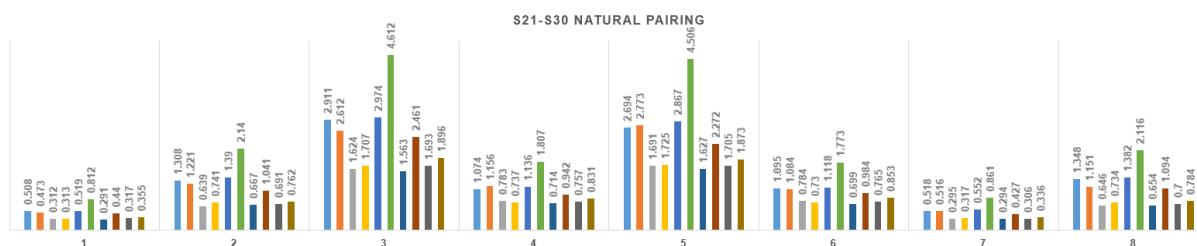


Table 18: Golden Ratios of Virus Genomes S21 to S30 (Natural pairing)

Seq. No.	Accession ID	Total length	A	T	G	C	Golden Ratios for Natural Pairing							
							A1	A2	A3	A4	A5	A6	A7	A8
S21	NC_009890.1	5077	1516	1252	1336	973	0.508	1.308	2.911	1.074	2.694	1.095	0.518	1.348
S22	NC_014609.1	7510	2239	1784	1672	1815	0.473	1.221	2.612	1.156	2.773	1.084	0.516	1.151
S23	NC_024151.1	5327	961	1251	1375	1740	0.312	0.639	1.624	0.783	1.691	0.784	0.295	0.646
S24	NC_025214.1	5322	1145	1111	1519	1547	0.313	0.741	1.707	0.737	1.725	0.73	0.317	0.734
S25	NC_027212.1	5704	1811	1359	1414	1120	0.519	1.39	2.974	1.136	2.867	1.118	0.552	1.382
S26	NC_030295.1	7788	2902	2249	1436	1201	0.812	2.14	4.612	1.807	4.506	1.773	0.861	2.116
S27	NC_030867.1	5124	1022	1058	1419	1625	0.291	0.667	1.563	0.714	1.627	0.699	0.294	0.654
S28	NC_035674.1	6203	1570	1551	1730	1352	0.44	1.041	2.461	0.942	2.272	0.984	0.427	1.094
S29	NC_038928.1	5194	1016	1172	1441	1563	0.317	0.691	1.693	0.757	1.705	0.765	0.306	0.7
S30	NC_038929.1	5228	1065	1271	1418	1474	0.355	0.762	1.896	0.831	1.873	0.853	0.336	0.784





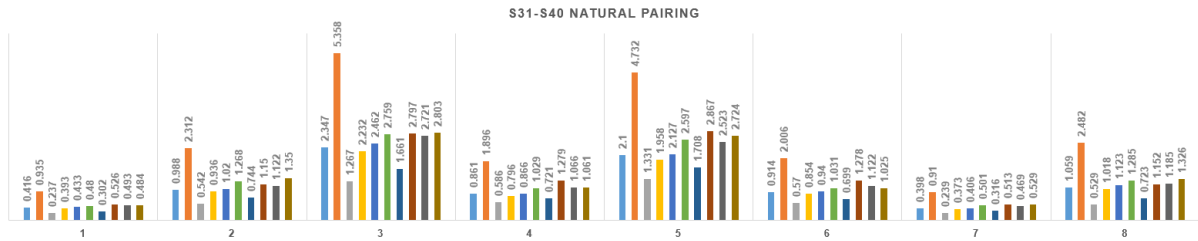


Table 20: Golden Ratios of Virus Genomes S41 to S50 (Natural pairing)

Seq. No.	Accession ID	Total length	A	T	G	C	Golden Ratios for Natural Pairing							
							A1	A2	A3	A4	A5	A6	A7	A8
S41	NC_001512.1	11835	3676	2440	2859	2860	0.427	1.199	2.423	1.026	2.567	0.939	0.489	1.112
S42	NC_001513.1	6211	1330	1748	973	2160	0.417	0.838	2.074	1.306	2.572	1.149	0.424	0.778
S43	NC_001564.2	10682	2618	2614	2919	2531	0.415	0.974	2.294	0.92	2.188	0.946	0.407	1.002
S44	NC_001642.1	6366	1925	1218	1339	1884	0.377	1.07	2.084	1.036	2.488	0.873	0.46	0.925
S45	NC_001728.1	6618	1990	2013	1441	1174	0.667	1.557	3.7	1.444	3.451	1.505	0.645	1.628
S46	NC_001948.1	8744	2430	2560	2075	1678	0.583	1.337	3.227	1.256	2.985	1.322	0.556	1.412
S47	NC_002604.1	6827	1689	1494	1405	2239	0.355	0.865	1.877	1	2.225	0.881	0.394	0.777
S48	NC_002729.1	7352	2511	2096	1571	1174	0.712	1.821	4.061	1.516	3.784	1.542	0.725	1.87
S49	NC_002795.1	8657	2306	2278	2149	1924	0.485	1.142	2.673	1.088	2.58	1.109	0.479	1.165
S50	NC_003557.1	8363	2282	2413	1943	1725	0.558	1.273	3.059	1.242	2.916	1.286	0.538	1.319

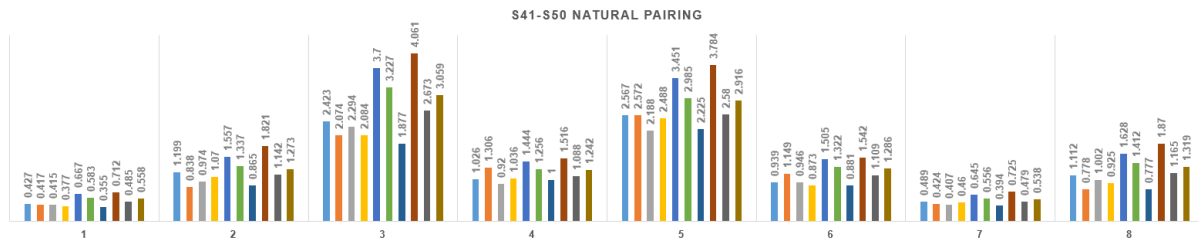


Table 21: Golden Ratios of Virus Genomes S51 to S60 (Natural pairing)

Seq. No.	Accession ID	Total length	A	T	G	C	Golden Ratios for Natural Pairing							
							A1	A2	A3	A4	A5	A6	A7	A8
S51	NC_003603.1	4019	970	812	1176	1061	0.333	0.847	1.867	0.759	1.85	0.746	0.348	0.836
S52	NC_003608.1	3911	975	1012	1007	917	0.448	1.03	2.454	1.008	2.366	1.034	0.436	1.058
S53	NC_003634.1	6673	1503	1588	874	2708	0.347	0.769	1.726	1.252	2.418	0.977	0.395	0.656
S54	NC_003679.1	12333	4007	2715	3203	2408	0.49	1.375	2.853	1.061	2.742	1.03	0.535	1.359
S55	NC_003852.1	6507	1949	1867	1520	1171	0.614	1.474	3.447	1.31	3.181	1.364	0.6	1.544
S56	NC_003900.1	11824	3462	2628	2828	2906	0.433	1.146	2.418	1.041	2.538	0.977	0.476	1.082
S57	NC_004724.1	16527	4250	4624	4224	3429	0.511	1.154	2.819	1.1	2.599	1.164	0.482	1.226
S58	NC_005062.1	10787	2772	2229	3361	2425	0.365	0.951	2.098	0.77	1.943	0.782	0.375	0.978
S59	NC_005132.1	6966	1813	1348	1288	2517	0.323	0.849	1.713	1	2.217	0.809	0.391	0.716
S60	NC_006939.1	3683	1041	868	900	874	0.448	1.137	2.49	1.047	2.531	1.014	0.474	1.105

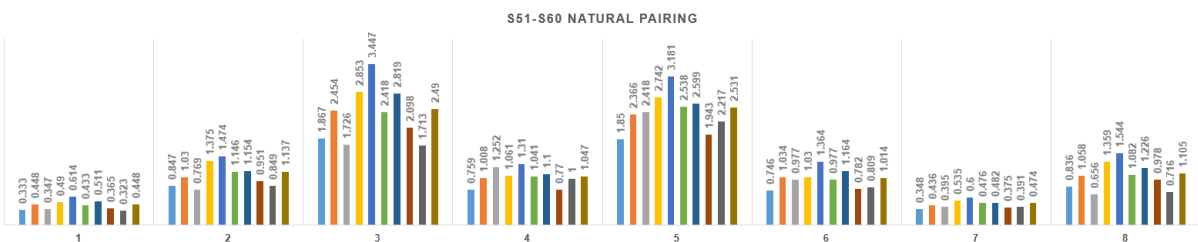


Table 22: Golden Ratios of Virus Genomes S61 to S70 (Natural pairing)

Seq. No.	Accession ID	Total length	A	T	G	C	Golden Ratios for Natural Pairing							
							A1	A2	A3	A4	A5	A6	A7	A8
S61	NC_007733.2	3962	1054	937	990	981	0.424	1.046	2.34	0.995	2.373	0.973	0.441	1.024
S62	NC_009028.2	10755	2903	2229	3004	2619	0.377	0.998	2.138	0.853	2.121	0.829	0.404	0.976
S63	NC_009892.1	9005	2392	2669	2042	1902	0.562	1.249	3.053	1.27	2.936	1.316	0.537	1.296
S64	NC_011535.1	4731	1243	1167	1319	1002	0.449	1.087	2.526	0.953	2.327	0.991	0.441	1.138
S65	NC_011538.1	6285	1223	1467	1210	2385	0.315	0.664	1.594	0.947	1.934	0.844	0.326	0.614
S66	NC_011552.1	7988	2439	2249	1908	1392	0.614	1.502	3.476	1.288	3.168	1.344	0.603	1.58
S67	NC_011559.1	6151	1437	1585	1154	1975	0.405	0.89	2.086	1.157	2.452	1.049	0.423	0.826
S68	NC_012533.1	10723	2922	2143	3219	2439	0.371	1.005	2.141	0.801	2.04	0.79	0.395	1.005
S69	NC_012534.1	10941	3190	2330	3088	2333	0.422	1.145	2.436	0.91	2.321	0.898	0.45	1.145
S70	NC_012812.1	12337	3945	2694	3266	2426	0.478	1.337	2.785	1.031	2.663	1	0.52	1.327

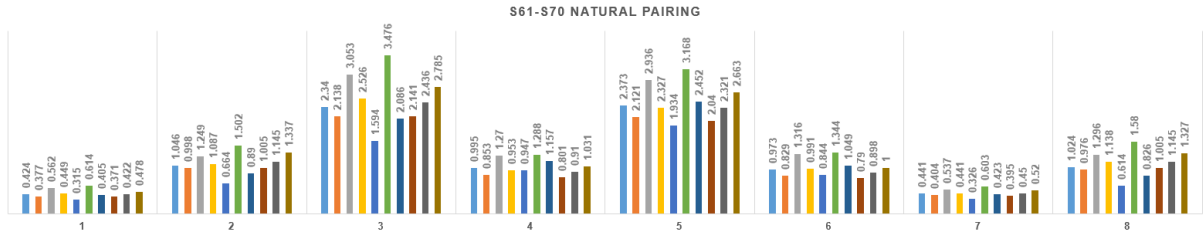


Table 23: Golden Ratios of Virus Genomes S71 to S80 (Natural pairing)

Seq. No.	Accession ID	Total length	A	T	G	C	Golden Ratios for Natural Pairing							
							A1	A2	A3	A4	A5	A6	A7	A8
S71	NC_013006.1	8517	2381	2215	2060	1857	0.5	1.211	2.771	1.129	2.705	1.136	0.505	1.219
S72	NC_015782.2	7259	2181	2230	1582	1266	0.676	1.573	3.758	1.455	3.479	1.525	0.65	1.655
S73	NC_016038.2	5666	1625	1300	1330	1411	0.438	1.131	2.426	1.062	2.554	1.001	0.476	1.071
S74	NC_016404.1	7488	2449	1558	1897	1584	0.462	1.328	2.68	1.043	2.69	0.979	0.523	1.27
S75	NC_016440.1	8638	2313	2473	2136	1716	0.546	1.244	3.022	1.173	2.784	1.24	0.518	1.32
S76	NC_016959.1	11724	3259	2588	3210	2632	0.418	1.091	2.375	0.923	2.297	0.913	0.439	1.088
S77	NC_018713.1	12292	3933	2728	3173	2458	0.485	1.345	2.807	1.059	2.716	1.028	0.527	1.326
S78	NC_020470.1	6337	1425	1742	892	2278	0.416	0.863	2.063	1.381	2.689	1.16	0.441	0.775
S79	NC_020471.1	6226	1344	1756	970	2154	0.421	0.848	2.094	1.318	2.599	1.159	0.429	0.786
S80	NC_023439.1	10688	2449	2280	3620	2339	0.346	0.847	1.984	0.697	1.736	0.744	0.333	0.917

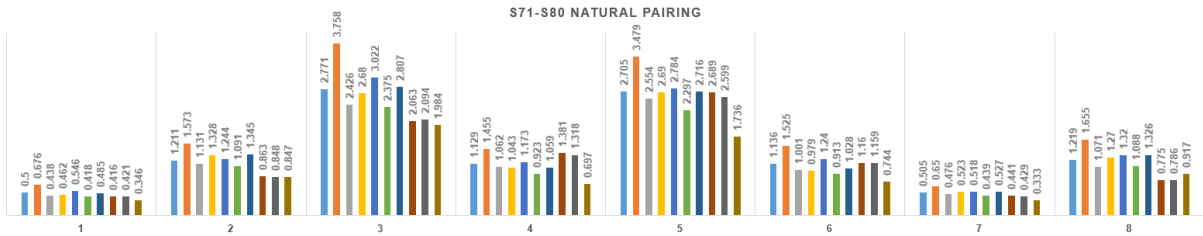


Table 24: Golden Ratios of Virus Genomes S81 to S90 (Natural pairing)

Seq. No.	Accession ID	Total length	A	T	G	C	Golden Ratios for Natural Pairing							
							A1	A2	A3	A4	A5	A6	A7	A8
S81	NC_023892.1	8659	2457	2086	2286	1829	0.467	1.184	2.643	1.018	2.513	1.027	0.478	1.202
S82	NC_024458.1	6677	1800	1465	1518	1894	0.389	0.993	2.122	1.003	2.351	0.918	0.43	0.915
S83	NC_024887.1	11550	3125	2313	3118	2994	0.363	0.973	2.045	0.852	2.106	0.806	0.399	0.927
S84	NC_026620.1	10125	2916	2599	2752	1858	0.517	1.287	2.959	1.059	2.643	1.111	0.508	1.369
S85	NC_028793.2	5851	1510	1427	1460	1413	0.435	1.043	2.388	1.006	2.381	1.001	0.441	1.038
S86	NC_030693.1	6863	1277	1476	1202	2908	0.277	0.591	1.387	0.904	1.795	0.762	0.297	0.528
S87	NC_031327.1	10588	2729	2629	2889	2341	0.442	1.058	2.47	0.96	2.315	0.992	0.435	1.097
S88	NC_040842.1	5839	1554	1260	1257	1768	0.375	0.956	2.024	1.013	2.334	0.902	0.422	0.862
S89	NC_040837.1	6060	1699	1942	1503	916	0.683	1.518	3.857	1.331	3.218	1.492	0.609	1.738
S90	NC_040800.1	8192	2847	2187	1884	1274	0.671	1.788	3.900	1.391	3.559	1.414	0.693	1.850

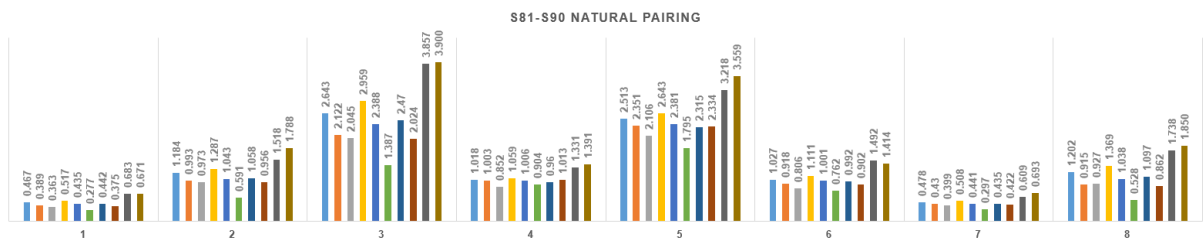


Table 25: Golden Ratios of Virus Genomes S91 to S100 (Natural pairing)

