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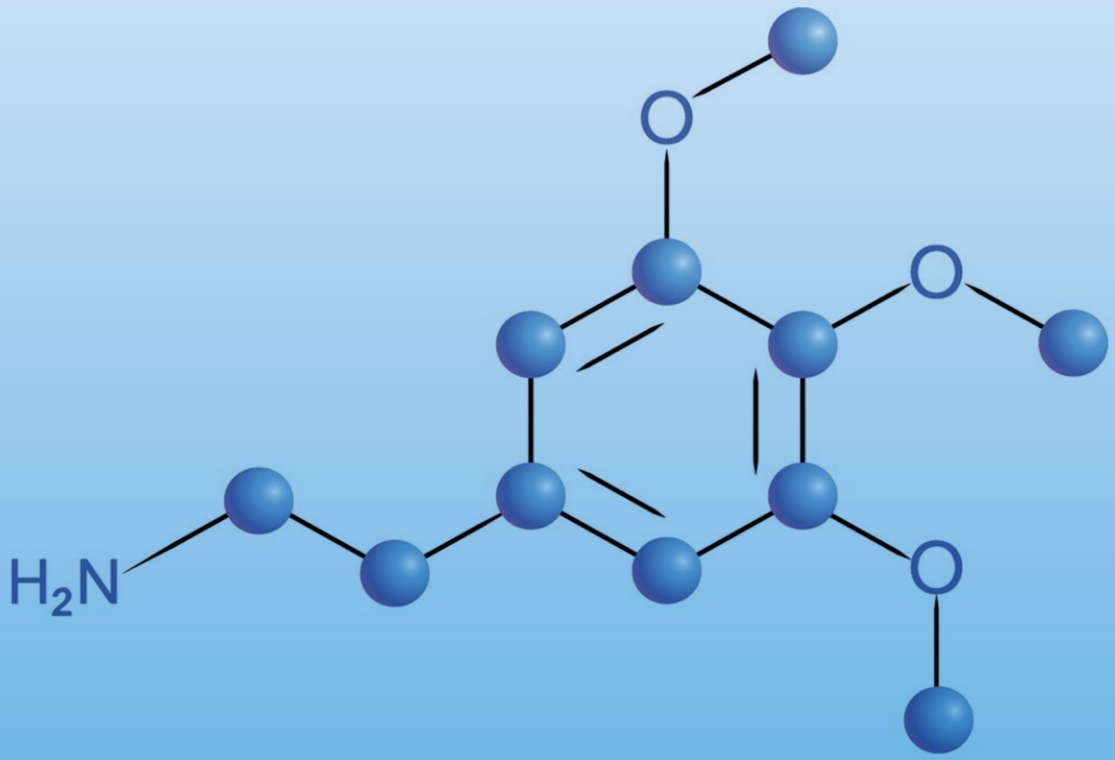

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Table of Contents

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Application of Graph Entropy in CRISPR and Repeats Detection in DNA Sequences

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Abstract

We analyzed DNA sequences using a new measure of entropy. The general aim was to analyze DNA sequences and find interesting sections of a genome using a new formulation of Shannon like entropy. We developed this new measure of entropy for any non-trivial graph or, more broadly, for any square matrix whose non-zero elements represent probabilistic weights assigned to connections or transitions between pairs of vertices. The new measure is called the graph entropy and it quantifies the aggregate indeterminacy effected by the variety of unique walks that exist between each pair of vertices. The new tool is shown to be uniquely capable of revealing CRISPR regions in bacterial genomes and to identify Tandem repeats and Direct repeats of genome. We have done experiment on 26 species and found many tandem repeats and direct repeats (CRISPR for bacteria or archaea). There are several existing separate CRISPR or Tandem finder tools but our entropy can find both of these features if present in genome.

Keywords

CRISPR, Graph Entropy, Tandem Repeats, DNA Sequences

1. Introduction

Deciphering the enormously long nucleotide sequences that are being uncovered in the human genome is one of the major challenges in our days. Along with serious ethical issues, we encounter a series of tremendously hard scientific problems. These problems mainly arise from the fact that although sequencing techniques are almost completely automatic controlled the analysis of the sequenced data is not. Hence, the major goal of the Human Genome Project is the extraction of biologically and medically relevant information from almost automatically sequenced DNA and RNA molecules. In prin-

ciple, biochemical methods are able to do this job, but since they are extremely expensive and time consuming, there is a high demand for alternative approaches to extract the information hidden in genome [1]. In this situation, concepts and techniques from information theory turned out to be welcoming tools to handle the problem of extracting valuable information from biosequences such as DNA, RNA, or amino acid chains. The main goal of our work is the presentation of a concept and method derived from information theory that will apply to problems of analysis of DNA.

