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Theory of Genetic Code

Randomized Block Designs

Highlights

Function on Fourier Cosine

Results on Bicomplex Matrices

Discovering Thoughts, Inventing Future

VOLUME 18 ISSUE 2 VERSION 1.0

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Topology and Dynamics of Terrorism

By U. S. Idiong & A. B. Ipinlaye
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Abstract- Terrorism is a social as well as an historical problem which has attracted great concerns in recent times. This paper discusses the mathematical perspective of terrorism and possible recommendations on nipping the problem in the bud.

Keywords: *connectedness, cluster point, neighbourhood, networks, terrorism.*

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Topology and Dynamics of Terrorism

U. S. Idiong [α] & A. B. Ipinlaye [σ]

Abstract- Terrorism is a social as well as an historical problem which has attracted great concerns in recent times. This paper discusses the mathematical perspective of terrorism and possible recommendations on nipping the problem in the bud.

Keywords: *connectedness, cluster point, neighbourhood, networks, terrorism.*

I. Introduction

Terrorism is a social as well as an historical problem that has posed a great threat to mankind. It is one of the greatest challenge of nations in the 21st century that has killed multitudes, rendered many able bodied persons invalid and displaced many households. Countries such as United States of America, Afghanistan, Pakistan, France, United Kingdom, Iraq, Somalia, Kenya, Nigeria etc. have been the worst hit on a daily basis when it comes to the scourge of Terrorism according to press daily reports. World organizations such as United Nations, the African Union and other government agencies are on a passionate search for a panacea to this perennial problem.

Terrorism is a very complex phenomenon that poses threat to international security. It affects every aspect of life. The economy of affected nations is under severe threat as no ready to invest in turbulent communities. Trade is put on hold because of violence. Agriculture and food security is also affected as no farmer will want to be exposed to attack in such areas. Health facilities cannot be sustained as this faceless group are hell-bent on total destruction of life and properties.

Not so many mathematicians have studied this perilous problem that has plagued vast populace of humanity. Among the few authors that have studied terrorism as a problem are Gutfrained [1, 2], Caulkins et.al [3], Woo [5], and Zhuang and Bier [7]. Also, Wright [6] in his paper, looks at terrorism as a thing of ideology than brute force. Stephen Trench [4] in his paper writes on how to fighting terrorism with Mathematics. The result discussed in this paper does not use the approach of previous discussants but adopts the topological strategy.

In what follows, it is necessary to outline what shall be presented in each section. In section two, we shall introduce the definitions of some fundamental concepts in topology required for this study. Section three contains the application of these concepts to the study of the problem. Section four shall reflect some recommendations on safety measures as well as counter-terrorism strategies.

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II. Fundamental Concepts

In this section, we introduce some important concepts in topology.

2.1 Definition: A set X is called a topological space if it is closed with respect to a family of its subsets $\tau \subseteq 2^X$ so that (i) $\emptyset, X \in \tau$ (ii)$\cup_{\alpha\in\mathcal{A}} U_\alpha \in \tau$ and (iii)$\cap_{i=1}^{n} U_i \in \tau$ where $\mathcal{A}$ is an indexing set.

In the above definition τ is called the topology of X and every open set $U \in \tau$ is called an open set.

2.2 Definition: A set $\mathcal{N}(x)$ is called the neighbourhood of $x \in X$ if there exists an open set $U \in \tau$ such that $x \in U \subseteq \mathcal{N}(x) \subset X$.

2.3 Definition: A point $x \in X$ is called a limit point, cluster point or accumulation point of S if $\mathcal{N}(x) \setminus \{x\} \cap S \neq \emptyset$.

2.4 Definition: A point $x \in X$ is called an isolation point of S if $\mathcal{N}(x) \setminus \{x\} \cap S = \emptyset$.

2.5 Definition: Let X and $\tilde{X}$ be topological spaces and $p : \tilde{X} \to X$ be continuous map. An open set $U \in \tau_X$ is said to be evenly covered by the map p if and only if

$$p^{-1}(U) = \coprod \{V : V \in \tau_{\tilde{X}}\}$$

each of which is mapped homeomorphically onto U by p. Then the map p is a covering map.

2.1 Theorem: (Lifting Lemma)**.** Let $p^{-1} : \tilde{X} \to X$ be a covering map and $f : (B, b_0) \to (X, x_0)$ a map from a base space (B, b_0) with a base point b_0 into the base space (X, x_0) with base point x_0. If $\tilde{x}_0$ is in the fibre of x_0 then there exists a unique map $\tilde{f} : (B, b_0) \to (\tilde{X}, x_0)$ such that $p \circ \tilde{f} = f$.

2.1 Remark: The map $\tilde{f}$ in Lemma 2.1 above is called the lift. When the base space (B, b_0) equals $(I, 0)$ a unit interval I based at 0 or any other path then $\tilde{f}$ is called a path lifting map. This principle is what is required when instead of engaging ground battle, air strikes could be adopted. The war airplanes serve as the lift.

III. Main Result

In this section, the application of the above concepts in the discussion of the problem of terrorism and the strategies for counter-terrorism operations is presented. In what follows, the topological space X shall be likened to regions susceptible to terror attack.

3.1 Theorem (Bomb ignition): An ignited bomb's point of impact affects its ignition point $x \in X$ and its neighbourhood $\mathcal{N}(x, \epsilon)$ bounded by the radius of impact ϵ.

3.1 Remark: The radius of impact ϵ of the bomb as a weapon of mass destruction at times ranges from $1m$ to $50m$ depending on its components.

Notes

3.2 Theorem (Risk of Casualties): Let the location of any potential risk victim be $y \in X$ then anyone at point $y \in \mathcal{N}(x, \epsilon)$ is at the risk of casualty.

3.2 Remark: By risk of casualty we mean that anyone at the point of impact is likely to suffer injuries and at worst will risk death.

Notes

3.3 Theorem: An isolation point which describes the location of a suicide bomber with no other person within the neighbourhood will have the minimum casuality impact of the bomb.

3.4 Theorem: A cluster point which describes a densely populated neighbourhood will record maximum casualty impact of the bomb.

3.5 Theorem: Let $y_i (i = 1, \ldots, m)$ denote the location of individuals in $\mathcal{N}(x, \epsilon)$ then minimum casualty will be recorded if $\mathcal{N}(x, \epsilon) \setminus \bigcap_{i=1}^{m} \{y_i\} = \{x\}$ where x is the location of the suicide bomber.

3.3 Remark: In other cases $\mathcal{N}(x, \epsilon) \setminus \bigcap_{i=1}^{m} \{y_i\} = \emptyset$ when x is the location of a timed bomb in the absence of a suicide bomber from $\mathcal{N}(x, \epsilon)$. Here, x is an isolated point.

Next, it is necessary to consider network topology because it is a well known fact that terrorist groups work in very intrinsic networks that make it difficult for security forces to crackdown on them. Terrorism is the worst kind of warfare because of its unpredictable nature. A network topology is the arrangement of a network, including its nodes and connecting lines. There are two ways of defining network geometry: the physical topology and the logical (or signal) topology (See Fig 1). In advanced technologies, drones technology is used in mapping out the networks of suspected terrorists using some of their known bio-data obtained in the course of interrogation. Though in actual modus operandi most crude terrorists operate using courier correspondence that are not electronic in nature. The reason for this is because such domains are trackable.

Sometimes the network topology allows one to loop points to a certain base point which helps the military to develop a strategy of counter-terrorism operations. (See fig 2).

3.6 Theorem: In counter terrorism operations, air raid can be carried out using a translated rotational triangular network loops from at least three surrounding air base where operations are taken in hourly permuted sequence group A_3 pattern with terms:

$$\imath, (12), (23), (13), (321), (213), (132), (312), (231)$$

Here, $\imath = (123)$ is the identity path.

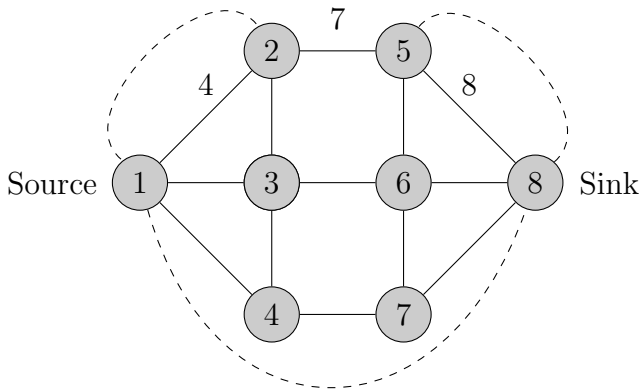

Figure 1: A Figure Showing An Example of Networks of Points in A Topological Space

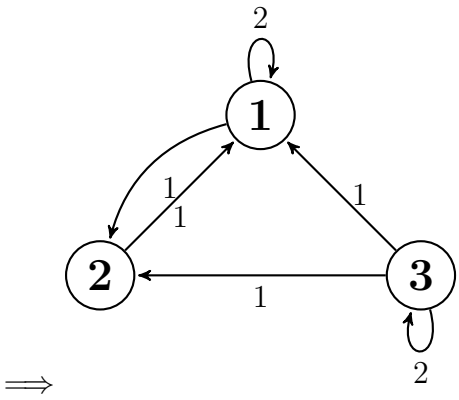

Figure 2: Figure Showing A simple loop of network of points called nodes

IV. Conclusion

This paper has discussed the safety and counter terrorism strategy for cubbing the menace and excesses of terrorist apart from the ideology and propaganda strategy. Other models for combating terrorist groups which can mesmerize them can be adopted using more advanced group permutations $A_{n,}$ $n > 3$.

V. Recommendations

The following recommendations can be deduced from this paper:

(a) Precautions should be taken by the Governments not to make inciting statements that could trigger violence.
(b) Government and Non-governmental agencies should use the mass media platforms to educate their citizenry to avoid cluster gatherings in highly susceptive areas.
(c) Places of high density such as markets, churches, mosques, etc. should be properly guarded by security agents well equipped with surveillance cameras, drowns, and bomb detectors.
(d) In counter terrorism feats, arial bombardments should be used more in dealing with concentrated hideouts of terrorists. The translated triangular symmetry model can be adopted to make their formation unpredictable by the insurgents.
(e) Intelligence gathering should also use satellite and drones technologies.

Notes

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Certain Results on Bicomplex Matrices

By Anjali & Amita
Dr. B. R. Ambedkar University

Abstract- This paper begins the study of bicomplex matrices. In this paper, we have defined bicomplex matrices, determinant of a bicomplex square matrix and singular and non-singular matrices in C_2. We have proved that the set of all bicomplex square matrices of order n is an algebra. We have given some definitions and results regarding adjoint and inverse of a matrix in C_2. We have defined three types of conjugates and three types of tranjugates of a bicomplex matrix. With the help of these conjugates and tranjugates, we have also defined symmetric and skew - symmetric matrices, Hermitian and Skew - Hermitian matrices in C_2.

Keywords: *bicomplex matrices, conjugates matrices, tranjugate matrices, Hermitian matrices, skew Hermitian matrices.*

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Certain Results on Bicomplex Matrices

Anjali [α] & Amita [σ]

Abstract- This paper begins the study of bicomplex matrices. In this paper, we have defined bicomplex matrices, determinant of a bicomplex square matrix and singular and non-singular matrices in C_2. We have proved that the set of all bicomplex square matrices of order n is an algebra. We have given some definitions and results regarding adjoint and inverse of a matrix in C_2. We have defined three types of conjugates and three types of tranjugates of a bicomplex matrix. With the help of these conjugates and tranjugates, we have also defined symmetric and skew - symmetric matrices, Hermitian and Skew - Hermitian matrices in C_2.

Keywords: bicomplex matrices, conjugates matrices, tranjugate matrices, Hermitian matrices, skew Hermitian matrices.

I. Introduction

In 1892, Corrado Segre (1860-1924) published a paper [8] in which he treated an infinite set of Algebras whose elements he called bicomplex numbers, tricomplex numbers,…., n-complex numbers. A bicomplex number is an element of the form $(x_1+i_1x_2) +i_2 (x_3+i_1x_4)$, where $x_1,\ldots, x_4$ are real numbers, $i_1^2 = i_2^2 = -1$ and $i_1i_2 = i_2i_1$.

Segre showed that every bicomplex number $z_1+i_2z_2$ can be represented as the complex combination

$$(z_1 - i_1z_2)\left[\frac{1+i_1i_2}{2}\right] + (z_1 + i_1z_2)\left[\frac{1-i_1i_2}{2}\right]$$

Srivastava [9] introduced the notations ${}^1\xi$ and ${}^2\xi$ for the idempotent components of the bicomplex number $\xi = z_1+i_2z_2$, so that

$$\xi = {}^1\xi\frac{1+i_1i_2}{2} + {}^2\xi\frac{1-i_1i_2}{2}$$

Michiji Futagawa seems to have been the first to consider the theory of functions of a bicomplex variable [2,3] in 1928 and 1932.

The hyper complex system of Ringleb [7] is more general than the Algebras; he showed in 1933 that Futagawa system is a special case of his own.

In 1953 James D. Riley published a paper [6] entitled "Contributions to theory of functions of a bicomplex variable".

Throughout, the symbols C_2, C_1, C_0 denote the set of all bicomplex, complex and real numbers respectively.

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a) Some special subset of C_2

We shall use notation C (i_1), C (i_2) and H for the following sets.

C(i_1) is the set of complex numbers with imaginary unit i_1.i. e.

$$C(i_1) = \{a + i_1 b;\ a, b \in C_0\}$$

and C (i_2) is the set of complex numbers with imaginary unit i_2.i. e.

$$C(i_2) = \{a + i_2 b;\ a, b \in C_0\}$$

The bicomplex number $\xi = (x_1 + i_1 x_2) + i_2 (x_3 + i_1 x_4)$ for which $x_2 = x_3 = 0$ is called a hyperbolic number.

The set of all hyperbolic numbers is denoted by H and defined as

$$H = \{a + i_1 i_2 b;\ a, b \in C_0\}$$

b) Idempotent elements in C_2

There are exactly four idempotent elements in C_2. Out of these, 0 and 1 are the trivial idempotent elements and two nontrivial idempotent elements denoted by e_1 and e_2 which are defined as

$$e_1 = \frac{1+i_1 i_2}{2} \text{ and } e_2 = \frac{1-i_1 i_2}{2}$$

Obviously $(e_1)^n = e_1$, $(e_2)^n = e_2$

$$e_1 + e_2 = 1,\ e_1.e_2 = 0$$

C_1 is a field but C_2 is not a field, since C_2 has divisor of zero for example $e_1\ e_2 = 0$ neither e_1 is zero nor e_2 is zero.

Every bicomplex number ξ has unique idempotent representation as complex combination of e_1 and e_2 as follows

$$\xi = z_1 + i_2 z_1 = (z_1 - i_1 z_2) e_1 + (z_1 + i_1 z_2) e_2$$

The complex numbers $(z_1 - i_1 z_2)$ and $(z_1 + i_1 z_2)$ are called idempotent component of ξ and are denoted by ${}^1\xi$ and ${}^2\xi$ respectively (cf. Srivastava [9]).

Thus $\xi = {}^1\xi\, e_1 + {}^2\xi\, e_2$

There are infinite numbers of element in C_2 which do not possess multiplicative inverse. A bicomplex number $\xi = z_1 + i_2 z_1$ is singular if and only if $|z_1^2 + z_2^2| = 0$

The set of all singular elements in C_2 is denoted by O_2.

Evidently a nonzero bicomplex number ξ is singular if and only if either ${}^1\xi = 0$ or ${}^2\xi = 0$ that is if and only if it is a complex multiple of either e_1 or e_2.

c) Algebraic properties of idempotent components

The idempotent representation is perfectly compatible with the algebraic structure of C_2 in the following way

For all ξ, η in C_2

$$\xi \pm \eta = ({}^1\xi e_1 + {}^2\xi e_2) \pm ({}^1\eta e_1 + {}^2\eta e_2)$$

$$= ({}^1\xi \pm {}^1\eta) e_1 + ({}^2\xi \pm {}^2\eta) e_2,$$

so that $^1(\xi \pm \eta) = {}^1\xi \pm {}^1\eta$ and $^2(\xi \pm \eta) = {}^2\xi \pm {}^2\eta$

$$\alpha\xi = \alpha\ ({}^1\xi e_1 + {}^2\xi e_2)$$

$$= \alpha\ ({}^1\xi)\ e_1 + \alpha\ ({}^2\xi)\ e_2,\ \forall \alpha \in C_1$$

so that $^1(\alpha\xi) = \alpha\ {}^1\xi$ and $^2(\alpha\xi) = \alpha\ {}^2\xi$ for $\alpha \in C_1$

$$\xi\eta = ({}^1\xi e_1 + {}^2\xi e_2).({}^1\eta e_1 + {}^2\eta e_2)$$

$$= ({}^1\xi\ {}^1\eta)e_1 + ({}^2\xi^2\eta)e_2,$$

so that $^1(\xi\eta) = {}^1\xi\ {}^1\eta$ and $^2(\xi\eta) = {}^2\xi\ {}^2\eta$

$$\frac{\xi}{\eta} = \left({}^1\xi e_1 + {}^2\xi e_2\right) \Big/ \left({}^1\eta e_1 + {}^2\eta e_2\right)$$

$$= \left({}^1\xi \Big/ {}_1\eta\right)e_1 + \left({}^2\xi \Big/ {}_2\eta\right)e_2, \quad \textit{provided}\ \eta \notin O_2$$

so that $^1\left(\xi/\eta\right) = {}^1\xi/{}_1\eta$ and $^2\left(\xi/\eta\right) = {}^2\xi/{}_2\eta$

d) Norm in C_2[5]

The norm of a bicomplex number

$$\xi = z_1 + i_2 z_2 = x_1 + i_1 x_2 + i_2 x_3 + i_1 i_2 x_4 = {}^1\xi\ e_1 + {}^2\xi\ e_2 \text{ is defined as}$$

$$\|\xi\| = (x_1^2 + x_2^2 + x_3^2 + x_4^2)^{1/2}$$

$$= (|z_1|^2 + |z_2|^2)^{1/2}$$

$$= \sqrt{\frac{\left|{}^1\xi\right|^2 + \left|{}^2\xi\right|^2}{2}}$$

C_2 becomes a modified Banach algebra, in the sense that $\xi, \eta \in C_2$, we have,
In general $\|\xi.\eta\| \leq \sqrt{2}\ \|\xi\|\|\eta\|$

e) Conjugates of a bicomplex number

Analogous to the concept of conjugate of a complex number, conjugates of a bicomplex number are also defined. As a bicomplex number is four dimensional, different types of conjugate arise.

In bicomplex space C_2, every number ξ possesses three types of conjugates. The i_1 conjugate, i_2 conjugate and $i_2 i_2$ conjugate of $\xi = z_1 + i_2 z_2 = x_1 + i_1 x_2 + i_2 x_3 + i_1 i_2 x_4 = {}^1\xi\ e_1 + {}^2\xi\ e_2$ are denoted by $\bar{\xi}$, $\xi^{\sim}$ and $\xi^{\#}$ respectively, therefore

$$\bar{\xi} = (x_1 - i_1 x_2) + i_2 (x_3 - i_1 x_4)$$

$$= (\bar{z}_1 + i_2 \bar{z}_2)$$

$$= (\overline{{}^2\xi} e_1 + \overline{{}^1\xi} e_2)$$

$$\xi^{\sim} = (x_1 + i_1 x_2) - i_2(x_3 + i_1 x_4)$$
$$= (z_1 - i_2 z_2)$$
$$= ({}^2\xi e_1 + {}^1\xi e_2)$$
$$\xi^{\#} = (x_1 - i_1 x_2) - i_2(x_3 - i_1 x_4)$$
$$= (\bar{z}_1 - i_2 \bar{z}_2)$$
$$= (\overline{{}^1\xi} e_1 + \overline{{}^2\xi} e_2)$$

Notes

II. Certain Results From Bicomplex Matrices

a) Some Definitions

2.1.1 Bicomplex matrices

A matrix $A = [\xi_{mn}]_{m\times n}$ whose entries belong in C_2, is said to be a bicomplex matrix i.e. we define

$$A = \begin{bmatrix} \xi_{11} & \xi_{12} & -- & \xi_{1n} \\ \xi_{21} & \xi_{22} & -- & \xi_{2n} \\ - & - & -- & - \\ \xi_{m1} & \xi_{m2} & -- & \xi_{mn} \end{bmatrix} \forall\, \xi_{pq} \in C_2$$

Where $1 \le p \le m$ and $1 \le q \le n$

Since every bicomplex number ξ has unique idempotent representation as complex combination of e_1 and e_2 as follows

$$\xi = z_1 + i_2 z_2 = (z_1 - i_1 z_2)e_1 + (z_1 + i_1 z_2)e_2$$

Therefore every bicomplex matrices $A = [\xi_{mn}]_{m\times n}$ can be expressed uniquely as ${}^1Ae_1 + {}^2Ae_2$ such that ${}^1A = [z_{mn}]_{m\times n}$ and ${}^2A = [w_{mn}]_{m\times n}$ are complex matrices.

2.1.2 Bicomplex square matrices

A bicomplex matrix in which the number of rows is equal to the number of columns is called a bicomplex square matrix. i.e.

$$A = \begin{bmatrix} \xi_{11} & \xi_{12} & ..... & \xi_{1n} \\ \xi_{21} & \xi_{22} & ..... & \xi_{2n} \\ ..... & ..... & ..... & ..... \\ \xi_{n1} & \xi_{n2} & .... & \xi_{nn} \end{bmatrix}; \xi_{pq} \in C_2;\ p, q = 1,2,\ldots,n$$

2.1.3 Bicomplex diagonal matrices

A bicomplex square matrix A is called a diagonal matrix if all its non-diagonal elements are zero i.e.

$$A = \begin{bmatrix} \xi_{11} & 0 & ..... & 0 \\ 0 & \xi_{22} & ..... & 0 \\ ..... & ..... & ..... & ..... \\ 0 & 0 & ..... & \xi_{nn} \end{bmatrix}, \quad \xi_{pq} \in C_2$$

Notes

2.1.4 Determinant of a bicomplex matrix

Let $A = [\xi_{ij}]_{n\times n}$ be a bicomplex square matrix of order n, where n is some positive integer. The determinant of A, is defined as

$$\det A = |A| = \left|[\xi_{ij}]\right|,\ \xi_{ij} \in C_2$$

$$detA = |A| = \sum_{\sigma \in S_n} Sig.(\sigma) \prod_{i=1}^{n} \xi_{i\,\sigma(i)}$$

Where S_n is the group of all permutation on 'n' symbols.

2.1.5 Transpose of a bicomplex matrix

If $A = [\xi_{m\ n}]_{m\times n}$ is any bicomplex matrix then A matrix of order $n \times m$ obtained from 'A' by changing its rows into columns and its columns into rows is called transpose of 'A' and is denoted by A^T.

2.1.6 Cofactor and adjoint matrix of a matrix in C_2

Let $A = [\xi_{ij}]_{n\times n}$ be a bicomplex square matrix of order n then cofactor of the entry ξ_{ij} is defined as $(-1)^{i+j}$ × the determinant obtained by leaving the row and the column(In the matrix A) passing through the entry $\xi_{ij} = \eta_{ij}$ (say).

