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A New Model of Permutation the Pieces of Nucleotides in DNA Sequences Using the Action of Dihedral Group and Graph Theory

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Abstract: ***In this paper, we givea new model of genetic algorithm using the action of largest subgroup Hof dihedral GroupD_n, $n = 3^m$, $m \in \mathbb{N}$, $m \geq 2$, bipartite graph, and a markov basisfor $\frac{n^2-3n}{3} \times 3 \times \frac{n}{3}$ - contingency tables with fixed two dimensional marginals such that $B$is H-invariant.***

Keywords: Computational algebraic statistics, sufficient statistics, linear transformation, connectedgraph, bipartite graph, dihedralgroup, algebra statistic, Markov basis.

1. Introduction

Let I be a finite set $n = |I|$ elements, we call an element of I a cell and denoted by $\boldsymbol{i} \in I$. $\boldsymbol{i}$ is often multi-index $\boldsymbol{i} = i_1 \dots i_m$. A non-negative integer $x_i \in \mathbb{N}$ denotes the frequency of a cell $\boldsymbol{i}$. The set of frequencies is called ***a contingency table and*** denoted as $\boldsymbol{x} = \{x_i\}_{i \in I}$, with an appropriate ordering of the cell, we treat a contingency table$\boldsymbol{x} = \{x_i\}_{i \in I} \in \mathbb{N}^n$ as a n-dimensional column vector of non-negative integers. Not that a contingency table can also be considered as a function from I to $\mathbb{N}$ defined as $\boldsymbol{i} \mapsto x_i$.The L_1-norm of $\boldsymbol{x} \in \mathbb{N}^n$ is called the samplesize and denoted as$|\boldsymbol{x}| = \sum_{i \in I} x_i$.We will denote $\mathbb{Z}$ be the set of integer numbers, also we denote to the $a_j \in \mathbb{Z}^n, j = 1, \dots, v,$ as fixed column vectors consisting of integers. A v-dimensional column vector $\boldsymbol{t} = (t_1, \dots, t_v)' \in \mathbb{Z}^v$ as $t_j = a'_j \boldsymbol{x}, j = 1, \dots, v$. Here $'$ denotes the transpose of a vector or matrix.We also define a $v \times p$ matrix A, with its j-row beinga'_jgiven by $A = \begin{bmatrix} a'_1 \\ \vdots \\ a'_v \end{bmatrix}$, and if $\boldsymbol{t} = A\boldsymbol{x}$ is a v-dimensional column vector, we define the set $T = \{\boldsymbol{t}: \boldsymbol{t} = A\boldsymbol{x}, \boldsymbol{x} \in \mathbb{N}^n\} = A\mathbb{N}^n \subset \mathbb{Z}^v$. In typical situations of a statistical theory,$\boldsymbol{t}$ is *sufficient statistic* for the nuisance parameter. The set of $\boldsymbol{x}$'s for a given $\boldsymbol{t}$, $A^{-1}[\boldsymbol{t}] = \{\boldsymbol{x} \in \mathbb{N}^n: A\boldsymbol{x} = \boldsymbol{t}\}$ ($\boldsymbol{t}$-fibers),is considered for performing *similar tests*, for the case of the independence model of two–way contingency tables, for example,$\boldsymbol{t}$is the row sums and column sums of $\boldsymbol{x}$, and $A^{-1}[\boldsymbol{t}]$is the set of $\boldsymbol{x}$'s with the same row sums and column sums to $\boldsymbol{t}$. The set of $\boldsymbol{t}$-fibers gives a decomposition of $\mathbb{N}^n$. An important observation is that $\boldsymbol{t}$-fiber depends on given only through its kernel, ker (A). For different A's with the same kernel, the set of $\boldsymbol{t}$-fibersare the same. In fact, if we define $\boldsymbol{x}_1 \sim \boldsymbol{x}_2 \Leftrightarrow \boldsymbol{x}_1 - \boldsymbol{x}_2 \in \ker(A)$,this relation is an equivalence relation and $\mathbb{N}^n$ is partitioned into disjoint equivalence classes. The set of $\boldsymbol{t}$-fibers is simply the set of these equivalence classes. Furthermore, $\boldsymbol{t}$ may be considered as labels of these equivalence classes.A n-dimensional column vector of integers $\boldsymbol{z} = \{z_i\}_{i \in I} \in \mathbb{Z}^n$is called a move if it is in the kernel of A, i.e. $A\boldsymbol{z} = 0$**[10]**.

