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Mathematical Modeling of Deterministic Systems: Insights from the Tenneti Theory

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Abstract: *Pair wise nucleotides[1] modelling act is a significant task in biological systems. This modelling act is crystal clear innovative mathematical act. It is based on attraction between nucleotides, basic arrangement of pattern and logics are taken from nature. Continuous modelling in the pair-wise nucleotides are stable, dynamic, spatial, periodic, auto assemblies, Chaotic and deterministic, it is possible to use both continuous and discrete modelling to interpret microbial behavior. In this version modelling are attached and detached due to thermodynamic attraction force between nucleotides and Chaotic order. It is a good mechanistic modelling act with clear predicting values. It explains various features of system like reverse patterns or biological patterns, modelling act and types of acts, existence and expanding cycles, how 24 micro units (pair wise nucleotides) are generated in the system, separating resulting patterns into groups, relationship with in group and between groups. micro-units, sub units, units, genetic units and pair wise modelling on DNA. How only 5 groups of micro units shall be combining combination and form into genetic code out of 6 groups? This modelling is aims to develop and use efficient algorithms, data structure, visualization communication tools with goal of computer modelling of biological systems. Equating this same modelling system is not possible in theory of probability[2] in random[3] manner. It creates more doubts than answers because theory of probability is not having perfect mathematical logic*.

Keywords: RHS Modeling. LHS Modelling. Existence cycle. Existence number, Expanding cycle. Expanding number. Micro unit. Sub unit. Unit. Genetic unit.

I. Introduction

THREE GREAT SCIENTIST THOUGHTS

1) In an article, Erwin Schrödinger4 described life as "Genetic code must be in the form of three general statements, (i) the nature of the genetic code is deterministic: (ii) The genetic code is conserved and universal: (iii) The genetic code is oldest known level of complexity in the evolution of living organisms that is accessible to our direct observation and experimental manipulations. In the same article he described "It is an aperiodic crystal. DNA is a crystal, and so is protein, note the pattern. The cleanest view than to the nature of genetic code is that".

2) In his work Anfinsen5,6 described life is "Due to thermodynamic molecular forces, polypeptides automatically assume unique, stable conformed ensembles. This might term the auto-assembly hypothesis of protein synthesis". And "For every sequence of amino acids there is a unique, defining conformational ensemble to which it must auto assembling"

3) According to Chaos7, life is "Chaotic systems appear to be disorder, even random. Beneath the random behavior is sense of order".

PRESENT SCENARIO - Science works by simplifying complexity, but in the case of genetic code we have over simplified it.

In fact, we still do not understand nature's nifty crystal-forming algorithms affectionately referred to as the genetic code.Codons8 are permutations of three nucleic acids. They have a specific configuration of set, which in this case has three members. Permutations are actual arrangements of symbols. For instance, the sequence of symbols XYZ is a permutation of the symbols X, Y and Z. other permutation of the same symbols are YZX, or ZYX, Taking the number of possible symbols, in this case 4 nucleic acids, and raising it to a power of the number of symbols in the permutation, in this case 3, determine the total set of permutations. Therefore, there are sixty-four (43=4*4*4=64). It is a fact that twenty amino acid set is standard set.

Using 64 codons to only assigned 20 amino acids is wasteful information. In this system, we are missing something?

Evaluating biological acts through theory of probability in a random manner create more doubts than answers. Because what kind of mechanism follows inside mother womb we don't know. I the same manner what type of arrangement act take lead role and other parameters like attraction forces in between nucleotides we did not understand. So present mathematical theory of probability cannot solve the problem. It creates puzzles in the mind.

Let us take four pairs of nucleotides the bases adenine (A), cytosine (C), guanine (G), and thymine (T) are as a blocks with four different colors. Black border with black letters blocks are belongs to egg group and red border blocks with red letters are belongs to mate group. This is case study for the type of arrangement and the role of attraction. They can arrange in three types. Reverse order (Figure-1A). Parallel order (Figure-1B). Random order (Figure-1C).

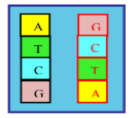
PAIR WISE NECLEOTIDES MODELING ACT WITH RESPECT TO TYPE OF PATTER & NUCLEOTIDES ATTRACTION FORCES:

Let us take four pairs of nucleotide the bases adenine (A),

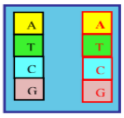
cytosine (C), guanine (G), and thymine (T) are as a blocks with four different colors. Black border with black letters blocks are belongs to egg group and red border blocks with red letters are belongs to mate group. This is case study for the type of arrangement and the role of attraction. They can arrange in three types. Reverse order (Figure-1A). Parallel order (Figure-1B). Random order (Figure-1C).

3.1 Figures and Tables

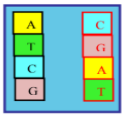
Place illustrations (figures, tables, drawings, and Taking concept attraction bond in between homologous nucleotides. Fig -2A, 2B and 2C explains about relation between pattern and attraction between homologous nucleotides. In reverse order, attraction lines pass through center point in X-Y plane, it have chance of nucleotides momentum in a balance manner. In parallel order attraction lines are in parallel, and in the random order attraction lines are in zigzag way. illustration numbers and caption under the illustration in 10 pt font. Do not allow illustrations to extend into the margins or the gap between columns (except 2-column illustrations may cross the gap). If your figure has two parts, include the labels "(a)" and "(b)".



Reverse order
Figure 1A



Parallel order,
Figure 1B



Random order,
Figure 1C

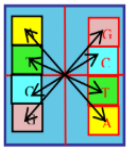
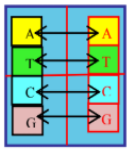


Figure-2A.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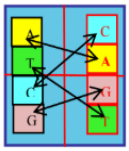


Figure-2C

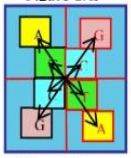


Figure-3A,

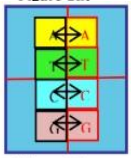


Figure-3B,

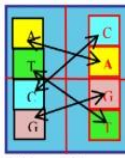


Figure-3C

Fig-3A explain further actions of homologous nucleotides in reverse order, attraction forces pass through center point, based on these forces the modelling of nucleotides form X shape. In parallel order (Fig-3B) homologous nucleotides are *INTRODUCING FOUR PAIRS NUCLEOTIDES MATHEMATICAL MODELLING ACT.*

Four pairs of nucleotides mean eight elements, they generate factorial 8 number of sequences, that is equal to 40320.

Separating patterns into groups is a new innovate thinking. The most abstract level in this hierarchy is the mathematical model. Here the behavior of a system is reproduced as a series of mathematical relationships which reflect and often predict its behavior. This is the required basic input data to separate the system in the Hamiltonian9 path of elements modeling and ends are free, which explains modeling act in mathematical determinism in polynomial time10,11,12 mathematical logics.