Seq. No.	Accession ID	Total length	A	T	G	C	Golden Ratios for Natural Pairing							
							A1	A2	A3	A4	A5	A6	A7	A8
S91	NC_040788.1	10311	2885	2271	3053	2102	0.422	1.112	2.444	0.879	2.235	0.895	0.434	1.151
S92	NC_040776.1	10794	2976	2169	3066	2583	0.374	1.013	2.138	0.839	2.112	0.811	0.405	0.990
S93	NC_039237.1	12513	4045	2783	3186	2499	0.491	1.367	2.842	1.078	2.765	1.042	0.537	1.342
S94	NC_039218.1	10376	2509	2139	3314	2414	0.346	0.877	1.975	0.729	1.819	0.749	0.349	0.910
S95	NC_039217.1	14072	4836	3986	2783	2467	0.703	1.799	3.946	1.590	3.896	1.564	0.736	1.776
S96	NC_038966.1	8881	2426	2429	2180	1846	0.523	1.225	2.894	1.148	2.737	1.186	0.510	1.268
S97	NC_036587.1	6692	2080	1479	1452	1681	0.454	1.233	2.525	1.147	2.782	1.036	0.519	1.125
S98	NC_035462.1	6930	2255	2046	1554	1075	0.708	1.747	4.035	1.460	3.623	1.532	0.694	1.854
S99	NC_035453.1	18848	5414	5495	4453	3486	0.600	1.402	3.345	1.282	3.077	1.347	0.577	1.480
S100	NC_035116.1	5877	1129	1730	1417	1601	0.430	0.817	2.231	1.024	2.188	1.079	0.380	0.875

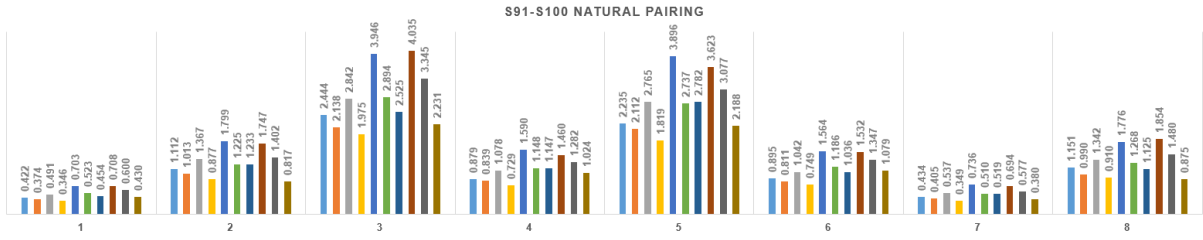


Table 26: Golden Ratios of Virus Genomes S101 to S110 (Natural pairing)

Seq. No.	Accession ID	Total length	A	T	G	C	Golden Ratios for Natural Pairing							
							A1	A2	A3	A4	A5	A6	A7	A8
S101	NC_035071.1	20414	6142	4537	4813	4922	0.445	1.193	2.495	1.071	2.624	1.000	0.494	1.122
S102	NC_034833.1	6958	2140	1572	1766	1480	0.471	1.270	2.688	1.052	2.648	1.020	0.508	1.244
S103	NC_034242.1	10370	2787	2704	2131	0.488	1.165	2.735	1.042	2.525	1.087	0.476	1.221	
S104	NC_034216.1	15098	5582	3901	3120	2495	0.692	1.911	3.988	1.527	3.895	1.476	0.754	1.873
S105	NC_034207.1	5953	1588	1380	1517	1468	0.417	1.039	2.309	0.970	2.330	0.949	0.435	1.018
S106	NC_034205.1	6730	1205	1598	1424	2498	0.308	0.620	1.558	0.879	1.798	0.819	0.303	0.596
S107	NC_033828.1	6612	1287	1277	1398	2650	0.259	0.597	1.339	0.777	1.648	0.673	0.284	0.534
S108	NC_033725.1	10203	2866	2441	2878	2018	0.463	1.177	2.655	0.964	2.416	0.996	0.465	1.231
S109	NC_033724.1	10215	2601	2229	3177	2208	0.384	0.973	2.201	0.797	1.996	0.825	0.384	1.020
S110	NC_033723.1	10251	2701	2209	3207	2134	0.392	1.015	2.266	0.803	2.039	0.830	0.395	1.066

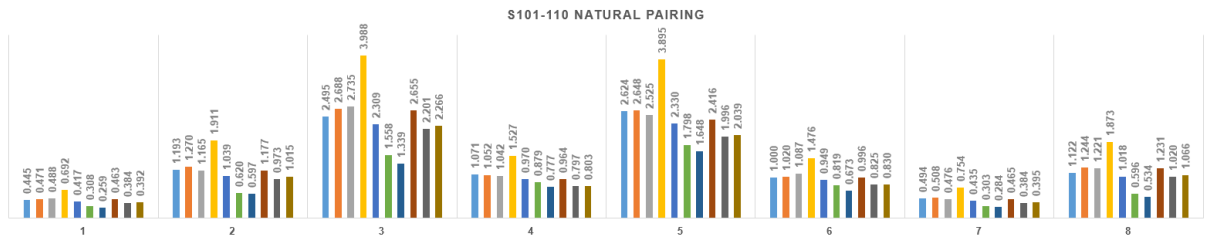


Table 27: Golden Ratios of Virus Genomes S111 to S120 (Natural pairing)

Seq. No.	Accession ID	Total length	A	T	G	C	Golden Ratios for Natural Pairing							
							A1	A2	A3	A4	A5	A6	A7	A8
S111	NC_033699.1	10173	2948	2319	2751	2155	0.449	1.179	2.566	0.976	2.448	0.973	0.470	1.185
S112	NC_033693.1	10173	2940	2338	2744	2151	0.452	1.180	2.579	0.982	2.457	0.980	0.471	1.189
S113	NC_032088.1	10864	2872	2395	2947	2650	0.394	1.002	2.206	0.895	2.185	0.880	0.412	0.989
S114	NC_031752.1	11557	4006	3151	2231	2169	0.670	1.748	3.748	1.574	3.842	1.505	0.723	1.679
S115	NC_031463.1	23635	9624	6181	4217	3613	0.811	2.318	4.683	1.845	4.734	1.728	0.917	2.208
S116	NC_031462.1	15207	4392	3640	3787	3388	0.468	1.195	2.625	1.063	2.598	1.044	0.490	1.179
S117	NC_043110.1	10182	2778	2274	2867	2263	0.415	1.068	2.357	0.901	2.242	0.904	0.428	1.080
S118	NC_008516.1	26660	8975	6143	3758	7784	0.501	1.362	2.664	1.594	3.55	1.249	0.627	1.123
S119	NC_026812.1	27004	8268	6892	3909	7929	0.507	1.264	2.649	1.579	3.413	1.299	0.594	1.083
S120	NC_038295.1	27318	9234	6954	4110	7020	0.572	1.498	3.058	1.676	3.792	1.405	0.677	1.292

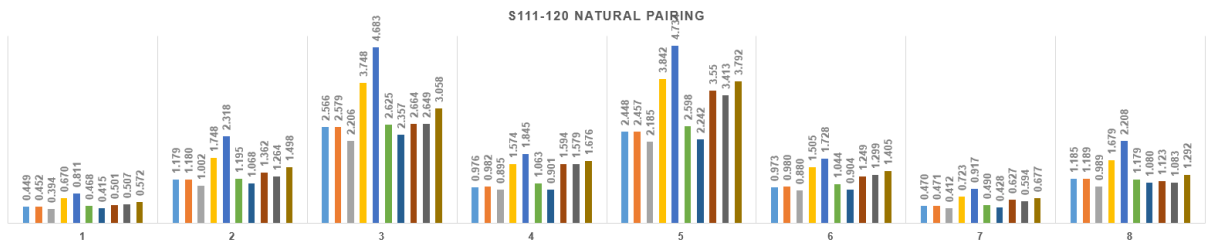
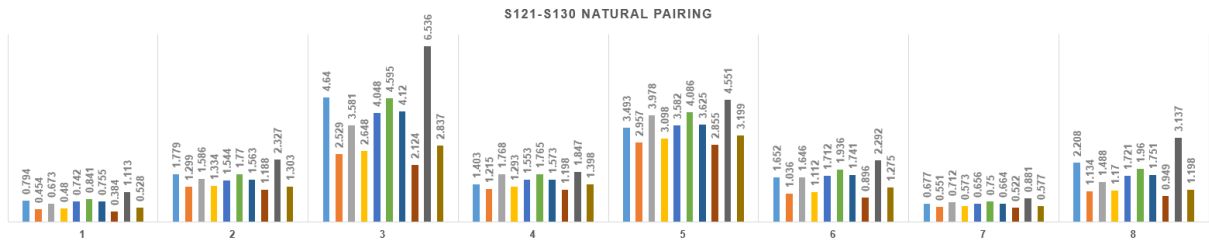


Table 28: Golden Ratios of Virus Genomes S121 to S130 (Natural pairing)

Seq. No.	Accession ID	Total length	A	T	G	C	Golden Ratios for Natural Pairing							
							A1	A2	A3	A4	A5	A6	A7	A8
S121	NC_027199.1	20261	5947	6839	5208	2266	0.794	1.779	4.64	1.403	3.493	1.652	0.677	2.208
S122	NC_024709.1	33452	11117	6932	6663	8740	0.454	1.299	2.529	1.215	2.957	1.036	0.551	1.134
S123	NC_033700.1	30353	9555	9194	4934	6670	0.673	1.586	3.581	1.768	3.978	1.646	0.712	1.488
S124	NC_035465.1	32399	10710	7139	6186	8364	0.48	1.334	2.648	1.293	3.098	1.112	0.573	1.17
S125	NC_007447.1	28475	7690	9959	6104	4718	0.742	1.544	4.048	1.553	3.582	1.712	0.656	1.721
S126	NC_022787.1	28301	8124	10267	5579	4331	0.841	1.77	4.595	1.765	4.086	1.936	0.75	1.96
S127	NC_034976.1	28487	7686	10072	6083	4646	0.755	1.563	4.12	1.573	3.625	1.741	0.664	1.751
S128	NC_046956.1	30742	10484	5273	5238	9747	0.384	1.188	2.124	1.198	2.855	0.896	0.522	0.949
S129	NC_046962.1	29409	8759	11760	6561	2328	1.113	2.327	6.536	1.847	4.551	2.292	0.881	3.137
S130	NC_046963.1	30859	9285	8097	5722	7755	0.528	1.303	2.837	1.398	3.199	1.275	0.577	1.198



Now, the GR values of all 130 virus genomes are analyzed based on ‘Assignments’ of values to the coefficients in the rational polynomial  $(x1A + x2T) / (x3G + x4C)$ . It has been observed (i) GR values of all 130 virus genomes remain almost the same for the assignments of A1 and A7 [Ref. Fig. 34], (ii) GR values of all 130 virus genomes remain almost the same but different from previous values for the assignments of A2 and A8 [Ref. Fig. 35], (iii) GR values of all 130 virus genomes remain almost the same but different from previous values for the assignments of A3 and A5 [Ref. Fig. 36] and (iv) GR values of all 130 virus genomes remain almost the same but different from previous values for the assignments of A4 and A6 [Ref. Fig. 37].

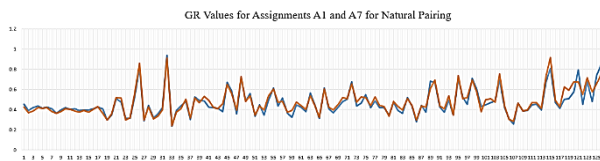


Fig. 34: GR values for assignments A1 and A7

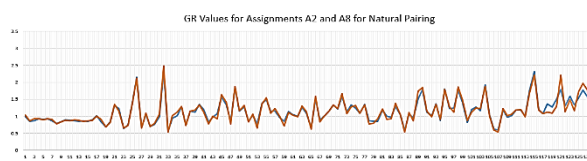


Fig. 35: GR values for assignments A2 and A8

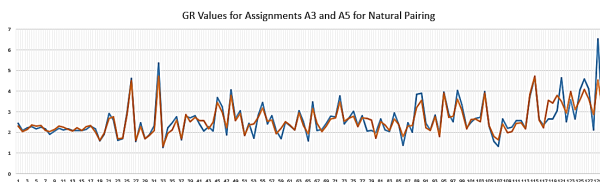


Fig. 36: GR values for assignments A3 and A5

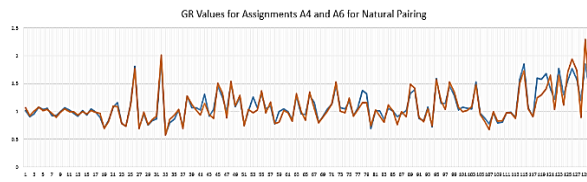


Fig. 37: GR values for assignments A4 and A6

Now, Golden Ratios of all 130 virus genome sequences are calculated for all eight assignments A1 to A8 in the context of ‘Unnatural Pairing’.

<b>Golden Ratio (GR)</b> of Viral Sequence obeying <b>Unnatural Pairing</b> may be treated as the solution of rational polynomial $(x1A + x4C) / (x2T + x3G)$ , where $x1, x2, x3$ and $x4$ denote the coefficients; A denotes the number of Adenines in the sequence; T denotes the number of Thymines in the sequence; G denotes the number of Guanines in the sequence; C denotes the number of Cytosines in the sequence. The term ‘ <b>Unnatural Pairing</b> ’ refers to pairing of (i) Adenine and Cytosine and (ii) Thymine and Guanine. The first assignment A1 refers to the numerical values of the coefficients in the rational polynomial $x1=1; x2=2; x3=3$ and $x4=4$ . Assignments A2, A3 and A4 refer to the cyclically permuted values. Assignments A5, A6, A7 and A8 refer to the graphical inverse and their cyclic permutations.	$x1$	$x2$	$x3$	$x4$	
	A1	1	2	3	4
	A2	4	1	2	3
	A3	3	4	1	2
	A4	2	3	4	1
	A5	4	3	2	1
	A6	1	4	3	2
	A7	2	1	4	3
	A8	3	2	1	4

Eight assignments of values, for instance, 1, 2, 3 and 4 to coefficients are considered here such that A1:  $x1=1, x2=2, x3=3$  and  $x4=4$ . One can cyclically permute the sequence of assigned values 1,2,3,4 as 4,1,2,3 and further permute as 3,4,1,2, and 2,3,4,1. One may have the graphical inverse of  $A1=1,2,3,4$  as  $A5=4,3,2,1$  and permute it as  $A6=1,4,3,2, A7=2,1,4,3$  and  $A8=3,2,1,4$ . Golden Ratios are obtained for all the eight assignments and results studied. The results are given below in tables 29 to 41 along with bar graphs.

Table 29: Golden Ratios of Virus Genomes S1 to S10 (Unnatural pairing)

Seria 1 No.	Accession ID	Total length	A	T	G	C	Golden Ratios for Unnatural Pairing							
							A1	A2	A3	A4	A5	A6	A7	A8
S1	NC_001639.1	14104	3244	3888	3646	3326	0.884	2.053	0.853	0.373	0.859	0.373	0.891	2.016
S2	NC_001961.1	15428	3353	3903	4047	4125	0.995	2.149	0.931	0.388	0.885	0.418	0.949	2.24
S3	NC_002532.2	12704	2692	3449	3305	3258	0.935	2.042	0.853	0.366	0.827	0.388	0.909	2.068
S4	NC_003092.2	15717	3534	4307	3556	4314	1.078	2.371	0.925	0.419	0.92	0.435	1.079	2.289
S5	NC_025112.1	14927	3476	3853	3404	4194	1.13	2.484	1	0.442	0.985	0.463	1.118	2.448
S6	NC_025113.1	14851	3456	3909	3398	4088	1.099	2.436	0.974	0.434	0.967	0.45	1.095	2.382
S7	NC_026439.1	14953	3238	3920	3944	3851	0.947	2.075	0.887	0.375	0.855	0.397	0.915	2.131
S8	NC_026509.1	15684	3364	3816	3688	4816	1.21	2.493	1.04	0.44	0.97	0.493	1.14	2.593
S9	NC_027124.1	15478	3291	4077	3623	4487	1.116	2.351	0.945	0.414	0.906	0.451	1.079	2.362
S10	NC_029053.1	14924	3311	4025	3333	4255	1.126	2.432	0.949	0.428	0.933	0.452	1.116	2.367

<b>Golden Ratio (GR)</b> of Viral Sequence obeying <b>Unnatural Pairing</b> may be treated as the solution of rational polynomial $(x1A + x4C) / (x2T + x3G)$ , where $x1, x2, x3$ and $x4$ denote the coefficients; A denotes the number of Adenines in the sequence; T denotes the number of Thymines in the sequence; G denotes the number of Guanines in the sequence; C denotes the number of Cytosines in the sequence. The term ' <b>Unnatural Pairing</b> ' refers to pairing of (i) Adenine and Cytosine and (ii) Thymine and Guanine. The first assignment A1 refers to the numerical values of the coefficients in the rational polynomial $x1=1; x2=2; x3=3$ and $x4=4$ . Assignments A2, A3 and A4 refer to the cyclically permuted values. Assignments A5, A6, A7 and A8 refer to the graphical inverse and their cyclic permutations.		$x1$	$x2$	$x3$	$x4$
	A1	1	2	3	4
	A2	4	1	2	3
	A3	3	4	1	2
	A4	2	3	4	1
	A5	4	3	2	1
	A6	1	4	3	2
	A7	2	1	4	3
	A8	3	2	1	4

Eight assignments of values, for instance, 1, 2, 3 and 4 to coefficients are considered here such that A1:  $x1=1, x2=2, x3=3$  and  $x4=4$ . One can cyclically permute the sequence of assigned values 1,2,3,4 as 4,1,2,3 and further permute as 3,4,1,2, and 2,3,4,1. One may have the graphical inverse of A1=1,2,3,4 as A5=4,3,2,1 and permute it as A6=1,4,3,2, A7=2,1,4,3 and A8=3,2,1,4. Golden Ratios are obtained for all the eight assignments and results studied. The results are given below in tables 29 to 41 along with bar graphs.