The motivation for this study is to analyze DNA sequences to determine interesting sections of genome that has repeating features using information theory tool.

In many organisms, the genomic DNA is highly repetitive accounting for close to 5% of the genome size [2] [3]. Repetitive DNA sequences are a major component of eukaryotic genomes and may account for up to 90% of the genome size [4]. The human genome itself has over two-thirds of the sequence consisting of repetitive elements [5]. The identification of repeats has proven to be of significance, as they provide insight into the functional and evolutionary roles of various organisms [6] [7] [8] [9] [10].

In our study we also focus on a family of repeats known as Clustered Regularly Inter Spaced Palindromic Repeats (CRISPRs) [11]. CRISPRs have attracted a great deal of interest recently in genome editing [12]. CRISPRs have been found only in the genomes of prokaryotes and are composed of short direct repeats currently known to range in sizes from 21 - 47 base pairs. This family of repeats is unique in that they are interspaced by non-repeating sequences of similar size, called spacers. CRISPRs were found in approximately 40% of bacterial genome investigated [13].

Several software applications are available for identifying various form of repeats in [14] [15] [16].

2. Graph Entropy Algorithm

A graph is an object that consists of a non-empty set of vertices and another set of edges. Vertices are often called nodes, and edges are referred as connections. The set of edges may be empty, in which case the graph is just a collection of points.

We say that two vertices i and j of a directed graph are connected if there is an edge from i to j or from j and i. Suppose we are given a directed graph with n vertices. We construct an $n \times n$ adjacency matrix A associated to it as follows: if there is an edge from vertex i to vertex j, we put 1 as the entry on row i, column j of the matrix A; if there is no edge, we put 0.

If one can walk from vertex i to vertex j along the edges of the graph then we say that there is a path from i to j. If we walked on k edges, then the path has length k. For matrices, we denote by A^k the matrix obtained by multiplying A with itself k times. The entry on row i, column j of A^2 corresponds to the number of paths of length 2 from vertex i to vertex j in the graph.

Let us consider a directed graph and a positive integer k. Then the number of directed walks from vertex i to vertex j of length k is the entry on row i and column j of the matrix A^k, where A is the adjacency matrix.

In this section, we will discuss entropy of such adjacency matrix *A*. Let $\{v_1, v_2, ..., v_n\}$ be a set of vertices of a direct graph. Let $A = (a_{ij})$ be the $n \times n$ adjacency matrix with at least one positive element.

Let $\sum_{i,j}^{n} a_{ij} = N$. Let $P = (P_{ij})$ be the matrix such that $P = \frac{A}{N}$. Hence $\sum_{i,j}^{n} p_{ij} = 1$. p_{ij} is the probability of having a path from vertex v_i to vertex v_j. Adding all elements of each row of P and placing them on the diagonal, we form a diagonal matrix

$$\theta = \begin{pmatrix} \sum_{k=1}^{n} p_{1k} & \cdots & 0 \\ \vdots & \cdots & \vdots \\ \vdots & \cdots & \vdots \\ \vdots & \cdots & \vdots \\ 0 & \cdots & \sum_{k=1}^{n} p_{nk} \end{pmatrix} = (\theta_{ij})$$

$1 - \theta_{jj} = \left(1 - \sum_{k=1}^{n} p_{jk}\right)$ is the probability for a randomly generated path to end at the vertex v_j. Let $Q_{ij}(l)$ be the probability for generating a path of length *l* that begins at v_i and ends at v_j for any integer *l*. For example, we have $Q_{ij}(1) = p_{ij}\left(1 - \sum_{k=1}^{n} p_{jk}\right)$ and $Q_{ij}(2) = (p_{i1}, p_{i2}, ..., p_{in}) \begin{pmatrix} p_{1j} \\ \vdots \\ p_{nj} \end{pmatrix} \left(1 - \sum_{k=1}^{n} p_{jk}\right)$. Let Q_l be the matrix whose *ij* element is $Q_{ij}(l)$. Then we have $Q_l = P^I (I - \theta)$. Finally, we define the asymptotic walk matrix $\Omega = (\Omega_{ij})$ as $\Omega \equiv \sum_{l=1}^{\infty} Q_l$, Where Ω_{ij} is the probability for generating a walk of any length from v_i to v_j.