For a move$\boldsymbol{z}$, the positive part $\boldsymbol{z}^+ = \{z^+_i\}_{i \in I}$and the negative part $\boldsymbol{z}^- = \{z^-_i\}_{i \in I}$ are defined by $z^+_i = \max(z_i, 0)$, $z^-_i = \max(-z_i, 0)$, respectively, Then $\boldsymbol{z} = \boldsymbol{z}^+ - \boldsymbol{z}^-$ and $\boldsymbol{z}^+, \boldsymbol{z}^- \in \mathbb{N}^n \boldsymbol{z}^+, \boldsymbol{z}^- \in \mathbb{N}^n$. Moreover, $\boldsymbol{z}^+$ and $\boldsymbol{z}^-$ are in the same $\boldsymbol{t}$-fiber, i.e., $\boldsymbol{z}^+, \boldsymbol{z}^- \in A^{-1}[\boldsymbol{t}]$ for $\boldsymbol{t} = A\boldsymbol{z}^+ = A\boldsymbol{z}^-$. We define the *degree* of $\boldsymbol{z}$ **as the sample size of** $\boldsymbol{z}^+$or $(\boldsymbol{z}^-)$ and denote it by $\deg(\boldsymbol{z}) = |\boldsymbol{z}^+| = |\boldsymbol{z}^-|$. In the following we denote the set of moves (for a given A) by $M = M_A = \mathbb{Z}^n \cap \ker(A)$**[1]**.

Let G be a group and W be a set. A left action of G in W is a function from $G \times W$ in to W, usually denote by $(g, w) \to w \in W$ such that $g(hw) = (gh)w$ and $ew = w$ for all $g, h \in G$and $w \in W$where e is the identity element of G. We also say that G acts on W on the left.

Let a group G act on a set W, and $U \subseteq W$, $G_{(U)} = \{g: gu = u, \forall u \in U\}$ is called the pointwise stabilizer of U.Let a group G acts on a set W, $U \subseteq W$, and $GU = \{gu: u \in U, g \in G\}$. We call U invariant under G (or G-invariant) if $GU = U$ **[9].**

Let $A: \mathbb{Z}^n \to \mathbb{Z}^v$be a linear transformation, $\boldsymbol{t} \in \mathbb{Z}^v$, and $A^{-1}[\boldsymbol{t}]$ be the set of $\boldsymbol{t}$-fibers, and let $B \subset ker_z(A)$, then we define $A^{-1}[\boldsymbol{t}]_B$ be the graph with vertex set $A^{-1}[\boldsymbol{t}]$ and $u - -v$ an edge if and only if $u - v \in \pm B$[12].Let$A^{-1}[\boldsymbol{t}] = \{\boldsymbol{x} \in \mathbb{N}^n: A\boldsymbol{x} = \boldsymbol{t}\}$. A set of finite moves B is called **Markov basis** if for all $\boldsymbol{t}$, $A^{-1}[\boldsymbol{t}]$ constitutes one B equivalence class,If $B \subseteq ker_z(A)$ is a set such that $A^{-1}[\boldsymbol{t}]_B$is connected for all$\boldsymbol{t}$, then B is a Markovbasis for A[1].

If a group G act on $A^{-1}[t]$ on the left, B is a Markov basis, and $G(B) = \{gz : z \in B, g \in G\}, B$ is called invariant under G (or G- invariant) if $G(B) = B$. We will denote to the polynomials in the p indeterminates (polynomial variables) $p_1, p_2, \dots, p_p$ over the complex field $\mathbb{C}$ by either $\mathbb{C}[p_1, p_2, \dots, p_p]$ or $\mathbb{C}[P]$, $P = (p_1, p_2, \dots, p_p)$. Let $A: \mathbb{Z}^n \to \mathbb{Z}^d$ be a linear transformation, the toric ideal I_A is the ideal $< P^u - P^v : u, v \in \mathbb{N}^n, A(u) = A(v) > \subseteq \mathbb{C}[P_1, \dots, P_p]$ where $P^u = P_1^{u_1} P_2^{u_2} \dots P_p^{u_p}$ [11].