Table 29: Golden Ratios of Virus Genomes S1 to S10 (Unnatural pairing)

Serial No.	Accession ID	Total length	A	T	G	C	Golden Ratios for Unnatural Pairing							
							A1	A2	A3	A4	A5	A6	A7	A8
S1	NC_001639.1	14104	3244	3888	3646	3326	0.884	2.053	0.853	0.373	0.859	0.373	0.891	2.016
S2	NC_001961.1	15428	3353	3903	4047	4125	0.995	2.149	0.931	0.388	0.885	0.418	0.949	2.24
S3	NC_002532.2	12704	2692	3449	3305	3258	0.935	2.042	0.853	0.366	0.827	0.388	0.909	2.068
S4	NC_003092.2	15717	3534	4307	3556	4314	1.078	2.371	0.925	0.419	0.92	0.435	1.079	2.289
S5	NC_025112.1	14927	3476	3853	3404	4194	1.13	2.484	1	0.442	0.985	0.463	1.118	2.448
S6	NC_025113.1	14851	3456	3909	3398	4088	1.099	2.436	0.974	0.434	0.967	0.45	1.095	2.382
S7	NC_026439.1	14953	3238	3920	3944	3851	0.947	2.075	0.887	0.375	0.855	0.397	0.915	2.131
S8	NC_026509.1	15684	3364	3816	3688	4816	1.21	2.493	1.04	0.44	0.97	0.493	1.14	2.593
S9	NC_027124.1	15478	3291	4077	3623	4487	1.116	2.351	0.945	0.414	0.906	0.451	1.079	2.362
S10	NC_029053.1	14924	3311	4025	3333	4255	1.126	2.432	0.949	0.428	0.933	0.452	1.116	2.367

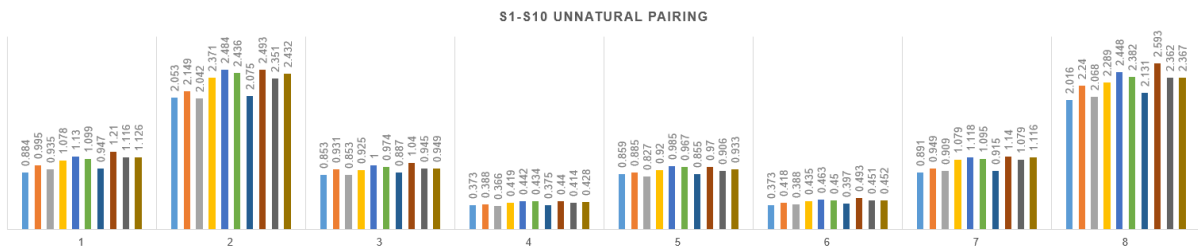


Table 30: Golden Ratios of Virus Genomes S11 to S20 (Unnatural pairing)

Serial No.	Accession ID	Total length	A	T	G	C	Golden Ratios for Unnatural Pairing							
							A1	A2	A3	A4	A5	A6	A7	A8
S11	NC_029992.1	15247	3450	3929	3457	4411	1.157	2.493	0.999	0.441	0.973	0.47	1.133	2.474
S12	NC_035127.1	13766	2948	3675	3438	3705	1.005	2.171	0.896	0.387	0.865	0.414	0.976	2.193
S13	NC_038291.1	15411	3345	3923	4036	4107	0.99	2.142	0.925	0.386	0.881	0.415	0.947	2.227
S14	NC_038293.1	15370	3406	3979	3502	4481	1.155	2.464	0.987	0.435	0.955	0.468	1.126	2.455
S15	NC_043487.1	15111	3247	3912	3815	4137	1.027	2.2	0.925	0.393	0.884	0.425	0.986	2.258
S16	NC_048209.1	15307	3454	4008	3431	4414	1.152	2.489	0.985	0.439	0.965	0.466	1.136	2.447
S17	NC_003555.1	6277	1606	1530	1565	1576	1.019	2.393	1.037	0.441	1.036	0.439	1.019	2.404
S18	NC_005883.1	5310	1076	1441	1465	1328	0.877	1.896	0.813	0.341	0.776	0.367	0.84	1.964
S19	NC_007523.1	4975	1008	1024	1416	1527	1.13	2.233	1.102	0.405	0.941	0.486	0.986	2.636
S20	NC_009224.1	5261	1232	1151	1392	1486	1.107	2.385	1.112	0.437	1.028	0.478	1.03	2.609

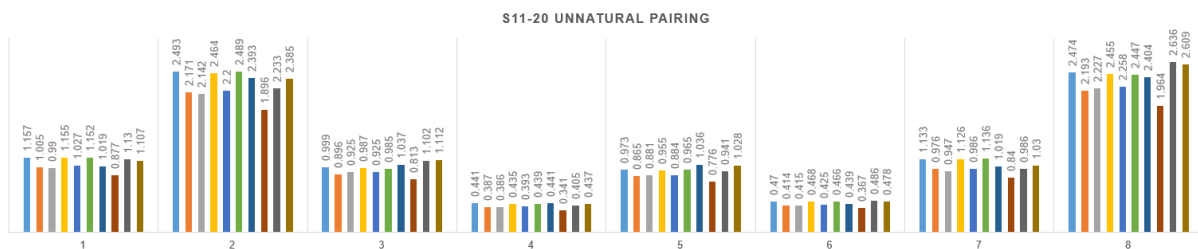




Table 31: Golden Ratios of Virus Genomes S21 to S30 (Unnatural pairing)

Serial No.	Accession ID	Total length	A	T	G	C	Golden Ratios for Unnatural Pairing							
							A1	A2	A3	A4	A5	A6	A7	A8
S21	NC_009890.1	5077	1516	1252	1336	973	0.83	2.289	1.023	0.44	1.094	0.383	0.902	2.197
S22	NC_014609.1	7510	2239	1784	1672	1815	1.106	2.808	1.174	0.522	1.238	0.482	1.171	2.667
S23	NC_024151.1	5327	961	1251	1375	1740	1.195	2.265	0.997	0.395	0.858	0.486	1.057	2.538
S24	NC_025214.1	5322	1145	1111	1519	1547	1.081	2.222	1.094	0.407	0.961	0.47	0.964	2.572
S25	NC_027212.1	5704	1811	1359	1414	1120	0.903	2.532	1.12	0.487	1.211	0.418	0.995	2.399
S26	NC_030295.1	7788	2902	2249	1436	1201	0.875	2.97	1.064	0.56	1.331	0.398	1.176	2.276
S27	NC_030867.1	5124	1022	1058	1419	1625	1.18	2.3	1.117	0.414	0.95	0.503	1.027	2.706
S28	NC_035674.1	6203	1570	1551	1730	1352	0.841	2.062	0.934	0.388	0.94	0.375	0.849	2.093
S29	NC_038928.1	5194	1016	1172	1441	1563	1.09	2.159	1.007	0.387	0.879	0.459	0.969	2.457
S30	NC_038929.1	5228	1065	1271	1418	1474	1.024	2.113	0.944	0.379	0.862	0.429	0.943	2.295

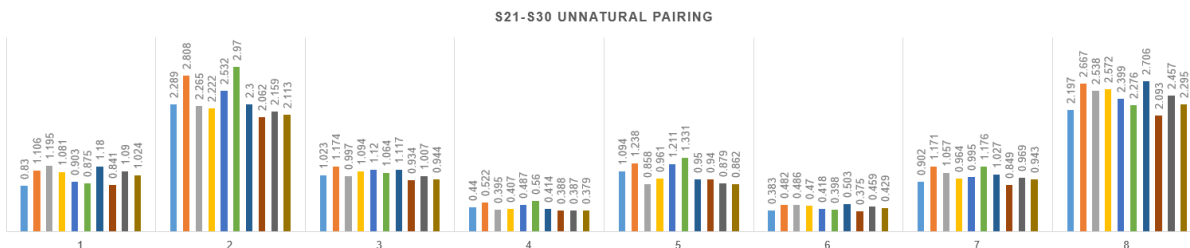


Table 32: Golden Ratios of Virus Genomes S31 to S40 (Unnatural pairing)

Serial No.	Accession ID	Total length	A	T	G	C	Golden Ratios for Unnatural Pairing							
							A1	A2	A3	A4	A5	A6	A7	A8
S31	NC_040431.1	4671	1147	1129	1401	994	0.792	1.925	0.917	0.365	0.901	0.359	0.783	2.027
S32	NC_040632.1	4947	1772	1606	947	622	0.703	2.558	0.889	0.484	1.148	0.325	1.002	1.876
S33	NC_040653.1	5281	929	959	1560	1833	1.252	2.259	1.195	0.404	0.925	0.539	1.021	2.909
S34	NC_040659.1	5082	1211	1188	1610	1073	0.763	1.829	0.908	0.349	0.872	0.35	0.739	1.988
S35	NC_040660.1	5160	1270	1282	1587	1021	0.73	1.827	0.871	0.349	0.869	0.334	0.734	1.901
S36	NC_040775.1	5941	1784	1389	1583	1185	0.866	2.347	1.081	0.452	1.134	0.403	0.922	2.314
S37	NC_040793.1	5206	1154	1029	1486	1537	1.12	2.306	1.166	0.425	1.015	0.493	0.992	2.711
S38	NC_046959.1	18410	4712	5381	3886	4431	1	2.443	0.905	0.437	0.973	0.409	1.085	2.175
S39	NC_000939.2	4415	1129	1206	1143	937	0.834	1.268	0.881	0.39	0.923	0.363	0.715	2
S40	NC_001461.1	12573	4049	2767	3233	2524	0.928	1.513	1.202	0.5	1.267	0.438	0.837	2.537

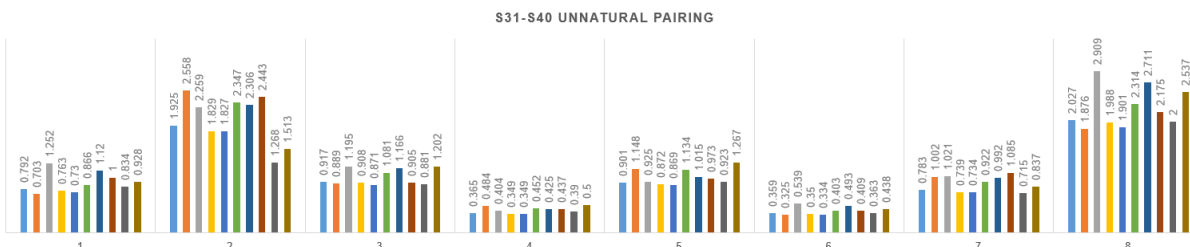
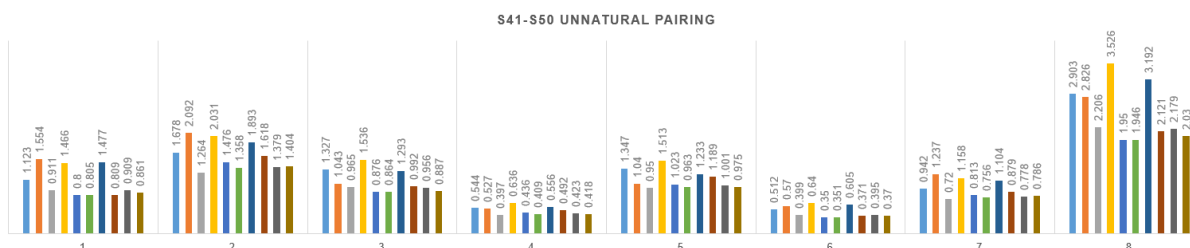


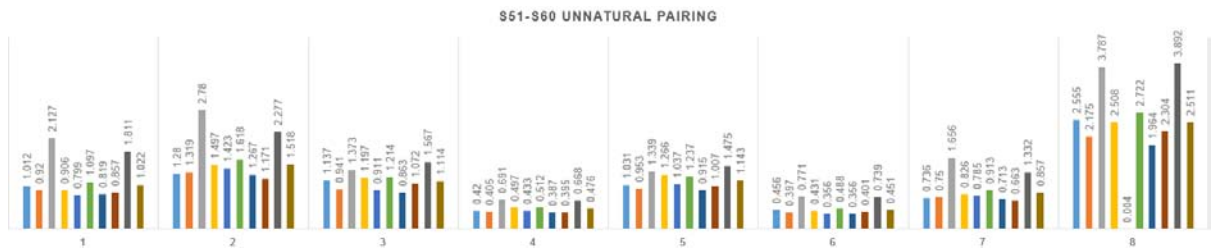
Table 33: Golden Ratios of Virus Genomes S31 to S50 (Unnatural pairing)

Serial No.	Accession ID	Total length	A	T	G	C	Golden Ratios for Unnatural Pairing							
							A1	A2	A3	A4	A5	A6	A7	A8
S41	NC_001512.1	11835	3676	2440	2859	2860	1.123	1.678	1.327	0.544	1.347	0.512	0.942	2.903
S42	NC_001513.1	6211	1330	1748	973	2160	1.554	2.092	1.043	0.527	1.04	0.57	1.237	2.826
S43	NC_001564.2	10682	2618	2614	2919	2531	0.911	1.264	0.965	0.397	0.95	0.399	0.72	2.206
S44	NC_001642.1	6366	1925	1218	1339	1884	1.466	2.031	1.536	0.636	1.513	0.64	1.158	3.526
S45	NC_001728.1	6618	1990	2013	1441	1174	0.8	1.476	0.876	0.436	1.023	0.35	0.813	1.95
S46	NC_001948.1	8744	2430	2560	2075	1678	0.805	1.358	0.864	0.409	0.963	0.351	0.756	1.946
S47	NC_002604.1	6827	1689	1494	1405	2239	1.477	1.893	1.293	0.556	1.233	0.605	1.104	3.192
S48	NC_002729.1	7352	2511	2096	1571	1174	0.809	1.618	0.992	0.492	1.189	0.371	0.879	2.121
S49	NC_002795.1	8657	2306	2278	2149	1924	0.909	1.379	0.956	0.423	1.001	0.395	0.778	2.179
S50	NC_003557.1	8363	2282	2413	1943	1725	0.861	1.404	0.887	0.418	0.975	0.37	0.786	2.03



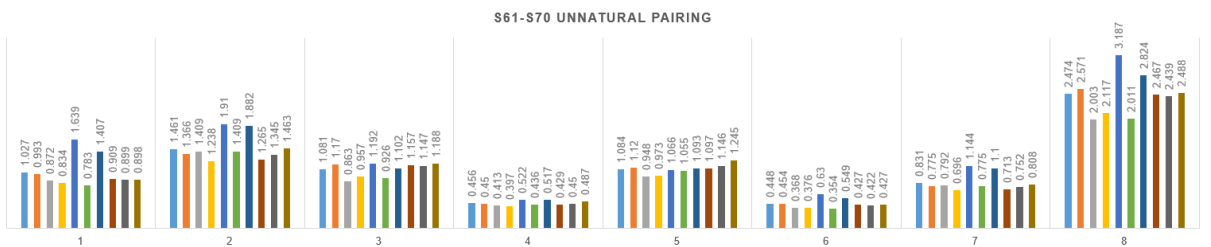
**Table 34:** Golden Ratios of Virus Genomes S51 to S60 (Unnatural pairing)

Serial No.	Accession ID	Total length	A	T	G	C	Golden Ratios for Unnatural Pairing							
							A1	A2	A3	A4	A5	A6	A7	A8
S51	NC_003603.1	4019	970	812	1176	1061	1.012	1.28	1.137	0.42	1.031	0.456	0.736	2.555
S52	NC_003608.1	3911	975	1012	1007	917	0.92	1.319	0.941	0.405	0.953	0.397	0.75	2.175
S53	NC_003634.1	6673	1503	1588	874	2708	2.127	2.78	1.373	0.691	1.339	0.771	1.656	3.787
S54	NC_003679.1	12333	4007	2715	3203	2408	0.906	1.497	1.197	0.497	1.266	0.431	0.826	2.508
S55	NC_003852.1	6507	1949	1867	1520	1171	0.799	1.423	0.911	0.433	1.037	0.356	0.785	0.004
S56	NC_003900.1	11824	3462	2628	2828	2906	1.097	1.618	1.214	0.512	1.237	0.488	0.913	2.722
S57	NC_004724.1	16527	4250	4624	4224	3429	0.819	1.267	0.863	0.387	0.915	0.356	0.713	1.964
S58	NC_005062.1	10787	2772	2229	3361	2425	0.857	1.171	1.072	0.395	1.007	0.401	0.663	2.304
S59	NC_005132.1	6966	1813	1348	1288	2517	1.811	2.277	1.567	0.668	1.475	0.739	1.332	3.892
S60	NC_006939.1	3683	1041	868	900	874	1.022	1.518	1.114	0.476	1.143	0.451	0.857	2.511



