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STUDY OF GENOME SEQUENCES USING GRAPH THEORY

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Abstract

This paper proposes a novel study of genome sequences using graph theoretic tools. A genome sequence is a characteristic sequence of four 'Nucleotides' such as 'Adenine', 'Thymine', Guanine, 'Cytosine'. These four macromolecules are represented by their first letters such as A, T, G and C respectively. Genome is entire set of DNA instructions found in a cell. Human genome consists of 23 pairs of chromosomes located in the cell's nucleus, as well as a small chromosome in the cell's mitochondria. Genome contains all relevant information needed for an individual to grow and function. Human genome contains about 3 billion nucleotides. A sequence of three consecutive nucleotides is called 'Codon', to be more specific, a 'Triplet Codon'. One can construct 64 triplet codons from four nucleotides. During protein synthesis inside a cell, the protein called 'Ribosome' makes use of sequence of triplet codons, chooses amino acids and builds required proteins. These triplet codons play a vital role in the cell action. In a codon sequence, adjacent codons overlap by one nucleotide or by two nucleotides. All hereditary properties of an individual are decided by these overlaps. This paper introduces the structure of overlapping and non-overlapping codons using graph theoretic tools.

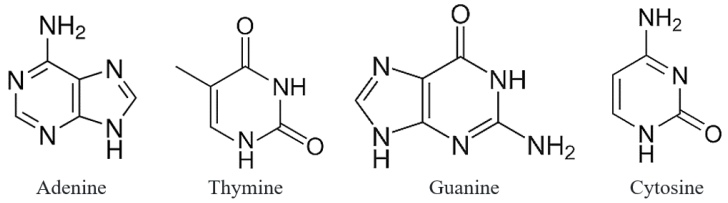
Keywords: Adenine', 'Thymine', Guanine,Codon,, 'Cytosine',DNA,RNA

1 Introduction

A codon is a DNA or RNA sequence of three nucleotides (a trinucleotide) that forms a unit of genomic information encoding a particular amino acid or signalling the termination of protein synthesis. There are 64 different codons, where 61 specify amino acids and 3 codons such as UAA, UAG and UGA are used as stop signal codons. The question that arises here is as to what extent graph theoretic tools could be used to study DNA/RNA sequences. Traditionally graphs were first used as a purely mathematical way to solve certain problems. One such problem was Königsberg Bridge Problem. 'Path Optimization and Logistics' is another application where graphs are used extensively. Computer networks are probably the easiest thing to represent as a graph since networking uses graphs to represent the layout of any computer network. Applications are many. Almost countless theorems and lemmas have been formulated since 1735. In spite of so much of work carried out in graph theory, it is hardly found in the literature, any application related to the study of DNA/RNA sequences. In fact, DNA/RNA sequences exhibit so much of geometric properties that advocate the effective use of graph theoretical concepts and tools for their analysis. This has been considered as a motivating factor for this research to be carried out.