II. Theory

THREE TYPES OF MATHEMATICS TO UNDERSTAND BIOLOGICAL ACTS.

1) Class-1 involves routine application of existing mathematical techniques to solve biological problem, for example mitosis cell division the cell division can explain in term of multiplying by using present mathematics.

2) Class-2 some fundamental issues in biology required all together new way of thinking quantitatively or analytically.

Creation of entirely new area of mathematics may be necessary before it will be possible to grapple successfully with the underlying biological problems. Examples are events in fertilization like egg selecting matured sperm, chromosomes cross-over, tree of life --- nucleotides arrangement on DNA.

3) Class-3, Third class is combining of known and un-known it is combining of mitosis and meiosis.

MODELLING ACT The modelling act is look like Riffle shuffling act but it fallows certain rules and regulations where shuffling act is in random. A common shuffling technique is called the riffle or dovetail shuffle, in which half of the deck is held in each hand with the thumb inward, then cards are released by the thumb so that they fall to the table interleaved. The Gilbert-Shannon-Reeds model provides a mathematical model of the random outcomes. Riffle shuffling is in between two groups.

KEY WORDS: RHS Modeling. LHS Modelling. Existence cycle. Existence number, Expanding cycle. Expanding number.

Micro unit. Sub unit. Unit. Genetic unit.

MODELLING ACT: A key function of the model therefore is to predict behavior. A model is only validated if such predictions are confirmed. Modeling is arrangement elements of two groups (four pairs) like Hamiltonian path in ascending manner. "Hamiltonian path is a traceable path is a path visit each nearest group vertex element exactly once in ascending manner". Reverse order taken for the experiment.

RULE-1 Modelling act is in between two groups of elements; each group must have equal numbers of elements. In a group each one of the nucleotide is one of homologous nucleotide. So number of elements are equal to 2N (N- indicate elements in each group) . in the case of three groups then total elements are 3N--- like wise.

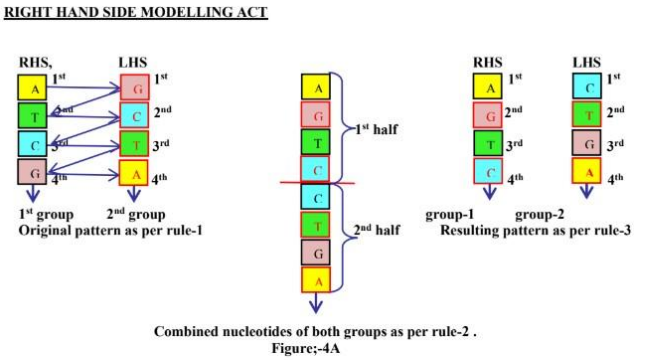
RULE-2 This rule explains combining of both group elements are based on "first come first serve principle". Modelling act in between two groups are as follows. Take first nucleotide of 1st group as 1st position. Second group 1st nucleotide occupies 2nd position. First group 2nd nucleotide as 3rd position. Second group 2nd nucleotide as 4th position, --- like wise first group last nucleotide is (2N-1)th position, and 2nd group last nucleotide as last or 2Nth position in combined group.

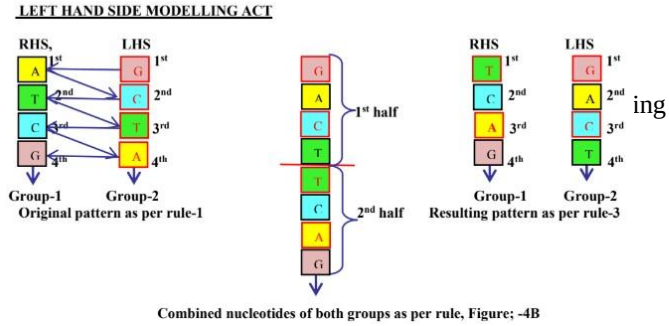
RULE-3 This rule explains separating of combined element group into two groups, in this process separating first half or four nucleotides as first group and second four nucleotides as second group, that result re-constitute pattern. In the case of more than two groups same rule applies with respect to

number of groups. This modelling act is two types RHS modelling act and LHS modelling act.

RHS MODELLING ACT Taking right hand side group as first- and left-hand side group as second and fallow the rules of modelling are mention above and carry out the modelling process is known as RHS modelling act.

LHS MODELLING ACT Taking left hand side group as first and right hand side group as second and fallow the rules of





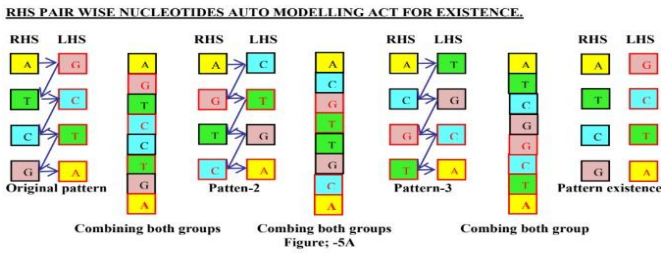
ing

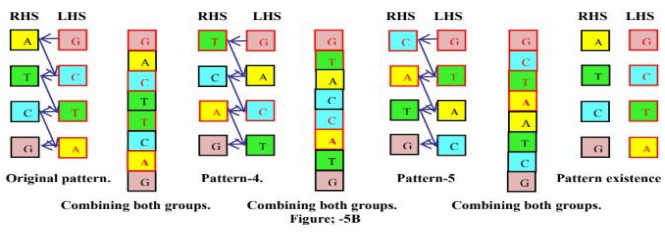
OBSERVATIONS

1) The process of system fallows Hamiltonian path in both RHS and LHS modelling.2) The system can predicable in easy manner.3) First group first nucleotide and second group last nucleotide not change their original place; remain nucleotides changes their original places in RHS modelling act.4) Second group first nucleotide and first group last nucleotide not change their original place; remain nucleotides changes their original places in LHS modelling act.

EXISTENCE CYCLE & EXISTENCE NUMBER.

The system is developed on the basis of nature rules and regulations so it is very important to understand complete system and system features.





For that repeating modelling act on resulting patterns is in both methods is very important. Repeating act on resulting reconstitute patterns till to the pattern became original or existence, this cycle of act known as Existence cycle. nucleotides auto arrangement acts are periodic or existence.

OBSVERVATIONS:

1) Either RHS or LHS arrangement or modelling, both systems are periodic auto-assemblies and system are predictable,where it is not possible in random shuffling.

2) In RHS modelling first group first nucleotide and second group last nucleotide never change its position.