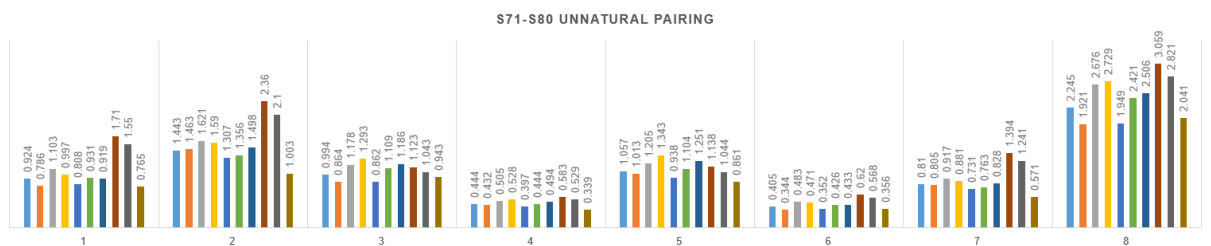
**Table 35:** Golden Ratios of Virus Genomes S61 to S70 (Unnatural pairing)

Serial No.	Accession ID	Total length	A	T	G	C	Golden Ratios for Unnatural Pairing							
							A1	A2	A3	A4	A5	A6	A7	A8
S61	NC_007733.2	3962	1054	937	990	981	1.027	1.461	1.081	0.456	1.084	0.448	0.831	2.474
S62	NC_009028.2	10755	2903	2229	3004	2619	0.993	1.366	1.17	0.45	1.12	0.454	0.775	2.571
S63	NC_009892.1	9005	2392	2669	2042	1902	0.872	1.409	0.863	0.413	0.948	0.368	0.792	2.003
S64	NC_011535.1	4731	1243	1167	1319	1002	0.834	1.238	0.957	0.397	0.973	0.376	0.696	2.117
S65	NC_011538.1	6285	1223	1467	1210	2385	1.639	1.91	1.192	0.522	1.066	0.63	1.144	3.187
S66	NC_011552.1	7988	2439	2249	1908	1392	0.783	1.409	0.926	0.436	1.055	0.354	0.775	2.011
S67	NC_011559.1	6151	1437	1585	1154	1975	1.407	1.882	1.102	0.517	1.093	0.549	1.1	2.824
S68	NC_012533.1	10723	2922	2143	3219	2439	0.909	1.265	1.157	0.429	1.097	0.427	0.713	2.467
S69	NC_012534.1	10941	3190	2330	3088	2333	0.899	1.345	1.147	0.45	1.146	0.422	0.752	2.439
S70	NC_012812.1	12337	3945	2694	3266	2426	0.898	1.463	1.188	0.487	1.245	0.427	0.808	2.488



**Table 36:** Golden Ratios of Virus Genomes S71 to S80 (Unnatural pairing)

Serial No.	Accession ID	Total length	A	T	G	C	Golden Ratios for Unnatural Pairing							
							A1	A2	A3	A4	A5	A6	A7	A8
S71	NC_013006.1	8517	2381	2215	2060	1857	0.924	1.443	0.994	0.444	1.057	0.405	0.81	2.245
S72	NC_015782.2	7259	2181	2230	1582	1266	0.786	1.463	0.864	0.432	1.013	0.344	0.805	1.921
S73	NC_016038.2	5666	1625	1300	1330	1411	1.103	1.621	1.178	0.505	1.205	0.483	0.917	2.676
S74	NC_016404.1	7488	2449	1558	1897	1584	0.997	1.59	1.293	0.528	1.343	0.471	0.881	2.729
S75	NC_016440.1	8638	2313	2473	2136	1716	0.808	1.307	0.862	0.397	0.938	0.352	0.731	1.949
S76	NC_016959.1	11724	3259	2588	3210	2632	0.931	1.356	1.109	0.444	1.104	0.426	0.763	2.421
S77	NC_018713.1	12292	3933	2728	3173	2458	0.919	1.498	1.186	0.494	1.251	0.433	0.828	2.506
S78	NC_020470.1	6337	1425	1742	892	2278	1.71	2.36	1.123	0.583	1.138	0.62	1.394	3.059
S79	NC_020471.1	6226	1344	1756	970	2154	1.55	2.1	1.043	0.529	1.044	0.568	1.241	2.821
S80	NC_023439.1	10688	2449	2280	3620	2339	0.765	1.003	0.943	0.339	0.861	0.356	0.571	2.041





S71-S80 UNNATURAL PAIRING

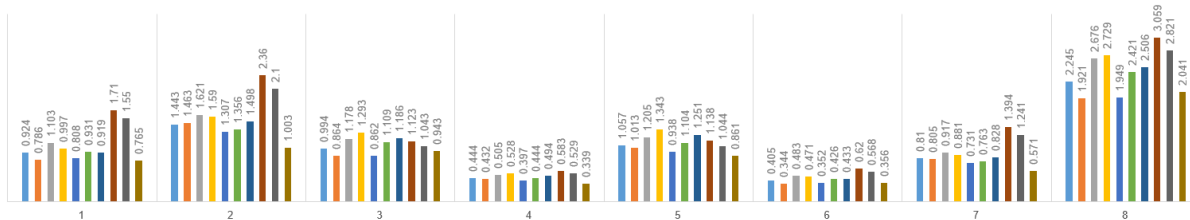


Table 37: Golden Ratios of Virus Genomes S81 to S90 (Unnatural pairing)

Serial No.	Accession ID	Total length	A	T	G	C	Golden Ratios for Unnatural Pairing							
							A1	A2	A3	A4	A5	A6	A7	A8
S81	NC_023892.1	8659	2457	2086	2286	1829	0.886	1.363	1.037	0.437	1.076	0.402	0.763	2.274
S82	NC_024458.1	6677	1800	1465	1518	1894	1.252	1.709	1.245	0.524	1.223	0.536	0.98	2.917
S83	NC_024887.1	11550	3125	2313	3118	2994	1.08	1.452	1.241	0.476	1.176	0.489	0.827	2.757
S84	NC_026620.1	10125	2916	2599	2752	1858	0.769	1.266	0.947	0.408	1.016	0.355	0.701	2.035
S85	NC_028793.2	5851	1510	1427	1460	1413	0.99	1.414	1.026	0.438	1.034	0.429	0.804	2.36
S86	NC_030693.1	6863	1277	1476	1202	2908	1.968	2.201	1.357	0.591	1.173	0.745	1.331	3.722
S87	NC_031327.1	10588	2729	2629	2889	2341	0.868	1.264	0.96	0.401	0.97	0.386	0.714	2.154
S88	NC_040842.1	5839	1554	1260	1257	1768	1.371	3.052	1.301	0.553	1.268	0.577	1.337	3.106
S89	NC_040837.1	6060	1699	1942	1503	916	0.638	1.928	0.747	0.364	0.873	0.287	0.772	1.626
S90	NC_040800.1	8192	2847	2187	1884	1274	0.792	2.554	1.042	0.494	1.225	0.374	0.978	2.179

S81-S90 UNNATURAL PAIRING

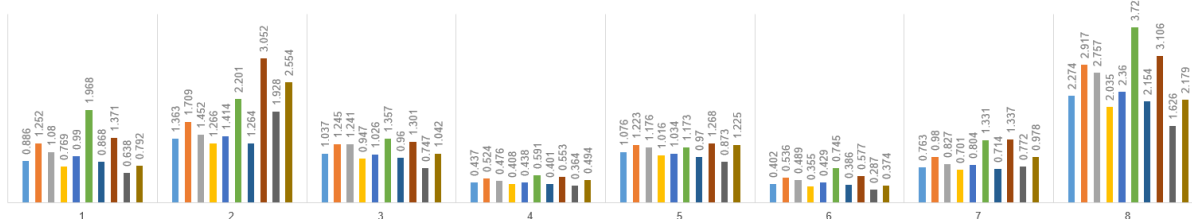


Table 38: Golden Ratios of Virus Genomes S91 to S100 (Unnatural pairing)

Serial No.	Accession ID	Total length	A	T	G	C	Golden Ratios for Unnatural Pairing							
							A1	A2	A3	A4	A5	A6	A7	A8
S91	NC_040788.1	10311	2885	2271	3053	2102	0.824	2.130	1.059	0.413	1.055	0.388	0.833	2.246
S92	NC_040776.1	10794	2976	2169	3066	2583	0.983	2.367	1.200	0.454	1.146	0.455	0.949	2.601
S93	NC_039237.1	12513	4045	2783	3186	2499	0.928	2.586	1.196	0.502	1.268	0.437	1.003	2.528
S94	NC_039218.1	10376	2509	2139	3314	2414	0.855	1.970	1.040	0.377	0.954	0.396	0.796	2.263
S95	NC_039217.1	14072	4836	3986	2783	2467	0.900	2.799	1.038	0.525	1.244	0.402	1.129	2.266
S96	NC_038966.1	8881	2426	2429	2180	1846	0.860	2.245	0.922	0.418	0.991	0.376	0.931	2.083
S97	NC_036587.1	6692	2080	1479	1452	1681	1.203	3.048	1.303	0.57	1.362	0.529	1.262	2.939
S98	NC_035462.1	6930	2255	2046	1554	1075	0.748	2.375	0.915	0.452	1.091	0.342	0.936	1.959
S99	NC_035453.1	18848	5414	5495	4453	3486	0.795	2.229	0.878	0.417	0.990	0.350	0.913	1.954
S100	NC_035116.1	5877	1129	1730	1417	1601	0.976	2.041	0.790	0.355	0.762	0.387	0.954	2.007

S91-S100 UNNATURAL PAIRING

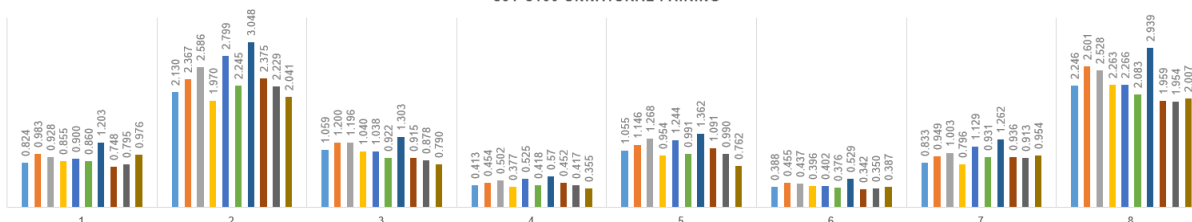


Table 39: Golden Ratios of Virus Genomes S101 to S110 (Unnatural pairing)

Serial No.	Accession ID	Total length	A	T	G	C	Golden Ratios for Unnatural Pairing							
							A1	A2	A3	A4	A5	A6	A7	A8
S101	NC_035071.1	20414	6142	4537	4813	4922	1.098	2.777	1.231	0.523	1.269	0.490	1.137	2.744
S102	NC_034833.1	6958	2140	1572	1766	1480	0.954	2.547	1.164	0.488	1.217	0.440	1.009	2.513
S103	NC_034242.1	10370	2787	2704	2748	2131	0.828	2.139	0.930	0.403	0.975	0.369	0.873	2.070
S104	NC_034216.1	15098	5582	3901	3120	2495	0.906	2.939	1.160	0.564	1.383	0.423	1.138	2.446
S105	NC_034207.1	5953	1588	1380	1517	1468	1.020	2.436	1.094	0.454	1.090	0.449	1.017	2.486
S106	NC_034205.1	6730	1205	1598	1424	2498	1.499	2.769	1.101	0.467	0.957	0.581	1.357	2.945
S107	NC_033828.1	6612	1287	1277	1398	2650	1.761	3.215	1.408	0.554	1.176	0.708	1.532	3.659
S108	NC_033725.1	10203	2866	2441	2878	2018	0.809	2.137	0.999	0.411	1.030	0.375	0.844	2.148
S109	NC_033724.1	10215	2601	2229	3177	2208	0.817	1.983	1.010	0.382	0.967	0.380	0.791	2.178
S110	NC_033723.1	10251	2701	2209	3207	2134	0.800	1.995	1.027	0.387	0.992	0.377	0.784	2.182

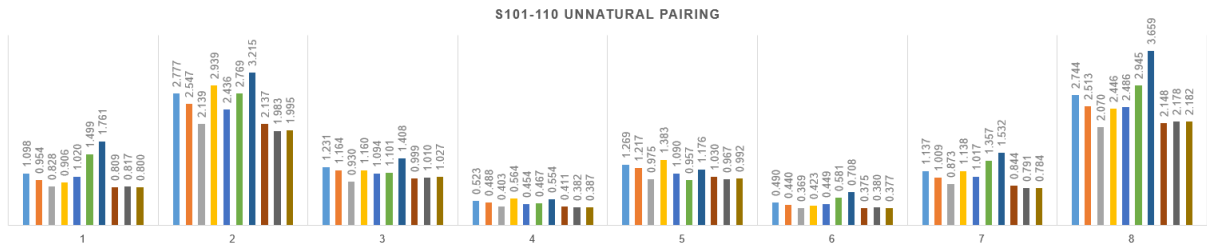


Table 40: Golden Ratios of Virus Genomes S111 to S120 (Unnatural pairing)

Serial No.	Accession ID	Total length	A	T	G	C	Golden Ratios for Unnatural Pairing							
							A1	A2	A3	A4	A5	A6	A7	A8
S111	NC_033699.1	10173	2948	2319	2751	2155	0.897	2.334	1.093	0.448	1.119	0.414	0.927	2.363
S112	NC_033693.1	10173	2940	2338	2744	2151	0.894	2.327	1.084	0.446	1.112	0.411	0.926	2.348
S113	NC_032088.1	10864	2872	2395	2947	2650	0.988	2.345	1.110	0.442	1.080	0.443	0.965	2.483
S114	NC_031752.1	11557	4006	3151	2231	2169	0.975	2.959	1.102	0.554	1.307	0.432	1.202	2.425
S115	NC_031463.1	23635	9624	6181	4217	3613	0.962	3.375	1.247	0.645	1.56	0.450	1.305	2.613
S116	NC_031462.1	15207	4392	3640	3787	3388	0.962	2.472	1.087	0.466	1.133	0.430	1.008	2.415
S117	NC_043110.1	10182	2778	2274	2867	2263	0.899	2.235	1.074	0.427	1.065	0.412	0.898	2.344
S118	NC_008516.1	26660	8975	6143	3758	7784	1.702	4.337	1.499	0.769	1.683	0.684	1.95	3.618
S119	NC_026812.1	27004	8268	6892	3909	7929	1.567	3.865	1.291	0.673	1.438	0.613	1.789	3.194
S120	NC_038295.1	27318	9234	6954	4110	7020	1.422	3.822	1.307	0.683	1.511	0.579	1.689	3.095

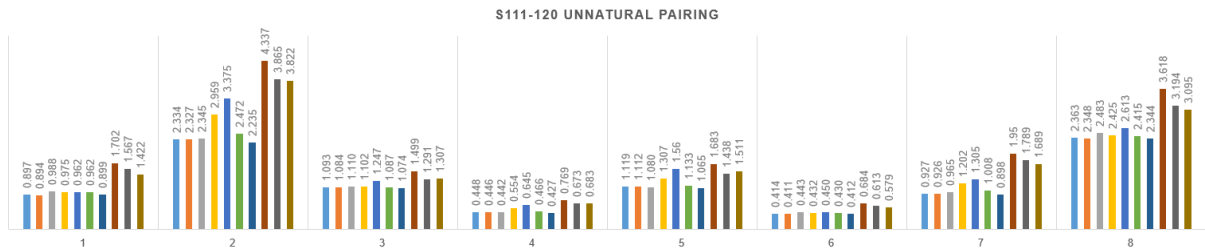
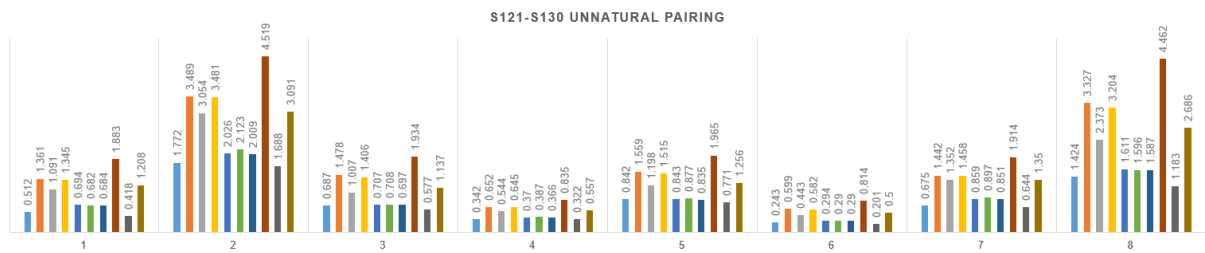


Table 41: Golden Ratios of Virus Genomes S121 to S130 (Unnatural pairing)

Serial No.	Accession ID	Total length	A	T	G	C	Golden Ratios for Unnatural Pairing							
							A1	A2	A3	A4	A5	A6	A7	A8
S121	NC_027199.1	20261	5947	6839	5208	2266	0.512	1.772	0.687	0.342	0.842	0.243	0.675	1.424
S122	NC_024709.1	33452	11117	6932	6663	8740	1.361	3.489	1.478	0.652	1.559	0.599	1.442	3.327
S123	NC_033700.1	30353	9555	9194	4934	6670	1.091	3.054	1.007	0.544	1.198	0.443	1.352	2.373
S124	NC_035465.1	32399	10710	7139	6186	8364	1.345	3.481	1.406	0.645	1.515	0.582	1.458	3.204
S125	NC_007447.1	28475	7690	9959	6104	4718	0.694	2.026	0.707	0.37	0.843	0.294	0.859	1.611
S126	NC_022787.1	28301	8124	10267	5579	4331	0.682	2.123	0.708	0.387	0.877	0.29	0.897	1.596
S127	NC_034976.1	28487	7686	10072	6083	4646	0.684	2.009	0.697	0.366	0.835	0.29	0.851	1.587
S128	NC_046956.1	30742	10484	5273	5238	9747	1.883	4.519	1.934	0.835	1.965	0.814	1.914	4.462
S129	NC_046962.1	29409	8759	11760	6561	2328	0.418	1.688	0.577	0.322	0.771	0.201	0.644	1.183
S130	NC_046963.1	30859	9285	8097	5722	7755	1.208	3.091	1.137	0.557	1.256	0.5	1.35	2.686



Now, the GR values of all 130 virus genomes are analyzed based on ‘Assignments’ of values to the coefficients in the rational polynomial  $(x1A + x2C) / (x3T + x4G)$ . It has been observed (i) GR values of all 130 virus genomes remain almost the same for the assignments of A1 and A7 [Ref. Fig. 38], (ii) GR values of all 130 virus genomes remain almost the same but different from previous values for the assignments of A2 and A8 [Ref. Fig. 39], (iii) GR values of all 130 virus genomes remain almost the same but different from previous values for the assignments of A3 and A5 [Ref. Fig. 40] and (iv) GR values of all 130 virus genomes remain almost the same but different from previous values for the assignments of A4 and A6 [Ref. Fig. 41].

