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Evolutions of Adjoints Sequences

Highlights

Simulation of Traffic Monitoring

Modeling and Simulation of Genome

Discovering Thoughts, Inventing Future

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A Novel Approach to Genome Editing using Cellular Automata Evolutions of Adjoints Sequences

By Prashanthi Govindarajan, Sathya Govindarajan & Ethirajan Govindarajan

Abstract- This paper proposes a novel method for genome editing using cellular automata evolutions of adjoints of Adenine, Thymine, Guanine, and Cytosine. The adjoints of the given a genome sequence are the characteristic binary string sequences. For example, the adjoint of Adenine of a given genome sequence is a binary string consisting of 0's and 1's where 1's corresponds to the presence of Adenine in the genome sequence. So, one can have four adjoint sequences of Adenine, Thymine, Guanine, and Cytosine corresponding to a given genome sequence. One-dimensional three neighborhood binary value cellular automata rules can be applied to an adjoint sequence and the desired number of evolutions could be obtained. This rule is defined by a linear Boolean function and one can have 256 such linear Boolean functions. Genome editing is carried out by superimposing the evolved adjoint sequence on the original genome sequence or on its successive evolutions. In this manner, one can have four ways of genome editing using four adjoint sequences and evolutions.

Keywords: *genome editing, cellular automata, evolutions of adjoints, linear boolean functions.*

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ANOVELAPPROACHTOGENOMEEDITINGUSINGCELLULARAUTOMATAEVOLUTIONSOFADJOINTSSEQUENCES

Strictly as per the compliance and regulations of:

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Prashanthi Govindarajan [α], Sathya Govindarajan [σ] & Ethirajan Govindarajan [ρ]

Abstract- This paper proposes a novel method for genome editing using cellular automata evolutions of adjoints of Adenine, Thymine, Guanine, and Cytosine. The adjoints of the given a genome sequence are the characteristic binary string sequences. For example, the adjoint of Adenine of a given genome sequence is a binary string consisting of 0's and 1's where 1's corresponds to the presence of Adenine in the genome sequence. So, one can have four adjoint sequences of Adenine, Thymine, Guanine, and Cytosine corresponding to a given genome sequence. One-dimensional three neighborhood binary value cellular automata rules can be applied to an adjoint sequence and the desired number of evolutions could be obtained. This rule is defined by a linear Boolean function and one can have 256 such linear Boolean functions. Genome editing is carried out by superimposing the evolved adjoint sequence on the original genome sequence or on its successive evolutions. In this manner, one can have four ways of genome editing using four adjoint sequences and evolutions.

Keywords: genome editing, cellular automata, evolutions of adjoints, linear boolean functions.

I. Introduction

Genome editing is essentially the process of introducing required changes in a given DNA. A protein or enzyme cuts certain portions of a given DNA and substitutes the target sequences of nucleotides by specific chains of nucleotides. For ages, people have been working on the notion of Genome editing. However, only recently, the spurt of activities has been reported in the literature about genome editing. Before getting into the details of the genome editing, it would be apt to reason out why genome editing is viewed as a significant activity. Genome editing is carried out as a health initiative to healeven the so-called incurable diseases associated with genetic problems. Clinically there are many methods of editing genomes among which CRISPR technique is recognized as a reliable technique ratified by the U.S. Food and Drug Administration, pushing in a new era of cancer treatment. CRISPR based therapy is designed to treat blood and bone marrow cancer, which usually affects children and young adults. This therapy is known as CAR-T therapy, and it has shown remarkable results in patients. By eliminating those genes which cause disease, physicians can treat various illnesses ranging from heart disease to Alzheimer's.

In addition to curing diseases, gene therapy (gene editing) could be used to stop inherited disease in its tracks to save endangered species, and more so, to resurrect extinct species. All such gene therapy techniques are clinical laboratory- based. Alternatively, one can try out the possibilities of developing some of them for genome editing using computational tools and concepts. Genome is a string of nucleotides, and its characteristic sequence is a sequence of A, T, G, and C. Gene editing, in the computer science point of view, is a pattern searching and substituting process, meaning, genome editing is essentially a string processing operation. A genome is a subset of a free monoid A* of an alphabet A which consists of the primitive symbols A, T, G and C. So, gene editing is viewed as a map ϕ that connects A* to A*.It is in this context, this paper introduces a novel concept of genome editing cellular automata evolutions of adjoint strings of a genome. Section 2 of this paper describes the fundamental notions of adjoints of a genome and their evolution using one-dimensional cellular automata rules defined by linear Boolean functions. Section 3 presents the technique of editing genome sequences using the cellular automata generations of adjoint sequences. Section 4 illustrates the concept with the help of a case study.

II. Adjoints of A Genome Sequence and their Evolutions using One-Dimensional three Neighborhood Cellular Automata

Adjoint of a particular nucleotide in a genome sequence is the binary sequence obtained by substituting the particular nucleotides in the genome sequence by 1's and the others by 0's. For example, let us consider a sample sequence of BrucellaSuis 1330 for a case study. The actual length of the genome sequence of BrucellaSuis 1330 is 5806. A cellular automaton is an idealized parallel processing system consisting of an array of numbers (1-D, 2-D and more) realized using updating rules based on certain

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neighborhood. For example, a one dimensional cellular automaton would consist of a finite length array as shown below.

---	---	---	i-1	i	i+1	---	---	---

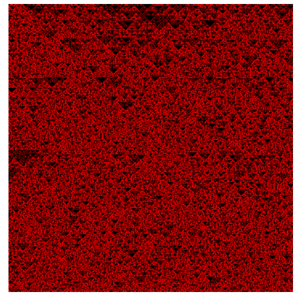
Consider an ith cell in the array. This cell has a neighbor i-1 on its left and another i+1 on its right. All three put together is called a three neighborhood. One can assign a site (cell) variable ξi-1, ξi, and ξi+1 to the three neighborhood cells. At a particular instant of time, these variables take on numerical values, say either a 0 or a 1. In such a case, the variables are denoted as ξti-1, ξti, and ξti+1. The value of the ith cell at the next instant of time is evaluated using an updating rule that involves the present values of the ith, (i-1)th and (i+1)th cells. This updating rule is basically a linear Boolean function of three variables. One can construct 256 linear Boolean functions, as updating rules of one-dimensional three-neighborhood binary- valued cellular automata. Each rule defines an automaton by itself. So, one dimensional binary-valued three-neighborhood cellular automata (123CA) rules could be used to model adjoints of a genome sequence. The first twenty linear Boolean functions of cellular automata 123CA are listed below with their decimal equivalents.

Linear Boolean Function	Decimal Equivalent
0	0
$(\bar{\xi}_{i-1}\bar{\xi}_i\bar{\xi}_{i+1})$	1
$(\bar{\xi}_{i-1}\bar{\xi}_i\xi_{i+1})$	2
$(\bar{\xi}_{i-1}\bar{\xi}_i)$	3
$(\bar{\xi}_{i-1}\xi_i\bar{\xi}_{i+1})$	4
$(\bar{\xi}_{i-1}\bar{\xi}_{i+1})$	5
$(\bar{\xi}_{i-1}\xi_i\bar{\xi}_{i+1})+(\bar{\xi}_{i-1}\bar{\xi}_i\xi_{i+1})$	6
$(\bar{\xi}_{i-1}\bar{\xi}_{i+1})+(\bar{\xi}_{i-1}\bar{\xi}_i)$	7
$(\bar{\xi}_{i-1}\xi_i\xi_{i+1})$	8
$(\bar{\xi}_{i-1}\bar{\xi}_i\bar{\xi}_{i+1}) + (\bar{\xi}_{i-1}\xi_i\xi_{i+1})$	9
$(\bar{\xi}_{i-1}\xi_{i+1})$	10
$(\bar{\xi}_{i-1}\bar{\xi}_i) + (\bar{\xi}_{i-1}\xi_{i+1})$	11
$(\bar{\xi}_{i-1}\xi_i)$	12
$(\bar{\xi}_{i-1}\bar{\xi}_{i+1}) + (\bar{\xi}_{i-1}\xi_i)$	13
$(\bar{\xi}_{i-1}\xi_i) + (\bar{\xi}_{i-1}\xi_{i+1})$	14
$(\bar{\xi}_{i-1})$	15
$(\xi_{i-1}\bar{\xi}_i\bar{\xi}_{i+1})$	16
$\overline{(\xi}_i\bar{\xi}_{i+1})$	17
$(\xi_{i-1}\bar{\xi}_i\bar{\xi}_{i+1}) + (\bar{\xi}_{i-1}\bar{\xi}_i\xi_{i+1})$	18
$\overline{(\xi}_i\bar{\xi}_{i+1}) + (\bar{\xi}_{i-1}\bar{\xi}_i)$	19
$(\xi_{i-1}\bar{\xi}_i\bar{\xi}_{i+1}) + (\bar{\xi}_{i-1}\xi_i\bar{\xi}_{i+1})$	20

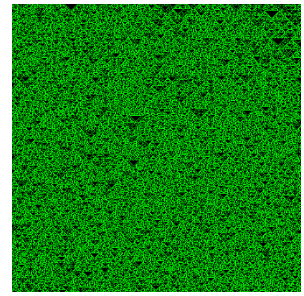
For the case study rule number 90 is applied to the adjoints of BrucellaSuis 1330 genome sequence and 500 evolutions generated. Rule 90 is shown below.

$(\xi_{i-1}\bar{\xi}_{i+1}) + (\bar{\xi}_{i-1}\xi_{i+1})$ 90

Since the image of the 500 evolutions of BrucellaSuis 1330 is quite large, a small portion of the images are presented in this paper. Fig. 1 shows evolutions of the adjoints of A(n) and T(n).



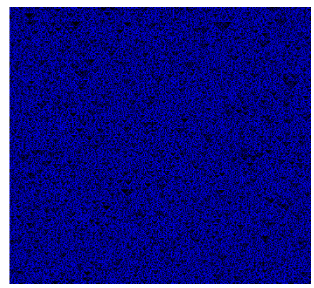
Evolution of Adjoint A(n) using rule 90 of 123CA



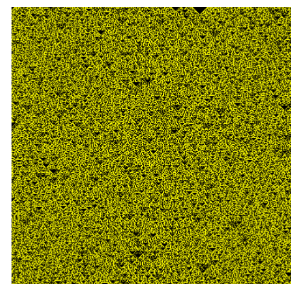
Evolution of Adjoint T(n) using rule 90 of 123CA

Fig. 1: Evolutions of A(n) and T(n)

Fig. 2 shows evolution of the adjoints of G(n) and C(n).



Evolution of Adjoint G(n) using rule 90 of 123CA



Evolution of Adjoint C(n) using rule 90 of 123CA

Fig. 2: Evolutions of G (n) and C (n)

III. Nucleotide Adjoints based Genome Editing

As outlined earlier, a genome sequence is a subset of a free monoid A* of an alphabet A which consists of the primitive symbols A, T, G and C and gene editing is a map ϕ that connects A * to A *. The map ϕ is a rule that transforms a sequence into another desired sequence. One can use four types of symbol to symbol substitution formulas given below for genome editing.

Symbol to be substituted		Substitution symbol	Formula Number
A∨T∨G∨C	→	A	1
A∨T∨G∨C	→	T	2
A∨T∨G∨C	→	G	3
A∨T∨G∨C	→	C	4

Where the symbol ∨ denotes the relation of logical OR. Application of formula #1 to any genome sequence is called A-latch. Similarly one can think of T-latch, G-latch and C-latch. A nucleotide latch would give rise to conversion of any genome sequence into a sequence consisting of that particular nucleotide in one step. This is called 'Nucleotide Saturation'. Thus one can have A-saturation, T-saturation,G-saturation,and C-saturation. To be precise, A-latching of any genome sequence transforms it into A-saturated sequence and it holds for other three types of latching also. The question that arises here is that whether it is possible to edit a genome sequence using nucleotide latching techniques at preferred locations in the sequence. One such possibility is latching of a genome sequence using cellular automata evolutions of adjoints. Once a genome sequence is latched, the resulting edited sequence is called its elementary transformation. Two types of latching are discussed here (i) latching of elementary transformations of a genome sequence with various cellular automata evolutions of adjoints and (ii) latching of original genome sequence with various cellular automata evolutions of adjoints. Fig. 3 portraits the first approach of latching of elementary transformations of a genome sequence with various cellular automata evolutions of adjoints.