Note that $\sum_{i,j} \Omega_{ij} = 1$. $\Omega \equiv \sum_{l=1}^{\infty} Q_l = P(I - \theta) + P^2 (I - \theta) + \cdots$

We noticed that the sum of all entrees of the matrix $P^{\lambda}(Q - P)$, for any integer λ, is 0. Since sum of all entrees of P is 1, sum of all entrees of Ω is also1. We therefore define the asymptotic entropy

$$H(P) = -\sum_{i,j} \Omega_{ij} \log(\Omega_{ij})$$

where $\Omega_{ij} \log(\Omega_{ij})$ is defined to be 0 for $\Omega_{ij} = 0$. This can also be called the graph entropy of the graph or entropy of the adjacency matrix *A*. For illustration, Let us consider a short sequence:

ATGCCTGATGCGACGC

Taking 2-letter nodes with one overlap, we can create a graph as following:

$$AT \to TG \to GC \to CC \to CT \to TG \to GA \to$$
$$AT \to TG \to GC \to CG \to GA \to AC \to CG \to GC$$

We draw a graph as in the Figure 1.

For our sequence, graph entropy

$$\mathrm{H}(P) = -\sum_{i,j} \Omega_{ij} \log(\Omega_{ij}) \approx 2.9614$$

3. Results

We have downloaded wide range of genome data, eukaryotes (animals, plants, insects, fungus) and prokaryotes (bacteria, archaea) from Gen Bank: ftp://ftp.ncbi.nlm.nih.gov/genomes/.

We have implemented the Graph Entropy Algorithm in MATLAB platform and converted data to MATLAB format. Then we have computed graph entropy using our Graph Entropy Algorithm by scanning the data with a typical sample size of 512 base pairs (bp) and step size of 10 bp taking 3 nodes with 1 overlap. We have drawn graphs of entropy versus genome length of Acidovorax bacteria in Figure 2, Salmonella-Typhi CT18 bacteria in Figure 3, Caldicellulosiruptor Kristianssonii bacteria in Figure 4 and Human Chromosome-21 in Figure 5. We have studied the intervals visually where entropy was low and found some repetitive pattern in the sequence. Once we have a string of repetitive pattern we used MATLAB "strfind" command to find out exact positions of the repetitive patterns. We have included few examples in this paper, only the ones we thought important.

In Figure 2 we looked at the lowest drop of entropy which is at: x: genome length = 871,100, y: entropy = 4.088. We took an interval (871,000, 871,600) around the lowest drop x = 871,100.

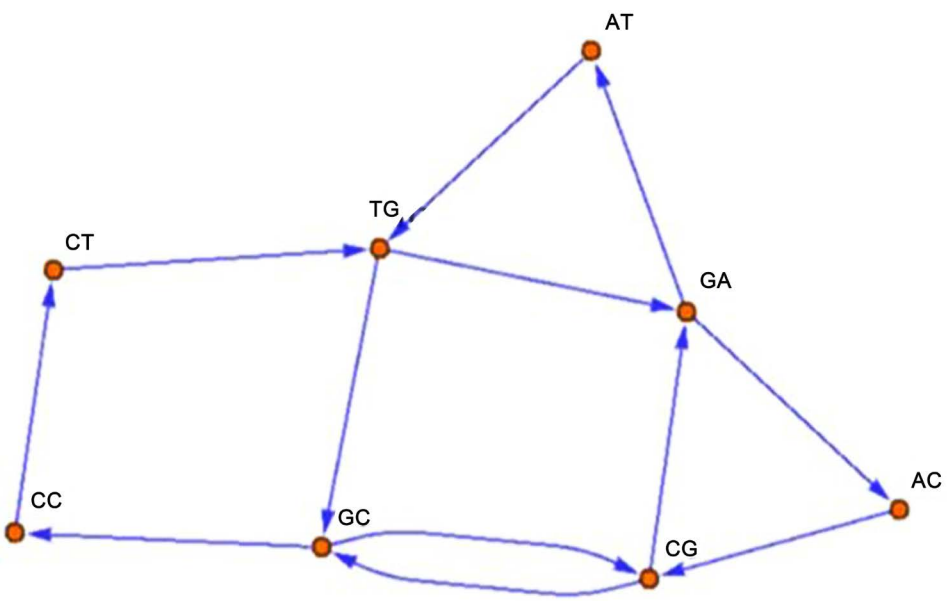

Figure 1. Example of DNA graph.