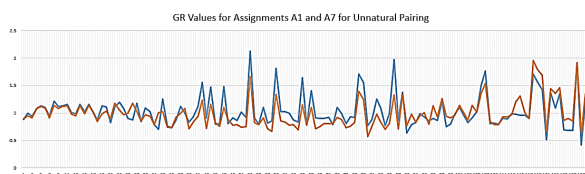


Fig. 38: GR values for assignments A1 and A7

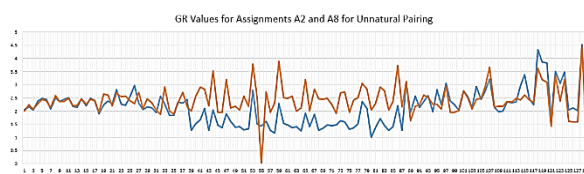


Fig. 39: GR values for assignments A2 and A8

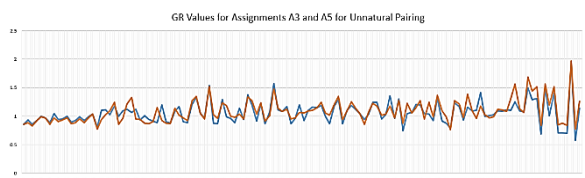


Fig. 40: GR values for assignments A3 and A5

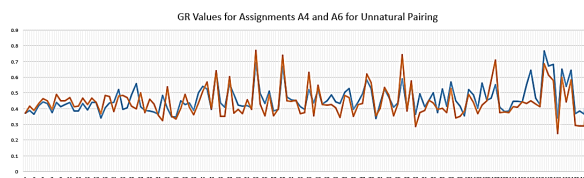


Fig. 41: GR values for assignments A4 and A6

This exercise of evaluating JCP Golden Ratios for all 130 virus genome sequences for A1=1,3,5,7, A2=7,1,3,5, A3=5,7,1,3, A4=3,5,7,1, A5=7,5,3,1, A6=1,7,5,3, A7=3,1,7,5 and A8=5,3,1,7 has been repeated and results compared with the previous ones. Due to space constraints, the results of this exercise are not provided.

**As per the definition of 'JCP Golden Ratios', their values are expected to remain within certain limits irrespective of the numerical values assigned to the coefficients in the formula  $(x1A + x2T) / (x3G + x4C)$ .** Table 42 presents the error values obtained using the formula  $A(1,2,3,4) - A(1,3,5,7)$ .

Table 42: Error values obtained using the formula  $A(1,2,3,4) - A(1,3,5,7)$

Sequences	A(1,2,3,4) – A(1,3,5,7)							
	A1	A2	A3	A4	A5	A6	A7	A8
S1	0.095	0.011	-0.733	0.002	-0.635	-0.012	0.099	-0.004
S2	0.082	0.010	-0.598	-0.005	-0.588	-0.011	0.086	0.004
S3	0.085	0.016	-0.648	-0.005	-0.601	-0.017	0.092	0.004
S4	0.092	0.018	-0.614	-0.022	-0.721	-0.021	0.097	0.017
S5	0.090	0.011	-0.583	-0.021	-0.712	-0.014	0.093	0.015
S6	0.091	0.013	-0.604	-0.019	-0.715	-0.014	0.095	0.014
S7	0.085	0.012	-0.635	-0.003	-0.590	-0.013	0.089	0.002
S8	0.078	0.012	-0.497	-0.024	-0.642	-0.014	0.082	0.016
S9	0.084	0.018	-0.556	-0.023	-0.664	-0.021	0.089	0.016
S10	0.089	0.018	-0.581	-0.027	-0.720	-0.022	0.094	0.019
S11	0.087	0.013	-0.559	-0.024	-0.704	-0.016	0.091	0.016
S12	0.085	0.016	-0.611	-0.011	-0.627	-0.018	0.090	0.009
S13	0.083	0.011	-0.601	-0.005	-0.590	-0.012	0.086	0.004
S14	0.085	0.015	-0.553	-0.025	-0.693	-0.018	0.090	0.017
S15	0.083	0.014	-0.588	-0.011	-0.613	-0.015	0.088	0.009
S16	0.088	0.015	-0.566	-0.026	-0.716	-0.018	0.092	0.018
S17	0.095	-0.004	-0.660	0.000	-0.673	0.003	0.094	-0.001
S18	0.082	0.017	-0.658	-0.001	-0.549	-0.017	0.088	-0.001
S19	0.065	0.002	-0.444	-0.005	-0.479	-0.003	0.065	0.004
S20	0.079	-0.003	-0.529	-0.004	-0.578	0.002	0.078	0.002
S21	0.117	-0.029	-0.930	0.027	-0.693	0.024	0.110	-0.043
S22	0.113	-0.018	-0.716	-0.001	-0.827	0.017	0.107	0.000
S23	0.065	0.017	-0.432	-0.021	-0.522	-0.019	0.069	0.015
S24	0.070	-0.001	-0.485	-0.001	-0.498	0.001	0.070	0.000
S25	0.124	-0.036	-0.915	0.026	-0.764	0.032	0.114	-0.037
S26	0.193	-0.048	-1.392	0.034	-1.223	0.044	0.179	-0.044
S27	0.064	0.004	-0.426	-0.009	-0.489	-0.005	0.066	0.007
S28	0.096	-0.008	-0.772	0.016	-0.593	0.006	0.095	-0.023
S29	0.067	0.009	-0.474	-0.008	-0.499	-0.010	0.070	0.006
S30	0.075	0.011	-0.539	-0.007	-0.538	-0.012	0.078	0.005
S31	0.091	-0.010	-0.765	0.020	-0.531	0.008	0.089	-0.032
S32	0.210	-0.042	-1.788	0.055	-1.169	0.034	0.199	-0.098
S33	0.053	0.003	-0.342	-0.009	-0.404	-0.005	0.052	0.006
S34	0.086	-0.012	-0.744	0.020	-0.484	0.009	0.083	-0.037
S35	0.094	-0.011	-0.833	0.023	-0.519	0.009	0.092	-0.044
S36	0.113	-0.032	-0.869	0.026	-0.678	0.028	0.105	-0.040

S37	0.069	-0.006	-0.467	0.000	-0.498	0.005	0.068	0.000
S38	0.113	0.015	-0.767	-0.018	-0.855	-0.017	0.118	0.014
S39	0.106	-0.001	-0.842	0.012	-0.668	-0.001	0.107	-0.018
S40	0.119	-0.044	-0.863	0.028	-0.727	0.038	0.106	-0.040
S41	0.107	-0.032	-0.677	0.010	-0.750	0.032	0.096	-0.011
S42	0.088	0.032	-0.460	-0.113	-0.982	-0.047	0.098	0.039
S43	0.091	-0.004	-0.692	0.009	-0.593	0.003	0.091	-0.012
S44	0.096	-0.023	-0.512	-0.018	-0.828	0.027	0.088	0.011
S45	0.146	-0.007	-1.144	0.020	-0.914	0.006	0.145	-0.027
S46	0.126	-0.002	-1.003	0.016	-0.787	0.001	0.126	-0.023
S47	0.083	0.001	-0.450	-0.038	-0.764	-0.003	0.082	0.020
S48	0.165	-0.038	-1.285	0.036	-0.982	0.032	0.154	-0.055
S49	0.108	-0.004	-0.796	0.009	-0.709	0.004	0.106	-0.011
S50	0.121	0.001	-0.917	0.008	-0.796	-0.002	0.121	-0.011
S51	0.077	-0.014	-0.550	0.009	-0.514	0.012	0.073	-0.011
S52	0.098	0.000	-0.728	0.006	-0.652	-0.001	0.098	-0.007
S53	0.078	0.020	-0.345	-0.158	-1.046	-0.033	0.085	0.037
S54	0.120	-0.046	-0.891	0.030	-0.722	0.040	0.107	-0.046
S55	0.136	-0.015	-1.086	0.025	-0.828	0.013	0.132	-0.035
S56	0.104	-0.021	-0.674	0.005	-0.743	0.021	0.097	-0.005
S57	0.109	0.001	-0.876	0.013	-0.685	-0.002	0.110	-0.018
S58	0.085	-0.023	-0.672	0.020	-0.499	0.019	0.079	-0.032
S59	0.080	-0.004	-0.380	-0.056	-0.828	0.005	0.077	0.023
S60	0.105	-0.016	-0.710	0.007	-0.721	0.015	0.100	-0.007
S61	0.097	-0.010	-0.667	0.003	-0.681	0.009	0.095	-0.004
S62	0.090	-0.022	-0.634	0.013	-0.584	0.020	0.084	-0.017
S63	0.120	0.008	-0.900	0.003	-0.812	-0.008	0.124	-0.004
S64	0.101	-0.013	-0.798	0.019	-0.603	0.011	0.097	-0.027
S65	0.068	0.020	-0.364	-0.067	-0.708	-0.026	0.074	0.027
S66	0.138	-0.021	-1.114	0.029	-0.811	0.019	0.132	-0.045
S67	0.089	0.017	-0.496	-0.060	-0.856	-0.022	0.095	0.029
S68	0.089	-0.029	-0.669	0.021	-0.537	0.025	0.081	-0.032
S69	0.102	-0.033	-0.762	0.024	-0.609	0.029	0.092	-0.036
S70	0.117	-0.045	-0.874	0.030	-0.698	0.034	0.105	-0.046
S71	0.113	-0.010	-0.820	0.010	-0.746	0.009	0.110	-0.012
S72	0.147	-0.006	-1.168	0.022	-0.913	0.006	0.146	-0.029
S73	0.104	-0.017	-0.670	0.001	-0.756	0.016	0.099	-0.002
S74	0.116	-0.046	-0.801	0.024	-0.738	0.041	0.103	-0.033
S75	0.117	-0.001	-0.940	0.015	-0.729	0.001	0.118	-0.021
S76	0.098	-0.024	-0.723	0.018	-0.619	0.020	0.092	-0.024
S77	0.119	-0.043	-0.868	0.028	-0.722	0.037	0.106	-0.040
S78	0.090	0.030	-0.437	-0.143	-1.083	-0.046	0.100	0.041
S79	0.089	0.032	-0.464	-0.115	-0.993	-0.046	0.099	0.039
S80	0.077	-0.014	-0.668	0.020	-0.427	0.011	0.073	-0.037
S81	0.108	-0.020	-0.814	0.020	-0.666	0.019	0.102	-0.026
S82	0.092	-0.010	-0.551	-0.013	-0.739	0.010	0.088	0.009
S83	0.088	-0.021	-0.584	0.008	-0.602	0.020	0.081	-0.010
S84	0.117	-0.024	-0.975	0.030	-0.659	0.020	0.111	-0.050
S85	0.098	-0.004	-0.686	0.003	-0.674	0.005	0.097	-0.003
S86	0.061	0.017	-0.297	-0.085	-0.707	-0.025	0.066	0.027
S87	0.098	-0.009	-0.763	0.015	-0.615	0.008	0.096	-0.020
S88	0.016	-0.259	-1.375	-0.036	-0.984	-0.124	0.035	-0.333
S89	0.076	-0.876	-2.210	-0.473	-2.824	-0.164	-0.128	-0.520
S90	0.160	0.010	-0.915	-0.170	-1.383	-0.061	0.120	0.158
S91	0.120	0.094	-0.412	-0.005	-0.556	0.029	0.109	0.149
S92	0.028	-0.194	-1.240	-0.121	-0.997	-0.146	0.032	-0.230
S93	0.148	0.161	-0.518	0.123	-0.331	0.094	0.165	0.126
S94	0.045	-0.163	-1.039	-0.050	-0.728	-0.060	0.038	-0.199
S95	0.407	0.806	1.028	0.815	1.396	0.755	0.435	0.720
S96	0.166	0.024	-0.621	0.209	-0.292	0.210	0.145	-0.004
S97	0.254	0.644	0.881	0.323	0.533	0.352	0.296	0.611

S98	0.464	1.149	2.106	0.530	1.198	0.685	0.462	1.282
S99	0.279	0.350	0.372	0.317	0.082	0.409	0.235	0.455
S100	-0.093	-1.151	-2.974	-0.466	-2.753	-0.346	-0.222	-1.049
S101	0.065	0.018	-1.099	0.047	-0.559	-0.078	0.124	-0.126
S102	0.114	-0.034	-0.808	0.020	-0.722	0.030	0.104	-0.027
S103	0.150	-0.052	-0.456	-0.023	-0.868	0.111	0.082	0.092
S104	0.346	1.124	1.132	0.481	1.064	0.362	0.468	1.014
S105	-0.052	-0.370	-2.086	-0.291	-1.551	-0.392	-0.012	-0.491
S106	-0.241	-1.158	-3.798	-0.543	-2.739	-0.689	-0.240	-1.322
S107	-0.084	-0.659	-1.856	-0.374	-1.989	-0.338	-0.132	-0.588
S108	0.055	-0.054	-1.119	-0.172	-1.058	-0.186	0.069	-0.054
S109	-0.154	-0.856	-2.912	-0.772	-2.976	-0.711	-0.197	-0.782
S110	0.125	0.120	-0.340	0.092	-0.248	0.096	0.121	0.128
S111	0.078	-0.231	-1.150	-0.074	-1.054	-0.031	0.041	-0.196
S112	0.168	0.140	-0.200	0.160	-0.232	0.193	0.148	0.178
S113	0.071	-0.140	-1.033	0.043	-0.616	0.009	0.069	-0.206
S114	0.157	-0.091	-1.428	0.227	-0.615	0.134	0.174	-0.245
S115	0.271	0.797	-0.508	0.551	0.755	0.239	0.451	0.400
S116	0.182	0.233	0.098	0.026	-0.503	0.149	0.154	0.332
S117	0.097	-0.023	-0.730	0.019	-0.595	0.019	0.090	-0.027
S118	0.127	-0.012	-0.577	-0.097	-1.358	0.016	0.120	0.036
S119	0.121	0.003	-0.586	-0.100	-1.285	-0.005	0.121	0.039
S120	0.140	-0.011	-0.710	-0.070	-1.345	0.013	0.134	0.033
S121	0.162	-0.019	-1.824	0.059	-0.745	0.013	0.161	-0.177
S122	0.116	-0.032	-0.637	-0.013	-0.958	0.034	0.105	0.008
S123	0.153	0.006	-0.914	-0.043	-1.278	-0.008	0.154	0.028
S124	0.121	-0.026	-0.662	-0.020	-1.013	0.029	0.112	0.012
S125	0.151	0.022	-1.291	0.017	-0.918	-0.021	0.158	-0.025
S126	0.172	0.021	-1.462	0.020	-1.050	-0.020	0.179	-0.030
S127	0.153	0.023	-1.321	0.018	-0.925	-0.022	0.161	-0.027
S128	0.105	-0.033	-0.467	-0.048	-1.063	0.041	0.092	0.020
S129	0.216	-0.006	-2.775	0.084	-0.906	0.003	0.220	-0.323
S130	0.123	-0.004	-0.720	-0.031	-1.034	0.003	0.121	0.020

