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Research Article

Codes over Lattice-Valued Intuitionistic Fuzzy Set Type-3 with Application to the Complex DNA Analysis

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In this article codes over lattice valued intuitionistic fuzzy set type-3 (LIFS-3) are defined. Binary block codes and linear codes are constructed over LIFS-3. Hamming distance and related properties of these newly established codes are examined. The research findings are applied to genetic codes. The set L of sixty-four codons is converted into a lattice and then codes are created over the set S of twenty amino acids by defining membership and nonmembership functions from the set of twenty amino acids to the sixty-four codon set. Comparison of codes over L-fuzzy set and LIFS-3 conducted in terms of hamming distance for codon system that ensures the efficiency of newly established codes.

1. Introduction

Probability theory was once believed to be an ideal tool to deal with any uncertain situation. However, there are many problems where the uncertainty appears as an imprecision and ambiguity rather than a statistical variation. The classical probability theory is not efficient and suitable for handling the uncertainties and imprecision that appear in pattern recognition. Zadeh [1] presented the notion of fuzzy set as an extension of the ordinary set. This notion is used for describing vagueness and ambiguity mathematically. The formulation of fuzzy sets over a nonempty set S is based on an allocation of a grade of membership to each element of S. The allocated grades are precisely the real numbers ranging between 0 and 1. Mathematically, a fuzzy set μ over S is characterized by a map $\mu\colon S \longrightarrow [0,1]$ termed as membership function and the value $\mu(x)$ as grade of membership of x in S. For instance, let X be the set of seven days of a week and $p(x)$ be the number of codes transmitted from a source center S and $q(x)$ be the number of codes received accurately at the receiver end R in the day $x \in X$. Then the function $\mu\colon X \longrightarrow [0,1]$ defined as $\mu(x) = q(x)/p(x)$, for all $x \in X$, provides a fuzzy set over X (that is, the collection of ordered pairs $(x, \mu(x))$). For example, if on x = Monday, 100 codes were transmitted from S and the supervisor at R reported that 75 codes were received properly at R, then $\mu(x) = 75/100 = 0.75$ would be the grade of membership of x in X, or we can say that the supervisor's statement's truth value was 0.75. According to classical probability, 25 codes were not received at R, but in real practice, mostly the interpreter at R can decode the partially transmitted codes for further processing. In this example, if ten partially received codes are processed, then the supervisor's statement's truth value increases from 0.75 to 0.85; the falsity value (nonmembership) decreases from 0.25 to 0.15. Let $\nu(x) = 0.15$ represent the falsity value of the supervisor's statement; then $1 - \{\mu(x) + \nu(x)\} = 0.10$ is the degree of uncertainty caused by the performance of interpreter at R. So, the membership grades are not enough to communicate the correct information in this case and need to introduce the idea of nonmembership grades; these grades should not be confused with the probability of non-occurrence $P(\overline{A}) = 1 - P(A)$ of an event A.

Atanassov [2], first introduced the notion of nonmenbership grages. The generalization of fuzzy sets that involves both the membership and nonmembership grades is known as the intuitionistic fuzzy set (IFS). Atanassov proposed fundamental properties, various arithmetic operations for his development in fuzzy sets. In continuation, Atanassov [3] presented the geometric interpretation of intuitionistic fuzzy objects. There are several other generalizations of fuzzy sets that mostly depend upon membership, nonmembership, hesitancy and indeterminacy grades. As in a fuzzy set, the grades $\mu(x)$ belong to the close interval $[0, 1]$, which is naturally endowed with a partial order. The assumption of order structures outside the unit interval laid the foundations of ordered fuzzy sets. Partial orderings and fuzzy uncertainties are features of many real-world problems. These kinds of problems are ill-posed most of the time, because either they have infinite solutions or no solutions at all. For instance, the selection of a grocery bundle from various packages is subjected to various contradictory and conflicting criteria. Nutritional value, quality, variety and above all cost, are some of the factors that a person can think about a bundle. Thus, the partial ordering of the bundles is an essential feature of this problem. Goguen [4] introduced the concept of L-fuzzy subsets of S where the interval $[0, 1]$ is replaced by a partially ordered set L. He discovered remarkable features of this generalized concept and concluded that L-fuzzy set theory works more efficiently in real-world problems. After IFS Atanassov and Stoeva [5] enrich the area and replaced the lattice [0, 1] by arbitrary complete lattice L, to relate membership and nonmembership functions $\mu, \nu\colon S \longrightarrow L$ he involved an involutive order reversing unary operation $N\colon L \longrightarrow L$. The new structure is known as lattice valued intuitionistic fuzzy set (LIFS-1). But it has certain limmitation mostly occurred due to the incorporation of the operator N. Gerstenkorn and Tepavcevic [6] made an attempt to upgrade Atanassov idea and proposed a new variant, that is, the lattice valued intuitionistic fuzzy set type 2 (LIFS-2) simply by exchanging the operator N with a linearization function $\ell\colon L \longrightarrow [0, 1]$. This modification is quite helpful in the establishment of decomposition theorem and synthesis but fails to deal with basic set operations. Choice of the linearization function is the main reseaon behind this failure. Finally, lattice homomorphism $\alpha\colon L \longrightarrow [0, 1]$ is used to relate membership and nonmembership functions and the new LIFS is called a lattice valued intuitionistic fuzzy set type-3 (LIFS-3). This new sturcture has certain advantages over the previously defined fuzzy sets and L-fuzzy sets mostly occurs due to the inclusion of lattices and lattice homomorphism. The lattice homomorphim is applicable to any collection of lattices unlike the unary operator N of LIFS-1 and satisfy all the basic set operations unlike the linearization function ℓ of LIFS-2.

A code is a system of rules used for data communication and information process. These rules are designed in the form of letters, symbols, images, sounds or numbers. Coding theory was established to study these rules mathematically and make them workable in daily communication. In communication, algebraic codes are used for data compression and error correction. Coding theory is concerned with the reliability of communication over a noisy channel. Algebraic codes are studied in a variety of domains and they have a wide range of applications across a large range of disciplines. Murugan and Ananthanarayana [7] presented the WordTrie, a specialised trie for storing words in order to facilitate fast coding. The code combination is generated in such a manner that the size of the WordCode for a word must be less than the entire size of the character coding. To improve the detection rate of NLOS nodes in any safety application of VANET, the WDHPBDS protocol was designed by Arjunan and Kaviarasan [8] in order to permit reliable delivery of emergency information to the targeted node in a timely manner. Nagaraju et al. [9] explored that by using a hybrid area exploration technique, mobility assisted localization for mission critical wireless sensor network applications can be achieved.

When data are transmitted through a noisy channel, some errors may arise. The vagueness in data transmission can be handled by involving theoretical fuzzy set concepts in the coding and decoding process. There are two ways to incorporate theoretical fuzzy set concepts in coding. One method was proposed by von Kaenel and Pierre [10], termed fuzzy code, and is defined as a fuzzy subset of n-dimensional vector space $\mathbb{F}^n$ over the field $\mathbb{F}$. He investigated the Hamming distance for newly established fuzzy codes. Kaenel's theory is based on the symmetric nature of the error—that is, the probability of $1 \longrightarrow 0$ crossover failure and $0 \longrightarrow 1$ is equally likely. However, in computer memories and VLSI circuits, the error may not be symmetric. Hall and Dial [11] discussed the asymmetric nature of fuzzy codes and generalized the results of Kaenel. They worked on the distance between fuzzy code words and proved that the distance is independent of the dimension of the vector space $\mathbb{F}^n$. Tsafack et al. [12] established a fuzzy linear code, fuzzy cyclic code over Gralois ring $\mathbb{Z}_{p^k}$. Amudhambigai and Neeraja [13] discussed arithmetic operations on fuzzy codes and introduced their super increasing sequences. Shijina [14] introduced multi-fuzzy code in terms of a multi-fuzzy subset of n-tuples over a set S, and produced some essential results for Hamming distance. Du [15] analyzed arithmetic operations of subtraction and division on intuitionistic fuzzy subsets that were induced by the Hamming distance. Ali et al. [16] developed soft algebraic codes over soft sets. They also defined soft canonical generator matrix and soft canonical parity check to decode these algebraic codes. Seselja and Tepavcevic [17] introduced another method of involving fuzzy theory in coding, which is based on defining a map $\overline{A}$ from a nonempty set $S = \{1, 2, \ldots, n\}$ for partially ordered set P. Seselja et al. [18] carried the concept and defined binary block codes over lattice valued fuzzy sets (L-fuzzy sets). Mališa and Lazarević [19] discussed the length and cardinality of block codes over L-fuzzy sets. The concepts of fuzzy codes and codes of ordered fuzzy sets are relatively new, but crucial for modifying the data communication and pattern recognition in deep learning [20] and fault detection for distributed components [21, 22]. However, these codes are unable to identify and handle any expected error in the information process while codes are transmitted in a noisy channel, for example, a spell

checker and machine reader. Moreover, the already existing fuzzy codes or codes over fuzzy sets are based solely on the degree of membership; the degree of nonmembership was not incorporated in any previous method. Lattice valued intuitionistic fuzzy set type-3 is a generalization of basic fuzzy set that incorporates both the degree of membership and the degree of nonmembership, so it is a more workable framework for modeling uncertain data. The effectiveness of LIFS-3 motivated us to construct codes over these fuzzy sets.