3) In LHS modelling second group first nucleotide and first group last nucleotide never change its position.

4) Either RHS or LHS modelling, both systems are existence after three iterations.

5) The difference is resulting reconstitute patterns are different compare RHS modelling with LHS modelling.

6) Modelling of existing cycle is also applicable to parallel and random patterns.

7) With respect to four pair nucleotides they also periodic auto segments and results reconstitute pattern are different with respect RHS and LHS modelling.

SELECTING NATURES BIOLOGICAL PATTERN OR MICRO UNITS-

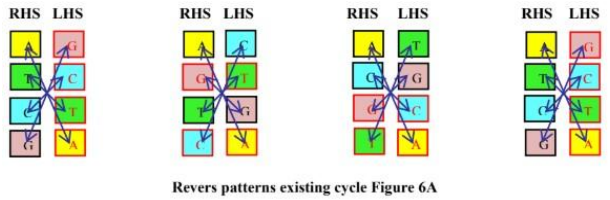
Taking four pairs of nucleotide as a micro-unit, how the nature micro-unit structure is play key role in genetic code? It is very important to the system because the overall code is combinations of twenty-four micro units. The micro-unit pattern can define in three existence cycle which are given below.

1) The first one is reverse modelling micro-unit where RHS group nucleotides modelling is reverse to LHS group nucleotides modelling.

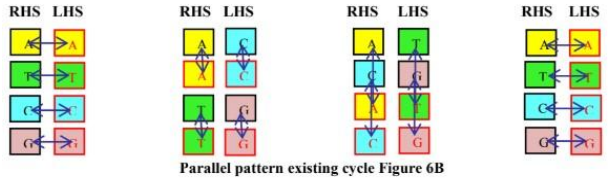
2) The second one is parallel modelling micro-unit where RHS group nucleotides modelling is parallel to LHS group nucleotides modelling.

3) The third one is random modelling micro-unit where RHS group nucleotides modelling is random to LHS group nucleotides modelling.

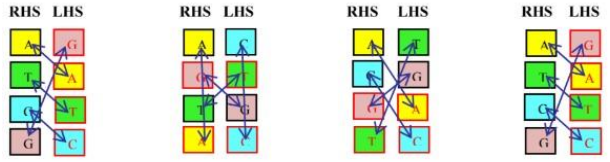
The most important part is which type of pattern modelling have a capacity to carry out a perfect genetic code. It is also important weather genetic code is developing with three nucleotides (as per present science) or some other modelling. But is true that four pair nucleotide arrangement or modelling on DNA calling as genetic code. In this case four pairs of nucleotides are taken as micro-unit in the system. It is smallest unit in genetic code. It is very important to understand micro-units, types of micro-units with respect to both end nucleotides, separating them into groups, examine them how they bond each other with in the group and selecting suitable possibility for bonding as sub units. How sub units further develop into group units. How group units are bond with other group units. All these home work is very important to understand how four pairs nucleotide modelling DNA.



Revers patterns existing cycle Figure 6A



Parallel pattern existing cycle Figure 6B



Random pattern existing cycle Figure 6C

OBSERVATIONS; - The fallowing observation are very important to study and understand features of micro-unit expansion cycles. From all three cycles (reverse existence cycle, parallel existence cycle and random existence cycle) which system is perfectly match for biological acts.

1) Incisional stage reverses order micro-unit, parallel order micro-unit and random order micro-unit their sequence of nucleotides are as per definition of pattern but one thing is common the is each group have four nucleotides, each one of nucleotide is one of the homologous nucleotides,

2) In the reverse micro unit, the attraction in between homologous nucleotides are in X-shape formation throughout the periodic cycle. That means the reverse system fallows same type modelling order in generated reconstitute micro-units. The modelling order is in such way each group have four nucleotides, each nucleotide is one of the homologous nucleotide.

3) In the case of parallel order, the result reconstitute micro-unit are not fallow parallel order arrangement. However homologous nucleotides are mixing up in each group. So no chances of parallel attraction in between homologous nucleotides.

4) In the case of random order, the result reconstitute micro-unit are fallow random order arrangement. However homologous nucleotides are not mixing up in each group. Random attraction in between homologous nucleotides.

Parallel order and random order micro-unit's existence cycles very clearly explains these micro-units modelling are not suitable for biological act. But with respect to reverse order it have special feature let study, understand, analyzing and compare the basic conditions are required for biological acts.

1) In entire existence cycle in reverse order, reconstitute micro-units fallow a systematic balancing, they are crystal clear to understanding each micro-unit structural formation or result modelling.

2) With homologous nucleotides attraction in micro-unit can create perfect equilibrium momentum in the systems.
Homologous nucleotides attraction is in diagonal. No chance of homologous nucleotides combined together.

3) Nature designs the system in such beautiful balance way, the system is perfectly static in normal condition. The code of micro-unit is unique and universal, same code can fallow to all creatures.

4) Diagonal attraction in between homologous nucleotides effect is easy to separate and easy to mutually interchange in biotical acts.

5) The combinations of micro-unit nucleotide arrangements and attraction in between homologous nucleotides create natures acts; those are auto sequences or auto micro-unit codes.

6) The folding capabilities are more in the system. It leads more compressive and easier to enlarge because diagonal attraction creates spiral way of formation in the system it is actual DNA shape. In the shape creates compressive ness due the same attraction in between them.

7) In the case of biological act crossing over the attraction with in the micro-unit transform to attract mate micro-unit.

8) At this stage the compressed chromosome enlarge and one strand separate from the system were same strand present in mate non-sister chromosome.

9) Crossing-over is in between one set of homologous chromosomes and 22 pairs of non-sister chromosomes. So homologous chromosomes have same genetic code throughout its length. Such a situation both chromosomes are enlarged and mutually inter change one strand from each. This modelling has all biological reasons to perform biological acts.

EXPANDING CYCLE & EXPANDING NUMBER,

Once the system is parodic or existence further modelling or further iteration has no use, the system keeps or repeating in both RHS & LHS modeling. To understand the system, resulting reconstitute patterns of RHS modeling cycle further carry out LHS modelling operation. In the same manner resulting reconstitute pattern of LHS modelling further carry out RHS modeling operation. In this situation the system generates more existing cycles. This is known as system expanding, it is better way to understand expanding cycle. Expanding cycle is defined as "Pool of reconstitute patterns are in a combination of number of existence cycles generate through alternative combination of RHS modeling and LHS modelling". This expanding cycle is mathematically explainable and equitable.

1) Suppose a pattern goes under RHS modelling and generate X-number of reconstitute pattern in a first generation, equal to (En-1).

2) (En-1) number of patterns further goes under LHS Modelling and generate (En-1)2 number of reconstitute patterns in second generation.

