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A PATENT ANALYSIS IN CISTRON EDITING USING STURDY ALPHA MATCHING TECHNIQUE ON FUZZYPLOTS

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Abstract:

This study investigates innovation in emerging technologies through both quantitative and qualitative patent analysis and citation trends. This paper deals with the cure of congential disease and emerging technology of cistron editing using sturdy alpha matching. Congential disorders are caused by cistrons when a cistron or cistrons has a problem with its code and this leads health problems. Such things happened as a mutation, deletion, translocation, an extra or missing chromosome and too few or too many sex chromosomes. There are different types of congential disorders found from the new born to teen agers. At present situation the congential disorders are cured by genome editing with many methods, like clustered regularly interspaced short palindromic repeatsclustered regularly interspaced short palindromic repeats is one of the most successful in medical field to edit the cistrons,in which is short for clustered regularly interspaced short palindromic repeats and clustered regularly interspaced short palindromic repeatsclustered regularly interspaced short palindromic repeats – associated protein 9.It creates lots of successful cistron editing in medical community since it is time wise, cost wise and more efficient than other methods. In this paper we introduce the technique of sturdy alpha matching in clustered regularly interspaced short palindromic repeatsclustered regularly interspaced short palindromic

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repeats – Cas 9 to provide the most efficient in cistron editing using fuzzyplots. Our findings reveal significant trends in patent activity, highlighting the most influential patents and emerging technological fields. This comprehensive approach provides valuable insights into the dynamics of innovation, guiding future research and policy – making in technology development.

Keywords: Fuzzy Set, Fuzzyplots, Fuzzy Alpha Cut, Fuzzy Alpha Matching, Cistron Editing.

Introduction:

Quantitative methods focus on the number of patents and their citation counts to identify key trends and influential technologies. Qualitative approaches examine the content and context of patent documents to understand the nature and impact of innovations. By combining these methods, we map the landscape of technological advancements and identify critical areas of innovation. In 2013, Feng Zhang narrated how clustered regularly interspaced short palindromic repeatsclustered regularly interspaced short palindromic repeats could be used to edit eukaryotic deoxyribonucleic acid. Since these finding out, clustered regularly interspaced short palindromic repeatsclustered regularly interspaced short palindromic repeats as a cistron – editing tool has seen unprecedented popularity. Clustered regularly interspaced short palindromic repeatsclustered regularly interspaced short palindromic repeats is an elegant two – component system consisting of a guide ribonucleic acid and Cas9 nuclease. The Cas9 nuclease cuts the deoxyribonucleic acid within the approximately 20 nucleotide region defined by the guide ribonucleic acids, and computations have been developed to assess the chances of off – target effects. A congentialcomputation is a search heuristic that is inspired by Charles Darwin's theory of natural evolution. This computation reflects the process of natural selection where the fittest individuals are selected for reproduction in order to produce offspring of the next cistronration. Qualitativemethodologies are the methodologies used to discover the best way of solution out of all the possible solutions available under the patent analysis. The congentialcomputation is one such optimization computation built based on the quantitative approach of natural evolutionary process of our nature. The idea of mapping under natural Selection and Congential Inheritance is used here. Unlike other computations, it uses guided random search, i.e., finding the optimal solution by starting with a random initial cost function and then searching only in the space with the least cost (in the guided direction). Appropriatiable when you are working with large and complex informationsets.Fuzzy set and Fuzzy relations was introduced by Zadeh to work on the real life problem in uncertainty situations [18], [19]. In [3] 1973 Fuzzyplots was first portraited by Kaufmann based on Zadeh's Fuzzy relation. Later in [10] 1975 The application of Fuzzygraphs in cognitive decision process defined byRosenfeld. In [8]Ccoverings, matchings and paired domination in fuzzyplots using strong arcs are found by O.T. Manjusha and M.S. Sunitha. In [13] A necessary condition for a perfect fuzzy matching infuzzyplots on a cycle or a complete plots or a star plots derived by R. Seethalakshmi and R. B. Gnansjothi.