2. Preliminaries

2.1. Bounded Lattice. A relation ϱ on a nonempty set L is precisely a subset of $L \times L$. The elements of ϱ are more commonly denoted by $a\varrho b$; a is ρ related to b. Based on the nature of elements in the relation ϱ, it can have different names. For instance, if $x\varrho x$ for all $x \in L$, then ϱ is called reflexive; if $x \rangle y \Longrightarrow y \rangle x$, then ϱ is called symmetric; if $x\varrho y$ and $y \succ x \Longrightarrow x = y$, then ϱ is called anti-symmetric; if $x\varrho y$ and $y \rangle z \Longrightarrow x \rangle z$, then ϱ is called transitive. A reflexive, anti-symmetric and transitive relation is called a partial order of L. In this case, the set L is called a partially ordered set. For example, " $\leq$ " (less than or equal) is a partial order on the set of real numbers. The symbol " $\leq$ " is used for partial order in general and is also used in this article for better understanding by a wider audience. A subset Y of a partially ordered set L is said to be bounded above (below) if there exists $\ell \in L$ such that $\ell' \leq \ell$ ($\ell \leq \ell'$) for all $\ell' \in Y$. The element ℓ is called an upper (lower) bound of Y. The set Y may possess more than one upper (lower) bound. The least (greatest) member in the set of upper (lower) bounds of Y is called the supremum (infimum) of Y denoted by $\sup(Y)$ ($\inf(Y)$). More precisely, if $\ell = \sup(Y)$ then. $\ell \leq \xi$ ($\xi \leq \ell$).

The partially ordered set L is called a *lattice* if $\inf\{l_1, l_2\}$ and $\sup\{l_1, l_2\}$ exist for any pair of elements $l_1, l_2 \in L$. The symbols $\wedge$ and $\vee$ are used to indicate the infimum and supremum of l_1 and l_2. Thus, we can write $l_1 \wedge l_2 = inf\{l_1, l_2\}$ and $l_1 \vee l_2 = \sup\{l_1, l_2\}$. The lattice L is said to be *complete* if and only if $\inf(Y)$ and $\sup(Y)$ exist for all $Y \subset L$. The lattice L is said to be *bounded* if it has a greatest a element T and a least element B. These elements are also called the *top* and *bottom* elements of L, respectively. Thus, in a bounded lattice $B \leq l \leq T$ for all $l \in L$. If $\vee$ and $\wedge$ are distributive over each other, then such a lattice is called a distributive lattice. A complemented distributive lattice is called a Boolean lattice.

A lattice L can be represented geometrically by means of a Hasse diagram whose vertices are labeled by elements of L, and any two vertices a and b are joined by a line segment or a curve that goes upward from a to b whenever $a < b$ and there is no member $c \in L$ between a and b. These edges may cross each other but must not touch any vertex other than their endpoints. Such a diagram uniquely determines the partial order defined on L. In a partial order, the existence of $l_1 \wedge l_2$ and $l_1 \vee l_2$ is essential for the formulation of lattices. Being nonempty sets, we can define several maps between any two lattices. Any map that preserves the three essential components that constitute a lattice is called a *lattice homomorphism*. Mathematically, a map α from a lattice L_1 into a lattice L_2 is called a lattice homomorphism if for all $l_1, l_1' \in L_1$, $\alpha(l_1 \wedge l_1') = \alpha(l_1) \wedge \alpha(l_1')$ and $\alpha(l_1 \vee l_1') = \alpha(l_1) \vee \alpha(l_1')$.

If L_1 is a bounded lattice with top element T_{L_1} and bottom element is a bounded lattice with $\alpha(T_{L_1})$ and $\alpha(B_{L_1})$ as top and bottom elements. If L_1 and L_2 both are bounded lattices, then α maps top and bottom elements of L_1 onto the top and bottom elements of L_2 respectively.

Example 1. Let $L = \{B, T, a, c, d, e, f, g, h, i, j, k\}$ be a lattice [6] with partial order presented by the Hasse diagram in Figure 1.

The map α: $L \longrightarrow [0, 1]$ de is a lattice homomorphism.

A filter F of a lattice L is a subset $F \subseteq L$ satisfying two conditions stated as

(i) If $\ell \in F$ and $\ell' \ell'$, then $\ell' \in F$;

(ii) If $\ell, \ell' \in F$, then $\ell \wedge \ell' \in F$.

Let L be a lattice. The principal filter denoted by $\uparrow p$ is de Clearly, the principal filter is the smallest filter that contains the given element p. Let L be a bounded lattice. If M is a subset of L, then M_p: $= \uparrow p \cap M$.

2.2. Lattice Valued Intuitionistic Fuzzy Set Type-3. Zadeh [1] formulated the fundamental definition of fuzzy sets. A fuzzy subset A of a nonempty set S is perhaps the collection of ordered pairs with first components from S, and second components are images of the map μ: $S \longrightarrow [0, 1]$ (called membership function). Mathematically, A can be written as $A = \{(x, \mu(x))\colon x \in S\}$. The grades of membership for elements of S under μ can be used to define crisp subsets of S termed level or cut sets. For any $\alpha \in [0, 1]$, the α-level set of μ is de. The idea of a fuzzy set is a major breakthrough in mathematical logic giving a better approximation than the classical probability theory. However, in real-life problems, membership is not the only option in all cases; there is the chance of nonmembership to handle as well. For such cases, Atanassov introduced the concept of the intuitionistic fuzzy set (IFS). An intuitionistic fuzzy set (IFS) A over S is a triplet (A, μ, ν), where μ, ν: $S \longrightarrow [0, 1]$ (called membership and nonmembership functions). Thus, the IFS A can be written as $A = \{\langle x, \mu(x), \nu(x)\rangle\colon x \in S\}$ with $0 \leq \mu(x) + \nu(x) \leq 1$. "Less than or equal to" ($\leq$) constitutes a natural partial order on the closed interval $[0, 1]$ and turns it into a lattice. The replacement of $[0, 1]$ by any other lattice L gives us the concept of L-fuzzy and L-intuitionistic fuzzy sets. A lattice valued intuitionistic fuzzy set type-1 (LIFS-1) [6] is the set (S, L, μ, ν, N), where S is a non empty set; L is a lattice; μ: $S \longrightarrow L$ and ν: $S \longrightarrow L$ are membership and nonmembership functions; and N: $L \longrightarrow L$ is an involutive order reversing unary operator on L such that $\mu(x) \leq N(\nu(x))$ for all $x \in S$. The replacement of unary operator N by the linearization map ℓ: $L \longrightarrow [0, 1]$ satisfying $\ell(\mu(x)) + \ell(\nu(x)) \leq 1$ for all $x \in S$ constitutes a lattice valued intuitionistic fuzzy set type-2 (LIFS-2). A lattice valued intuitionistic fuzzy set type-3 (LIFS-3) is the quintuplet (S, L, μ, ν, α), where S is a nonempty set; L is a bounded lattice with top element T and bottom element B; μ: $S \longrightarrow L$

