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Closure operators in terms of chromosomal mutations

Abd El Fattah El Atik[1], **Mohammed S. Badr**[2]

[1]Department of Mathematics
Faculty of Science
Tanta University
Tanta, Egypt

[2]Department of Mathematics
Faculty of Science
New Valley University
El Kharga, Egypt

email: aelatik55@yahoo.com, m.shaban@sci.nvu.edu.eg

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Abstract

Topology provides an easy mathematical method to express some problems and helps to access a mathematical model to find solutions of these problems. The aim of this paper is to provide a mathematical model of chromosomal mutations in terms of mathematical and topological methods. Moreover, we verify the validity of the mathematical model through topological operators by matching the properties of the resulting spaces with the biological properties of each of the chromosomal mutations.

1 Introduction and preliminaries

There are two types of mutations: mutations that occur on chromosomes called chromosomal mutations and mutations that occur on the genes called

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gene mutation [4,6]. In a previous study, gene mutations were used. There are five types of chromosomal mutations: Deletion, Duplication, Inversion, Translocation and NonDisjunction mutations. A chromosome is a molecule of DNA made up of a group of genes and contains part or all of the genetic material [2,5,11]. Humans have 23 pairs of chromosomes with each parent sharing one chromosome. All chromosomes are inherited under normal conditions [10]. When DNA is duplicated, problems may occur and these problems may self solve or mutations occur [1].

Closure operators have been studied and applied extensively in various fields such as topology and computer science. There had been increased interest in the applications of generalized topological spaces, in particular, through the identification of new spaces and knowledge of their properties from knowledge of the type of topological spaces, image analysis, and related fields [3]. It is easily modified and leads to a general closure of neighborhood operators that fit the requirement of digital topology [8].

In this paper, we define a function for each mutation is defined and we introduce a closure operator on this function. Moreover, we discuss the topological structure from the conditions of a closure operator. Finally, we investigate the mathematical modeling by matching the biological properties to the mathematical topological properties.

Definition 1.1. [7] *Let X be a non-empty set and consider the closure operator $cL : P(X) \to P(X)$ such that:*

(i) $cL(\emptyset) = \emptyset$;

(ii) $A \subseteq B \Rightarrow cL(A) \subseteq cL(B)$;

(iii) $A \subseteq cL(A)$;

(iv) $cL(A \cup B) = cL(A) \cup cL(B)$; ;

(v) $cL(cL(A)) = cL(A)$;

(vi) $\bigcup_{i \in I} cl(A_i) = cL(\bigcup_{i \in I}(A_i))$.

Definition 1.2. [9]. *Let $F = C(n)$ be a set of all Boolean vectors of size n, $a = (a_1, a_2, ..., a_n) \in C(n)$, where $a_i \in 0, 1 \forall i$ and $|C(n)| = 2^n$. Then X_i is a set of one point crossover operator for $1 \leq i \leq n$ defined as:*
$X_i : C(n) \times C(n) \to C(n)$, with $(a_1, a_2, ..., a_n) x_i (b_1, b_2, ..., b_n) = (a_1, , a_i, b_{i+1}, ..., b_n)$

2 Mutations through their closure operators

Now, we will study chromosomal deletion and chromosomal duplication.

2.1 Chromosomal deletion

In a chromosomal deletion mutation, one or more genes are lost (deletion of one or more genes) as in Figure 1, a mathematical model of this mutation is given and the comparison between mathematical and biological results will be verified.

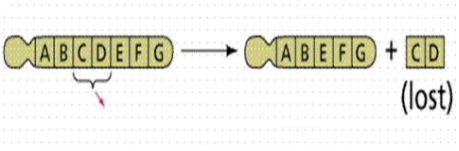

Figure 1: One or more gene removed.

Definition 2.1. *Let X be a non empty set of chromosomes and let L be set of all linear combination of X. We define the Chromosomal Deletion function as:*
$D : X \to SpanX$, *Since* $SpanX = L = \{l_1, l_2, l_3, \cdots, l_m\}$ *and* $m = \sum_{k=1}^{n} \begin{pmatrix} n \\ k \end{pmatrix}$,$k > 0$ *and* $k < n$ *or* $1 \leq k \leq n$

Proposition 2.2. *The number of deletion mutation* $m = \sum_{k=1}^{n} \begin{pmatrix} n \\ k \end{pmatrix} = 2^n - 1$, $k > 0$ *and* $k < n$ *or* $1 \leq k \leq n$.