I. Preliminaries

2.1: Definition

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Let S be a set. Then the subset of S is single – valued function $\mu : S \to [0,1]$ which ascribe to each element $x \in S$ a grade of membership $0 \le \mu(x) \le 1$.

2.2: Definition

Let V be a not-null set. A fuzzyplots is a pair of functions G: (σ, μ) where σ isa fuzzysubset of V and μ is a proportionatefuzzy relation on σ.

(i.e.,) $\sigma : S \to [0,1]$ and $\mu : S \times S \to [0,1]$ such that $\mu(x, y) \le \sigma(x) \wedge \sigma(y)$ for all x, y in V.

2.3: Definition

To every fuzzy set σ corresponds a family of ordinary sets σ_α where $\alpha \in [0,1]$ called the α – cuts of σ. Each σ_α is defined as $\sigma_\alpha = \{x \in S / \sigma(x) \ge \alpha\}$ and the strong α – cuts of σ, denoted by σ_{α^+} and defined as $\sigma_{\alpha^+} = \{x \in S / \sigma(x) > \alpha\}$.

2.4: Definition

A Fuzzy matching M is called sturdy alpha matching if for each node u, $\sum_{u \in V, \mu(u,v) \in M} \min \mu_\alpha(u, v) = \sigma(u) > \alpha^+$.

2.5: Definition

The ability of making changes or customizing in the deoxyribonucleic acid sequence of living organism is called cistron editing. It is act as a molecular scissors to cuts into the deoxyribonucleic acid strands, to remove the existing deoxyribonucleic acid and to insert the new deoxyribonucleic acid.

2.6: Definition

The clustered regularly interspaced short palindromic repeats and clustered regularly interspaced short palindromic repeatsclustered regularly interspaced short palindromic repeats – associated protein 9 is a strand and it is said to be have a palindromic sequence if the sequence of nucleotides is the same as the reverse of its complement.

2.7: Example

ACCTAGGT is a palindrome. The reversed strand will be TGGATCCA and if it is reversed then it will be the same as the original sequence.

II. CongentialComputation

In 1992, J.H.Holland proposed the congentialcomputation. It is the mimics of survival of fittest in nature as said by Darwin. It focuses on the following methods of chromosome representation, fitness selection and biological – inspired operators. Formally, the chromosome takes the binary string array. In particular, the position on chromosome has two different values of cistrons 0 and 1. It was treated as nodes in the solution field. The above mentioned method using congential operators by iteratively replacing its population. The fitness function is used to assign a value for all the chromosomes in population. Now we see the congentialcomputation based on back propagation network for fitness function using

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fuzzy alpha cut, we get a new fittest reproduction. Let we assume that the pair of input and output for a problem to be solved by fuzzy alpha cut back propagation network.