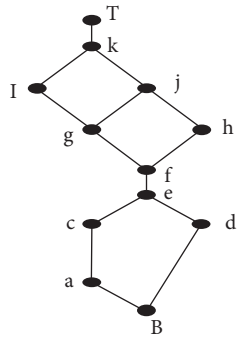

Figure 1: Lattice $L = \{B, T, a, c, d, e, f, g, h, i, j, k\}$.

and $\nu: S \longrightarrow L$ are membership and nonmembership functions; and $\alpha: L \longrightarrow [0,1]$ is a lattice homomorphism with $\alpha(\mu(x)) + \alpha(\nu(x)) \leq 1$ for all $x \in S$. For $p \in L$, two level sets in LIFS-3 are defined as:

$$\mu_p = \{X \in S \mid \mu(x) \geq p\}; \nu_p = \{X \in S \mid \nu(x) \geq p\}. \quad (1)$$

Two level functions generally called characteristics functions $\overline{\mu}_p$ and $\overline{\nu}_p$ are defined as:

$$\overline{\mu}_p(x) = 1 \Longleftrightarrow \mu(x) \geq p, \overline{\nu}_p(x) = 1 \Longleftrightarrow \nu(x) \geq p. \quad (2)$$

Proposition 1. *[6] Let S be a nonempty set and (S, L, μ, ν, α) be an LIFS-3. Then the following statements are true:*

(i) Let L be a lattice with bottom element B. Then $\mu_B = \nu_B = S$.

(ii) If $p \leq q$, then $\mu_q \subseteq \mu_p$ and $\nu_q \subseteq \nu_p$.

(iii) If $Z \subseteq L$, then $\wedge\{\mu_P | p \in Z\} = \mu_{\vee\{p|p\in Z\}}$ and $\wedge\{\nu_P | p \in Z\} = \nu_{\vee\{p|p\in Z\}}$.

Remark 1. The functions μ: S $\longrightarrow$ L and ν: S $\longrightarrow$ L define a partitioning of L under the equivalence relation $\sim$ defined as $g \sim h$ if and only if $\mu_g = \mu_h$ and $\nu_g = \nu_h$.

For every $g \in L$, the equivalence class of g is $[g]_\sim = \{h \in L | g \sim h\}$. As we know, the join (supremum) of a set may or may not be an element of that set, but for these classes $\vee [g] \sim \in [g] \sim$.

3. Codes over LIFS-3

Let $S = \{1, 2, \ldots, r\}$ and $S^{\alpha}_{L\mu\nu} = (S, L, \mu, \nu, \alpha)$ be an LIFS-3. For $p \in L$, define $\overline{\mathscr{C}}_p: S \longrightarrow \{0,1\}$ as:

$$\begin{aligned} \overline{\mathscr{C}}_p &= \overline{\mu}_p \wedge \overline{\nu}_p \\ &= u_p \wedge v_p \\ &= (a_1, \ldots, a_n) \wedge (b_1, \ldots, b_n) \\ &= (a_1 \wedge b_1)(a_2 \wedge b_2) \ldots (a_n \wedge b_n), \end{aligned} \quad (3)$$

where u_p and v_p are the codewords—also called vectors—for the element $p \in L$. The map $\overline{\mathscr{C}}_p$ is called a binary block codeword over $S^{\alpha}_{L\mu\nu}$. The LIFS-3 codewords inherit a partial order from the lattice L in such a way that $a_1 \ldots a_n \leq b_1 \ldots b_n$ if and only if $a_1 \geq b_1, a_2 \geq b_2, \ldots, a_n \geq b_n$ in L. The number of elements in S that are mapped onto $p \in L$ under μ and ν are called the degrees of u_p and v_p denoted by $s(u_p)$ and $s(v_p)$. Moreover, the degree of c_p is exactly equal to the sum of the maxima of $s(u_p)$ and $s(v_p)$. For a binary block code $\mathscr{C} \subseteq \{0,1\}^n$, a nonempty set S, a lattice L and lattice homomorphism $\alpha: L \longrightarrow [0,1]$, the set $S^{\alpha}_{L\mu\nu\mathscr{C}}$ is an LIFS-3 if the binary block code constructed on it is equal to $\mathscr{C}$.

Example 2. Let us consider a nonempty set $S = \{x, y, z\}$ and lattice L described in example 1. Define membership and nonmembership functions as

$$\mu = \begin{pmatrix} x & y & z \\ a & g & e \end{pmatrix} \nu = \begin{pmatrix} x & y & z \\ f & \mathrm{d} & j \end{pmatrix}. \quad (4)$$

Clearly, for all $s \in S$, the lattice homomorphism α satisfies $0 \leq \alpha(\mu(s)) + \alpha(\nu(s)) \leq 1$. Now for $a \in L$, $\overline{\mu}_a = 111$ and $\overline{\nu}_a = 101$ because $a \leq \mu(x), a \leq \mu(y), a \leq \mu(z)$ and $a \leq \nu(x)$, $a \geq \nu(y), a \leq \nu(z)$. Thus, $\mathscr{C}_a = (1 \wedge 1)(1 \wedge 0)(1 \wedge 1) = 101$.

Codewords corresponding to other elements of L can be computed in a similar fashion and are presented in Table 1.

As $s(u_a) = 1$ and $s(v_a) = 0$, the degree of a code word $c_a \subseteq \mathscr{C}$ is. $s(c_a) = \max\{s(u_a), s(v_a)\} = \max\{1, 0\} = 1$.

Theorem 1. *The binary block code $\mathscr{C} \subseteq \{0,1\}^n$ constitutes a lattice valued intuitionistic fuzzy set type-3 if and only if code $\mathscr{C}$ is closed under an intersection and the identity vector $11 \ldots 1$ belongs to $\mathscr{C}$.*

Proof. Let $\mathscr{C} \subseteq \{0,1\}^{\mathrm{n}}$ be a code and $S^{\alpha}_{L\mu\nu\mathscr{C}}$ be the corresponding LIFS-3. As L is a lattice, the families $\{\mu_p: p \in L\}$ and $\{\nu_p: p \in L\}$ are closed under a set theoretical intersection, which implies that the code $\mathscr{C}$ is closed. Hence, binary block code is closed under intersection. Moreover, $\mu_B = S$ and $\nu_B = S$ imply that $11 \ldots 1 \in \overline{\mu}_B$ and $11 \ldots 1 \in \overline{\nu}_B$ for the bottom element $B \in L$. Thus $\overline{\mathscr{C}}_B = \overline{\mu}_B \wedge \overline{\nu}_B = 11 \ldots 1$ belongs to $\mathscr{C}$. Conversely, suppose that $\mathscr{C}$ is closed under a set theoretical intersection and non-zero codeword $11 \ldots 1 \in \mathscr{C}$. Now we show that there is an LIFS-3 corresponding to the code $\mathscr{C}$. Consider $S = \{1, 2, \ldots, n\}$. The complements of the subsets of S obtained by the codewords of $\mathscr{C}$ in terms of characteristic functions constitute a lattice L with inclusion as a partial order. Now for $p \in L$, $\overline{\mathscr{C}}_p$ is a codeword such that $\overline{\mu}_p(i) = \overline{\nu}_p(i) = 0$ if and only if $i \in p$. The collection $\overline{\mathscr{C}}_p: p \in L$ gives an LIFS-3 having cod for all $x \in S$. □

3.1. Hamming Distance. The Hamming distance $d(s,t)$ defined in [23] is the number of places in which the two vectors (codewords) s and t differ. In other words, $d(s,t)$ represents the component-wise difference of the two codewords s and t. That is,

$$d(s,t) = \left|\{i: s_i = t_i\}\right|. \quad (5)$$

Consider a code $\mathscr{C}$. Then the distance $d(\mathscr{C})$ of a code $\mathscr{C}$ is defined in [23] as the minimum distance between two

Table 1: Codewords over LIFS-3.

$\overline{\mu}_p$	$\overline{\nu}_p$	$\overline{\mathscr{C}}_p = \overline{\mu}_p \wedge \overline{\nu}_p$	$\overline{\mu}_p$	$\overline{\nu}_p$	$\overline{\mathscr{C}}_p = \overline{\mu}_p \wedge \overline{\nu}_p$	$\overline{\mu}_p$	$\overline{\nu}_p$	$\overline{\mathscr{C}}_p = \overline{\mu}_p \wedge \overline{\nu}_p$
111	101	101	010	101	000	000	001	000
011	101	001	010	001	000	000	000	000
011	111	011	000	001	000	111	111	111
011	101	001	000	000	000	000	000	000

distinct codewords in $\mathscr{C}$. The number of non-zero components of a codeword is known as its Hamming weight denoted by $\|c_p\|$.