Proof. The proof follows easily by induction. □

Definition 2.3. *Let X be a non empty set of chromosomes and let L be the set of linear combinations of X. We define the General Chromosomal Deletion function as follows:* $D : X \to P(L)$
Since $L = \{l_1, l_2, l_3, \cdots, l_m\}$ *and* $m = \sum_{k=1}^{n} \begin{pmatrix} n \\ k \end{pmatrix}$

Definition 2.4. *Let $H \subseteq X$. Define the deletion closure operator of H by* $cl_D(H) = \bigcup_{x_i \in H} D(H)$ *(All possible deletions).*

Proposition 2.5. *The deletion closure space (X, cl_D) arising from chromosomal deletion function has the following properties:*

(i) $cl_D(\emptyset) = \emptyset$;

(ii) If $H \subseteq K$, *then* $cl_D(H) \subseteq cl_D(K)$ *(Isotonic)*

(iii) $H \subseteq cl_D(H)$ *(Expanding)*

(iv) $cl_D(H \cup K) \supseteq cl_D(H) \cup cl_D(K)$

(v) $cl_D(cl_D(H)) = cl_D(H)$ *(Idempotent). (We call* (X, cl_D) *a deletion convex closure structure).*

Proof. (i) Since no chromosome (no genes) implies no deletion $cl_D(\emptyset) = \emptyset$.

(ii) If $H \subseteq K$, then Span H$\subseteq$ span K. Thus $\bigcup_{x_i \in H} D(H) \subseteq \bigcup_{x_i \in H} D(H)$. Therefore, $cl_D(H) \subseteq cl_D(K)$.

(iii) Since $H \subseteq spanH$ ($cl_D(H)$ denotes all possible deletions). Hence $H \subseteq cl_D(H)$.

(iv) Suppose that $\| H \| = n_1$ and $\| K \| = n_n$. Then $\| H \cup K \| \leq n_1 + n_2$,$n_1 + n_2 \geq n_1$ and $n_1 + n_2 \geq n_1$ such that $\| cl_D(H) \| = 2^{n_1} - 1$ and $\| cl_D(K) \| = 2^{n_2} - 1$. Then $\| cl_D(H \cup K) \| \geq 2^{n_1} + 2^{n_2} - 2$. Therefore, $cl_D(H \cup K) \supseteq cl_D(H) \cup cl_D(K)$.

(v) Assume that $cl_D(H) = \{L_1, L_2, L_3, \cdots, L_n\}$, $cl_D(\{L_1, L_2, L_3, \cdots, L_n\}) = L_1, L_2, L_3, \cdots, L_n$. Consequently, $cl_D(cl_D(H)) = cl_D(H)$. □

Lemma 2.6. *Consider a Chromosome* $X = \{A, B, C\}$, $H = \{A, B\}$ *and* $K = \{C\}$. *Then* $cl_D(H) = \{\{A\}, \{B\}, \{A, B\}\}$, $cl_D(K) = \{C\}$ *and* $cl_D(X) = \{\{A\}, \{B\}, \{C\}, \{A, B\}, \{A, C\}, \{B, C\}, X\}$. *Thus* $cl_D(H \cup K) \neq cl_D(H) \cup cl_D(K)$.

These topological properties apply to properties with biological meaning.

2.2 Chromosomal Duplication

In a chromosomal duplication mutation, one or more genes are copied and added to the chromosome as Figure 2 shows. We will construct a mathematical model of chromosomal duplication mutation. We represent a chromosome by a set H and duplication chromosome by a multiset H_i.

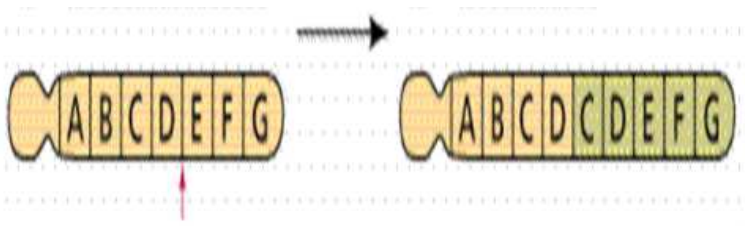

Figure 2: A segment of genes is copied twice and added to the chromosome.

Definition 2.7. *Let $H \subseteq X$. Then the duplication closure operator of H is $cl_{Du}(H) = \bigcup_i^n H_i =$ since H_j is a set containing the j-repeat of genes.*

Proposition 2.8. *The duplication closure space (X, cl_{Du}) arising from a chromosomal duplication function satisfies the following statements:*

(i) $cl_{Du}(\emptyset) = \emptyset$;

(ii) If $H \subseteq K$, *then* $cl_{Du}(H) \subseteq cl_{Du}(K)$
((X, cl_{Du}) is called a Duplication extended structure).