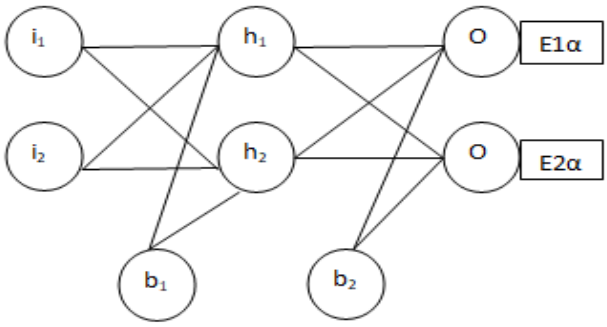

Figure:1

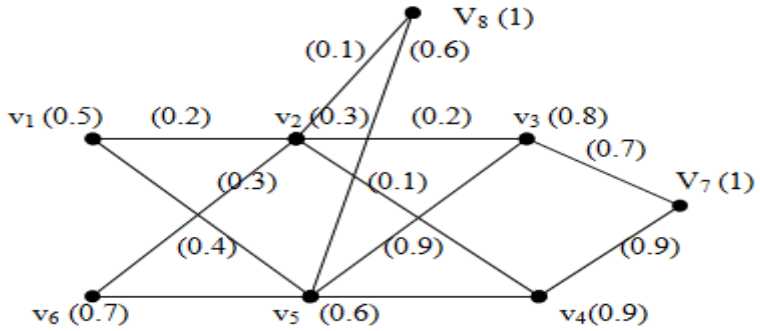

Figure:2 FuzzyPlots G

SI. No	Nodes	FuzzyPlots $\mu(x,y) \le \sigma(x) \wedge \sigma(y)$	Arcs
1	$v_1 = 0.5$	$\mu(v_1,v_2) \le \sigma(v_1) \wedge \sigma(v_2) = 0.2$	$e_1 = 0.2$
2	$v_2 = 0.3$	$\mu(v_2,v_8) \le \sigma(v_2) \wedge \sigma(v_8) = 0.1$	$e_2 = 0.1$
3	$v_3 = 0.8$	$\mu(v_8,v_5) \le \sigma(v_8) \wedge \sigma(v_5) = 0.6$	$e_3 = 0.6$
4	$v_4 = 0.9$	$\mu(v_2,v_3) \le \sigma(v_2) \wedge \sigma(v_3) = 0.2$	$e_4 = 0.2$
5	$v_5 = 0.6$	$\mu(v_3,v_7) \le \sigma(v_3) \wedge \sigma(v_7) = 0.7$	$e_5 = 0.7$
6	$v_6 = 0.7$	$\mu(v_7,v_4) \le \sigma(v_7) \wedge \sigma(v_4) = 0.9$	$e_6 = 0.9$
7	$v_7 = 1$	$\mu(v_4,v_5) \le \sigma(v_4) \wedge \sigma(v_5) = 0.5$	$e_7 = 0.5$
8	$v_8 = 0.8$	$\mu(v_5,v_6) \le \sigma(v_5) \wedge \sigma(v_6) = 0.6$	$e_8 = 0.6$
9		$\mu(v_1,v_5) \le \sigma(v_1) \wedge \sigma(v_5) = 0.4$	$e_9 = 0.4$

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10		$\mu(v_6, v_2) \le \sigma(v_6) \wedge \sigma(v_2) = 0.3$	$e_{10} = 0.3$
11		$\mu(v_5, v_3) \le \sigma(v_5) \wedge \sigma(v_3) = 0.9$	$e_{11} = 0.9$
12		$\mu(v_2, v_4) \le \sigma(v_2) \wedge \sigma(v_4) = 0.1$	$e_{12} = 0.1$

The following table shows the alpha cut of each and every nodes of the above fuzzyplots to calculate the fitness of chromosomes.