Proposition 2. *For any code $\mathscr{C}$, $d(\mathscr{C}) \geq min_{p\in\overline{\mu}(s),\overline{\nu}(s)}\, s(c_p)$.*

Proof. Let L be a lattice and $\mathscr{C}$ be a binary block code over $S^{\alpha}_{L\mu\nu}$. Then for any $p \in L$ and codeword c_p, the degree of c_p is equal to the maximum of $s(\mu_p)$ and $s(\nu_p)$. Ultimately if c_p differs at the i^{th} coordinate, then it will differ at each j^{th} coordinate, which is an outcome of some $x \in S$ mapped onto p under μ and ν. Thus, the distance of code $\mathscr{C}$ is at least equal to $s(c_p)$. □

Proposition 3. *For any $c_p \in \mathscr{C}$, the Hamming weight*

$$\left\|c_p\right\| \geq \max\left\{s\left(c_q\right) :\ q \in \mu(S), \nu(S) \text{ and } c_p \leq c_q\right\}. \tag{6}$$

Proof. Let $S^{\alpha}_{L\mu\nu}$ be an LIFS-3. Then $\overline{u}_q(x) = \overline{v}_q(x) = 1$ if $\mu(x), \nu(x) \geq q \Rightarrow c_q(x) = 1$ if $p = \mathscr{C}(x) \geq q$. Hence, $c_q(x)$ is non-zero if both $u_q(x)$ and $v_q(x)$ are non-zero, implying that the number of non-zero coordinate is equal to or greater than the degree of $s(c_q)$. □

Proposition 4. *Let $c_p, c_q \in \mathscr{C}$, such that $?_p \leq ?_q$. Then, $d(c_p, c_q) = \sum_{c_t \in T} s(c_t)$ where*

$$T = \left\{c_t \in \mathscr{C} :\ c_t \geq c_p \text{ and } c_t \leq c_q\right\}. \tag{7}$$

Proof. Let $S^{\alpha}_{L\mu\nu}$ be an LIFS-3. Let $\overline{u}_p$ and $\overline{u}_q$ be two vectors corresponding to the membership function. For $c_p \leq c_q$ we have $\overline{u}_p \leq \overline{u}_q$; this implies that the number of non-zero elements in $\overline{u}_q$ is not more than the number of non-zero elements in $\overline{u}_p$. Let $t \in \mu(S)$ such that $\overline{u}_t \geq \overline{v}_p$ and $\overline{u}_t \leq \overline{v}_q$. Then for each element $x \in S$ which is mapped onto t, we have $u_p(x) = 1$ and $u_q(x) = 0$.

A similar argument for the nonmembership function implies. $v_p(x) = 1$ and $v_q(x) = 0$.

Hence $c_p(x) = u_p(x) \wedge v_p(x) = 1$ and. $c_q(x) = u_q(x) \wedge v_q(x) = 0$.

As $c_p \leq c_q$, for each $x \in S$ there exist non-zero coordinates in c_q that belong to c_p and are mapped onto t. □

Theorem 2. *If c_p and c_q are two different codewords, then $d(c_p, c_q) = d(c_p, c_{p\vee q}) + d(c_q, c_{p\vee q})$.*

Proof. Suppose we have two vectors $\overline{u}_p$ and $\overline{v}_p$ corresponding to the membership and nonmembership functi in this case $p \vee q = q$, and $d(c_p, c_q) = d(c_p, c_{p\vee q}) + d(c_q, c_{p\vee q})$. Now let us consider the case when two vectors $\overline{u}_p$ and $\overline{u}_q$ are non-comparable. Then any coordinate which is non-zero in $\overline{u}_{p\vee q}$ will be non-zero in $\overline{u}_p$ and $\overline{u}_q$. A similar case exists for two vectors $\overline{v}_p$ and $\overline{v}_q$ corresponding to the nonmembership function. Let m be the coordinates at which two code words $\overline{u}_p$ and $\overline{u}_q$ and $\overline{v}_p$ and $\overline{v}_q$ differ, that is, $u_q(m) = 1$ and $u_p(m) = 0$.

In addition, $v_q(m) = 1$ and $v_p(m) = 0$, imply $c_q(m) = 1, c_p(m) = 0$.

Hence, c_p and c_q differ at m. If $\mu(m) = t$, then. $\overline{u}_t \geq \overline{u}_q$ and $\overline{u}_t \leq \overline{u}_p$.

If $\nu(m) = t$, then $\overline{v}_t \geq \overline{v}_q$ *an d* $\overline{v}_t \leq \overline{v}_p$. Hence $\overline{u}_t \leq \overline{u}_{p\vee q}, u_{p\vee q}(m) = 0$ and. $\overline{v}_t \leq \overline{v}_{p\vee q}, v_{p\vee q}(m) = 0$

Imply

$$c_{p\vee q}(m) = 0. \tag{8}$$

Hence c_q and $c_{p\vee q}$ differ at the coordinate m. □

3.2. Linear Codes over LIFS-3. A linear (n, k) code is defined in [23] is a k-dimensional subspace of a vector space $\{0, 1\}^n$ under the binary operation $\oplus$ of componentwise addition modulo 2.

Theorem 3. *Let $\mathscr{C}$ be a linear (r, k) code satisfying the conditions of Theorem 1. Then the lattice L of $S^{\alpha}_{L\mu\nu}$ corresponding to $\mathscr{C}$ is Boolean.*

Proof. Let $\mathscr{C}$ be a linear (r, k) code satisfying the conditions of Theorem 1. Then, corresponding to code $\mathscr{C}$, we have an LIFS-3, where L consists of all the elements which are the complement of subsets of the set S. The lattice is distributive and the elements 0 and 1 are in L. As in distributive lattice, every element has a unique complement and $\overline{r} = r \oplus 11 \ldots 1$, so this lattice is complemented, and hence it is a Boolean lattice.

The relation in Remark 2.4. is modified in the following result. □

Theorem 4. *If for μ: $S \longrightarrow L$ and ν: $S \longrightarrow L$ in $S^{\alpha}_{L\mu\nu}$ we have $M = \mu(S)$ and $N = \nu(S)$, then for any pair of elements p,q in $Lp \sim q$ if and only if $M_p = M_q$ and $N_p = N_q$.*

Proof. For $S^{\alpha}_{L\mu\nu}$, the relation $\sim$ defined by $p \sim q$ if and only if $\mu_p = \mu_q$ and $\nu_p = \nu_q$ is an equivalence relation on L. As $\mu_p = \{x \in S | \mu_P = 1\} = \{x \in S | \mu_P \in \uparrow p\}$ and $\nu_p = \{x \in S | \nu_P = 1\} = \{x \in S | \nu_P \in \uparrow p\}$. We get that

$$\begin{aligned} p \sim q &\Leftrightarrow \mu_p = \mu_q, \\ \nu_p &= \nu_q \\ \Leftrightarrow \{x \in S | \mu(x) \in \uparrow p\} &= \{x \in S | \mu(x) \in \uparrow q\}, \\ \{x \in S | \nu(x) \in \uparrow p\} &= \{x \in S | \nu(x) \in \uparrow q\}, \\ \Leftrightarrow \uparrow p \cap M &= \uparrow q \cap M \\ \uparrow p \cap N &= \uparrow q \cap N, \\ \Leftrightarrow M_p &= M_q, \\ N_p &= N_q. \end{aligned} \tag{9}$$

Thus for $g, h \in L$, $g \neq h$ implies $\uparrow g \cap M \neq \uparrow h \cap M$ turns out to be the necessary and sufficient condition for an equivalence class to be a singleton. □

Theorem 5. *The sets $\mu(S)$ and $\nu(S)$ consists of all coatoms of the Boolean lattice L of lattice valued intuitionistic fuzzy set type-3 $S^{\alpha}_{L\mu\nu}$ constituted by a linear (r, k) code.*

Proof. Let $S^{\alpha}_{L\mu\nu}$ be an LIFS-3 corresponding to the linear code $\mathscr{C}$. From Theorem 4. if $x \neq y \in L$, then.