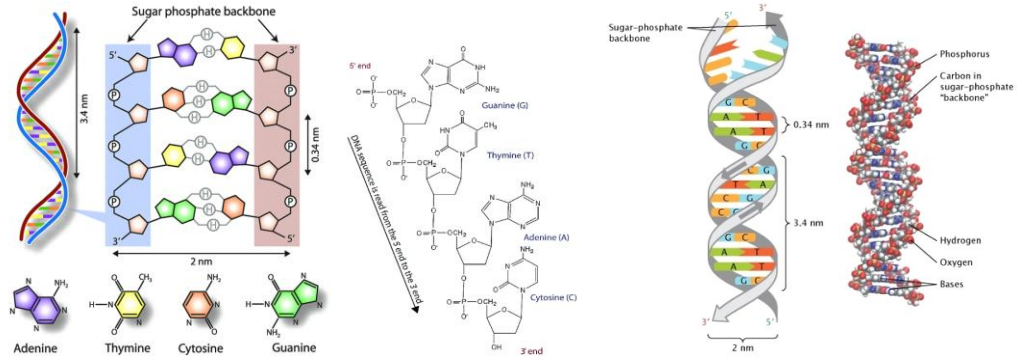
2. GENETIC CODE – A BRIEF DESCRIPTION

Let us denote a finite set of vertices by V. Let us denote the set of edges by E. Then e_1, e_2, e_3,..., e_n are edges, where E $\{\{v_i, v_j\} | v_i, v_j \in V$ and $v_i \neq v_j\}$. For example, let us consider the 64 triplet codons of a genome sequence. The molecular structures of four macromolecules known as 'Nucleotides' (i) Adenine, (ii) Thymine, (iii) Guanine and (iv) Cytosine are given below. These nucleotides concatenated chemically with what is called as 'Phosphodiester' bond in order to make a genome sequence. A genome sequence is represented as a characteristic sequence consisting of the symbols A (Adenine), T (Thymine), G (Guanine) and C (Cytosine).

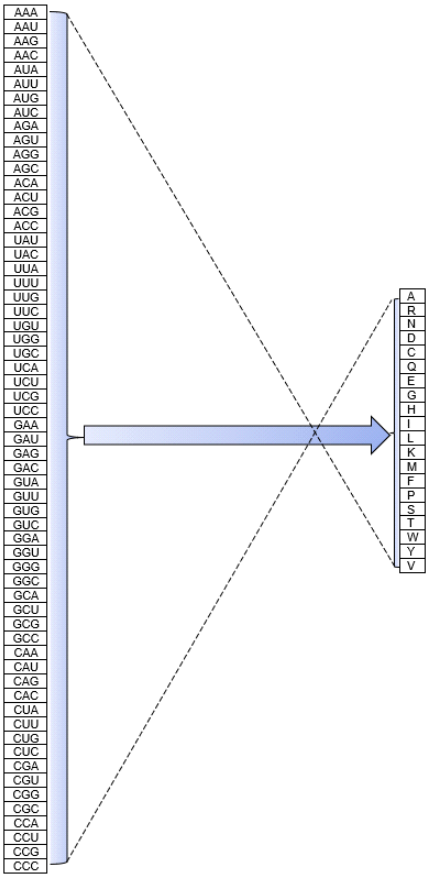


Molecular structures of purines and pyrimidines

Phospho-diester bond that builds a Genome Sequence and the double helical Structure of a Genome Sequence are shown in the figure given below. In terms of cellular molecular biology 'genome is a pair of DNA strands of nucleotides entwined in the form of a double helical structure. Each strand is made up of nucleotides chained with the help of 'phosphodiester bonds' and both the strands are entwined with the help of hydrogen bonds. Adenine (A) in one strand weekly pairs up with Thymine (T) in the other strand with the help of hydrogen bond. Similarly, Guanine (G) in one strand weekly pairs up with Cytosine in the other strand with the help of hydrogen bond. Even if the strands of the pair of a genome are separated forcibly inside the cell, they pair up once again with the help of hydrogen bonds. RNA polymerase (a protein inside a cell) makes use of one of the strands of the DNA double helix as template and synthesizes mRNA. This mRNA undergoes several processes and finally becomes a sequence of triplet 'codons'. As per the 'genetic code' dictated by DNA and represented by mRNA, amino acids are added one by one and get translated into polypeptidic sequences.



An RNA (codon sequence) consisting of N nucleotides would contain N/3 triplet codons, N/2 2-tuple codons and N single codons. Thus, one can construct $64^{N/3}$ triplet codon sequences, $64^{N/2}$ 2-tuple codon sequences and 64^{N} single codon sequences. A total of $(64^{N/3}+64^{N/2}+64^{N})$ of RNAs is said to constitute what we call as a finite 'Codon Space'. An infinite 'Codon Space' denoted by the symbol C is potentially realized as the limit of N of $(64^{N/3}+64^{N/2}+64^{N})$. Of all the 64 codons, three are known as termination codons or stop codons, which do not code for any amino acid. They are UAA, UAG and UGA. They act as stop signals for protein synthesis. Remaining 61 codons actually code for 20 amino acids. Refer to figure given below.