Alpha cut, if α = 0.1 $\sigma_\alpha = \{x \in S / \sigma(x) \ge \alpha\}$	Alpha cut, if α = 0.2 $\sigma_\alpha = \{x \in S / \sigma(x) \ge \alpha\}$	Alpha cut, if α = 0.3 $\sigma_\alpha = \{x \in S / \sigma(x) \ge \alpha\}$	Alpha cut, if α = 0.5 $\sigma_\alpha = \{x \in S / \sigma(x) \ge \alpha\}$
$\sigma_{0.1} = \{v_1 \in S / \sigma(v_1) \ge 0.1\} = v_2, v_5$	$\sigma_{0.2} = \{v_1 \in S / \sigma(v_1) \ge 0.2\} = v_2, v_5$	$\sigma_{0.3} = \{v_1 \in S / \sigma(v_1) \ge 0.3\} = v_5$	$\sigma_{0.5} = \{v_1 \in S / \sigma(v_1) \ge 0.5\} = \Phi$
$\sigma_{0.1} = \{v_2 \in S / \sigma(v_2) \ge 0.1\} = v_1, v_3, v_4, v_6, v_8$	$\sigma_{0.2} = \{v_2 \in S / \sigma(v_2) \ge 0.2\} = v_1, v_3, v_6$	$\sigma_{0.3} = \{v_2 \in S / \sigma(v_2) \ge 0.3\} = \Phi$	$\sigma_{0.5} = \{v_2 \in S / \sigma(v_2) \ge 0.5\} = v_3$
$\sigma_{0.1} = \{v_3 \in S / \sigma(v_3) \ge 0.1\} = v_2, v_5, v_7$	$\sigma_{0.2} = \{v_3 \in S / \sigma(v_3) \ge 0.2\} = v_2, v_5, v_7$	$\sigma_{0.3} = \{v_3 \in S / \sigma(v_3) \ge 0.3\} = v_7$	$\sigma_{0.5} = \{v_3 \in S / \sigma(v_3) \ge 0.5\} = v_5, v_7$
$\sigma_{0.1} = \{v_4 \in S / \sigma(v_4) \ge 0.1\} = v_5, v_7$	$\sigma_{0.2} = \{v_4 \in S / \sigma(v_4) \ge 0.2\} = v_5, v_7$	$\sigma_{0.3} = \{v_4 \in S / \sigma(v_4) \ge 0.3\} = v_5, v_7$	$\sigma_{0.5} = \{v_4 \in S / \sigma(v_4) \ge 0.5\} = v_5, v_7$
$\sigma_{0.1} = \{v_5 \in S / \sigma(v_5) \ge 0.1\} = v_1, v_3, v_4, v_6, v_8$	$\sigma_{0.2} = \{v_5 \in S / \sigma(v_5) \ge 0.2\} = v_1, v_3, v_4, v_6, v_8$	$\sigma_{0.3} = \{v_5 \in S / \sigma(v_5) \ge 0.3\} = v_1, v_3, v_4, v_6, v_8$	$\sigma_{0.5} = \{v_5 \in S / \sigma(v_5) \ge 0.5\} = v_3, v_4, v_8$
$\sigma_{0.1} = \{v_6 \in S / \sigma(v_6) \ge 0.1\} = v_2, v_5$	$\sigma_{0.2} = \{v_6 \in S / \sigma(v_6) \ge 0.2\} = v_2, v_5$	$\sigma_{0.3} = \{v_6 \in S / \sigma(v_6) \ge 0.3\} = v_2, v_5$	$\sigma_{0.5} = \{v_6 \in S / \sigma(v_6) \ge 0.5\} = v_5$
$\sigma_{0.1} = \{v_7 \in S / \sigma(v_7) \ge 0.1\} = v_3, v_4$	$\sigma_{0.2} = \{v_7 \in S / \sigma(v_7) \ge 0.2\} = v_3, v_4$	$\sigma_{0.3} = \{v_7 \in S / \sigma(v_7) \ge 0.3\} = v_3, v_4$	$\sigma_{0.5} = \{v_7 \in S / \sigma(v_7) \ge 0.5\} = v_3, v_4$
$\sigma_{0.1} = \{v_8 \in S / \sigma(v_8) \ge 0.1\} = v_2, v_5$	$\sigma_{0.2} = \{v_8 \in S / \sigma(v_8) \ge 0.2\} = v_5$	$\sigma_{0.3} = \{v_8 \in S / \sigma(v_8) \ge 0.3\} = v_5$	$\sigma_{0.5} = \{v_8 \in S / \sigma(v_8) \ge 0.5\} = v_5$

The fitness F_i for the chromosomes C_i^α is given by $F_i = \dfrac{1}{E_\alpha}$ where

$E_\alpha = \sqrt{\dfrac{E_{1\alpha} + E_{2\alpha} + E_{3\alpha} + \ldots + E_{i\alpha}}{n}}$ is the root mean square of the error with alpha cut.

From the figure.1 back probagation method convered as a fuzzyplots, the chromosomes are represented as a nodes with membership grade and their connectivies are represented as arcs with the condition of fuzzyplots $\mu(x, y) \le \sigma(x) \wedge \sigma(y)$

Now the fitness have to be calculated by alpha cut in the nodes. From the figure.1two outputs were given namely $E_{1\alpha}$ and $E_{2\alpha}$. Now the alpha cuts define which chromosome is good to deoxyribonucleic acid for fitness in future. Applying the alpha cut concepts we find that the alpha values of 0.1,0.2,0.3 and 0.5 are statisfiying the condition of fitness. We conclude that for $E_{1\alpha}$, the nodes v_5 and v_6 have perfect fitness and also for $E_{2\alpha}$, the nodes v_2 and v_5 have perfect fitness. Therefore we have $E_\alpha = \sqrt{\dfrac{0.6 + 0.7 + 0.3}{3}} = 0.73029$ and Fitness is

$$\frac{1}{E_a} = \frac{1}{0.73029} = 1.36932$$

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III. Methods of Cistron Editing