$$\begin{aligned} [x) \cap \mu(S) &\neq [y) \cap \mu(S), \\ [x) \cap \nu(S) &\neq [y) \cap \nu(S). \end{aligned} \tag{10}$$

Hence, the top element 1_L of the lattice L does not belong to $\mu(S)$ and $\nu(S)$ otherwise, the code $\mathscr{C}$ does not contain the codeword $00\ldots0$, which contradicts the linearity of the code. Now on the contrary, suppose that one co-atom, say, y, is not present in $\mu(S)$ and $\nu(S)$; then

$$\begin{aligned} [y) \cap \mu(S) &= [1) \cap \mu(S), \\ [y) \cap \nu(S) &= [1) \cap \nu(S). \end{aligned} \tag{11}$$

Thus $|\mathscr{C}| < |L|$, which leads to a contradiction. In fact, each codeword that corresponds to a co-atom has only non-zero coordinates, and forms a basis for the code $\mathscr{C}$. Let t be an element in $\mu(S)$ and $\nu(S)$ but not a co-atom. Then each codeword corresponding to t has a zero coordinate. If $\overline{c}_t$ is a codeword corresponding to t, then it is linearly independent of all those elements which are in the base that are not true. Hence $\mu(S)$ and $\nu(S)$ will consist of all co-atoms of a Boolean lattice. □

Theorem 6. *The linear (r, k)-code $\mathscr{C}$ corresponds to an LIFS-3 if and only if $\mathscr{C}$ is closed under intersection and for each $j \in \{1, \ldots, r\}$ there is a codeword in $\mathscr{C}$ having a non-zero j th coordinate.*

Proof. Let $S^{\alpha}_{L\mu\nu}$ be the LIFS-3 corresponding to $\mathscr{C}$. Then by Theorem 3, $\mathscr{C}$ is closed under an intersection, and non-zero vector $11\ldots1$ belongs to the families $\overline{\mu}_p$ and $\overline{\nu}_p$ for an element $p \in L$. As codeword $\overline{c}_p \in \mathscr{C}$ is a meeting of these two families, it is a non-zero vector contained in $\mathscr{C}$. Hence, satisfies the required condition. Conversely, suppose $\mathscr{C}$ is a linear (r, k) code satisfying the given conditions. The closeness of $\mathscr{C}$ under intersection ensures the existence of $11\ldots1$ in $\mathscr{C}$, which implies the constitution of LIFS-3. □

Theorem 7. *Let $S^{\alpha}_{L\mu\nu}$ be an LIFS-3 over a Boolean lattice L. If $\mu(S)$ and $\nu(S)$ include the maximum element of the set of all co-atoms of L, then the code constructed on $S^{\alpha}_{L\mu\nu}$ is linear.*

Proof. Consider $S^{\alpha}_{L\mu\nu}$ over a Boolean lattice L. The codewords corresponding to the maximum elements of co-atoms of a boolean lattice are linearly independent and thus can be extended to a basis that will be used to generate other codewords from the former codewords. If, corresponding to a maximum number of co-atoms, we have n codewords, then the code $\mathscr{C}$ consists of exactly 2^n codewords. Thus $\mathscr{C}$ is closed under the binary operation $\oplus$, and hence it is linear. □

Example 3. Consider the lattice $L = \{0, 1, a, b, c, d, e, f\}$ with partial order presented in Figure 2.

Construct an LIFS-3 on $S = \{1, 2\}$ by defining μ and ν as $\mu = \begin{pmatrix} 1 & 2 \\ e & f \end{pmatrix}$ and $\nu = \begin{pmatrix} 1 & 2 \\ f & d \end{pmatrix}$. Then a linear code is obtained as shown in Table 2.

Theorem 8. *Let $\mathscr{C}$ be a linear code over where a set T consists of maximum elements of the classes of co-atoms of Boolean lattice.*

Proof. For the linear code $\mathscr{C}$ over $S^{\alpha}_{L\mu\nu}$, the sets $\mu(S)$ and $\nu(S)$ consist of all the maximum elements of co-atoms. Hence $\mu(S) = \nu(S) = T$ and by Proposition 2.

$$d(\mathscr{C}) \geq \min_{p \in \overline{\mu}(s), \overline{\nu}(s)} s\left(c_p\right). \tag{12}$$

As for $s(u_p)$ and $s(v_p)$, this distance is equal to the minimum value on the codeword corresponding to the class of the co-atoms with minimal degree, and thus $s(c_p)$ is also attained its minimum. □

4. Application

Proteins are the most diverse class of biomolecules, both structurally and functionally, and they carry out many tasks. They are polymers of amino acids which are attached via peptide bonds and arranged in the form of long polypeptide chains [24]. Proteins have an extremely wide range of different functions, and they do not act by themselves. They usually interact with other proteins or macromolecules to form fully functional complexes, and these protein complexes are responsible for carrying out many different functions [25]. Nucleic acids are giant biomolecules made of monomers called nucleotides. Nucleic acids refer to the genetic material present in cells that transfer all the hereditary and transmissible information from parents to offspring. Deoxyribonucleic acid (DNA) and ribonucleic acid (RNA) are the two types of nucleic acids. The key task of nucleic acids is to use their stored genetic information for the synthesis of proteins via processes commonly known as translation and transcription. DNA is transcribed to RNA and then translated into a protein. The translation

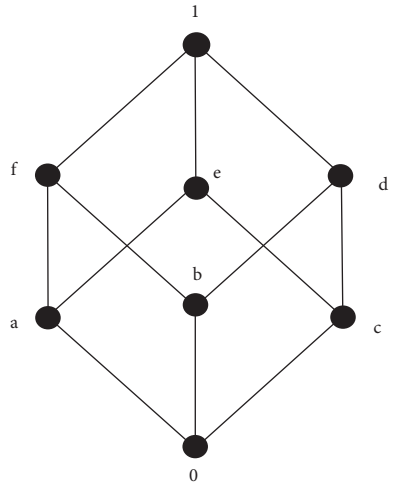

Figure 2: Lattice $L = \{0, 1, a, b, c, d, e, f\}$.

Table 2: Linear code over LIFS-3.

$\overline{\mu}_p$	$\overline{\nu}_p$	$\mathscr{C}$	$\overline{\mu}_p$	$\overline{\nu}_p$	$\mathscr{C}$	$\overline{\mu}_p$	$\overline{\nu}_p$	$\mathscr{C}$	$\overline{\mu}_p$	$\overline{\nu}_p$	$\mathscr{C}$
00	00	00	10	10	10	01	00	00	01	01	01
10	10	10	00	11	00	11	01	01	11	11	11

machinery includes tRNA, mRNA and ribosomes. A ribosomal subunit attaches to an mRNA molecule; then, tRNA molecules that have three complementary bases in their anticodon regions recognize and bind to specific codon sequences on the mRNA molecule. The ribosome moves along the mRNA, matching three base pairs at a time and adding the amino acids to the polypeptide chain [24, 25].

All living cells use a genetic code to translate the information encoded within the genetic material (DNA and RNA) into proteins. The genetic code describes the set of trios of nucleotides which specify particular amino acids (three nucleotides to one amino acid). There are twenty amino acids typically used to build proteins. As there are four bases, there are 64 possible base triplets [26]. A genetic code is a list of codons, and a codon is a consecutive series of three nucleotides. A codon set is an extension of the four letter-alphabet of DNA. There are four DNA bases, adenine (A), guanine (G), cytosine (C) and thymine (T), and thymine is replaced by uracil in RNA. The base guanine is the complementary base of cytosine, and adenine is that of thymine. Each codon corresponds to a specific type of amino acid; for example, the sequence of nucleotides "GUU" corresponds to a specific amino acid known as valine [27]. Two or more different codons can correspond to the same amino acid, making the genetic code degenerate, and such codons are known as synonymous codons. In a coding sequence, the synonymous codons are not used with equal frequencies in many organisms. This phenomenon is called synonymous codon usage bias (SCUB), and this shows that during the translation of genes to proteins, there is nonuniform usage of synonymous codons encoding the same amino acid; e.g., UGC and UGU are two different sequences corresponding to the same amino acid, cysteine [28].