Figs. 42 to 57 show the values of  $A(1,2,3,4)$  and  $A(1,3,5,7)$  and their differences

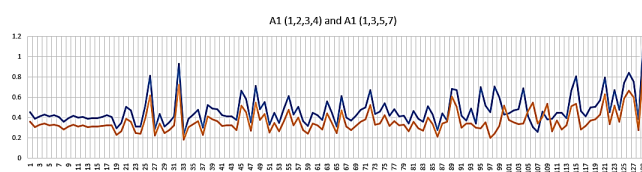


Fig. 42:  $A1(1,2,3,4)$  and  $A1(1,3,5,7)$

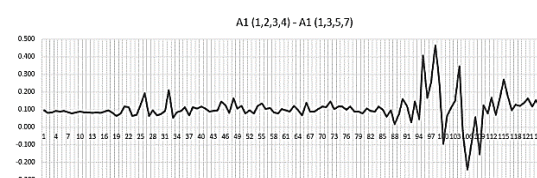


Fig. 43:  $A1(1,2,3,4) - A1(1,3,5,7)$

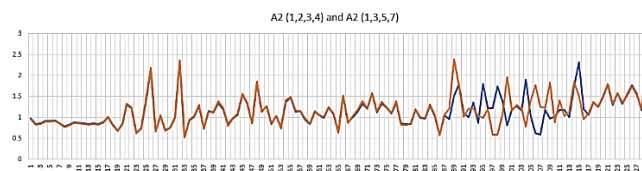


Fig. 44:  $A2(1,2,3,4)$  and  $A2(1,3,5,7)$

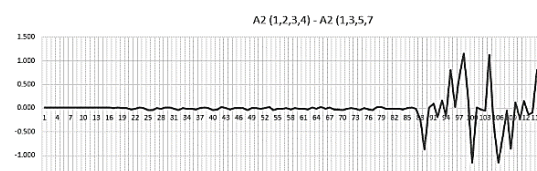


Fig. 45:  $A2(1,2,3,4) - A2(1,3,5,7)$

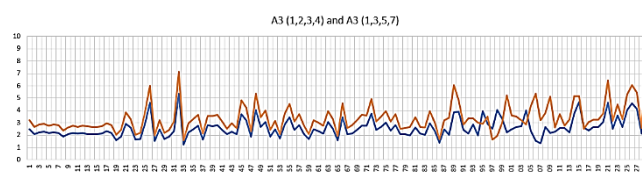


Fig. 46:  $A3(1,2,3,4)$  and  $A3(1,3,5,7)$



Fig. 47:  $A3(1,2,3,4) - A3(1,3,5,7)$



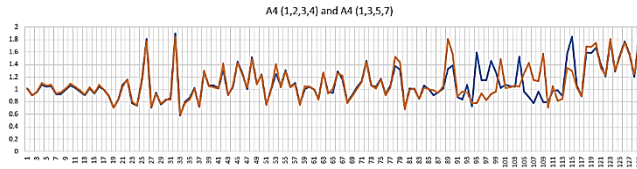


Fig. 48: A4(1,2,3,4) and A4(1,3,5,7)

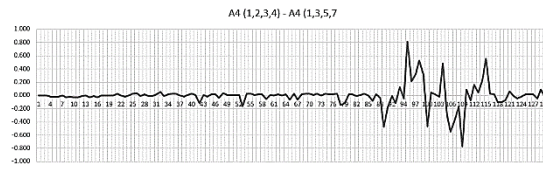


Fig. 49: A4(1,2,3,4) – A4(1,3,5,7)

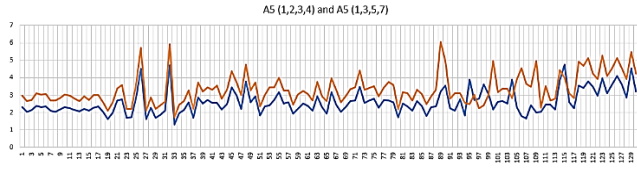


Fig. 50: A5(1,2,3,4) and A5(1,3,5,7)

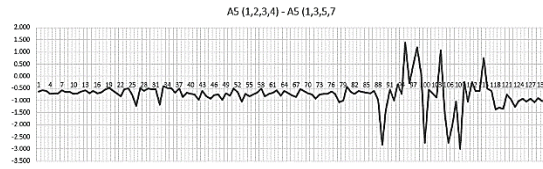


Fig. 51: A5(1,2,3,4) – A5(1,3,5,7)

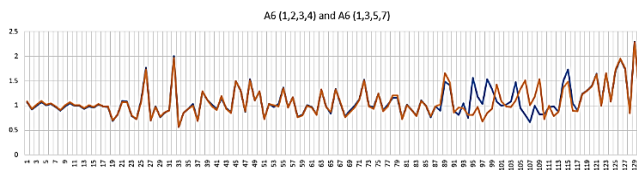


Fig. 52: A6(1,2,3,4) and A6(1,3,5,7)

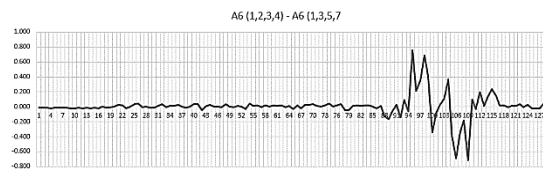


Fig. 53: A6(1,2,3,4) – A6(1,3,5,7)

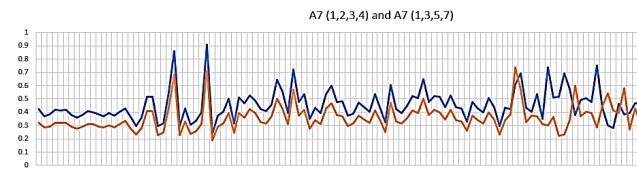


Fig. 54: A7(1,2,3,4) and A7(1,3,5,7)

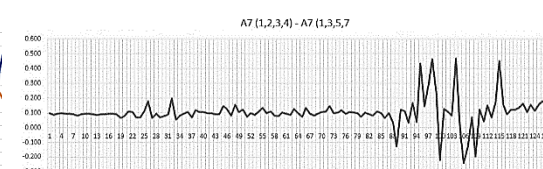


Fig. 55: A7(1,2,3,4) – A7(1,3,5,7)

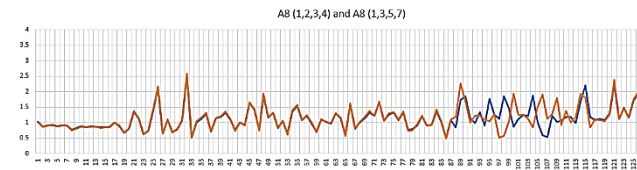


Fig. 56: A8(1,2,3,4) and A8(1,3,5,7)

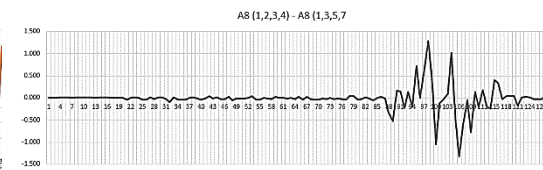


Fig. 57: A8(1,2,3,4) – A8(1,3,5,7)

With reference to table 42 and Figs. 42 to 57, one would observe that virus sequences S26 and S32 show considerable errors in their GR values  $A1(1,2,3,4) - A1(1,3,5,7)$ ,  $A3(1,2,3,4) - A3(1,3,5,7)$ ,  $A5(1,2,3,4) - A5(1,3,5,7)$  and  $A7(1,2,3,4) - A7(1,3,5,7)$ . These error values are given below highlighted in red color.

S26	0.193	-0.048	-1.392	0.034	-1.223	0.044	0.179	-0.044
S32	0.210	-0.042	-1.788	0.055	-1.169	0.034	0.199	-0.098

Once again with reference to table 42 and Figs. 42 to 57, one would observe that many of the virus sequences in the band S88 and S130 show considerable errors in their GR values. The gray colored rows in table 43 do not show considerable errors, whereas the remaining sequences exhibit large errors.

Table 43: Maximum error values obtained using the formula  $A(1,2,3,4) - A(1,3,5,7)$

Sequences	$A(1,2,3,4) - A(1,3,5,7)$							
	A1	A2	A3	A4	A5	A6	A7	A8
S88	0.016	-0.259	-1.375	-0.036	-0.984	-0.124	0.035	-0.333
S89	0.076	-0.876	-2.21	-0.473	-2.824	-0.164	-0.128	-0.52
S90	0.16	0.01	-0.915	-0.17	-1.383	-0.061	0.12	0.158
S91	0.12	0.094	-0.412	-0.005	-0.556	0.029	0.109	0.149
S92	0.028	-0.194	-1.24	-0.121	-0.997	-0.146	0.032	-0.23
S93	0.148	0.161	-0.518	0.123	-0.331	0.094	0.165	0.126
S94	0.045	-0.163	-1.039	-0.05	-0.728	-0.06	0.038	-0.199
S95	0.407	0.806	1.028	0.815	1.396	0.755	0.435	0.72





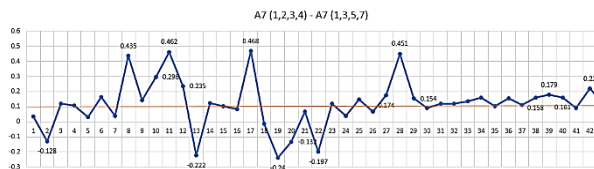


Fig. 64: A7(1,2,3,4) – A7(1,3,5,7)

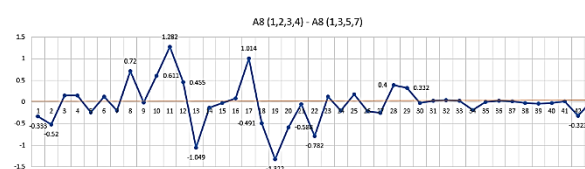


Fig. 65: A8(1,2,3,4) – A8(1,3,5,7)

**Observations**

1. Among the 43 sequences, the following 17 sequences do not show wide differences:  
S92, S93, S94, S101, S102, S103, S111, S113, S117, S118, S119, S120, S122, S124, S125, S128, S130
2. Among the 43 sequences, the following 26 sequences show wide differences:  
S88, S89, S90, S91, S95, S96, S97, S98, S99, S100, S104, S105, S106, S107, S108, S109, S110, S112, S114, S115, S116, S121, S123, S126, S127, S129
3. Among the remaining 87 sequences, the following 2 sequences show wide differences  
S26, S32.
4. Among the 130 sequences, the following 85 sequences do not show any difference:  
S1, S2, S3, S4, S5, S6, S7, S8, S9, S10, S11, S12, S13, S14, S15, S16, S17, S18, S19, S20, S21, S22, S23, S24, S25, S27, S28, S29, S30, S31, S33, S34, S35, S36, S37, S38, S39, S40, S41, S42, S43, S44, S45, S46, S47, S48, S49, S50, S51, S52, S53, S54, S55, S56, S57, S58, S59, S60, S61, S62, S63, S64, S65, S66, S67, S68, S69, S70, S71, S72, S73, S74, S75, S76, S77, S78, S79, S80, S81, S82, S83, S84, S85, S86, S87

Based on above observations on GR values, one could classify all 130 virus sequences in four categories. Table 44 presents these four categories.

Table 44: Classification of 130 Virus Sequences Based on JCP Golden Ratios

Category	Virus Sequences	Remarks
1	S1, S2, S3, S4, S5, S6, S7, S8, S9, S10, S11, S12, S13, S14, S15, S16, S17, S18, S19, S20, S21, S22, S23, S24, S25, S27, S28, S29, S30, S31, S33, S34, S35, S36, S37, S38, S39, S40, S41, S42, S43, S44, S45, S46, S47, S48, S49, S50, S51, S52, S53, S54, S55,	All these 85 sequences satisfy Golden Ratio Property (GRP). Different value assignments to nucleotides have not affected GRP. This means that these virus sequences have not changed their structures due to value assignments and hence
	S56, S57, S58, S59, S60, S61, S62, S63, S64, S65, S66, S67, S68, S69, S70, S71, S72, S73, S74, S75, S76, S77, S78, S79, S80, S81, S82, S83, S84, S85, S86, S87	<b>mutation possibility among these 85 sequences is very remote.</b>
2	S88, S89, S90, S91, S95, S96, S97, S98, S99, S100, S104, S105, S106, S107, S108, S109, S110, S112, S114, S115, S116, S121, S123, S126, S127, S129	All these 26 sequences do not satisfy Golden Ratio Property (GRP). Different value assignments to nucleotides have affected GRP. This means that these virus sequences have changed their structures due to value assignments and hence <b>mutation possibility among these 26 sequences is likely.</b>
3	S92, S93, S94, S101, S102, S103, S111, S113, S117, S118, S119, S120, S122, S124, S125, S128, S130	All these 17 sequences do not satisfy Golden Ratio Property (GRP). Different value assignments to nucleotides have affected GRP. This means that these virus sequences have changed their structures due to value assignments and hence <b>mutation possibility among these 17 sequences is likely.</b>
4	S26, S32	Both of these 2 sequences do not satisfy Golden Ratio Property (GRP). Different value assignments to nucleotides have affected GRP. This means that these virus sequences have changed their structures due to value assignments and hence <b>mutation possibility among these 2 sequences is likely.</b>

**Final Observation**

From the results presented above, it is clear that one could classify any given set of virus genomes based on (i) Auto Correlation Measures, (ii) Percentage Concentration of Nucleotides and Pairwise Correlation Coefficients and Golden Ratio (GR) values of the sequences.

**Inference**

After analyzing more than 70,000 virus genome sequences provided in the NCBI web site, most of the patterns of results so far obtained indicate the possibility of creating any desired virus apart from natural ones and also the possibility of creating engineered versions of natural viruses – *A Subjective Understanding by the Research Team*

## V. SONIC ATTACK – A FEASIBLE SOLUTION TO BREAK THE STRUCTURE OF A VIRUS GENOME

DNA molecule is the most evolved and most complex molecule created by nature and its primary role is long-term storage of genetic information. **Genetic modification could be carried out under the influence of acoustic, electromagnetic, and scalar waves, meaning genetic code of a DNA could be read and possibly rewritten.**

### 5.1 Natural Frequencies of DNA

Mobin Marvi & Majid Ghadiri have proposed ‘A Mathematical model for Vibration Behavior Analysis of DNA and Using a Resonant frequency of DNA for Genome engineering’ ([www.nature.com/scientificreports](http://www.nature.com/scientificreports)). In this model, the mass of the nucleobases in the DNA structure, the effects of the fluid surrounding the DNA (nucleoplasm) and the effects of temperature changes are also considered. A set of governing equations have been derived from Hamilton’s principle and by solving these equations using the generalized differential quadrature method (GDQM), the frequency and mode shape of the DNA has been obtained. An interesting but important topic called “**wave genome**” has been mooted by some Russian scientists, which states that DNA could be affected by acoustic, electromagnetic, and scalar waves. **Under the influence of these waves, the genetic code can be read or rewritten.** Konstantin Meyl has adapted the scalar waves described by ‘Nicola Tesla’ to biology and proposed a relationship between the scalar waves and DNA. Braddon et al investigated the manipulability of DNA from human emotions also. **Rein and Mccraty studied the impact of music on the DNA. Another study was carried out on the effect of sound waves on the synthesis and genes of chrysanthemum.** Peter Garjajev and his research group proved that DNA can be reprogrammed by words and using the correct resonant frequencies of DNA. Russian quantum biologist Poponin tried to prove that human DNA has a direct effect on the physical world and he also found out that DNA can cause disturbing patterns in the vacuum, thus producing magnetized microscopic wormholes. Nobel Laureate Luc Montagnier known for his study on HIV and AIDS, has demonstrated that DNA can be generated by teleportation through quantum imprint and also showed that DNA emits electromagnetic signals that teleport the DNA to other places, such as water molecules, a shocking revelation. Mobin Marvi & Majid Ghadiri has advocated the PBD (Peyrard-Bishop-Dauxois) model for describing DNA. Fig. 66 shows the shape of a DNA before reaching its resonant frequency and its shape distortions after reaching its resonant frequency.