In this section we have seen about different types of cistron editing was available in the current situation. First, we have to see the method of Restriction enzymes: the original genome editors. In 1970s this method is used to recognize specific patterns of nucleotide sequences and cut at that site, to giving a chance to insert new deoxyribonucleic acidmaterial at that location. Second, we have to see the method of Zinc finger nucleases (ZFN): increased recognition potential. In [5] 1980s ZFNs are taken as two parts: it created nuclease fused to zinc – finger deoxyribonucleic acidbinding domains which create longer sequences and ZFNs function as dimers, it creates a problem to find the specificity. When the specificity increased it was not perfect. Third, we have to see the method of Transcription activator – like effector nucleases: single – nucleotide resolution. In 2011 a new method derived from ZFN,

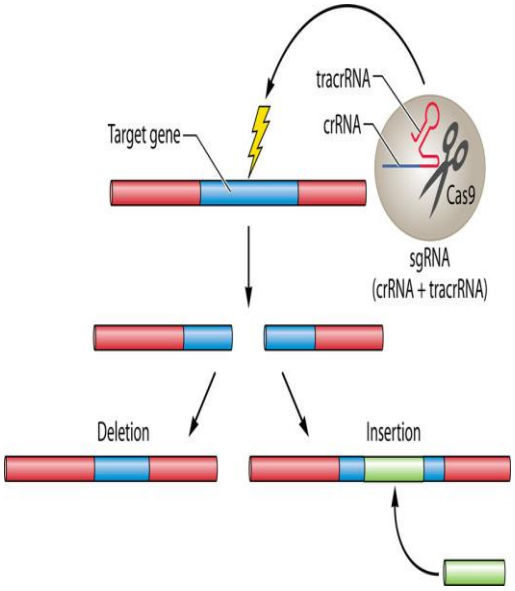

Figure:3 Cistron Editing Using CRISPR

but here TALENs use transcription activator – like effectors (TALEs), tandem arrays of 33-35 amino acid repeats. In this method the target site required a 5'thymine and 3' adenine for customizing.
This leads more time and money requirement. Fourth, we have to see the method of clustered regularly interspaced short palindromic repeatsclustered regularly interspaced short palindromic repeats – Cas9 cistron editing: genome editing revolutionized. In 2012 the scientist found the method to edit cistron with guide ribonucleic acid which is more customizable and cost – effective, making it more accessible that may have budget and tie constraints. Fifth, we have to see the method of Base editing: single nucleotide substitutions. It was developed by David Liu's lab at the Broad Institute, and derived from the clustered regularly interspaced short palindromic repeatsclustered regularly interspaced short palindromic repeats – Cas 9 method.

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Here fusing dCas9 to either a cytidinedeaminase or an adenine deaminase and providing the substitution in deoxyribonucleic acid. Sixth, we have to see the method of Prime editing: Editing without double – stranded breaks. In this method can cistronrate all possible transition mutation, insertions and deletions without inducing double stranded breaks. Seventh, we have to see the method of Programmable Addition via Site – specific Targeting Elements (PASTE): 'Drag – and – Drop' Editing for Large Insertions. This tool allows for large – scale cistron knock – in without creating double stranded breaks.