3) (En-1)2 number of patterns further goes under RHS modelling and generate (En-1)3 number of reconstitute patterns in third generation--- likewise the system keeps on expanding.

4) After some generations reconstitute pattern and existence cycles are keeps on repeating in both modellings. So further expanding is not having any logic.

5) The number of reconstitute patterns are in the system is more important.

6) The total number of reconstitute patterns in the system is known as expanding number.

The system equitation = 1+(En-1) +(En-1)2+(En-1)3

From ancient society to modern silicon society our mathematical logic is polynomial, it is based on mathematical verbs adding (+), subtraction (-), multiplication (x) and dividing (/). Apart from present mathematical verbs, there are other mathematical
acts are present in nature like modeling. The modeling act is not shuffling11 act in random12 manner. Because random systems are not predicting next patterns, systems existence and total patterns (Factorial N) separating them into groups. In this situation the system creates more doubts than answers, feeding random logic to the computer create computational complexity13.
Micro-units expanding cycles explains how the system works in defined deterministic manner. The cells generation in stage by stage is fallows same method in the chromosomes crossing-over act in a large scale, because the number of chromosomes in human cell equal to 23 pairs. The expanding number in human chromosomes expanding cycle is equal to cells present in human body. To develop such a bigger human chromosome expanding cycle further needs a group research with biologists and software developers to development of suitable software.

FIRST PAIR WISE NUCLEOTIDES EXPANDING CYCLE.

This expanding cycle is combination of 15 existence cycles. in the expanding cycle only 12 patterns are generating (X1, X2,X3----X12). Further expanding, system repeats same patterns. System expanding number is 12. All sequence in the systems are in reverse order.

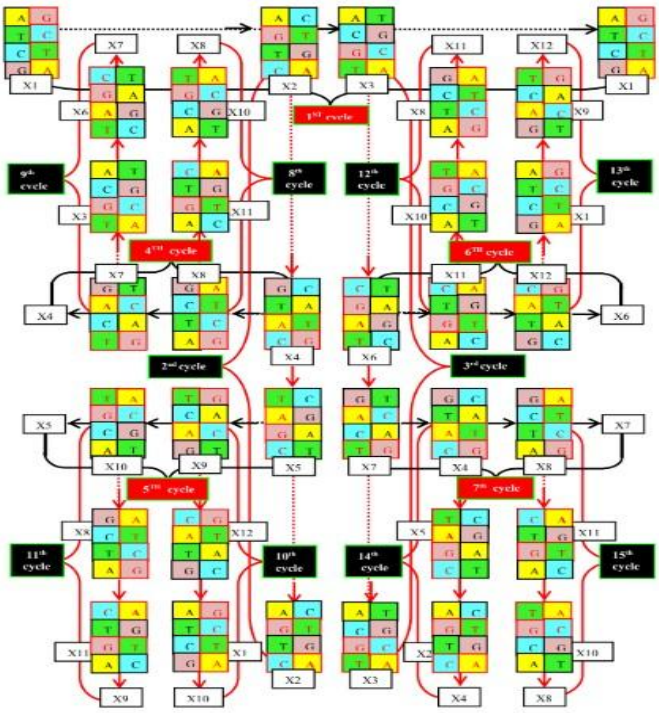


Figure-7A

SECOND PAIR WISE NUCLEOTIDES EXPANDING CYCLE.

The system is combination of 15 existence cycles. Only 12 patterns are generating in the system (Y1, Y2, Y3----Y12). Further expanding results same patterns are repeats. Each pattern in the system fallows a one basic principle, which is reverse order.

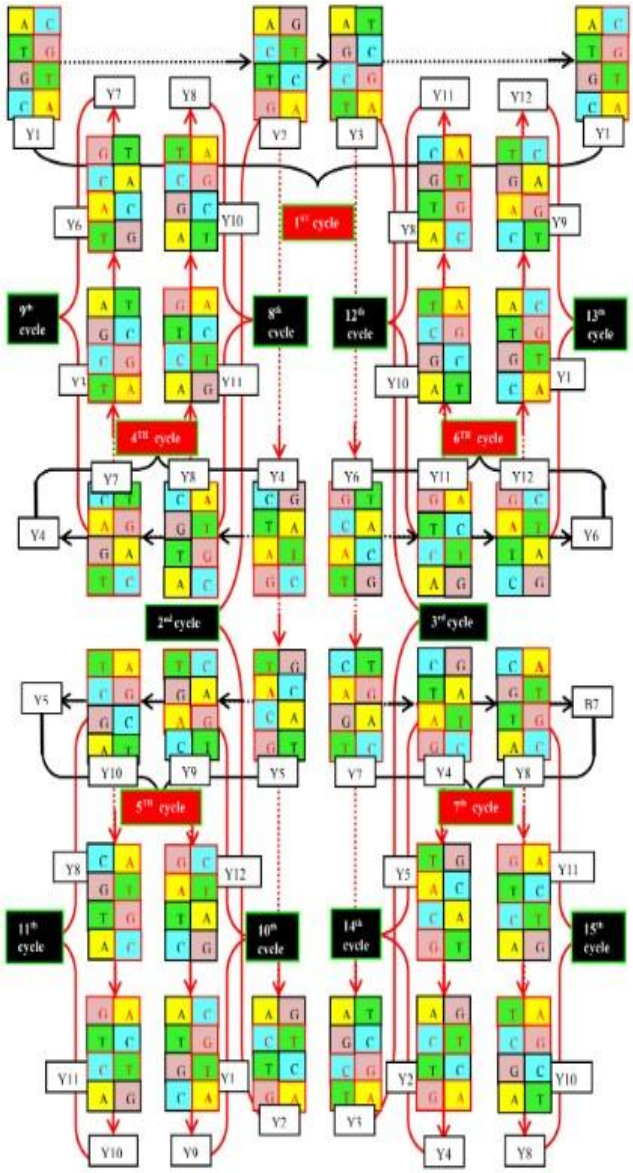
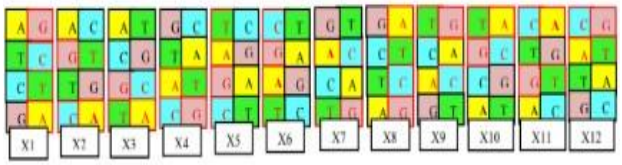


Figure -7B

RECONSTITUTE PATTERNS FROM EXPANDING CYCLE-1



Figure; -8A

RECONSTITUTE PATTERNS FROM EXPANDING CYCLE-2

Figure; -8B

WHY SYSTEM NEED TWO EXPANDING CYCLES

The answer is the fallowing reasons.