In [4] H. H. Abbass and H. S. Mohammed Hussein found a Markov basis **B** and toric ideals for $\frac{n^2-3n}{3} \times 3 \times \frac{n}{3}$ -contingency tables with fixed two dimensional marginals, n is a multiple of 3 greater than or equal 6, also they [5] found the largest subgroup H of dihedral Group D_{3^m}, m ∈ ℕ, such that **B** is H-invariant.

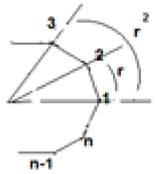
In this paper, we use the Markov basis **B** and action of the subgroup H of dihedral Group D_n on these contingency tables to give a new model of permutation the pieces of nucleotides in DNA sequences.

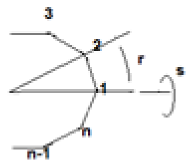
2. Preliminaries

In this section, we review some basic definitions and notations of dihedralgroup,connected graph, bipartite graph,moves, Markov basis, and toric ideals that we need in our work.

Definition 1(see[12]). Let n be a positive integer greater than or equal 3. The group of all symmetries of the regular polygon with n sides, including both rotations and reflections, is called **dihedral group** and denoted by D_n . If we center the regular polygon at origin then the elements of the dihedral group acts as linear transformation of the plane. Lets us represent the elements of D_n as matrix, with composition multiplication. Dihedral groups are among simplest examples of finite groups and they play an important role in group theory, geometry, and chemistry. The set of rotations is generated by r- counterclockwise rotation with angle $2\pi/n$ of order n, and the set of reflections is of order 2 and every element sr^j generates $\{e, sr^j\}$, where e is the identity element in Dn . The 2n elements in D_n can be written as: $\{e, r, r^2, \dots, r^{n-1}, s, sr, sr^2, \dots, sr^{n-1}\}$.In general, we can write D_n as: $D_n = \{s^j r^k : 0 \le k \le n-1, 0 \le j \le 1\}$ which has the following properties: $r^n = 1, sr^k s = r^{-k}$, $(sr^k)^2 = 1$, $for\ all\ 0 \le k \le n-1$ .The composition of two elements of the D_n is given by $r^i r^j = r^{i+j}$, $r^i s r^j = sr^{j-i}$, $sr^i r^j = sr^{i+j}$, $sr^i s r^j = r^{i-j}$.

Remark 2(see [12]). If we label the vertices (of the regular n-gon) 1 to n in a counterclockwise direction around n-gon then the elements of D_n can be written as permutations of vertices, let r be a counterclockwise rotation, and let S be the reflection of the n-gon about an axis through the center and vertex 1 , as indicated in below . The element r generates the cyclic group of order n Cn which is a normal cyclic subgroup of D_n. In all cases, addition and subtraction should be performed using modular arithmetic with modulus n.


Elements of Cn


Elements of Dn

Any symmetry will fix the origin and is determined by the image of two adjacent vertices , say 1 and 2 .The vertex 1 can be taken to any of n vertices and then the vertex 2 must be taken to one of the two vertices adjacent to the image of 1. Hence, D_n is a non abelian group of order $2n$ generated by r and s.

Now, we give some concepts about the action of a group on a set that we use later.

Definition 3 (see**[3]**). A graph G is connected if for every pair of distinct vertices $u, v \in V(G)$, where $V(G)$ be the set of vertices of the graph G, the graph G has a u, v-path. Otherwise, we say the graph is disconnected.

Definition 4(see**[3]**).A graph G is a bipartite graph if there are $X, Y \subseteq V(G)$ meeting the following conditions:
1. $V(G) = X \cup Y$,
2. $X \cap Y = \Phi$,
3. $G[X]$ and $G[Y]$ are both null graphs, where $G[X]$ and $G[Y]$ are subgraphs of the graph G induced by the set of vertices $X, Y \subseteq V(G)$ respectively.

Theorem 5(see**[3]**).
For a graph G the following statements are equivalent:
1. G is bipartite.
2. Every cycle in G has an even length.