Then the matrix $[\eta_{ij}]_{n\times n}$ is defined as the cofactor matrix of A and the transpose of cofactor matrix of A is known as adjoint matrix of A. i.e. AdjA=$[\eta_{ij}]^T{}_{n\times n}$

2.1.7 Bicomplex singular and non-singular matrix

A bicomplex Square matrix is said to be non-singular if $|A| \notin O_2$ (set of all singular element in C_2).

and If $|A| \in O_2$ then it is called singular matrix.

b) Algebraic structure of bicomplex Matrices

Let S be the set of all bicomplex square matrices of order n. Define binary compositions over S called addition "+" , scalar multiplication "." and multiplication "×" as follows:

$$\text{Let} A = \begin{bmatrix} \xi_{11} & \xi_{12} & \cdots & \xi_{1n} \\ \xi_{21} & \xi_{22} & \cdots & \xi_{2n} \\ \cdots & \cdots & \cdots & \cdots \\ \xi_{n1} & \xi_{n2} & \cdots & \xi_{nn} \end{bmatrix} \text{and}$$

$$B = \begin{bmatrix} \eta_{11} & \eta_{12} & \cdots & \eta_{1n} \\ \eta_{21} & \eta_{22} & \cdots & \eta_{2n} \\ \cdots & \cdots & \cdots & \cdots \\ \eta_{n1} & \eta_{n2} & \cdots & \eta_{nn} \end{bmatrix}$$

be the arbitrary member of S and $\alpha \in F$, where F is either field of real numbers or complex numbers.

$$A + B = \begin{bmatrix} \xi_{11}+\eta_{11} & \xi_{12}+\eta_{12} & ..... & \xi_{1n}+\eta_{1n} \\ \xi_{21}+\eta_{21} & \xi_{22}+\eta_{22} & ..... & \xi_{2n}+\eta_{2n} \\ ..... & ..... & ..... & ..... \\ \xi_{n1}+\eta_{n1} & \xi_{n2}+\eta_{n2} & ..... & \xi_{nn}+\eta_{nn} \end{bmatrix}$$

$$\alpha.A = \begin{bmatrix} \alpha\xi_{11} & \alpha\xi_{12} & ..... & \alpha\xi_{1n} \\ \alpha\xi_{21} & \alpha\xi_{22} & ..... & \alpha\xi_{2n} \\ ..... & ..... & ..... & ..... \\ \alpha\xi_{1n} & \alpha\xi_{2n} & ..... & \alpha\xi_{nn} \end{bmatrix}. \text{ and } A\times B = \begin{bmatrix} \xi_{11}\eta_{11}+.....+\xi_{1n}\eta_{n1} & --- & \xi_{11}\eta_{1n}+.....+\xi_{1n}\eta_{nn} \\ \xi_{21}\eta_{11}+.....+\xi_{2n}\eta_{n1} & --- & \xi_{21}\eta_{1n}+....+\xi_{2n}\eta_{nn} \\ --- & --- & --- \\ \xi_{n1}\eta_{11}+.....+\xi_{nn}\eta_{n1} & --- & \xi_{n1}\eta_{1n}+....+\xi_{nn}\eta_{nn} \end{bmatrix}$$

2.2.1 Theorem: The set of all bicomplex square matries i.e "S" forms an algebra.

Proof:

a. *Additive abelian group structure*

- *Associativity:*

Let A $=[\xi_{ij}]_{n\times n}$, B $= [\eta_{ij}]_{n\times n}$ and C $= [\varsigma_{ij}]_{n\times n}$ be the member of S and $\alpha, \beta \in F$ then

$$A+(B+C) = \begin{bmatrix} \xi_{11}+(\eta_{11}+\varsigma_{11}) & ..... & \xi_{1n}+(\eta_{1n}+\varsigma_{1n}) \\ \xi_{21}+(\eta_{21}+\varsigma_{21}) & ..... & \xi_{2n}+(\eta_{2n}+\varsigma_{2n}) \\ ..... & ..... & ..... \\ \xi_{n1}+(\eta_{n1}+\varsigma_{n1}) & ..... & \xi_{nn}+(\eta_{nn}+\varsigma_{nn}) \end{bmatrix}$$

$$(A+B)+C = \begin{bmatrix} (\xi_{11}+\eta_{11})+\varsigma_{11} & ..... & (\xi_{1n}+(\eta_{1n})+\varsigma_{1n} \\ (\xi_{21}+\eta_{21})+\varsigma_{21} & ..... & (\xi_{2n}+\eta_{2n})+\varsigma_{2n} \\ ..... & ..... & ..... \\ (\xi_{n1}+\eta_{n1})+\varsigma_{n1} & ..... & (\xi_{nn}+\eta_{nn})+\varsigma_{nn} \end{bmatrix}$$

Since C_2 is an algebra

Therefore A + (B +C) = (A + B)+ C

Identity: $\forall$ A $\in$ S $\exists$ null matrix "0" $\in$ S then A + 0 =A i.e

$$\begin{bmatrix} \xi_{11} & \xi_{12} & ..... & \xi 1n \\ \xi_{21} & \xi_{22} & ..... & \xi_{2n} \\ ..... & ..... & ..... & ..... \\ \xi_{n1} & \xi_{n2} & ..... & \xi_{nn} \end{bmatrix} + \begin{bmatrix} 0 & 0 & ..... & 0 \\ 0 & 0 & ..... & 0 \\ ..... & ..... & ..... & ..... \\ 0 & 0 & ..... & 0 \end{bmatrix} = \begin{bmatrix} \xi_{11} & \xi_{12} & ..... & \xi 1n \\ \xi_{21} & \xi_{22} & ..... & \xi_{2n} \\ ..... & ..... & ..... & ..... \\ \xi_{n1} & \xi_{n2} & ..... & \xi_{nn} \end{bmatrix}$$

So 0 is the additive identity.

- Inverse:

$\forall$ A $\in$ S $\exists$ - A $\in$ S such that $-$A +A = 0 i.e.

$$\begin{bmatrix} -\xi_{11} & -\xi_{12} & ..... & -\xi 1n \\ -\xi_{21} & -\xi_{22} & ..... & -\xi_{2n} \\ ..... & ..... & ..... & ... \\ -\xi_{n1} & -\xi_{n2} & ..... & -\xi_{nn} \end{bmatrix} + \begin{bmatrix} \xi_{11} & \xi_{12} & ..... & \xi 1n \\ \xi_{21} & \xi_{22} & ..... & \xi_{2n} \\ ..... & ..... & ..... & ..... \\ \xi_{n1} & \xi_{n2} & ..... & \xi_{nn} \end{bmatrix}. = \begin{bmatrix} 0 & 0 & ..... & 0 \\ 0 & 0 & ..... & 0 \\ ..... & ..... & ..... & ..... \\ 0 & 0 & ..... & 0 \end{bmatrix}$$

Notes

Therefore "–A" is the additive inverse of A.

- *Commutative:*

Since

$$A + B = \begin{bmatrix} \xi_{11}+\eta_{11} & \xi_{12}+\eta_{12} & ..... & \xi_{1n}+\eta_{1n} \\ \xi_{21}+\eta_{21} & \xi_{22}+\eta_{22} & ..... & \xi_{2n}+\eta_{2n} \\ ..... & ..... & ..... & ..... \\ \xi_{n1}+\eta_{n1} & \xi_{n2}+\eta_{n2} & ..... & \xi_{nn}+\eta_{nn} \end{bmatrix}$$

And

$$B + A = \begin{bmatrix} \eta_{11}+\xi_{11} & \eta_{12}+\xi_{12} & ..... & \eta_{1n}+\xi_{1n} \\ \eta_{21}+\xi_{21} & \eta_{22}+\xi_{22} & ..... & \eta_{2n}+\xi_{2n} \\ ..... & ..... & ..... & ..... \\ \eta_{n1}+\xi_{n1} & \eta_{n2}+\xi_{n2} & ..... & \eta_{nn}+\xi_{nn} \end{bmatrix}$$

Therefore A + B = B+A as C_2 is an algebra.
So S is abelian group under addition

b. *Ring structure*

- *Closure:*

Since

$$A\times B = \begin{bmatrix} \xi_{11}\eta_{11}+.....+\xi_{1n}\eta_{n1} & --- & \xi_{11}\eta_{1n}+.....+\xi_{1n}\eta_{nn} \\ \xi_{21}\eta_{11}+.....+\xi_{2n}\eta_{n2} & --- & \xi_{21}\eta_{1n}+....+\xi_{2n}\eta_{nn} \\ --- & --- & --- \\ \xi_{n1}\eta_{11}+.....+\xi_{nn}\eta_{n1} & --- & \xi_{n1}\eta_{1n}+....+\xi_{nn}\eta_{nn} \end{bmatrix}$$

Therefore it is evident that A×B ∈ S
Therefore S is closed under multiplication

- *Associativity:*

∀ A, B, C ∈S

Let A =$[\xi_{ij}]_{n\times n}$, B = $[\eta_{ij}]_{n\times n}$ and C = $[\varsigma_{ij}]_{n\times n}$

The $i^{th}j^{th}$ entry of (A×B)×C = [i^{th}row of (A×B)]×[j^{th} column of C]

=[i^{th} row of A]×B×[j^{th}column of C]

Now the $i^{th}j^{th}$ entry of A×(B×C) = [i^{th} row of A]×[j^{th} column of (B×C)]

=[i^{th} row of A] × B × [j^{th}column of C]

Therefore the $i^{th}j^{th}$ entry of (A×B)×C =$i^{th}j^{th}$ entry of A×(B×C)

Hence (A×B)×C = A×(B×C)

Distribution law:

We can easily show that

(A + B)×C = A×C+B×C and A×(B+C)=A×B+A×C

c. *Linear space structure*

$$\alpha.(A+B)=\alpha.\begin{bmatrix}\xi_{11}+\eta_{11} & \xi_{12}+\eta_{12} & \ldots.. & \xi_{1n}+\eta_{1n}\\ \xi_{21}+\eta_{21} & \xi_{22}+\eta_{22} & \ldots.. & \xi_{2n}+\eta_{2n}\\ \ldots.. & \ldots.. & \ldots.. & \ldots..\\ \xi_{n1}+\eta_{n1} & \xi_{n2}+\eta_{n2} & \ldots.. & \xi_{nn}+\eta_{nn}\end{bmatrix} \quad (1)$$

$$=\begin{bmatrix}\alpha(\xi_{11}+\eta_{11}) & \alpha(\xi_{12}+\eta_{12}) & \ldots.. & \alpha(\xi_{1n}+\eta_{1n})\\ \alpha(\xi_{21}+\eta_{21}) & \alpha(\xi_{22}+\eta_{22}) & \ldots.. & \alpha(\xi_{2n}+\eta_{2n})\\ \ldots.. & \ldots.. & \ldots.. & \ldots..\\ \alpha(\xi_{n1}+\eta_{n1}) & \alpha(\xi_{n2}+\eta_{n2}) & \ldots.. & \alpha(\xi_{nn}+\eta_{nn})\end{bmatrix}=\begin{bmatrix}\alpha\xi_{11} & \alpha\xi_{12} & \ldots.. & \alpha\xi_{1n}\\ \alpha\xi_{21} & \alpha\xi_{22} & \ldots.. & \alpha\xi_{2n}\\ \ldots.. & \ldots.. & \ldots.. & \ldots..\\ \alpha\xi_{n1} & \alpha\xi_{n2} & \ldots.. & \alpha\xi_{nn}\end{bmatrix}+$$

$$\begin{bmatrix}\alpha\eta_{11} & \alpha\eta_{12} & \ldots.. & \alpha\eta_{1n}\\ \alpha\eta_{21} & \alpha\eta_{22} & \ldots.. & \alpha\eta_{2n}\\ \ldots.. & \ldots.. & \ldots.. & \ldots.._{-}\\ \alpha\eta_{n1} & \alpha\eta_{n2} & \ldots.. & \eta_{nn}\end{bmatrix}=\alpha.\begin{bmatrix}\xi_{11} & \xi_{12} & \ldots.. & \xi 1n\\ \xi_{21} & \xi_{22} & \ldots.. & \xi_{2n}\\ \ldots.. & \ldots.. & \ldots.. & \ldots..\\ \xi_{n1} & \xi_{n2} & \ldots.. & \xi_{nn}\end{bmatrix}+\alpha.\begin{bmatrix}\eta_{11} & \eta_{12} & \ldots.. & \eta_{1n}\\ \eta_{21} & \eta_{22} & \ldots.. & \eta_{2n}\\ \ldots.. & \ldots.. & \ldots.. & \ldots..\\ \eta_{n1} & \eta_{n2} & \ldots.. & \eta_{nn}\end{bmatrix}$$

Therefore $\alpha.(A+B)=\alpha.A+\alpha.B$

$$(\alpha\beta).A=(\alpha\beta).\begin{bmatrix}\xi_{11} & \xi_{12} & - & \xi_{1n}\\ \xi_{21} & \xi_{22} & - & \xi_{2n}\\ - & - & - & -\\ \xi_{n1} & \xi_{n2} & - & \xi_{nn}\end{bmatrix}=\begin{bmatrix}(\alpha\beta)\xi_{11} & (\alpha\beta)\xi_{12} & - & (\alpha\beta)\xi_{1n}\\ (\alpha\beta)\xi_{21} & (\alpha\beta)\xi_{22} & - & (\alpha\beta)\xi_{2n}\\ - & - & - & -\\ (\alpha\beta)\xi_{n1} & (\alpha\beta)\xi_{n2} & - & (\alpha\beta)\xi_{nn}\end{bmatrix}(\alpha\beta).A=\alpha.\begin{bmatrix}\beta\xi_{11} & \beta\xi_{12} & - & \beta\xi_{1n}\\ \beta\xi_{21} & \beta\xi_{22} & - & \beta\xi_{2n}\\ - & - & - & -\\ \beta\xi_{1n} & \beta\xi_{2n} & - & \beta\xi_{nn}\end{bmatrix} \quad (2)$$

Therefore $(\alpha\beta).A=\alpha.(\beta.A)$

$$(\alpha+\beta).A=(\alpha+\beta).\begin{bmatrix}\xi_{11} & \xi_{12} & \ldots.. & \xi_{1n}\\ \xi_{21} & \xi_{22} & \ldots.. & \xi_{2n}\\ \ldots.. & \ldots.. & \ldots.. & \ldots..\\ \xi_{n1} & \xi_{n2} & \ldots.. & \xi_{nn}\end{bmatrix}=\alpha.\begin{bmatrix}\xi_{11} & \xi_{12} & \ldots. & \xi_{1}n\\ \xi_{21} & \xi_{22} & \ldots. & \xi_{2n}\\ \ldots. & \ldots.. & \ldots. & \ldots.\\ \xi_{n1} & \xi_{n2} & \ldots. & \xi_{nn}\end{bmatrix}+\beta.\begin{bmatrix}\xi_{11} & \xi_{12} & \ldots.. & \xi_{1}n\\ \xi_{21} & \xi_{22} & \ldots.. & \xi_{2n}\\ \ldots.. & \ldots.. & \ldots.. & \ldots..\\ \xi_{n1} & \xi_{n2} & \ldots.. & \xi_{nn}\end{bmatrix} \quad (3)$$

Therefore $(\alpha+\beta).A=\alpha.A+\beta.A$

(4) It is evident that $1.A=A$ for all A in S and $1\in F$

d. Consistency between multiplication and scalar multiplication

$$\alpha.(A\times B)=(\alpha.A)\times B=A\times(\alpha.B)$$

$$\alpha.(A\times B)=\alpha.\left\{\begin{bmatrix}\xi_{11} & \xi_{12} & \ldots. & \xi_{1n}\\ \xi_{21} & \xi_{22} & \ldots. & \xi_{2n}\\ \ldots. & \ldots. & \ldots. & \ldots.\\ \xi_{n1} & \xi_{n2} & \ldots. & \xi_{nn}\end{bmatrix}\times\begin{bmatrix}\eta_{11} & \eta_{12} & \ldots. & \eta_{1n}\\ \eta_{21} & \eta_{22} & \ldots. & \eta_{2n}\\ \ldots. & \ldots. & \ldots. & \ldots.\\ \eta_{1n} & \eta_{2n} & \ldots. & \eta_{nn}\end{bmatrix}\right\}$$

$$\alpha.(A\times B)=\alpha.\begin{bmatrix}\xi_{11}\eta_{11}+.....+\xi_{1n}\eta_{n1} & --- & \xi_{11}\eta_{1n}+.....+\xi_{1n}\eta_{nn}\\ \xi_{21}\eta_{11}+.....+\xi_{2n}\eta_{n2} & --- & \xi_{21}\eta_{1n}+....+\xi_{2n}\eta_{nn}\\ --- & --- & ---\\ \xi_{n1}\eta_{11}+.....+\xi_{nn}\eta_{n1} & --- & \xi_{n1}\eta_{1n}+....+\xi_{nn}\eta_{nn}\end{bmatrix}$$

$$=\begin{bmatrix}\alpha(\xi_{11}\eta_{11})+.....+\alpha(\xi_{1n}\eta_{n1}) & --- & \alpha(\xi_{11}\eta_{1n})+.....+\alpha(\xi_{1n}\eta_{nn})\\ \alpha(\xi_{21}\eta_{11})+.....+\alpha(\xi_{2n}\eta_{n2}) & --- & \alpha(\xi_{21}\eta_{1n})+....+\alpha(\xi_{2n}\eta_{nn})\\ --- & --- & ---\\ \alpha(\xi_{n1}\eta_{11})+.....+\alpha(\xi_{nn}\eta_{n1}) & --- & \alpha(\xi_{n1}\eta_{1n})+....+\alpha(\xi_{nn}\eta_{nn})\end{bmatrix}$$

Since C_2 is an algebra

Therefore $\alpha.(A\times B)=(\alpha.A)\times B=A\times(\alpha.B)$

Hence it proves that S is an algebra.

2.2.2 Theorem: Let $A = [\xi_{ij}]_{n\times n}$ be a bicomplex square matrix then $\det A = (\det^1 A)\, e_1 + (\det^2 A)\, e_2$.

Proof:

Let

$$A = \begin{bmatrix}\xi_{11} & \xi_{12} & ..... & \xi_{1n}\\ \xi_{21} & \xi_{22} & .... & \xi_{2n}\\ ..... & ..... & ..... & .....\\ \xi_{n1} & \xi_{n2} & ..... & \xi_{nn}\end{bmatrix}$$

From 2.1.4,

$$|A| = \left|\begin{bmatrix}\xi_{11} & \xi_{12} & ..... & \xi_{1n}\\ \xi_{21} & \xi_{22} & ..... & \xi_{2n}\\ ..... & ..... & ..... & .....\\ \xi_{n1} & \xi_{n2} & ..... & \xi_{nn}\end{bmatrix}.\right|$$

$$\therefore detA = |A| = \sum_{\sigma\in S_n} Sig.(\sigma)\prod_{i=1}^{n}\xi_{i\,\sigma(i)}$$

$$=\left[\sum_{\sigma\in S_n} Sig.(\sigma)\prod_{i=1}^{n}{}^1\xi_{i\,\sigma(i)}\right]e_1+\left[\sum_{\sigma\in S_n} Sig.(\sigma)\prod_{i=1}^{n}{}^2\xi_{i\,\sigma(i)}\right]e_2$$

As $\xi.\eta = ({}^1\xi{}^1\eta)\, e_1 + ({}^2\xi{}^2\eta)\, e_2$ and $\xi+\eta = ({}^1\xi+{}^1\eta)\, e_1 + ({}^2\xi+{}^2\eta)\, e_2$

Since $\det {}^1A = \left|\left[{}^1\xi_{ij}\right]_{n\times n}\right|$

$$= \left[\sum_{\sigma \in S_n} Sig.(\sigma) \prod_{i=1}^{n} {}^{1}\xi_{i\,\sigma(i)} \right]$$

And $\det {}^{2}A = \left| \left[{}^{2}\xi_{ij} \right]_{n \times n} \right|$

$$= \left[\sum_{\sigma \in S_n} Sig.(\sigma) \prod_{i=1}^{n} {}^{2}\xi_{i\,\sigma(i)} \right]$$

Therefore $\det A = (\det {}^{1}A)\, e_1 + (\det {}^{2}A)\, e_2$

2.2.3 Theorem: If the determinant of A is non-singular then $\left| {}^{1}A \right| \neq 0$ and $\left| {}^{2}A \right| \neq 0$.

Proof:

Suppose

$$A = \begin{bmatrix} \xi_{11} & \xi_{12} & \cdots & \xi_{1n} \\ \xi_{21} & \xi_{22} & \cdots & \xi_{2n} \\ \cdots & \cdots & \cdots & \cdots \\ \xi_{n1} & \xi_{n2} & \cdots & \xi_{nn} \end{bmatrix}$$

From 2.2.2,

$\det A = (\det {}^{1}A)\, e_1 + (\det {}^{2}A)\, e_2$

since det A is non-singular

therefore $\det A = [(\det {}^{1}A)\, e_1 + (\det {}^{2}A)\, e_2] \notin O_2$

(Since $({}^{1}\xi e_1 + {}^{2}\xi e_2) \notin O_2$ then ${}^{1}\xi e_1$ and ${}^{2}\xi e_2$ both are non-zero)

Hence $\left| {}^{1}A \right| \neq 0$ and $\left| {}^{2}A \right| \neq 0$

2.2.4 Theorem: Let A be a bicomplex matrix then $A^{T} = {}^{1}A^{T}\, e_1 + {}^{2}A^{T}\, e_2$.

Proof:

Let $A = [\xi_{ij}]_{m \times n}$ be a bicomplex matrix then

$$A^{T} = \begin{bmatrix} \xi_{11} & \xi_{21} & \cdots & \xi_{m1} \\ \xi_{12} & \xi_{22} & \cdots & \xi_{m2} \\ \cdots & \cdots & \cdots & \cdots \\ \xi_{1n} & \xi_{2n} & \cdots & \xi_{mn} \end{bmatrix}$$

$$A^{T} = \begin{bmatrix} {}^{1}\xi_{11} & {}^{1}\xi_{21} & \cdots & {}^{1}\xi_{m1} \\ {}^{1}\xi_{12} & {}^{1}\xi_{22} & \cdots & {}^{1}\xi_{m2} \\ \cdots & \cdots & \cdots & \cdots \\ {}^{1}\xi_{1n} & {}^{1}\xi_{2n} & \cdots & {}^{1}\xi_{mn} \end{bmatrix} e_1 +$$

$$\begin{bmatrix} {}^2\xi_{11} & {}^2\xi_{21} & ..... & {}^2\xi_{m1} \\ {}^2\xi_{12} & {}^2\xi_{22} & ..... & {}^2\xi_{m2} \\ ..... & .... & .... & .... \\ {}^2\xi_{1n} & {}^2\xi_{2n} & .... & {}^2\xi_{mn} \end{bmatrix} e_2$$

Notes

Therefore $A^T = {}^1A^T e_1 + {}^2A^T e_2$

2.2.5 Theorem: Let A be a bicomplex square matrix then cofactor matrix of A = (cofactor matrix of ${}^1A$) e_1+(cofactor matrix of ${}^2A$) e_2.

Proof:

Let $A = [\xi_{ij}]_{n \times n}$ be a bicomplex square matrix then

${}^1A = [{}^1\xi_{ij}]_{n \times n}$ and ${}^2A = [{}^2\xi_{ij}]_{n \times n}$

Now the i^{th} j^{th} entry of cofactor matrix of A

=cofactor of the entry ξ_{ij}

$=(-1)^{i+j} \times$ the determinant obtained by leaving the row and the column(in the matrix A) passing through the entry ξ_{ij}

$= (-1)^{i+j} \times$ [{the determinant obtained by leaving the row and the column(in the matrix ${}^1A$) passing through the entry ${}^1\xi_{ij}$}e_1 +{the determinant obtained by leaving the row and the column(in the matrix ${}^2A$) passing through the entry ${}^2\xi_{ij}$}e_2]

= (cofactor of the entry ${}^1\xi_{ij}$ in the matrix ${}^1A$) e_1 +(cofactor of the entry ${}^2\xi_{ij}$ in the matrix ${}^2A$) e_2

Therefore the i^{th} j^{th} entry of cofactor matrix of A = (The i^{th} j^{th} entry of cofactor matrix of ${}^1A$) e_1 + (The i^{th} j^{th} entry of cofactor matrix of ${}^2A$) e_2

Hence it proves that cofactor matrix of A = (cofactor matrix of ${}^1A$) e_1+(cofactor matrix of ${}^2A$) e_2

Theorem 2.2.4 and 2.2.5 submerge together to give a new corollary which is started below.

2.2.6 Corollary: If $A= [\xi_{ij}]_{m \times n}$ is a bicomplex square matrix then adj A=[adj ${}^1A$]e_1 +[adj ${}^2A$] e_2.

c) Inversion of bicomplex matrix by two techniques

2.3.1 Inverse of a bicomplex square matrix with the help of adjoint matrix

Let $A = [\xi_{ij}]_{n \times n}$ be a square and non-singular matrix whose elements are in C_2 and From 2.1.1, 2.2.2 and 2.2.6

We have $A = {}^1A e_1 + {}^2A e_2$, $|A| = |{}^1A| e_1 + |{}^2A| e_2$

And adj A = [adj ${}^1A$] e_1 + [adj ${}^2A$] e_2

Now

$A \times (Adj.A) = [{}^1A e_1 + {}^2A e_2] \times [Adj.({}^1A)e_1 + Adj.({}^2A)e_2]$

$= ({}^1A.Adj.{}^1A) e_1 + ({}^2A.Adj.{}^2A) e_2$ (since $e_1.e_2 = 0$)

$= (|{}^1A|.I) e_1 + (|{}^2A|.I) e_2$,

Since ${}^1A$, ${}^2A$ and I are complex matrices.

Therefore $A\times(\text{Adj.}A)=(\left|{}^1A\right|\ e_1+\left|{}^2A\right|e_2).I$, where the matrix I is a bicomplex matrix.(since there is no difference between the identity matrix in C_1 and the identity matrix in C_2 of same order.)

Therefore $A\times(\text{Adj.}A)=|A|.I$

$$\because |A|\notin O_2$$

$$\therefore A\times\frac{AdjA}{|A|}=I$$

$$\Rightarrow A^{-1}=\frac{AdjA}{|A|}$$

$$\because\left(\left|{}^1A\right|\neq 0 \text{and} \left|{}^2A\right|\neq 0\right)$$

Now construct

$$\frac{{}^1A.(\text{Adj }{}^1A)}{\left|{}^1A\right|}e_1+\frac{{}^2A.(\text{Adj }{}^2A)}{\left|{}^2A\right|}e_2$$

$$=({}^1A\ {}^1A^{-1})\ e_1+({}^2A\ {}^2A^{-1})\ e_2$$

$$=I\ e_1+I\ e_2=I$$

$$=A\times\frac{AdjA}{|A|}$$

Hence $A^{-1}=\frac{AdjA}{|A|}$ and

$$A\times\frac{AdjA}{|A|}=\frac{{}^1A.(\text{Adj}{}^1A)}{\left|{}^1A\right|}e_1+\frac{{}^2A.(\text{Adj}{}^2A)}{\left|{}^2A\right|}e_2$$

2.3.2 Inverse of bicomplex square matrix with the help of idempotent technique

If $M=[\xi_{ij}]_{n\times n}$ is a square and nonsingular bicomplex matrix of order n

Therefore $M={}^1M\ e_1+{}^2M\ e_2$

Since $|M|\notin O_2$ therefore $\left|{}^1M\right|\neq 0$ and $\left|{}^2M\right|\neq 0$

i.e. ${}^1M$ and ${}^2M$ are invertible. Let the inverse of both ${}^1M$ and ${}^2M$ be $[z_{ij}]_{n\times n}$ and $[w_{ij}]_{n\times n}$ respectively. Now construct a new matrix with the help of $[z_{ij}]_{n\times n}$ and $[w_{ij}]_{n\times n}$ as

$$[z_{ij}]_{n\times n}e_1+[w_{ij}]_{n\times n}e_2=[\eta_{ij}]_{n\times n}\ \ (\text{say})$$

Now we claim that $[\eta_{ij}]_{n\times n}$ is the inverse of M.