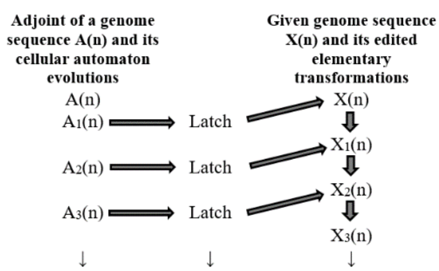


Fig. 3: Editing of elementary transformations of a genome sequence

Fig. 4 portraits the second approach of latching of original genome sequence with various cellular automata evolutions of adjoints.

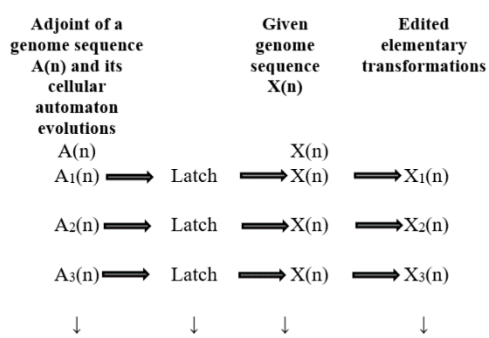


Fig. 4: Editing of original genome sequence

IV. Case Study

The characteristic sequence of BrucellaSuis 1330 genome sequence is used here for the case study. The length of this sequence is 5806. Rule number 90 is used here for the study. The linear Boolean function corresponding to this rule is

$$(\xi_{i-1}\bar{\xi}_{i+1}) + (\bar{\xi}_{i-1}\xi_{i+1})$$

Approach #1

Editing of elementary transformations of a genome sequence with various cellular automata evolutions of adjoints

Figs. 5 to 8 portrait the first approach of latching of elementary transformations of a genome sequence with various cellular automata evolutions of adjoints.

Fig. 5 shows the result of A-latching the genome sequence, that is, Adenine based genome editing. Since the image is quite large, a small portion of it is shown here. It was observed that the A-saturation of the genome sequence occurred while editing the previous elementary transformation of the genome sequence using the 32nd evolution of the A(n).

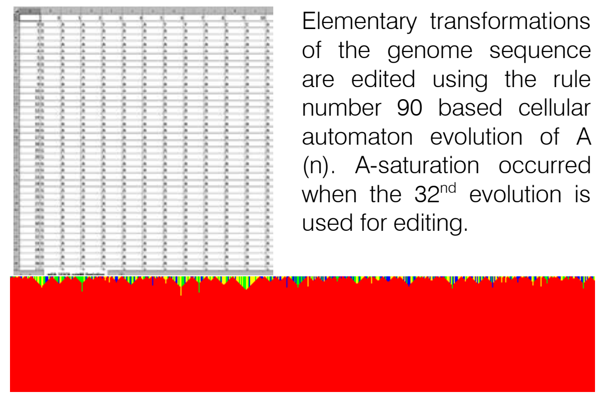


Fig. 5: Adenine based genome editing (A-saturation at 32nd evolution)

Fig. 6 shows the result of T-latching the genome sequence, that is, Thymine based genome editing. Since the image is quite large, a small portion of it is shown here. It was observed that the T-saturation of the genome sequence occurred while editing the previous elementary transformation of the genome sequence using the 40th evolution of the A(n).

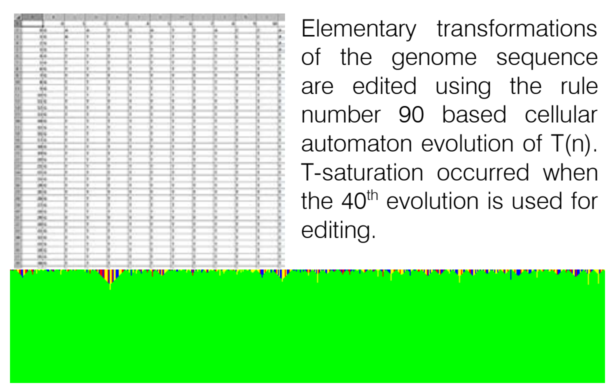
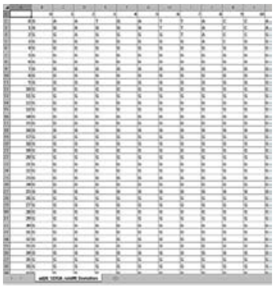


Fig. 6: Thymine based genome editing (T-saturation at 40th evolution)

Fig. 7 shows the result of G-latching the genome sequence, that is, Guanine based genome editing. Since the image is quite large, a small portion of it is shown here. It was observed that the G-saturation of the genome sequence occurred while editing the previous elementary transformation of the genome sequence using the 15th evolution of the G(n).



Elementary transformations of the genome sequence are edited using the rule number 90 based cellular automaton evolution of GT(n). G-saturation occurred when the 15th evolution is used for editing.

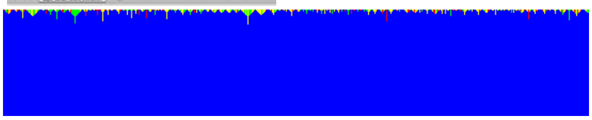
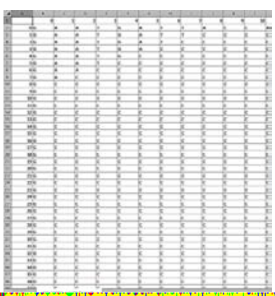


Fig. 7: Guanine based genome editing (G-saturation at 15th evolution)

Fig. 8 shows the result of C-latching the genome sequence, that is, Cytosine based genome editing. Since the image is quite large, a small portion of it is shown here. It was observed that the C-saturation of the genome sequence occurred while editing the previous elementary transformation of the genome sequence using the 21stevolution of the C(n).



Elementary transformations of the genome sequence are edited using the rule number 90 based cellular automaton evolution of C(n). C-saturation occurred when the 21st evolution is used for editing.

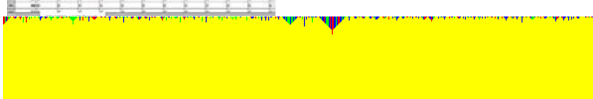
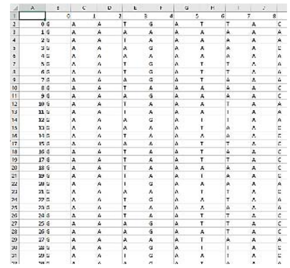


Fig. 8: Cytosine based genome editing (C-saturation at 21st evolution)

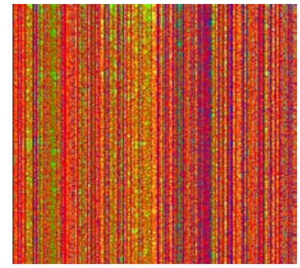
Approach #2

Editing of a genome sequence with various cellular automata evolutions of adjoints

Figs. 9 to 14 portrait the second approach of latching of a given genome sequence with rule number 90 based cellular automata evolutions of adjoints. Figs. 9 shows Adenine based genome editing on original sequence both in Text Form and in Image Form. The Image Form is obtained using a color coding scheme which paints a red color for Adenine, green color for Thymine, blue color for Guanine and yellow color for Cytosine. Fig. 10 shows the predominant horizontal lines and vertical lines of the image of the edited genome separately. An image processing tool of line detector is used for this purpose.

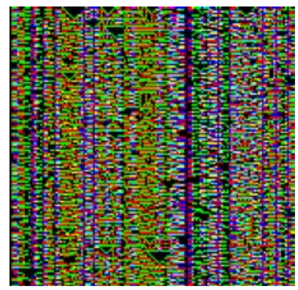


Adenine based genome editing on original sequence (Text Form)

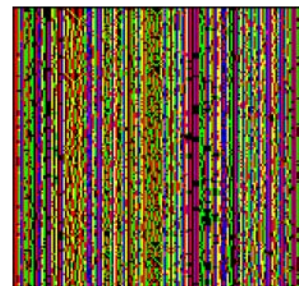


Adenine based genome editing on original sequence (Image Form)

Fig. 9: Edited genome using evolutions of A(n)



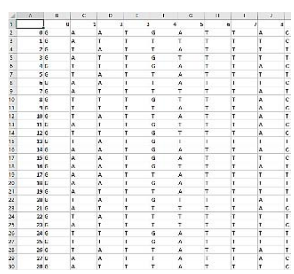
Adenine based genome editing on original sequence Horizontal lines Detected



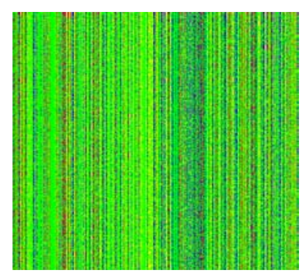
Adenine based genome editing on original sequence Vertical lines Detected

Fig. 10: Horizontal and Vertical lines of A-latch detected

Figs. 11 shows Thymine based genome editing on original sequence both in Text Form and in Image Form. Fig. 12 shows the predominant horizontal lines and vertical lines of the image of the edited genome separately.

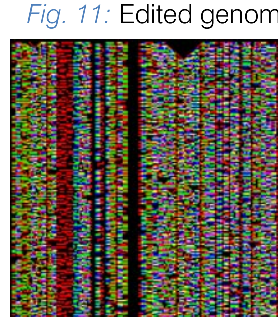


Thymine based genome editing on original sequence (Text Form)

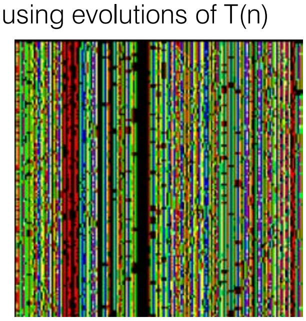


Thymine based genome editing on original sequence (Image Form)

Fig. 11: Edited genome using evolutions of T(n)



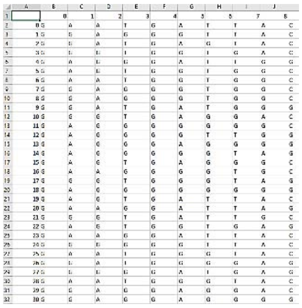
Thymine based genome editing on original sequence Horizontal lines Detected



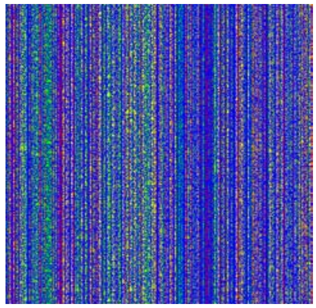
Thymine based genome editing on original sequence Vertical lines Detected

Fig.12: Horizontal and Vertical lines of T-latch detected

Figs. 13 shows Guanine based genome editing on original sequence both in Text Form and in Image Form. Fig. 14 shows the predominant horizontal lines and vertical lines of the image of the edited genome separately.

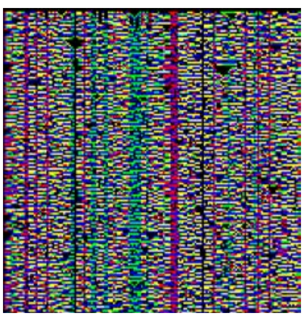


Guanine based genome editing on original sequence (Text Form)

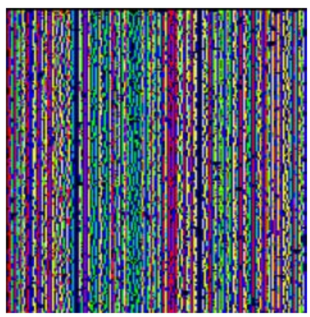


Guanine based genome editing on original sequence (Image Form)

Fig.13: Edited genome using evolutions of G(n)

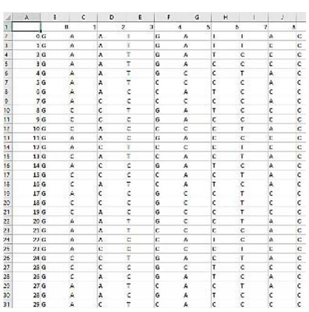


Guanine based genome editing on original sequence Horizontal lines Detected

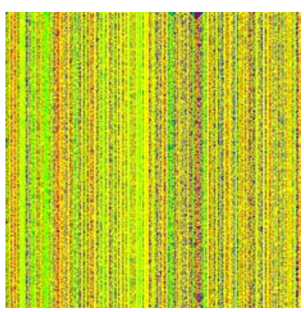


Guanine based genome editing on original sequence Vertical lines Detected

Fig.14: Horizontal and Vertical lines of G-latch detected



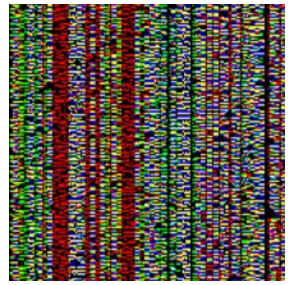
Cytosine based genome editing on original sequence (Text Form)



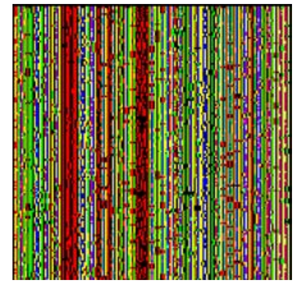
Cytosine based genome editing on original sequence (Image Form)

Fig.15: Edited genome using evolutions of C(n)

Figs. 15 shows Cytosine based genome editing on original sequence both in Text Form and in Image Form. Fig. 16 shows the predominant horizontal lines and vertical lines of the image of the edited genome separately.