Definition 6 (see [3]). Let $B \subset M_A$ be the set of moves and let $x_1, x_2 \in A^{-1}[t]$. We say that x_2 accessible from x_1 by B if there exists a sequance of moves $z_1, \dots, z_k \in B$ and $\varepsilon_k \in \{-1, 1\}$, $k = 1, \dots, K$, such that

$$x_2 = x_1 + \sum_{k=1}^{K} \varepsilon_k z_k,$$

$$x_1 + \sum_{k=1}^{K} \varepsilon_k z_k \in A^{-1}[t] \text{ for } 1 \le k \le K.$$

Remark 7 (see [4]). Let n be a multiple of 3 such that $n \ge 6$, and let $\boldsymbol{x}_j \in A^{-1}[t]$, $j = 1, \dots, k$ be the representative elements of the set of $3 \times \frac{n}{3}$ −contingency tables and $\mathbf{B} = \{\mathbf{z}_1, \mathbf{z}_2, \dots, \mathbf{z}_k\}$ such that each $\mathbf{z}_j$

,$j = 1,2,\ldots,k$, is a matrix of dimension $3 \times \frac{n}{3}$ either has two columns $(1,-1,0)', (-1,1,0)'$ ($(1,0,-1)', (-1,0,1)'$ or either $(0,1,-1)', (0,-1,1)'$) and the other columns are zero denoted by $+\boldsymbol{z}_j$, or it two columns $(1,-1,0)', (-1,1,0)'$ ($(1,0,-1)', (-1,0,1)'$ or either $(0,1,-1)', (0,-1,1)'$) and the other columns are zero denoted by $+\boldsymbol{z}_j$, or it has two columns $(-1,0,1)', (1,0,-1)'$($(-1,0,1)', (1,0,-1)'$ or $(0,-1,1)', (0,1,-1)'$) and the other columns are zero denoted by $-\boldsymbol{z}_j$,like

$$\begin{bmatrix}1&-1&0\\-1&1&0\\0&0&0\end{bmatrix}, \quad \begin{bmatrix}1&-1&0\\0&0&0\\-1&1&0\end{bmatrix}$$
$$\begin{bmatrix}0&0&0\\1&-1&0\\-1&1&0\end{bmatrix}, \quad \begin{bmatrix}-1&1&0\\1&-1&0\\0&0&0\end{bmatrix}$$
$$\begin{bmatrix}-1&1&0\\0&0&0\\1&-1&0\end{bmatrix}, \quad \begin{bmatrix}0&0&0\\-1&1&0\\1&-1&0\end{bmatrix}.$$

Also, we can write all elements of $\mathbf{B}$as one-dimensional column vectoras follows:

$\boldsymbol{z_j} = (z_1,\ldots,z_n)', j = 1,\ldots,k$and $z_t = 1$ or -1 or 0 such that

$If\, t = 1,2,\ldots,\frac{n}{3}$

$$z_t = \begin{cases} 1 \;\; if\; z_{t+\frac{n}{3}} + z_{t+\frac{2n}{3}} = -1 \; and \sum_{\substack{i=1\\ i\neq t}}^{\frac{n}{3}} z_i = -1 \\ -1 \;\; if\; z_{t+\frac{n}{3}} + z_{t+\frac{2n}{3}} = 1 \; and \sum_{\substack{i=1\\ i\neq t}}^{\frac{n}{3}} z_i = 1 \\ 0 \;\; if\; z_{t+\frac{n}{3}} + z_{t+\frac{2n}{3}} = 0 \; and \sum_{\substack{i=1\\ i\neq t}}^{\frac{n}{3}} z_i = 0 \end{cases}$$

If $t = \frac{n}{3}+1, \frac{n}{3}+2, \ldots, \frac{2n}{3}$

$$z_t = \begin{cases} 1 \;\; if\; z_{t-\frac{n}{3}} + z_{t+\frac{n}{3}} = -1 \; and \sum_{\substack{i=\frac{n}{3}+1\\ i\neq t}}^{\frac{2n}{3}} z_i = -1 \\ -1 \;\; if\; z_{t-\frac{n}{3}} + z_{t+\frac{n}{3}} = 1 \; and \sum_{\substack{i=\frac{n}{3}+1\\ i\neq t}}^{\frac{2n}{3}} z_i = 1 \\ 0 \;\; if\; z_{t-\frac{n}{3}} + z_{t+\frac{n}{3}} = 0 \; and \sum_{\substack{i=\frac{n}{3}+1\\ i\neq t}}^{\frac{2n}{3}} z_i = 0 \end{cases}$$