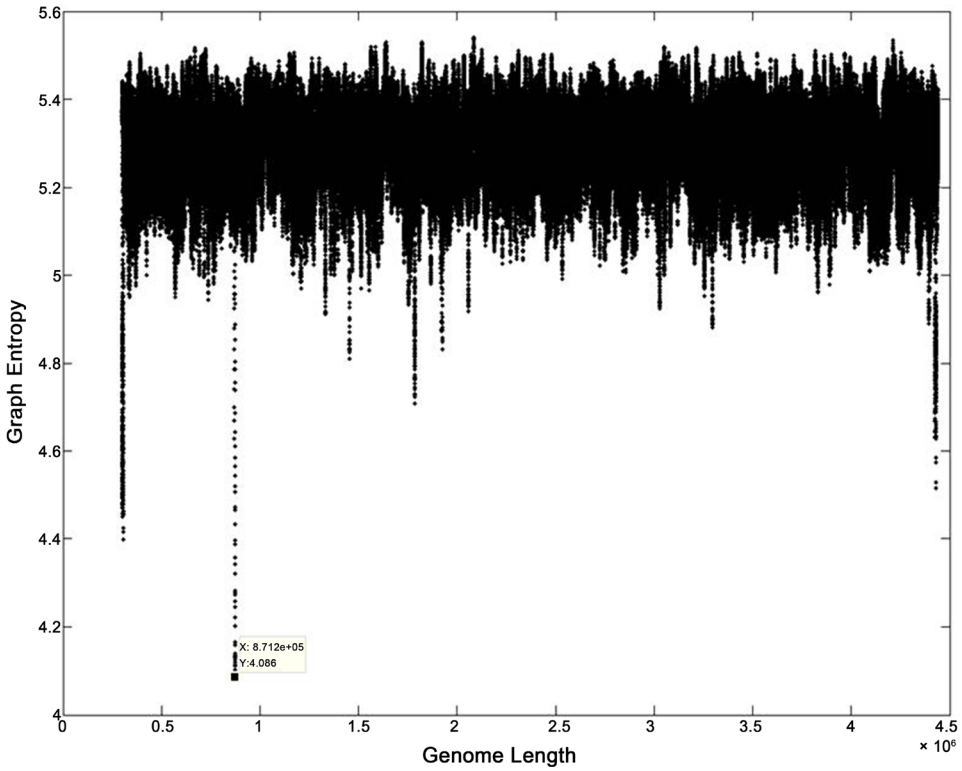

Figure 2. Acidovorax (bacteria) genome length vs entropy.

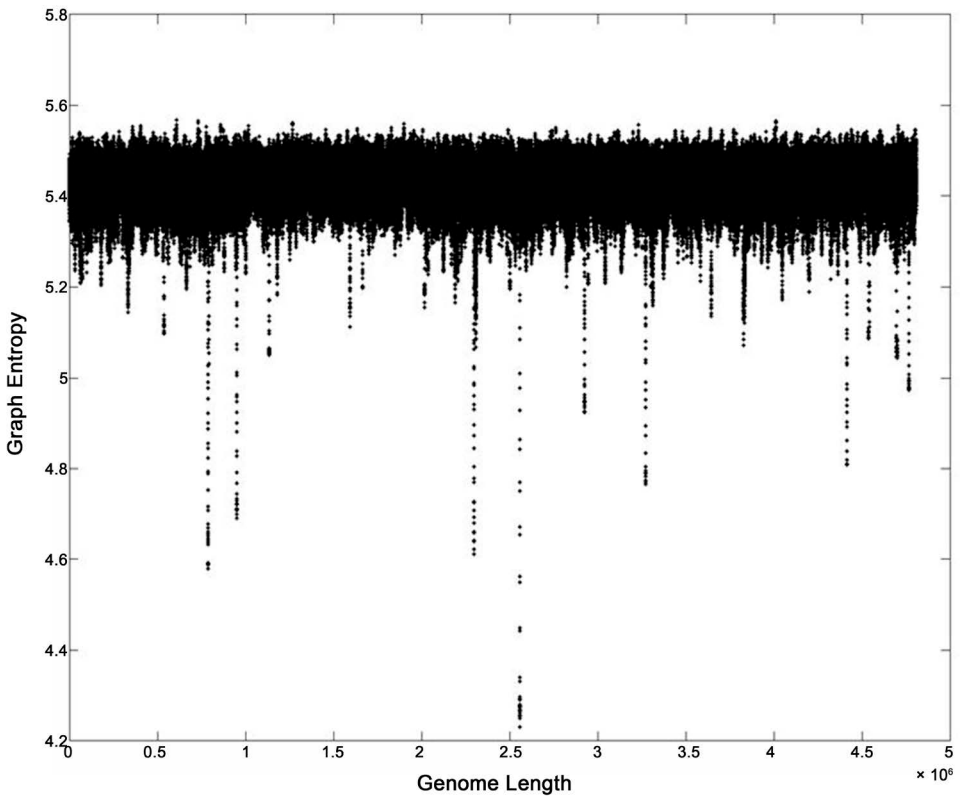

Figure 3. Salmonella-typhi CT18 (bacteria).