Cytosine based genome editing on original sequence Horizontal lines Detected

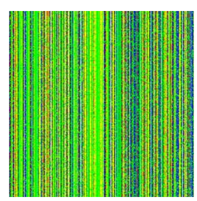


Cytosine based genome editing on original sequence Vertical lines Detected

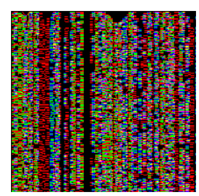
Fig.16: Horizontal and Vertical lines of C-latch detected

Dyadic Operations among edited genomes

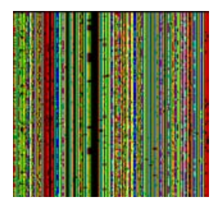
Two relational operations 'max' and 'min' are carried out on the A-latch, T-latch, G-latch and C-latch edited genomes. Adenine is represented by the number 1, Thymine by 2, Guanine by 3 and Cytosine by 4. Now, the relation max(x,y) of two nucleotides is evaluated as the maximum of the numerical values of the nucleotides under comparison. Similarly, the relation min(x,y) of two nucleotides is evaluated as the minimum of the numerical values of the nucleotides under comparison. Fig. 17 shows the result of comparing A-latch and T-latch of BrucellaSuis 1330 genome with the max operator along with its horizontal and vertical lines.



AT Max



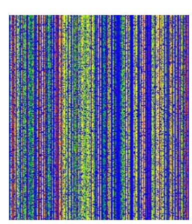
AT Max Horizontal line



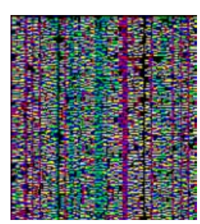
AT Max Vertical line

Fig.17: Max of A and T latches and its horizontal and vertical lines

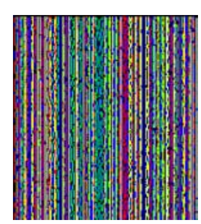
Fig. 18 shows the result of comparing A-latch and C-latch of BrucellaSuis 1330 genome with the max operator along with its horizontal and vertical lines.



AG Max



AG Max Horizontal line



AG Max Vertical line

Fig.18: Max of A and G latches and its horizontal and vertical lines

Fig. 19 shows the result of comparing A-latch and C-latch of BrucellaSuis 1330 genome with the max operator along with its horizontal and vertical lines.

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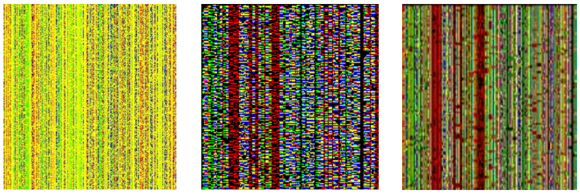
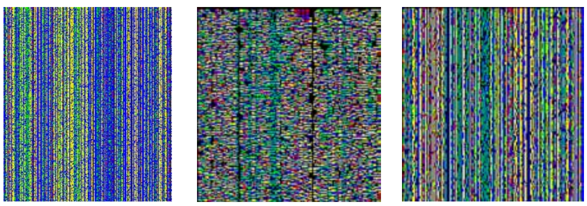


AC Max | AC Max Horizontal line | AC Max Vertical line

Fig.19: Max of A and C latches
and its horizontal and vertical lines

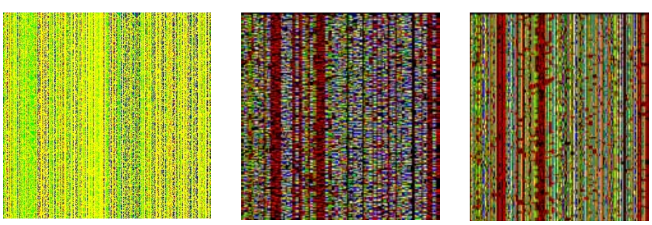
Fig. 20 shows the result of comparing T-latch and G-latch of BrucellaSuis 1330 genome with the max operator along with its horizontal and vertical lines.



TG Max | TG Max Horizontal line | TG Max Vertical line

Fig. 20: Max of T and G latches
and its horizontal and vertical lines

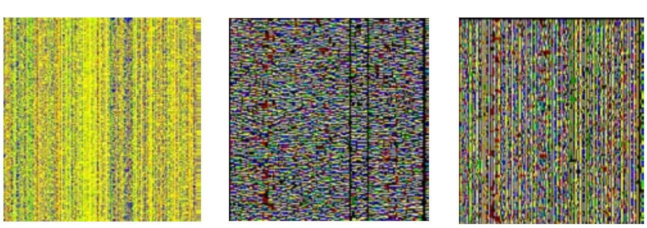
Fig. 21 shows the result of comparing T-latch and C-latch of BrucellaSuis 1330 genome with the max operator along with its horizontal and vertical lines.



TC Max | TC Max Horizontal line | TC Max Vertical line

Fig. 21: Max of T and C latches
and its horizontal and vertical lines

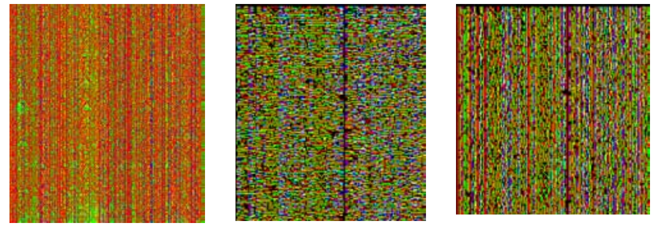
Fig. 22 shows the result of comparing G-latch and C-latch of BrucellaSuis 1330 genome with the max operator along with its horizontal and vertical lines.



GC Max | GC Max Horizontal line | GC Max Vertical line

Fig. 22: Max of G and C latches
and its horizontal and vertical lines

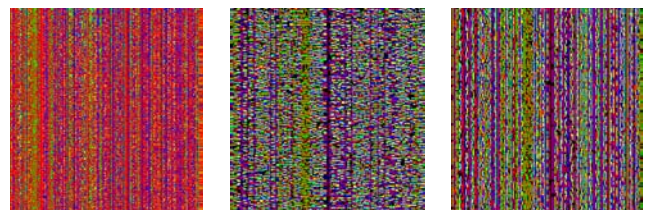
Fig. 23 shows the result of comparing A-latch and T-latch of BrucellaSuis 1330 genome with the min operator along with its horizontal and vertical lines.



AT Min | AT Min Horizontal line | AT Min Vertical line

Fig. 23: Min of A and T latches
and its horizontal and vertical lines

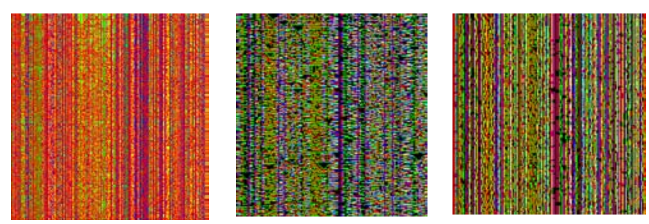
Fig. 24 shows the result of comparing A-latch and G-latch of BrucellaSuis 1330 genome with the min operator along with its horizontal and vertical lines.



AG Min | AG Min Horizontal line | AG Min Vertical line

Fig. 24: Min of A and G latches
and its horizontal and vertical lines

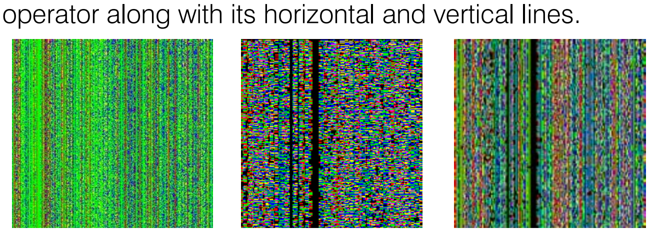
Fig. 25 shows the result of comparing A-latch and C-latch of BrucellaSuis 1330 genome with the min operator along with its horizontal and vertical lines.



AC Min | AC Min Horizontal line | AC Min Vertical line

Fig. 25: Min of A and C latches
and its horizontal and vertical lines

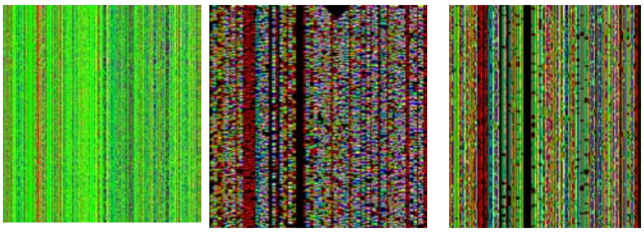
Fig. 26 shows the result of comparing T-latch and G-latch of BrucellaSuis 1330 genome with the min operator along with its horizontal and vertical lines.



TG Min | TG Min Horizontal line | TG Min Vertical line

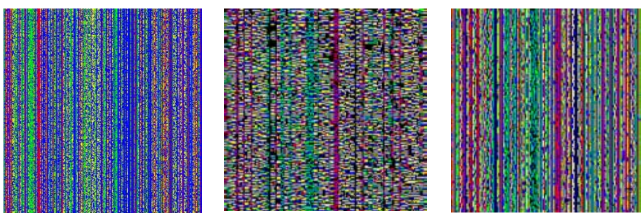
Fig. 26: Min of T and G latches
and its horizontal and vertical lines

Fig. 27 shows the result of comparing T-latch and C-latch of BrucellaSuis 1330 genome with the min operator along with its horizontal and vertical lines. Fig. 28 shows the result of comparing G-latch and C-latch of BrucellaSuis 1330 genome with the min operator along with its horizontal and vertical lines.



TC Min | TC Min Horizontal line | TC Min Vertical line

Fig. 27: Min of T and C latches and its horizontal and vertical lines



GC Min | GC Min Horizontal line | GC Min Vertical line

Fig. 28: Min of G and C latches and its horizontal and vertical lines

V. Results and Discussions

The following observations are made from the case study.

1. Editing a genome is a map or a function that transforms a genome into a desired genome sequence
2. Two approaches could be undertaken for genome editing (i) Editing of elementary transformations of a genome sequence with various cellular automata evolutions of adjoints and(ii) Editing of the given genome sequence with various cellular automata evolutions of adjoints
3. Using approach 1, one would end up with saturation in short steps. Using approach 2, one would be able to generate edited versions that exhibit periodicities and generic evolutions.
4. Relational operations like ‘max’ and ‘min’ could be carried out on various latches. One can have 11 such max operations like (i) A-latch and T-latch, (ii) A-latch and G-latch, (iii) A-latch and C-latch, (iv) T-latch and G-latch, (v) T-latch and C-latch, (vi) G-latch and C-latch, (vii) A-latch, T-latch and G-latch (viii) A-latch, T-latch and C-latch(ix) A-latch, G-latch and C-latch, (x)T-latch, G-latch and C-latch, (xi) A-latch,T-latch, G-latch and C-latch. In the same manner, one can have 11 min operations.
5. The result of each operation exhibits unique behavior in periodicity and generic form.
6. Interpretation of these properties could be made in a better way only by an expert in genetic Engineering

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The Current State of Fake News in the D.R. Congo and Socials Impacts

By Eliud Aganze & Riphin Kusinza
Kivu Hub & Hope Africa University

Abstract- In the media industry, the propagation of fake news is becoming a booming topic and challenge. On social media, website and written press the spread of this is so fast to keep track of confusing reader on what is fake and also causing damage in different sector of life [1] in response, social media platforms have announced actions to limit the spread of false content. Rapid speed of fake news poses an increasing risk to society's worldwide to counter this more need to done.