Note that

$$[\xi_{ij}]_{n\times n}\times[\eta_{ij}]_{n\times n}=\left(\left[{}^1\xi_{ij}\right]_{n\times n}e_1+\left[{}^2\xi_{ij}\right]_{n\times n}e_2\right)\times\left(\left[{}^1\eta_{ij}\right]_{n\times n}e_1+\left[{}^2\eta_{ij}\right]_{n\times n}e_2\right)$$

$$=\left(\left[{}^1\xi_{ij}\right]_{n\times n}\left[{}^1\eta_{ij}\right]_{n\times n}\right)e_1+\left(\left[{}^2\xi_{ij}\right]_{n\times n}\left[{}^2\eta_{ij}\right]_{n\times n}\right)e_2$$

Since $\left[{}^{1}\eta_{ij}\right]_{n\times n} = \left[z_{ij}\right]_{n\times n}$ and $\left[{}^{2}\eta_{ij}\right]_{n\times n} = \left[w_{ij}\right]_{n\times n}$

$$\therefore \left[\xi_{ij}\right]_{n\times n} \times \left[\eta_{ij}\right]_{n\times n} = I\, e_1 + I\, e_2 = I$$

Hence $\left[\eta_{ij}\right]_{n\times n}$ is the inverse of M.

Notes

III. Some Special Bicomplex Matrices

a) Conjugates of a bicomplex matrix

As there are three types of conjugates of a bicomplex number, we have defined three types of conjugates of a bicomplex matrix.

3.1.1 Definition: i_1 Conjugate of a bicomlex matrix

Let $A = \left[\xi_{ij}\right]_{m\times n}$ be the bicomplex matrix then the i_1 conjugate of matrix A written as $\bar{A}$ is the matrix obtained from A by taken i_1 conjugate of each entry of A. i.e.

$$\overline{A} = \begin{bmatrix} \overline{\xi}_{11} & \overline{\xi}_{12} & \ldots\ldots & \overline{\xi}_{1n} \\ \overline{\xi}_{21} & \overline{\xi}_{22} & \ldots\ldots & \overline{\xi}_{2n} \\ \ldots\ldots & \ldots\ldots & \ldots\ldots & \ldots\ldots \\ \overline{\xi}_{m1} & \overline{\xi}_{m2} & \ldots\ldots & \overline{\xi}_{mn} \end{bmatrix}$$

The idempotent representation of $\bar{A}$ can be obtained as follows

$$\overline{A} = \begin{bmatrix} \overline{{}^{2}\xi}_{11} & \overline{{}^{2}\xi}_{12} & \ldots\ldots & \overline{{}^{2}\xi}_{1n} \\ \overline{{}^{2}\xi}_{21} & \overline{{}^{2}\xi}_{22} & \ldots\ldots & \overline{{}^{2}\xi}_{2n} \\ \ldots\ldots & \ldots\ldots & \ldots\ldots & \ldots\ldots \\ \overline{{}^{2}\xi}_{m1} & \overline{{}^{2}\xi}_{m2} & \ldots\ldots & \overline{{}^{2}\xi}_{mn} \end{bmatrix} e_1 + \begin{bmatrix} \overline{{}^{1}\xi}_{11} & \overline{{}^{1}\xi}_{12} & \ldots\ldots & \overline{{}^{1}\xi}_{1n} \\ \overline{{}^{1}\xi}_{21} & \overline{{}^{1}\xi}_{22} & \ldots\ldots & \overline{{}^{1}\xi}_{2n} \\ \ldots\ldots & \ldots\ldots & \ldots\ldots & \ldots\ldots \\ \overline{{}^{1}\xi}_{m1} & \overline{{}^{1}\xi}_{m2} & \ldots\ldots & \overline{{}^{1}\xi}_{mn} \end{bmatrix} e_2$$

It is evident that

(a) $\overline{[(\bar{A})]} = A$

(b) $\overline{kA} = \bar{k}\,\bar{A}$ where $k \in C_2$

Similarly the definition of i_2 and i_1i_2 conjugate of a bicomplex matrix is following.

3.1.2 Definition: i_2 Conjugate of a bicomlex matrix

Let $A = \left[\xi_{ij}\right]_{m\times n}$ be the bicomplex matrix then the i_2 conjugate of matrix A written as $A^{\sim}$ is the matrix obtained from A by taken i_2 conjugate of each entry of A. i.e.

$$A^{\sim} = \begin{bmatrix} \tilde{\xi}_{11} & \tilde{\xi}_{12} & \ldots\ldots & \tilde{\xi}_{1n} \\ \tilde{\xi}_{21} & \tilde{\xi}_{22} & \ldots\ldots & \tilde{\xi}_{2n} \\ \ldots\ldots & \ldots\ldots & \ldots\ldots & \ldots\ldots \\ \tilde{\xi}_{m1} & \tilde{\xi}_{m2} & \ldots\ldots & \tilde{\xi}_{mn} \end{bmatrix}$$

The idempotent representation of $A^{\sim}$ can be obtained as follows:

$$A^{\sim} = \begin{bmatrix} {}_2\xi_{11} & {}_2\xi_{12} & \ldots & {}_2\xi_{1n} \\ {}_2\xi_{21} & {}_2\xi_{22} & \ldots & {}_2\xi_{2n} \\ \ldots & \ldots & \ldots & \ldots \\ {}_2\xi_{m1} & {}_2\xi_{m2} & \ldots & {}_2\xi_{mn} \end{bmatrix} e_1$$

$$+ \begin{bmatrix} {}_1\xi_{11} & {}_1\xi_{12} & \ldots & {}_1\xi_{1n} \\ {}_1\xi_{21} & {}_1\xi_{22} & \ldots & {}_1\xi_{2n} \\ \ldots & \ldots & \ldots & \ldots \\ {}_1\xi_{m1} & {}_1\xi_{m2} & \ldots & {}_1\xi_{mn} \end{bmatrix} e_2$$

It is evident that

(a) $(A^{\sim})^{\sim} = A$

(b) $(k\,A)^{\sim} = k^{\sim} A^{\sim}$ *where* $k \in C_2$

3.1.3 Definition: i_1i_2Conjugate of a bicomplex matrix

Let $A = [\xi_{ij}]_{m\times n}$ be the bicomplex matrix then the i_1i_2 conjugate of matrix A written as $A^{\#}$ is the matrix obtained from A by taken i_1i_2 conjugate of each entry of A. i.e.

$$A^{\#} = \begin{bmatrix} \xi_{11}^{\#} & \xi_{12}^{\#} & \ldots & \xi_{1n}^{\#} \\ \xi_{21}^{\#} & \xi_{22}^{\#} & \ldots & \xi_{2n}^{\#} \\ \ldots & \ldots & \ldots & \ldots \\ \xi_{m1}^{\#} & \xi_{m2}^{\#} & \ldots & \xi_{mn}^{\#} \end{bmatrix}$$

The idempotent representation of $A^{\#}$ can be obtained as follows:

$$A^{\#} = \begin{bmatrix} \overline{{}_1\xi}_{11} & \overline{{}_1\xi}_{12} & \ldots & \overline{{}_1\xi}_{1n} \\ \overline{{}_1\xi}_{21} & \overline{{}_1\xi}_{22} & \ldots & \overline{{}_1\xi}_{2n} \\ \ldots & \ldots & \ldots & \ldots \\ \overline{{}_1\xi}_{m1} & \overline{{}_1\xi}_{m2} & \ldots & \overline{{}_1\xi}_{mn} \end{bmatrix} e_1 + \begin{bmatrix} \overline{{}_2\xi}_{11} & \overline{{}_2\xi}_{12} & \ldots & \overline{{}_2\xi}_{1n} \\ \overline{{}_2\xi}_{21} & \overline{{}_2\xi}_{22} & \ldots & \overline{{}_2\xi}_{2n} \\ \ldots & \ldots & \ldots & \ldots \\ \overline{{}_2\xi}_{m1} & \overline{{}_2\xi}_{m2} & \ldots & \overline{{}_2\xi}_{mn} \end{bmatrix} e_2$$

It is evident that

(a) $(A^{\#})^{\#} = A$

(b) $(k\,A)^{\#} = k^{\#}A^{\#}$, $k \in C_2$

b) Tranjugate of a bicomplex matrix

The transpose of conjugate of a bicomplex matrix is defined as the tranjugate of the matrix. There are three types of tranjugates of a bicomplex matrix.

3.2.1 Definition: i_1 tranjugate of a bicomplex matrix

The transpose of the i_1 conjugate of a bicomplex matrix is defined as the $i_1$tranjugate of the matrix.

i.e. If $A = [\xi_{ij}]_{m\times n}$ then

$$i_1 \text{ tranjugate of } A=[\overline{A}]^T = \begin{bmatrix} \overline{\xi}_{11} & \overline{\xi}_{21} & \cdots & \overline{\xi}_{m1} \\ \overline{\xi}_{12} & \overline{\xi}_{22} & \cdots & \overline{\xi}_{m2} \\ \cdots & \cdots & \cdots & \cdots \\ \overline{\xi}_{1n} & \overline{\xi}_{2n} & \cdots & \overline{\xi}_{mn} \end{bmatrix}$$

Similarly

3.2.2 Definition: i_2 tranjugate of a bicomplex matrix

The transpose of the i_2 conjugate of a bicomplex matrix is defined as the i_2 tranjugate of the matrix.

i.e. If $A = [\xi_{ij}]_{m\times n}$ then

$$i_2 \text{ tranjugate of } A=[A^{\sim}]^T = \begin{bmatrix} \xi_{11}^{\sim} & \xi_{21}^{\sim} & \cdots & \xi_{m1}^{\sim} \\ \xi_{12}^{\sim} & \xi_{22}^{\sim} & \cdots & \xi_{m2}^{\sim} \\ \cdots & \cdots & \cdots & \cdots \\ \xi_{1n}^{\sim} & \xi_{2n}^{\sim} & \cdots & \xi_{mn}^{\sim} \end{bmatrix}$$

3.2.3 Definition: i_1i_2 tranjugate of a bicomplex matrix

The transpose of the i_1i_2 conjugate of a bicomplex matrix is defined as the i_1i_2 tranjugate of the matrix.

i.e. If $A = [\xi_{ij}]_{m\times n}$ then

$$i_1i_2 \text{ tranjugate of } A=[A^{\#}]^T = \begin{bmatrix} \xi_{11}^{\#} & \xi_{21}^{\#} & \cdots & \xi_{m1}^{\#} \\ \xi_{12}^{\#} & \xi_{22}^{\#} & \cdots & \xi_{m2}^{\#} \\ \cdots & \cdots & \cdots & \cdots \\ \xi_{1n}^{\#} & \xi_{2n}^{\#} & \cdots & \xi_{mn}^{\#} \end{bmatrix}$$

c) Symmetric and skew – symmetric matrix in C_2

3.3.1 Definition: Symmetric matrix

A bicomplex square matrix $A = [\xi_{ij}]_{n\times n}$ is said to be symmetric if $A = [A]^T$. Thus for a symmetric matrix A, we have $\xi_{ij} = \xi_{ji}$ for all i and j

3.3.2 Definition: Skew-symmetric matrix

A bicomplex square matrix $A = [\xi_{ij}]_{n\times n}$ is said to be skew-symmetric if $A = -[A]^T$. Thus for a skew-symmetric matrix A, we have $\xi_{ij} = -\xi_{ji}$ for all i and j

3.3.3 Theorem: The elements of principal diagonal of skew-symmetric matrix are zero.

Proof:

We know that a matrix $A = [\xi_{ij}]_{n\times n}$ is skew - symmetric if and only if $\xi_{ij} = -\xi_{ji}$ for all i and j. For diagonal element we have $\xi_{ii} = -\xi_{ii}$ therefore

If $\xi_{ii} = z_{ii} + i_2w_{ii}$ then $(z_{ii} + i_2w_{ii}) = -(z_{ii} + i_2w_{ii})$

Therefore $z_{ii} = 0$, $w_{ii} = 0$

i.e. $\xi_{ii} = 0$ for all i

d) Hermitian matrix in C_2

Corresponding to the three types of conjugates in C_2,there are three types of Hermitian matrix in C_2.

3.4.1 Definition: i_1 Hermitian matrix

A bicomplex square matrix A is said to be i_1Hermitian matrix if $A = [\bar{A}]^T$

3.4.2 Theorem: The elements of principal diagonal of an i_1 Hermitian matrix are members of $C(i_2)$.

Proof:

Recall that $A = [\xi_{ij}]_{n\times n}$ is i_1Hermitian matrix if and only if $\xi_{ij} = \bar{\xi}_{ji}\ \forall$i and j.

For diagonal element we have

$$\xi_{kk} = \bar{\xi}_{kk}$$

$$\text{If } \xi_{kk} = z_{kk} + i_2 w_{kk} \text{ then}$$

$$z_{kk} + i_2 w_{kk} = \bar{z}_{kk} + i_2 \bar{w}_{kk}$$

$$\Rightarrow z_{kk} \in C_0 \text{ and } w_{kk} \in C_0$$

$$\Rightarrow \xi_{kk} \in C(i_2)$$

3.4.3 Definition: i_2 Hermitian matrix

A bicomplex square matrix A is said to be i_2 Hermitian matrix if $A = [A^{\sim}]^T$

3.4.4 Theorem: The elements of principal diagonal of an i_2 Hermitian matrix are members of C (i_1).

Proof:

$A = [\xi_{ij}]_{n\times n}$ is i_2Hermitian matrix if and only if $\xi_{ij} = \xi_{ji}^{\sim}\ \forall$i and j.

For diagonal element we have

$$\xi_{kk} = \xi_{kk}^{\sim}$$

$$\text{If } \xi_{kk} = z_{kk} + i_2 w_{kk}$$

$$\Rightarrow z_{kk} + i_2 w_{kk} = z_{kk} - i_2 w_{kk}$$

$$\Rightarrow \xi_{kk} \in C(i_1)$$

3.4.5 Definition: $i_1 i_2$ Hermitian matrix

A bicomplex square matrix A is said to be $i_1 i_2$ Hermitian matrix if $A = [A^{\#}]^T$

3.4.6 Theorem: The elements of principal diagonal of an $i_1 i_2$ Hermitian matrix are members of H.

Proof:

$A = [\xi_{ij}]_{n\times n}$ is $i_1 i_2$ Hermitian matrix if and only if $\xi_{ij} = \xi_{ji}^{\#}\ \forall$i and j.

For diagonal element we have

$$\xi_{kk} = \xi_{kk}^{\#}$$

If $\xi_{kk} = z_{kk} + i_2 w_{kk}$

$$\Rightarrow z_{kk} + i_2 w_{kk} = \bar{z}_{kk} - i_2 \bar{w}_{kk}$$

$$\Rightarrow z_{kk} \in C_0 \text{ and } w_{kk} \text{ is in the form of } i_1 y \text{ where } y \text{ in } C_0$$

$$\Rightarrow \xi_{kk} \in H$$

e) Skew-Hermitian matrix in C_2

Analogous to the theory of Hermitian matrices, we have defined three types of skew-Hermitian matrices in C_2.

3.5.1 Definition: i_1 skew-Hermitian matrix

A bicomplex square matrix A is said to be i_1 skew-Hermitian matrix if $A = -[\bar{A}]^T$

3.5.2 Theorem: The elements of principal diagonal of an i_1 skew-Hermitian matrix are of the type of $(i_1 \times s)$, where $s \in C(i_2)$.

Proof:

Let $A = [\xi_{ij}]_{n\times n}$ be an i_1 skew-Hermitian matrix then $\xi_{ij} = -\bar{\xi}_{ji}$; for all i and j.

For diagonal element we have

$$\xi_{kk} = -\bar{\xi}_{kk}$$

If $\xi_{kk} = z_{kk} + i_2 w_{kk}$ then

$$z_{kk} + i_2 w_{kk} = -(\bar{z}_{kk} + i_2 \bar{w}_{kk})$$

Therefore $z_{kk} = -\bar{z}_{kk}$ *and* $w_{kk} = -\bar{w}_{kk}$

Hence $\xi_{kk} = i_1\{\text{Im}(z_{kk})\} + i_2 i_1\{\text{Im}(w_{kk})\} = i_1.s$ where $s \in C(i_2)$

3.5.3 Definition: i_2 skew-Hermitian matrix

A bicomplex square matrix A is said to be i_2 skew-Hermitian matrix if $A = -[A^{\sim}]^T$

3.5.4 Theorem: The elements of principal diagonal of an i_2 skew-Hermitian matrix are of the type of $(i_2 \times s)$, where $s \in C(i_1)$.

Proof:

$A = [\xi_{ij}]_{n\times n}$ is an i_2 skew-Hermitian matrix if and only if $\xi_{ij} = -\xi_{ji}^{\sim}$; for all i and j.

For diagonal element we have

$$\xi_{kk} = -\xi_{kk}^{\sim}$$

If $\xi_{kk} = z_{kk} + i_2 w_{kk}$ then

$$z_{kk} + i_2 w_{kk} = -(z_{kk} - i_2 w_{kk})$$

Therefore $z_{kk} = -z_{kk}$ i.e. $z_{kk} = 0$

Hence $\xi_{kk} = i_2(w_{kk}) = i_2.s$ where $s = w_{kk} \in C(i_1)$

3.5.5 Definition: i_1i_2 skew-Hermitian matrix

A bicomplex square matrix A is said to be i_1i_2 skew-Hermitian matrix if $A = -[A^{\#}]^T$

3.5.6 Theorem: The elements of principal diagonal of an i_1i_2 skew-Hermitian matrix are of the type of $(i_1 \times s)$, where $s \in H$.

Proof:

$A = [\xi_{ij}]_{n\times n}$ is an $i_1i_2$skew-Hermitian matrix if and only if $\xi_{ij} = -\xi_{ji}^{\#}$; for all i and j.

For diagonal element we have

$$\xi_{kk} = -\xi_{kk}^{\#}$$

$$\text{If } \xi_{kk} = z_{kk} + i_2w_{kk} \text{ then}$$

$$z_{kk} + i_2w_{kk} = -(\bar{z}_{kk} - i_2\bar{w}_{kk})$$

Therefore $z_{kk} = -\bar{z}_{kk}$ and $w_{kk} = \bar{w}_{kk}$

Hence $$\xi_{kk} = i_1\{\text{Im}(z_{kk})\} + i_2\{\text{Re}(w_{kk})\}$$

i.e. $$\xi_{kk} = i_1\{\text{Im}(z_{kk})\} + i_1i_1^{-1}i_2\{\text{Re}(w_{kk})\}$$

$$= i_1[\text{Im}(z_{kk}) - i_1i_2\text{Re}(w_{kk})]$$

$$= i_1.s; \text{ where } s \in H$$

3.5.7 Theorem: A is i_1 Hermitian matrix if and only if i_1 A is i_1 skew - Hermitian matrix.

Proof:

Let A be an i_1 Hermitian matrix therefore

$$A = [\bar{A}]^T$$

$$\text{Now } [\overline{i_1A}]^T = [\bar{i}_1\bar{A}]^T \quad \ldots[\text{by 3.1.1}]$$

$$= -i_1[\bar{A}]^T$$

$$= -i_1A$$

i.e. $i_1A = -[\overline{i_1A}]^T$

$\Rightarrow i_1$ A is i_1 skew - Hermitian matrix.

Converse:

Let i_1 A be an i_1 skew - Hermitian matrix

i.e. $$i_1A = -[\overline{i_1A}]^T$$

$$= -[\bar{i}_1\bar{A}]^T$$

$$= i_1[\bar{A}]^T$$

i.e. $$A = [\bar{A}]^T$$

Hence A is i_1 Hermitian matrix.

3.5.8 Theorem: A is i_2 Hermitian matrix if and only if i_2 A is i_2 skew - Hermitian matrix.

Proof:

Let A be an i_2 Hermitian matrix therefore

$$A = [A^{\sim}]^T$$

Now $$[(i_2A)^{\sim}]^T = i_2{}^{\sim}[A^{\sim}]^T \quad \text{...[by 3.1.2]}$$

$$= -i_2 A$$

i.e. $$i_2A = -[(i_2A)^{\sim}]^T$$

$\Rightarrow i_2$ A is i_2 skew - Hermitian matrix.

Converse:

Let i_2 A be an i_2 skew - Hermitian matrix

i.e. $$i_2 A = -[(i_2A)^{\sim}]^T$$

$$= -[i_2{}^{\sim}A^{\sim}]^T$$

$$= i_2[A^{\sim}]^T$$

i.e. $$A = [A^{\sim}]^T$$

Hence A is i_2 Hermitian matrix.

3.5.9 Theorem: A is i_1i_2 Hermitian matrix if and only if i_1i_2 A is i_1i_2 Hermitian matrix.

Proof:

Let A be an i_1i_2 Hermitian matrix therefore

$$A = [A^{\#}]^T$$

Now $$[(i_1i_2A)^{\#}]^T = i_1{}^{\#}i_2{}^{\#}[A^{\#}]^T \quad \text{...[by 3.1.3]}$$

$$= (-i_1)(-i_2)A$$

$$= i_1i_2A$$

$\Rightarrow i_1i_2$ A is i_1i_2 Hermitian matrix.

Converse:

Let i_1i_2 A be i_1i_2 Hermitian matrix

i.e. $$i_1i_2A = [i_1i_2A]^{\#}$$

$$= i_1{}^{\#}i_2{}^{\#}[A^{\#}]^T$$

$$= (-i_1)(-i_2)[A^{\#}]^T$$

$$= i_1i_2[A^{\#}]^T$$

i.e. $$A = [A]^{\#}$$

Hence A is i_1i_2 Hermitian matrix.

It is evident that if A is i_1i_2 skew-Hermitian matrix then i_1i_2A will be also i_1i_2 skew-Hermitian matrix and vice versa.

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Notes

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Probability and Entanglement

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Abstract- Here the concept of "TRUE" is defined according to Alfred Tarski, and the concept "OCCURING EVENT" is derived from this definition.

From here, we obtain operations on the events and properties of these operations and derive the main properties of the CLASSICAL PROBABILITY. PHYSICAL EVENTS are defined as the results of applying these operations to DOT EVENTS.

Next, the 3 + 1 vector of the PROBABILITY CURRENT and the EVENT STATE VECTOR are determined.

The presence in our universe of Planck's constant gives reason to presume that our world is in a CONFINED SPACE. In such spaces, functions are presented by Fourier series. These presentations allow formulating the ENTANGLEMENT phenomenon.

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1. Tarski, A. The Semantic Conception of Truth and the Foundations of Semantics, *Philosophy and Phenomenological Research*, 4, 1944.

Probability and Entanglement

G. Quznetsov

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The presence in our universe of Planck's constant gives reason to presume that our world is in a CONFINED SPACE. In such spaces, functions are presented by Fourier series. These presentations allow formulating the ENTANGLEMENT phenomenon.

I. Truth

Science presents its ideas and results with language texts. Therefore, we will begin by considering narrative sentences:

By Alfred Tarski [1]

A sentence $\ll \Theta \gg$ is *true* if and only if Θ.

For example, sentence $\ll$It is raining$\gg$ is true if and only if it is raining

A sentence $\ll \Theta \gg$ is *false* if and only if there is not that Θ.

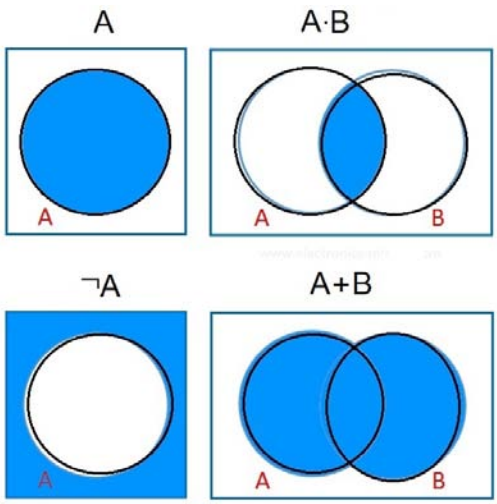

Figure 1: The Venn diagrams for A, B events

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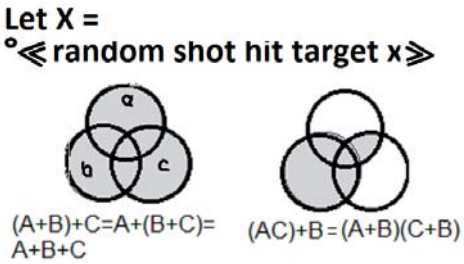

Figure 2: The Venn diagrams the associativity and the distribution

For example, $\ll 2 + 3 = 4 \gg$.

