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A RESIDUE NUMBER SYSTEM (RNS) ANTI-CODON TABLE FOR PROTEIN SYNTHESIS

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ABSTRACT

Purpose: This study aims to optimise the representation and processing of genetic information through RNS encoding.
Design/Methodology/Approach: The RNS anti-codon table is constructed as a table of RNS genetic code using the concept of number trees. The complementarity of bases suggests the swap of bases leading to the generation of 64 anti-codons for all possible codons of the genetic code. These are algorithmically reduced to less than 40 known anti-codons due to wobbling.
Findings: The finding indicates that the decimal values change as the moduli sets vary, but the residue digits remain the same. Codons and anti-codons are static with some bases, in this case, moduli set and vary with the third base.
Research Limitations: The current RNS implementation may experience overflow issues when dealing with extensive protein sequences and difficulty in verifying results across different organism types
Practical Implications: This research answers the compelling cases of a quarternary number system in molecular biology applications. In the era of Artificial Intelligence (AI) and machine learning and the desire for gene editing, gene therapy, and personalised medicine, digital implementations are enhanced with number systems.
Social Implication: The findings demonstrate the far-reaching impact of implementing RNS anti-codon tables in protein synthesis, highlighting the need for careful consideration and planning in its deployment and integration into society.

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Originality/ Value: This research represents a significant departure from conventional approaches to genetic information processing, introducing multiple layers of innovation that advance theoretical understanding and practical applications in the field.

Keywords: *Algorithmically. anti-codons. genetic. protein synthesis. wobbling*

INTRODUCTION

Recent developments in genetic sequencing and molecular biology have broadened our knowledge of the significance of codons and anticodons in protein synthesis and unlocked a plethora of potential uses for anticodons. (Weiss et al., 2024)One of the most researched RNA molecules is transfer RNA (tRNA). It mediates the transfer of amino acids to ribosomes, making it a crucial component of the machinery that produces proteins.

Messenger (mRNA), transfer RNA (tRNA), and ribosomal (rRNA) RNA are the primary trio of RNAs that facilitate the passage of genetic information from DNA to proteins. Transfer RNAs (tRNAs), non-coding RNAs, play a significant role in translation. As such, the amino acid that tRNA is associated with is determined by the mRNA codon, whereas rRNA is necessary for forming peptide bonds between aminoacylated tRNA substrates. In this context, tRNA has two distinct qualities. It carries an anticodon that matches the mRNA codon, and in a process that is aided by a particular aminoacyl-tRNA synthetase enzyme, it binds to the correct amino acid (Ganesh & Maerkl, 2022).

Accordingly, tRNA is a crucial molecule that connects the worlds of RNA and proteins (Mohamed, 2022). Thus, the mRNA codon specifies the amino acid to which tRNA is attached, but the synthesis of peptide bonds between aminoacylated tRNA substrates requires rRNA. In this case, tRNA has two distinct qualities. It has an anticodon that matches the mRNA codon, and when an aminoacyl-tRNA synthetase enzyme of a certain kind catalyses a reaction, it binds to the necessary amino acid. Accordingly, tRNA is a crucial molecule that connects the worlds of RNA and proteins.

Biological information is ascribed to digital and computational meaning with the well-known binary number system (Marshall, 2021). These considerations are static and not structured in an entire number system space. The integration of computers and mathematics is revolutionising the field of molecular biology, resulting in computational biology and bioinformatics.

An advanced digital representation of molecular biological concepts like the tRNA holds transformative potential for molecular biological processes and analyses. A well-structured and

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innovative approach, aligned with computational algorithms, is needed to enhance molecular biology practices (Zahoor et al., 2024). Their static nature, the fact that these approaches are not structured within an entire number system framework, and binary constraints in digital applications limit their effectiveness. This study aims to optimise the representation and processing of genetic information through RNS encoding.