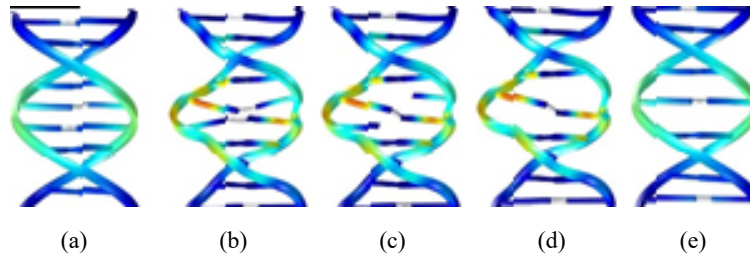


Fig. 66: Original DNA and engineered DNA

#### Legend:

- (a) Shape of DNA before reaching resonant frequency
- (b) Shape after reaching resonant frequency
- (c) Formation of hydrogen bond between a nucleobase to adjacent nucleobase
- (d) Removal of certain nucleobases
- (e) New shape for the DNA – DNA engineered

The mathematical model for vibration behavior analysis of DNA and using a resonant frequency of DNA due to Mobin Marvi and Majid Ghadiri is given by two governing equations of DNA considering the effects of the cellular fluid and temperature change. Appropriate details about the formulation of these two governing equations could be obtained from [www.nature.com/scientificreports](http://www.nature.com/scientificreports).

$$\begin{aligned}
 & \left( \begin{matrix} \mathbf{e}_{01}^T \mathbf{Y}_{e_0A} \\ \mathbf{e}_{11}^T \mathbf{Y}_{e_1I_2} \\ \mathbf{e}_{21}^T \mathbf{Y}_{e_2I_1} \end{matrix} - \begin{matrix} \mathbf{e}_{02}^T \mathbf{Y}_{e_0A} \\ \mathbf{e}_{12}^T \mathbf{Y}_{e_1I_2} \\ \mathbf{e}_{22}^T \mathbf{Y}_{e_2I_1} \end{matrix} - (e_0a)^2 \left( \begin{matrix} \mathbf{e}_{01}^T \mathbf{Y}_{e_0A} \\ \mathbf{e}_{11}^T \mathbf{Y}_{e_1I_2} \\ \mathbf{e}_{21}^T \mathbf{Y}_{e_2I_1} \end{matrix} + 2 \begin{matrix} \mathbf{e}'_{01} \mathbf{Y}_{e_0A} \\ \mathbf{e}'_{11} \mathbf{Y}_{e_1I_2} \\ \mathbf{e}'_{21} \mathbf{Y}_{e_2I_1} \end{matrix} \right) \right) \begin{Bmatrix} \mathbf{r}_1 \\ \mathbf{r}_1 \end{Bmatrix} \\
 & - \left( \begin{matrix} \mathbf{e}_{02}^T \mathbf{Y}_{e_0A} \\ \mathbf{e}_{12}^T \mathbf{Y}_{e_1I_2} \\ \mathbf{e}_{22}^T \mathbf{Y}_{e_2I_1} \end{matrix} + 2(e_0a)^2 \begin{matrix} \mathbf{e}'_{01} \mathbf{Y}_{e_0A} \\ \mathbf{e}'_{11} \mathbf{Y}_{e_1I_2} \\ \mathbf{e}'_{21} \mathbf{Y}_{e_2I_1} \end{matrix} \right) \begin{Bmatrix} \mathbf{r}'_1 \\ \mathbf{r}'_1 \end{Bmatrix} \\
 & + (\mathbf{K}(\mathbf{r}_1 - \mathbf{r}_2) - (e_0a)^2 \mathbf{K}(\mathbf{r}'_1 - \mathbf{r}'_2)) \\
 & - ((\mathbf{O}_2^T \mathbf{Y}_{A_s_2} \alpha \Delta \mathbf{TO}_2) \mathbf{r}_1 - (e_0a)^2 (\mathbf{O}_2^T \mathbf{Y}_{A_s_2} \alpha \Delta \mathbf{TO}_2) \mathbf{r}'_2) \\
 & - \rho \omega^2 (\mathbf{r}_1 \mathbf{A} - (e_0a)^2 \mathbf{r}'_1 \mathbf{A}) - m_K \omega^2 (\mathbf{r}_1 - (e_0a)^2 \mathbf{r}'_1) \\
 & + \omega (\mathbf{C}_a (\mathbf{r}_1 - \mathbf{r}_2) - (e_0a)^2 \mathbf{C}_a (\mathbf{r}'_1 - \mathbf{r}'_2)) \\
 & + \omega (\rho_n \mathbf{r}_1 (\mathbf{A}_{s_1} + \mathbf{A}_{s_2}) - (e_0a)^2 \rho_n \mathbf{r}'_1 (\mathbf{A}_{s_1} + \mathbf{A}_{s_2})) = 0
 \end{aligned}
 \tag{Equation #1}$$

$$\begin{aligned}
 & \left( \begin{matrix} \mathbf{e}_{01}^T \mathbf{Y}_{e_0A} \\ \mathbf{e}_{11}^T \mathbf{Y}_{e_1I_2} \\ \mathbf{e}_{21}^T \mathbf{Y}_{e_2I_1} \end{matrix} - \begin{matrix} \mathbf{e}_{02}^T \mathbf{Y}_{e_0A} \\ \mathbf{e}_{12}^T \mathbf{Y}_{e_1I_2} \\ \mathbf{e}_{22}^T \mathbf{Y}_{e_2I_1} \end{matrix} - (e_0a)^2 \left( \begin{matrix} \mathbf{e}_{01}^T \mathbf{Y}_{e_0A} \\ \mathbf{e}_{11}^T \mathbf{Y}_{e_1I_2} \\ \mathbf{e}_{21}^T \mathbf{Y}_{e_2I_1} \end{matrix} + 2 \begin{matrix} \mathbf{e}'_{01} \mathbf{Y}_{e_0A} \\ \mathbf{e}'_{11} \mathbf{Y}_{e_1I_2} \\ \mathbf{e}'_{21} \mathbf{Y}_{e_2I_1} \end{matrix} \right) \right) \begin{Bmatrix} \mathbf{r}_2 \\ \mathbf{r}_2 \end{Bmatrix} \\
 & - \left( \begin{matrix} \mathbf{e}_{02}^T \mathbf{Y}_{e_0A} \\ \mathbf{e}_{12}^T \mathbf{Y}_{e_1I_2} \\ \mathbf{e}_{22}^T \mathbf{Y}_{e_2I_1} \end{matrix} + 2(e_0a)^2 \begin{matrix} \mathbf{e}'_{01} \mathbf{Y}_{e_0A} \\ \mathbf{e}'_{11} \mathbf{Y}_{e_1I_2} \\ \mathbf{e}'_{21} \mathbf{Y}_{e_2I_1} \end{matrix} \right) \begin{Bmatrix} \mathbf{r}'_2 \\ \mathbf{r}'_2 \end{Bmatrix} \\
 & - (\mathbf{K}(\mathbf{r}_1 - \mathbf{r}_2) - (e_0a)^2 \mathbf{K}(\mathbf{r}'_1 - \mathbf{r}'_2)) \\
 & - ((\mathbf{O}_1^T \mathbf{Y}_{A_s_1} \alpha \Delta \mathbf{TO}_1) \mathbf{r}_2 - (e_0a)^2 (\mathbf{O}_1^T \mathbf{Y}_{A_s_1} \alpha \Delta \mathbf{TO}_1) \mathbf{r}'_2) \\
 & - \rho \omega^2 (\mathbf{r}_2 \mathbf{A} - (e_0a)^2 \mathbf{r}'_2 \mathbf{A}) - m_K \omega^2 (\mathbf{r}_2 - (e_0a)^2 \mathbf{r}'_2) \\
 & - \omega (\mathbf{C}_a (\mathbf{r}_1 - \mathbf{r}_2) - (e_0a)^2 \mathbf{C}_a (\mathbf{r}'_1 - \mathbf{r}'_2)) \\
 & + \omega (\rho_n \mathbf{r}_2 (\mathbf{A}_{s_1} + \mathbf{A}_{s_2}) - (e_0a)^2 \rho_n \mathbf{r}'_2 (\mathbf{A}_{s_1} + \mathbf{A}_{s_2})) = 0
 \end{aligned}
 \tag{Equation #2}$$

Based on these governing equations, Mobin Marvi and Majid Ghadiri have evaluated the mechanical and geometrical properties of DNA, which are presented in Fig. 67.

Mechanical or thermal properties	Symbol	Quantity	Reference
Young modulus	$E$	0.3 (GPa)	
Poisson's ratio	$\nu$	0.5	
Shear modulus	$G$	0.1 (GPa)	$G = \frac{E}{2(1+\nu)}$
Density	$\rho$	1.7 (g/m <sup>3</sup> )	
Mass of Adenine	$M$	226 * 10 <sup>-27</sup> (Kg)	
Mass of Thymine	$M$	211 * 10 <sup>-27</sup> (Kg)	
Mass of Guanine	$M$	252 * 10 <sup>-27</sup> (Kg)	
Mass of Cytosine	$M$	185 * 10 <sup>-27</sup> (Kg)	
Hydrogen bond strength	Between Adenine-Thymine ( $k_{AT}$ )	19.5 (N/m)	
	Between Guanine-Cytosine ( $k_{GC}$ )	56.3 (N/m)	
Damper constant	$C$	0.05 (N s/m)	
Density of nucleoplasm	$\rho_n$	0.14 (g/cm <sup>3</sup> )	
Viscosity of nucleoplasm	$\mu_n$	1.35 (cP) or 0.135 * 10 <sup>-2</sup> ( $\frac{N \cdot s}{m^2}$ )	
Osmotic pressure	$P$	4 (atm)	
Thermal conductivity	$k_t$	$k = 150 \frac{W}{mK}$	
Specific heat capacity	$c_p$	$C_p = 40 \frac{cal}{molK}$ or $2.56 * 10^{-4} \frac{KJ}{gK}$	
Thermal diffusivity	$\alpha$	$\alpha = 3.44 * 10^{-8} \frac{m^2}{s}$ $\alpha = \frac{k}{\rho c_p}$	

Geometry	Quantity	Reference
Pitch/turn of helix	34 (Å)	
Rise/bp along axis	3.4 (Å)	
Radius	10 (Å)	
Rotation/bp	34.3°	
Curvature	0.008 * 10 <sup>10</sup>	$\kappa = \frac{radius}{\sqrt{radius^2 + pitch^2}}$
Twist	0.027 * 10 <sup>10</sup>	$\tau = \frac{pitch}{\sqrt{radius^2 + pitch^2}}$
Straight and open length	7.14 * 10 <sup>-9</sup>	$L = \sqrt{(2\pi r)^2 + (pitch)^2}$
Length of Adenine	2 * 5.8 (Å)	
Length of Thymine	2 * 4.8 (Å)	
Length of Guanine	2 * 5.7 (Å)	
Length of Cytosine	2 * 4.7 (Å)	
Distance between Adenine-Thymine	2.83 (Å)	

Thickness	Width
0.98 (Å)	3.17 (Å)

Cross-section of DNA strands

Adenine	Thymine	Guanine	Cytosine
0.53	0.5	0.55	0.45

Sectional radius of nucleobases (Å)

Fig. 67: Mechanical and geometrical properties of DNA

Courtesy: www.nature.com/scientificreports

Moreover, the authors have estimated the natural frequencies of DNA in terms of its length. The estimated values are shown in Fig. 68.

Number of Nucleobases	Number of turn of helix	Natural frequency (Hz)		
		First mode	Second mode	Third mode
10	1	5.0198 * 10 <sup>9</sup>	7.0444 * 10 <sup>9</sup>	9.6939 * 10 <sup>9</sup>
20	2	1.4375 * 10 <sup>9</sup>	2.6497 * 10 <sup>9</sup>	3.8139 * 10 <sup>9</sup>
30	3	5.2032 * 10 <sup>8</sup>	1.1533 * 10 <sup>9</sup>	1.8835 * 10 <sup>9</sup>
40	4	6.6750 * 10 <sup>8</sup>	6.8998 * 10 <sup>8</sup>	1.3232 * 10 <sup>9</sup>
50	5	5.3081 * 10 <sup>8</sup>	5.4125 * 10 <sup>8</sup>	1.0504 * 10 <sup>9</sup>
60	6	4.3337 * 10 <sup>8</sup>	4.5284 * 10 <sup>8</sup>	8.6065 * 10 <sup>8</sup>
70	7	3.7059 * 10 <sup>8</sup>	3.8425 * 10 <sup>8</sup>	7.3720 * 10 <sup>8</sup>
80	8	3.2702 * 10 <sup>8</sup>	3.3004 * 10 <sup>8</sup>	6.5024 * 10 <sup>8</sup>

Fig. 68: Variations in natural frequencies with respect to DNA lengths

Based on the details given above, one would wonder whether it is possible to develop a formal method of dealing with Corona viruses using sonic frequencies with the idea of causing a physical disruption in the virus structure. In this context, this paper first points out to a work carried out by Mark D. Temple, for generating sonic frequencies artificially in order to express Corona viruses. Subsequently, a novel technique for artificially generating sonic bursts is proposed for the purpose of physically dismembering Corona viruses, for that matter any real time viral genome.

### 5.2 Sonic frequencies artificially generated to express corona viruses

“Mark D. Temple describes in his paper (<https://bmcbioinformatics.biomedcentral.com/articles/10.1186/s12859-020-03760-7>), a real-time audio and visual display of the Coronavirus genome wherein he uses a combination of sonification and an animated display to inquire into the SARS-CoV-2 genome. The audio data is generated in real time from a variety of RNA motifs that are known to be important in the functioning of RNA. Additionally, metadata relating to RNA translation and transcription has been used to shape the auditory and visual displays. Together these tools provide a unique approach to further understand the metabolism of the viral RNA genome. This audio signal provides a further means to represent the function of the RNA in addition to traditional written and visual approaches. Sonification of the SARS-CoV-2 genomic RNA sequence results in a complex auditory stream composed of up to 12 individual audio tracks. Each auditory motive is derived from the actual RNA sequence or from metadata. This approach has been used to represent transcription or translation of the viral RNA genome.

Observations:

1. As the DNA length increases, the natural frequency decreases. This need not be true in all cases because the natural frequencies depend on various factors like helical turns, viscosity, density and temperature of the fluid surrounding the RNA.
2. It is expected that the natural frequency associated with a Corona virus RNA could be of the order of kilo hertz.
3. Frequency varies between various modes need not be uniform.

The display highlights the real-time interaction of functional RNA elements. The sonification of codons derived from all three reading frames of the viral RNA sequence in combination with sonified metadata provide the framework for this display. Functional RNA motifs such as transcription regulatory sequences and stem loop regions have also been sonified. Using the tool, audio can be generated in real-time from either genomic or sub-genomic representations of the RNA. Given the large size of the viral genome, a collection of interactive buttons has been provided to navigate to regions of interest, such as cleavage regions in the polyprotein, untranslated regions or each gene. These tools are available through an internet browser and the user can interact with the data display in real time. Each nucleotide generates a note on every beat whereas each di-nucleotide generates a note every second beat. Each codon (in an ORF) generates a note every third beat. Together these notes are syncopated to create a characteristic sound during peptide translation that is distinct from the surrounding untranslated region. Audio from the GC tracks are only triggered when the GC ratio changes by an increment of 0.1. If a note sequence has identical adjacent notes then the length of the note is extended rather than being repeated. This creates space and clarity for other notes layered in the auditory display. Table xxx provides scale degrees and instrumentation used for the RNA features that are sonified". **Reproduced verbatim from <https://bmcbioinformatics.biomedcentral.com/articles/10.1186/s12859-020-03760-7>**

Table 45: Scale degrees and instrumentation of the RNA features being sonified

Sonified motif	Instrument	Pan	Translation Scale Bb aeolian mode		Transcription Scale C Lydian mode		
			Scale degrees		Octave	Scale degrees	Octave
			Nucleotide	Synth	L	1, 3	2, 3
Di-nucleotide	Synth	R	1, 4, 5, 6	1, 2, 3, 4	1, 3, 5	1	
GC Content (10 bp)	AM synth + delay	L	1, 3, 6, 7	2,3	1, 3, 5, 7	4, 5	
GC Content (100 bp)	AM synth + delay	R	1, 3, 6, 7	2, 3	1, 3, 5, 7	4, 5	
3 bp repeat	Synth	L	1, 3	4	1, 4, 5	6	
Codon Frame 1 (translation)	FM synth + distortion	L	1, 3, 4, 5, 7	2, 3, 4, 5	–	–	
Codon Frame 2 (translation)	FM synth + distortion	C	1, 3, 4, 5, 7	2, 3, 4, 5	–	–	
Codon Frame 3 (translation)	FM synth + distortion	R	1, 3, 4, 5, 7	2, 3, 4, 5	–	–	
Tri-nucleotide (transcription)	FM synth + distortion	L	–	–	1, 3, 4, 5, 7	3, 4, 5	
Untranslated regions	AM synth	R	1, 2, 3	5	1, 4, 6, 7	3	
Transcription regulating sequences (TRS)	AM synth	L	1, 2, 4, 5, 6	5	1, 2, 3, 4, 5, 6, 7	6	
Cleavage sites in the polyprotein	AM synth + distortion	L	1, 6, 7	4	1, 2, 3	6	
Stem and loop regions (SL)	AM synth + delay + distortion	R	1, 2, 6, 7	5	1, 4, 5, 7		
Nucleotide	Synth	L	1, 3	2, 3	1, 5	2, 3	
Di-nucleotide	Synth	R	1, 4, 5, 6	1, 2, 3, 4	1, 3, 5	1	
GC Content (10 bp)	AM synth + delay	L	1, 3, 6, 7	2,3	1, 3, 5, 7	4, 5	
GC Content (100 bp)	AM synth + delay	R	1, 3, 6, 7	2, 3	1, 3, 5, 7	4, 5	
3 bp repeat	Synth	L	1, 3	4	1, 4, 5	6	
Codon Frame 1 (translation)	FM synth + distortion	L	1, 3, 4, 5, 7	2, 3, 4, 5	–	–	
Codon Frame 2 (translation)	FM synth + distortion	C	1, 3, 4, 5, 7	2, 3, 4, 5	–	–	
Codon Frame 3 (translation)	FM synth + distortion	R	1, 3, 4, 5, 7	2, 3, 4, 5	–	–	
Tri-nucleotide (transcription)	FM synth + distortion	L	–	–	1, 3, 4, 5, 7	3, 4, 5	
Untranslated regions	AM synth	R	1, 2, 3	5	1, 4, 6, 7	3	
Transcription regulating sequences (TRS)	AM synth	L	1, 2, 4, 5, 6	5	1, 2, 3, 4, 5, 6, 7	6	
Cleavage sites in the polyprotein	AM synth + distortion	L	1, 6, 7	4	1, 2, 3	6	
Stem and loop regions (SL)	AM synth + delay + distortion	R	1, 2, 6, 7	5	1, 4, 5, 7		