If $t = \frac{2n}{3}+1, \frac{2n}{3}+2, \ldots, n$

$$z_t = \begin{cases} 1 \;\; if\; z_{t-\frac{2n}{3}} + z_{t-\frac{n}{3}} = -1 \; and \sum_{\substack{i=\frac{2n}{3}+1\\ i\neq t}}^{n} z_i = -1 \\ -1 \;\; if\; z_{t-\frac{2n}{3}} + z_{t-\frac{n}{3}} = 1 \; and \sum_{\substack{i=\frac{n}{3}+1\\ i\neq t}}^{n} z_i = 1 \\ 0 \;\; if\; z_{t-\frac{2n}{3}} + z_{t-\frac{n}{3}} = 0 \; and \sum_{\substack{i=\frac{n}{3}+1\\ i\neq t}}^{n} z_i = 0 \end{cases}$$

Theorem 8 (see [4]). The number of elements in $\mathbf{B}$ equal to $\frac{n^2-3n}{3}$.

Remark 9(see [4]). Given a contingency table= $(x_1, x_2, \ldots, x_n)'$, the entry of the matrix A in the column indexed by$x_1, x_2, \ldots, x_n$ respectively and its rows indexed by

$$\sum_{i=1}^{\frac{n}{3}} x_i, \sum_{i=\frac{n}{3}+1}^{\frac{2n}{3}} x_i, \sum_{i=\frac{2n}{3}+1}^{n} x_i, x_1 + x_{\frac{n}{3}+1} + x_{\frac{2n}{3}+1}, x_2 + x_{\frac{n}{3}+2} + x_{\frac{2n}{3}+2}, \ldots, x_{\frac{n}{3}} + x_{\frac{2n}{3}} + x_n$$

respectively. The entry in the column indexed by x_i in the matrix **A** will be equal to one, if x_ia pears in the index of its row, and otherwise it will be zero. Then

A

$$= \begin{bmatrix} 1&1&\cdots&1&1&0&0&\ldots&0&0&0&0&\cdots&0&0\\ 0&0&\cdots&0&0&1&1&\cdots&1&1&0&0&\cdots&0&0\\ 0&0&\cdots&0&0&0&0&\cdots&0&0&1&1&\cdots&1&1\\ 1&0&\cdots&0&0&1&0&\cdots&0&0&1&0&\cdots&0&0\\ 0&1&\cdots&0&0&0&1&\cdots&0&0&0&1&\cdots&0&0\\ \vdots&\vdots&\cdots&\vdots&\vdots&\vdots&\vdots&\cdots&\vdots&\vdots&\vdots&\vdots&\cdots&\vdots&\vdots\\ 0&0&\cdots&0&1&0&0&\cdots&0&1&0&0&\cdots&0&1 \end{bmatrix}_{\frac{n+9}{3}\times n}$$

Theorem 10 (see [4]). The set $\mathbf{B} = \{\boldsymbol{z}_1, \ldots, \boldsymbol{z}_{\frac{n^2-3n}{3}}\}$ is a set of moves.

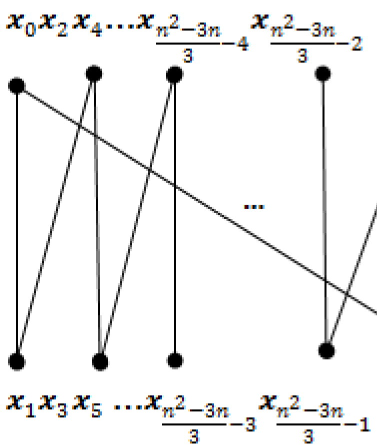
Corollary 11 (see [4]). Theset $\mathbf{B}$ of moves in theorem10 is a Markov basis**.**

Corollary 12 (see [4]). The toric ideal I_A for $\frac{n^2-3n}{3} \times 3 \times \frac{n}{3}$ -contingency tables are $I_A = < P_{i+l}P_{j+k} - P_{j+l}P_{i+k}\colon i,j = 1,2,\ldots,\frac{n}{3}$ and $l,k = 0,\frac{n}{3},\frac{2n}{3}$, such that $i < j$ and $l < k > \subset \mathbb{C}[P_1, P_2, \ldots, P_n]$.