1) Twelve reconstitute patterns are not sufficient to explain biological act, assume nature working with two expanding cycles.

2) In a reverse order keeping one group completely egg nucleotides another as sperm nucleotides, system can format in 24 combinations but all combinations result only 24 patterns.

BINARY HEAP

Pattern expanding in the system is like a binary heap, each pattern has at most two children. Which are referred as the right child and left child. A recursive definition using just set theory notions is that a binary tree is a triple (R. S. L), where R is RHA act result reconstitute sequences (in black branches), L is LHA act result reconstitute sequences (in red branches), S is a singleton set's original pattern. It is mostly similar like binary heap; it is complete binary tree that is in all levels of the tree, the level is mathematical mention as iteration. In the case of binary heap except possibly the last one (deepest) fully filled and last level of the tree is not complete. But in this case of expanding cycle, expanding cycle is combination of existence cycles,

existence cycles are endless so last level of tree is complete, and all nodes are equal. In the binary heap only 12 sequences are keep on repeating, those mention in doted boundaries.

PATTERN EXPANDING SYSTEM IN THE FORM OF BINARY HEAP.

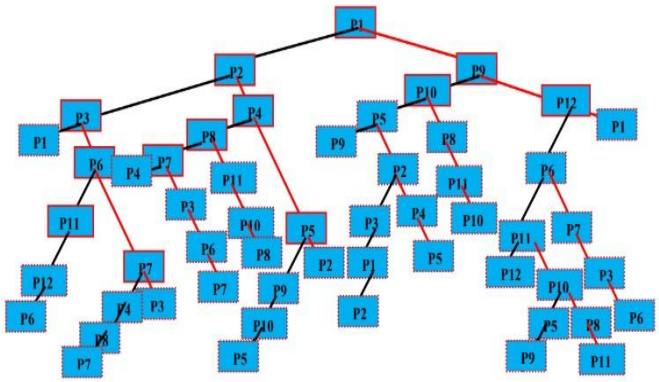


Figure- 9

HAMILTONIAN CYCLE

Hamiltonian circuit, vertex tour or graph cycle is cycle that visits each vertex exactly once (except for the vertex that is both the start and end, which is visited twice). In the arrangement act sequence or reconstitute patterns are developing one after another in periodic formats. In the above figure-9 capital A, B, C---L represent to P1, P2, P3---- P12 because of space

constrains. Black circles or cycles are representing to RHA act and yellow circles or cycles are representing to LHA act, and arrows directions represent to the way of reconstitute patterns are generating. Sequences are developing in the form of Hamiltonian path or cycles sequences are traced in a single direction, the vertices are connected with arrows and the edges traced "tail –to -head, it is proof for Hamiltonian cycles.

PATTERN EXPANDING CYCLE IN THE FORM OF HAMILTONIAN CYCLE.

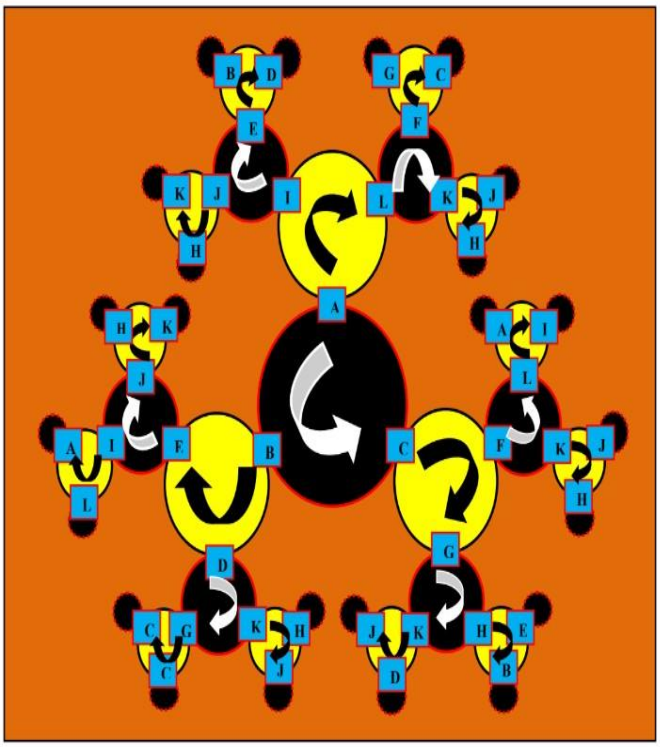


Figure-10

Polynomial-time equations; - A mathematical expression that involves N's and N2 s and N's raised to other powers is called a polynomial-time, and that's what the "P" in "P = NP" stands for. P is the set of problems whose solution times are proportional to

polynomials involving N's. NP-class problems include many pattern-matching and optimization problems that are of great practical interest, such as determining the optimal arrangement of transistors on a silicon chip, developing accurate financial-forecasting models, or analyzing protein-folding behavior in a cell.

All patterns are not possible to equate, there are some series of patterns are only possible to equate, which are based on relationship in between the series. The relationship is with respect to columns and rows.

Equation-1: For example Columns are P and rows are Q, which is equal to P, or columns and rows are equal (P= T1 and Q=T1), then existence number= 1+1=2, that means after 2nd iteration the system become original.

Equation-2: The relation between columns and rows are mathematically express that involves to the raised to powers with both columns and rows bases are equal, those series are equitable. For better understanding; A pattern has Tn columns and Tm rows (columns, P=Tn and rows=Q=Tm), then the existence number equal to combining of to the power= n+m), that means the system existence after (n + m) iterations. Columns P= Tn, Rows Q=Tm then Existence number of the order= (n + m)

Equation for expanding no. for equitable series = Existence number *Number of elements in order/2, (Note - This equation is just imagination based on 2 columns and 4 rows this equation is to further equate perfectly).

NECESSARY CONDITIONS FOR PAIR WISE NUCLEOTIDE MODELLING ON DNA

Fertilization is a natural event; the role of man and woman is up to sex only. Later what is happing inside mother womb no one don't know. We are assuming and praying for good results. Even doctor's biologist knows only symptoms. Natures events are not based on freewill or random. Natures selection is only determined. This nature's determinism is part of every micro-unit, sub units, units, genetic units, chromosomes, cells, cells generation to zygote. Mother womb has perfect determined mathematical chain of events, which are developing output in fixed time. For this determinism has necessary conditions.

1) Natures genetic code must be deterministic; it must be conserved and universal.

2) Genetic code an aperiodic crystal, the combination of code and thermodynamic molecular forces developing unique, stable conformed ensembles.

3) For every sequence of amino acids there is a unique, defining conformational ensemble to which it must auto assembling.

4) The code shall be static, dynamic, spatial, symmetric, most compressed, enlargeable and easy to mutually inter changeable.