The lack of digital literacy may play a big role in spread of fake news in the DRC were less than 20% have access to internet never less access to social media is also low few how have access don't have computer literacy skills to distinguish and decide what to share. With growing number for the last decade, the challenge will be more complicated with a population estimated to 80 million in 2017, if 75% will be able to access social media platform in 2030 the problem will far great than what it is now.

Keywords: *fake news, misinformation, social media, public health, election, digital literacy.*

GJCST-G Classification: *H.5.1*

THECURRENTSTATEOFFAKENEWSINTHEDRCONGOANDSOCIALSIMPACTS

Strictly as per the compliance and regulations of:

The Current State of Fake News in the D.R. Congo and Socials Impacts

Eliud Aganze [α] & Riphin Kusinza [σ]

Abstract- In the media industry, the propagation of fake news is becoming a booming topic and challenge. On social media, website and written press the spread of this is so fast to keep track of confusing reader on what is fake and also causing damage in different sector of life [1] in response, social media platforms have announced actions to limit the spread of false content. Rapid speed of fake news poses an increasing risk to society's worldwide to counter this more need to done.

The lack of digital literacy may play a big role in spread of fake news in the DRC were less than 20% have access to internet never less access to social media is also low few how have access don't have computer literacy skills to distinguish and decide what to share. With growing number for the last decade, the challenge will be more complicated with a population estimated to 80 million in 2017, if 75% will be able to access social media platform in 2030 the problem will far great than what it is now.

Keywords: fake news, misinformation, social media, public health, election, digital literacy.

I. Introduction

In the media industry, the propagation of fake news is becoming a booming topic and challenge. On social media, website and written press the spread of this is so fast to keep track of confusing reader on what is fake and also causing damage in different sector of life [1]

In an age of where almost half of all news consumers and share their news from online sources [13] fake news can reach large audience thought social media platform rapidly from one person to another [14] Van Der linden, S "The conspiracy-effect: exposure to conspiracy to conspiracy theory(about global warming) decreases pro-social behaviors and science acceptance. Personality and individuals' differences, 87, 171-173", 2015. following an age of post trust [28] Some previous research indicated that 31% of kids age 10 to 18 have shared online at least one news story that tend to be fake. this situation raised concerned related to digital literacy a specially in country with low access to Internet around 3.1% in 2016 statistics from internet live stats and education such as the Democratic Republic of The Congo [34]

In the DRC a study published in the lancet found that "nearly Ralph of respondents believe Ebola didn't not exists or was invented to destabilize the region or make money" this turned to be fake news which resulted in more than 5000 infected and more than 2000 dead with Ebola.

Currently day social media reputation and access keeps growing at fast rate , the quality of contents is raising the issue of fake news with more users sharing unverified contents leading to misinformation campaign used by some nation to influence they foreign policies , the Russia fake news campaign launched during the year 2018 in several Africa nation include the DR. Congo in favor of their candidate during the DR. Congo election has showed how social media can be used to spread fake news [3]. Other proposed solution ranges from making digital literacy a primary pillar of education [17], to prevent false information going viral in first place.

As stating point of this research, relevant literature including theoretical background were reviewed. Based on the review of existing literature, we developed our research framework to guide a survey study, which be developed and tested with pilot study sample. Actual data will be collected through an online survey form targeting social media users and internet users. Regression analysis will be conducted based on collected data. Finally, we will interpret and discuss about data analysis based on research framework.

II. Theoretical Review of Fake News

In the current state of proliferation multiple source of information, fake news is spreading fast and it becoming increasingly hard and harder to detect what is authentic and fake news despite technology advancement but fake news spread faster the all detections technology available. In some countries they are no policies regulating the type of digital contents such our case the DR. Congo which has seen an increase of social media and mobile access.

a) Social Media Source of Fake News

Fake news is defined as "the deliberate creation and sharing of false and/or manipulated information that intended to deceive and mislead audience, either for purposes of causing harm, or for political, personal and financial gain.[1]. The world economic forums rank misinformation and fake news among the world top risk. [12].

Most of nowadays news consumption has shifted towards online social media, where it is more com- for table to ingest, share and further discuss news with friends or other readers [32]

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Recent report by Stanford internet observatory regarding Russia influence in in recent political election in Africa , the report stated that Russia used fake news to influence political environment by creating fake Facebook page to influence their political agenda which campaign was targeted countries such as Sudan, Libya, Central Africa republic , Madagascar, Mozambique and the Democratic republic of Congo. Regarding the DRC they were several pages created in the eve of 2018 elections to influence voters. The report stated that they have been indication that Russia interest in the DRC and their heavy involvement in the neighbor Central Africa Republic. This Russia operation took place against the backdrop of fragile domestic political situation after mention elections December 2018, in which opposition candidate Martin Fayulu and numerous observers claimed that the cote count was manipulated , the DRC settle into an uneasy balance , in which Felix Tshisekedi governed as president while outgoing president Joseph Kabila's party retained a majority in the national assembly, lead observers to speculate that he would continue to rule behind the scenes. [27]. The two pages provided by Facebook "Congo Actu" and "Patriotism Congolaise" were created one day part in august 2019 and have clear commonalities. The other page, "les Echos RDC," was created earlier and differs in some significant ways. Congo acts had one-page manager in Madagascar since then. The page has published 123 posts and revived 94,400 interaction. Les Echos RDC and Patriotisme congolais had both 2.427 and 5.534 followers, both managed in Madagascar and their average interactions 944 and 628. [27]

With an internet penetration of less than 7%, word of mouth remains the most common way for rumors to spread in DRC. These have included speculation that people who died from Ebola are deliberately being killed in treatment center. The spread of harmful rumors thought social media had tragic consequences for Congolese frontline workers, many of whom have been accused of profiting from the crisis. There have been more than 1300 attacks on healthcare facilities, during which dozens of people have been killed. [19] as we can fake new spread from social media has impact health care in some region of the DRC.

In response, Facebook and other social media companies have made a range of algorithmic and policy changes to limit the spread of false content. In the appendix, we list twelve announcements by Facebook and five by Twitter aimed at reducing the circulation of misinformation on their platforms since the 2016 election [29]

Majority of social media companies have their approaches to deal with spams accounts, Facebook's approach involves detecting inauthentic behaviors [14]. it is used to detect operated bots. Also, twitter's initiative on election integrity focused on giving users more transparency on us federal political campaigning ads.[15] twitter does this by reaving billing information, ad spend, impression data allowing to make an educated decision [13]

b) Fake News in Drc Ebola Outbreak

'Fake News': 'Fake news', was chosen in 2017 as the word of the year by the Oxford University. In line with previous research, this paper avoids the term except when directly mentioned by interviewees. The main reasons for this, as highlighted in Nielsen and Grave, 2018 and the Report commissioned by the European Commission in March 2018, is that the term is inadequate to capture the complex problem of disinformation. As argued elsewhere, the term has also been appropriated by some politicians and pundits to undermine independent news media. Therefore, as previously mentioned the term *disinformation*, which includes an array of practices not only to produce but also to disseminate fabricated or false information, is preferred here. [33]

In the DRC a study published in the lancet found that "nearly Ralph of respondents believe Ebola didn't not exists or was invented to destabilize the region or make money" this turned to be fake news which resulted in more than 5000 infected and more than 2000 dead with Ebola [11].

Some people were affected by fake news and as we can hear from one victim who never believed in Ebola diseases a real testimony If Floride Kayindo hadn't contracted Ebola herself. She would not believe that it existed. The 36 years old prints with bemusement thinking about the rumors she's heard. "she thought it was not a real illness, it was brought in by white people to make money out", she explains, "white people are evil, that's what people in community believe, "Kayindo tells TIME. "Before Ebola white people were around, but now they're thinking white people came with Ebola, Kayindo was declared Ebola free in November 2018[19]. Misinformation has contributed to the difficulties containing the virus in the DRC, where more than 1300 people have now died in the second largest outbreak in the DRC history. These rumors lead to destruction of medical centers and death of health workers.

According to Diallo senior UNICEF Ebola coordinator interviewed by the TIME says "the lack of information leads the community to ask a lot of question about the Ebola virus". Also, other people believe that international aid organization are behind the outbreak. The belief has been compounded by the amount of the money that suddenly seems to be flowing into DRC east of the help assist efforts to contain Ebola. They argue they got little relief from conflict and other health and other health issues before this, and ask why Ebola would be any different.

c) Digital Literacy and Misinformation Spread

We can define digital literacy according to the European Union is “the skills required to achieve digital competences [26] emphasizing “‘he confident and critical use of digital technology’ which implies ‘knowledge ‘. After checking different sources, we can also define digital literacy, “in additional to ICT competence, implies a critical assessment of impact of digital technology on personal development and society; in an addition to ICT competence, it incorporates the three pillars: smart use, nurturing values and an understanding of the digital age. [24], according to the research by Target DRC, we have seen an increase of 84% of Congolese having access to internet through mobile device [35]

Misinformation is defined as information that is inaccurate or misleading [30. It could spread un-intentionally [31] due to honest reporting mistakes or incorrect interpretations [31]. The digital age poses many opportunities and challenges for its citizens. While it that digital native has the self-developed skills required to take advantage and harness risks of the digital environment. Developments in the digital field caller systematic upgrade of literacy to the level of digital competence. [23] In a time when we increasing implement digitalization at work, estimates show that 65% of child in primary school will jobs which do not exist today [25]

To ensure responsible behavior of digital natives in the environment, and ultimately create responsible and competent digital citizens, it is of utmost importance to address and bring closer the concept of digital literacy to educators [25].

The key to success is therefore to increase the level of education and education itself. It is also necessary to build and increase the digital literacy of individuals. Which is related to searching, processing, sorting and sharing information through new media and ICT. In addition to more specific digital literacy. It is necessary to increase media literacy itself and improve the social status of media literacy as set of technical, knowledge, civil and creative capabilities that allow access to and critical perception of media. [22].

III. Research Framework

Information disorder theoretical framework [16], which define three types of false or harmful information:

- *Mis-information:* False information that shared inadvertently, without meaning to cause harm.
- *Dis-information:* Intending to cause harm, by deliberately sharing false information.
- *Mal-information:* Genuine information or opinion shared to cause harm, e.g. Hate speech, harassment. [20],

In [9], Piotrkowicz studied the impart of the linguistics of major headline of news stories on their popularity, also [10] similar discussed the impact of fake news in recent US election Spread of fake new on Facebook and twitter.

IV. Research Design and Method

The survey was completed by a nationally representative sample of 1500 representative for age, gender and job. The research tool the survey online to allow respondents to answer at their convenience, which results in a more considered response. The X question survey covered a range of topics around news consumption, including;

- Trust /distrust News sources
- News format
- Example of fake new

It is important for general users to continue to pay attention to information and misinformation they encounter on the web and social media platform. In this section, we discuss how research results and their publicizing lead over time to change in design features of these systems addressing the exhibited weakness.

We will use survey method to conduct this research [8], the survey questionnaire will be developed for influence of fans news in the DR. Congo. The survey data will be collected through online survey, the population study focuses on the social media/internet users in the DR. Congo, and the sample population which we collect is target 150 participants. The sample will be collected using free survey response platform. We will use students, journalist, media professional, IT professional, academic and blogger in this survey. Later, we can generalize the result of this research to a population of general internet/social media users.

After getting the final data set, we will clean the survey data set by removing invalid data. [7], The descriptive data analysis will show some demographic information about the respondents. In regard to statistical analysis, factors analysis and multiple regression measurements of six different variables. Correlation will be used to see the relationships among all research variables. [6]

Regression result

Regression coefficients represents the mean change in response variable for one unit of change in predictor variable while holding other predictors in the model of constant was used, as his control that regression provides is important because it isolates the role of variable from all of the others in the model [8] look for documentation.

V. Conclusion

The purpose of this study is to understand the factors which the current state of fake news in the D.R. Congo and socials impacts. We focus on both gratification research and adoption to answer our research question.