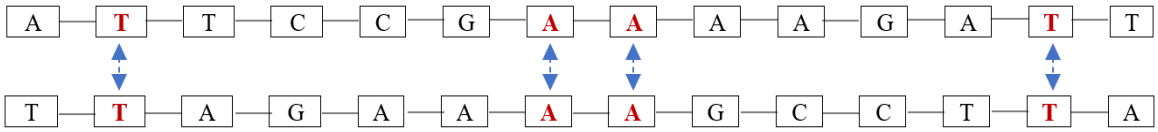


The graph $K_{61,20}$ shown above shows 1220 edges. This means there are 1220 correspondences between 61 codons and 20 amino acids. The combinatorics of 1220 correspondences having one at a time, two at a time, and so on up to 1220 at a time amounts to ${}^{1220}C_1 + {}^{1220}C_2 + {}^{1220}C_3 + \ldots + {}^{1220}C_{1220}$ edges (correspondences). This is called '**Genetic Code**'.

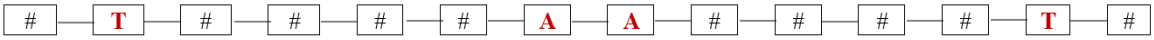
20 Amino Acids			
• alanine - ala - A • arginine - arg - R • asparagine - asn - N • aspartic acid - asp - D • cysteine - cys - C	• glutamine - gln - Q • glutamic acid - glu - E • glycine - gly - G • histidine - his - H • isoleucine - ile - I	• leucine - leu - L • lysine - lys - K • methionine - met - M • phenylalanine - phe - F • proline - pro - P	• serine - ser - S • threonine - thr - T • tryptophan - trp - W • tyrosine - tyr - Y • valine - val - V

3. DYADIC INTERSECTION OF LINEAR UNDIECTED GRAPH AND ITS INVERSE

Here we consider a finite genome sequence as a linear undirected graph with 14 vertices and 13 edges and its graphical inverse as shown below. Let us compare these two graphs, vertices wise, and match the vertices and study the properties.



Let us retain the matching vertices and replace the vertices which are not matching by the symbol #. The resulting graph is shown below. The sequence of matched vertices forms a palindrome sequence.



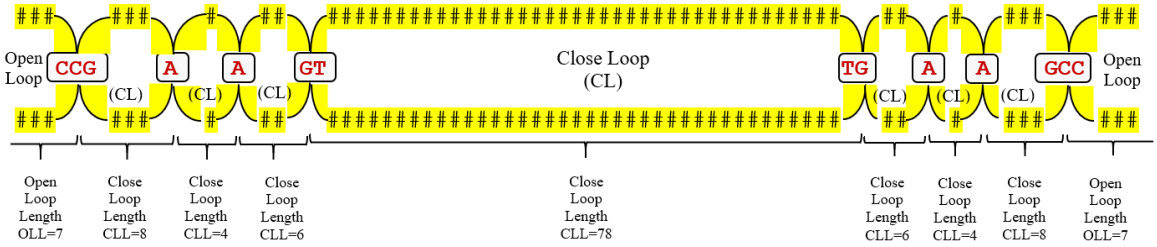
The following proposition holds for any type of alphanumerical sequence.

Proposition 1: "Given any arbitrary numerical or alphanumerical sequence x_1 of length N, one may obtain its graphical inverse as x^{-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".

The above proposition has been verified to be correct by testing 130 virus genome sequences drawn from the NCBI website https://www.ncbi.nlm.nih.gov/. Let us consider the first 70 nucleotides of a virus genome sequence S_1 and its graphical inverse S_1^{-1}. Let us compare the first 70 nucleotides of the virus genome S_1 and its inverse S_1^{-1}.

S_1	ATTCCGAAAA GATTGTGTGA ACCCGTGCGG TAACCGTCTA TTTCAAGGAG CCACTGGGAC AGTGGCCCGC
S_1^{-1}	CGCCCGGTGA CAGGGTCACC GAGGAACTTT ATCTGCCAAT GGCGTGCCCA AGTGTGTTAG AAAAGCCTTA

The pairwise intersection of S_1 and S_1^{-1} denoted as $S_1S_1^{-1}$ is **CCGAAGTTGAAGCC**. This sequence could be seen to be a palindrome sequence. The unmatched symbols are denoted by the don't care symbol #. With reference to the figure given below, the resulting pair of sequences is represented as:

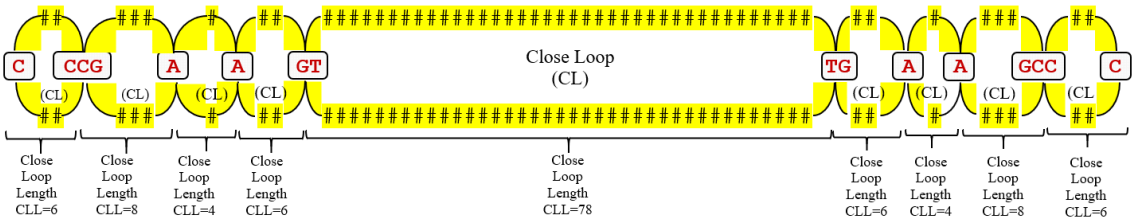


where # refers to don't care symbol, OLL refers to 'Open Loop Length', and CLL refers to 'Closed Loop Length'. The value of an OLL is calculated as 2n+1, where 'n' is the number of don't care symbols present in the pair of sequences. The value of a CLL is calculated as 2n+2, where 'n' is the number of don't care symbols present in a single strand. The OLL and CLL values calculated for the above example pair $S_1S_1^{-1}$ 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 $S_1S_1^{-1}$ is an open-ended pair**. Now the graphical inverse of the sequence $S_1S_1^{-1}$ denoted as $(S_1S_1^{-1})^{-1}$ is **CCGAAGTTGAAGCC**. It is observed that $S_1S_1^{-1} \doteq (S_1S_1^{-1})^{-1}$, where the symbol $\doteq$ denotes the binary relation '**graphical equivalence**', meaning the sequence is a palindrome. Moreover, the sequence of loop values {7, 8, 4, 6, 78, 6, 4, 8, 7} also exhibits palindrome property. In this case, the maximum CLL value is 78 and the minimum CLL value is 4.

Let us consider another sequence S_2 and its inverse S_2^{-1}

S_2	CTTCCGAAAA GATTGTGTGA ACCCGTGCGG TAACCGTCTA TTTCAAGGAG CCACTGGGAC AGTGGCCCGC
S_2^{-1}	CGCCCGGTGA CAGGGTCACC GAGGAACTTT ATCTGCCAAT GGCGTGCCCA AGTGTGTTAG AAAAGCCTTC

The pairwise intersection of S_2 and S_2^{-1} denoted as $S_2S_2^{-1}$ is **CCCGAAGTTGAAGCCC**. Now the graphical inverse of the sequence $S_2S_2^{-1}$ denoted as $(S_2S_2^{-1})^{-1}$ is **CCCGAAGTTGAAGCCC**. It is observed that $S_2S_2^{-1} \doteq (S_2S_2^{-1})^{-1}$, where the symbol $\doteq$ 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 $S_2S_2^{-1}$ is given as {CLL=6, CLL=8, CLL=4, CLL=6, CLL=78, CLL=6, CLL=4, CLL=8, OLL=6} or simply written as {6, 8, 4, 6, 78, 6, 4, 8, 6}. **Note that the sequence pair $S_2S_2^{-1}$ is a close-ended pair.** In this case also, the maximum CLL value is 78 and the minimum CLL value is 4.

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)**'.

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

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, $x_2 \doteq x_2^{-1}$. 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: One can interpret a discrete Hibert space l_N: (N), 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 3: Every SSI based subspace of the discrete Hibert space l_N: (N) is potentially denumerable. This proposition is a self-evidential truth.

5. DYADIC PAIRING OF NUCLEOTIDES IN A SEQUENCE AND ITS INVERSE

The following proposition holds for any type of genome sequence.

Proposition 4: Given any arbitrary nucleotides sequence x_1 of length N, one may obtain its inverse as x^{-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 <A,T>, <T,A>, <G,C> and <C,G> forms a palindrome sequence.
Let us consider the example sequence S_1 and its inverse S_1^{-1}. Let us carry out natural pairing of the sequence S_1 and its inverse S_1^{-1} and form the sequence of natural pairs as shown below.