The algebraic structures of the genetic code are essential to understanding the information and applications which are stored within the code. There are various conventional mathematical models of the genetic code, which include binary representations of the DNA bases. The representations of the four DNA bases by Jimenez-Montano et al. [29] are: ?=00, $G = 01$, $U = 10$ and $C = 11$. Stambuk [30] presented the universal metric properties of the human genetic code and described it by using the nucleotide base representation on the square having U or $T = 00$, $C = 01$, $G = 10$ and $A = 11$. A model for topological coding of proteins was proposed by Karasev and Stefanov [31], using: $C = 00$, $U = 01$, $G = 10$ and $A = 11$. Sánchez et al. [32] described the Boolean lattice of the genetic code and showed that the Boolean lattice of the genetic code can be obtained as the third power of the initial lattice. He used two types of lattices, the primal $(B(X), \sup, \inf)$ and the dual $(B(X), \inf, \sup)$, with $X = \{U, C, G, A\}$. The representations of the four bases given to primal lattice are: $G = 00$, $A = 01$, $U = 10$ and $C = 11$. Similarly, for the dual lattice: $C = 00, U = 01, A = 10$ and $G = 11$. A Hasse diagram of the genetic Boolean lattice is presented in the following Figure. It shows that the codons with uracil as a second base encode hydrophobic amino acids, and the codons with adenine as the second base encode hydrophilic amino acids. Additionally, the Hamming distances between pairs of codons reveal distinct hydrophobicities among their encoded amino acids. If XYZ and $X_1Y_1Z_1$ are two codons, then $XYZ \leq X_1Y_1Z_1$ only if $X \leq X_1, Y \leq Y_1$, $Z \leq Z_1$, and we can say that the codons are comparable.

In recent years, a paradigm shift for "new biology" has taken place as a direct result of an expanded awareness of the fuzziness of the processes that occur in biological systems. There is a lot of evidence to suggest that many biological processes are not deterministic but rather include an inherent element of uncertainty. Many studies and observations have shown that fuzzy effects are a very important part of how living things develop and work in their physiology and evolution. Both fuzzy set theory and fuzzy logic, along with many other approaches to computational intelligence, have the potential to solve a numerous challenges that arise in the field of bioinformatics. An analysis of protein sequences can be performed using fuzzy set theory and fuzzy logic. A method was devised to predict the solvent accessibility of each amino acid in a protein sequence by using a k-nearest neighbour approach [33]. In addition, the FKNN algorithm has been used to predict a protein's subcellular location [34], which refers to the region of the cell in which the protein is found (including extracellular, cytoplasm, nucleus). In this study, a class membership function was used in accordance with the dipeptide composition of a protein sequence. Fuzzy logic was used in conjunction with neural networks to describe how protein motifs can change [35].

An information-theoretic-based fuzzy inference engine was created to predict coding areas, or the sequence segments that correspond to proteins, for genomic sequences (DNA) [36]. Polynucleotides (words made up of the letters A, T, C, and G) were also employed by researchers as fuzzy

Table 3: Amino acids and RNA codons.

Amino acid	RNA codons	Abb	Amino acid	RNA codons	Abb
Isoleucine	AUU, AUC, AUA	I	Phenylalanine	UUU, UUC	F
Valine	GUA, GUC, GUG, GUU	V	Lysine	AAA, AAG	K
Tryptophan	UGG	W	Methionine	AUG	M
Alanine	GCA, GCC, GCG, GCU	A	Glycine	GGA, GGC, GGG, GGU	G
Cysteine	UGC, UGU	C	Tyrosine	UAC, UAU	Y
Proline	CCA, CCC, CCG, CCU	P	Threonine	ACA, ACC, ACG, ACU	T
Serine	UCA, UCC, UCG, UCU, AGC, AGU	S	Histidine	CAC, CAU	H
Glutamic acid	GAA, GAG	E	Asparagine	AAC, AAU	N
Glutamine	CAA, CAG	Q	Aspartic acid	GAC, GAU	D
Leucine	CUA, CUC, CUG, CUU, UUA, UUG	L	Arginine	CGA, CGC, CGG, CGU, AGA, AGG	R

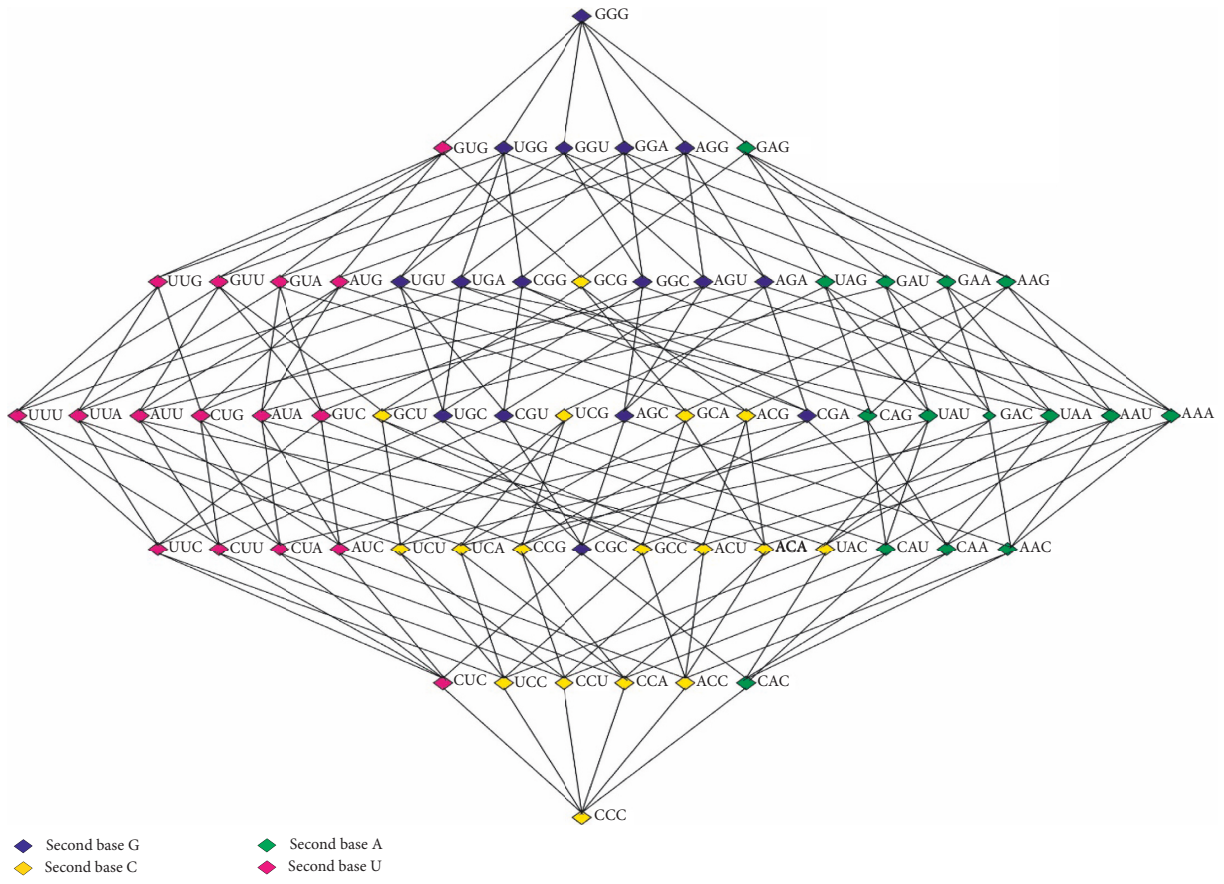

Figure 3: The Boolean lattice of 64 codons.

sets, and they developed a method for calculating the distances between them as points in a hypercube [37, 38]. The procedure served as a tool for comparing various genetic sequences. Additionally, operons, an important structure in bacterial genomes, were predicted using fuzzy scoring functions based on various biological information (e.g., genome sequences, functional annotations, and conservation across multiple genomes) [39]. An operon is a closely related group of neighbouring genes on a DNA sequence.