On the basis of system requirement to further formulate pairwise arrangement on DNA. Separating both expanding cycles into groups based on end nucleotides. It is very important to understand each group; they can combine together to form into genetic code. How many groups can combine all these are important questions?

DEFINITION MICRO-UNIT; - Micro unit is nothing but a pattern or reconstitute pattern, each pattern has two groups, each group have four nucleotides, each nucleotide in any one group is one of the homologous nucleotide. The nucleotide arrangement sequence in reverse order. That mean any one of the group nucleotides arrangement sequence is reverse to other group nucleotides sequence. Total micro units are 24. Length of each micro unit is four letters.

MICRO UNITS MODELLING; -The process of lining up any one of group micro units to achieves maximum level of identity and conservation for nucleotides sequences for the purpose of assessing degree of similarity and the possibility of homology. In any case pair wise nucleotides pattern never change.

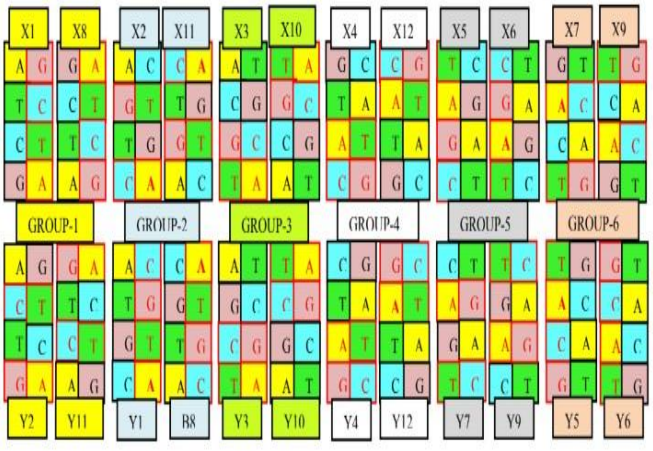


Figure-11,

The above figure explains four pair wise nucleotides modelling patterns further separates into six groups based on patterns both end nucleotides.

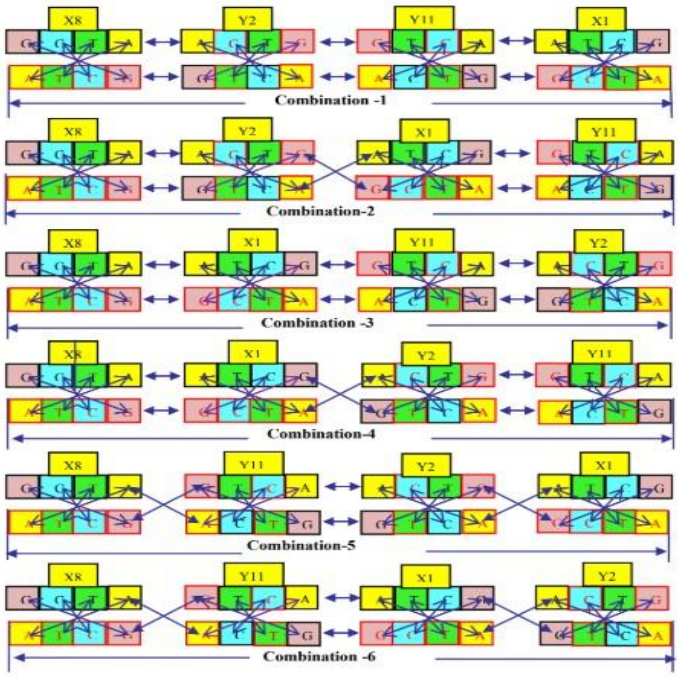
1) Micro Units X1, X8, Y2&Y11 are 1st group.
2) Micro Units X2, X11, Y1 & Y8 are 2nd group.
3) Micro Units X3, X10, Y3 & Y10 are 3rd group.
4) Micro Units X4, X12, Y4 & Y12 are 4th group.
5) Micro Units X5, X6 Y9, & Y7are 5th group.
6) Micro Units X7, X9, Y5 &Y6 are 6th group.

EXAMINE MICRO UNITS' NUCLEOTIDES BONDING WITH IN GROUP.

DEFINITION OF SUB UNIT - Combining combination of micro units within the group with respect to nucleotide attraction forces, which are suitable to conditions like static, dynamic, spatial, symmetric, most compressed, enlargeable and easy to mutually inter changeable.

For this experiment group-1 micro units are taken as samples. All results combinations are not suitable for sub units as definition. Out of all combinations some of them are suitable. The goal is select to some of them.

parentheses.



Figure; -12

1) micro units four are developing six combinations which are shown above.

2) Out of six combinations two or 1/3 combinations are 100% parallel attraction bond in between micro units.

3) Another two combinations or 1/3 combinations are 1/3% diagonal attraction and 2/3% are parallel attraction in between micro units.

4) Remain two combinations or 1/3 combinations are 2/3% diagonal attraction and 1/3% are parallel attraction in between micro units.

CASE STUDY BASED ON BIOLIGICAL CONDITIONS ARE REQUIRED

1) In this innovative work, the system is deterministic, universal, aperiodic crystal where all possibilities are fallows.

2) Parallel attraction in between reconstitute patterns are more suitable for biological act because one is the system is more static, and gene length will be longer, easy to separate,

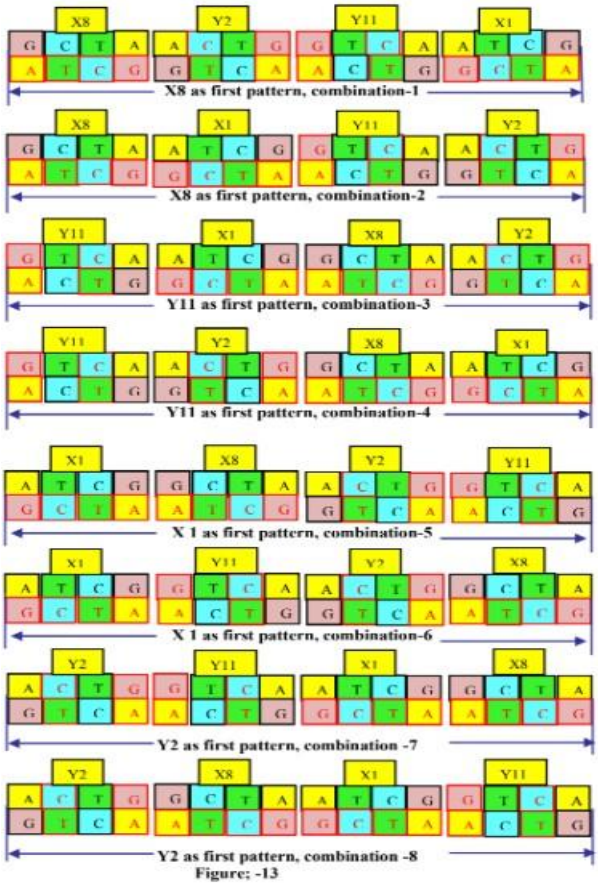
easy to interchange,

3) The system is dynamic, spatial, symmetric, most compressed, enlargeable and easy.