S_1	ATTCCGAAAA GATTGTGTGA ACCCGTGCGG TAACCGTCTA TTTCAAGGAG CCACTGGGAC AGTGGCCCGC
S_1^{-1}	CGCCCGGTGA CAGGGTCACC GAGGAACTTT ATCTGCCAAT GGCGTGCCCA AGTGTGTTAG AAAAGCCTTA

The sequence of natural pairs of nucleotides along with don't care symbols is given below.
#######<A,T>########<G,C><T,A><G,C>###<C,G><C,G>#<T,A><G,C>### <T,A><A,T>##<C,G><G,C>##<T,A><A,T>###<C,G><A,T>#<G,C><G,C>###<C ,G><A,T><C,G>########<T,A>#######

Now, the sequence of natural pairs of nucleotides along with loop lengths is given below, and this could be seen to be a palindrome sequence.
15<A,T>18<G,C><T,A><G,C>8<C,G><C,G>4<T,A><G,C>8<T,A><A,T>6<C,G><G,C>6<T,A><A,T>8<C,G><A,T>
4<G,C><G,C>8<C,G><A,T><C,G>18<T,A>15

Proposition 5: Given any arbitrary nucleotides sequence x_1 of length N, one may obtain its inverse as x^{-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 <A,C>, <C,A>, <T,G> and <G,T> forms a palindrome sequence.

Let us consider the same example sequence S_1 and its inverse S_1^{-1}. Let us carry out unnatural pairing of the sequence S_1 and its inverse S_1^{-1} and form the sequence of unnatural pairs as shown below.

S_1	**AT**TCCGAAAA GA**TT**GTGTG**A** A**C**CCGTGC**GG** TA**A**CCGT**C**TA **TT**TCAAGG**A**G **C**CACTG**GG**AC AGTGGCCC**GC**
S_1^{-1}	**CG**CCCGGTGA CA**GG**GTCAC**C** G**A**GGAACT**TT** AT**C**TGCC**A**AT **GG**CGTGCC**C**A **A**GTGTG**TT**AG AAAAGCCT**TA**

The sequence of unnatural pairs of nucleotides along with don't care symbols is given below.
<A,C><T,G>##########<T,G><T,G>#####<A,C>#<C,A>######<G,T><G,T>##<A,C>####<C,A>##<T,G><T,G>######<A,C>#<C,A>#####<G,T><G,T>##########<G,T><C,A>
The sequence of unnatural pairs of nucleotides along with loop lengths is given below, and this could be seen to be a palindrome sequence.
<A,C><T,G>22<T,G><T,G>12<A,C>4<C,A>14<G,T><G,T>6<A,C>10<C,A>6<T,G><T,G>14<A,C>4<C,A>12<G,T>
<G,T>22<G,T><C,A>

6. CASE STUDY

A Python based computational tool for dyadic intersection of a sequence and its inverse is applied to 130 actual virus genome sequences drawn from NCBI website. All the five propositions stated in this paper were found to be correct. The list of 130 virus genomes is given below.
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 Chalara 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 GmGlV1-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

 Volume 21 | Issue 1 | Compilation 1.0 41
London Journal of Research in Computer Science and Technology
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
Keywords: corona type viruses, golden ratios, percentage concentrations of nucleotides, artificial intelligence, sonic bursts.

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_012533.1 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 tymo-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 Phaseolus 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 Bouboui 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

Piscanivirinae

S118. >NC_008516.1 White bream virus, complete genome
42 Volume 21 | Issue 1 | Compilation 1.0 © 2021 London Journals Press London Journal of Research in Computer Science and Technology
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
S119. >NC_026812.1 Chinook salmon bafinivirus isolate NIDO, complete genome
S120. >NC_038295.1 Fathead minnow nidovirus replicase polyprotein 1ab (pp1ab), replicase polyprotein 1a (pp1a), spike
glycoprotein (S), membrane protein (M), and nucleocapsid protein (N) genes, complete cds