In regard to the possible result s of this research, first we found/believe FIST FINDING, second, third. The analysis of survey results will help us validating the new model and understand individual user "the factors which the current state of fake news in the D.R. Congo and socials impacts"

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Modeling and Simulation of Genome Evolution Using Linear Boolean Functions Associated with One Dimensional Cellular Automata

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Abstract- Structural and functional behavior of genomes could be studied using one dimensional binary-valued three neighborhood cellular automata updating rules. These updating rules are linear Boolean functions, and they are applied to the adjoint sequences of adenine, (A), Thymine (T), Guanine (G) and Cytosine (C) corresponding to the characteristic sequence of a genome. This paper proposes the use of linear Boolean functions, and demonstrates the textural or fractal behavior of genome evolution in terms of nucleotide adjoints.

Keywords: *linear boolean functions, cellular automata, genome evolution.*

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Prashanthi Govindarajan [α], Sathya Govindarajan [σ] & Ethirajan Govindarajan [ρ]

Abstract- Structural and functional behavior of genomes could be studied using one dimensional binary-valued three neighborhood cellular automata updating rules. These updating rules are linear Boolean functions, and they are applied to the adjoint sequences of adenine, (A), Thymine (T), Guanine (G) and Cytosine (C) corresponding to the characteristic sequence of a genome. This paper proposes the use of linear Boolean functions, and demonstrates the textural or fractal behavior of genome evolution in terms of nucleotide adjoints.

Keywords: linear boolean functions, cellular automata, genome evolution.

I. Introduction

The four nucleotides A, T, G, and C get connected by phosphodiester bonds to form strands. Strand formation depends on innumerable factors related to inter and intra cellular parameters and functions. One cannot precisely say that a particular strand gets formed using such and such rules. The infinite possibilities of strand formation cannot be determined experimentally or in the framework of classical genetics. One can alternatively formulate a notion of "Language of Genomes" wherein one can finitely specify infinite strands, Fig. 1 shows a finitely generated quaternary tree structure of strand formation of nucleic acids.

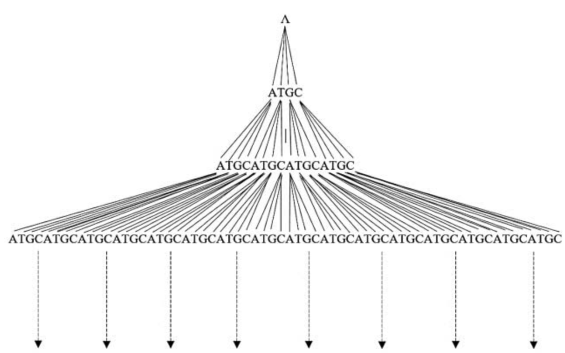

Fig. 1: Quaternary tree structure for strand formation

To be precise, Fig. 1 shows three levels of nucleotides. One can generate 64 strands of length 3. As the length increases, the number of strands increases as per the formula 4n, where n is the length of the strand. Strands of length three are called triplet codons or 3-tuple codons. Similarly, one can think of n-tuple codons where n is any number.

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Parallel Prediction of Nucleotides using One Dimensional Cellular Automata

A genome sequence is a chain of four nucleotides A, T, G and C. The numerical representation of a genome sequence is a sequence of four numbers 1, 2, 3 and 4. Linear prediction of a strand could be carried out using linear prediction algorithms from a sub sequence of length 8. Alternatively, one can evolve generations of genome sequences from a given full-length genome sequence using one-dimensional cellular automata rules. Section 2 describes the notions of adjoints of nucleotides corresponding to a genome sequence. Section 3 describes the notions of cellular automata and linear Boolean functions. Section 4 provides the results of applying linear Boolean functions on adjoint strings of nucleotides. Section 5 demonstrates the results of combining evolution patterns of adjoint sequences dyadically. Section 6 presents various observations made from the study and proposes future perspectives of cellular automata-based genome analytics.

II. Adjoints of Nucleotides

Adjoint of a particular nucleotide in a genome sequence is the binary sequence obtained by substituting the particular nucleotides in the genome sequence by 1's and the others by 0's. For example, let us consider a sample sequence G, A, A, T, G, A, T, T, A, C, C, A, A, G, G, C of length 16. Now the adjoint of adenine (A) is the binary string A(n) = 0, 1, 1, 0, 0, 1, 0, 0, 1, 0, 0, 1, 1, 0, 0, 0. The adjoint of thymine (T) is the binary string T(n) = 0, 0, 0, 1, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0. The adjoint of guanine (G) is the binary string G(n) = 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 1, 1, 0, 0. The adjoint of cytocine (C) is binary string C(n) = 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 0, 0, 0, 0, 1. The first segment of 40 nucleotides of a genome sequence of Brucella Suis 1330 is considered here for a case study. The actual length of the genome sequence of Brucella Suis 1330 is 5806. The sample sequence is given below.

GAATGATTACCAAGGCCAAGCTCAAGCTCTCCTTCCTTGG

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Now the adjoints of this sample sequence of length 40 are given below.

A(n) = 0110010010011000011000011000000000000000
T(n) = 00010011000000000000001000001010011001100
G(n) = 1000100000000110000100000100000000000011
C(n) = 0000000001100001100010100010101100110000

A cellular automaton is an idealized parallel processing system consisting of an array of numbers (1-D, 2-D and more) realized using updating rules based on certain neighborhood. For example, a one-dimensional cellular automaton would consist of a finite length array as shown below.

III. Cellular Automata and Linear Boolean Functions

A cellular automaton is an idealized parallel processing system consisting of an array of numbers (1-D, 2-D and more) realized using updating rules based on certain neighborhood. For example, a one dimensional cellular automaton would consist of a finite length array as shown below.

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Consider an ith cell in the array. This cell has a neighbor i-1 on its left and another i+1 on its right. All three put together is called a three-neighborhood. One can assign a site (cell) variable ξi-1, ξi, and ξi+1 to the three-neighborhood cells. At a particular instant of time, these variables take on numerical values, say either a 0 or a 1. In such a case, the variables are denoted as ξti-1, ξti, and ξti+1. The value of the ith cell at the next instant of time is evaluated using an updating rule that involves the present values of the ith, (i-1)th and (i+1)th cells. This updating rule is essentially a linear Boolean function of three variables. One can construct 256 linear Boolean functions as updating rules of one-dimensional three-neighborhood binary-valued cellular automata. Each rule defines an automaton by itself. So, one-dimensional binary-valued three-neighborhood cellular automata (123CA) rules could be used to model adjoints of a genome sequence. The first thirty linear Boolean functions of cellular automata 123CA are listed below with their decimal equivalents.

Linear Boolean Function	Decimal Equivalent
0	0
$(\bar{\xi}_{i-1}\bar{\xi}_i\bar{\xi}_{i+1})$	1
$(\bar{\xi}_{i-1}\bar{\xi}_i\xi_{i+1})$	2
$(\bar{\xi}_{i-1}\bar{\xi}_i)$	3
$(\bar{\xi}_{i-1}\xi_i\bar{\xi}_{i+1})$	4
$(\bar{\xi}_{i-1}\bar{\xi}_{i+1})$	5
$(\bar{\xi}_{i-1}\xi_i\bar{\xi}_{i+1})+(\bar{\xi}_{i-1}\bar{\xi}_i\xi_{i+1})$	6
$(\bar{\xi}_{i-1}\bar{\xi}_{i+1})+(\bar{\xi}_{i-1}\bar{\xi}_i)$	7
$(\bar{\xi}_{i-1}\xi_i\xi_{i+1})$	8
$(\bar{\xi}_{i-1}\bar{\xi}_i\bar{\xi}_{i+1}) + (\bar{\xi}_{i-1}\xi_i\xi_{i+1})$	9
$(\bar{\xi}_{i-1}\xi_{i+1})$	10
$(\bar{\xi}_{i-1}\bar{\xi}_i) + (\bar{\xi}_{i-1}\xi_{i+1})$	11
$(\bar{\xi}_{i-1}\xi_i)$	12
$(\bar{\xi}_{i-1}\bar{\xi}_{i+1}) + (\bar{\xi}_{i-1}\xi_i)$	13
$(\bar{\xi}_{i-1}\xi_i) + (\bar{\xi}_{i-1}\xi_{i+1})$	14
$(\bar{\xi}_{i-1})$	15
$(\xi_{i-1}\bar{\xi}_i\bar{\xi}_{i+1})$	16
$(\bar{\xi}_i\bar{\xi}_{i+1})$	17
$(\xi_{i-1}\bar{\xi}_i\bar{\xi}_{i+1}) + (\bar{\xi}_{i-1}\bar{\xi}_i\xi_{i+1})$	18
$(\bar{\xi}_i\bar{\xi}_{i+1}) + (\bar{\xi}_{i-1}\bar{\xi}_i)$	19
$(\xi_{i-1}\bar{\xi}_i\bar{\xi}_{i+1}) + (\bar{\xi}_{i-1}\xi_i\bar{\xi}_{i+1})$	20
$(\bar{\xi}_i\bar{\xi}_{i+1}) + (\bar{\xi}_{i-1}\bar{\xi}_{i+1})$	21
$(\xi_{i-1}\bar{\xi}_i\bar{\xi}_{i+1}) + (\bar{\xi}_{i-1}\xi_i\bar{\xi}_{i+1}) + (\bar{\xi}_{i-1}\bar{\xi}_i\xi_{i+1})$	22
$(\bar{\xi}_i\bar{\xi}_{i+1}) + (\bar{\xi}_{i-1}\bar{\xi}_{i+1}) + (\bar{\xi}_{i-1}\bar{\xi}_i)$	23
$(\xi_{i-1}\bar{\xi}_i\bar{\xi}_{i+1}) + (\bar{\xi}_{i-1}\xi_i\xi_{i+1})$	24
$(\bar{\xi}_{i-1}\xi_i\xi_{i+1}) + (\bar{\xi}_i\bar{\xi}_{i+1})$	25
$(\xi_{i-1}\bar{\xi}_i\bar{\xi}_{i+1}) + (\bar{\xi}_{i-1}\xi_{i+1})$	26
$(\bar{\xi}_i\bar{\xi}_{i+1}) + (\bar{\xi}_{i-1}\xi_{i+1})$	27
$(\xi_{i-1}\bar{\xi}_i\bar{\xi}_{i+1}) + (\bar{\xi}_{i-1}\xi_i)$	28
$(\bar{\xi}_i\bar{\xi}_{i+1}) + (\bar{\xi}_{i-1}\xi_i)$	29
$(\xi_{i-1}\bar{\xi}_i\bar{\xi}_{i+1}) + (\bar{\xi}_{i-1}\xi_i) + (\bar{\xi}_{i-1}\xi_{i+1})$	30

IV. Cellular Automata Evolutions of Genome Adjoints

The genome sequence of Brucella Suis 1330 is considered here for a case study. Due to space limitations, a part of the genome sequence and its adjoints are shown below. As defined already, adjoint of genome sequence concerning a particular nucleotide is the binary string obtained by marking a '1' in the place of that particular nucleotide and by marking a '0' in the places of other nucleotides. A segment consisting of 60 nucleotides of Brucella Suis 1330 is shown below.