Remark 13 (see [4]). Now, we will construct a connected graph by using the elements of $\mathbf{B}$. Let $\boldsymbol{z}_m$ be an element of $\mathbf{B}$such that$\boldsymbol{z}_m = \boldsymbol{x}_m - \boldsymbol{x}_{m-1}$,$m = 1,2,\ldots,\frac{n^2-3n}{3}$is an edgeconnected $\boldsymbol{x}_m$ and $\boldsymbol{x}_{m-1}$, …, and $\boldsymbol{z}_{\frac{n^2-3n}{3}} = \boldsymbol{x}_0 - \boldsymbol{x}_{\frac{n^2-3n}{3}-1}$ is an edge connect $\boldsymbol{x}_0$ and $\boldsymbol{x}_{\frac{n^2-3n}{3}-1}$,where$\boldsymbol{x}_i \in A^{-1}[t]$, $i = 0,2,\ldots,\frac{n^2-3n}{3} - 1$.Then we canconnected all $\frac{n^2-3n}{3} \times 3 \times \frac{n}{3}$ - contingency tables with fixed two dimensional marginals by $\frac{n^2-3n}{3}$ edges by applying moves from $\mathbf{B}$ one by one and go from $\boldsymbol{x}_0$ to

$\boldsymbol{x}_{\frac{n^2-3n}{3}-1}$ without causing negative cell frequencies on the way, and also from $\boldsymbol{x}_{\frac{n^2-3n}{3}-1}$ to $\boldsymbol{x}_0$, of this type, by forming undirected graph $G = (R, W, \mathbf{B}) = \mathrm{A}^{-1}[\boldsymbol{t}]_{\mathbf{B}}$, where the contingency tables interpreted as vertices and connecting moves are interpreted as edges of a graph, $R = \{\boldsymbol{x}_0, \boldsymbol{x}_2, \dots, \boldsymbol{x}_{\frac{n^2-3n}{3}-2}\}$ and $W = \{\boldsymbol{x}_1, \boldsymbol{x}_3, \dots, \boldsymbol{x}_{\frac{n^2-3n}{3}-1}\}$ as shown in figure 1

Figure1. The graph $G = (R, W, \mathbf{B}) = \mathrm{A}^{-1}[\boldsymbol{t}]_{\mathbf{B}}$.



In [5] H. H. Abbass and H. S. Mohammed Hussein assumed $n = 3^m, m \in \mathbb{N}$, and $m \geq 2$, and H is the subgroup $\{e, r^{\frac{n}{3}}, r^{\frac{2n}{3}}, sr, sr^{\frac{n}{3}+1}, sr^{\frac{2n}{3}+1}\}$ of dihedral group D_n, where $r = (1\ 2\ 3\ \dots n)$ and $s = (2\ \ n)(3\ \ n-1)\dots(\frac{n+1}{2}\frac{n+3}{2})$.

Theorem 14 (see [4]). The graph $G = (R, W, \mathbf{B})$is a connected bipartite graph (up to graph isomorphism).

Theorem 15 (see [5]). The Markov basis$\mathbf{B}$is H-invariant.

Corollary16 (see [5]). The subgroup $H$is the Largest Subgroup ofthe group $\boldsymbol{D}_{3^m}$ such that the Markov basis$\mathbf{B}$is H-invariant.