Still an example: Obviously, the following sentence isn't true and isn't false [2]:

≪This sentense is false. ≫

Those sentences which can be either true, or false, are called as *meaningful* sentences. The previous example sentence is meaningless sentence.

Further, we consider only meaningful sentences which are either true, or false.

Sentences A and B are *equal* (design.: $A = B$) if A is true, if and only if B is true.

II. Events

A set $\mathtt{B}$ of sentences is called *an event, expressed by sentence* C, if the following conditions are fulfilled:

1. $C \in \mathtt{B}$;
2. if $A \in \mathtt{B}$ and $D \in \mathtt{B}$ then $A = D$;
3. if $D \in \mathtt{B}$ and $A = D$ then $A \in \mathtt{B}$.

In this case let us denote: $\mathtt{B} := {}^{\circ}C$.

An event $\mathtt{B}$ *occures* if a true sentence A exists such that $A \in \mathtt{B}$.

Events $\mathtt{A}$ and $\mathtt{B}$ *equal* (denote: $\mathtt{A} = \mathtt{B}$) if $\mathtt{A}$ occures if and only if $\mathtt{B}$ occures.

Event $\mathtt{C}$ is called *product* of event $\mathtt{A}$ and event $\mathtt{B}$ (denote: $\mathtt{C} = (\mathtt{A} \cdot \mathtt{B})$) if $\mathtt{C}$ occures if and only if $\mathtt{A}$ occures and $\mathtt{B}$ occures.

Events $\mathtt{C}$ is called *complement* of event $\mathtt{A}$ (denote: $\mathtt{C} = (\neg \mathtt{A})$) if $\mathtt{C}$ occures if and only if $\mathtt{A}$ does not occure.

$(\mathtt{A} + \mathtt{B}) := (\neg((\neg \mathtt{A}) \cdot (\neg \mathtt{B})))$. Event$(\mathtt{A} + \mathtt{B})$ is called *sum* of event $\mathtt{A}$ and event $\mathtt{B}$.

Therefore, a sum of event occures if and only if there at least one of the addends occures.

Events obey following properties (you can test these formulas by Venn diagrams – see Figure 1, Figure 2. Venn diagrams):

1. associarivity: $(\mathtt{A} \cdot \mathtt{B}) \cdot \mathtt{C} = \mathtt{A} \cdot (\mathtt{B} \cdot \mathtt{C}) = \mathtt{A} \cdot \mathtt{B} \cdot \mathtt{C}$,

$$(\mathtt{A} + \mathtt{B}) + \mathtt{C} = \mathtt{A} + (\mathtt{B} + \mathtt{C}) = \mathtt{A} + \mathtt{B} + \mathtt{C};$$

2. distributiviy: $(\mathtt{A} \cdot \mathtt{B}) + \mathtt{C} = (\mathtt{A} + \mathtt{C})\,(\mathtt{B} + \mathtt{C})$,

$$(\mathtt{A} + \mathtt{B}) \cdot \mathtt{C} = (\mathtt{A} \cdot \mathtt{C}) + (\mathtt{B} \cdot \mathtt{C});$$

3. if $\mathtt{C}$ occures then for every $\mathtt{A}$: $(\mathtt{A} \cdot \mathtt{C}) = \mathtt{A}$;
4. $(\neg\,(\neg \mathtt{A})) = \mathtt{A}$
5. cummutativity: $(\mathtt{A} \cdot \mathtt{B}) = (\mathtt{B} \cdot \mathtt{A})$, $(\mathtt{A} + \mathtt{B}) = (\mathtt{B} + \mathtt{A})$.

III. Classical Probability

Let $\mathsf{P}(X)$ be *a probability function*[3, pp.49–57] defined on the set of events.

Hence,
1. this function has values on the real numbers segment $[0;1]$;
2. for all events $\mathtt{A}$ and $\mathtt{B}$: $\mathsf{P}(\mathtt{A}\cdot\mathtt{B})+\mathsf{P}(\mathtt{A}\cdot(\neg\mathtt{B}))=\mathsf{P}(\mathtt{A})$;
3. for ever event $\mathtt{A}$: if $\mathsf{P}(\mathtt{A})=1$ then $\mathtt{A}$ occures.

Let there exists an event $\mathtt{C}_0$ such that $\mathsf{P}(\mathtt{C}_0)=1$.

By this definition: $\mathsf{P}(\mathtt{C}_0\cdot\mathtt{B})+\mathsf{P}(\mathtt{C}_0\cdot(\neg\mathtt{B}))=\mathsf{P}(\mathtt{C}_0)=1$.
Because $\mathtt{C}_0\cdot\mathtt{B}=\mathtt{B}$ and $\mathtt{C}_0\cdot(\neg\mathtt{B})=(\neg\mathtt{B})$ then

$$\mathsf{P}(\mathtt{B})+\mathsf{P}(\neg\mathtt{B}))=1 \tag{1}$$

Let us calculate:
$\mathsf{P}(\mathtt{A}+\mathtt{B})=\mathsf{P}(\neg((\neg\mathtt{A})\cdot(\neg\mathtt{B})))=1-\mathsf{P}((\neg\mathtt{A})\cdot(\neg\mathtt{B}))=$
$=1-(\mathsf{P}(\neg\mathtt{A})-\mathsf{P}((\neg\mathtt{A})\cdot\mathtt{B}))=1-\mathsf{P}(\neg\mathtt{A})+\mathsf{P}((\neg\mathtt{A})\cdot\mathtt{B})=$
$=1-1+\mathsf{P}(\mathtt{A})+\mathsf{P}(\mathtt{B})-\mathsf{P}(\mathtt{A}\cdot\mathtt{B})$
Hence,

$$\mathsf{P}(\mathtt{A}+\mathtt{B})=\mathsf{P}(\mathtt{A})+\mathsf{P}(\mathtt{B})-\mathsf{P}(\mathtt{A}\cdot\mathtt{B}) \tag{2}$$

this is *the formula for adding probabilities.*
The events $\mathtt{A}$ and $\mathtt{B}$ are *incompatible* if and if only $\mathsf{P}(\mathtt{A}\cdot\mathtt{B})=0$.
The formula for adding probabilities for incompatible events:

$$\mathsf{P}(\mathtt{A}+\mathtt{B})=\mathsf{P}(\mathtt{A})+\mathsf{P}(\mathtt{B}) \tag{3}$$

The events $\mathtt{A}$ and $\mathtt{B}$ are *independent* if $\mathsf{P}(\mathtt{A}\cdot\mathtt{B})=\mathsf{P}(\mathtt{A})\cdot\mathsf{P}(\mathtt{B})$.

IV. Physics Events

Events of the type ° ≪At the point $(t.\mathbf{x})$ $\mathtt{A}$ ≫ (for example, ° ≪At the point $(t.\mathbf{x})$ the temperature dropped to 0C≫) are called *dot events. Physical events* are dot events and events derived from physical events by the "$\cdot$", "$+$", and "$\neg$" operations.

Let[1] $\langle X_{\mathtt{A},0},X_{\mathtt{A},1},X_{\mathtt{A},2},X_{\mathtt{A},3}\rangle$ be random coordinates of event $\mathtt{A}$.
Let $F_{\mathtt{A}}$ be a *Cumulative Distribution Function* i.e.:

$$F_{\mathtt{A}}(x_0,x_1,x_2,x_3)=\mathsf{P}((X_{\mathtt{A},0}<x_0)\wedge(X_{\mathtt{A},1}<x_1)\wedge(X_{\mathtt{A},2}<x_2)\wedge(X_{\mathtt{A},3}<x_3)).$$

If

$$j_0 := \frac{\partial^3 F}{\partial x_1\partial x_2\partial x_3},$$

$$j_1 := -\frac{\partial^3 F}{\partial x_0\partial x_2\partial x_3},$$

$$j_2 := -\frac{\partial^3 F}{\partial x_0\partial x_1\partial x_3},$$

$$j_3 := \frac{\partial^3 F}{\partial x_0\partial x_1\partial x_2}$$

then $\langle j_0,j_1,j_2,j_3\rangle$ is *a probability current vector of event.*
If $\rho:=j_0/\mathrm{c}$ then ρ is *a a probability density function.*

If $\mathbf{u}_{\mathtt{A}}:=\mathbf{j}_{\mathtt{A}}/\rho_{\mathtt{A}}$ then vector $\mathbf{u}_{\mathtt{A}}$ is *a velocity of a probability* of $\mathtt{A}$ propagation.

(for example for u_2:

$$u_2=\frac{j_2}{\rho}=\frac{\left(-\frac{\partial^3 F}{\partial x_0\partial x_1\partial x_3}\right)c}{\left(\frac{\partial^3 F}{\partial x_1\partial x_2\partial x_3}\right)}=\left(-\frac{\Delta_{013}F}{\Delta_{123}F}\frac{\Delta x_2}{\Delta x_0}\right)c$$

)

Probability, for which $u_1^2+u_2^2+u_3^2\leq\mathrm{c}$ are called *traceable probability.*

[1] $x_0=ct$

Denote:

$$1_2 := \begin{bmatrix} 1 & 0 \\ 0 & 1 \end{bmatrix}, 0_2 := \begin{bmatrix} 0 & 0 \\ 0 & 0 \end{bmatrix}, \beta^{[0]} := -\begin{bmatrix} 1_2 & 0_2 \\ 0_2 & 1_2 \end{bmatrix} = -1_4,$$

the Pauli matrices

$$\sigma_1 = \begin{bmatrix} 0 & 1 \\ 1 & 0 \end{bmatrix}, \sigma_2 = \begin{bmatrix} 0 & -\mathrm{i} \\ \mathrm{i} & 0 \end{bmatrix}, \sigma_3 = \begin{bmatrix} 1 & 0 \\ 0 & -1 \end{bmatrix}.$$

A set $\widetilde{C}$ of complex $n \times n$ matrices is called *a Clifford set of rank n* [4] if the following conditions are fulfilled:

if $\alpha_k \in \widetilde{C}$ and $\alpha_r \in \widetilde{C}$ then $\alpha_k\alpha_r + \alpha_r\alpha_k = 2\delta_{k,r}$;

if $\alpha_k\alpha_r + \alpha_r\alpha_k = 2\delta_{k,r}$ for all elements α_r of set $\widetilde{C}$ then $\alpha_k \in \widetilde{C}$.

If $n = 4$ then a Clifford set either contains 3 matrices (*a Clifford triplet*) or contains 5 matrices (*a Clifford pentad*).

For example, *light pentad* β:

$$\beta^{[k]} := \begin{bmatrix} \sigma_k & 0_2 \\ 0_2 & -\sigma_k \end{bmatrix}, \gamma^{[0]} := \begin{bmatrix} 0_2 & 1_2 \\ 1_2 & 0_2 \end{bmatrix}, \beta^{[4]} := \mathrm{i} \cdot \begin{bmatrix} 0_2 & 1_2 \\ -1_2 & 0_2 \end{bmatrix}$$

The following set of four real equations with eight real unknowns: b^2 with $b > 0$, α, β, χ, θ, γ, υ, λ:

$$\left\{ \begin{array}{c} b^2 = \rho_{\mathtt{A},}, \\ b^2\left(\cos^2(\alpha)\sin(2\beta)\cos(\theta-\gamma) - \sin^2(\alpha)\sin(2\chi)\cos(\upsilon-\lambda)\right) = -\frac{j_{\mathtt{A},1}}{\mathrm{c}}, \\ b^2\left(\cos^2(\alpha)\sin(2\beta)\sin(\theta-\gamma) - \sin^2(\alpha)\sin(2\chi)\sin(\upsilon-\lambda)\right) = -\frac{j_{\mathtt{A},2}}{\mathrm{c}}, \\ b^2\left(\cos^2(\alpha)\cos(2\beta) - \sin^2(\alpha)\cos(2\chi)\right) = -\frac{j_{\mathtt{A},3}}{\mathrm{c}}. \end{array} \right| \tag{4}$$

has solutions for any traceable $\rho_{\mathtt{A}}$ and $j_{\mathtt{A},k}$[3, pp.62–63].

If

$$\begin{aligned} \varphi_{\mathtt{A}.1} &:= b\exp(\mathrm{i}\gamma)\cos(\beta)\cos(\alpha), \\ \varphi_{\mathtt{A},2} &:= b\exp(\mathrm{i}\theta)\sin(\beta)\cos(\alpha), \\ \varphi_{\mathtt{A},3} &:= b\exp(\mathrm{i}\lambda)\cos(\chi)\sin(\alpha), \\ \varphi_{\mathtt{A},4} &:= b\exp(\mathrm{i}\upsilon)\sin(\chi)\sin(\alpha) \end{aligned} \tag{5}$$

then you can calculate that

$$\rho_{\mathtt{A}} = \sum_{s=1}^{4} \varphi^*_{\mathtt{A},s}\varphi_{\mathtt{A},s}, \tag{6}$$

$$\frac{j_{\mathtt{A},\alpha}}{\mathrm{c}} = -\sum_{k=1}^{4}\sum_{s=1}^{4} \varphi^*_{\mathtt{A},s}\beta^{[\alpha]}_{s,k}\varphi_{\mathtt{A},k}$$

Function $\varphi_{\mathtt{A}}$ is *a state vector* of event $\mathtt{A}$.

V. Entanglement

The presence in our universe of Planck's constant gives reason to presume that our world is in a confined space: $|\mathbf{x}| \leq \pi\mathrm{c}/\mathrm{h}$. Functions

Ref

4. For instance, Madelung, E., *Die Mathematischen Hilfsmittel des Physikers.* Springer Verlag, (1957) p.29.

$$\phi_{\mathbf{n}}(\mathbf{x}) := \left(\frac{h}{2\pi c}\right)^{\frac{3}{2}} \exp\left(-\mathrm{i}\frac{\mathrm{h}}{\mathrm{c}}(\mathbf{nx})\right).$$

form an orthonormal basis of this space with scalar product of the following shape:

$$(\widetilde{\varphi}(t), \widetilde{\chi}(t)) := \int_{-\frac{\pi c}{h}}^{\frac{\pi c}{\mathrm{h}}} dx_1 \int_{-\frac{\pi c}{h}}^{\frac{\pi c}{\mathrm{h}}} dx_2 \int_{-\frac{\pi c}{h}}^{\frac{\pi c}{\mathrm{h}}} dx_3 \cdot \widetilde{\varphi}(t, \mathbf{x})^{\dagger} \widetilde{\chi}(t, \mathbf{x}).$$

For the state vector:

$$(\varphi_{\mathtt{A}}(t), \varphi_{\mathtt{A}}(t)) = \mathsf{P}(\mathtt{A}(t)).$$

Let

$$\varphi_{\mathtt{A}}(t, \mathbf{x}) = \sum_{\mathbf{n}} a_{\mathtt{A},\mathbf{n}}(t)\, \phi_{\mathbf{n}}(\mathbf{x})$$

be a Fourier series of $\varphi_{\mathtt{A}}\ \ t, \mathbf{x}$
That is:

$$\mathsf{P}(\mathtt{A}(t)) = \sum_{\mathbf{n}} a^{\dagger}_{\mathtt{A},\mathbf{n}}(t)\, a_{\mathtt{A},\mathbf{n}}(t) = \sum_{\mathbf{n}} \mathsf{P}(\mathtt{A}_{\mathbf{n}}(t)).$$

Hence,

$$\mathtt{A}(t) = \sum_{\mathbf{n}} \mathtt{A}_{\mathbf{n}}(t).$$

there $\mathtt{A}_n(t)$ are incompatible, independent events:Therefore, if $\mathsf{P}(\mathtt{A}(t)) = 1$ then $\mathtt{A}(t)$ occures. Hence, one among $\mathtt{A}_{\mathbf{n}}(t)$ occures.

Operator $\check{r}$, defined on the state function φ set and has values on this set, is *an realization operator* if $(\check{r}\varphi, \check{r}\varphi) = 1$.

This operator can act in the measurement process or as a result of some other external disturbance.

Let $\varphi_{\mathtt{A},\mathtt{B}}((t, \mathbf{x})(\tau, \mathbf{y}))$ be a state vector of event $\mathtt{A}(t, \mathbf{x})$ **and** event $\mathtt{B}(\tau, \mathbf{y})$.
In this case the basis of space present the following functions:

$$\phi_{\mathbf{n},\mathbf{s}}(\mathbf{x}, \mathbf{y}) := \left(\frac{h}{2\pi c}\right)^{3} \exp\left(-\mathrm{i}\frac{\mathrm{h}}{\mathrm{c}}(\mathbf{nx} + \mathbf{sy})\right).$$

The scalar product has the following shape:

$$(\widetilde{\varphi}(t, \tau), \widetilde{\chi}(t, \tau)) :=$$

$$\int_{-\frac{\pi c}{h}}^{\frac{\pi c}{\mathrm{h}}} dx_1 \int_{-\frac{\pi c}{h}}^{\frac{\pi c}{\mathrm{h}}} dx_2 \int_{-\frac{\pi c}{h}}^{\frac{\pi c}{\mathrm{h}}} dx_3 \int_{-\frac{\pi c}{h}}^{\frac{\pi c}{\mathrm{h}}} dy_1 \int_{-\frac{\pi c}{h}}^{\frac{\pi c}{\mathrm{h}}} dy_2 \int_{-\frac{\pi c}{h}}^{\frac{\pi c}{\mathrm{h}}} dy_3 \cdot$$

$$\widetilde{\varphi}(t, \tau, \mathbf{x}, \mathbf{y})^{\dagger} \widetilde{\chi}(t, \tau, \mathbf{x}, \mathbf{y}).$$

The Fourier series:

$$\varphi_{\mathtt{A},\mathtt{B}}((t, \mathbf{x})(\tau, \mathbf{y})) = \sum_{\mathbf{n}} \sum_{\mathbf{s}} a_{\mathtt{A},\mathtt{B},\mathbf{n},\mathbf{s}}(t, \tau)\, \phi_{\mathbf{n},\mathbf{s}}(\mathbf{x}, \mathbf{y}).$$

Hence,

$$\begin{aligned}
(\varphi_{\mathtt{A},\mathtt{B}}(t, \tau), \varphi_{\mathtt{A},\mathtt{B}}(t, \tau)) &= \sum_{\mathbf{n}} \sum_{\mathbf{s}} a^{\dagger}_{\mathtt{A},\mathtt{B},\mathbf{n},\mathbf{s}}(t, \tau)\, a_{\mathtt{A},\mathtt{B}.\mathbf{n},\mathbf{s}}(t, \tau), \\
(\varphi_{\mathtt{A},\mathtt{B}}(t, \tau), \varphi_{\mathtt{A},\mathtt{B}}(t, \tau)) &= \mathsf{P}(\mathtt{A}(t) \cdot \mathtt{B}(\tau)), \\
\mathsf{P}(\mathtt{A}(t) \cdot \mathtt{B}(\tau)) &= \sum_{\mathbf{n}} \sum_{\mathbf{s}} \mathsf{P}\left(\mathtt{A}_{\mathbf{n}}(t) \cdot \mathtt{B}_{\mathbf{s}}(\tau)_{,}\right).
\end{aligned}$$

For example: Let

$$\varphi_{\mathtt{A},\mathtt{B}}\left((t,\mathbf{x})\left(\tau,\mathbf{y}\right)\right)=$$
$$a_{\mathtt{A},\mathtt{B},\mathbf{1},\mathbf{4}}\left(t,\tau\right)\phi_{\mathbf{1},\mathbf{4}}\left(\mathbf{x},\mathbf{y}\right)+a_{\mathtt{A},\mathtt{B},\mathbf{2},\mathbf{3}}\left(t,\tau\right)\phi_{\mathbf{2},\mathbf{3}}\left(\mathbf{x},\mathbf{y}\right)+$$
$$a_{\mathtt{A},\mathtt{B},3,\mathbf{2}}\left(t,\tau\right)\phi_{3,\mathbf{2}}\left(\mathbf{x},\mathbf{y}\right)+a_{\mathtt{A},\mathtt{B},4,\mathbf{1}}\left(t,\tau\right)\phi_{4,\mathbf{1}}\left(\mathbf{x},\mathbf{y}\right).$$

Such event called *entangled* if $a_{\mathtt{A},\mathtt{B},\mathbf{n},\mathbf{s}}$ are not factorized.
In that case:

$$\left(\varphi_{\mathtt{A},\mathtt{B}}\left(t,\tau\right),\varphi_{\mathtt{A},\mathtt{B}}\left(t,\tau\right)\right)=$$
$$a^{\dagger}_{\mathtt{A},\mathtt{B},\mathbf{1},\mathbf{4}}\left(t,\tau\right)a_{\mathtt{A},\mathtt{B}.\mathbf{1},\mathbf{4}}\left(t,\tau\right)+a^{\dagger}_{\mathtt{A},\mathtt{B},\mathbf{2},\mathbf{3}}\left(t,\tau\right)a_{\mathtt{A},\mathtt{B}.\mathbf{2},\mathbf{3}}\left(t,\tau\right)+$$
$$a^{\dagger}_{\mathtt{A},\mathtt{B},3,\mathbf{2}}\left(t,\tau\right)a_{\mathtt{A},\mathtt{B}.3,\mathbf{2}}\left(t,\tau\right)+a^{\dagger}_{\mathtt{A},\mathtt{B},4,\mathbf{1}}\left(t,\tau\right)a_{\mathtt{A},\mathtt{B}.4,\mathbf{1}}\left(t,\tau\right).$$

$$\mathtt{P}\left(\mathtt{A}\left(t\right)\cdot\mathtt{B}\left(\tau\right)\right)=$$
$$\mathtt{P}\left(\mathtt{A}_{\mathbf{1}}\left(t\right)\cdot\mathtt{B}_{\mathbf{4}}\left(\tau\right)_{,}\right)+\mathtt{P}\left(\mathtt{A}_{\mathbf{2}}\left(t\right)\cdot\mathtt{B}_{\mathbf{3}}\left(\tau\right)_{,}\right)+$$
$$\mathtt{P}\left(\mathtt{A}_{\mathbf{3}}\left(t\right)\cdot\mathtt{B}_{\mathbf{2}}\left(\tau\right)_{,}\right)+\mathtt{P}\left(\mathtt{A}_{\mathbf{4}}\left(t\right)\cdot\mathtt{B}_{\mathbf{1}}\left(\tau\right)_{,}\right).$$

Let to $\varphi_{\mathtt{A},\mathtt{B}}\left((t,\mathbf{x})\left(\tau,\mathbf{y}\right)\right)$ acts realization operator: $(\check{r}\varphi,\check{r}\varphi)=1$. Then $\mathtt{A}\left(t\right)\cdot\mathtt{B}\left(\tau\right)$ occures. Therefore, in accordance with the sum definition, one among events $\mathtt{A}_{\mathbf{n}}\left(t\right)\cdot\mathtt{B}_{\mathbf{s}}\left(\tau\right)$ occures.

VI. Conclusion

Hence, events of entangled pair can occure in any time moments.

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Notes

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On the Efficiency of Some Selected Designs: A Case of Randomized Block Designs

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Abstract- This work examines the Relative Efficiency (RE) of some selected Randomized Complete Block Designs $(RCBD)$.The efficiency of the selected designs showed that design B was the most preferable having Mean Square Error of 6.14, followed by design C with Mean Square Error of 9.11 and design A with Mean Square Error of 18.08. The results from the pair-wise relative efficiency of the selected designs show that $RE(B,A) = 0.34$ with the smallest relative efficiency value and $RE(A,B) = 2.94$ with the largest relative efficiency value. We recommended design B as the best design for this particular problem since its mean square error remains the smallest.

Keywords: *RCBD, efficiency, missing value and estimation.*

GJSFR-F Classification: *MSC 2010: 13P25*

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On the Efficiency of Some Selected Designs: A Case of Randomized Block Designs

Asogwa, O. C. [α] & Eze, C. M. [σ]

Abstract- This work examines the Relative Efficiency (RE) of some selected Randomized Complete Block Designs ($RCBD$). The efficiency of the selected designs showed that design B was the most preferable having Mean Square Error of 6.14, followed by design C with Mean Square Error of 9.11 and design A with Mean Square Error of 18.08. The results from the pair-wise relative efficiency of the selected designs show that $RE(B,A) = 0.34$ with the smallest relative efficiency value and $RE(A,B) = 2.94$ with the largest relative efficiency value. We recommended design B as the best design for this particular problem since its mean square error remains the smallest.

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I. Introduction

The basic concepts of the statistical design of experiments and data analysis were discovered as early as 20th century as a cost effective research design tool to improve researches, for instance in agriculture and every other fields of study where experimentation is possible. Moreover, an experiments performed by an investigators or a researchers virtually in all the fields of inquiry, are usually, to discover something about a particular process or system, in relative to cost effectiveness.

However, the missingness of observation is common in scientific experiments. In statistical planning, it is never possible to anticipate beforehand which of the observations are going to be missing after the experiment. With this regards, the experimenter cannot redo the experiment with a different design because it costs money, time and effort, etc. One of such experimental designs in which missing observation can occur is a randomized block design. A randomized block design is a set together with a family of subsets whose members are chosen to satisfy some set of properties that are deemed useful for a particular application.

Complete block design may encounter missing observation at the process of experimentation because of some known causes which ranges from the carelessness of the experimenter, lack of response, questionable response, mixed up of values from different experimental plots, or the death of an experimental units, etc. This missing observation could inadvertently occur in various kinds of experiments, like in Agriculture, Ecology, Biology, Animal trials, etc.

