A Survey of the Combinatorial Paraphernalia in Protein Synthesis

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Abstract

Statement of the Problem: *The combinatorial paraphernalia in protein synthesis to be surveyed are multifarious, embracing, phenomena, processes, activities and materials, all characterized by plurality and dissimilarity. The materials usable are phenomenal and must be a set of discrete plural and dissimilar objects, e.g. the RNA four bases of Adenine, Uracil, Guanine, Cytosine (A,U,G,C) for the activity of permutation for building genetic code. Sequences for protein type sequence composition, proliferation and diversification as inherent in protein synthesis.*

Methodology and Theoretical Orientation: *We are in for combinatorics which is the scientific study of the phenomenon of input/output productivity exhibited by a duality of numeral entities as in permutation of specified set (n) of dissimilar discrete plural. Things and selection (r) of them. The Dalina apparatus of Input/Output Multiplicative Replication system equipped with Square Kinematics View Mixing Technique sourced from inchoate Numeration Science literature being developed by this author is in use for the computation of 4 from 4 permutations of RNA four bases, A,U,G,C constituting the 24 quadruplet genetic code as the workforce in protein synthesis.*

Findings: *The combinatorial paraphernalia in protein synthesis identified and surveyed comprise 14 characteristics, 3 materials and 11 processes/operatives.*

Conclusion and Significance: *The relevance of the several identified and surveyed combinatorial paraphernalia in protein synthesis has been demonstrated by the test of agreeability with the working of the Dalina apparatus of Input/Output Multiplicative Replication Combinatorial System using the Square Kinematics View Mixing technique for the computation of permutations of RNA four bases A,U,G,C making up the 24 quadruplet genetic code as the workforce in protein synthesis for the substance of all plants and animals throughout CREATION.*

Introduction

Protein synthesis, with the Reader's Digest Great Encyclopedic Dictionary meaning of synthesis given as putting together of parts or elements to make up complex whole, is a stupendous natural process engaged in protein type composition, protein type proliferation and diversification. The same dictionary gives the meaning of paraphernalia as personal belong; accessories; odds and ends; hence it is the requirement of our topic to identify the personal belongs, accessories and odds and ends of protein synthesis that are combinatorial, that is to say belonging to combinatorics, and get them surveyed; in other words, examined in detail, as the meaning given by our cherished dictionary of reference.

Identification of Paraphernalia

This starts with the imperative of combinatorial, which of course is a derivative of combinatorics. Combinatorial is the pivot of the basis of the paraphernalia and combinatorics is the scientific study of the phenomenon of input/output productivity exhibited for example by a duality of numeral entities as in permutation of specified set (n) and selection (r) arrayed the Dalina input/output mul-

tiplicative replication combinatorial system. The output sequence consists of a specific population of the input set, which can both be calculated and computed in terms of membership of factorial complements in the case of a specified set (n) and selection (r). The population (p) of permutation factorial complements of set (n) and selection (r) is given by the formula nPr, where (n) is the leading factor in tower multiplication and (r) is the number of consecutive decreasing factors in the multiplication array. On the other hand, the membership of the factorial complements population can be computed or shown forth by Square Kinematic View Mixing Technique of three techniques all sourced from Numeration Science and identified by name respectively as Square Kinematics View Mixing (direct method for 4 from 4 only), Successive Collateral Posting (SCP), (indirect method), Solid State View Mixing (direct method).

The principal agent in the phenomenal Dalina input/output multiplicative replication combinatorial system is the input set which must needs be characterized by plurality, discreteness, dissimilarity etc as presented in Table 1, captioned as Roll-call of Combinatorial paraphernalia. Protein synthesis is serviced by this Dalina input/output multiplicative replication system employing Square Kinematics View Mixing technique for computing 4 from 4 permutations of RNA four bases A,U,G,C for the formation of the 24 quadruplet genetic code responsible for protein type composition, diversification and proliferation. With protein type being constituted by any sequence of 20 amino acids, the proliferation and diversification of protein may well be accomplished by the use of one protein type of 20 amino acids sequence as the input set in