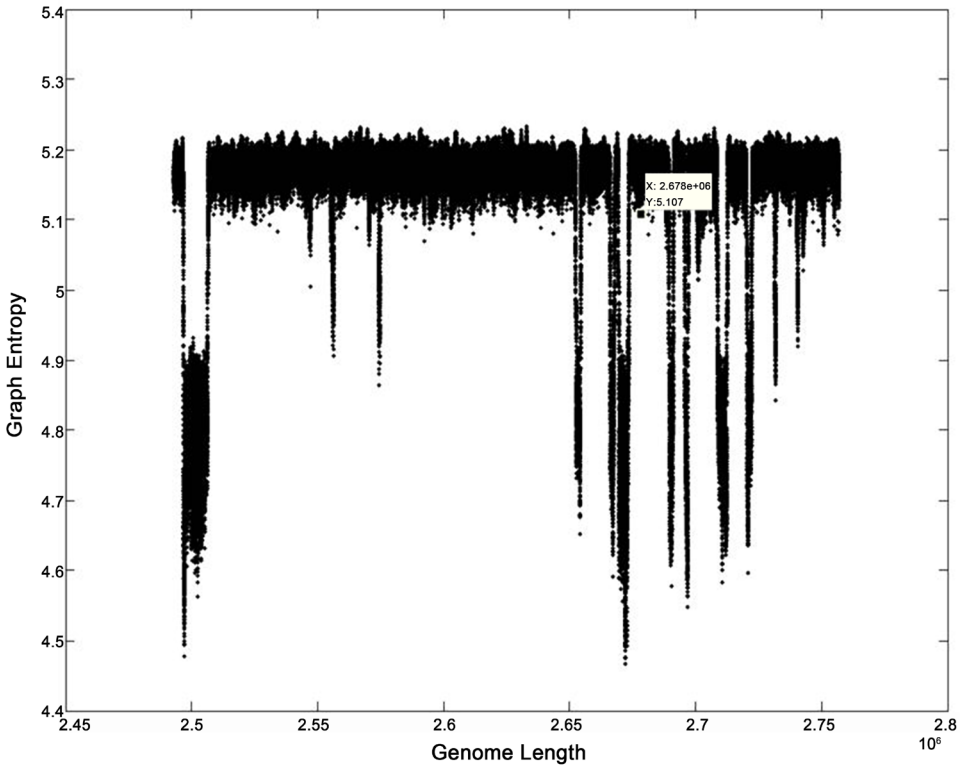

Figure 4. Caldicellulosiruptor kristianssonii (bacteria).

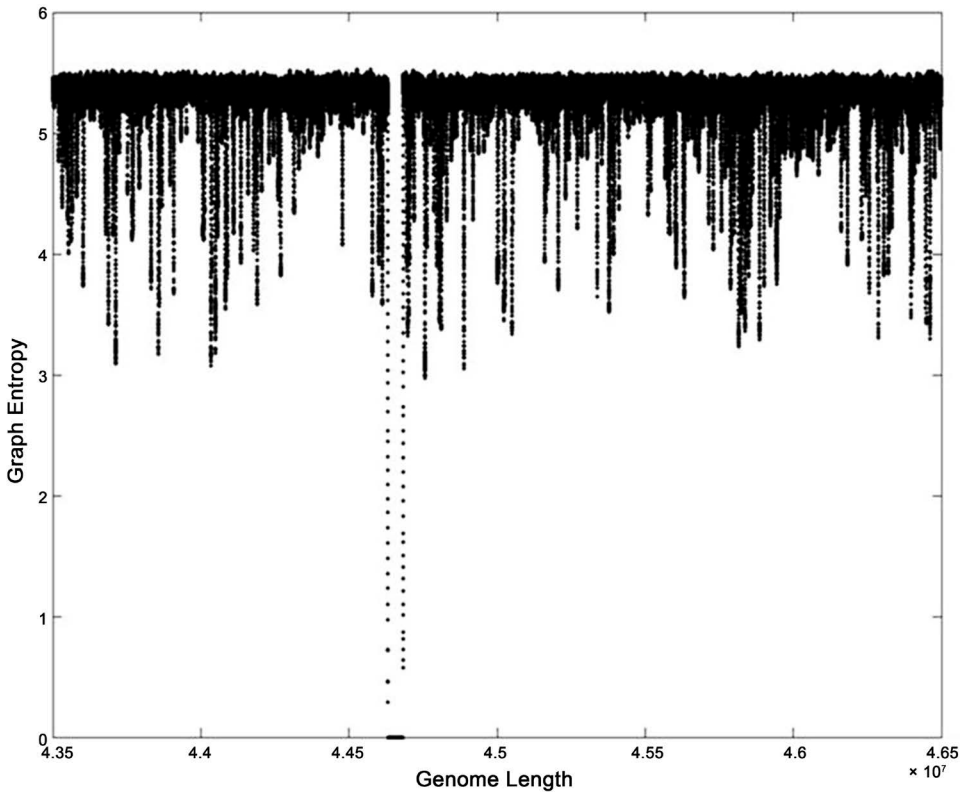

Figure 5. Human chromosome-21.