The anti-codon table can be represented uniquely by utilising a three-moduli set RNS and the number tree model (based on Gamow's postulation). A three-modulus RNS that buttresses the quest for a quaternary number system for molecular biological applications is considered. This model uses number trees, uniquely categorising all RNS digits into blocks (Yu et al., 2022). These blocks mimic the codon blocks of the genetic code, as the first two digits of each block have the uniqueness of being the same. The number tree concept and the principle of complementarity of nitrogenous bases are the foundation for generating an anticodon table (Rosandić & Paar, 2021). This categorises all anti-codons in the family box and algorithmically sorts the required anti-codons, thus achieving the required anti-codons due to wobbling.

LITERATURE REVIEW

Residue Number System (RNS)

A growing body of research examines the Residue Number System (RNS) as a potential contender for many digital applications. The number system is not weighted and offers some advantages in these applications compared with the weighted number systems – binary number system (Afriyie, 2021). Thus, there has been a resurgence in the area of RNS in the past years, and various interesting findings have been made to support the need to adopt RNS to achieve a much faster arithmetic computation, error control coding, and fault-tolerance computing (Akanni, 2022). Digital applications are necessary to provide biological features with some computational relevance. The well-known binary number system has served the digital world for a long time until some limiting features like carry and borrow chain and ordered significance were figured out. RNS has, therefore, resurfaced to offer solutions to myriad challenges limiting the potential of digital applications (Chervyakov et al., 2020). Consider the set of N positive, pairwise relatively prime moduli $\{m_1; m_2;...; m_N\}$. Let M be the moduli product, defined as $M = m_1 \times m_2 \times \ldots \times m_N$. [0; M-1] is the range of representation, while M is the dynamic range. The representation of X is in the form $< x_1; x_2; \ldots; x_N >$ where $xi = |X| mi$

Example Consider the residue system {3, 4, 5}, then the dynamic range M= (3 x 4 x 5) = 60

20 is represented as < 2, 0, 0 >. , Thus, $20mod3 = 6r2$, $20mod4 = 5r0$ and $20mod5 = 4r0$.

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Hence, a concatenation of the residues constitutes the number 20.

Also, 29 is represented as < 2, 1, 4 >

From $29mod3 = 7r2$, $29mod4 = 7r1$and $29mod5 = 5r4$.

Also, 20 +29 becomes < 2, 0, 0 > + < 2, 1, 4 >

$(2 + 2)mod3 = 4mod3 = 1$

$(0 + 1)mod4 = 1mod4 = 1$

$(0 + 4)mod5 = 4mod5 = 4$

The result is < 1, 1, 4 >

This is confirmed as$49mod3 = 13r1$, $49mod4 = 12r1$, $49mod5 = 9r4 =>$ < 1, 1, 4>

Thus, RNS lacks the ordered significance of digits and does not generate carry or borrow propagation in its arithmetic (Olsen, 2018). In general, number representation impacts all design abstraction layers, ranging from algorithms to hardware architecture, in any digital system. Therefore, an application's workload is influenced by the complexity and quantity of operations needed to complete specific specialised tasks, which are dictated by the number of systems used for the hardware implementation (Khanam et al., 2024). Notably, a residue number system will not be unique if the moduli sets are not pairwise relatively prime representations. Thus, two or more numbers will be the same.

Protein Synthesis

The genetic information transmitted by DNA and RNA determines the fundamental structure of proteins found in biological organisms (Sun et al., 2021). Twenty amino acid chains comprise each codified protein (Dubey et al., 2024). A codon, or triplet, is a group of three adjacent nitrogenous nucleotides arranged along an RNA or DNA filament. There are twenty different types of amino acids, which are the building blocks of proteins. A proper sequence of genetic triplets defines an amino acid sequence in a protein chain. These 20 amino acids are combined in various ways to create proteins. The initial stage in the creation of proteins is transcription, which is the process of translating genetic information from DNA to RNA (Mejía-Almonte et al., 2020). The cytoplasmic ribosome sites, situated externally to the nucleus, are the sites of protein synthesis. While RNA is

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single-stranded and small enough to pass through the nuclear pores in the nucleus, DNA is too big to exit the nucleus due to its double-stranded nature.