Row Number	Column 1	Column 2	Column 3	Column 4	Column 5	Column 6
1.	GAATGATTAC	CAAGGCCAAG	CTCAAGCTCT	CCTTCCTTGG	GCTGAGCTTT	TGCCTTTGCA
2.	ATTCGTCATT	TTTTTTCTGT	CACTGCTGAC	GAAAGACCCA	GCCAGCCGGG	CCCAAGTCGT
3.	CTGTCTGCCT	GAGCCTTGAG	TCCAGATCGC	AGCAGCCCCT	GATGCTCGGC	TCCTTTGCCT
4.	CCGAGCGTCT	TCGGTCCAGC	CTCCTGACCT	CTGCCCCTTG	CTCATCGCCC	TCTCTTTCCT
5.	GCCCCCTCCC	AGGGCACCTC	TGTCGGACGC	GGCCCACGGA	CCTGGTGTTT	GTTGTGGACA
6.	GCTCGCGCAG	CGTGCGGCCA	GTGGAGTTTG	AGAAGGTGAA	GGTGTTCCTG	TCCCAGGTCA
7.	TCGAGTCCCT	GGACGTGGGG	CCCAATGCCA	CCCGCGTGGG	CCTGGTCAAC	TACGCCAGCG
8.	CCGTGAAGCA	GGAGTTCCCG	CTGCGGGCCC	ACGGCTCCAA	GGCCGCGCTG	CTGCAGGCCG
9.	TGCGCCGCAT	CCAGCCACTG	TCCACGGGGA	CCATGACGGG	CCTGGCCATC	CAGTTTGCCA
10.	TCACCAGGGC	CTTCAGTGAA	GCCGAGGGCG	GTCGCGCCAG	GTCCCCCGAC	ATCAGCAAGG
11.	TGCGTGCCCG	CCCTGCTGGG	TTCCCGCTGT	TTGTCGCTCC	CACTTGTGCT	AAGAACTCTT
12.	GCCGGCACGC	TCTTTGGTTC	TCCCGCACAC	CCCCGCGATG	GCCGTTTTAC	TTCGGGGACC
13.	AGACCCAACT	AAGAGAACGA	CGGCTGACGC	TGGGATCGAA	CCCCTCTTTA	CCCACCTTCC
14.	GACCCCAGGC	CTCACAATGG	GGTGACGATG	ATTTCAGGGT	GGTTGACCTT	GGCTCCCCCG
15.	CCCCGTCTGA	GCTCCTCGAA	CGCACAGCGA	GAGGGTGCAG	ATGCTTATGT	GATGGTCAGG
16.	GGCGTGGACA	CTGCCGCCGG	CCTGTCCACG	TTCAAGCCCC	GGCTCCACCA	CACCAGCTGT
17.	GCCTCCCTGA	GCAGGAGCTT	CAGCCCGTGC	GCCTCAGTTT	CCTCACCTAC	AAAATGGGAG
18.	CAACACAGCG	CCTTCTCAGA	GGGCCGCAGG	CAGGACTAAA	CGAGTTCATC	TGCTGAAGGC
19.	GCTCAGCACA	GCGCCTCGGA	CCCAACAGGC	CCCATGGAGG	CGTTAGCTGA	GTTTGTATTT
20.	AGTACGCCTT	TGAGGGGGAG	GGGCTCAGAA	ACGCAAAGCA	ATGCCCCCAA	GTCACACTGG

The adjoints of the genome sequence segment are given below.

Adjoint A(n)

Row Number	0olumn 1	0olumn 2	0olumn 3	0olumn 4	0olumn 5	0olumn 6
1.	0110010010	0110000110	0001100000	0000000000	0000100000	000000001
2.	1000000100	0000000000	0100000010	0111010001	0001000000	0001100000
3.	0000000000	0100000010	0001010000	1001000000	0100000000	0000000000
4.	0001000000	0000000100	0000001000	0000000000	0001000000	0000000000
5.	0000000000	1000010000	0000001000	000001000	0000000000	000000101
6.	0000000010	0000000001	0000100000	1011000011	0000000000	000010001
7.	0001000000	0010000000	000110000	0000000000	0000000110	010001000
8.	000001100	0010000000	0000000000	1000000011	0000000000	000010000
9.	0000000010	0010001000	000100000	0010010000	0000000100	010000001
10.	0010010000	000010001	0000100000	0000000010	0000000010	1001001100
11.	0000000000	0000000000	0000000000	0000000000	0100000000	1101100000
12.	0000001000	0000000000	0000001010	0000000100	0000000010	000000100
13.	1010001100	110101100	0000001000	000010001	000000001	0001000000
14.	0100001000	0001011000	0000100100	1000010000	0000010000	0000000000
15.	000000001	000000001	0001010001	0100000010	1000001000	010000100
16.	000000101	0000000000	0000000100	0001100000	0000001001	0100100000
17.	000000001	0010010000	0100000000	0000010000	0000100010	1111000010
18.	0110101000	000000101	0000000100	0100100111	0010000100	0000011000
19.	0000100101	000000001	0001101000	0001000100	0000100001	000001000
20.	1001000000	0010000010	000001011	100011001	100000011	0001010000

Adjoint T(n)

Row Number	0olumn 1	0olumn 2	0olumn 3	0olumn 4	0olumn 5	0olumn 6
1.	0001001100	0000000000	0100000101	0011001100	0010000111	1000111000
2.	0110010011	1111110101	0001001000	0000000000	0000000000	0000001001
3.	0101010001	0000011000	1000001000	0000000001	0010010000	1001110001
4.	0000000101	1000100000	0100100001	0100000110	0100100000	1010111001
5.	0000001000	0000000010	1010000000	0000000000	0010010111	0110100000
6.	0010000000	0010000000	0100001110	0000001000	0010110010	1000000100
7.	1000010001	0000010000	0000010000	0000001000	0010010000	1000000000
8.	0001000000	0000110000	0100000000	0000010000	0000000010	0100000000
9.	1000000001	0000000010	1000000000	0001000000	0010000010	0001110000
10.	1000000000	0110001000	0000000000	0100000000	0100000000	0100000000
11.	1000100000	0001001000	1100000101	1101000100	0001101001	0000001011
12.	0000000000	1011100110	1000000000	0000000010	0000111100	1100000000
13.	0000000001	0000000000	0000100000	1000010000	0000010110	0000001100
14.	0000000000	0100000100	0010000010	0111000001	0011000011	0001000000
15.	0000010100	0010010000	0000000000	0000010000	0100110101	0010010000
16.	0000100000	0100000000	0010100000	1100000000	0001000000	0000000101
17.	0001000100	0000000011	0000000100	0001000111	0010000100	0000100000
18.	0000000000	0011010000	0000000000	0000001000	0000110010	1001000000
19.	0010000000	0000010000	0000000000	0000100000	0011000100	0111010111
20.	0010000011	1000000000	0000100000	0000100000	0100000000	0100000100

Adjoint G(n)

Row Number	0olumn 1	0olumn 2	0olumn 3	0olumn 4	0olumn 5	0olumn 6
1.	1000100000	0001100001	0000010000	0000000011	1001010000	0100000100
2.	0000100000	0000000010	0000100100	1000100000	1000100111	0000010010
3.	0010001000	1010000101	0000100010	0100100000	1001000110	0000001000
4.	0010101000	0011000010	0000010000	0010000001	0000001000	0000000000
5.	1000000000	0111000000	0100110010	1100000110	0001101000	1001011000
6.	1000101001	0101011000	1011010001	0100110100	1101000001	0000011000
7.	0010100000	1100101111	0000001000	0001010111	0001100000	0001000101
8.	0010100100	1101000001	0010111000	0011000000	1100101001	0010011001
9.	0101001000	0001000001	0000011110	0000100111	0001100000	0010001000
10.	0000001110	0000010100	1001011101	1001010001	1000000100	0000100011
11.	0101010001	0000100111	0000010010	0010010000	0000010100	0010000000
12.	1001100010	0000011000	0000100000	0000101001	1001000000	0001111000
13.	0100000000	0010100010	0110010010	0111000100	0000000000	0000000000
14.	1000000110	0000000011	1101001001	0000001110	1100100000	1100000001
15.	0000100010	1000000100	0100001010	1011101001	0010000010	1001100011
16.	1101011000	0010010011	0001000001	0000010000	1100000000	0000010010
17.	1000000010	1001101000	0010001010	1000001000	0000000000	0000011101
18.	0000000101	0000000010	1110010011	0011000000	0101000000	0100100110
19.	1000010000	1010000110	0000000110	0000011011	0100010010	1000100000
20.	0100010000	0101111101	1110000100	0010000100	0010000000	1000000011

Adjoint C(n)

Row Number	1olumn 1	1olumn 2	1olumn 3	1olumn 4	1olumn 5	1olumn 6
1.	0000000001	1000011000	1010001010	1100110000	0100001000	0011000010
2.	0001001000	0000001000	1010010001	0000001110	0110011000	1110000100
3.	1000100110	0001100000	0110000101	0010011110	0000101001	0110000110
4.	1100010010	0100011001	1011000110	1001111000	1010010111	0101000110
5.	0111110111	0000101101	0001000101	0011101000	1100000000	0000000010
6.	0101010100	1000100110	0000000000	0000000000	0000001100	0111000010
7.	0100001110	0001000000	1110000110	1110100000	1100001001	0010110010
8.	1100000010	0000001110	1001000111	0100101100	0011010100	1001000110
9.	0010110100	1100110100	0110100000	1100001000	1100011001	1000000110
10.	0101100001	1001000000	0110000010	0010101100	0011111001	0010010000
11.	0010001110	1110010000	0011101000	0000101011	1010000010	0000010100
12.	0110010101	0100000001	0111010101	1111010000	0110000001	0010000011
13.	0001110010	0000000100	1001000101	0000001000	1111010000	1110110011
14.	0011110001	1010100000	0000010000	0000100000	0000001100	0010111110
15.	1111001000	0101101000	1010100100	0000000100	0001000000	0000001000
16.	0010000010	1001101100	1100011010	0010001111	0010110110	1011001000
17.	0110111000	0100000100	1001110001	0110100000	1101011001	0000000000
18.	1001010010	1100101000	0001101000	1000010000	1000001001	0010000001
19.	0101001010	0101101000	1110010001	1110000000	1000001000	0000000000
20.	0000101100	0000000000	0001010000	0101000010	0001111100	0010101000

Cellular automata evolutions of adjoints of a genome are carried out using 256 rules of 123CA. As an example, rule number 137 of 123CA, that is, $(\bar{\xi}_{i-1}\bar{\xi}_i\bar{\xi}_{i+1}) + (\xi_i\xi_{i+1})$ is applied to adjoints of Brucella Suis 1330 genome and results shown below in Fig. 2.

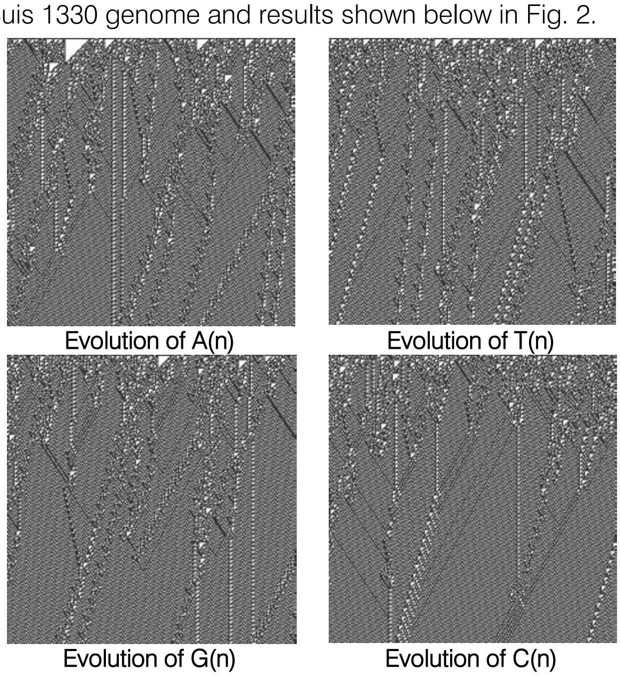


Fig. 2: Evolution of adjoints using rule 137 of 123CA

The size of the images shown in Fig. 2 is 500x500, though the actual size is 5806x500. The first 500 columns of the actual images are clipped and presented here for visual clarity. From Fig. 2, it is clear that the evolution pattern of each adjoint is different. One can observe that there are certain fractal patterns in the evolutions and such fractals are distributed in the images very differently. For instance, the zoomed in versions of the evolution patterns of A(n), T(n), G(n) and C(n) using rule 137 are shown in Figs. 3, 4, 5 and 6 respectively.