This research basically aims at comparing the efficiency, as well as the relative efficiency of the selected designs, $(A, B, \& C)$. Design A analyzed the data as an incomplete design. Design B and design C computed the data when the missing

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observation has been estimated by the Correct Least Square Method and the Inversion Method, respectively. Test of significances of the individual designs were equally evaluated at some levels of significance.

[5] compared the relative efficiency of two statistical experimental designs based on mean square error. The result showed that lattice design is better off than randomized complete block design. [1] studied the effect of a range of uniform plant populations on yield and yield components of canola. The result indicated a significance difference in the seed yield. More literatures can be seen in, [4], [10], [2]. Etc.

II. The Correct Least Square Approach (CLSA)

This approach stipulates that the block(s) in which the missing value(s) occur(s) is /are removed from the data and then analyzed using the available observations. This removal will normally reduce the number of available blocks to the number of blocks in which missing observation occurred. The estimates of the experimental effects realized here are always unbiased. The major drawback encounters in this approach is that the analysis is more complicated than the case when no missing observation(s) occur.

III. The Inversion Method (IM)

In this case the missing observation(s) is/are first estimated from the remaining data and the experiment is then analyzed as in the complete data case. However, there is a loss of a unit(s) in the degree of freedom due to the error, depending on the number of missing observations present. This method equally has a setback when the numbers of missing observations are many.

IV. Estimation of Missing Observations

The general procedure is to replace the missing observation by its estimate under the model. This can only be achieved if the following steps are adhered to;

- Write down the linear model for the design under consideration.
- Write down the parametric equation involving the missing observation and this identify the parameter whose estimates are required to estimate the missing observation.
- Apply the least square method to obtain the estimates of the unknown parameter.

In the case where $m > 1$, where m signifies the number of missing observation in different blocks, set up estimates for each of them using the general expression for one missing observation. In setting up the estimate each observation is treated as if it is the only one that is missing and the rest are assigned values $x_1, x_2, \ldots, x_{n-1}$. This approach leads to a system of equation in n unknown whose solution gives estimate of the missing observations.

V. Randomized Compete Block Design (RCBD)

Randomized complete block design which is one of the most widely used experimental designs [8], which has its primary interest as to reduce or minimize the error or variability arising from the known nuisance sources, has been widely used in agricultural and industrial researches for many decades. It makes the experimental error or variability as small as possible by the help of its unique nature, which is blocking the variables according to their homogeneity. The blocks restrict the randomization here in the sense that randomization of the treatments is within the blocks. Usually they are more powerful, have higher external validity, are less subject to bias, and produce more

Ref

5. Irum, Raza and Masood, M. A. (2009). *Pakistan Journal of Agriculture Research.* **20**, 101.

reproducible results than the completely randomized designs typically used in research involving laboratory animals, [7].

VI. Efficiency

In mathematical or scientific terms, efficiency is a measure of the extent to which input is well used for an intended output. It measures the goodness of a design, [6]. However, In the comparison of various statistical procedures, efficiency is a measure of quality of an estimator, of an experimental design, [3] or of a hypothesis testing procedure, [9]. Essentially, a more efficient estimator, experiment, or test needs fewer observations than a less efficient one to achieve a given performance. In fact, efficiencies are often defined using the variance or mean square error (minimal) as the measure of desirability, [3].

VII. Relative Efficiency (RE)

Relative efficiency which is often used to indicate how much saving in cost can be envisaged from a design, can be symbolized as RE, which stands for relative efficiency. The relative efficiency of two procedures is the ratio of their efficiencies. If statistic X has a smaller variance than statistic Y, then statistic X is more efficient than statistic Y. The relative efficiency of two designs X and Y are expressed as $RE(A,B)$ and if this realization is greater than 1, this implies that design A is a better design than design B and this is computed generally as:

$$(a) \quad RE(A,B) = \frac{\sigma^2_{\varepsilon(B)}}{\sigma^2_{\varepsilon(A)}} \ \ldots (*) \qquad (b) \quad RE(A,B) = \frac{SS_B / d_{f_B}}{SS_A / d_{f_A}}, \text{ if } d_{f_A} \geq 20 \ \ldots (**)$$

$$(c) \quad RE(A,B) = \frac{\{(d_{f_A}+1)(d_{f_B}+3)\}MS_B}{\{(d_{f_B}+1)(d_{f_A}+3)\}MS_A}, \text{ if } \ d_{f_A} < 20 \ \ldots (***)$$

Where: MS_A is the mean square error of design A, d_{f_A} is the degree of freedom for the error term of design A, MS_B is the mean square error of design B, d_{f_B} is the degree of freedom for the error term of design B. SS_A and SS_B are the sum of squares for design A and B respectively.

VIII. Materials and Methodology

The data used in this study are secondary and were collected from the National Root Crops Research Institute (NRCRI) Umudike, Abia State, Nigeria. The data are on yield of cassava with different rations (kg) of Nitrogen, Phosphorous and Potassium (NPK) application. The experimenter was interested in the yield of four varieties of cassava when four different rates of NPK fertilizer were administered on them. It was administered in such manner that the fertilizer rations (kg) were blocked by the varieties of cassava. The data were arranged by the experimenter in a Randomized Complete Block Design (RCBD) layout. This arrangement was made, because Randomized Complete Block Design was deemed appropriate for the study.

a) The Statistical model of the design

The statistical model is given as:

$$Y_{ij} = I + \alpha_i + \beta_j + \varepsilon_{ij} \ ; \quad i = 1,2,3; \ j = 1,2,3.$$

3. Everitt, B. S. (2002). *The Cambridge Dictionary of Statistics.* Cambridge University Press. *ISBN 0-521-81099-X.*

$$\varepsilon_{ij} \sim N(0,1); \sum_{i}^{a} \alpha_i = 0; \sum_{j}^{b} \beta_j = 0;$$

Where Y_{ij} is the observed response of the ith level of the NPK on the jth yield. I is the universal constant. α_i is the effect of the ith NPK. β_j is the jth effect of the yield. ε_{ij} is the random error. The model was based on the assumptions of normality, constant variance and independence.

The data layout of the Randomized Complete Block Design is presented in table 1 below;

b) The table of the observed values

Table 1: Table of extracted data for this study (Source: NRCRI, Umudike, Abia State, Nigeria)

Fertilizers (NPK)	Cassava (Yield)			
05kg	7	8	6	Y_{14}
10kg	10	9	12	14
15kg	20	15	25	26

The missing observation in table 1above was estimated and replaced in the table 2 below;

c) Data layout with the missing observations replaced

Table 2: Table with the estimated value of of Y_{2A}

Fertilizers (NPK)	Cassava (Yield)			
05kg	7	8	6	Y_{14}= (12)
10kg	10	9	12	14
15kg	20	15	25	26

The descriptive ANOVA table of Randomized Complete Block Design is represented in the table 3 below;

d) The ANOVA Table

Table 3: ANOVA Table for the design (Randomized Complete Block Design)

Source of Variation	Degree of freedom	Sum of squares	Mean square	F-ratio
NPK$\{\alpha_i\}$	$\{p-1\}$	SS_α	MS_α	$F_\alpha = MS_\alpha/MS_e$
Yield$\{\beta_j\}$	$\{n-1\}$	SS_β	MS_β	$F_\beta = MS_\beta/MS_e$
Error $\{e\}$	$\{p-1\}\{n-1\}$	SS_e	MS_e	-
Total	$N-1$	SS_T	-	-

IX. Presentation of Tables of the Results

The result gotten when design A was analyzed is being presented in the table 4 below;

a) Table of result for design A

Table 4: ANOVA table for design A (the data were analyzed as an incomplete design)

Source of Variation	Degree of Freedom	Sum of Squares	Mean Squares	F-ratio	F-tabulated	
					$\alpha = 0.01$	$\alpha = 0.05$
Fertilizer(kg) $\{\alpha_i\}$	2	540.20	270.10	$F = 14.94$	$F_v = 10.90$	$F_v = 5.14$
Yields(tons) $\{\beta_j\}$	3	22.03	7.34	$F = 0.46$	$F_d = 9.78$	$F_d = 4.76$
Error $\{\varepsilon_{ij}\}$	6	108.47	18.08			
Total	11	670.70				

Below in table 5, the result of the analyses of design B was presented.

b) Table of result of design B

Table 5: ANOVA table for design B (the missing value in the datum was estimated & analyzed)

Source of Variation	Degree of Freedom	Sum of Squares	Mean Squares	F-ratio	F-tabulated	
					$\alpha = 0.01$	$\alpha = 0.05$
Fertilizer(kg) $\{\alpha_i\}$	2	386.20	193.10	$F = 30.12$	$F_j = 10.90$	$F_j = 5.14$
Yields(tons) $\{\beta_j\}$	3	74.03	24.68	$F = 3.85$	$F_q = 9.78$	$F_q = 4.76$
Error $\{\varepsilon_{ij}\}$	6	38.47	6.41			
Total	11	498.70				

The result of the analyses of design C was equally displayed in table 6 below;

c) Table of result of design C

Table 6: ANOVA table for design C (the block with the missing value is deleted from the design & analyzed

Source of Variation	Degree of Freedom	Sum of Squares	Mean Squares	F-ratio	F-tabulated	
					$\alpha = 0.01$	$\alpha = 0.05$
Fertilizer(kg) $\{\alpha_i\}$	2	273.55	136.78	$F = 15.01$	$F_u = 18.00$	$F_u = 6.94$
Yields(tons) $\{\beta_j\}$	2	20.22	10.11	$F = 1.11$	$F_i = 18.00$	$F_i = 6.94$
Error $\{\varepsilon_{ij}\}$	4	36.45	9.11			
Total	8	330.22				

The result of the efficiency comparisons of designs A, B and C was presented in the table 7 below;

d) Table of result comparisons of the three designs

Table 7: Tabulation of the result of the hypotheses carried out in this study

Designs	Eff. (MS_ϵ)	Sig $\alpha_i, 0.01$	Sig $\beta_j, 0.01$	Sig $\alpha_i, 0.05$	Sig $\beta_j, 0.05$
Design A	18.08	Sig	Not sig	Sig	Not sig
Design B	6.14	Sig	Not sig	Sig	Not sig
Design C	9.11	Not sig	Not sig	Sig	Not sig

It can be observed that in table 8, the result of the relative efficiency of the pair wise designs were presented;

e) The pair wise comparisons of the relative efficiency

Table 8: Table that compared the relative efficiency of all the possible pairs of the designs

Relative Efficiency	Values	Comparisons of the Designs
$R(A,B)$	2.94	Design A is better than Design B
$R(A,C)$	2.16	Design A is better than Design C
$R(B,C)$	0.73	Design C is better than Design B
$R(B,A)$	0.34	Design A is better than Design B
$R(C,A)$	0.46	Design A is better than Design C
$R(C,B)$	1.36	Design C is better than Design B

X. Summary and Discussion

The randomized complete block design is undoubtedly one of the most fundamental and useful tool in the analysis of variance models. The major advantage of using a randomized complete block design is that it makes reduction in error variance its primary target. The widely accepted relative precision measure is purported to evaluate the relative efficiency in terms of the ratio of error variances of both designs.

However, this relative precision measure does not take account of the loss in error degrees of freedom in a randomized complete block design with complete observations as compared with that in a randomized complete block design with a missing observation.

Unlike other researches that examine parameter values; this one focuses on the estimates of the relative efficiency measure that possess immediate applicability and practical importance. In this research, the selected randomized complete block designs presented different values of efficiency and relative efficiency, depending on the pair-wise combination of the designs considered, as can be seen in table 7, which enveloped the results of table 4, 5 and 6. This efficiency value was evaluated in terms of (1) comparing the precisions, (2) comparing the observed significance levels, while the relative efficiency was evaluated by taking the ration of the efficiencies of all the possible pair-wise combination of the selected designs with replacement.

It can be observed in table 7 that at different levels of significance considered, the treatments which is the level of the administered NPK fertilizer to the cassava (yield) is significant for all the designs, except design C at 0.01, while blocking were all not significant. The mean square error (MSE) for the selected designs showed that design B has the least (smallest) mean square error of 6.14, followed by design C and design A, with 9.11 and 18.08 values respectively and this recommend design B as the best of all. Finally, table 8, which evaluated a pair-wise relative efficiency presented $R(B,A) = 0.34$, which is the smallest (< 1) and best recommended and $R(A,B) = 2.94$, which is the largest (> 1) and least recommended. Both $R(B,A)$ and $R(A,B)$ agree with an existing literature like [10], which suggest design B as the best design for our problem.

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Polynomial Function on Fourier Cosine and Sine Transform

By Feyissa Kaba Wakene & Getachew Abiye Salilew
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Abstract- Aim of this study is to provide properties of a polynomial function on Fourier cosine and Fourier sine transform. Authors presented general properties of a polynomial function on Fourier cosine and Fourier sine transform by applying known results.

Keywords: *fourier cosine and sine transform, polynomial function.*

GJSFR-F Classification: *MSC 2010: 26D05, 11F30*

Strictly as per the compliance and regulations of:

1. M. Ziaul Haque, Solutions Manual to Introduction to Differential Equations with Dynamical Systems, Princeton University Press, 2008.

Polynomial Function on Fourier Cosine and Sine Transform

Feyissa Kaba Wakene [α] & Getachew Abiye Salilew [σ]

Abstract- Aim of this study is to provide properties of a polynomial function on Fourier cosine and Fourier sine transform. Authors presented general properties of a polynomial function on Fourier cosine and Fourier sine transform by applying known results.

Keywords: *fourier cosine and sine transform, polynomial function.*

I. Introduction

The theory of Fourier series and the Fourier transform is concerned with dividing a function into a superposition of sine and cosine, its components of various frequencies. It is a crucial tool for understanding waves, including water waves, sound waves and light waves. Fourier analysis is a mathematical technique which enables us to decompose an arbitrary function into a superposition of oscillations which can be resolved into a sum of sine and cosine. The theory of Fourier series can be used to analyze the flow of heat in a bar and the motion of a vibrating string. Fourier series in the work of Euler and D. Bernoulli on vibrating strings but the theory of Fourier series truly began with the profound work of Fourier on heat conduction at the beginning of the 19th century. Joseph Fourier a 21 years old mathematician and engineer announced a thesis which began a new chapter in the history of mathematics. Fourier's original investigations which led to the theory of Fourier series were motivated by an attempt to understand heat flow [1-2]. Nowadays, the notion of dividing a function into its components with respect to an appropriate orthonormal basis of functions is one of the key ideas of applied mathematics, useful not only as a tool for solving partial differential equations but also for many other purposes as well. In this study, we presented presumably new general interesting properties of a polynomial function on Fourier cosine and Fourier sine transform, by using known results.

II. Materials and Methods

The basic materials for this study are Fourier transforms. For now we will consider only the concepts of Fourier cosine and sine transform with some mathematical methods to do this paper. We use also methods such as techniques of integration, higher order derivative of a one variable function.

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Definition 2.1. The Fourier cosine and Fourier sine transform of the function $f(x)$ be given respectively as:

$$\mathcal{F}_c(f(x)) = \sqrt{\frac{2}{\pi}} \int_0^\infty f(x)\cos(x\omega)dx \text{ and } \mathcal{F}_s(f(x)) = \sqrt{\frac{2}{\pi}} \int_0^\infty f(x)\sin(x\omega)dx.$$

The Fourier transform of the function $f(x)$ is given by

$$\mathcal{F}(f(x)) = \frac{1}{\sqrt{2\pi}} \int_0^\infty f(x)e^{-ix\omega}dx.$$

Where $0 \leq \omega < \infty$, c and s represent cosine and sine respectively [3-4].

Definition 2.2. The derivative of a function such as $\frac{d^n}{dx^n}(f(x))$ for $n \in \mathbb{N}$ is called nth order derivative of a function $f(x)$ which is also called higher order derivative for $n \geq 2$.

Lemma 2.1. Let $f(x)$ has both Fourier cosine and sine transform. For an even natural number n, we have:

$$\mathcal{F}_c(x^n f(x)) = (-1)^{\frac{n}{2}} \frac{d^n}{d\omega^n}[\mathcal{F}_c(f(x))].$$

And for an odd natural number n, we have:

$$\mathcal{F}_c(x^n f(x)) = (-1)^{(\frac{n+3}{2})} \frac{d^n}{d\omega^n}[\mathcal{F}_s(f(x))].$$

For these properties we have equivalent properties such as for an even natural number n, we have:

$$\mathcal{F}_s(x^n f(x)) = (-1)^{\frac{n}{2}} \frac{d^n}{d\omega^n}[\mathcal{F}_s(f(x))].$$

And for an odd natural number n, we have:

$$\mathcal{F}_s(x^n f(x)) = (-1)^{(\frac{n+1}{2})} \frac{d^n}{d\omega^n}[\mathcal{F}_c(f(x))].$$

Proof (2.1). Using the recent work [5-6], proofs of all properties are straight forward. We omit the details.

III. Main Results

Theorem 3.1. Consider a polynomial function, $P_n(x) = a_n x^n + a_{n-1}x^{n-1} + a_{n-2}x^{n-2} + ... + a_2x^2 + a_1x + a_0$, where coefficients are numbers and assume that $f(x)$ has both Fourier cosine and sine transform. Then the Fourier sine transform of a new function, $P_n(x)f(x)$, given as follows. For whole numbers such as $n = 0, 1, 2, 3, ..., 2m$, for some m in the set of whole numbers, we have:

Ref
3. James R. Brannan, William E. Boyce, Differential equations, 2nd edition.

$$\mathcal{F}_s(P_n(x)f(x)) = \sum_{k=0}^{n} a_k(-1)^{\frac{k}{2}} \frac{d^k}{d\omega^k}[\mathcal{F}_s(f(x))] + \sum_{l=1}^{n-1} a_l(-1)^{(\frac{l+1}{2})} \frac{d^l}{d\omega^l}[\mathcal{F}_c(f(x))].$$

Where $l = 1, 3, 5, ..., n-1$; $k = 0, 2, 4, 6, ..., n$.

For whole numbers such as $n = 0, 1, 2, 3, ..., 2m-1$, for some m in the set of natural numbers, we have:

$$\mathcal{F}_s(P_n(x)f(x)) = \sum_{l=1}^{n} a_l(-1)^{(\frac{l+1}{2})} \frac{d^l}{d\omega^l}[\mathcal{F}_c(f(x))] + \sum_{k=0}^{n-1} a_k(-1)^{\frac{k}{2}} \frac{d^k}{d\omega^k}[\mathcal{F}_s(f(x))].$$

Where $l = 1, 3, 5, ..., n$; $k = 0, 2, 4, 6, ..., n-1$.

Proof (3.1). Consider that the function $f(x)$ has both Fourier cosine and Fourier sine transform for whole numbers such as $n = 0, 1, 2, 3, ..., 2m$, m is from whole number, we have:

$$P_n(x) = a_n x^n + a_{n-1}x^{n-1} + a_{n-2}x^{n-2} + ... + a_2x^2 + a_1x + a_0$$

$$P_n(x) = (a_n x^n + a_{n-2}x^{n-2} + ... + a_2x^2 + a_0) + (a_{n-1}x^{n-1} + a_{n-3}x^{n-3} + ... + a_3x^3 + a_1x).$$

$$\Longrightarrow P_n(x) = h(x) + g(x).$$

Where $h(x) = a_n x^n + a_{n-2}x^{n-2} + ... + a_2x^2 + a_0$ implies that all powers of variable x are even and $g(x) = a_{n-1}x^{n-1} + a_{n-3}x^{n-3} + ... + a_3x^3 + a_1x$ implies all powers of variable x are odd. The Fourier sine transform of a new function, $h(x)f(x)$, is given by

$$\mathcal{F}_s(h(x)f(x)) = \sqrt{\frac{2}{\pi}} \int_0^\infty h(x)f(x)\sin(x\omega)dx$$

$$\mathcal{F}_s(h(x)f(x)) = \sqrt{\frac{2}{\pi}} \int_0^\infty (a_n x^n + a_{n-2}x^{n-2} + ... + a_2x^2 + a_0)f(x)\sin(x\omega)dx.$$

By using lemma and arranging the powers of suitable terms, after simplification, we obtain

$$\mathcal{F}_s(h(x)f(x)) = a_0\mathcal{F}_s(f(x)) - a_2\frac{d^2}{d\omega^2}[\mathcal{F}_s(f(x))] + ... + a_n(-1)^{\frac{n}{2}} \frac{d^n}{d\omega^n}[\mathcal{F}_s(f(x))]$$

$$\mathcal{F}_s(h(x)f(x)) = \sum_{k=0}^{n} a_k(-1)^{\frac{k}{2}} \frac{d^k}{d\omega^k}[\mathcal{F}_s(f(x))]. \tag{1}$$

Where $k = 0, 2, 4, 6, ..., n$.

Similarly the Fourier sine transform of a new function, $g(x)f(x)$, given by

$$\mathcal{F}_s(g(x)f(x)) = \sqrt{\frac{2}{\pi}}\int_0^\infty g(x)f(x)\sin(x\omega)dx$$

$$\mathcal{F}_s(g(x)f(x)) = \sqrt{\frac{2}{\pi}}\int_0^\infty (a_{n-1}x^{n-1}+a_{n-3}x^{n-3}+...+a_3x^3+a_1x)f(x)\sin(x\omega)dx.$$

Using lemma and arranging the powers of suitable terms, after little algebra, we obtain

$$\mathcal{F}_s(g(x)f(x)) = -a_1\frac{d}{d\omega}[\mathcal{F}_c(f(x))]+a_3\frac{d^3}{d\omega^3}[\mathcal{F}_c(f(x))]-...+a_{n-1}(-1)^{\frac{n}{2}}\frac{d^{n-1}}{d\omega^{n-1}}[\mathcal{F}_c(f(x))]$$

$$\mathcal{F}_s(g(x)f(x)) = \sum_{l=1}^{n-1} a_l(-1)^{(\frac{l+1}{2})}\frac{d^l}{d\omega^l}[\mathcal{F}_c(f(x))]. \quad (2)$$

Where $l = 1, 3, 5, ..., n-1$.

Combining (1) and (2), the Fourier sine transform of a new function, $P_n(x)f(x)$, obtained as:

$$\mathcal{F}_s(P_n(x)f(x)) = \sum_{k=0}^{n} a_k(-1)^{\frac{k}{2}}\frac{d^k}{d\omega^k}[\mathcal{F}_s(f(x))] + \sum_{l=1}^{n-1} a_l(-1)^{(\frac{l+1}{2})}\frac{d^l}{d\omega^l}[\mathcal{F}_c(f(x))].$$

Where $l = 1, 3, 5, ..., n-1$; $\quad k = 0, 2, 4, 6, ..., n$.

Similarly let $f(x)$ has Fourier cosine and sine transform for numbers such as $n = 0, 1, 2, 3, ..., 2m-1$, m is from natural number, we have:

$$P_n(x) = a_nx^n + a_{n-1}x^{n-1} + a_{n-2}x^{n-2} + ... + a_2x^2 + a_1x + a_0$$

$$P_n(x) = (a_nx^n+a_{n-2}x^{n-2}+...+a_3x^3+a_1x)+(a_{n-1}x^{n-1}+a_{n-3}x^{n-3}+...+a_2x^2+a_0).$$

$$\Longrightarrow P_n(x) = q(x) + r(x).$$

Where $q(x) = a_nx^n + a_{n-2}x^{n-2} + ... + a_3x^3 + a_1x$ implies that all powers of variable x are odd and $r(x) = a_{n-1}x^{n-1} + a_{n-3}x^{n-3} + ... + a_2x^2 + a_0$ gives all powers of variable x are even. Then using the previous suitable properties with simplification of little algebra the Fourier sine transform of a new functions, $q(x)f(x)$ and $r(x)f(x)$, are given by

$$\mathcal{F}_s(q(x)f(x)) = \sum_{l=1}^{n} a_l(-1)^{(\frac{l+1}{2})}\frac{d^l}{d\omega^l}[\mathcal{F}_c(f(x))] \quad and$$

$$\mathcal{F}_s(r(x)f(x)) = \sum_{k=0}^{n-1} a_k(-1)^{\frac{k}{2}}\frac{d^k}{d\omega^k}[\mathcal{F}_s(f(x))]$$

Notes

respectively. Thus the Fourier sine transform of a new functions, $P_n(x)f(x)$, is given by

$$\mathcal{F}_s(P_n(x)f(x)) = \mathcal{F}_s([q(x) + r(x)]f(x))$$

$$\mathcal{F}_s(P_n(x)f(x)) = \sum_{l=1}^{n} a_l(-1)^{(\frac{l+1}{2})}\frac{d^l}{d\omega^l}[\mathcal{F}_c(f(x))] + \sum_{k=0}^{n-1} a_k(-1)^{\frac{k}{2}}\frac{d^k}{d\omega^k}[\mathcal{F}_s(f(x))].$$

Notes

Where $l = 1, 3, 5, ..., n$; $k = 0, 2, 4, 6, ..., n-1$. Hence we complete the proof of (3.1).

IV. Conclusions

The objective of this paper is to provide a brief representation of any function in the integral form. Fourier cosine and sine transform of a function after multiplying the given function by a polynomial function with coefficient are numbers provide the relationship between Fourier cosine and sine transform. Significance of this study will help to represent the solutions of ODEs, PDEs, and integral equations that involving polynomial function terms in the integral form of simper functions of cosine and sine. This study may be a base for generating other new findings or researches.