A portion of the DNA unzips and is employed as a template for assembling complementary nucleotides (tRNA) into messenger RNA (mRNA). Affixed to the ribosome, the mRNA exits the nucleus via pores containing the DNA code. Protein synthesis involves two steps, the second of which is translation—the process of translating mRNA into a protein. Proteins from the cytoplasm are transferred to the ribosome via a transfer RNA. Each amino acid in an mRNA molecule is coded for by three (3) neighbouring nucleotides known as codons (Das et al., 2021). The three nucleotides of each transfer RNA are complementary to the codon in the mRNA. At the ribosome site, the tRNA carrying amino acids (anticodons) and the mRNA carrying DNA instructions (codons) combine to facilitate translation. Some codons can code for the same amino acids, termed degeneracy, which accounts for genetic variations. Also, some codons can be paired with one anticodon, resulting from wobbling, which reduces translation errors. Thus, fewer anticodons are required to translate all known codons successfully. This gives rise to the anticodon table in the known family box of codons.

Anti-Codons

A specific form of RNA molecule called transfer ribonucleic acid (tRNA) makes it easier for a messenger RNA (mRNA) sequence to be translated into a protein (Elias, 2014). mRNA's nucleotide sequence dictates which amino acids are incorporated into the protein product. Protein synthesis results from a 3-nucleotide tRNA anticodon complementing a 3-nucleotide codon in an mRNA. Amino acids are thus transported by tRNA to the machinery involved in protein synthesis. Every transfer molecule is linked to a particular amino acid, and the tRNA determines which sequence in the genetic code corresponds to which amino acid (Gao et al., 2024). A distinct tRNA recognises each codon, a three-nucleotide or triplet sequence on mRNA that codes for a particular amino acid during translation. The tRNA molecule has a sequence known as the anticodon, which is made up of three nucleotides and binds via base pairing to a corresponding mRNA codon, which can determine and decode an mRNA codon (Wu et al., 2022; Mohanta et al., 2022).

In the code of life, 64 possible codons should require 64 anticodons for translation. However, there are 61 sense codons, and since 3 out of the 64 codons are stop codons, they terminate the translation process. Less than forty kinds of tRNA, or anticodons, are found in most species (Salman et al., 2024). The wobble hypothesis explains this feature: the first base of a tRNA anticodon can couple with the third base of an mRNA codon in a non-Watson-Crick base pairing. Every sense codon has a tRNA, and for a one-to-one relationship between tRNA molecules and the mRNA codons

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that designate amino acids, 61 different forms of tRNA are needed since the normal genetic code consists of 61 sense codons. A table with 61 anticodon RNAs may exist to translate all 61 sense codons unambiguously. By using the wobbling principles to identify every sense codon in mRNA, less than 40 tRNAs are required. That is to say, some anti-codons pair with more than one codon. Figures 1 (a) and (b) represent the canonical anticodon and the anticodon table due to wobbling, respectively.

Table of DNA Base Triplets, RNA Codons & Anticodons

AMINO ACID	DNA BASE TRIPLETS	M-RNA CODONS	T-RNA ANTICODONS
alanine	CGA, CGG, CGT, CGC	GCU, GCC, GCA, GCG	CGA, CGG, CGU, CGC
arginine	GCA, GCG, GCT, GCC TCT, TCC	CGU, CGC, CGA, CGG AGA, AGG	GCA, GCG, GCU, GCC UCU, UCC
asparagine	TTA, TTG	AAU, AAC	UUA, UUG
aspartate	CTA, CTG	GAU, GAC	CUA, CUG
cysteine	ACA, ACG	UGA, UGC	ACA, ACG
glutamate	CTT, CTC	GAA, GAG	CUU, CUC
glutamine	GTT, GTC	CAA, CAG	GUU, GUC
glycine	CCA, CCG, CCT, CCC	GGU, GGC, GGA, GGG	CCA, CCG, CCU, CCC
histidine	GTA, GTG	CAU, CAC	GUA, GUG
isoleucine	TAA, TAG, TAT	AUU, AUC, AUA	UAA, UAG, UAU
leucine	AAT, AAC, GAA, GAG GAT, GAC	UUA, UUG, CUU, CUC CUA, CUG	AAU, AAC, GAA, GAG GAU, GAC
lysine	TTT, TTC	AAA, AAG	UUU, UUC
methionine	TAC	AUG	UAC
phenylalanine	AAA, AAG	UUU, UUC	AAA, AAG
proline	GGA, GGG, GGT, GGC	CCU, CCC, CCA, CCG	GGA, GGG, GGU, GGC
serine	AGA, AGG, AGT, AGC TCA, TCG	UCU, UCC, UCA, UCG AGU, AGC	AGA, AGG, AGU, AGC UCA, UCG
Stop	ATG, ATT, ACT	UAA, UAG, UGA	AUG, AUU, ACU
threonine	TGA, TGG, TGT, TGC	ACU, ACC, ACA, ACG	UGA, UGG, UGU, UGC
tryptophan	ACC	UGG	ACC
tyrosine	ATA, ATG	UAU, UAC	AUA, AUG
valine	CAA, CAG, CAT, CAC	GUU, GUC, GUA, GUG	CAA, CAG, CAU, CAC