our aforementioned combinatorial input/output system. The output sequence would be given by 20 from 20 permutations i.e. 20P20 = 20! = 20 x 19 x 18 … 3 x 2 x 1 = 2 432 902 008 176 640 000 … (i) (a nineteen-digit figure) of units of 20 digits per unit, so very highly proliferated and diversified to meet the enormous demand for protein for sustenance of all plants and animals in terms of the living sector of creation. But how convenient is this unwieldy nineteen digit figure for human intellectual capacity in usage? The all-knowing CREATOR by grace substituted the RNA of four bases A,U,G,C (Adenine, Uracil, Guanine, Cytosine) for the sequence of 20 amino acids as the input set in our favoured input/output system to give 4 from 4 permutation i.e. 4P4 = 4! = 4x3x2x1 = 24 quadruplets only (ii) so by reason of convenience smallness in terms of fewness, equation (ii) product representing the genetic code, is preferred to equation (i) product as combinatorial paraphernalia in protein synthesis. The rest of the identified combinatorial paraphernalia are listed in Table 1 at columns 1, 2 and 3, covering characteristics materials and paraphernalia respectively for the intended survey.

The survey have two-fold bases:
a. One based on the possession of the combinatorial characteristics in Table 1 Column 1 by the identified three materials in Table 1 Column 2; and
b. The other based on the interaction between the identified three combinatorial materials in Table 1 Column 2 and the identified eleven combinatorial processes/operatives in Table 1 Column 3, in protein synthesis.

Table 1: Roll-call of the combinatorial characteristics, materials, processes and operatives as paraphernalia in protein synthesis.

Combinatorial Characteristics		Combinatorial Materials		Combinatorial Process/Operatives	
1	Substantive	1	Set of RNA four bases, A,U,G,C.	1	Dalina Input/Output multiplicative replication combinatorial system
2	Permanence	2	24-quadruplet genetic code	2	Permutation
3	Discrete	3	20 amino acids for protein	3	Alignment of 20 amino acids with four signals
4	Plural			4	Affinity based pairing between 20 of the 24 quadruplet codons of the genetic code and 20 amino acids of protein
5	Dissimilar			5	Auto-sequence replication
6	Compatible			6	Viviparous delivery
7	Motile			7	Monogamous partnership
8	Potency			8	Protein type composition
9	Uniqueness			9	Protein type diversification
10	Integrity			10	Protein type proliferation
11	Visible			11	Protein folding and packaging
12	Distinct			12	
13	Completeness			13	
14	Composite			14	
Column 1		Column 2		Column 3	

The Survey Proper

Substantive: The three combinatorial materials in Column 2 of Table 1 all possess components that are substantive, meaning having separate existence in the sense of being recognizable individually, which is a necessary point in combinatorial operations/computations. This is true of the four RNA bases A,U,G,C (Adenine, Uracil, Guanine, Cytosine) of item 1, likewise of the 24 quadruplet codons of the genetic code of item 2, and also of the 20 amino acids of protein, item 3.

Permanence: The identified three combinatorial materials in Table 1, Column 2 as paraphernalia in protein synthesis all possess components that exhibit durability in the context of the Dalina input/output multiplicative replication system and beyond e.g. the set of RNA four bases A,U,G,C likewise the 24 quadruplet codons of the genetic code; and lastly the 20 amino acids of protein.

Discrete: Discrete meaning separate and distinct is descriptive of the components of the identified materials that belong to the combinatorial paraphernalia in protein synthesis in the context of the Dalina input/output multiplicative replication system and beyond. In effect RNA four bases A,U,G,C item 1 of Table 1, Column 2 are discrete; likewise the 24 quadruplet codons of the genetic code, item 2 in Column 2, Table 1 are discrete components; and lastly the 20 amino acids of protein, item 3 in Column 2, Table 1 are equally discrete.