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Mathematical Theory of Genetic Code

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Abstract- On the basis of studying of genes new properties of a genetic code were established and its major integrated characteristics are calculated. Two groups of such characteristics were allocated. The first group treats integrated characteristics for the DNA areas where genes are in pairs blocked and all 5 cases of the overlappings allowed by structure of DNA were investigated. The second group of characteristics treats most DNA extended areas in which there are no genetic overlappings. The interrelation of the established integrated characteristics in the called groups is established. Were as a result found a number of unknown before effects. It was succeeded to establish two functions in which all codons reassignment participate in mitochondrial genetic codes (human and other organisms), and also essential distinction in integrated characteristics of such codes by comparison with a standard code. Other properties of structure of the genetic code, following from the received results are established also.On the basis of the constructed theory, the problem of calculating the genetic code was set (in 1992) and the first complete publication was published recently [26].

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26. Kozlov. N. N. (2017) Computation of the Genetic Code: Full Version. Journal Computer and Communications, 5, 78-94 https://doi.org/10.4236/jcc.2017.510008.

Mathematical Theory of Genetic Code

Математическая теория генетического кода

N. N. Kozlov

Abstract- On the basis of studying of genes new properties of a genetic code were established and its major integrated characteristics are calculated. Two groups of such characteristics were allocated. The first group treats integrated characteristics for the DNA areas where genes are in pairs blocked and all 5 cases of the overlappings allowed by structure of DNA were investigated. The second group of characteristics treats most DNA extended areas in which there are no genetic overlappings. The interrelation of the established integrated characteristics in the called groups is established. Were as a result found a number of unknown before effects. It was succeeded to establish two functions in which all codons reassignment participate in mitochondrial genetic codes (human and other organisms), and also essential distinction in integrated characteristics of such codes by comparison with a standard code. Other properties of structure of the genetic code, following from the received results are established also.On the basis of the constructed theory, the problem of calculating the genetic code was set (in 1992) and the first complete publication was published recently [26].

Abstract- **На основе изучения генов были установлены новые свойства генетического кода и вычислены важнейшие его интегральные характеристики. Были выделены две группы таких характеристик. Первая группа относится к интегральным характеристикам для областей ДНК, где гены попарно перекрываются и были исследованы все 5 случаев перекрытий, разрешенных структурой ДНК. Вторая группа характеристик относится к наиболее протяженным областям ДНК, в которых нет генетических перекрытий. Устанавливается взаимосвязь установленных интегральных характеристик в названных группах. В результате были обнаружены ряд неизвестных ранее эффектов. Удалось установить две функции, в которых участвуют все переосмысленные кодоны в митохондриальных генетических кодах (человека и других организмов), а также существенное различие в интегральных характеристиках таких кодов по сравнению со стандартным кодом. Установлены также другие свойства структуры генетического кода, вытекающие из полученных результатов. На основе построенной теории была поставлена (в 1992 году) и решена задача расчета генетического кода и первая полная публикация опубликована недавно: [26].**

I. Introduction

По результатам многолетних исследований автором была разработана математическая теория генетического кода, кратко представленная в статье N.N. Kozlov and T.M. Eneev. Fundamentals of a Mathematical Theory of Genetic Code. Doklady Mathematics 2017, Volume 95, № 2, pp. 144-146. Данная работа представляет собой расширенную версию этой статьи. Основное внимание будет уделяться вопросам, получившим строгое математическое обоснование. Мы пытались дать материал в виде, доступном для широкого круга математиков, поэтому введены два первых вводных пункта. Задача упрощается тем, что расширенные версии некоторые из главных

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результатов были опубликованы в ряде статей, которые процитированы в списке литературы. Однако принципиально важно представить такие результаты в их взаимосвязи, ведь они касаются загадок одной и той же таинственной структуры - генетического кода. Следует отметить, что ни один из приведенных результатов не был обнаружен автором в других публикациях, причем как в отечественных, так и в зарубежных.

II. Генетический Код

История открытия генетического кода достаточно подробно описана М. Ичасом [1, 2]- одним из участников пионерских исследований по этой проблеме. Он пишет: «… расшифровка биологического кода действительно революционизирующее событие, ее, быть может, уместно сравнить с другим событием, вызвавшим переворот в науке сто лет назад с появлением дарвиновского «Происхождения видов¸ [1]. Самым трудным в проблеме кода было понять, что код существует. На это потребовалось почти целое столетие. Отсчет его ведется от работы Менделя [3], который показал, что наследственные признаки передаются дискретными частицами, которые мы сегодня называем генами. Эта работа, как известно, почти не вызвала интереса. «Из всего того, что нам известно, складывается впечатление, что Менделю были, в общем-то, безразличны отклики на его работу. Опубликовав свой главный труд, он посчитал свой долг исполненным: если на нее не обратили внимания, то тем хуже для читателей, а не для автора¸. [2, стр. 142]. В 1900 году три независимых исследователя одновременно своими опытами подтвердили результаты, полученные Менделем. Только завершив работу, они узнали, что 34 года назад их опередил Мендель. После 1900 года генетика стала развиваться быстро и непрерывно.

Впервые идея молекулярно-биологического подхода к проблемам генетики была сформулирована известным физиком Э. Шредингером в книге «Что такое жизнь? С точки зрения физика¸ [4], которая в оригинале увидела свет в 1945 году. На странице 28 читаем представление о коде (за 21 год до его окончательной разгадки!): «Называя структуру хромосомных нитей шифровальным кодом, мы подразумеваем, что всеохватывающий ум, вроде такого, который некогда представлял себе Лаплас и которому каждая причинная связь непосредственно открыта, мог бы, исходя из структуры хромосом, сказать, разовьется ли яйцо при благоприятных условиях в черного петуха или в крапчатую курицу, в муху или растение маиса, в рододендрон, жука, мышь или человека¸. Помимо этого и других блистательных предвидений следует отметить, что эта книга сыграла решающую роль в судьбе ряда физиков-теоретиков. Назову лишь две фамилии, о которых будет идти речь в дальнейшем. Это Ф. Крик, который в 1946 году оставил теоретическую физику и обратился к задачам биологии после прочтения этой книги. Его Нобелевская лекция была посвящена проблеме кода, а не структуре ДНК, за которую он был удостоен Нобелевской премии (F.Crick - Nobel Lecture, Dec. 11, 1962: On the Genetic Code, Internet). У истоков проблемы кода стоял также физик Г. Гамов, на которого Ф.Крик ссылается на первой странице указанной лекции. Однако на финальном этапе исследований именно

Ref

1. Ичас М. Биологический код/– М.: Мир, 1971, 359 с. англ. пер.: Ycas M. The biological code//Amsterdam – London. – 1969. – 359P.

биохимики экспериментально установили генетический код и указали его роль в биосинтезе белка. За этот результат Х. Корана, М. Ниренберг и Р. Холли получили Нобелевскую премию в 1968г.

Но сначала была решена проблема структуры ДНК. Аспиранту Д. Уотсону понадобилось примерно полтора года, чтобы совместно с руководителем Ф. Криком решить одну из важнейших проблем биологии, которая в настоящее время считается одной из главных фундаментальных проблем, решенных в прошлом столетии. Речь идет о структуре молекул ДНК, которую мир впервые увидел 25 апреля 1953 года: работа [5], объемом в одну (!) страницу журнала «Nature¸ поставила точку на дискуссии относительно роли ДНК в передаче наследственной информации. Описания, которые дают для ДНК сегодня, различны. Для наших целей достаточно упрощенного описания. Модель двойной спирали ДНК представляет собой две нити, закрученные друг относительно друга (рис. 1.).

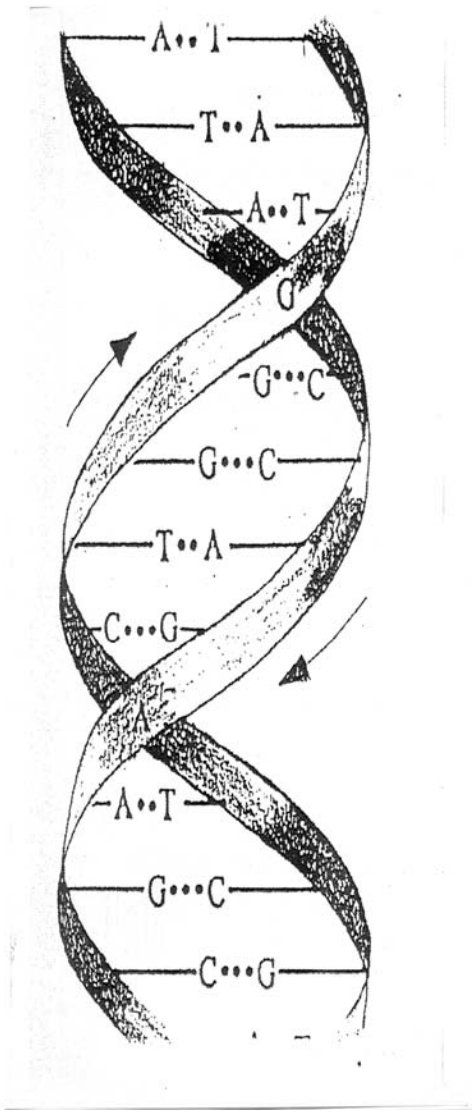

Рис. 1: Модель двойной спирали ДНК. Чтение текста гена указано стрелками по одной цепи - сверху вниз, по другой - снизу вверх

Ref

5. Watson, J.D., Crick, F.H.C. A structure for Deoxyribose Nucleic Accid//Nature. – 1953. – V.171. – P. 737-738.

По сути дела, это – двойная винтовая линия, а не какая ни спираль. Алфавит ДНК содержит всего 4 буквы: A, C, G, T. Это четыре нуклеотида: аденин, цитозин, гуанин, и тимин соответственно. Точки между этими буквами на рис. 1. указывают на количество водородных связей: две связи между A и T и три - между C и G. Именно эта блестящая догадка Уотсона, который ввел эти комплиментарные пары [6], и позволила объяснить важнейшие свойства передачи наследственной информации. (Эти связи существуют между двумя спиралями ДНК). ДНК измеряют по- разному, в том числе, и количеством пар нуклеотидов. Например, для ДНК человека их около 3.2 миллиардов (ftp://ftp.ncbi.nih.gov/refseq/H_sapiens/).

Тайна гена была окончательно разгадана в 1966 году (к столетию работы Менделя [3]), когда в ходе экспериментальных исследований было окончательно установлено, что гены есть однонитевые участки ДНК и содержат информацию о белке в закодированном виде. Оказалось, что каждая из 20 аминокислот - элементов, из которых состоят все известные белки, кодируется определенными тройками нуклеотидов - кодонами или триплетами. Для четырех букв: A, C, G, T, имеем 64 кодона: AAA, AAC, AAG, …, TTT. Смысл всех этих кодонов был экспериментально установлен и представлен в таблице генетического кода, причем кодировка, которую выбрала природа, оказалась своеобразной. В табл. 1. она представлена полностью.

Таблица 1: Стандартныйгенетическийкод.

	1	2	3
1	Met	1	ATG
2	Trp	1	TGG
3	Phe	2	TTY
4	Tyr	2	TAY
5	His	2	CAY
6	Asn	2	AAY
7	Asp	2	GAY
8	Cys	2	TGY
9	Gln	2	CAX
10	Lys	2	AAX
11	Glu	2	GAX
12	Ile	3	ATM
13	Val	4	GTN
14	Pro	4	CCN
15	Thr	4	ACN
16	Ala	4	GCN
17	Gly	4	GGN
18	Ser	6	TCN, AGY
19	Leu	6	CTN, TTX
20	Arg	6	CGN, AGX
	ter(*)	3	TAX, TGA

Примечание. Для каждой из аминокислот приводятся: 1 – стандартные трехбуквенные сокращения, 2 – число кодонов-синонимов, 3 – трехбуквенные нуклеотидные представления кодонов. Обозначение: X: A, G; Y: T, C; M: T, C, A; N: A, G, T, C. В последней строке приводятся три терминаторных кодона – ter, каждый из которых обозначает останов синтеза белка.

Ref

3. Mendel G. Versuche über Pflanzenhybriden, Verhandl//Naturforsch. Ver. Brünn. – 1866. – V.4, – P. 3–47.

Notes

Оказалось, что только две аминокислоты - метионин (Met) и триптофан (Trp) кодируются однозначно кодонами ATG и TGG соответственно. Все остальные аминокислоты кодируются более чем одним кодоном (это кодоны-синонимы), но не более чем шестью. Последнее наблюдается только для трех аминокислот: серин (Ser), лейцин (Leu), аргинин (Arg). Такие три кодировки названы нерегулярными, в отличие от 17-и других, регулярных для которых каждые 1-ая и 2-ая позиции одинаковы в соответствующем наборе кодонов-синонимов. Полное число смысловых кодонов или троек, кодирующих какую-либо аминокислоту, равно 61. Кодоны терминации ter (*) не соответствуют никаким аминокислотам, каждый из них останавливает синтез белка. В виду важности этих

Кодонов при дальнейшем анализе выделим их в (1):

$$\text{ter: TAA, TAG, TGA.} \qquad (1)$$

Укажем, что помимо вырожденности (т.е., когда одной и той же аминокислоте соответствуют, как правило, несколько кодонов-синонимов) важнейшим свойством кода является его универсальность: код одинаков для почти всех живых организмов. Однако к настоящему времени обнаружены ряд отклонений кода от стандартного, что является одной из наиболее загадочных особенностей кода (см. табл.2).

Таблица 2: Стандартный – K^0 и нестандартные генетические коды K^1- K^{14} и их характеристики p

1	2	3	p	p
K^0	The standard code		16	
K^1	The Vertebrate Mitochondrial Code	TGA(ter)→Trp, ATA(Ile)→Met, AGX(Arg)→ter	7	
K^2	The Invertebrate Mitochondrial Code	TGA(ter)→Trp, ATA(Ile)→Met, AGX(Arg)→Ser	7	
K^3	The Echinoderm and Flatworm Mitochondrial Code	TGA(ter)→Trp, AAA(Lys)→Asn, AGX(Arg)→Ser	5	
K^4	The Mold, Protozoan, and Coelenterate Mitochondrial Code and the Mycoplasma / Spiroplasma Code	TGA(ter)→Trp	6	
K^5	The Ciliate, Dasycladacean and Hexamita Nuclear Code	TAX (ter)→Gln	5	
K^6	The Euplotid Nuclear Code	TGA(ter)→Cys	5	
K^7	The Alternative Yeast Nuclear Code	CTG(Leu)→Ser	16	
K^8	The Ascidian Mitochondrial Code	TGA(ter)→Trp, ATA(Ile)→Met, AGX(Arg)→Gly	7	
K^9	The Alternative Flatworm Mitochondrial Code	TGA(ter)→Trp, AAA(Lys)→Asn, TAA(ter)→Tyr, AGX (Arg) →Ser	0	
K^{10}	Blepharisma Nuclear Code	TAG(ter)→Gln	10	
K^{11}	Chlorophycean Mitochondrial Code	TAG(ter)→Leu	10	
K^{12}	Trematode Mitochondrial Code	TGA(ter)→Trp, AAA(Lys)→Asn, ATA(Ile)→Met, AGX (Arg) →Ser	6	
K^{13}	Scenedesmus Obliquus Mitochondrial Code	TAG(ter)→Leu, TCA (Ser) →ter	10	
K^{14}	Thraustochytrium Mitochondrial Code	TTA (Leu)→ter	21	

Примечание.

1- коды K^0- K^{14}, 2 – их названия, 3- отклонения от стандартного кода
Колонки 2 и 3 получены на основе: http://www.ncbi.nlm.nih.gov/Taxonomy/Utils/wprintgc.cgi?mode=t

III. Перекрывающиеся Гены

Математический анализ структуры генетического кода, прежде всего, опирается на исследование некоторых необычных способов записи генов, кодирующих белки. Необычный способ записи генов состоит в том, что один и тот же участок цепи ДНК, кодирующий белок, может читаться со сдвигом фазы на +1 либо -1 нуклеотид либо с другой цепи ДНК (с подобными сдвигами либо без них). Иными словами один и тот же указанный участок ДНК может кодировать два, и более белков, вплоть до шести. Такие гены были названы перекрывающимися. Отметим, что как показывают эксперименты, такое чтение оказывается разрешенным лишь в некоторых случаях, а в подавляющем большинстве случаев существует запрет на указанные альтернативные чтения. Этот запрет состоит в том, что указанные сдвиги приводят к совершенно иным последовательностям кодонов отличным от исходной последовательности (когда сдвигов нет). Но было установлено, что в подобных альтернативных последовательностях непременно возникают какие-либо кодоны из (1); так устроен ген кодирующий белок, или так выбраны соответствующие кодировки аминокислот вследствие вырожденности кода. Из-за роли названных трех кодонов (они останавливают (блокируют) белковый синтез), белок при альтернативном чтении не синтезируется. Был сделан вывод о мощной биологической защите: природе не нужны эфемерные белки, она не синтезирует белки соответствующие сдвинутым позициям (например, если в ходе мутаций начальная точка сдвинется). Тем самым были введены в рассмотрение две рамки считывания - РС: открытая рамка считывания (ОРС) - последовательность кодонов, не содержащая кодонов терминации и блокированная РС - БРС, когда такие кодоны встречаются [7]. На рис. 2 белок соответствует ОРС, сдвинутые позиции нуклеотидных последовательностей, как +1 так и -1 - БРС.

```
сдвиг -1  AsnGlyGlyLeuLeu *  * AlaGlu...          БРС
сдвиг +1    TrpArgLeuArgIleValGly * ...            БРС

белок →   MetGlnAlaCysTyrSerArgLeuLys...           ОРС
ген →     AATGGAGGCTTGCTATAGTAGGCTGAAG...
           •            ↑   ↑   ↑
                        C   C   C
```

Рис. 2: Участок белковой последовательности (первая аминокислота - Met) закодирован в гене начиная с ATG (первый нуклеотид A в этом триплете помечен жирной точкой) и случаи сдвигов на +1 либо -1 нуклеотид

В сдвинутых состояниях получим другие последовательности кодонов (две другие РС), в каждой из которых будет неоднократно присутствовать кодоны терминации ter, которые на рис.2 помечены одним и тем же символом символом *. Это будут две РС с блокировками - БРС. Можно видеть, что с помощью трех нуклеотидных замен на один и тот же нуклеотид C (позиции замен указаны под текстом гена), ни один из трех кодонов ter (символ *) на заданном участке гена

не возникнет, причем при таких заменах белковая последовательность не изменится т.к. указанные три замены соответствуют трем заменам кодонов на их синонимы. Однако типичный ген устроен так, чтобы указанные сдвиги давали именно две БРС [7]. Оказалось, что лишь для перекрывающихся генов такого запрета не существует. Впервые этот эффект был установлен экспериментально в 1976 году в ходе исследований по чтению первого целого генома - вируса бактерии ФХ 174 [8]. После этих исследований их руководитель F.Sanger становится единственным в истории двукратным лауреатом Нобелевской премии по химии. F.Sanger проявил интерес к одной из первых наших работ В письме к нему я сформулировал новое свойство первого целого генома. Оно состоит в том, что для записи такого генома требуется использовать все 61 смысловых кодонов- это из-за перекрытий генов, впервые обнаруженные в этом геноме. Я просил представить этот результат в NAURE. Его ответ приводится в файле Sanger. Полная нуклеотидная последовательность кольцевой одноцепочечной ДНК ФХ174 (по-видимому фактор одноцепочности ДНК, установленный ранее экспериментально и явился решающим для чтения первого целого генома) содержит 5386 нуклеотидов [10], однако общее число аминокислотных остатков в последовательностях всех белков умноженное на 3 (с учетом не кодирующих участков) превышает это число нуклеотидов. Было показано, что ген Е содержит 273 нуклеотида и локализуется внутри гена D [8]. Это первое экспериментально обнаруженное перекрытие представлено на рис.3.

Ref

8. Barrell B.G., Air G.M. and Hutchison C.A. III. Overlapping genes in bacteriophage ФХ17 Nature. – 1976. – V. 264. – P. 34-41.

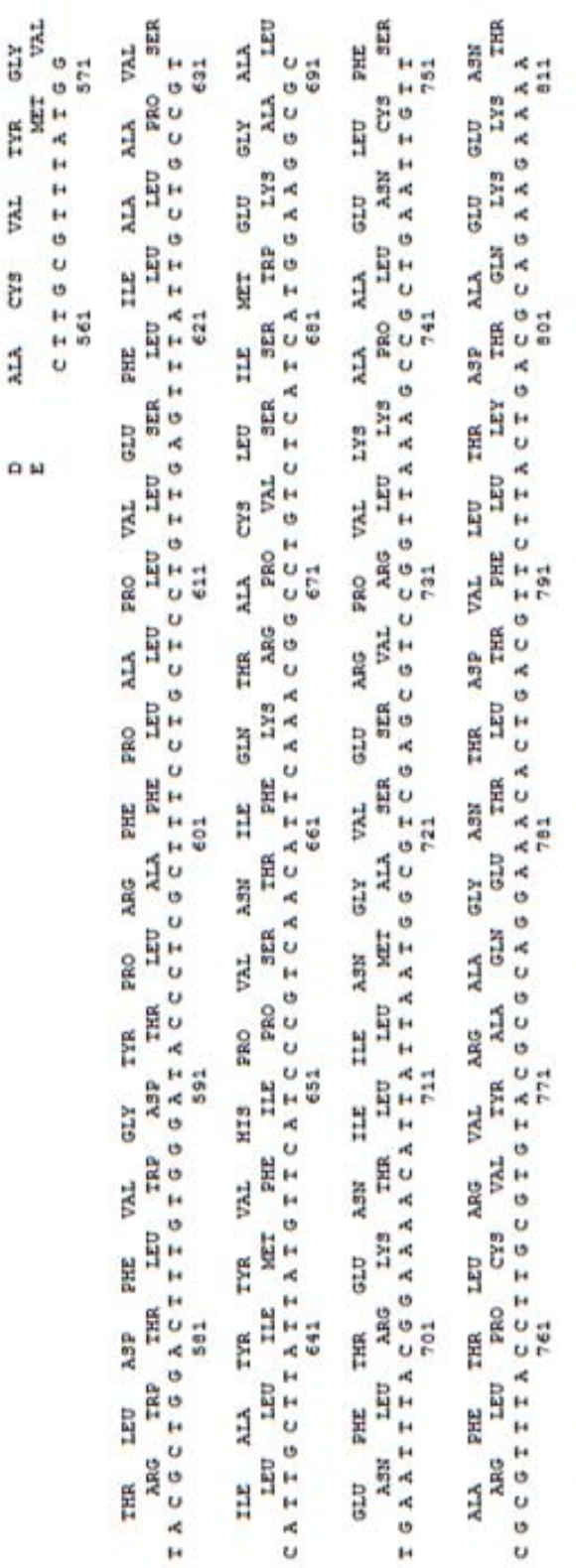

Рис. 3: Первое генетическое перекрытие, обнаруженное экспериментально [8].Рисунок представлен в формате публикации полного текста первого целого генома для бактериофага ФХ 174 [10]. Видим, что начиная с позиции 568 и до позиции 840, была установлена кодировка нового белка E на участке нуклеотидной последовательности другого белка - белка D

Ref

10. Sanger F., Coulson A.R., Friedmann T., Air G.M., Barrell B.G., Brown N.L., Fiddes J.C., Hutchison C.A., III, Slocombe P.M., Smith M. The Nucleotide Sequence of Bacteriophage ΦX174//J. Mol. Biol. – 1978. – V.125. – P.225-246.

В настоящее время считается, что перекрывающиеся гены представляют собой хотя и необычный, но все, же довольно распространенный элемент организации генома. В расшифрованном человеческом геноме обнаружены множественные генетические перекрытия [11]- их оказалось около 1700. Накопленный обширный материал по генетическим перекрытиям выдвинул задачу их тщательного и всестороннего анализа. Остановимся на некоторых результатах, полученных нами на основе математического анализа.

Можно видеть, что различающихся случаев перекрытий генов, разрешенных структурой ДНК, всего 5 (рис.4), из которых первые два относятся к перекрытиям генов из одной и той же цепи ДНК, а оставшиеся 3- к перекрытиям генов, взятых из разных цепей ДНК.

Ref

11. Nakayama T., Asai S., Takahashi Y., Nishida Y. Overlapping of Genes in the Human. Genome //Nevill Juvenile Bonfire Society 2007, vol.3, no. 1, p. 14-19.