4) In this code every sequence is unique, defined conformational ensemble, and auto assembling.

5) Diagonal combinations are not suitable in this act because length is small, the role of interchange not predicable, the role of compressed and enlargeable not predicable.

To understand the system in better way let us study all parallel combinations of any one group micro units, which explains further unknown information for suitable biological conditions.



Figure; -13

III) OBSERVATIONS

1) Group-A reconstitute micro units are developing eight sub units in parallel end nucleotide attraction combinations.

2) These combinations further recognize as two sets,

3) Each set sub units can bond further in parallel manner, but with other set they bond diagonal. Considering parallel combination is the most suitable for genetic coding

4) Further these each group subunits bonding that is combining them based on parallel attraction of nucleotides, then they
called as group units.

5) Total number of sub units are in each group is 2X4=8

6) Total sub units in the overall system is 2X4X6 =48

DEFINITION OF GROUP UNITS - Combining combination of sub units within the group with respect to end nucleotide bond, which are suitable to conditions like static, dynamic, spatial, symmetric, most compressed, enlargeable and easy to

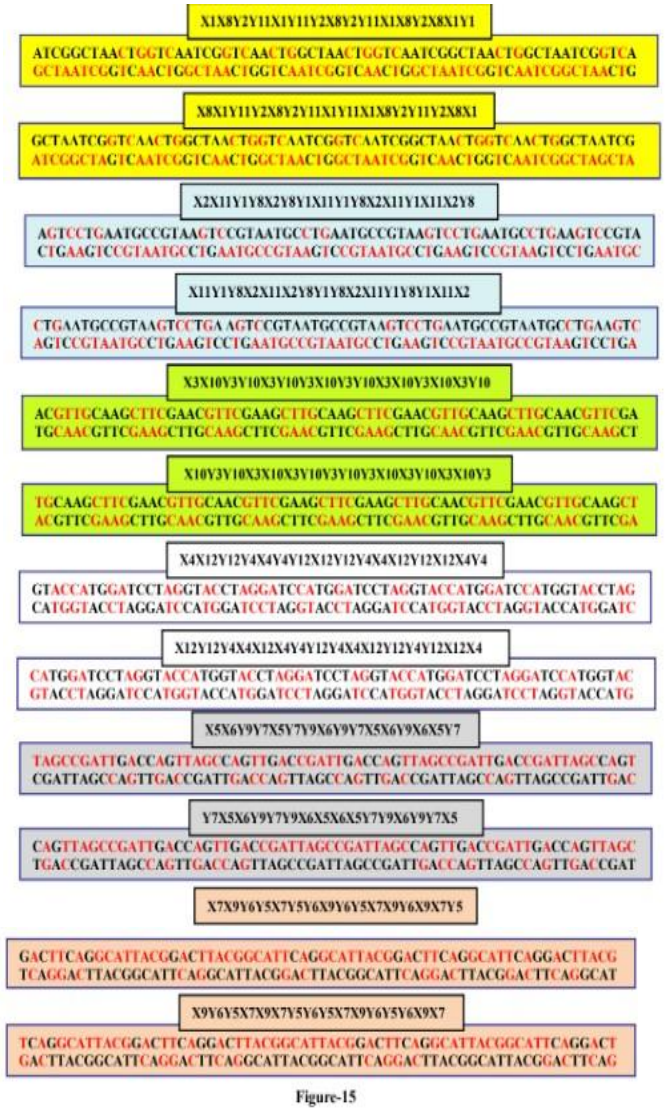


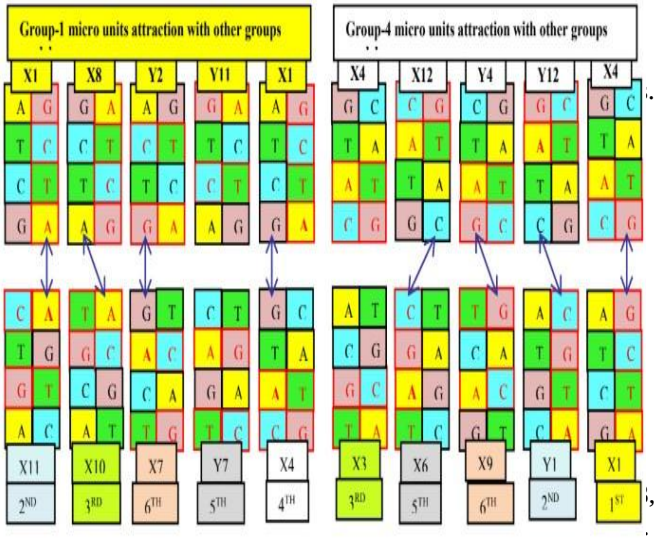
Figure-15

IMPORTANCE OF GENETIC CODE

Science says that proteins are the end products of the decoding process that start with the information in cellular DNA. As workhorses of the cell. Proteins compose structural and motor elements in the cell, they serve as the catalysts for virtually every biochemical reaction that occurs in living things. This incredible array of functions derives from a startlingly simple code that specifies a hugely diverse set of structures. In fact, each gene in cellular DNA contains the code a unique protein structure. Not only are these proteins assembled with different amino acid sequences, but they also are held together by different bonds and folded into a variety of three-dimensional structures. The folding shape, or conformation, depends directly on the liner amino acid sequence of the protein. It is very important to understand that how micro units further develops into sub units, sub units further form into units.

These all modellings are part with in the group or with in the groups. But it is equally important how micro units combine with other groups micro units and form into hugely diverse set of structures. To understand the protein structure, it is important to equally understanding how the system works.

MICRO UNITS END NUCLEOTIDES ARRACTION IN BETWEEN OTHER GROUPS MICRO UNITS.



Figure; - 16

2) Group-2 micro units have a bond with group-1, group-3 group-4 and group-5 micro-units except group-6 micro-units.
3) Group-3 micro units have a bond with group-1, group-2, group-5, and group-6 micro units except group-4 micro units.
4) Group-4 micro-units have a bond with group-1, group-2 group-5 and group-6 micro units except group-3 micro-units.
5) Group-5 micro units have a bond with group-2, group-3, group-4 and group-6 micro units except group-1 micro units.
6) Group-6 micro units have a bond with group-1, group-3, group-4 and group-5 micro units expect group-2 micro units.