Remotovirinae

S121. >NC_027199.1 Bovine nidovirus TCH5, complete genome

Serpentovirinae

S122. >NC_024709.1 Ball python nidovirus strain 07-53, complete genome
S123. >NC_033700.1 Xinzhou toro-like virus strain XZSJSC65757 1ab, putative glycoprotein, and hypothetical protein genes,
complete cds
S124. >NC_035465.1 Morelia viridis nidovirus strain S14-1323_MVNV, complete genome

Torovirinae

S125. >NC_007447.1 Breda virus, complete genome
S126. >NC_022787.1 Porcine torovirus strain SH1, complete genome
S127. >NC_034976.1 Goat torovirus strain SZ, complete genome
S128. >NC_046956.1 Bellinger River virus isolate J248, complete genome
S129. >NC_046962.1 Hainan hebius popei torovirus strain LPSC33749 1ab protein, spike protein, and hypothetical protein genes, complete cds
S130. >NC_046963.1 Guangdong red-banded snake torovirus strain LPSF30546 1ab protein, spike protein, hypothetical protein, and putative glycoprotein genes, complete cds

Courtesy: https://www.ncbi.nlm.nih.gov/genomes/GenomesGroup.cgi

7. RESULTS AND CONCLUSIONS

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 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 (MLL) 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
1	S1	58	3
2	S2	54	4
3	S3	46	3
4	S4	50	3
5	**S5**	**70**	3
6	S7	66	4
7	S8	52	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

1	**S6**	**88**	4
2	S10	56	4
3			4
4	S15	58	4
5	S16	66	4
6			4
7	S18	58	4
8			4
9			4
10	S40	64	4
11	S48	70	4
12	**S75**	**42**	4
13			4
14			4
15			4
16	**S87**	**52**	4
17	**S94**	**44**	4
18	S96	72	4
19	S99	62	4
20	S105	54	4
21			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

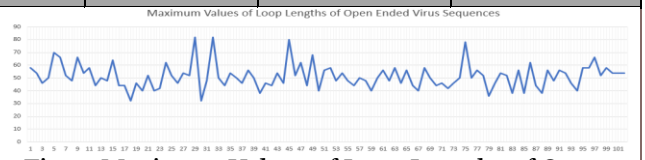


Fig. 1: Maximum Values of Loop Lengths of Open-Ended Sequences

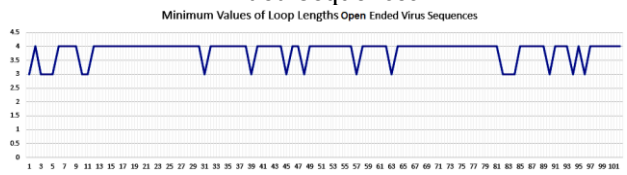


Fig. 2: Minimum Values of Loop Lengths of Open-Ended Sequences

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
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

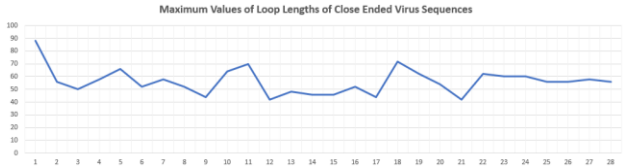


Fig. 3: Maximum Values of Loop Lengths of Close-Ended Sequences

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.

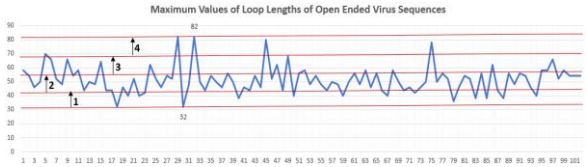


Fig. 4: MLL values of open-ended virus genomes with four levels

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) 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

98	S123	52	4
99	S125	58	4
100	S126	54	4
101	S127	54	4
102	S130	54	4

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.

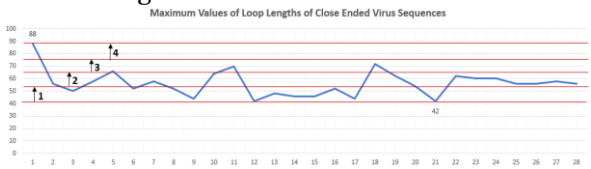


Fig. 5: MLL values of close-ended virus genomes with four levels

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

- 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.
- 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.
- 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.
- 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.

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