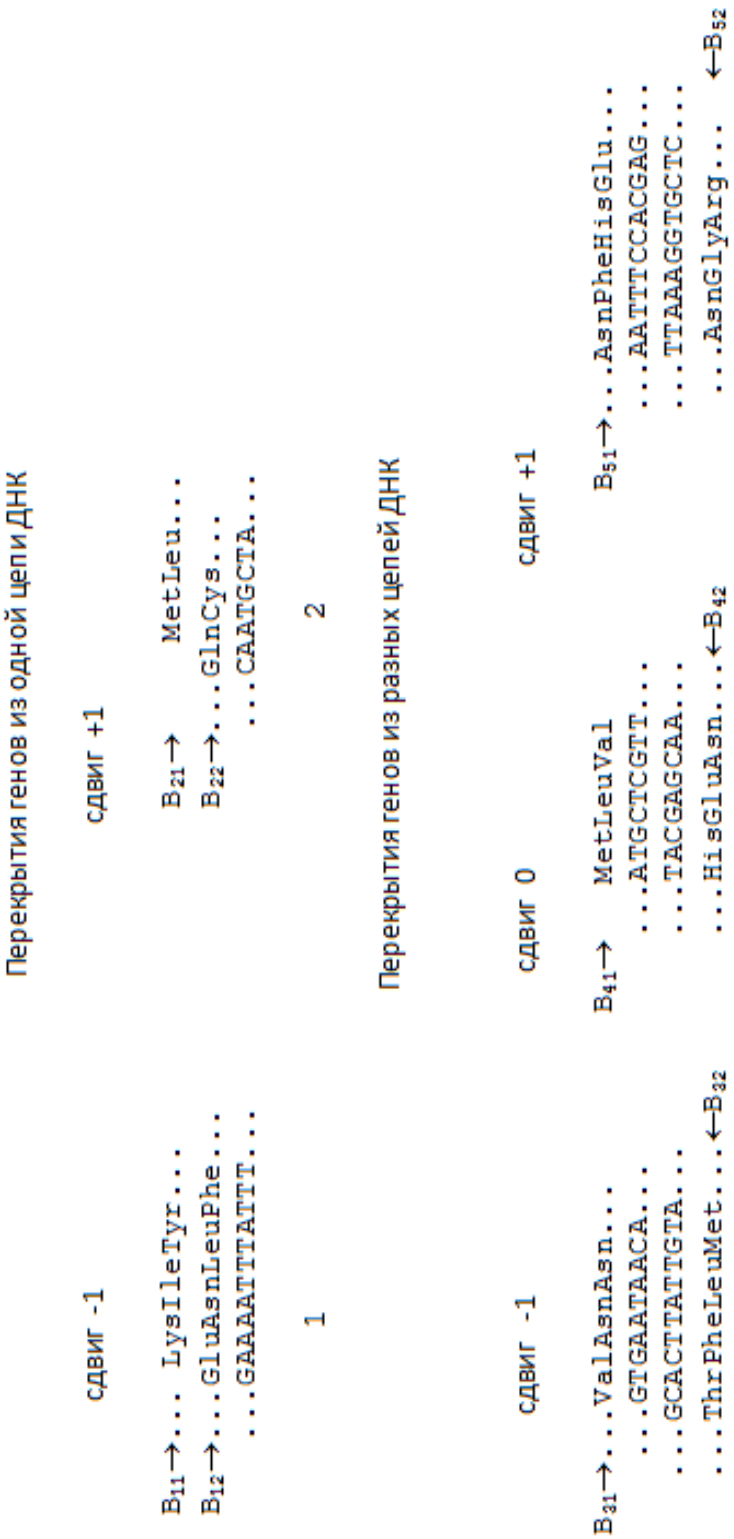

Рис. 4: Пять возможных случаев перекрытий генов, соответствующих одной (1,2) либо двум цепям ДНК (3-5). Чтение текстов при этом осуществляется в разных направлениях (указано стрелкой): слева направо для B_{11}, B_{12}, B_{21}, B_{22}, B_{31}, B_{41}, B_{51} и справа налево для B_{32}, B_{42}, B_{52}. В этих фрагментах присутствуют только канонические пары ДНК: CG и AT

Notes

На рис.4. представлены лишь небольшие фрагменты реальных перекрытий, причем полная протяженность некоторых из них достигает почти 1300 нуклеотидов. Кроме того, суммарная протяженность перекрытий может достигать более половины размера генома (вирус GSHV).

Следует подчеркнуть, что именно анализ множественных взаимосвязей кодонов в генетических перекрытиях и является главным инструментом проведенных исследований.

IV. Вырожденность Кода

Одна из задач, которая была поставлена нами, относится к фундаментальной проблеме генетического кода: зачем нужна вырожденность кода, когда для одной и той же аминокислоты имеют место, как правило, более одной кодировки, вплоть до 6-и кодировок. Было изучено участие всех смысловых кодонов в перекрытиях генов. Оказалось, что существует множество геномов с перекрытиями, в которых непременно должны участвовать все 61 смысловых кодонов, и при исключении хотя бы одного кодона обнаруженная в экспериментах запись генетических перекрытий представляется невозможной. Одним из таких геномов является первый целый геном для вируса бактерии ФХ174, содержащий перекрытия для 814 нуклеотидов [10]. Наша статья [9], а также статья, сопутствующая ей, были процитированы не менее чем по 100 раз каждая. (см. файл 300 citation).

V. Нерегулярности Кода

Следующая наша задача была связана с анализом кодонов, отклоняющих генетический код от однородной структуры. Это одна из наиболее загадочных особенностей генетического кода. Как показал анализ добавочные кодонные представления из табл.1, или нерегулярности, для Ser это AGY, для Leu это TTX, для Arg это AGX, позволяют в принципе «организовать¸ перекрытия в ряде геномов либо существенно расширить диапазоны генетических перекрытий как для двойных (для генома ФХ 174 в 7 раз), так и для тройных (для HIV-2 [12] в 5 раз) перекрытий, если бы они были организованы с использованием однородного кода, или кода без нерегулярностей.

Потенциальные возможности кода для построения множества генетических перекрытий.

Далее нами была поставлена задача о том, каков же потенциал генетического кода для создания всех указанных случаев перекрытий. Ответ оказался следующим - феноменальный потенциал!, Этот результат оценил Лауреат Нобелевской премии.de Duve to me (see the file) Оказалось, что только 16 пар аминокислот из возможных 400 могут создавать препятствия для построения всех 5-и случаев перекрытий. Это пары аминокислот всего для трех случаев перекрытий:

в случае 2 это 5 пар:

$$\text{MetMet, MetAsn, MetLys, MetIle, MetThr,} \qquad (2)$$

в случае 3 это 6 пар:

Ref

10. Sanger F., Coulson A.R., Friedmann T., Air G.M., Barrell B.G., Brown N.L., Fiddes J.C., Hutchison C.A., III, Slocombe P.M., Smith M. The Nucleotide Sequence of Bacteriophage ΦX174//J. Mol. Biol. – 1978. – V.125. – P.225-246.

PheTyr, TyrTyr, HisTyr, AsnTyr, AspTyr, CysTyr, (3)

в случае 5 это 5 пар:

PheMet, PheAsn, PheLys, PheIle, PheThr. (4)

Иными словами создается впечатление, что генетический код как бы подобран под перекрытия. Так ли это? Ответ на этот вопрос будет дан ниже.

Итак, нами установлена первая интегральная характеристика генетического кода, которую обозначим через p и которая равна 16 для стандартного кода:

$$p = 16 \quad (5)$$

VI. Общее Свойство Всех Природных Кодов

Полученный результат привел к остановке новых задач. Каково значение p для нестандартных (девиантных) кодов, число которых равно 14 и продолжает расти? Отметим, что первый нестандартный код, был обнаружен в 1979 году в клетке человека в отдельной органелле – в митохондрии: гены митохондриальной ДНК – mtДНК были записаны таким кодом [13]. Переосмысленными оказались всего 4 кодона. Расчеты показали, что значение p для всех 14 девиантных кодов не превышает значения 22 или около 5% полного числа пар аминокислот[14], см. Табл.2. При этом запретными оказались все те же самые три случая перекрытий, как и для стандартного кода и кроме того был обнаружен один код с нулевым значением p.Таким образом все природные генетические коды имеют малое число запретов на построение генетических перекрытий. Это может рассматриваться как общее свойство всех природных кодов, известных к настоящему времени. Возникает вопрос: почему природные коды этому соответствуют, в то время как число записей генов с перекрытиями неизмеримо меньше чем обычных неперекрывающихся генов и какова роль переосмысленных кодонов? Оба эти вопроса были решены.

VII. Одна Математическая Аналогия

При решении первого из этих вопросов была установлена важнейшая математическая аналогия между перекрытиями генов из разных цепей ДНК и важнейшими структурными единицами. Как известно, ген считывается с ДНК, происходит в его тексте множественная модификация нуклеотидов T на U (урацил) и образуется матричная РНК, которая в свою очередь структурируется. Важнейшими элементами такой структуры являются стебли – фрагменты, содержащие связи подобные связям в ДНК. На рис. 5 дается один из стеблей самой известной вторичной структуры матричной РНК- RNA MS2 [15], которая содержит более 130 стеблей. Структура была полностью нами проанализирована, и полученные результаты представлены в моей монографии [25].

Ref
13. Barrell B.G., Bankier A.T., Drouin J. A different genetic code in human mitochondria//Nature. – 1979. – V. 282. – P.189-194.

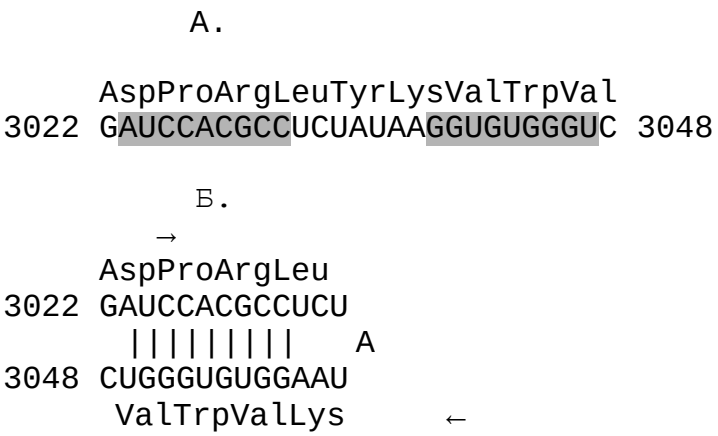

Рис. 5: Стебель вторичной структуры матричной RNA MS2. Вверху (А) дан линейный текст – это фрагмент в диапазоне 3022-3048. а заштрихованные участки соответствуют стеблям вторичной структуры. Под текстом (Б) указан фрагмент вторичной структуры. Показано присутствие неканонической пары GU (они были обнаружен экспериментально в структурах РНК), помимо канонической CG в ДНК, и аналога канонической -AU

На рис.5 изображен один стебель этой вторичной структуры (Б), представлен также фрагмент А, в диапазоне 3022-3048 первичной структуры в стилистике процитированной статьи. Однако во фрагменте Б, дана запись не только нуклеотидов, но и соответствующих аминокислот согласно А. Стебель из рис.5Б соответствует перекрытию фрагментов как будто бы взятых из разных цепей ДНК. Направление чтения на стебле Б (стрелки) становится различным и этот фрагмент вторичной структуры эквивалентен перекрытию заштрихованных в А участков, взятых из разных цепей ДНК (случай перекрытия 4). Однако здесь нет никаких разных цепей. Этот эффект - поворот исходного направления чтения (→) (нижняя строка рис. 5Б (←)) обусловлен присутствием, так называемой шпилечной петли UCUAUAA – последовательность не входящую в стебель.

Какова же роль малости первой характеристики p? Дело в том, что ее малое значение позволяет строить феноменальное разнообразие генетических перекрытий генов, и тем самым это позволяет строить феноменальное разнообразие вторичных структур, в том числе также функционально значимые участки вторичных структур мРНК для всех генов, записанных как стандартным, так и любым из известных девиантных кодов. Увеличение указанной характеристики для кода, отклоненного от стандартного (например, на порядок, как это было показано для гипотетического кода из монографии), приводит к значительному сокращению такого разнообразия. Тем самым установлено, что малое значение p выполняет две функции: позволяет строить как феноменальное множество генетических перекрытий, так и феноменальное разнообразие вторичных структур матричных РНК для всех генов.

VIII. О Роли Переосмысленных Кодонов

Рассмотрим теперь вопрос о роли переосмысленных кодонов. Нами был поставлен вопрос о возможной взаимосвязи ограничений на перекрываемость (2)-(4) с вариабельностью кода, наблюдаемой у ряда организмов. Анализ показал, что такая взаимосвязь существует, и она выражается в том, что для ряда девиантных кодов (примеры для некоторых из них, обнаруженных в митохондриальных ДНК, представлены на рис.6), природные переосмысления кодонов приводят к возможности построения генетических перекрытий, запретных для стандартного кода.

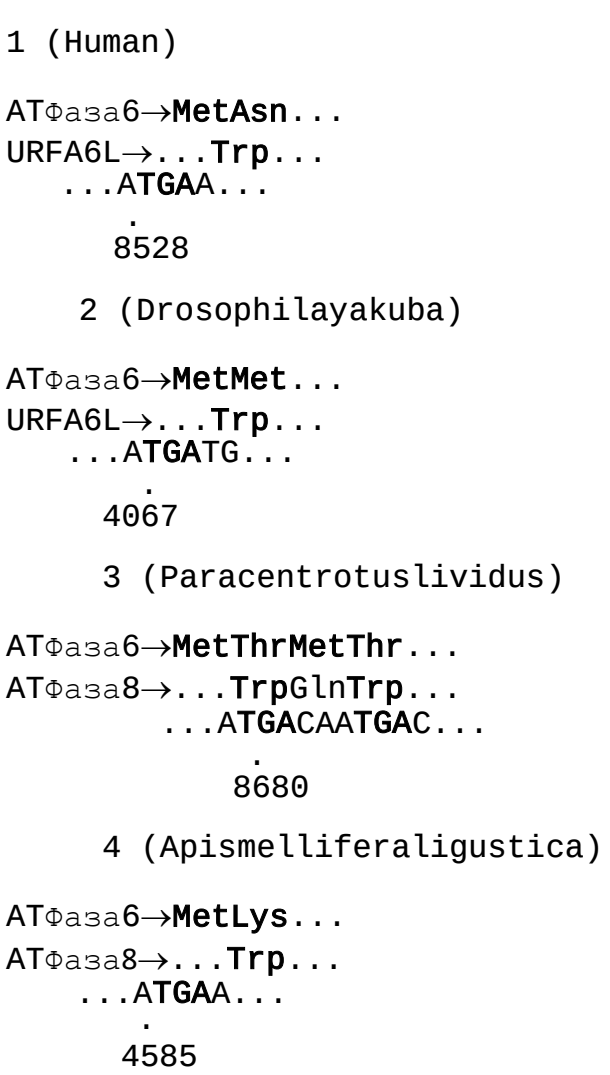

Рис. 6: Фрагменты генетических перекрытий, обнаруженные в митохондриях четырех организмов, гены которых записаны кодами, отклоненными от кода стандартного. Это перекрытия в одной цепи ДНК. Фрагменты и названия белков даны по публикациям[16]-[19]. Число под нуклеотидом указывает его номер в геноме

В каждом из четырех фрагментов перекрытий, приведенных на рис. 3 показана роль одной и той же перестановки: TGA(ter)→Trp. Эта природная перестановка наблюдается для трех девиантных кодов, которым соответствуют приведенные фрагменты соответственно; второй и четвертый фрагмент записаны одним и тем же

Ref

19. Crozier R.H., Crozier Y.C. The Mitochondrial Genome of the Honeybee Apis mellifera: Complete Sequence and Genome Organization // Genetics. – 1993. – V.133 – P.97 – 117.

Notes

девиантным кодом. Причем указанная перестановка присутствует во всех трех девиантных кодах. Оказалось, что такая перестановка делает возможными перекрытия для пар MetAsn (рис.6.1, этот случай соответствует ДНК митохондрии человека), MetMet (рис.6.2), дважды MetThr (рис.6.3) и MetLys, которые являются запретными для стандартного кода, см. (2) Указанные пары нуклеотидов и переосмысленные кодоны выделены. Тем самым размер геномов сокращается за счет возможности построения перекрытий генов, которые невозможны для стандартного кода. Такое сокращение для живой клетки может быть достаточно большим, т.к. число митохондрий, как правило, больше 1 и может достигать миллиона. Проведенное исследование процитировано не менее 100 раз (см файл 300 citation).

Полученные результаты позволили обратиться к анализу экспериментальных данных по всем девиантным генетическим кодам, или кодам, отклоненным от кода стандартного. Однако в рамках генетических перекрытий мне не удалось объяснить функциональную значимость всех переосмысленных кодонов во всех девиантных кодах. Требуемое решение было найдено при исследовании областей ДНК, где гены не перекрываются, а таких генов – подавляющее большинство.

IX. О Двух Интегральных Характеристиках Кода

Речь идет о природной блокировке генов, когда все 5 последовательностей кодонов, альтернативных последовательности гена ли рамок считывания - РС, содержат многократные остановки синтеза белка, или кодоны из набора (1). На рис.7 это показано для участка гена. См.также ранний упрощенный рис.2.

```
ОРС0        MetSerIleLysLeuSerTyrArgGluSerPheSerIleLeuGluGluVal…

БРС1 (-1) TyrGluHis * Thr * Leu * ArgValIle * TyrIleArgGlyGly…

БРС2 (+1)     * AlaLeuAsnLeuValIleGluSerHisLeuValTyr * ArgArgPhe…

→          TATGAGCATTAAACTTAGTTATAGAGAGTCATTTAGTATATTAGAGGAGGTTTA…
←          ATACTCGTAATTTGAATCAATATCTCTCAGTAAATCATATAATCTCCTCCAAAT…

БРС3 (-1) IleLeuMetLeuSerLeu * LeuSerAspAsnLeuIleAsnSerSerThr …

БРС4 (0)   HisAlaAsnPheLysThrIleSerLeu * LysThrTyr * LeuLeuAsn…

БРС5 (+1)   SerCys * Val * AsnTyrLeuThrMet * TyrIleLeuProProLys…
```

Рис. 7: Шесть РС для фрагмента гена (начало с кодона ATG(Met), направление чтения указано стрелкой → из которых одна РС является открытой – ОРСО (в ней 17 смысловых кодонов), а 5 РС – альтернативные РС являются блокированными: БРС1-БРС5. При этом БРС3-БРС5 соответствуют другой цепи ДНК и чтение последовательностей кодонов осуществляется в обратном направлении (←). В скобках указан сдвиг в нуклеотидах относительно ОРСО. Символом * были обозначены каждый из трех кодонов ter из (1)

Установлен потенциал такой блокировки для стандартного генетического кода: было показано, что для такого кода в процессе блокировки участвуют лишь не более 210 пар аминокислот из 400 возможных. Показано также, что 31 пара из них дает неизбежные блокировки, которые имеют место при любых кодировках аминокислот, содержащихся в этих парах. Тем самым была введена в рассмотрение вторая интегральная характеристика генетического кода [20] содержащая две компоненты:

$$q: \quad q_{min}=31, \qquad q_{max}=210 \tag{6}$$

С учетом этого, помимо неизбежных, были введены в рассмотрение возможные блокировки, возникающие для ограниченного числа кодировок; эти блокировки - главная составляющая 210 блокировок, куда включены также 31 неизбежная блокировка.

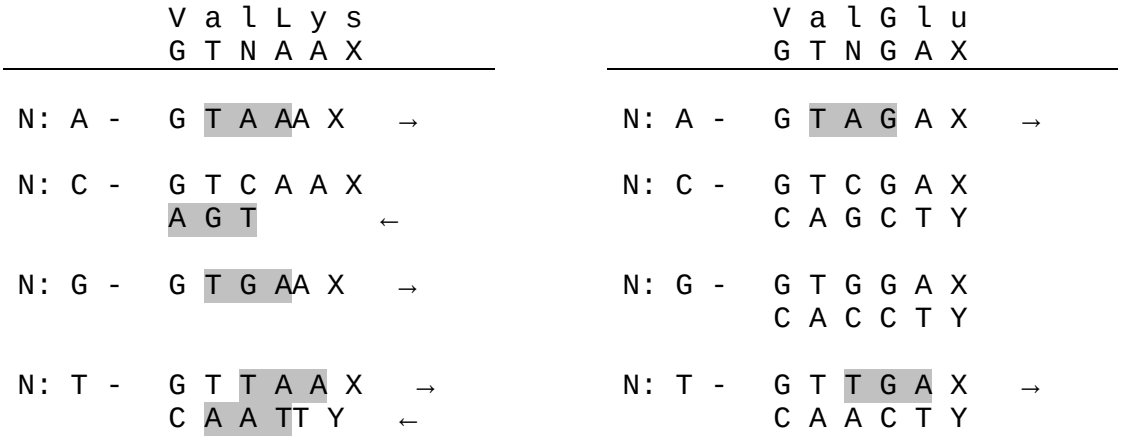

Рис. 8: Неизбежные блокировки для пары аминокислот ValLys (слева) и воз-можные блокировки для пары аминокислот ValGlu (справа). Кодоны ter из (1) заштрихованы. Стрелки указывают направление чтения. Полный перечень неизбежных блокировок представлен в табл.3

Таб 3: Полный перечень пар аминокислот, вызывающих неизбежную блокировку (столбец 1), с указанием номеров РС, которые блокируются (столбец 2)

№	1	2	№	1	2
1	MetMet	2	17	IleMet	2,5
2	MetAsn	2	18	ValMet	2,5
3	MetLys	2	19	LeuMet	2,4,5
4	MetIle	2	20	IleAsn	1,2,5
5	MetThr	2	21	ValAsn	1,2,5
6	PheTyr	3	22	LeuAsn	1,2,4,5
7	TyrTyr	3	23	IleLys	1,2,5
8	HisTyr	3	24	ValLys	1,2,5
9	AsnTyr	3	25	LeuLys	1,2,4,5
10	AspTyr	3	26	IleIle	2,5
11	CysTyr	3	27	ValIle	2,5
12	PheMet	5	28	LeuIle	2,4,5
13	PheAsn	1,5	29	IleThr	2,5
14	PheLys	1,5	30	ValThr	2,5
15	PheIle	5	31	LeuThr	2,4,5
16	PheThr	5			

Ref
20. Козлов Н.Н. Интегральные характеристики генетического кода. Математическое моделирование,т.22.№9.С.51-66.,2010.; анг.пер.: N.N. Kozlov. Integral characteristics of genetic code.Mathematical Models and Computer Simulations April 2011, Volume 3, Issue 2, pp 123-134.

В столбце 2 этой таблицы указываются номера РС для которых (потенциально) может иметь место блокировка. Число таких РС, в зависимости от пары, меняется от 1 до 4. Представим множество этих пар в виде двух подмножеств. К первому отнесем пары неизбежно блокирующие одну и ту же РС. Таких пар оказалось всего 16- это первые 16 пар из табл.3. Имеем РС2 неизбежно блокируют 5 пар аминокислот, которые совпадают с набором (2), определенным выше, поскольку в РС2 образуется кодон ter – TGA. Для РС3 имеем 6 блокирующих пар, совпадающих с набором (3), а в РС3 образуется один из кодонов ter: TAA или TAG.Особо следует сказать о блокировке для 5-и пар с номерами 12-16, которые совпадают с парами из (4), определенные выше..Отметим лишь, что каждая из этих последних пар неизбежно блокирует РС5, поскольку в РС5 образуется один из кодонов ter: TAA или TGA .Однако в парах PheAsn, PheLys помимо РС5 в табл.3 указывается также РС1. Однако последняя РС не соответствует неизбежной блокировке в отличие от РС5. Таким образом, пары 1-16 из табл.3 образуют набор пар аминокислот, запретных для перекрытий двух генов и были установлены выше. На основе п.2 была введена в рассмотрение числовая характеристика, которая была обозначена буквой p, и которая соответствует числу различающихся блокировочных пар из (2)-(4), имеем значение p из (5.) Тем самым использование подмножества неизбежных блокировок позволяет установить связь изучаемых характеристик: имеет место неравенство:

$$0 \le p \le q_{\min} \qquad (7)$$

Иными словами интегральная характеристика генетического кода p не является независимой, а определяется выбором характеристики $q_{\min,}$ которая используется в решении совершенно другой задачи – в блокировке не перекрывающихся генов.

При рассмотрении только одной задачи – перекрывания пар генов можно было бы сделать вывод о том, что генетический код был «выбран¸ под перекрытия генов, поскольку только 16 пар из 400 возможных запретны для перекрытий. Это справедливо для всех 5 способов парных перекрытий генов, разрешенных структурой ДНК. Однако, при рассмотрении двух задач и двух интегральных характеристик p и q оказалось, с учетом связи (7), что генетический код был ориентирован на «выбор¸ двухкомпонентной интегральной характеристики (6), одна из компонент которой согласно неравенству (7) определяет область значения другой интегральной характеристики p. Таким образом, малость интегральной характеристики p является следствием более общего принципа, связанного с выбором всего набора неизбежных пар аминокислот, создающих блокировки. Т.е. пары аминокислот соответствующие характеристике p могут быть «выбраны¸ только из этого ограниченного набора соответствующего $q_{\min}$, а не из полного набора 400 пар аминокислот. По какому критерию произошел предполагаемый «выбор¸ генетического кода пока остается неясным.

В связи с анализом задачи о блокировках, нами были исследованы ряд геномов с общим числом генов более 200 000. Рассказ об этой работе требует отдельного рассмотрения, более подробный анализ представлен в [21]. Отметим лишь один

Ref

21. Н.Н. Козлов. О некоторых новых характеристиках больших геномов. Математическое моделирование, т. 24, № 10.С.98-108, 2012.; англ. пер.: N.N. Kozlov. Some New Characteristics of Large Genomes Mathematical Models and Computer Simulations 2013, Volume 5, Issue 3, pp 220-228.

результат, полученный для генома человека. Из 25613 генов в этом геноме три гена вовсе не содержат никаких блокировок: Для каждого из них рисунки аналогичные рис.8 не содержат ни одного кодона терминации, ни в одной из пяти альтернативных РС. Это гены MT1G и MT1M из хромосомы 16 и KLK8 из хромосомы 19 (см. рис.9).