Plural: Meaning more than one in number, is a basic requirement of materials due to undergo the permutation aspect of combinatorics involved in protein synthesis in view of the expression of the formula for the calculation of factorial complements e.g. nPr, meaning set of (n) dissimilar things and selection of (r) of these dissimilar things, so that when n = 4, and r = 4 in the case of derivation of the genetic code, the workforce of 24 quadruplet codons, from the RNA four bases A,U,G,C, would be easily and readily accomplished by $4P4 = 4! = 4 \times 3 \times 2 \times 1 = 24$ quadruplets. In the formula nPr, n indicates the leading factor and r the number of factors descending from n in the tower multiplication array. Computation of the membership of the 24 quadruplets by view mixing techniques is now available from inchoate Numeration Science literature being developed by this author. Plurality of the components of the three named materials in Table 1, Column 2 items 1, 2, 3 is evident in terms of 4 RNA bases, 24 quadruplet codons of the genetic code and 20 amino acids of protein.

Dissimilar: Dissimilarity is a basic characteristic requirement in combinatorics embodying permutation and combinations of specified set (n) and selection (r) so far as the materials are concerned. Indeed all the four RNA bases, adenine, uracil, guanine, cytosine (A,U,G,C) are different by name and nature for distinction. Likewise, all the 24 quadruplet codons of the genetic code comprising the RNA four bases per codon are dissimilar and different in sequence. The 20 amino acids of protein are equally dissimilar by name and texture.

Compatible: Things that are compatible can always coexist without neigbourhood preferences, especially in lines. As materials for combinatorics, all the RNA four bases exhibit compatibility in linear formations, that is, they can always stand in any order

to yield a quadruplet RNA codon. Likewise, all the 24 quadruplet codons of the RNA four bases can stand in any order to give a genetic code of unique sequence. Also the 20 amino acids of protein can stand in any order to give a protein type that is unique in sequence. Compatibility is best illustrated with multi-digital numbers, whereby each sequence of dissimilar digits makes a sense in terms of numerical value, e.g. 123, 321, 213 etc as well as being distinct numerical entities. So as permutations cannot do without compatibility of material items.

Motile: To be motile means to be movable, so as to be placed in any person in a sequence. This also is a basic requirement in permutations of combinatorics that must be satisfied by any material for use.

Potency: The Dalina input/output multiplicative replication combinatorial system subsists on potency, whereby any input set replicates itself in the output sequence to a particular value given by the formula nPr or nPn. Whence the 24 quadruplet genetic code is the evidence of the potency of the input set of RNA four bases in a particular sequence. Every sequence of the input set of 4 RNA bases is therefore capable of generating the 24 quadruplet genetic code in a unique sequence in demonstration of the potency requirement of the material for combinatorial operation/computation. In this connection all components of the input material set must be dissimilar, that is to say potency in this case subsists on dissimilarity of the items concerned.

Uniqueness: Uniqueness is the characteristic of distinction between individuals of a kind or set, e.g. the RNA four bases, where A,U,G,C can be seen as different from one mother, hence unique. Uniqueness in the case of the 24 quadruplet genetic code material is applicable to the quadruplet codons, whereby they respectively fit into the design of mutuality for pairing between a quadruplet RNA codon and an amino acid/one of four time and place based start/stop signals in the setting of collinearity between 24 codons and 20 amino acids/four signals during protein synthesis.

Integrity: Embracing wholeness, soundness and uprightness in meaning involves maintaining one's own characteristic features through and across changes affecting time and space or environment. Thus integrity is to ensure that individual materials in use in computation of permutation factorial complements retain their identity in different locations or positions in divers sequences for validity of products.

Visible: Visibility of course is inevitable in human experience and any physical endeavour of his no less applicable in combinatorics operations/ computations involving materials in use in academics.

Distinct: Meaning clearly perceptible, definite, positive, separate, different in quality or kind according to the Reader's Digest Pocket Dictionary is a necessary condition for materials to satisfy in order to be used in combinatorial operations/computations. It is the strength of individuals in a plural assembly, such as the output sequence of products replication system of combinatorics. Completeness is a remarkable characteristic in combinatorics on account of the specifications of set (n) and selection (r) for permutations to guarantee the fullness of operation and accomplishment of popu-

lation desired. Hence for example the expression, permutation of 4 from 4 i.e. 4P4, meaning set of 4 dissimilar things and selection of 4 of these dissimilar, involves a specific population of the permutation, factorial complements. So completeness is required in each of specified set, selection and the product for correctness of calculated and computed population of permutation factorial complements, as illustrated below. Completeness as a combinatorial characteristic is encapsulated in formula viz 4 from 4 given by 4P4 = 4! = 4x3x2x1 = 24 quadruplets.