(Courtesy: <https://bmcbioinformatics.biomedcentral.com/articles/10.1186/s12859-020-03760-7>),

### 5.3 Sonic frequencies artificially generated to dismember corona viruses

What is intended in this section is to explore the possibility of generating sonic frequencies in order to dismember corona viruses. The basic idea that is used here is that one can assign four of the heptonic scales to the four nucleotides. The seven svaras of the saptak are the fundamentals of heptatonic scales or melakarta ragas and thaats in Carnatic and Hindustani classical music. The seven svaras are Shadja (षड्ज), Rishabh (ऋषभ), Gandhara (गान्धार), Madhyama (मध्यम), Panchama (पंचम), Dhaivata (धैवत) and Nishada (निषाद). The frequencies corresponding to the svaras are determined as shown here. Shadja is realized as the fundamental frequency  $f_s$ , which may be in any suitable scale. Then the remaining svaras are realized as the frequencies given by  $f_r = f_s + 33\text{Hz}$ ,  $f_g = f_s + 69\text{Hz}$ ,  $f_m = f_s + 88\text{Hz}$ ,  $f_p = f_s + 131\text{Hz}$ ,  $f_d = f_s + 179\text{Hz}$ ,  $f_n = f_s + 233\text{Hz}$ , and the Shadja of the next octave  $f_{ss} = f_s + 254\text{Hz}$ . For example, if one chooses 50Hz for  $f_s$ , then  $f_r = 83\text{Hz}$ ,  $f_g = 119\text{Hz}$ ,  $f_m = 138\text{Hz}$ ,  $f_p = 181\text{Hz}$ ,  $f_d = 229\text{Hz}$ ,  $f_n = 283\text{Hz}$ , and the Shadja of the next octave  $f_{ss} = 304\text{Hz}$ . For convenience, four frequencies such as  $f_s$ ,  $f_m$ ,  $f_p$  and  $f_{ss}$  are chosen and allotted to the four nucleotides such as Adenine (A), Thymine (T), Guanine (G) and Cytosine (C) respectively. Table 46 shows frequency allocation to the nucleotides and a sample frequency allocation.

Table 46: Frequency allocation to nucleotides

Nucleotides	A	T	G	C	Nucleotides	A	T	G	C
Frequencies	$f_s$	$f_m$	$f_p$	$f_{ss}$	Sample Frequencies	$f_s = 50\text{Hz}$	$f_m = 138\text{Hz}$	$f_p = 181\text{Hz}$	$f_{ss} = 304\text{Hz}$



For example, let us consider the first 30 nucleotides in S1: >NC\_001639.1 Lactate dehydrogenase-elevating virus, complete genome. Then the frequency allocation for the nucleotides is given in Table 47.

Table 47: Frequency allocation to 30 nucleotides ( $s1$  to  $s30$ ) in the sequence S1: >NC\_001639.1

Sample Number	$s1$	$s2$	$s3$	$s4$	$s5$	$s6$	$s7$	$s8$	$s9$	$S10$
Nucleotide	c	t	a	c	c	c	a	g	g	a
Frequency Allotted	$f_{SS} = 304\text{Hz}$	$f_M = 138\text{Hz}$	$f_S = 50\text{Hz}$	$f_{SS} = 304\text{Hz}$	$f_{SS} = 304\text{Hz}$	$f_{SS} = 304\text{Hz}$	$f_S = 50\text{Hz}$	$f_P = 181\text{Hz}$	$f_P = 181\text{Hz}$	$f_S = 50\text{Hz}$
Sample Number	$s11$	$s12$	$s13$	$s14$	$s15$	$s16$	$s17$	$s18$	$s19$	$s20$
Nucleotide	a	a	a	g	c	c	a	a	c	c
Frequency Allotted	$f_S = 50\text{Hz}$	$f_S = 50\text{Hz}$	$f_S = 50\text{Hz}$	$f_P = 181\text{Hz}$	$f_{SS} = 304\text{Hz}$	$f_{SS} = 304\text{Hz}$	$f_S = 50\text{Hz}$	$f_S = 50\text{Hz}$	$f_{SS} = 304\text{Hz}$	$f_{SS} = 304\text{Hz}$
Sample Number	$s21$	$s22$	$s23$	$s24$	$s25$	$s26$	$s27$	$s28$	$s29$	$s30$
Nucleotide	a	a	c	c	t	c	g	a	t	c
Frequency Allotted	$f_S = 50\text{Hz}$	$f_S = 50\text{Hz}$	$f_{SS} = 304\text{Hz}$	$f_{SS} = 304\text{Hz}$	$f_M = 138\text{Hz}$	$f_{SS} = 304\text{Hz}$	$f_P = 181\text{Hz}$	$f_S = 50\text{Hz}$	$f_M = 138\text{Hz}$	$f_{SS} = 304\text{Hz}$

Fig. 69 shows the pure tones generated programmatically.

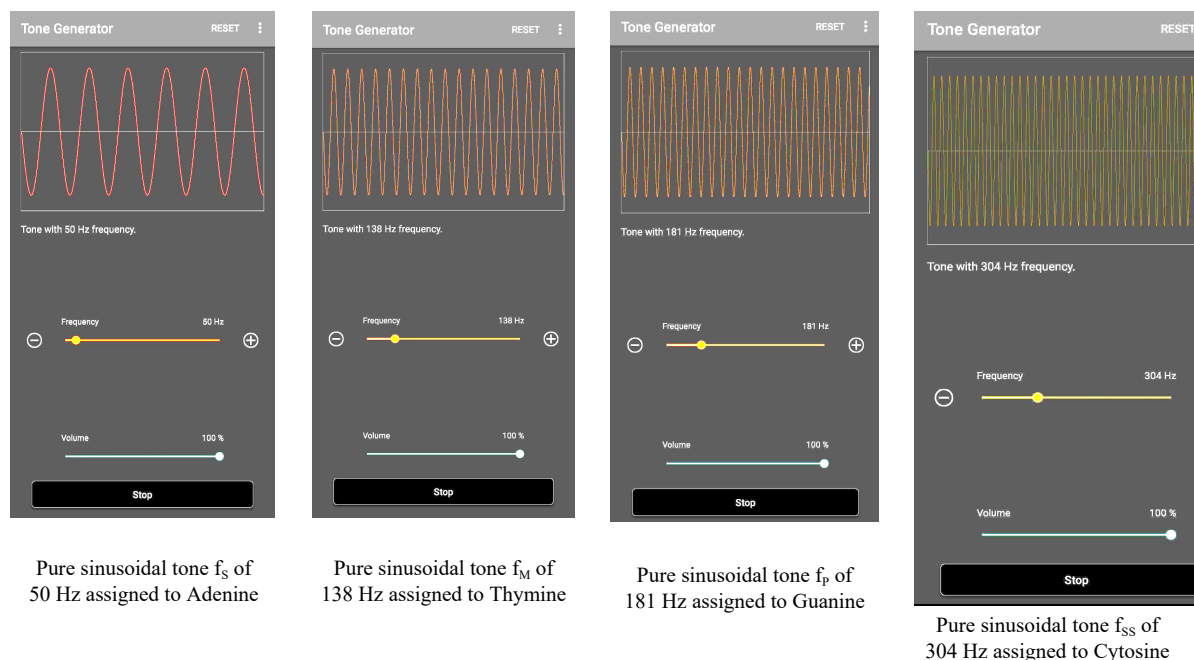


Fig. 69: Pure tones generated programmatically

Now let us consider the first thirty nucleotides in the viral genome S1: >NC\_001639.1 and allot the four frequencies to the respective nucleotides. Fig. 70 shows the audio frequency bursts for first 30 nucleotides of S1: >NC\_001639.1 virus sequence.

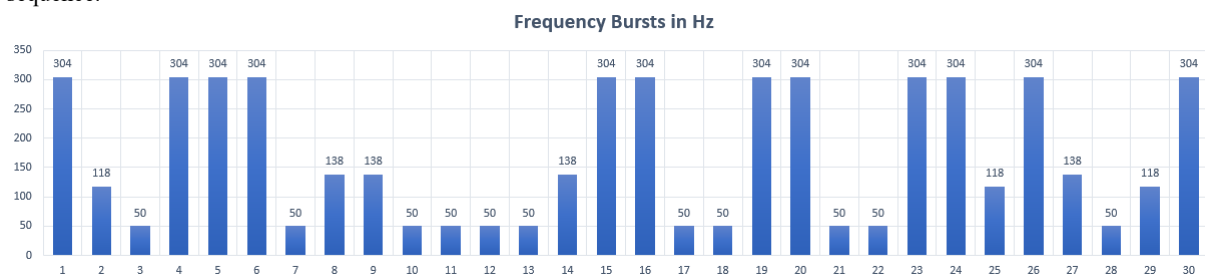


Fig. 70: Audio frequency bursts for first 30 nucleotides of S1: >NC\_001639.1 virus sequence



The waveform of the audio signal is described mathematically as  $s(t) = A(t) \cdot \sin[2\pi f(t) \cdot t + \phi(t)]$ . In our case,  $A(t)$  is a constant and the audio burst is on for time  $\tau$ . The function of time is determined by the pulse repetition frequency and the duty cycle. The frequency spectrum of such a sequence of rectangular pulses is represented by a  $(\sin x)/x$  function. Fig. 71 shows a sequence of rectangular amplitude modulated pulses and its frequency spectrum.

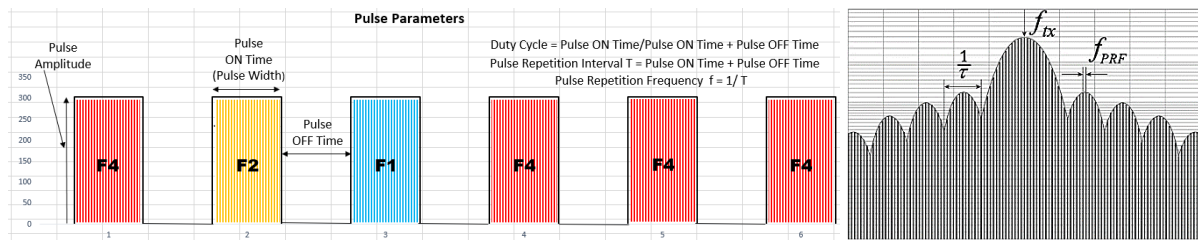


Fig. 71: Frequency spectrum of a sequence of rectangular amplitude modulated pulses

The essential parts of the audio transmission power are in a region  $B_{HF} = 2/\tau$  in the vicinity of the pulse frequency  $f_k$ . The audio burst bandwidth  $B_{HF}$  increases with decreasing pulse width like  $B_{HF} = \tau^{-1}$ . The shortening of the pulses limits the maximum range in the case of simple pulse modulation. Under these conditions, the pulse energy  $E_p$  is increased only by the pulse power  $P_s$  at a required virus target range. For the maximum range, the pulse energy is crucial, and not its pulse power:

$$E_p = P_s \cdot \tau = P_{av} \cdot T = \frac{P_{av}}{f_{PRF}} \quad \text{where} \quad \begin{array}{l} E_p = \text{energy content of the pulse} \\ P_s = \text{transmission pulse power} \\ P_{av} = \text{average power} \end{array}$$

Significant improvements could be achieved with the internal modulation of the transmitted pulse (intra-pulse modulation). The intra-pulse modulation is carried out in this case, using the frequencies  $f_s$ ,  $f_M$ ,  $f_p$  and  $f_{SS}$ . Due to intra-pulse modulation, the frequency spectrum would keep changing and the changes occur as per the nucleotides present in a virus genome. For example, let us consider the meta data of S1: >NC\_001639.1 Lactate dehydrogenase-elevating virus, complete genome. Then the bursts of sonic frequencies generated for the virus metadata mentioned above, are shown below as a sequence of frequency components separated with a timing symbol  $\sim$  that denotes the burst OFF time duration. This pulse OFF time duration could be varied from pulse to pulse, if needed. As outlined earlier, four discrete frequencies of  $f_s = 50\text{Hz}$ ,  $f_M = 138\text{Hz}$ ,  $f_p = 181\text{Hz}$ , and  $f_{SS} = 304\text{Hz}$  corresponding to the nucleotides Adenine, Thymine, Guanine and Cytosine are used here. Each pulse ON time and OFF time could be varied depending on prevailing context. In what is given below, the basic frequency of 50 Hz is assigned to Adenine. However, one can as well change the basic frequency as per the need. In fact, significant improvements have been achieved with this internal pulse modulation using the frequencies  $f_s$ ,  $f_M$ ,  $f_p$  and  $f_{SS}$ . The frequency spectrum changes occur as per the nucleotides present in the target virus genome S1: >NC\_001639.1 and the sequence of frequencies shown above is meant for dismembering it. These frequencies resonate with the natural frequencies of nucleotides and cause considerable physical change in the structure of the entire genome. **The efficacy of this technique of deactivating virus genome by sonic attack has to be checked, real time, by transmitting generated pulses to the actual target genome and by observing the changes in the shape of the genome.** The control parameters are (i) pulse width, (ii) pulse OFF time, (iii) amplitude of pulse and (iv) frequencies embedded inside the pulses.

### 5.3.1 Use of Ultrasound for deactivating virus genomes

What has been shown above is just an example to explain the 'Sonic Attack' technique. In fact, one should avoid audio signals of frequencies less than 10,000Hz because these sounds may cause damage to ears. Moreover, these signals are subharmonic, whereas the actual frequencies to be used to destroy a virus genome of length more than 20,000 bases should be near or ultrasonic frequencies above 10,000Hz. We have found that the base frequency  $f_s = 20,000\text{Hz}$  together with  $f_M = 20,088\text{Hz}$ ,  $f_p = 20,131\text{Hz}$  and  $f_{SS} = 20,254\text{Hz}$  would do a perfect job of dismembering the structure of virus genome. It is to be noted that one would require different frequency sequences for different virus genomes like F1 for S1, F2 for S2, F3 for S3 and so on, up to F130 for S130.

### 5.3.2 Pulse to Pulse Frequency Agile System

Alternatively, one could develop a random frequency sequence generator to produce only four discrete frequencies of  $f_s$ ,  $f_M$ ,  $f_p$  and  $f_{SS}$  and tune the generator to deactivate any real time virus genome. Fig. 72 shows a hypothetical block diagram that is self explanatory as to how to produce random frequency sequences. Apart from this, Phase Shift Keying (PSK) could also be incorporated as a part of intra-pulse modulation scheme to improve efficacy of the system.































2. Pairwise Spectral Correlation of SARS-Corona Viruses, London Journal of Research in Computer Science and Technology, London Journals Press, Volume 20 | Issue 2 | Compilation 1.0 Year 2020, pp 81-148

In this paper, a set of 130 virus genomes obtained from NCBI web site <https://www.ncbi.nlm.nih.gov/genbank/sars-cov-2-seqs/> has been analyzed and classified based on three quantificational measures (i) Four Level Auto Correlation Measures (ACMs), (ii) Percentage Concentration of Nucleotides and Pairwise Correlation Coefficients and (iii) JCP Golden Ratio (GR) values of the sequences. Moreover, a novel technique called '**Sonic Attack**' has been introduced which is expected to destroy the shape and structure of any kind of virus genome, be it inside the body or in the environment.

SARS-Corona like virus has been described in ancient ayurvedic scriptures about 5,000 years ago in a chapter called 'Krimi' i.e., infections, in the '**Charak Samhita**' that describes an infection exactly like the novel coronavirus. In the chapter 'Krimi', there is mention of a term called '**Sleshma Krimi**', which is described as something that cannot be seen by the naked eye as they are '**Maha Sukshma**' which means they are so minute that one needs a special instrument to see that.

ॐ त्र्यम्बकं यजामहे सुगन्धिं पुष्टिवर्धनम् ।  
उर्वारुकमिव बन्धनान् मृत्योर्मुक्षीय मामृतात् ॥

Om, We Worship the Tryambaka (the Three-Eyed One, Lord Shiva)  
Who is Fragrant (as the Spiritual Essence), Increasing the Nourishment (of our Spiritual Core);  
From these many Bondages (of Samsara) similar to Cucumbers (tied to their Creepers),  
May I be Liberated from Death (Attachment to Perishable Things), So that I am not separated from the perception  
of Immortality (Immortal Essence pervading everywhere)

ओम शांति शांति शांति ॥