Ordinary fuzzy sets are used in the literature to model numerous bioinformatics-related problems. In a conventional fuzzy set, the degree of belongingness to the set under discussion is indicated by the membership function, which assigns a number from the unit interval to each element of the discourse universe. A LIFS-3, on the other hand, is distinguished by two functions that, express the degree of belongingness and the degree of non-belongingness. This concept, which is a natural generalization of an ordinary fuzzy set, appears to be helpful in simulating a variety of real-world scenarios. Thus, the idea of LIFS-3 can be used to study biological problems in a more significant way.

In this paper we investigate the genetic code further by considering a lattice valued intuitionistic fuzzy set. We consider S to be the set of 20 amino acids: x_1 = Phenylalanine, x_2 = Leucine, x_3 = Isoleucine, x_4 = Methionine, x_5 = Valine, x_6 = Serine, x_7 = Proline,

Table 4: Genetic codes over LIFS-3.

p	$\overline{\mu}_p$	$\overline{\nu}_p$	$\overline{\mathscr{C}}_p = \overline{\mu}_p \wedge \overline{\nu}_p$
CCC	1111111111111111111	1111111111111111111	1111111111111111111
CUC	11111000000000001111	11111100000000001111	11111000000000001111
UCC	11001100110000111111	11001100110000111101	11001100110000111101
CCU	10111111111010101111	01010000000101010100	00010000000000000101
CCA	01010000000101010110	01010000000101010110	01010000000101010110
ACC	00111001100011110011	00111001100011110011	00111001100011110011
CAC	00000000011111111111	00000000011111111111	00000000011111111111
UUC	11001000000000001101	10010000000000001101	11001000000000001101
CUU	10111000000000001101	01010000000000000111	00010000000000000111
CUA	01010000000000000110	01010000000000000110	01010000000000000110
AUC	00111000000000000011	00111000000000000011	00111000000000000011
UCU	10001100110000101101	01000000000000010101	00000000000000000101
UCA	01000000000000010100	00100000000000010100	01000000000000000100
CCG	00010000000000000100	01010100000100010110	00010000000000010110
CGC	00000000000000000111	00000000000000001111	00000000000000000111
GCC	00001000100000110001	00001000100000110001	00001000100000110001
ACU	00111001100010100001	00010000000001010011	00010000000000000001
ACA	00010000000001010010	00100000000011101010	00010000000001010010
UAC	00000000010000111101	00000000010000111111	00000000110000111101
CAU	00000000000101010111	00000000001000101011	00000000000000000101
CAA	00000000001010110110	00000000000101010110	00000000000101010110
AAC	00000000000011110011	00000000000011110011	00000000000011110011
UUU	10000110000000001101	01000000000000000100	00000000000000000100
UUA	01000000000000000100	01000000000000000100	01100000000000000100
AUU	00111000000000100001	00010000000000000010	00010000000000000001
CUG	00010000000000000100	01010000000000000110	00010000000000000100
AUA	00010000000000000010	00010000000000000010	00010000000000000010
GUC	00000000000000110001	00000000000000110001	00000000000000110001
GCU	00001000100000010001	00000000000000010000	00000000000000000000
UGC	00000000000000001111	00000000000000001111	00000000000000001111
CGU	00000000000000000100	00000000000000000100	00000000000000000100
UCG	00000000000000000100	00000000000000000100	00000000000000000100
AGC	00000000000000000011	00000000000000000011	00000000000000000011
GCA	00000000000000010000	00000000000000010000	00000000000000010000
ACG	00010000000000000000	00010000000001010010	00010000000000000000
CGA	00000000000000000110	00000000000000000110	00000000000000000110
CAG	00000000000000000100	00000000000100010110	00000000000000000100
UAU	00000000010000101101	00000000000000000101	00000000000000000101
GAC	00000000000000110001	00000000000000110001	00000000000000110001
UAA	00000000000000010100	00000000000000010100	00000000000000010100
AAU	00000000000010100001	00000000000000010010	00000000000000000000
AAA	00000000000001010010	00000000000001010010	00000000000001010010
UUG	00000000000000000100	01000000000000001100	00000000000000000100
GUU	00001000000000000001	00000000000000000000	00000000000000000000
GUA	00000000000000000000	00000000000000000000	00000000000000000000
AUG	00010000000000000000	00010000000000000000	00010000000000000000
UGU	00000000000000001101	00000000000000000101	00000000000000000100
UGA	00000000000000000100	00000000000000000100	00000000000000000100
CGG	00000000000000000100	00000000000000000110	00000000000000000100
GCG	00000000000000000000	00000000000000010000	00000000000000000000
GGC	00000000000000000001	00000000000000000001	00000000000000000001
AGU	00000000000000000001	00000000000000000010	00000000000000000000
AGA	00000000000000000010	00000000000000000010	00000000000000000010
UAG	00000000000000000100	00000000000000010100	00000000000000000100
GAU	00000000000000100001	00000000000000010000	00000000000000000000
GAA	00000000000000110000	00000000000000010000	00000000000000010000
AAG	00000000000000000000	00000000000000010010	00000000000000000000
GUG	00000000000000000000	00000000000000000000	00000000000000000000
UGG	00000000000000000100	00000000000000000100	00000000000000000100
GGU	00000000000000000001	00000000000000000000	00000000000000000000

Table 4: Continued.

p	$\overline{\mu}_p$	$\overline{\nu}_p$	$\overline{\mathscr{C}}_p = \overline{\mu}_p \wedge \overline{\nu}_p$
GGA	00000000000000000000	00000000000000000000	00000000000000000000
AGG	00000000000000000100	00000000000000000100	00000000000000000100
GAG	00000000000000000000	00000000000000010000	00000000000000000000
GGG	00000000000000000000	00000000000000000000	00000000000000000000

Table 5: Hamming distance between pairs of Amino acids.

Amino acid	G	W	C	R	S	V	L	F	M	I	E	D	Y	K	N	Q	H	A	T	p
G	0	1.5	2.8	1.8	3.2	1.4	3.8	5.2	1.7	2.5	1	2.9	2.5	2	3	3.5	6	2.4	4.5	8.6
W	1.5	0	1	0.6	2.7	3	2.8	5	2	4	2	2.5	2	2.5	4	2	5.5	2.5	5.5	8.2
C	2.8	1	0	1.2	2.8	2.3	2.8	5.8	3	3.7	3	3	2	3.6	4	2.5	5	3.1	5.4	8
R	1.8	0.6	1.2	0	3.1	2.5	2.8	4.8	2.5	3.5	2	2.8	3	2.5	4.3	2.3	5.5	2.9	5.3	7.9
S	3.2	2.7	2.8	3.1	0	3.8	3.0	5.3	4.0	4.2	3.3	2.9	3.3	4	4.6	3.6	6.5	3.8	5.7	8.5
V	1.4	3	2.3	2.5	3.8	0	4.3	6.2	2	3.7	1.2	1.8	2.8	2.2	3	3.6	6.2	1.6	4.6	8
L	3.8	2.8	2.8	2.8	3.0	6.2	0	6.5	3.2	3.9	4	4.8	3.5	4.8	5.9	4.3	7	4.3	6.3	7.8
F	5.2	5	5.8	4.8	5.3	6.2	6.5	0	7	6.8	6	6	5	5.3	5	5	8	5.8	8.3	8.5
M	1.7	4	3	2.5	4	2	3.2	7	0	2	1.5	2.5	4	2.5	4	4	7.5	2	3.5	8.7
I	2.5	4	3.7	3.5	4.2	3.7	3.9	6.8	2	0	3	4	4.5	3.8	6.3	5.3	7.3	3.6	3.8	4.5
E	1	2	3	2	3.3	1.2	4	6	1.5	3	0	2	3	2	3.5	3.5	7.3	2.2	5.1	8.3
D	2.9	2.5	3	2.8	2.9	1.8	4.8	6	2.5	4	2	0	2.5	2.8	3.3	3.5	6	2	4.6	8.1
Y	2.5	2	2	3	3.3	2.8	3.5	5	4	4.5	3	2.5	0	4	4.2	3.5	4.5	3.6	5.4	8.2
K	2	2.5	3.6	2.5	4	2.2	4.8	5.3	2.5	3.8	2	2.8	4	0	3	4.5	5.3	2.6	5.1	8.4
N	3	4	4	4.3	4.6	3	5.9	5	4	6.3	3.5	3.3	4.2	3	0	4.3	5.5	4.3	4.8	8.6
Q	3.5	2	2.5	2.3	3.6	3.6	4.3	5	4	5.3	3.5	3.5	3.5	4.5	4.3	0	5.5	5	5.8	7.2
H	6	5.5	5	5.5	6.5	6.2	7	8	7.5	7.3	7.3	6	4.5	5.3	5.5	5.5	0	6	8.1	7.2
A	2.4	2.5	3.1	2.9	3.8	1.6	4.3	5.8	2	7.3	2.2	2	3.6	2.6	4.3	5	6	0	4.7	4.5
T	4.5	5.5	5.4	5.3	5.7	4.6	6.3	8.3	3.5	3.8	5.1	4.6	5.4	5.1	4.8	5.8	8.1	4.7	0	4.5
P	8.6	8.2	8	7.9	8.5	9	7.8	8.5	8.7	4.5	8.3	8.1	8.2	8.4	8.6	7.2	4.5	7.2	8.9	0