Composite meaning consisting of different parts or materials is descriptive all the three named materials of Table 1 Column 2, items 1, 2, and 3.

Composite thrives on completeness of constituent parts and it is a needful state in the Dalina input/output multiplicative replication system that is operational in protein synthesis and as exemplified by the three identified combinatorial materials in Table 1 Column 2, namely: RNA set of 4 bases, Genetic code of 24 quadruplets, and lastly protein type of 20 amino acids.

Summary of survey (a) based on the possession of the combinatorial characteristics (1) – (14) of the three identified combinatorial materials; Table 2.

Table 2: All-in-view of survey (a) above.

	Combinatorial Characteristic	Combinatorial Materials			
		Set of RNA 4 bases	Genetic code of 24 quadruplets	Protein type of 20 amino acids	Remarks
1	Substantive	✓	✓	✓	Remarkable compliance by materials in favour of protein synthesis based on permutation aspect of combina-torics
2	Permanence	✓	✓	✓	
3	Discrete	✓	✓	✓	
4	Plural	✓	✓	✓	
5	Dissimilar	✓	✓	✓	
6	Compatible	✓	✓	✓	
7	Motile	✓	✓	✓	
8	Potency	✓	✓	✓	
9	Uniqueness	✓	✓	✓	
10	Integrity	✓	✓	✓	
11	Visible	✓	✓	✓	
12	Distinct	✓	✓	✓	
13	Completeness	✓	✓	✓	
14	Composite	✓	✓	✓	

With the survey (a) based on the possession of the combinatorial characteristics by the identified materials of paraphernalia in protein synthesis done, we now proceed to the last lap (b) of the survey based on the use of the identified three materials in the operations/operatives listed in Table 1 Column 3 as paraphernalia in protein synthesis, involving the Dalina Input/Output multiplicative replication combinatorial system.

The Dalina input/output system: sourced from inchoate Numeration Science Literature, is the resource for generating the productivity of combinatorics and of digibreed of specified base strength. It is serviced by Square Kinematics View Mixing Scheme for 4 from 4 permutations, being one of three techniques as illustrated in Appendix 1.

Permutation: Permutation as an aspect of arrangement in combinatorics consists of component called factorial complements usually embodied in its nominal expression in terms of specified set (n) and selection (r), e.g. nPr meaning selection of (r) dissimilar things from a set (n) of dissimilar things. For example, permuta-

tion of 4 from 4 requires calculation to give the numerical population of the factorial complements and computation to display the entire membership of the factorial complements population in the case of our example of 4 from 4 is given by the formula 4P4 = 4! = 4x3x2x1 = 24 quadruplets, involving lower multiplication. On the other hand the computation of the membership of 24 quadruplets is illustrated in Appendix 1 sourced from Numeration Science Literature being developed by this author. The set of RNA four bases can as the input set, while the 24 quadruplet genetic code is the output product in the Dalina input/output system.

Alignment of 20 amino acids with four interspersed fallow portions: The significance of this process in the context of protein synthesis is that the protein type of 20 amino acids composed or fixed by the genetic code of 24 quadruplet codons is of relative commensurate length with the genetic code itself, in the sense that 20 of the 24 quadruplet codons take responsibility in fixing 20 amino acids based on natural affinity in a sequence with four portions fallow due to four signals lacking affinity with the amino acids and concerned with four place and time based start/stop control in

the midst of the sequence of 20 amino acids of protein concerned. So a protein type is of relative commensurate length with its fixer genetic code of 24 quadruplets with four interspersed flaccid portions later serve as flexible portions in the folding of protein types during packaging of proteins for transportation.