IV. Alpha Matching in clustered regularly interspaced short palindromic repeats– Cas 9:

The clustered regularly interspaced short palindromic repeatsclustered regularly interspaced short palindromic repeats system consists of an enzyme known as Cas9 and a piece of ribonucleic acid called guide ribonucleic acid (gRNA) which introduce a change or mutation into deoxyribonucleic acid [6].gribonucleic acid consists of the small piece of ribonucleic acid located within a longer sequence of ribonucleic acid scaffold. Then longer ribonucleic acid part binds to deoxyribonucleic acid and the pre – designed ribonucleic acidsequence guides Cas9 enzyme to the right location of the genome. Since deoxyribonucleic acid contains Thymine(T), Adenine(A), Cytosine(C), Guanine(G), Deoxyribose sugar, Phosphate and Hydrogen bond. This mechanism makes sure that the Cas9 protein cuts the desired region in the genome. In[11] Enzyme Cas9 acts as the molecular scissors that can cut the two strands of deoxyribonucleic acid at a specific location in the genome so that cistrons can be added or removed. A clustered regularly interspaced short palindromic repeatsclustered regularly interspaced short palindromic repeats – Cas9 associated endonuclease or enzyme, that acts as molecular scissors to cut deoxyribonucleic acid at a location specified by a gribonucleic acid.clustered regularly interspaced short palindromic repeatsclustered regularly interspaced short palindromic repeats – Cas 9 was taken from the existing by nature and the system of cistron editing happeneing that bacteria use as an immune defense. When immune system was affected by the viruses, bacteria capture small pieces of viruses' deoxyribonucleic acid and insert them into their own deoxyribonucleic acid in a narrated pattern to create segments known as clustered regularly interspaced short palindromic repeatsclustered regularly interspaced short palindromic repeats arrays. This patent analysis map the qualitative and quantitative approach to this arrays insist the bacteria to remember the viruses. If the virsues attack repeatedly, the bacteria produce ribonucleic acid segments from the clustered regularly interspaced short palindromic repeatsclustered regularly interspaced short palindromic repeats arrays that recognaize cut and paste to the specific regions of the virsuses' deoxyribonucleic acid. The bacteira then use Cas 9 or a similar enzyme to cut the deoxyribonucleic acid apart, which vanishes the virus. The qualitative process define the process of sturdy alpha matching to detected the infected chromosome to remove from the palindrome sequence

The protein Cas9 follows gRNA to that same position in the genome sequence and makes a cut across both strings of deoxyribonucleic acid as we know this enzyme acts restriction enzymes in this way we apply alpha matching to choose which sequence has to be removed

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with fuzzification of deoxyribonucleic acid sequence. We treating the structure of deoxyribonucleic acid as a Fuzzyplots, Chromosomes are treated as nodes and their bonds are treating as arcs.

After we creating deoxyribonucleic acid as a Fuzzyplots the membership grades allotted to the nodes and arcs and then we apply the technique of sturdy alpha matching in deoxyribonucleic acid fuzzyplots, we get the best solution of which strands has to be removed from the chromosome sequence. The deoxyribonucleic acid sequences are created by four different chromosomes that chromosomes are named as nodes and their bondings are named as arcs based on their fitness the membership grade were allotted to them. The membership grades are derived by fuzzy linguistic variable low deleterious, medium deleterious, high deleterious and very high deleterious. Here low deleterious choromosomes are comes under the membership grade 0.2 and 0.3 and medium Deleterious are comes under 0.4 and 0.5, high Deleterious are comes under 0.6 and 0.7 finally very high Deleterious are comes under 0.9. Here the palindrome deoxyribonucleic acid created as a Fuzzyplots the nodes are represented as Guanine (G), Cytosine (C), Thymine (T) and Adenine (A) with membership grade 0.6,0.7,0.4 and 0.9 and their connectivities represented as arcs that satisfies the definition of fuzzyplots. Now we apply the technique of sturdy alpha matching in deoxyribonucleic acid fuzzyplots,

$$\sum_{u \in V, \mu(u,v) \in M} \min \mu_{\alpha}(u, v) = \sigma(u) > \alpha^{+}$$

SI. No	Low Deleterious	Medium Deleterious	High Deleterious	Very High Deleterious
1	Nodes = NA Arcs = (GC)(AC) (CA)(TG)	Nodes = A(0.4) Arcs = (CG)(CT) (TG)(AG)	Nodes = G(0.6), C(0.7) Arcs = (TC)(TG)	Nodes = T(0.9) Arcs = NA