The following is the sequence in the interval taken. The colored string is repeating.

ATAAAAAAACCCGGTGCATGCACCGGGTGGGACCAGCCCCGCGGGCGG
GGCGGCTGGCTGCTGTCGTCGCTCAGGGCTTGGTGCCCGTCGGGAAGGG
CCATGCGGCCTGCGGGTTCAGCGTGGTCTGTGCTGCGGGTGCAGGCGCA
GGGGCAGAGGCCTTGGAGGCCGCCTTTTTCGGGGCAGCCTTCTTCGGTG
CAGCGGCCTTGGTCGTGCCGGTGGCCTTCTTCGCCGGTGCAGCTGCCTTC
TTGGTGGAGGCTGCGGCCTTCTTTGCCGGTGCAGCTGCCTTCTTGGCGG
GGGCTGCGGCCTTCTTCGCCGGTGCAGCTGCCTTCTTGGCGGGGGCTGC
GGCCTTCTTTGCCGGTGCAGCTGCCTTCTTGGCAGGAGCTGCGGCCTTCT
TTGCCGGTGCAGCTGCCTTCTTGGCGGGGGCTGCGGCCTTCTTTGCCGGT
GCAGCTGCCTTCTTGGCAGGAGCTGCGGCCTTCTTTGCCGGTGCAGCTG
CCTTCTTGGCAGGAGCTGCGGCCTTCTTTGCCGGTGCAGCTGCCTTCTTG
GCGGGGGCTGCAGCCTTCTTCGCCGGAGCGGCCTTCTTCGTCGTGGCGG
CGGCCTTCTT

Strfind(g,'GCCGGTGCAGCTGCCTTCTTGG') command gave us the following positions of those repeats in the sequence.

871227 871269 871311 871353 871395 871437 871479 871521

The spacers are almost identical. These are tandem repeats.

Similarly in the **Figure 3** we looked at the lowest drop of entropy which is at x = 2926000 y = 4.923.

We looked at the DNA sequence in the interval (2926000:2926650) around x = 2926000. The following is the sequence in the interval taken. The colored string is repeating.

AAAAATGCATCCTTCCCGAACGGCAATAGCTGGCACGACGTACGGCTTG
ATAATCAACAGCATATAGACAAGGCGCTGCCAGGGCGGATTGAGCGCCG
TAGCCGCGATGTAGTGCGGATAATGCTGCCGTTGGTAAAAGAGCTGGCG
AAGGCGGAAAAAACGTCCTGATATGCTGGTGAAACGTGTTTATCCCCGC
TGGCGCGGGGAACACGGACAGCAACCCGTGTCGGATATCAGACAGATCG
GTTTATCCCCGCTGGCGCGGGGAACACACGCGAATCGCCAATCGCCGCC
GCGTGAATTGCGGTTTATCCCCGCTGGCGCGGGGAACACCCACGATGTA
TGCCGACCGTGATTTTTACCGCCGGTTTATCCCCGCTGGCGCGGGGAAC
ACAGATACGCCTTTACGTCGCCCTCTTTGGCGCGCGGTTTATCCCCGCTG
GCGCGGGGAACACTAAAACACCGGTTGCGCAACCTCCGCGGGGATCGGT
TTATCCCCGCTGGCGCGGGGATCGGTTTATCCCCGCTGGCGCGGGGATC
GGTTTATCCCCGCTGGCGCGGGGAACACTCTAAATCTACCCAATTGAATT
TAAATACTTTTTTAGCGCACAAAAAACCCACCAACTTTTCCTAATTTTTA
AAGATCTCTAA

We used strfind(g,'CGGTTTATCCCCGCTGGCGCGGGGAACAC') in MatLab and found more repeats outside the interval.

2926243 2926304 2926365 2926426 2926539 2943184 (does not be-

long to this region).

length('CGGTTTATCCCCGCTGGCGCGGGGAACAC')=29

strfind(g,'GTGTTTATCCCCGCTGGCGCGGGGAACAC'): 2926182

strfind(g,'CGGTTTATCCCCGCTGGCGCGGGGATCGG') 2926487 2926513.

Starts: 2926182 Ends: 2926567.