Affinity based pairing between 20 of the 24 quadruplet codons of the genetic code and the 20 amino acids of protein with four spare codons: This affinity or mutuality between the components of the two entities is a natural design to ensure protein synthesis through effective pairing arrangement for linear disposition in sequencing of products, in terms of parallels – one of the genetic code codons and the other of the amino acids with four interspersed fallow portions due to four place and time based start/stop signals during protein synthesis. This parallelism is occasioned by auto-sequence replication by the genetic code. Collinearity between 24 quadruplet codons of the genetic code and 20 amino acids of protein/ four fallow portions due to four control signals in protein synthesis. This accounts for the collinearity between the genetic code (fixer) and the protein type (fixed) whereby 20 of the 24 quadruplet codons engage the 20 amino acids of protein based on affinity and mutuality, while four spare quadruplet codons as signals take charge of four place and time based start/stop control during protein synthesis, featuring gaps' (flaccid portions) in the sequence of the protein type.
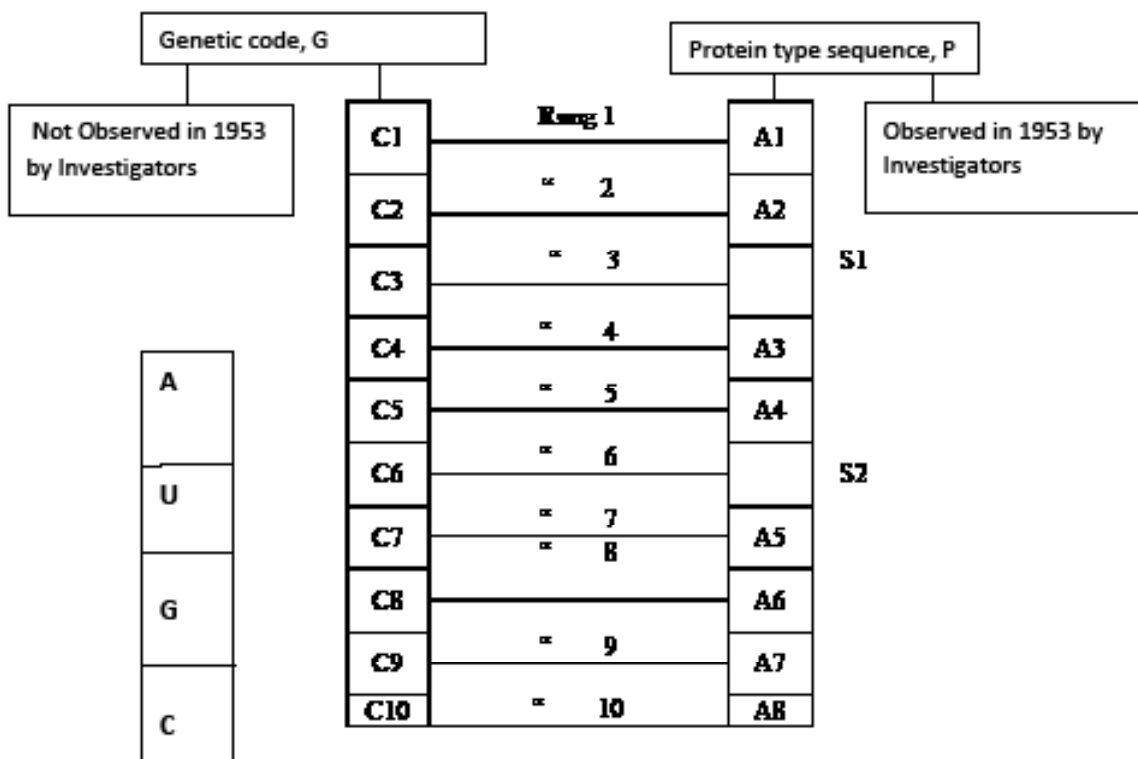
Auto-sequence replication: meaning own-sequence reproduction is the working principle of the quadruplet genetic code in protein synthesis, whereby every one of the constituent 24 quadruplet codons of unique sequence can serve as input set in the Dalina input/ output system to yield a genetic code output of unique sequence which in turn generates a protein type of unique sequence akin to that of genetic code responsible for its formation, via the affinity based pairing between 20 of the 24 quadruplets of the genetic code and the 20 amino acids of protein. Auto-sequence replication by the quadruplet genetic code in protein type composition is the essence of protein synthesis geared to proliferation and diversification of protein types characterized by unique sequences. The three materials of Table 1, Column 2 are evidently reflected in this combinatorial process of auto-sequence replication identified as paraphernalia in protein synthesis.