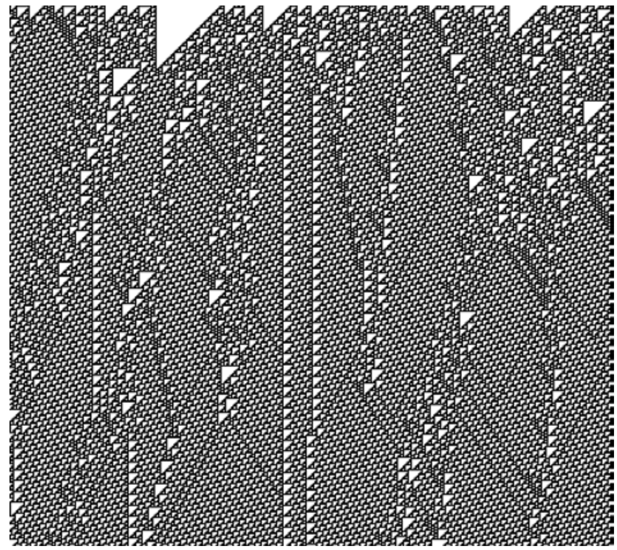


Fig. 3: Zoomed in version of evolution pattern of A(n)

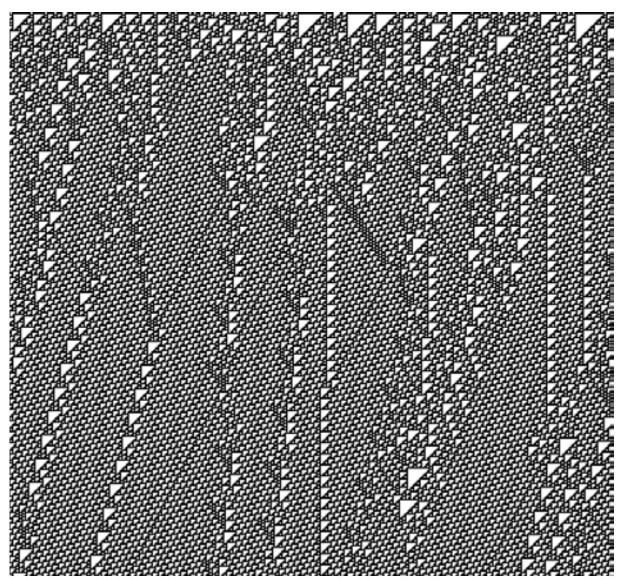


Fig. 4: Zoomed in version of evolution pattern of T(n)

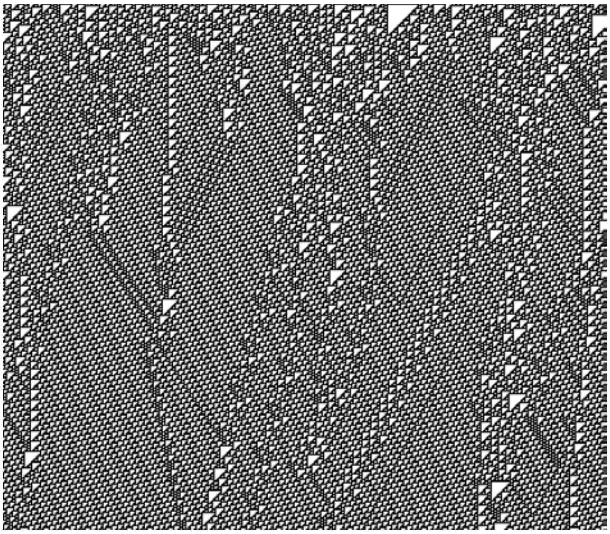


Fig. 5: Zoomed in version of evolution pattern of G(n)

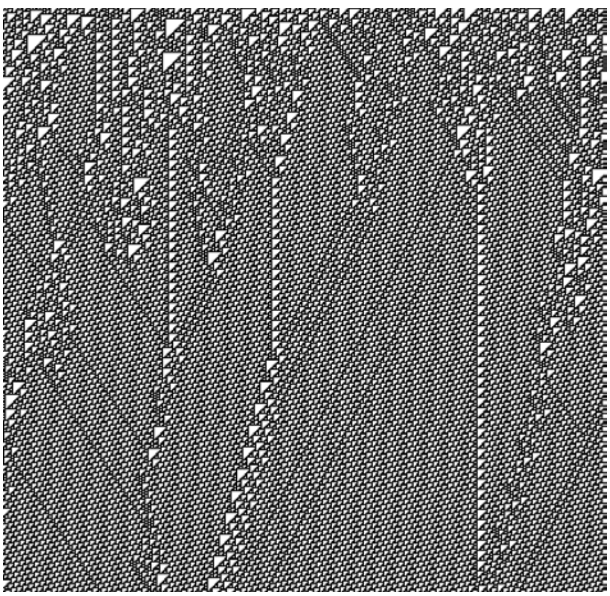
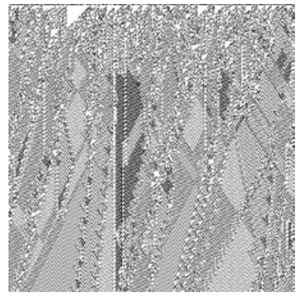


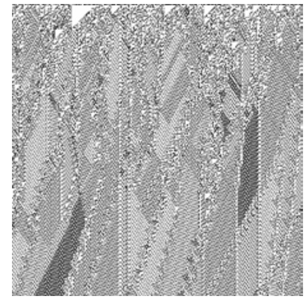
Fig. 6: Zoomed in version of evolution pattern of C(n)

V. Dyadic Operations between Cellular Automata Evolutions of Genome Adjoints

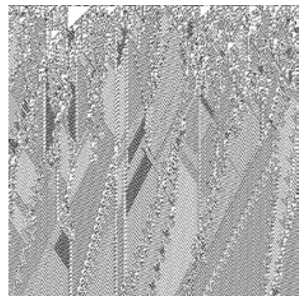
It is a matter of an empirical study to examine the conjoint behavior of various evolution patterns of adjoints and it could be carried out by combining evolution patterns of adjoints dyadically. The various dyadic operations are (i) Boolean addition, (ii) Boolean subtraction, (iii) Boolean multiplication, (iv) Boolean division, (v) Dyadic relation of maximum and (vi) Dyadic relation of minimum. Out of these six different dyadic operations and relations, the Boolean operation of binary addition is considered here for the intended study.



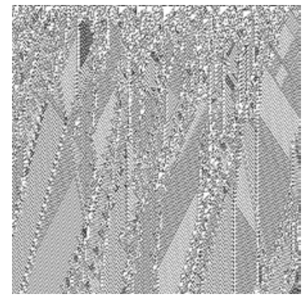
Addition of patterns of A and T



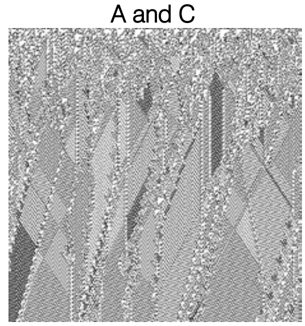
Addition of patterns of A and G



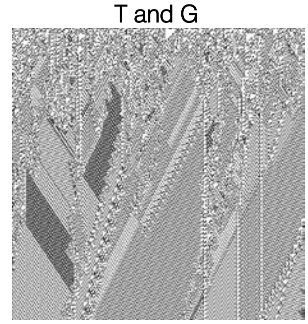
Addition of patterns of A and C



Addition of patterns of T and G



Addition of patterns of T and C



Addition of patterns of G and C

Fig. 7: Boolean addition of evolution patterns of adjoints

The zoomed in versions of the Boolean additions of evolution patterns of A(n), T(n), G(n) and C(n) using rule 137 are shown in Figs. 7, 8, 9 and 10 respectively.

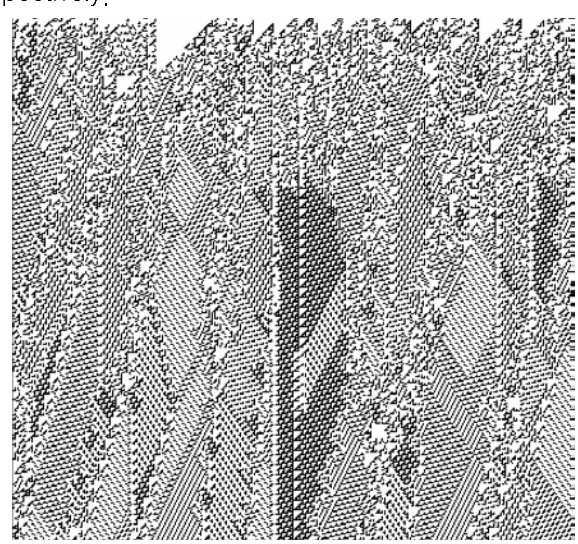


Fig. 8: Zoomed in version of addition of patterns of A and T

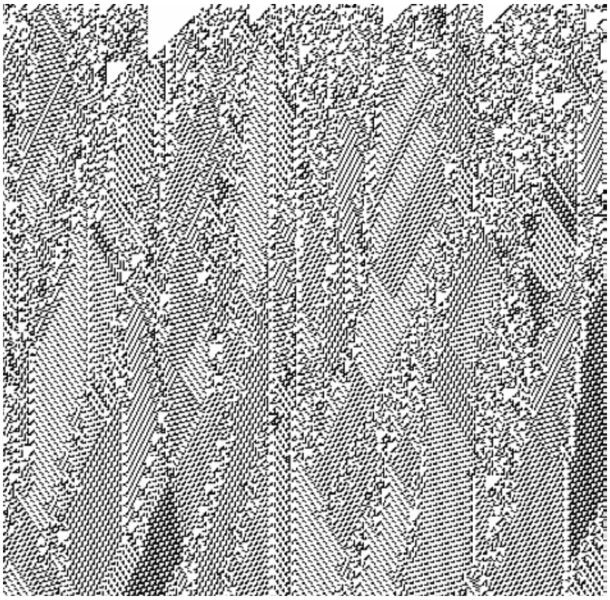


Fig. 9: Zoomed in version of addition of patterns of A and G

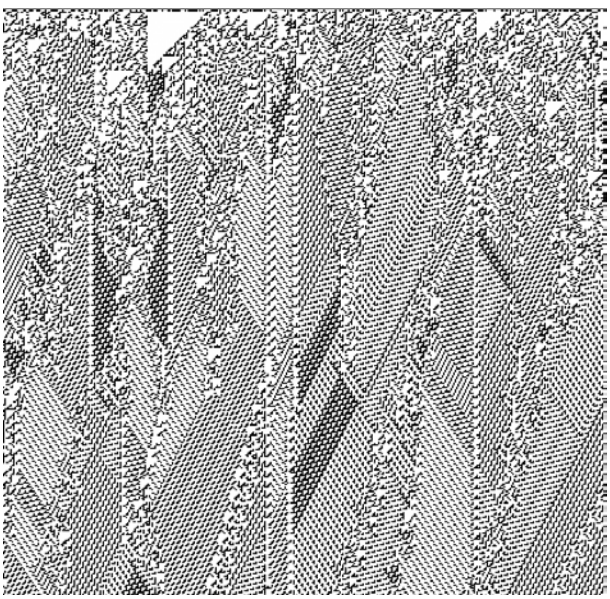


Fig. 10: Zoomed in version of addition of patterns of A and C

VI. Observations and Conclusions

From the above empirical study, it is observed that cellular automata modeling and simulation of evolutions of adjoints of a given genome sequence and the inter-pattern operations and relations exhibit distinct patterns of fractals and fractal distributions. The novel technique and results presented in this paper are outcome of prolonged research carried out in the mathematical modeling of genomes and their evolutions. It is evident that one can as well look into the possibilities of genome editing using such cellular automata tools.

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Verbs have to be in agreement with their subjects. In a research paper, do not start sentences with conjunctions or finish them with prepositions. When writing formally, it is advisable to never split an infinitive because someone will (wrongly) complain. Avoid clichés like a disease. Always shun irritating alliteration. Use language which is simple and straightforward. Put together a neat summary.

14. Arrangement of information: Each section of the main body should start with an opening sentence, and there should be a changeover at the end of the section. Give only valid and powerful arguments for your topic. You may also maintain your arguments with records.

15. Never start at the last minute: Always allow enough time for research work. Leaving everything to the last minute will degrade your paper and spoil your work.

16. Multitasking in research is not good: Doing several things at the same time is a bad habit in the case of research activity. Research is an area where everything has a particular time slot. Divide your research work into parts, and do a particular part in a particular time slot.

17. Never copy others' work: Never copy others' work and give it your name because if the evaluator has seen it anywhere, you will be in trouble. Take proper rest and food: No matter how many hours you spend on your research activity, if you are not taking care of your health, then all your efforts will have been in vain. For quality research, take proper rest and food.

18. Go to seminars: Attend seminars if the topic is relevant to your research area. Utilize all your resources.

19. Refresh your mind after intervals: Try to give your mind a rest by listening to soft music or sleeping in intervals. This will also improve your memory. Acquire colleagues: Always try to acquire colleagues. No matter how sharp you are, if you acquire colleagues, they can give you ideas which will be helpful to your research.