In the interval (2926182, 2926513) we find three strings differing by 2 to 4 letters.

These repeats are called CRISPR. This is only CRISPR so far known for this strain of the bacteria.

Again, we studied the pattern of the DNA sequence of Caldicellulosiruptor Kristianssonii (Bacteria) in intervals around the points of low entropy and found repetitive patterns. In **Figure 4**, we considered the drop at x = 2,672,000, y = 4.46. Following is the sequence in the interval (2671900, 2672600) around this drop. The repeats are shown in red color.

TATTGCAATTATTGTCCTATGCACAGAGTTTGTAGCCTTCCCGTTGGGGA
TTGAAACATAGATTTCATTTCGCAGCCAATAGAGCGGTTTATAGTTTGTA
GCCTTCCCGTTGGGGATTGAAACCTCAATTTCTGTTTCTCTTTTCTCAATT
ATTCTTGAGTTTGTAGCCTTCCCGTTGGGGATTGAAACTATAATAGCCCA
TTCATCAAAAACTTTTTCATCGAAGTTTGTAGCCTTCCCGTTGGGGATTG
AAACTATAATAGCCCATTCATCAAAAACTTTTTCATCGAAGTTTGTAGCC
TTCCCGTTGGGGATTGAAACCACAAAATTATAGTTTGGCGCAATGTAAA
CACGAACAGTTTGTAGCCTTCCCGTTGGGGATTGAAACTCTATGTCTTCT
TCAAGATACATATCGAGCAGCTTATTGTTTGTAGCCTTCCCGTTGGGGAT
TGAAACATACTTTTTTTCTCACGGTCTGTATGGCCTGTTCAGT

We notice repeats and use Matlab to find the exact locations of that string.

strfind(g,'GTTTGTAGCCTTCCCGTTGGGGATTGAAAC')

Columns 1 through 61

2666352 2666419 2666484 2666551 2666616 2666682 2666748 2666813
2666879 2666947 2667014 2667081 2667147 2667213 2667278 2667344
2667410 2667476 2667544 2667611 2667676 2667741 2667805 2667872
2667939 2670817 2670882 2670949 2671016 2671081 2671147 2671214
2671279 2671345 2671411 2671476 2671544 2671610 2671675 2671740
2671805 2671871 2671936 2672001 2672070 2672135 2672201 2672267
2672333 2672399 2672466 2672534 2672599 2672666 2672733 2672798
2672864 2672930 2672996 2673523 2673590

Length ('GTTTGTAGCCTTCCCGTTGGGGATTGAAAC')=30

61 repeats of length of 30, unique spacers

Starts: 2666352 Ends: 2673620 Period: 65/66/67 Total Length = 7268

These repeats are CRISPR.

In **Figure 5**, we considered the drop at x = 44010000, y = 4.13 and the interval (44009900, 44010500). Following is the sequence of Human Chromosome-21in that interval. We also found repeats.

CCGTTTATATCCACGCAGGCGTTTCCCCTTACCTGCACCGAGCCTCCATT
CCCGTTTATATCCACGCAGGCGTTTCCCCTTACCTGCACCGAGCCTCCCG
CCCCGTTTACATCCACGCAGGCGTTTCCCCTTACCTGCACCGAGCCTCCA
TTCCCGTTTATATCCACGCAGGCGTTTCCCCTTACCTGCACCGAGCCTCC
CGCCCCGTTTACATCCACGCAGGCGTTTCCCCTTACCTGCACCGAGCCTC
CATTCCCGTTTATATCCACGCAGGCGTTTCCCCTTACCTGCACCGAGCCT
CCCGCCCCGTTTACATCCACGCAGGCGTTTCCCCTTACCTGCACCGAGCC
TCCATTCCCGTTTATATCCACGCAGGCGTTTCCCCTTACCTGCACCGAGC
CTCCATTCCCGTTTATATCCACGCAGGCGTTTCCCCTTACCTGCACCGAG
CCTCCATTCCCGTTTATATCCACGCAGGCGTTTCCCCTTACCTGCACCGA
GCCTCCCGCCCCGTTTATATCCACGCAGGCGTTTCCCCTTACCTGCACCG
GGCCTGCCGCCCCGTTTACATCCACGCATGCGTTTCCCCTTACCTGCACT
G

strfind(g,'TTTCCCCTTACCTGCACCGAGCCTCCATTCCCGTTTATATCCACGCAGGCG')

Columns 1 through 18

44007626 44008952 44009105 44009156 44009258 44009360 44009462 44009513 44009615 44009717 44009819 44009870 44009921 44010023 44010125 44010227 44010278 44010329

The spacers are almost identical with this string except 4 letters (in purple). We also find the spacer string.