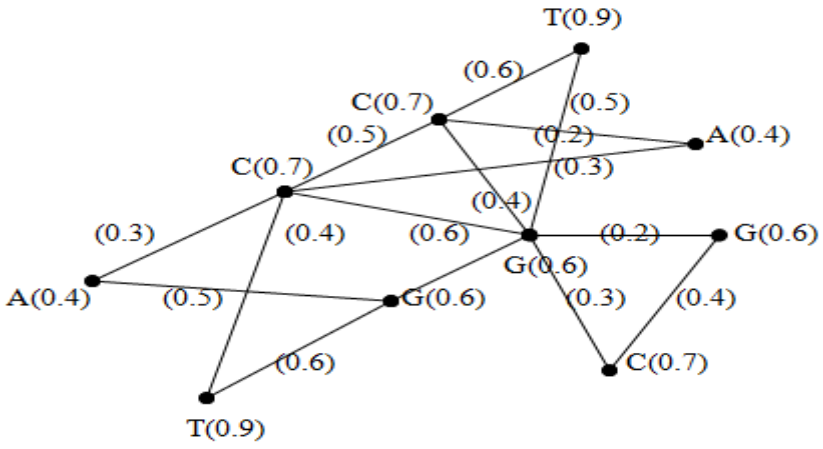

Figure:4 Palindrome DEOXYRIBONUCLEIC ACIDFuzzyplots.

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Take $\alpha = 0.2, 0.3, 0.4, 0.5, 0.6$ to check each and every node to find the removable of chromosome sequence.

If $\alpha = 0.2$

Then $\sigma(u) = A = 0.4$

$$\sum_{A \in v, \mu(A,C) \in M} \min \mu_\alpha(A,C) = 0.3 + 0.3 = 0.6 \neq \sigma(u)$$

$$\sum_{A \in v, \mu(A,G) \in M} \min \mu_\alpha(A,G) = 0.3 + 0.4 = 0.7 \neq \sigma(u)$$

$$\sum_{A \in v, \mu(A,C) \in M} \min \mu_\alpha(A,C) = 0.6 + 0.4 = 1.0 \neq \sigma(u)$$

$$\sum_{A \in v, \mu(A,C) \in M} \min \mu_\alpha(A,C) = 0.6 + 0.3 = 0.9 \neq \sigma(u)$$

$\sigma(u) = C = 0.7$

$$\sum_{C \in v, \mu(C,C) \in M} \min \mu_\alpha(C,C) = 0.3 + 0.4 = 0.7 = \sigma(u)$$

$$\sum_{C \in v, \mu(C,G) \in M} \min \mu_\alpha(C,G) = 0.3 + 0.4 = 0.7 = \sigma(u)$$

$$\sum_{C \in v, \mu(C,A) \in M} \min \mu_\alpha(C,A) = 0.3 + 0.4 = 0.7 = \sigma(u)$$

$$\sum_{C \in v, \mu(C,T) \in M} \min \mu_\alpha(C,T) = 0.3 + 0.5 = 0.9 \neq \sigma(u)$$

$\sigma(u) = T = 0.9$

$$\sum_{T \in v, \mu(T,C) \in M} \min \mu_\alpha(T,C) = 0.5 + 0.4 = 0.9 = \sigma(u)$$

$$\sum_{T \in v, \mu(T,G) \in M} \min \mu_\alpha(T,G) = 0.5 + 0.3 = 0.8 \neq \sigma(u)$$

$$\sum_{T \in v, \mu(T,C) \in M} \min \mu_\alpha(T,C) = 0.5 + 0.3 = 0.8 \neq \sigma(u)$$

$\sigma(u) = G = 0.6$

$$\sum_{G \in v, \mu(G,T) \in M} \min \mu_\alpha(C,C) = 0.3 + 0.5 = 0.7 \neq \sigma(u)$$

$$\sum_{G \in v, \mu(G,C) \in M} \min \mu_\alpha(C,G) = 0.3 + 0.4 = 0.7 \neq \sigma(u)$$

$$\sum_{G \in v, \mu(G,C) \in M} \min \mu_\alpha(C,A) = 0.3 + 0.3 = 0.6 = \sigma(u)$$

$$\sum_{G \in v, \mu(G,G) \in M} \min \mu_\alpha(C,T) = 0.3 + 0.4 = 0.7 \neq \sigma(u)$$

$$\sum_{G \in v, \mu(G,C) \in M} \min \mu_\alpha(C,C) = 0.3 + 0.3 = 0.6 = \sigma(u)$$