Viviparous delivery. Both the 24 quadruplet genetic code and the 20 amino-acid sequence of protein type are examples of serial viviparous delivery: the 24 quadruplet genetic code brought forth fully developed from the input quadruplet set of RNA four bases; followed by the protein type of 20 amino acids also brought forth fully developed from the 24 quadruplet genetic code via auto-sequence replication characterized by uniparous setting.

Monogamous partnership: Monogamous partnership is the order in Dalina input/output system, one quadruplet input set yielding one genetic code output sequence; likewise, one protein type to one genetic code in protein synthesis.

Protein type composition: This results from the linear alignment of the 20 amino acids of protein by 20 of the 24 quadruplet codons that bear affinity with the 20 amino acids of protein and enjoy pairing relationship in the fashion of the two hand rails of a ladder connected by a set of 24 rungs as depicted in Fig. 1, Protein type composition by the 24 quadruplet genetic code, involving auto-sequence replication.
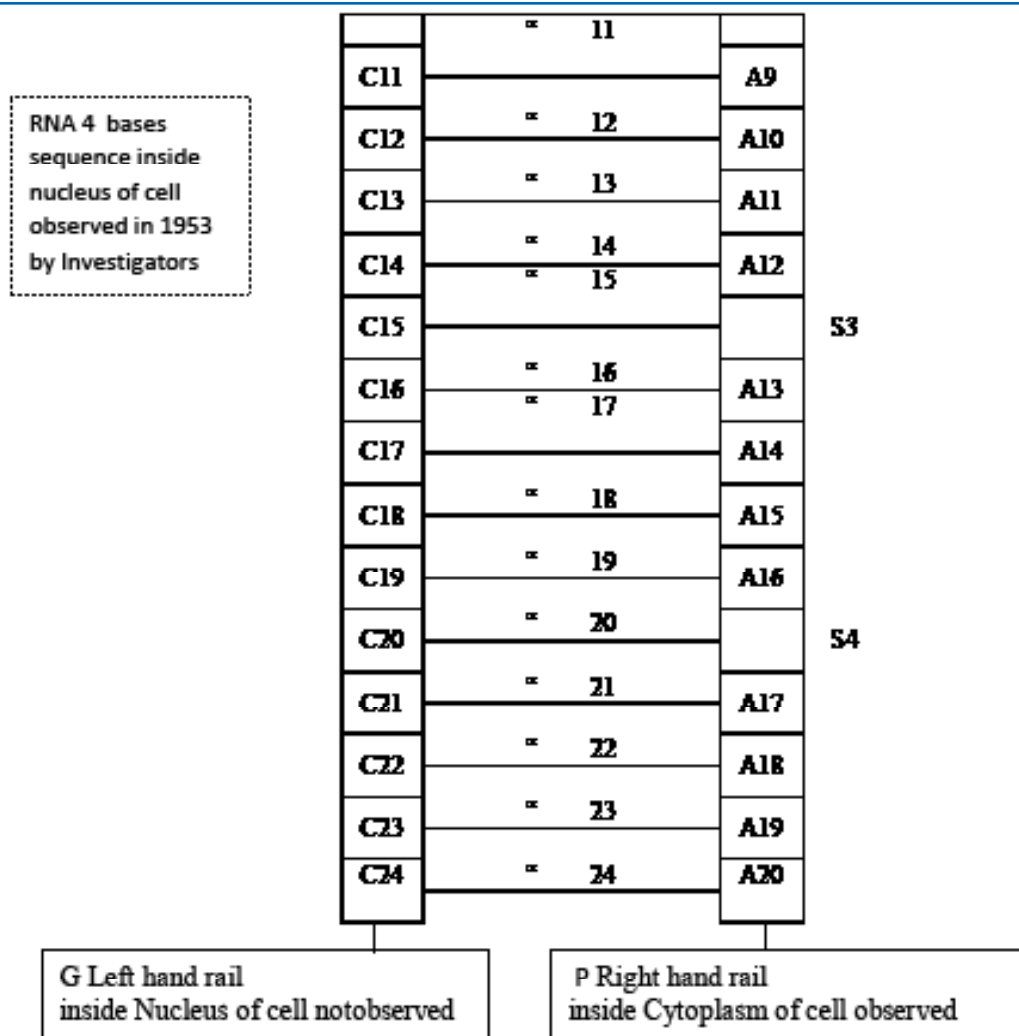
Figure 1: Protein type composition by the 24 quadruplet genetic code, involving auto-sequence replication