20. Think technically: Always think technically. If anything happens, search for its reasons, benefits, and demerits. Think and then print: When you go to print your paper, check that tables are not split, headings are not detached from their descriptions, and page sequence is maintained.

21. Adding unnecessary information: Do not add unnecessary information like "I have used MS Excel to draw graphs." Irrelevant and inappropriate material is superfluous. Foreign terminology and phrases are not apropos. One should never take a broad view. Analogy is like feathers on a snake. Use words properly, regardless of how others use them. Remove quotations. Puns are for kids, not grunt readers. Never oversimplify: When adding material to your research paper, never go for oversimplification; this will definitely irritate the evaluator. Be specific. Never use rhythmic redundancies. Contractions shouldn't be used in a research paper. Comparisons are as terrible as clichés. Give up ampersands, abbreviations, and so on. Remove commas that are not necessary. Parenthetical words should be between brackets or commas. Understatement is always the best way to put forward earth-shaking thoughts. Give a detailed literary review.

22. Report concluded results: Use concluded results. From raw data, filter the results, and then conclude your studies based on measurements and observations taken. An appropriate number of decimal places should be used. Parenthetical remarks are prohibited here. Proofread carefully at the final stage. At the end, give an outline to your arguments. Spot perspectives of further study of the subject. Justify your conclusion at the bottom sufficiently, which will probably include examples.

23. Upon conclusion: Once you have concluded your research, the next most important step is to present your findings. Presentation is extremely important as it is the definite medium though which your research is going to be in print for the rest of the crowd. Care should be taken to categorize your thoughts well and present them in a logical and neat manner. A good quality research paper format is essential because it serves to highlight your research paper and bring to light all necessary aspects of your research.

Informal Guidelines of Research Paper Writing

Key points to remember:

- Submit all work in its final form.
- Write your paper in the form which is presented in the guidelines using the template.
- Please note the criteria peer reviewers will use for grading the final paper.

Final points:

One purpose of organizing a research paper is to let people interpret your efforts selectively. The journal requires the following sections, submitted in the order listed, with each section starting on a new page:

The introduction: This will be compiled from reference matter and reflect the design processes or outline of basis that directed you to make a study. As you carry out the process of study, the method and process section will be constructed like that. The results segment will show related statistics in nearly sequential order and direct reviewers to similar intellectual paths throughout the data that you gathered to carry out your study.

The discussion section:

This will provide understanding of the data and projections as to the implications of the results. The use of good quality references throughout the paper will give the effort trustworthiness by representing an alertness to prior workings.

Writing a research paper is not an easy job, no matter how trouble-free the actual research or concept. Practice, excellent preparation, and controlled record-keeping are the only means to make straightforward progression.

General style:

Specific editorial column necessities for compliance of a manuscript will always take over from directions in these general guidelines.

To make a paper clear: Adhere to recommended page limits.

Mistakes to avoid:

- Insertion of a title at the foot of a page with subsequent text on the next page.
- Separating a table, chart, or figure—confine each to a single page.
- Submitting a manuscript with pages out of sequence.
- In every section of your document, use standard writing style, including articles ("a" and "the").
- Keep paying attention to the topic of the paper.
- Use paragraphs to split each significant point (excluding the abstract).
- Align the primary line of each section.
- Present your points in sound order.
- Use present tense to report well-accepted matters.
- Use past tense to describe specific results.
- Do not use familiar wording; don't address the reviewer directly. Don't use slang or superlatives.
- Avoid use of extra pictures—include only those figures essential to presenting results.

Title page:

Choose a revealing title. It should be short and include the name(s) and address(es) of all authors. It should not have acronyms or abbreviations or exceed two printed lines.

Abstract: This summary should be two hundred words or less. It should clearly and briefly explain the key findings reported in the manuscript and must have precise statistics. It should not have acronyms or abbreviations. It should be logical in itself. Do not cite references at this point.

An abstract is a brief, distinct paragraph summary of finished work or work in development. In a minute or less, a reviewer can be taught the foundation behind the study, common approaches to the problem, relevant results, and significant conclusions or new questions.

Write your summary when your paper is completed because how can you write the summary of anything which is not yet written? Wealth of terminology is very essential in abstract. Use comprehensive sentences, and do not sacrifice readability for brevity; you can maintain it succinctly by phrasing sentences so that they provide more than a lone rationale. The author can at this moment go straight to shortening the outcome. Sum up the study with the subsequent elements in any summary. Try to limit the initial two items to no more than one line each.

Reason for writing the article—theory, overall issue, purpose.

- Fundamental goal.
- To-the-point depiction of the research.
- Consequences, including definite statistics—if the consequences are quantitative in nature, account for this; results of any numerical analysis should be reported. Significant conclusions or questions that emerge from the research.

Approach:

- Single section and succinct.
- An outline of the job done is always written in past tense.
- Concentrate on shortening results—limit background information to a verdict or two.
- Exact spelling, clarity of sentences and phrases, and appropriate reporting of quantities (proper units, important statistics) are just as significant in an abstract as they are anywhere else.

Introduction:

The introduction should "introduce" the manuscript. The reviewer should be presented with sufficient background information to be capable of comprehending and calculating the purpose of your study without having to refer to other works. The basis for the study should be offered. Give the most important references, but avoid making a comprehensive appraisal of the topic. Describe the problem visibly. If the problem is not acknowledged in a logical, reasonable way, the reviewer will give no attention to your results. Speak in common terms about techniques used to explain the problem, if needed, but do not present any particulars about the protocols here.

The following approach can create a valuable beginning:

- Explain the value (significance) of the study.
- Defend the model—why did you employ this particular system or method? What is its compensation? Remark upon its appropriateness from an abstract point of view as well as pointing out sensible reasons for using it.
- Present a justification. State your particular theory(-ies) or aim(s), and describe the logic that led you to choose them.
- Briefly explain the study's tentative purpose and how it meets the declared objectives.

Approach:

Use past tense except for when referring to recognized facts. After all, the manuscript will be submitted after the entire job is done. Sort out your thoughts; manufacture one key point for every section. If you make the four points listed above, you will need at least four paragraphs. Present surrounding information only when it is necessary to support a situation. The reviewer does not desire to read everything you know about a topic. Shape the theory specifically—do not take a broad view.

As always, give awareness to spelling, simplicity, and correctness of sentences and phrases.

Procedures (methods and materials):

This part is supposed to be the easiest to carve if you have good skills. A soundly written procedures segment allows a capable scientist to replicate your results. Present precise information about your supplies. The suppliers and clarity of reagents can be helpful bits of information. Present methods in sequential order, but linked methodologies can be grouped as a segment. Be concise when relating the protocols. Attempt to give the least amount of information that would permit another capable scientist to replicate your outcome, but be cautious that vital information is integrated. The use of subheadings is suggested and ought to be synchronized with the results section.

When a technique is used that has been well-described in another section, mention the specific item describing the way, but draw the basic principle while stating the situation. The purpose is to show all particular resources and broad procedures so that another person may use some or all of the methods in one more study or referee the scientific value of your work. It is not to be a step-by-step report of the whole thing you did, nor is a methods section a set of orders.

Materials:

Materials may be reported in part of a section or else they may be recognized along with your measures.

Methods:

- Report the method and not the particulars of each process that engaged the same methodology.
- Describe the method entirely.
- To be succinct, present methods under headings dedicated to specific dealings or groups of measures.
- Simplify—detail how procedures were completed, not how they were performed on a particular day.
- If well-known procedures were used, account for the procedure by name, possibly with a reference, and that's all.

Approach:

It is embarrassing to use vigorous voice when documenting methods without using first person, which would focus the reviewer's interest on the researcher rather than the job. As a result, when writing up the methods, most authors use third person passive voice.

Use standard style in this and every other part of the paper—avoid familiar lists, and use full sentences.

What to keep away from:

- Resources and methods are not a set of information.
- Skip all descriptive information and surroundings—save it for the argument.
- Leave out information that is immaterial to a third party.

Results:

The principle of a results segment is to present and demonstrate your conclusion. Create this part as entirely objective details of the outcome, and save all understanding for the discussion.

The page length of this segment is set by the sum and types of data to be reported. Use statistics and tables, if suitable, to present consequences most efficiently.

You must clearly differentiate material which would usually be incorporated in a study editorial from any unprocessed data or additional appendix matter that would not be available. In fact, such matters should not be submitted at all except if requested by the instructor.

Content:

- Sum up your conclusions in text and demonstrate them, if suitable, with figures and tables.
- In the manuscript, explain each of your consequences, and point the reader to remarks that are most appropriate.
- Present a background, such as by describing the question that was addressed by creation of an exacting study.
- Explain results of control experiments and give remarks that are not accessible in a prescribed figure or table, if appropriate.
- Examine your data, then prepare the analyzed (transformed) data in the form of a figure (graph), table, or manuscript.

What to stay away from:

- Do not discuss or infer your outcome, report surrounding information, or try to explain anything.
- Do not include raw data or intermediate calculations in a research manuscript.
- Do not present similar data more than once.
- A manuscript should complement any figures or tables, not duplicate information.
- Never confuse figures with tables—there is a difference.

Approach:

As always, use past tense when you submit your results, and put the whole thing in a reasonable order.

Put figures and tables, appropriately numbered, in order at the end of the report.

If you desire, you may place your figures and tables properly within the text of your results section.

Figures and tables:

If you put figures and tables at the end of some details, make certain that they are visibly distinguished from any attached appendix materials, such as raw facts. Whatever the position, each table must be titled, numbered one after the other, and include a heading. All figures and tables must be divided from the text.

Discussion:

The discussion is expected to be the trickiest segment to write. A lot of papers submitted to the journal are discarded based on problems with the discussion. There is no rule for how long an argument should be.

Position your understanding of the outcome visibly to lead the reviewer through your conclusions, and then finish the paper with a summing up of the implications of the study. The purpose here is to offer an understanding of your results and support all of your conclusions, using facts from your research and generally accepted information, if suitable. The implication of results should be fully described.

Infer your data in the conversation in suitable depth. This means that when you clarify an observable fact, you must explain mechanisms that may account for the observation. If your results vary from your prospect, make clear why that may have happened. If your results agree, then explain the theory that the proof supported. It is never suitable to just state that the data approved the prospect, and let it drop at that. Make a decision as to whether each premise is supported or discarded or if you cannot make a conclusion with assurance. Do not just dismiss a study or part of a study as "uncertain."

Research papers are not acknowledged if the work is imperfect. Draw what conclusions you can based upon the results that you have, and take care of the study as a finished work.

- o You may propose future guidelines, such as how an experiment might be personalized to accomplish a new idea.
- o Give details of all of your remarks as much as possible, focusing on mechanisms.
- o Make a decision as to whether the tentative design sufficiently addressed the theory and whether or not it was correctly restricted. Try to present substitute explanations if they are sensible alternatives.
- o One piece of research will not counter an overall question, so maintain the large picture in mind. Where do you go next? The best studies unlock new avenues of study. What questions remain?
- o Recommendations for detailed papers will offer supplementary suggestions.

Approach:

When you refer to information, differentiate data generated by your own studies from other available information. Present work done by specific persons (including you) in past tense.

Describe generally acknowledged facts and main beliefs in present tense.

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Abstract	Clear and concise with appropriate content, Correct format. 200 words or below	Unclear summary and no specific data, Incorrect form Above 200 words	No specific data with ambiguous information Above 250 words
Introduction	Containing all background details with clear goal and appropriate details, flow specification, no grammar and spelling mistake, well organized sentence and paragraph, reference cited	Unclear and confusing data, appropriate format, grammar and spelling errors with unorganized matter	Out of place depth and content, hazy format
Methods and Procedures	Clear and to the point with well arranged paragraph, precision and accuracy of facts and figures, well organized subheads	Difficult to comprehend with embarrassed text, too much explanation but completed	Incorrect and unorganized structure with hazy meaning
Result	Well organized, Clear and specific, Correct units with precision, correct data, well structuring of paragraph, no grammar and spelling mistake	Complete and embarrassed text, difficult to comprehend	Irregular format with wrong facts and figures
Discussion	Well organized, meaningful specification, sound conclusion, logical and concise explanation, highly structured paragraph reference cited	Wordy, unclear conclusion, spurious	Conclusion is not cited, unorganized, difficult to comprehend
References	Complete and correct format, well organized	Beside the point, Incomplete	Wrong format and structuring

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