Strfind(g,"TTTCCCCTTACCTGCACCGAGCCTCC**CGC**CCCGTTTA**C**ATCCACGCAGGCG").

Columns 1 through 23

44007575 44007677 44007728 44007779 44007830 44007881 44007983 44008034 44008289 44008493 44008646 44008697 44008799 44008850 44008901 44009207 44009309 44009564 44009666 44009768 44009972 44010074 44010176

This is a repeat of a string without any gap in the region (44007575, 44010329).

Discussion

The importance of identifying repetitive sequences is clear; however, the considerable size of many genomes makes fast and efficient repeat detection very challenging. In this paper, we have presented a new algorithm for finding repeats in DNA sequences. The algorithm is based on our new measure of entropy for any non-trivial graph. In [15], an algorithm were presented for finding tandem repeats in DNA sequences based on the detection of k-tuple matches. It uses a probabilistic model of tandem repeats and a collection of statistical criteria based on that model. Whereas in [14] and [16] a new tool was introduced for the automatic detection of CRISPR elements in genome. The main advantage of our tool is it will detect both tandem repeats and CRISPR or any other repeats. The main disadvantage of our tool is lack of complete automation and hence it is less efficient compared to the other tools. Our detection technique convert sequences to

an alternative representation (namely, graph as it is given in [17]) in an attempt to make analysis more efficient. Future research plans are to modify the presented algorithm so that it is also able to identify repeats efficiently. Our code will be available to the reader upon request through email to one of the authors.

4. Conclusions

We have studied the following species:

Eukaryotes: Homo sapiens chromosome 19 & 21, Anopheles gambiae, Caenorhabditis elegans, Plasmodium falciparum Saccharomyces cerevisiae.

Prokaryotes: Acidovorax, Ammonifex, Caldicellulosiruptor kristjanssonii, E.Coli, Salmonella Typhi, Listeria Monocyto genes, Bacillus clausii KSM, Chlamydia muridarum Nigg, Cyanobacterium aponinum, Gluconacetobacter diazotrophicus, Haemophilus influenzae R2866, Mycobacterium tuberculosis, Mycoplasma genitalium, Neisseria meningitidis, Streptococcus pneumoniae, Thermosipho africanus, Truepera radiovictrix (Bacteria), A. fulgidus (Archaea).

Viruses: HIV, Hepatitis B. After analyzing the DNA sequence at the points of low entropy for all these species, we conclude that low entropy in a genome graph corresponds to high repeatability in the sequence. These repeats can be classified as CRISPR or Tandem Repeats or something else.

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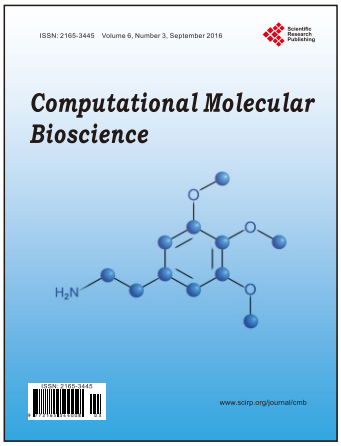

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- Combined Quantum Mechanical and Molecular Mechanical Methods (QM/MM)
- Computational Chemistry of Biomolecules, Ligands and Drugs
- Computational Drug Design: Structure-Based; Ligand-Based; Rational; *De Novo*
- Computational Modelling of Biomolecular Structures Interactions and Processes
- Computational Systems Biology and Chemistry
- Development and Applications of Monte Carlo Methods
- Development and Design of New Biological and Chemical Databases and Data Mining Techniques
- Development, Testing and Applications to Biomolecular Systems
- Enzymatic Reaction Mechanisms and Inhibition
- High Performance Computing in Molecular and Biomolecular Sciences
- Ligand Binding and Free Energy Calculations
- Modelling of Membrane Processes and Protein-Membrane Interactions
- Modelling Protein Structure, Conformational Dynamics an Interactions
- Molecular Mechanics, Force Field Development and Evaluation
- Molecular Visualizations and Data Analysis
- Multilevel Computational Simulations
- Nucleic Acids Structure, Dynamics and Interactions with Ligands
- Protein Folding
- Protein Ligand Docking New Algorithm, Codes and Applications
- Protein-Nucleic Acids Interactions
- Quantitative Structure-Activity Relationships (QSAR)
- Semiempirical Electronic Structure Calculations
- Structural Bioinformatics and Homology Modelling

We are also interested in: 1) Short Reports—2-5 page papers where an author can either present an idea with theoretical background but has not yet completed the research needed for a complete paper or preliminary data; 2) Book Reviews—Comments and critiques.

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