(a)

Ala		Arg		Asp		Asn		Cys	
GCC	CGG	AGA	UCU	GAC	CUG	AAC	UUG	UGC	ACG
GCU		AGG		GAU		AAU		UGU	
GCA	CGU	CGA	GCU						
GCG		CGG							
		CGU	GCG						
		CGC							
Glu		**Gln**		**Gly**		**His**		**Ile**	
GAA	CUU	CAA	GUU	GGA	CCU	CAC	GUG	AUA	UAU
GAG		CAG		GGG		CAU			
								AUC	UAG
				GGC	CCG			AUU	
				GGU					
Leu		**Lys**		**Met**		**Phe**		**Pro**	
UUA	AAU	AAA	UUU	AUG	UAC	UUC	AAG	CCA	GGU
UUG		AAG				UUU		CCG	
CUA	GUA							CCU	GGG
CUG								CCC	
CUU	GUG								
CUC									
Ser		**Thr**		**Trp**		**Tyr**		**Val**	
AGC	UCG	ACA	UGU	UGG	ACC	UAC	AUG	GUA	CAU
AGU		ACG				UAU		GUG	
UCA	AUG	ACU	UGA					GUC	CAG
UCG								GUU	
UCC	AGG								
UCU									
Amber Suppressor		**Ochre Suppressor**		**Opal Suppressor**					
UAG	AUC	UAA (UAG)	AUU	UGA (UGG)	ACU				

(b)

Figure 1: Codon – Anticodon Table
Source: (Taylor & Coates 1989).

METHODOLOGY

This research, therefore, presents a three (3) moduli set Residue Number System (RNS) anti-codon table for protein synthesis. When RNS is constructed as a tree, it results in a forest with a unique outlook for generating the genetic code (codon table) and anti-codon table.

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The concept is to design a tree (forest) of residue numbers from the generated residue numbers with appropriate roots, nodes, and leaves. The number of roots in the forest is defined by the first moduli set, while the number of blocks in each row is dictated by the second moduli set. The third modulus determines the number of inner fields or columns in each block.

This design uniquely categorises the residue numbers into specialised blocks of residue digits from which the genetic code and the anti-codon table can be generated. The concatenation of the root, child, and leaves of a three (3) moduli set RNS represents a codon or amino acid, m_1, m_2, m_3. These blocks display certain unique characteristics, in that digits are uniquely categorised into their family codon blocks that have been exploited to generate the genetic code and the anti-codon table. The complementarity of the nitrogenous bases serves as the foundation for generating the anticodon table. Guanine complements Cytosine, while Adenine complements Uracil.

In generating the RNS genetic code, the nitrogenous bases are assigned to residue digits; thus, U is assigned residue digit 0, Cytosine is assigned residue digit 1, Adenine is assigned residue digit 2, and Guanine is assigned residue digit 3. The principle of complementarity is the genesis of generating the anticodons. Thus, as opposed to the codons of the genetic code, Uracil is assigned residue digit 2, and Adenine is assigned residue digit zero since they are complementary pairs. Cytosine is also assigned residue digit three, and guanine is assigned residue digit one since they are complementary pairs. This enables the generation of 64 possible anti-codons for all the 64 codons. This makes it possible to construct an anticodon table for all the possible codons in RNS and further reduce the table to the required anticodons due to wobbling. This is built following the same concept of number trees, which categorises all anti-codons in the family box and algorithmically sorts the anticodons needed for each set of codons. This offers a better platform for protein synthesis analysis in the RNS space. The succeeding headings describe the block diagram and the algorithm designed to achieve the results of the RNS anticodon table.