Key to Figure 1

C1 … C24 = quadruplet codons of sequence G

C1 = Quadruplet codon of RNA four bases in unique sequence

C2 = Quadruplet codon of RNA four bases in unique sequence.

A1 … A20 = 20 amino acids of protein = Sequence P.

S1 … S4 = Four signals for four time and place based start/stop control;

Flaccid segments interspersed in the sequence of the 20 amino acids of protein type due to control signals that have no affinities with amino acids of protein.

Rung 1 …Rung 24 = 24 affinity linkages between 20 amino acids of protein and 20 of the 24 quadruplet genetic codons and between 4 of the non-amino acid fixing quadruplet codons and the flaccid segments S1 – S4 interspersed in the protein type sequence.

Rungs 1 – 24 of laddes of collinearity.

N.B. Affinity linkages not necessarily physical connectives, of course.

Sequence P is auto-sequence replication by sequence.

AUGC sequence of RNA four bases giving rise to 24 quadruplet genetic code of unique sequence responsible for the fixing of protein type of 20 amino acids in corresponding unique sequence.

Figure 1, is a pictorial presentation of the molecular biologists' observation in 1953 that the sequence of the RNA four bases in the nucleus of a cell influenced the sequence of the twenty amino acids of protein in the cytoplasm, even though the genetic code sequence in between the said two sequences responsible for the correlation between them was not mentioned in the said observation.

(9/10) Now is the turn of protein type proliferation and protein type diversification to be taken together, because they are inseparable twins in protein synthesis. They simultaneously emerge in the product as each of the 24 unique quadruplet codons of the genetic code serve as input set in the Dalina input/output multiplicative replication combinatorial system. They seem to represent the

two faces of the coin of multiplicative replication accomplished in protein synthesis. They are however non-identical twins. They happen to be bye-products of each other in that as proliferation of factorial complements is pursued towards completeness amongst the demands of permutation, diversification is yielded. Likewise, when diversification of factorial complements is pursued towards completeness amongst the demands of permutation, proliferation is also yielded profitably. Of course completeness of membership and variants amongst the demands of permutation is pursued as each of the intermediary genetic code is made to serve as input set in the indomitable Dalina input/output combinatorial system serviced by square kinematics view mixing scheme sourced from Numeration Science Literature now in the making by this author.

Protein folding and packaging: as terminal process in protein synthesis is facilitated by the four codon-size flaccid segments interspersed in each protein type, serving as flexible portions in each protein type of 20 named amino acids.

Summary of survey (b) of combinatorial paraphernalia based on the intervention between the identified three combinatorial materials in Table 1 Column 2 and the identified eleven combinatorial processes/operatives in Table 1 Column 3, ref. Table 3.

Table 3: All-in-view of survey (b) above.