OBSERVATIONS

1) As per this theory, the system has 24 micro units each unit can produce one amino acid and total amino acids are 24 in numbers.
2) These 24 micro units can separate into six groups based on end nucleotides.
3) It is possibility that only five groups micro units are having a bond together out of six groups. That means each group shall
bond with other four groups micro units.
4) Mature proves that only 20 micro units are part in each genetic code and they generate only 20 amino acids in genome it is protein.
5) Genome is pool of genetic codes, likewise many other codes generate other sets of 20 amino acids for other applications.
6) One thing is true that each protein has 20 amino acid set, but it is not clear that all proteins are combination of only 20 amino acids or combination 20 amino acids out of 24 amino acid set in natures determinism. Biologist must give this
answer. As per science proteins are built from a set of only twenty amino acids, each of which has a unique side chain. The side chains of amino acids have different chemistries. The largest group of amino acids have nonpolar side chains. Several other amino acids have side chains with positive or negative charges, while others have polar but uncharged side chains. The chemistry of amino acid side chains is critical to protein structure because these side chains can bond with one another to hold a length of protein in a certain shape or conformation. but they also are held together by different bonds and folded into a variety of three-dimensional structures. The folded shape, or conformation, depends directly on the linear amino acid sequence of the protein. Science says the typical confirmed human gene has 12 exons of an average length of 236 base pairs each, separated by introns of an average length of 5,478 base pairs. As a consequence, the average intron length is about twice the average transcript length. Basically, every cell pro with respect to all biological acts genetic unit must follow some rules; the order must fit in the frame of double helix structure. For better coil folding each genetic code is to base on any one of the group's units, the unit to be boundary for other four. group's units and base unit to be same or any one of the combinations of 24 units in entire gene. And other sub unit must be same throughout length of gene, which helps perfect coiling. The arrangement must be dynamic, spatial, and symmetric. Easy to mutual inter change at meiosis stage, easy to enlarge, and easy to compress at mitosis stage
and in three dimensional.

GENETIC UNIT: Genetic unit is defined as combination group units in a parallel bonding, of all possible bonding groups. Considering 20 set of amino acids are results production of genetic unit the format of bonding shall be mention below. The format is imaginary format. It is not original, for that lot of observation and experience is required in micro-biological field but I am not belonging to such a discipline.

SAMPLE GENETIC UNIT:

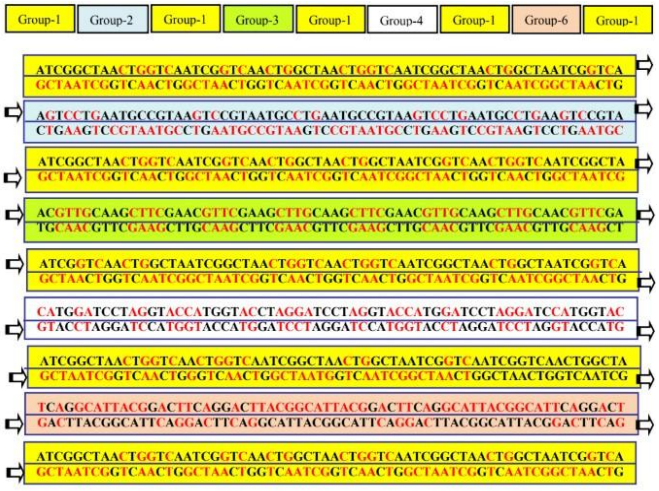
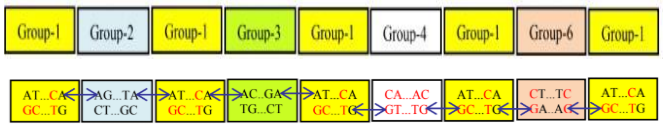


Figure-17



How five group unit are combining together and form into assumed sample genetic unit in a parallel bond.

IV) CONCLUSIONS:

Natures determinism act pays a key role on natural events and an important role on creatures. Several natures act shall have predetermined before they occur. Pre determinism is the idea that all events are determined in advance. The best way to understand natures pre- determinism is like arrangement act or modelling act in a single group. In the universal existence of events is based on planets rotation in orbit, time and gravitational, and other forces. These events are accurate

and can be equated in computer system. Earth is revolving around the Sun results the seasons like summer, spring, rainy, and winter. All seasons come one after another in periodic manner; this is one mega cycle in a year. With respect to the mega cycle, billions of creatures start their life cycle on Mother Earth. Re-production is the main events in a creature's life to generate their off springs. In this process two gametes generate required number of cells for creatures' zygote. This is natures modelling act in between two sets of chromosomes. It is possible to nature act to generate perfect genetic sequences. but computers cannot evaluate system because present mathematics are not suitable.

Fertilization is un-broken chains of events from egg selection to offspring in the interval of 9 months an average; it is similar like a modern car manufacture company where each car comes out of the factory in the interval of one hour. For this process every operation in all mega systems to micro-systems have time frame, very well defined and in perfect mathematical model. Any small mistake in any one of system cannot give planned results. This system cannot possible to think in the random order. Similar-way each micro-biological act to mega-act is in perfect mathematical model. Nature modelling act is based on chromosomes attraction forces and reverse of chromosomes. These modelling must be static, dynamic determined, spatial, symmetric, most compressed, enlargeable, and easy to mutually inter-changeable.

ANSWERS FOR UN SOLVED QUESTIONS IN SCIENCE AS PER NATURES DETERMINISM THEORY
IN MICRO BIOLOGY

1) How egg attract matured sperm.
2) Gametes further develops reconstitute cells.
3) Chromosomes cross-over.
4) Cells generation in the combination of meiosis and mitosis.
5) Twin tree of life.
6) How the resulting off-springs as a boy or girl or hermaphrodite in perfect fertilization.
7) Fertilization and natural problems.
8) Due to natural problems results fertilization as twins, twins as boys, twins as a girl, twins as boy and girl but not hermaphrodites.
9) Combined twins and more twins.

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Tenneti Vijay Kumar received his B.E. degree in Mechanical Engineering from Andhra University, Visakhapatnam, in 1981. He worked as a mechanical engineer in various national and international companies, gaining over four decades of professional experience. Since 1982, he has dedicated himself to developing the Tenneti Theory of Determinism, a novel mathematical framework inspired by shuffling rules and deterministic systems. His work explores applications in computer complexity, P vs NP problems, anti-piracy solutions, and innovative technologies. In 2011, he authored *Tenneti Theory of Determinism*, providing insights into mathematical patterns in fertilization and deterministic processes. Despite lacking formal degrees in related sciences, he continues to seek collaboration to contribute his findings to global research.

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