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Block Diagram of Rns Anti-Codon Design Flow

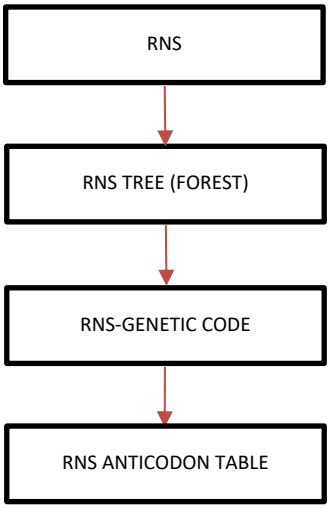

Figure 2: RNS Anti-codon Flow

Design Algorithm

AntiCodonTable(m_1,m_2,m_3)
Input: Three relatively prime numbers m_1, m_2, m_3
Output: RNS Genetic code Anticodon Reference Table

```
1    M ← m1 * m2 * m3
2    N ← 64    //  number of codons
3    Array GeneticCode[N, 6]
4    wobbleCount ← 0
5    wobbler ← 3
6    count ← 0
7    for i ← 0 to M-1
8            if ((x < 4) && (y < 4) && (z < 4))
9                    GeneticCode[count, 0] ← AntiCodon(x)
10                   GeneticCode[count, 1] ← AntiCodon(y)
11                   GeneticCode[count, 2] ← wobbler
12                   GeneticCode[count, 3] ← AminoAcid(AntiCodon(x),
                     AntiCodon(y), wobbler)
```

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```
13                  GeneticCode[count, 4] ← CodonName(x,y,z)
14                  GeneticCode[count, 5] ← i
15                  count ← count + 1
16                  if (wobbleCount < 2)
17                      wobbler ← 3
18                  else
19                        wobbler ← 0
20                  if (wobbleCount > 3)
21                      wobbleCount ← 0
22                  wobleCount ← wobbleCount + 1
23          x ← x + 1
24          y ← y + 1
25          z ← z + 1
26          if (x = m1)
27                  x ← 0
28          if (y = m2)
29                  y ← 0
30          if (z = m3)
31                  z ← 0
32  return GeneticCode
```

Anticodon(codon)

Input:Codon

Output: An Anti-Codon (A)