Proof. Since $cl_{Du}(H) = \bigcup_i^n H_i \subseteq \bigcup_i^n K_i = cl_{Du}(K)$, such that $H \subseteq K$. □

Corollary 2.9. *(i)* $H \nsubseteq cl_{Du}(H)$;

(ii) $cl_{Du}(H \cup K) \neq cl_{Du}(H) \cup cl_{Du}(K)$;

(iii) $cl_{Du}(cl_{Du}(H)) \neq cl_{Du}(H)$;

Lemma 2.10. *Consider a chromosome $M = \{A, B, C\}$, $H = \{A, B\}$ and $K = \{C\}$. Then $cl_D(H) = \{\{A, A, B\}, \{A, B, B\}, \{A, B, A, B\}\}$,$cl_D(K) = \{C, C\}$, $cl_D(cl_D(K)) = \{\{C, C, C\}, \{C, C, C, C\}\}$ and $cl_D(X) = \{\{A, A, B\}, \{A, B, B\}, \{A, B, A, B\}, \{A, B, C, C\}, \{A, B, A, B, c\}, \{A, B, C, B, C\}, \{A, B, C, A, B, C, \}\}$. Consequently, $cl_D(H \cup K) \neq cl_D(H) \cup cl_D(K)$.*

2.3 More on modeling chromosomal duplication

We follow Stadler [9] for the definition of the chromosomal duplication mutation in a mathematical model and its properties.

Definition 2.11. *Let L be any chromosome, $\| L \| = n$ and $L = (a_1, a_2, a_3, ..., a_n)$, since a_i is a gene for a chromosome L. We define $\{X_i\}$, a set of one point chromosomal duplication, for $0 \leq i \leq n$. $X_i : L \times L \to C(n+1)$, with $(a_1, a_2, a_3, ..., a_n)X_i(a_1, a_2, a_3, , a_n) = (a_1, a_2, a_3, ..., a_i, a_i, ..., a_n)$, where a set$C(n+1)$ is a collection of vectors (chromosomes) induced by chromosomal duplication.*

Remark 2.12. *From Definition 2.11, the chromosomal duplication operator satisfies $ax_ia \neq a$ and $ax_\Omega a = \{a_1, a_1, a_2, a_2, a_1, ..., a_i, a_i, ..., a_n, a_n, \} \neq 2a$, since x_Ω is a uniform duplication. With X_0 representing the null chromosomal duplication, $aX_0a = a$. The set of all possible duplications of a chromosome is called the duplication closure operator.*

Proposition 2.13. *The Duplication closure space (X, cl_{D_u}) arising from a chromosomal duplication function satisfies the following:*

(i) $cl_{D_u}(\emptyset) = \emptyset$,

(ii) $L \subseteq cl_{D_u}(L)$ *(Expanding),*

(iii) If $H \subseteq K$ *then* $cl_{Du}(H) \subseteq cl_{Du}(K)$ *(Isotonic).*

Proof. Since X_0 is the null chromosomal duplication, $LX_0L = L$. Hence $L \subseteq cl_{D_u}(L)$. □

Definition 2.14. *(Chromosomal duplication on two points) Let* L *be any chromosome,* $\| L \| = n$ *and* $L = (a_1, a_2, a_3, ..., a_n)$*, since* a_i *is a gene* L*. We define* $\{X_{ij}\}$*, a set of two points chromosomal duplication, for* $0 \leq i \leq n$*.* $X_i : L \times L \to C(n+2)$*, with* $(a_1, a_2, a_3, ..., a_n)X_ij(a_1, a_2, a_3, ..., a_n) = (a_1, a_2, a_3, ..., a_i, a_i, ..., a_j, a_j, ..., a_n)$*. (In* $C(n+2)$*, two indicates that the two chromosome duplications had been made).*

Remark 2.15. *If* X_{ij}=$X_i \circ X_j$*, then* $ax_\Omega = X_1 \circ X_2 \circ X_3.... \circ X_n\ a = \{a_1, a_1, a_2, a_2, a_1, ..., a_i, a_i, , ..., a_n, a_n, \} \neq 2a$*, where* x_Ω *is a uniform duplication.*

Proposition 2.16. *If* $S = a \times_i a$,$T = a \times_j a$*, then* $S \circ T = a \times_{ij} a$

Proof. Since $S = a \times_i a = (a_1, a_2, a_3, ..., a_i, a_i, ..., a_n)$ and $T = a \times_j a = (a_1, a_2, a_3, ..., a_j, a_j, ..., a_n)$. Then $S \circ T = S((a_1, a_2, a_3, ..., a_j, a_j, ..., a_n)) = (a_1, a_2, a_3, ..., a_i, a_i, ..., a_j, a_j, ..., a_n) = a \times_{ij} a$ □

3 Conclusion

We constructed a mathematical model for a chromosomal mutation using topology and verified its validity. In the future, we plan to transfer this mutation to agriculture and other fields in order to benefit from it.

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