x_{81} = Threonine, x_9 = Alanine, x_{10} = Tyrosine, x_{11} = Histidine, x_{12} = Glutamine, x_{13} = Aspartic, x_{14} = Lysine, x_{15} = Asparagine, x_{16} = Glutamic, x_{17} = Cysteine, x_{18} = Tryptophan, x_{19} = Arginine, x_{20} = Glycine. The codons related to amino acids are listed in Table 3.

Let L be the lattice (see Figure 3.) consisting of 64 codons. As two or more codons can encode the same amino acid e.g., UUU and UUC encode the same amino acid, phenylalanine we put $\overline{\mu}(x_1) = \text{UUU}$ and $\overline{\nu}(x_1) = \text{UUC}$, where x_1 =phenylalanine. Similarly, we can assign a codon for every other amino acid, and we ha where

$$\begin{aligned}
&a_1 = \text{UUU} \quad a_2 = \text{UUA} \quad a_3 = \text{AUU} \quad a_4 = \text{AUG} \quad a_5 = \text{GUU}\\
&a_6 = \text{UCU} \quad a_7 = \text{CCU} \quad a_8 = \text{ACU} \quad a_9 = \text{GCU} \quad a_{10} = \text{UAC}\\
&a_{11} = \text{CAU} \quad a_{12} = \text{CAA} \quad a_{13} = \text{AAU} \quad a_{14} = \text{AAA} \quad a_{15} = \text{GAU}\\
&a_{16} = \text{GAA} \quad a_{17} = \text{UGU} \quad a_{18} = \text{UGG} \quad a_{19} = \text{AGA} \quad a_{20} = \text{GGU}\\
&b_1 = \text{UUC} \quad b_2 = \text{UUG} \quad b_3 = \text{AUC} \quad b_4 = \text{AUG} \quad b_5 = \text{GUC}\\
&b_6 = \text{UCC} \quad b_7 = \text{CCC} \quad b_8 = \text{ACC} \quad b_9 = \text{GCU} \quad b_{10} = \text{UAC}\\
&b_{11} = \text{CAU} \quad b_{12} = \text{CAG} \quad b_{13} = \text{AAC} \quad b_{14} = \text{AAG} \quad b_{15} = \text{GAC}\\
&b_{16} = \text{GAG} \quad b_{17} = \text{UGC} \quad b_{18} = \text{UGG} \quad b_{19} = \text{AGG} \quad b_{20} = \text{GGC}
\end{aligned} \tag{13}$$

Consider a representation of four bases as $C = 00$, $U = 01$, $A = 10$ and $G = 11$. Let $p = CCC$ be an element of a lattice L. Then, $\overline{\mu}_{CCC}(x_1) = \mu(x_1) \geq CCC$. Now, by using definition of a level function, $\overline{\mu}_{CCC}(x_1) = 1$. Similarly, $\overline{\mu}_{CCC}(x_2), \ldots, \overline{\mu}_{CCC}(x_{20}) = 1$. Thus $\mu_{CCC} = 1111111111111111111$ is a codeword relative to the codon CCC. In similar fashion, the remaining codewords corresponding to the other codewords can be found, which are shown in Table 4.

Hence, we have a binary code corresponding to 64 codons having length 20. Furthermore, the difference

Table 6: Hamming distance between hydrophobic and hydrophilic Amino acids.

Codewords	$\mathscr{C}_{XAZ}$	$\mathscr{C}_{XUZ}$	Codewords	$\mathscr{C}'_{XAZ}$	$\mathscr{C}'_{XUZ}$
$\mathscr{C}_{XAZ}$	8.2	11	$\mathscr{C}'_{XAZ}$	7.6	9.3
$\mathscr{C}_{XUZ}$	9.5	6.5	$\mathscr{C}'_{XUZ}$	9.3	6.1

between two codewords can be calculated by using well known Hamming distance. That is,

$$d_H(\mathscr{C}_{CUC}, \mathscr{C}_{UCC}) = d_H(1111100000000000111, 1100110011000011110) = 8. \quad (14)$$

If we consider only membership values μ_p from the above table, then it is an L-fuzzy code [28]. The distances between different amino acids pairs can be computed in terms of mean distances between their respective codons. For instance, the amino acids glycine (G) and methionine (M) are encoded by the bases GGA, GGC, GGG, GGU and AUG. Thus, the distance between G and M means the distances between the codewords ($\mathscr{C}_{GGA}$, $\mathscr{C}_{GGC}$, $\mathscr{C}_{GGU}$, $\mathscr{C}_{CUG}$ and $\mathscr{C}_{AUG}$) relative to their codons. The distances between all the 20 pairs of amino acids are shown in Table 5.

The Hamming distance between two codons reflects the variations among the physico-chemical properties of the relative amino acids. Amino acids can be categorized by two types, hydrophobic amino acids (codons having U in second base) and hydrophilic amino acids (codons having A in the second base). Consider the collections of codewords $\mathscr{C}_{XAZ}$, $\mathscr{C}_{XUZ}$, $\mathscr{C}'_{XAZ}$ and $\mathscr{C}'_{XUZ}$, where $X, Y, Z \in \{A, C, G, U\}$ over LIFS-3 and L-fuzzy set, respectively. Table 6 shows the Hamming distances between these sets.

It can be seen that the distances between amino acids with larger differences in physico-chemical properties are larger in an LIFS-3 environment than a L-fuzzy set.

5. Conclusion

The authors' main focus was to construct codes over lattice valued intuitionistic fuzzy set type-3. Binary and binary Linear codes are commonly defined in terms of subspaces of $\mathbb{Z}_2^n$. Different attempts were made to incorporate the imprecisions in data into the coding process by involving theoretical fuzzy set concepts. Using membership and nonmembership functions, codes were designed over LIFS-3. Distances of code were examined in relation with the degrees of the codewords. It was concluded that binary block and binary linear codes can be constructed over LIFS-3, and conversely, from any given binary block code, we can formulate an LIFS-3. Code over a lattice valued intuitionistic fuzzy set type-3 was constructed by considering the lattice of a 64-codon system, and we found that the physico-chemical differences can be interpreted by computing the Hamming distances between codewords. In the case of LIFS-3, the Hamming distances between codewords were greater than the Hamming distances between codewords in L-fuzzy sets, which indicates the efficiency of the LIFS-3 compared to the L-fuzzy set. In the future, a variety of extensions will be possible. One of the major directions of this work will be to study the already existing codes, such as Hamming code and Hadamard code, by introducing the concept of LIFS-3. This may be done by encoding the messages by using the decomposition of LIFS-3, which gives the family of characteristic functions. Furthermore, the developed application could be used for the further study of the structure of genetic code. As found in the literature, the variations among different physio-chemical properties of amino acids are described by the Hamming distances between the codons. In LIFS-3 codes, this Hamming distance is related to the degrees of code words (or classes), so we can extend it by incorporating these degrees along with the Hamming distances. Moreover, there are several practically useful generalizations of fuzzy sets including the picture fuzzy sets [40], Pythagorean fuzzy sets [41], hesitant fuzzy sets [42] and neutrosophic sets [43] where the replacement of the interval [0, 1] by lattices L can play a vital role in the development and application of fuzzy coding theory.

Data Availability

No data is used to support this study.

Conflicts of Interest

The authors declare that there were no conflicts of interest regarding the publication of this article.

Authors' Contributions

All authors contributed equally to the preparation of this manuscript.

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