	Combinatorial processes/ operatives	Combinatorial Materials			Remarks
		Set of RNA four bases A,U,G,C	24 quadruplet genetic code	20 amino acids of protein	
1	Dalina Input/ Output multiplicative replication system	✓	✓	✓	Remarkable compliance by materials in favour of protein synthesis based on permutation aspect of combinatorics
2	Permutation	✓	✓	✓	
3	Alignment of 20 amino acids with four signals	✓	✓	✓	
4	Affinity based pairing between 20 of the 24 quadruplet codons of genetic code and 20 amino acids of protein	✓	✓	✓	
5	Auto-sequence replication	✓	✓	✓	
6	Viviparous delivery	✓	✓	✓	
7	Monogamous partnership	✓	✓	✓	
8	Protein type composition	✓	✓	✓	
9	Protein type diversification	✓	✓	✓	
10	Protein type proliferation	✓	✓	✓	
11	Protein folding and packaging	✓	✓	✓	
Col	1	2	3	4	5

Results

The combinatorial paraphernalia in protein synthesis identified and surveyed numbered up to 14 characteristics, 3 materials and 11 processes/operatives as listed in the roll call in Table 1

Discussion

The combinatorial paraphernalia in protein synthesis were categorized into characteristics, materials and processes/operatives for some light on the composition in the context of Dalina input/output multiplicative replication combinatorial system performance as fueled by Square Kinematics View Mixing Technique in the production of permutations of 4 from 4 RNA bases surnamed the 24 quadruplet genetic code, the workforce in protein synthesis!

The characteristics category of the combinatorial paraphernalia in protein synthesis is still a complex that can be subjected to further categorization in two folds covering bipartite and tripartite.
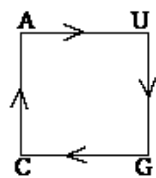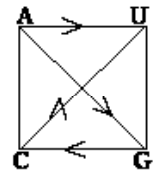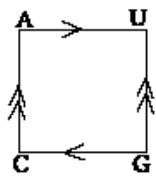
The bipartite categories of the characteristics fall into patent and latent, while the tripartite categories of characteristics fall into innate {inborn}, inherited and acquired. This means the 14 listed characteristics in Table 1 can be so categorized meaningfully in relation to the materials and processes/operatives in the fashion of Tables 2 and 3.

Conclusion and Significance: The combinatorial paraphernalia in protein synthesis are very well accommodated and utilized in omnium gatherum, (miscellaneous and assemblage) in furtherance of protein synthesis, one of the most demanding tasks in support of the living as per all plants and animals on planet Earth throughout creation.

Recommendation: Let experimental experts in molecular biology help with the spelling of the 24 quadruplet genetic code to render it fit for adoption in protein synthesis studies.

Appendix 1: The Dalina Input/Output multiplicative replication combinatorial system at work via Square Kinematics View Mixing Technique for computing 4 from 4 permutations of RNA four bases A,U,G,C. Ref. Chart 1.

Chart 1. Square Kinematics View Mixing Technique with input sequence A,U,G,C.

Fig. 1 (a) Sides Deployment	Viewing from A Clockwise	AUGC	Line 1
	Fro	CGUA	" 2
	Viewing from U Clockwise	UGCA	" 3
	Fro	ACGU	" 4
	Viewing from G Clockwise	GCAU	" 5
	Fro	UACG	" 6
	Viewing from C Clockwise	CAUG	" 7
	Fro	GUAC	" 8
Fig. 1 (b) Diagonals Deployment	Viewing from A Clockwise	AGCU	" 9
	Fro	UCGA	" 10
	Viewing from U Clockwise	UCAG	" 11
	Fro	GACU	" 12
	Viewing from G Clockwise	GAUC	" 13
	Fro	CUAG	" 14
	Viewing from C Clockwise	CUGA	" 15
	Fro	AGUC	" 16
Fig. 1 (c) Parallels Deployment	Parallels AU//CG become	AUCG	" 17
	Fro	GCUA	" 18
	Parallels UA//GC become	UAGC	" 19
	Fro	CGAU	" 20
	Parallels CA//GU become	CAGU	" 21
	Fro	UGAC	" 22
	Parallels GC//UA become	GCUA	" 23
	Fro	AUCG	" 24

Lines 1 – 24 = 24 quadruplet genetic code derived from RNA four bases A,U,G,C.

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