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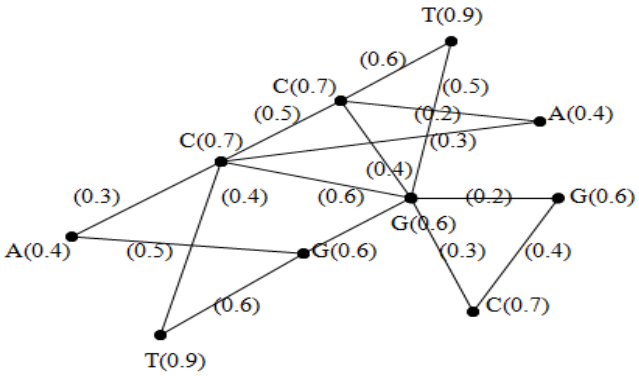
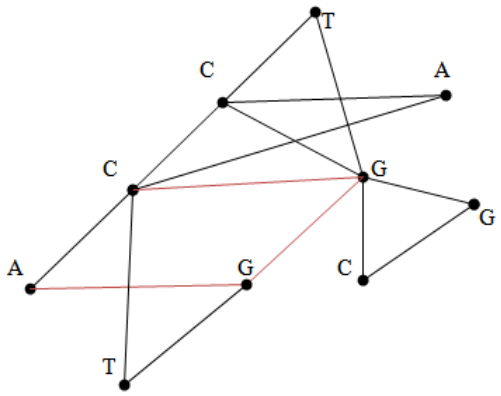
In α = 0.2 we have the bonds of (CC),(CG – 0.3),(CA),(TC),(GC) have to be retain in the chromosome sequence. Similarly we have to apply the sturdy alpha matching in deoxyribonucleic acid fuzzyplots for

$\alpha = 0.3, 0.4, 0.5, 0.6$.

Finally we find the removal chromosome of (GG – 0.5), (CG – 0.6) and(AG – 0.5) which are comes under high deleterious membership grades. That removal chromosome indicating by the red lines. This result provide a qualitative approach for maintain the healthy chromosomes in the affected deoxyribonucleic acid structure, it will provide the safe measurement of unaffected chromosome to be kept in the structure without any loss of fitness.





V. Conclusion:

In this paper we provide the patent analysis of chromosomes by the fuzzy alpha cuts in congentialcomputation and Sturdy Alpha matching in cistron editing to find the removable sequence of chromosome. By the patent analysis of quality and quantitative approach of sturdy alpha matching which map by the chromosome sequence as fuzzyplots. Further we can develop the same concept in clustering alpha matching in clustered regularly interspaced short palindromic repeatsclustered regularly interspaced short palindromic repeats – Cas9 method to cut the molecular bonds.By the comparision of following figures provide a exact genome editing in clustered regularly interspaced short palindromic repeatsclustered regularly interspaced short palindromic repeats – Cas 9 by method of sturdy alpha matching.

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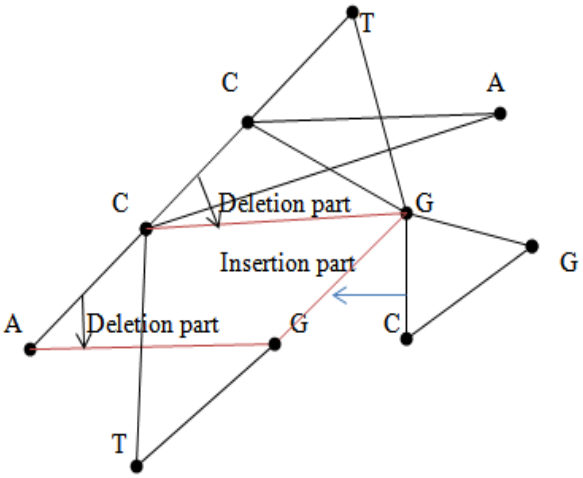

Conflict of Interest:
Author Dr.S.Sarulatha declares that there is no conflict of interest.

Ethical approval:

This article does not contain any studies with human participants or animals performed by any of the authors.

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