```
1   string A
2   if (codon == 0)
3     A = 2
4   if (codon == 1)
5     A = 3
6   if (codon == 2)
7     A = 0
8   if (codon == 3)
```

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9 A = 1
10 Return A

RESULTS AND DISCUSSION

RNS GENETIC CODE			
000	010	020	030
001	011	021	031
002	012	022	032
003	013	023	033
100	110	120	130
101	111	121	131
102	112	122	132
103	113	123	133
200	210	220	230
201	211	221	231
202	212	222	232
203	213	223	233
300	310	320	330
301	311	321	331
302	312	322	332
303	313	323	333

(a)

GENETIC CODE - mRNA codon			
UUU	UCU	UAU	UGU
UUC	UCC	UAC	UGC
UUA	UCA	UAA	UGA
UUG	UCG	UAG	UGG
CUU	CCU	CAU	CGU
CUC	CCC	CAC	CGC
CUA	CCA	CAA	CGA
CUG	CCG	CAG	CGG
AUU	ACU	AAU	AGU
AUC	ACC	AAC	AGC
AUA	ACA	AAA	AGA
AUG	ACG	AAG	AGG
GUU	GCU	GAU	GGU
GUC	GCC	GAC	GGC
GUA	GCA	GAA	GGA
GUG	GCG	GAG	GGG

(b)

RNS GENETIC CODE [4 5 7]			
0	56	112	28
120	36	92	8
100	16	72	128
80	136	52	108
105	21	77	133
85	1	57	113
65	121	37	93
45	101	17	73
70	126	42	98
50	106	22	78
30	86	2	58
10	66	122	38
35	91	7	63
15	71	127	43
135	51	107	23
115	31	87	3

(c)

RNS GENETIC CODE [5 6 7]			
0	175	140	105
120	85	50	15
30	205	170	135
150	115	80	45
126	91	56	21
36	1	176	141
156	121	86	51
66	31	206	171
42	7	182	147
162	127	92	57
72	37	2	177
192	157	122	87
168	133	98	63
78	43	8	183
198	163	128	93
108	73	38	3

(d)

Figure 3: Codon Table (a) RNS digits (b) Nitrogenous Bases (c) RNS-decimal value [4 5 7] (d) RNS-decimal values [5 6 7]

Figure 3 generally describes an RNS codon table, with (a) describing a three-moduli set RNS representation of the codon table and (b) representing the nitrogenous base representation of the codon table. Figure 3 (c), on the other hand, shows the decimal representation of the codon with moduli sets 4, 5 and 7, whereas (d) captures the decimal value representation of the codon table with moduli sets 5, 6 and 7. This shows that the decimal values will change as the moduli sets are varied, but the residue digits will always remain the same. Thus, the generation of the codon table is universal across the entire RNS number space. The blocks are in quartets and a single anticodon codes for each codon. (Schiessel, 2021).

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RNS - Anti-Codon Table			
2 2 2	2 3 2	2 0 2	2 1 2
2 2 3	2 3 3	2 0 3	2 1 3
2 2 0	2 3 0	2 0 0	2 1 0
2 2 1	2 3 1	2 0 1	2 1 1
3 2 2	3 3 2	3 0 2	3 1 2
3 2 3	3 3 3	3 0 3	3 1 3
3 2 0	3 3 0	3 0 0	3 1 0
3 2 1	3 3 1	3 0 1	3 1 1
0 2 2	0 3 2	0 0 2	0 1 2
0 2 3	0 3 3	0 0 3	0 1 3
0 2 0	0 3 0	0 0 0	0 1 0
0 2 1	0 3 1	0 0 1	0 1 1
1 2 2	1 3 2	1 0 2	1 1 2
1 2 3	1 3 3	1 0 3	1 1 3
1 2 0	1 3 0	1 0 0	1 1 0
1 2 1	1 3 1	1 0 1	1 1 1

(a)

tRNA Anti-codons			
AAA	AGA	AUA	ACA
AAG	AGG	AUG	ACG
AAU	AGU	AUU	ACU
AAC	AGC	AUC	ACC
GAA	GGA	GUA	GCA
GAG	GGG	GUG	GCG
GAU	GGU	GUU	GCU
GAC	GGC	GUC	GCC
UAA	UGA	UUA	UCA
UAG	UGG	UUG	UCG
UAU	UGU	UUU	UCU
UAC	UGC	UUC	UCC
CAA	CGA	CUA	CCA
CAG	CGG	CUG	CCG
CAU	CGU	CUU	CCU
CAC	CGC	CUC	CCC

(b)

RNS - Anti-Codon Table [4 5 7]			
2	58	30	86
122	38	10	66
42	98	70	126
22	78	50	106
107	23	135	51
87	3	115	31
7	63	35	91
127	43	15	71
72	128	100	16
52	108	80	136
112	28	0	56
92	8	120	36
37	93	65	121
17	73	45	101
77	133	105	21
57	113	85	1

(c)

RNS - Anti-Codon Table [5 6 7]			
2	177	72	37
122	87	192	157
182	147	42	7
92	57	162	127
128	93	198	163
38	3	108	73
98	63	168	133
8	183	78	43
170	135	30	205
80	45	150	115
140	105	0	175
50	15	120	85
86	51	156	121
206	171	66	31
56	21	126	91
176	141	36	1

(d)

Figure 4: Ideal Anti-codon Table (a) RNS digits (b) Nitrogenous bases (c) RNS-decimal values [4 5 7] (d) RNS-decimal values [5 6 7]

Figure 4 is the ideal anti-codon table, where (a) shows the table in RNS format and (b) depicts the nature of the ideal anticodon table in a nitrogenous base. Figure 4 (c) describes the ideal anticodon table with the decimal representation of the moduli sets 4, 5 and 7, while (d) captures the decimal representation with moduli sets 5, 6 and 7. It can be observed from this that while the residue digits stay constant, the decimal values vary with the moduli sets. Therefore, over the whole RNS number space, the anticodon table generation is universal. Codons and anti-codons are static with some bases, in this case, moduli set and vary with the third base; thus, the third moduli sets account for the wobble hypothesis (Panawala, 2017).