Рис. 9: Ген KLK8 из человеческого генома и 5 альтернативных РС. Каждая из этих РС не содержит ни одного кодона терминации.(сравни с рис.8)

В связи с полученным результатом было выдвинуто ряд гипотез, из которых простейшая – это не что иное, как случаи перекрытий 6 генов.

X. Математический Анализ Девиантности Кода

Задача исследования блокировок для девиантных кодов позволила завершить анализ одной из важнейших фундаментальных проблем, связанных с ролью всех переосмысленных кодонов. Данные были получены для mtДНК двух организмов: H.Sapiens (код K^1) и A.Mellifera (код K^2) .Обратимся к Табл.4.

Таб 4: Сводная таблица участия переосмысленных кодонов в двух функциях: в блокировке (в столбце 1 знак + соответствует участию, знак− неучастию), либо в гене - тическом перекрытии (столбец 2). Данные были получены для mtДНК двух организмов: H.Sapiens (код K^1) и A.Mellifera (код K^2). Переосмысленные кодоны ука заны в столбце: отклонения от стандартного кода

Организм	Отклонения от стандартного кода	1	2
H.Sapiens (K^1)	ATA(Ile)→Met	+	−
	TGA(ter)→Trp	+	+
	AGA(Arg)→ter	+	−
	AGG(Arg)→ter	+	−
A.Mellifera (K^2)	ATA(Ile)→Met	+	+
	TGA(ter)→Trp	−	+
	AGA(Arg)→Ser	+	−
	AGG(Arg)→Ser	+	−

Из таблицы следует, что для mtДНК H.Sapiens(K^1) имеет место участие всех переосмысленных кодонов(ATA(Ile)→Met, TGA(ter)→Trp, AGA(Arg)→ter, AGG(Arg)→ter) в процессе блокировки, а также переосмысленный кодон TGA(ter)→Trp участвует кроме того и в перекрытии генов, запретном для стандартного кода. Для mtДНК A.Mellifera (K^2) в процессе блокировки участвуют все переосмысленные кодоны (AGA(Arg)→Ser, AGG(Arg)→Ser, ATA(Ile)→Met), кроме того в перекрытиях участвуют два подобных кодона: TGA(ter)→Trp и ATA(Ile)→Met. Тем самым нами показано, что все переосмысленные кодоны в каждом из указанных двух девиантных кодов были использованы либо в процессе блокировки, либо в процессе перекрытий генов (разумеется, запрещенных для стандартного кода), либо и в том и другом процессах.

XI. Произволен Ли Код?

Полученные результаты приводит к тому выводу, что отклонения кода от стандартного не носит случайного характера, а несут совершенно четкую функциональную нагрузку (ср. «Переосмысление кодонов указывают на то, что в генетическом коде митохондрий могут происходить случайные перемены¸, см. [22]. В последней монографии также читаем «The code seem to have been selected arbitrarile[22]…¸ («Код, по-видимому, был «выбран¸ произвольно…¸). Из приведенных результатов следует, возможность для всех смысловых кодонных семейств, практически беспрепятственно записывать две белковые последовательности одним и тем же участком ДНК, причем для этого может быть использован наиболее благоприятный (по сочетанию аминокислот в перекрытии) один из 5-и вариантов такой компактной записи генов (5 случаев перекрытий). Категорический запрет существует не более чем для около 5% пар аминокислот, как для стандартного кода, так и для всех 14-и известных на сегодня нестандартных кодов. Т.е. 15 таблиц кодов удовлетворяют одному и тому же общему свойству. Это не оставляет никаких шансов для какой-либо произвольности, случайности.

XII. О Множествах Элементарных Перекрытий

Основные рабочие множества в данной теории – это множества элементарных генетических перекрытий, полностью представленные в Приложении. Элементарные перекрытия- это перекрытия по одиночным аминокислотам. Такие множества многократно использовались в ходе построения данной теории. Прежде всего-в доказательстве теоремы для генетического кода и далее эти множества были модифицированы 14 раз (по числу девиантных кодов) для получения первой интегральной характеристики этих 14 кодов, которые представлены на рис.2. Важнейший этап исследований был связан с математическим анализом неоднозначностей в этих множествах Компонентами исследуемого множества являются элементарные генетические перекрытия– это перекрытия для одиночных аминокислот. Анализ показал, что множество содержат особенности, которые были названы неоднозначностями. Исследуемые неоднозначности, соответствуют случаям, когда для одной и той же пары аминокислот имеет место более одного элементарного

Ref

22. Alberts, B., Bray, D., Lewis, J., Raff, M., Roberts, K., Watson, J., Molecular Biology of the Cell. //- New Jork, London: Gorland Publishing, Inc., 1994. 1294p.

перекрытия. Как и всякие особые случаи в математике этот феномен привлек наше пристальное внимание. Принципиально важно, что полученные результаты применимы для всего многообразия живой природы, белки которой записаны практически одним и тем же генетическим кодом. Анализ показал, что неоднозначности имеют место только для случаев перекрытий генов, принадлежащих различным цепям ДНК. Число неоднозначных элементарных перекрытий оказалось относительно небольшим–всего 6. Проведенное исследование позволило выявить три функции возможного использования указанных неоднозначностей. Этих функций оказалось три [23]. Одна из функций неоднозначностей исследовалась в новой модели, предложенной ране автором. Она состоит в том, что перекрытия пар генов, принадлежащие различным цепям ДНК, являются математическими аналогами стеблей вторичной структуры матричной РНК. Показывается, что за счет неоднозначности можно «регулировать¸ величину свободной энергии стебля функционально значимую биохимическую характеристику [24]. Теперь о других двух характеристиках согласно [23]. Первая из них связана с решением задачи о потенциальных позициях молчащих мутаций для случаев перекрытий генов, принадлежащих различным цепям ДНК. Вторая связана с расширением возможности построения множеств генетических перекрытий более двух генов; анализируются структуры возможных перекрытий 6-и генов в геноме человека.

Изучение пространственной структуры ДНК показало, что кроме трех семейств форм двойных спиралей с антипараллельной ориентацией нитей возможно образование двойных спиралей ДНК с параллельной взаимной ориентацией нитей. Математический анализ подобных случаев представлен в п.4.4 из [25], где были проанализированы все три новых случая перекрытий пар генов.

XIII. Заключение

На основе построенной теории была решена одна из прорывных задач - задача расчета генетического кода. Подобные задачи в мире неизвестны и могли быть поставлены только в 21 веке. Один из подходов к решению этой задачи дается в статье [26]. Впервые представлено подробное описание метода расчета генетического кода, идея которого впервые опубликована ранее, а выбор одного из главных множеств для расчетов опирался на статью. Такое множество соответствует полному набору аминокислотных представлений из множества тройных перекрытий генов, принадлежащих одной и той же цепи ДНК. Отдельный вопрос был связан с начальным приближением, запускающим итерационный процесс поиска всех кодов по представленным начальным данным. Математический анализ показал, что указанное множество содержит некоторые неоднозначности, которые были установлены на основе предложенного нами сжатого представления множества. В итоге разработанный метод расчета сводился к двум главным этапам исследований, где на первом этапе в расчетах были использованы только области однозначности. Предложенный подход позволил значительно сократить объем вычислений на каждом шаге в этой сложнейшей дискретной структуре. Математическая теория генетического кода непрерывно развивается. Укажем на последние две работы в этом направлении. Первая относится к анализу потенциала генетического кода для построения перекрытий шести генов [27].

Вторая связана с проведенным математическим анализом, который позволил сформулировать свойство тройки терминаторных кодонов стандартного генетического кода, при сравнении с другими теоретически возможными тройками [28].

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The ' MARSS ' title is accorded to a selected professional after the approval of the Editor-in-Chief / Editorial Board Members/Dean.

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MARSS designated members are entitled to avail a 25% discount while publishing their research papers (of a single author) in Global Journals Inc., if the same is accepted by our Editorial Board and Peer Reviewers. If you are a main author or co-author of a group of authors, you will get discount of 10%.

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We shall provide you intimation regarding launching of e-version of journal of your stream time to time.This may be utilized in your library for the enrichment of knowledge of your students as well as it can also be helpful for the concerned faculty members.

The MARSS member can apply for approval, grading and certification of standards of their educational and Institutional Degrees to Open Association of Research, Society U.S.A.

Once you are designated as MARSS, you may send us a scanned copy of all of your credentials. OARS will verify, grade and certify them. This will be based on your academic records, quality of research papers published by you, and some more criteria.

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AUXILIARY MEMBERSHIPS

Institutional Fellow of Global Journals Incorporation (USA)-OARS (USA)

Global Journals Incorporation (USA) is accredited by Open Association of Research Society, U.S.A (OARS) and in turn, affiliates research institutions as "Institutional Fellow of Open Association of Research Society" (IFOARS).

The "FARSC" is a dignified title which is accorded to a person's name viz. Dr. John E. Hall, Ph.D., FARSC or William Walldroff, M.S., FARSC.

The IFOARS institution is entitled to form a Board comprised of one Chairperson and three to five board members preferably from different streams. The Board will be recognized as "Institutional Board of Open Association of Research Society"-(IBOARS).

The Institute will be entitled to following benefits:

The IBOARS can initially review research papers of their institute and recommend them to publish with respective journal of Global Journals. It can also review the papers of other institutions after obtaining our consent. The second review will be done by peer reviewer of Global Journals Incorporation (USA) The Board is at liberty to appoint a peer reviewer with the approval of chairperson after consulting us.

The author fees of such paper may be waived off up to 40%.

The Global Journals Incorporation (USA) at its discretion can also refer double blind peer reviewed paper at their end to the board for the verification and to get recommendation for final stage of acceptance of publication.

The IBOARS can organize symposium/seminar/conference in their country on behalf of Global Journals Incorporation (USA)-OARS (USA). The terms and conditions can be discussed separately.

The Board can also play vital role by exploring and giving valuable suggestions regarding the Standards of "Open Association of Research Society, U.S.A (OARS)" so that proper amendment can take place for the benefit of entire research community. We shall provide details of particular standard only on receipt of request from the Board.

The board members can also join us as Individual Fellow with 40% discount on total fees applicable to Individual Fellow. They will be entitled to avail all the benefits as declared. Please visit Individual Fellow-sub menu of GlobalJournals.org to have more relevant details.

We shall provide you intimation regarding launching of e-version of journal of your stream time to time. This may be utilized in your library for the enrichment of knowledge of your students as well as it can also be helpful for the concerned faculty members.

After nomination of your institution as "Institutional Fellow" and constantly functioning successfully for one year, we can consider giving recognition to your institute to function as Regional/Zonal office on our behalf.
The board can also take up the additional allied activities for betterment after our consultation.

The following entitlements are applicable to individual Fellows:

Open Association of Research Society, U.S.A (OARS) By-laws states that an individual Fellow may use the designations as applicable, or the corresponding initials. The Credentials of individual Fellow and Associate designations signify that the individual has gained knowledge of the fundamental concepts. One is magnanimous and proficient in an expertise course covering the professional code of conduct, and follows recognized standards of practice.

Open Association of Research Society (US)/ Global Journals Incorporation (USA), as described in Corporate Statements, are educational, research publishing and professional membership organizations. Achieving our individual Fellow or Associate status is based mainly on meeting stated educational research requirements.

Disbursement of 40% Royalty earned through Global Journals : Researcher = 50%, Peer Reviewer = 37.50%, Institution = 12.50% E.g. Out of 40%, the 20% benefit should be passed on to researcher, 15 % benefit towards remuneration should be given to a reviewer and remaining 5% is to be retained by the institution.

We shall provide print version of 12 issues of any three journals [as per your requirement] out of our 38 journals worth $ 2376 USD.

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The individual Fellow and Associate designations accredited by Open Association of Research Society (US) credentials signify guarantees following achievements:

- The professional accredited with Fellow honor, is entitled to various benefits viz. name, fame, honor, regular flow of income, secured bright future, social status etc.

- In addition to above, if one is single author, then entitled to 40% discount on publishing research paper and can get 10%discount if one is co-author or main author among group of authors.
- The Fellow can organize symposium/seminar/conference on behalf of Global Journals Incorporation (USA) and he/she can also attend the same organized by other institutes on behalf of Global Journals.
- The Fellow can become member of Editorial Board Member after completing 3yrs.
- The Fellow can earn 60% of sales proceeds from the sale of reference/review books/literature/publishing of research paper.
- Fellow can also join as paid peer reviewer and earn 15% remuneration of author charges and can also get an opportunity to join as member of the Editorial Board of Global Journals Incorporation (USA)
- • This individual has learned the basic methods of applying those concepts and techniques to common challenging situations. This individual has further demonstrated an in–depth understanding of the application of suitable techniques to a particular area of research practice.

Note :

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- In future, if the board feels the necessity to change any board member, the same can be done with the consent of the chairperson along with anyone board member without our approval.
- In case, the chairperson needs to be replaced then consent of 2/3rd board members are required and they are also required to jointly pass the resolution copy of which should be sent to us. In such case, it will be compulsory to obtain our approval before replacement.
- In case of "Difference of Opinion [if any]" among the Board members, our decision will be final and binding to everyone.

"

Preferred Author Guidelines

We accept the manuscript submissions in any standard (generic) format.

We typeset manuscripts using advanced typesetting tools like Adobe In Design, CorelDraw, TeXnicCenter, and TeXStudio. We usually recommend authors submit their research using any standard format they are comfortable with, and let Global Journals do the rest.

Alternatively, you can download our basic template from https://globaljournals.org/Template.zip

Authors should submit their complete paper/article, including text illustrations, graphics, conclusions, artwork, and tables. Authors who are not able to submit manuscript using the form above can email the manuscript department at submit@globaljournals.org or get in touch with chiefeditor@globaljournals.org if they wish to send the abstract before submission.

Before and during Submission

Authors must ensure the information provided during the submission of a paper is authentic. Please go through the following checklist before submitting:

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2. Authors must accept the privacy policy, terms, and conditions of Global Journals.
3. Ensure corresponding author's email address and postal address are accurate and reachable.
4. Manuscript to be submitted must include keywords, an abstract, a paper title, co-author(s') names and details (email address, name, phone number, and institution), figures and illustrations in vector format including appropriate captions, tables, including titles and footnotes, a conclusion, results, acknowledgments and references.
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7. Manuscript submitted *must not have been submitted or published elsewhere* and all authors must be aware of the submission.

Declaration of Conflicts of Interest

It is required for authors to declare all financial, institutional, and personal relationships with other individuals and organizations that could influence (bias) their research.

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- Findings
- Writings
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- Graphs
- Illustrations
- Lectures

- Printed material
- Graphic representations
- Computer programs
- Electronic material
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2. Drafting the paper and revising it critically regarding important academic content.
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The corresponding author should mention the name and complete details of all co-authors during submission and in manuscript. We support addition, rearrangement, manipulation, and deletions in authors list till the early view publication of the journal. We expect that corresponding author will notify all co-authors of submission. We follow COPE guidelines for changes in authorship.

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Unless specified in the notification, the Editorial Board's decision on publication of the paper is final and cannot be appealed before making the major change in the manuscript.

Acknowledgments

Contributors to the research other than authors credited should be mentioned in Acknowledgments. The source of funding for the research can be included. Suppliers of resources may be mentioned along with their addresses.

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Authors can submit papers and articles in an acceptable file format: MS Word (doc, docx), LaTeX (.tex, .zip or .rar including all of your files), Adobe PDF (.pdf), rich text format (.rtf), simple text document (.txt), Open Document Text (.odt), and Apple Pages (.pages). Our professional layout editors will format the entire paper according to our official guidelines. This is one of the highlights of publishing with Global Journals—authors should not be concerned about the formatting of their paper. Global Journals accepts articles and manuscripts in every major language, be it Spanish, Chinese, Japanese, Portuguese, Russian, French, German, Dutch, Italian, Greek, or any other national language, but the title, subtitle, and abstract should be in English. This will facilitate indexing and the pre-peer review process.

The following is the official style and template developed for publication of a research paper. Authors are not required to follow this style during the submission of the paper. It is just for reference purposes.

Manuscript Style Instruction (Optional)

- Microsoft Word Document Setting Instructions.
- Font type of all text should be Swis721 Lt BT.
- Page size: 8.27" x 11'", left margin: 0.65, right margin: 0.65, bottom margin: 0.75.
- Paper title should be in one column of font size 24.
- Author name in font size of 11 in one column.
- Abstract: font size 9 with the word "Abstract" in bold italics.
- Main text: font size 10 with two justified columns.
- Two columns with equal column width of 3.38 and spacing of 0.2.
- First character must be three lines drop-capped.
- The paragraph before spacing of 1 pt and after of 0 pt.
- Line spacing of 1 pt.
- Large images must be in one column.
- The names of first main headings (Heading 1) must be in Roman font, capital letters, and font size of 10.
- The names of second main headings (Heading 2) must not include numbers and must be in italics with a font size of 10.

Structure and Format of Manuscript

The recommended size of an original research paper is under 15,000 words and review papers under 7,000 words. Research articles should be less than 10,000 words. Research papers are usually longer than review papers. Review papers are reports of significant research (typically less than 7,000 words, including tables, figures, and references)

A research paper must include:

a) A title which should be relevant to the theme of the paper.
b) A summary, known as an abstract (less than 150 words), containing the major results and conclusions.
c) Up to 10 keywords that precisely identify the paper's subject, purpose, and focus.
d) An introduction, giving fundamental background objectives.
e) Resources and techniques with sufficient complete experimental details (wherever possible by reference) to permit repetition, sources of information must be given, and numerical methods must be specified by reference.
f) Results which should be presented concisely by well-designed tables and figures.
g) Suitable statistical data should also be given.
h) All data must have been gathered with attention to numerical detail in the planning stage.

Design has been recognized to be essential to experiments for a considerable time, and the editor has decided that any paper that appears not to have adequate numerical treatments of the data will be returned unrefereed.

i) Discussion should cover implications and consequences and not just recapitulate the results; conclusions should also be summarized.
j) There should be brief acknowledgments.
k) There ought to be references in the conventional format. Global Journals recommends APA format.

Authors should carefully consider the preparation of papers to ensure that they communicate effectively. Papers are much more likely to be accepted if they are carefully designed and laid out, contain few or no errors, are summarizing, and follow instructions. They will also be published with much fewer delays than those that require much technical and editorial correction.

The Editorial Board reserves the right to make literary corrections and suggestions to improve brevity.

Format Structure

It is necessary that authors take care in submitting a manuscript that is written in simple language and adheres to published guidelines.

All manuscripts submitted to Global Journals should include:

Title

The title page must carry an informative title that reflects the content, a running title (less than 45 characters together with spaces), names of the authors and co-authors, and the place(s) where the work was carried out.

Author details

The full postal address of any related author(s) must be specified.

Abstract

The abstract is the foundation of the research paper. It should be clear and concise and must contain the objective of the paper and inferences drawn. It is advised to not include big mathematical equations or complicated jargon.

Many researchers searching for information online will use search engines such as Google, Yahoo or others. By optimizing your paper for search engines, you will amplify the chance of someone finding it. In turn, this will make it more likely to be viewed and cited in further works. Global Journals has compiled these guidelines to facilitate you to maximize the web-friendliness of the most public part of your paper.

Keywords

A major lynchpin of research work for the writing of research papers is the keyword search, which one will employ to find both library and internet resources. Up to eleven keywords or very brief phrases have to be given to help data retrieval, mining, and indexing.

One must be persistent and creative in using keywords. An effective keyword search requires a strategy: planning of a list of possible keywords and phrases to try.

Choice of the main keywords is the first tool of writing a research paper. Research paper writing is an art. Keyword search should be as strategic as possible.

One should start brainstorming lists of potential keywords before even beginning searching. Think about the most important concepts related to research work. Ask, "What words would a source have to include to be truly valuable in a research paper?" Then consider synonyms for the important words.

It may take the discovery of only one important paper to steer in the right keyword direction because, in most databases, the keywords under which a research paper is abstracted are listed with the paper.

Numerical Methods

Numerical methods used should be transparent and, where appropriate, supported by references.

Abbreviations

Authors must list all the abbreviations used in the paper at the end of the paper or in a separate table before using them.

Formulas and equations

Authors are advised to submit any mathematical equation using either MathJax, KaTeX, or LaTeX, or in a very high-quality image.

Tables, Figures, and Figure Legends

Tables: Tables should be cautiously designed, uncrowned, and include only essential data. Each must have an Arabic number, e.g., Table 4, a self-explanatory caption, and be on a separate sheet. Authors must submit tables in an editable format and not as images. References to these tables (if any) must be mentioned accurately.

Figures

Figures are supposed to be submitted as separate files. Always include a citation in the text for each figure using Arabic numbers, e.g., Fig. 4. Artwork must be submitted online in vector electronic form or by emailing it.

Preparation of Eletronic Figures for Publication

Although low-quality images are sufficient for review purposes, print publication requires high-quality images to prevent the final product being blurred or fuzzy. Submit (possibly by e-mail) EPS (line art) or TIFF (halftone/ photographs) files only. MS PowerPoint and Word Graphics are unsuitable for printed pictures. Avoid using pixel-oriented software. Scans (TIFF only) should have a resolution of at least 350 dpi (halftone) or 700 to 1100 dpi (line drawings). Please give the data for figures in black and white or submit a Color Work Agreement form. EPS files must be saved with fonts embedded (and with a TIFF preview, if possible).

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Tips for Writing a Good Quality Science Frontier Research Paper

Techniques for writing a good quality Science Frontier Research paper:

1. Choosing the topic: In most cases, the topic is selected by the interests of the author, but it can also be suggested by the guides. You can have several topics, and then judge which you are most comfortable with. This may be done by asking several questions of yourself, like "Will I be able to carry out a search in this area? Will I find all necessary resources to accomplish the search? Will I be able to find all information in this field area?" If the answer to this type of question is "yes," then you ought to choose that topic. In most cases, you may have to conduct surveys and visit several places. Also, you might have to do a lot of work to find all the rises and falls of the various data on that subject. Sometimes, detailed information plays a vital role, instead of short information. Evaluators are human: The first thing to remember is that evaluators are also human beings. They are not only meant for rejecting a paper. They are here to evaluate your paper. So present your best aspect.

2. Think like evaluators: If you are in confusion or getting demotivated because your paper may not be accepted by the evaluators, then think, and try to evaluate your paper like an evaluator. Try to understand what an evaluator wants in your research paper, and you will automatically have your answer. Make blueprints of paper: The outline is the plan or framework that will help you to arrange your thoughts. It will make your paper logical. But remember that all points of your outline must be related to the topic you have chosen.

3. Ask your guides: If you are having any difficulty with your research, then do not hesitate to share your difficulty with your guide (if you have one). They will surely help you out and resolve your doubts. If you can't clarify what exactly you require for your work, then ask your supervisor to help you with an alternative. He or she might also provide you with a list of essential readings.

4. Use of computer is recommended: As you are doing research in the field of science frontier then this point is quite obvious. Use right software: Always use good quality software packages. If you are not capable of judging good software, then you can lose the quality of your paper unknowingly. There are various programs available to help you which you can get through the internet.

5. Use the internet for help: An excellent start for your paper is using Google. It is a wondrous search engine, where you can have your doubts resolved. You may also read some answers for the frequent question of how to write your research paper or find a model research paper. You can download books from the internet. If you have all the required books, place importance on reading, selecting, and analyzing the specified information. Then sketch out your research paper. Use big pictures: You may use encyclopedias like Wikipedia to get pictures with the best resolution. At Global Journals, you should strictly follow here.

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7. Revise what you wrote: When you write anything, always read it, summarize it, and then finalize it.

8. Make every effort: Make every effort to mention what you are going to write in your paper. That means always have a good start. Try to mention everything in the introduction—what is the need for a particular research paper. Polish your work with good writing skills and always give an evaluator what he wants. Make backups: When you are going to do any important thing like making a research paper, you should always have backup copies of it either on your computer or on paper. This protects you from losing any portion of your important data.

9. Produce good diagrams of your own: Always try to include good charts or diagrams in your paper to improve quality. Using several unnecessary diagrams will degrade the quality of your paper by creating a hodgepodge. So always try to include diagrams which were made by you to improve the readability of your paper. Use of direct quotes: When you do research relevant to literature, history, or current affairs, then use of quotes becomes essential, but if the study is relevant to science, use of quotes is not preferable.

10. Use proper verb tense: Use proper verb tenses in your paper. Use past tense to present those events that have happened. Use present tense to indicate events that are going on. Use future tense to indicate events that will happen in the future. Use of wrong tenses will confuse the evaluator. Avoid sentences that are incomplete.

11. Pick a good study spot: Always try to pick a spot for your research which is quiet. Not every spot is good for studying.

12. Know what you know: Always try to know what you know by making objectives, otherwise you will be confused and unable to achieve your target.

13. Use good grammar: Always use good grammar and words that will have a positive impact on the evaluator; use of good vocabulary does not mean using tough words which the evaluator has to find in a dictionary. Do not fragment sentences. Eliminate one-word sentences. Do not ever use a big word when a smaller one would suffice.

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.

- You may propose future guidelines, such as how an experiment might be personalized to accomplish a new idea.
- Give details of all of your remarks as much as possible, focusing on mechanisms.
- 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.
- 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?
- 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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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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