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Codon (mRNA) - Anti-codon (tRNA)							
UUU		UCU		UAU		UGU	
UUC	AAG	UCC	AGG	UAC	AUG	UGC	ACG
UUA		UCA		UAA	AUU	UGA	ACU
UUG	AAU	UCG	AGU	UAG	AUC/AUU	UGG	ACU/ACC
CUU		CCU		CAU		CGU	
CUC	GAG	CCC	GGG	CAC	GUG	CGC	GCG
CUA		CCA		CAA		CGA	
CUG	GUA	CCG	GGU	CAG	GUU	CGG	GCU
AUU		ACU	UGA	AAU		AGU	
AUC	UAG	ACC	UGG	AAC	UUG	AGC	UCG
AUA	UAU	ACA		AAA		AGA	
AUG	UAC	ACG	UGU	AAG	UUU	AGG	UCU
GUU		GCU		GAU		GGU	
GUC	CAG	GCC	CGG	GAC	CUG	GGC	CCG
GUA		GCA		GAA		GGA	
GUG	CAU	GCG	CGU	GAG	CUU	GGG	CCU

(a)

RNS Codon (mRNA) - Anti-codon (tRNA)							
000		010		020		030	
001	223	011	233	021	203	031	213
002		012		022	200	032	210
003	220	013	230	023	201/200	033	210/211
100		110		210		130	
101	323	111	333	211	303	131	313
102		112		212		132	
103	320	113	330	213	300	133	310
200		210	032	220		230	
201	023	211	033	221	003	231	013
202	020	212		222		232	
203	021	213	030	223	000	233	010
300		310		320		330	
301	123	311	133	321	103	331	113
302		312		322		332	
303	120	313	130	323	100	333	110

(b)

Figure 5: Wobbling Codon-Anticodon: (a) Nitrogenous bases (b) RNS digits

The codon-anticodon table is shown in Figure 5(a) in its nitrogenous base form, illustrating how the codon-anticodon relationship is wobbling. This is also displayed in RNS format, representing the RNS anticodon table. In Figure 5(b), the algorithmically sorted anti-codons and corresponding codons are thus shown. It is demonstrated here that a single anti-codon can code for several codons in RNS, leading to a less than 40 RNS anti-codon table (Harrison et al., 2022) .

CONCLUSION

Modern molecular biological applications are digitally implemented in the binary number system, which is widely recognised. Since the known nitrogenous bases are four (4), molecular biology and bioinformatics experts have presented compelling cases for implementing a quarternary number system in molecular biology applications.

This work presents a robustly simple RNS anticodon table that is flexible over the whole residue number system space, suitable for quarternary number system consideration, and universal. The complementarity of bases and number trees makes the design more straightforward to build algorithmically.

Furthermore, it is universal since any three sets of relatively prime moduli can generate an anticodon table successfully. The tree approach adopted in this research uniquely presents the moduli digits in each codon block. Therefore, regardless of the moduli sets selected, the moduli

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digits in each codon block will always be the same, but the decimal values will vary. In the era of Artificial Intelligence (AI) and machine learning and the desire by molecular biologists for gene editing, gene therapy, and personalised medicine, a number system which forms the core for digital implementation that suites molecular biological applications is much desired. A complementary base (anticodons) designed with RNS adds a piece to the jigsaw.

These practical implications demonstrate the wide-ranging impact of implementing RNS anti-codon tables in protein synthesis. Implementation strategies and resource allocation must be carefully considered to ensure successful adoption and utilisation in various settings.

The findings demonstrate the far-reaching impact of implementing RNS anti-codon tables in protein synthesis, highlighting the need for careful consideration and planning in its deployment and integration into society.

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