Remark 17 (see [5]). Let $\boldsymbol{t} = \left(t_1, t_2, t_3, \dots, t_{\frac{n}{3}+3}\right)'$, $\boldsymbol{x}_i \in \mathrm{A}^{-1}[\boldsymbol{t}]andg \in H$.
Then$g\boldsymbol{x}_i \in \mathrm{A}^{-1}[g\boldsymbol{t}]$where
$g\boldsymbol{t} = \left(g t_1, g t_2, g t_3, \dots, g t_{\frac{n}{3}+3}\right)'$, $\mathrm{A}^{-1}[g\boldsymbol{t}] = \{\boldsymbol{x} \in \mathbb{N}^n : \boldsymbol{A}\boldsymbol{x} = g\boldsymbol{t}\}$. So, we have six types of $g\boldsymbol{t}$-fibers $\mathrm{A}^{-1}[\boldsymbol{t}]$, $\mathrm{A}^{-1}\left[r^{\frac{n}{3}}\boldsymbol{t}\right]$, $\mathrm{A}^{-1}\left[r^{\frac{2n}{3}}\boldsymbol{t}\right]$, $\mathrm{A}^{-1}[sr\boldsymbol{t}]$, $\mathrm{A}^{-1}\left[sr^{\frac{n}{3}+1}\boldsymbol{t}\right]and\mathrm{A}^{-1}\left[sr^{\frac{2n}{3}+1}\boldsymbol{t}\right]$.

Theorem 18 (see [5]). If $g \in H$, then $\mathbf{B}$is a Markov basis for $\frac{n^2-3n}{3}$ contingency tables$g\boldsymbol{x}_0, g\boldsymbol{x}_1, \dots, g\boldsymbol{x}_{\frac{n^2-3n}{3}-1}$ in $\mathrm{A}^{-1}[g\boldsymbol{t}]$.

Corollary 19 (see [5]). The toric ideal for $\frac{n^2-3n}{3} \times 3 \times \frac{n}{3}$ - contingency table in $\mathrm{A}^{-1}[g\boldsymbol{t}]$is

$I_{\mathrm{A}} =< P_{g(i+l)}P_{g(j+k)} - P_{g(j+l)}P_{g(i+k)} : i, j = 1, 2, \dots, \frac{n}{3}$ and $l, k = 0, \frac{n}{3}, \frac{2n}{3}$, such that $i < j$ and $l < k > \subset C[P_1, P_2, \dots, P_n]$, for all $g \in H$.

3. The Main Results

Let $n = 3^m, m \in \mathbb{N}$ and $m \geq 2$, $g\boldsymbol{x}_j \in A^{-1}[g\boldsymbol{t}]$, $j = 0, \dots, \frac{n^2-3n}{3} - 1$and $g \in H$ be representative elements of the set of $3 \times \frac{n}{3}$ –contingency tables. Then we write g as $n \times n$ permutation matrix $T_g = \{P_{ij}\} = \{\delta_i, g(i)\}$, where δ is the Kronecker's delta such that $T_{g_1 g_2} = T_{g_1}T_{g_2}$ for $g_1, g_2 \in H$, and $T_{g^{-1}} = T_g{}'$. The identity matrix of the order n denoted by E_n fur the unit element e.
Now, we consider a left action of dihedral group D_n, $n = |I|$, on $A^{-1}[t]$ the set of $\frac{n^2-3n}{3} \times 3 \times \frac{n}{3}$ - contingency tables, and the action of dihedral group D_n on the set of Markov basis $\mathbf{B}$.

Theorem 20. Let $\boldsymbol{x}_i, \boldsymbol{x}_j \in \mathrm{A}^{-1}[\boldsymbol{t}]$, if $g \in H$. Then $\boldsymbol{x}_i$ accessible from $\boldsymbol{x}_j$by $\mathbf{B}$ if and only if $T_g\boldsymbol{x}_i$ accessible from $T_g\boldsymbol{x}_j$by $\mathbf{B}$, for all $i, j = 1, 2, \dots, \frac{n^2-3n}{3}$.

Proof: If $\boldsymbol{x}_i$ accessible from $\boldsymbol{x}_j$by$\mathbf{B}$,then there exists a sequence of moves $\boldsymbol{z}_1, \dots, \boldsymbol{z}_k \in \mathbf{B}$ and $\varepsilon_k \in \{-1, 1\}$, $k = 1, \dots, \frac{n^2-3n}{3}$, such that

$\boldsymbol{x}_i = \boldsymbol{x}_j + \sum_{k=1}^{\frac{n^2-3n}{3}} \varepsilon_k \boldsymbol{z}_k, \boldsymbol{x}_j + \sum_{k=1}^{\frac{n^2-3n}{3}} \varepsilon_k \boldsymbol{z}_k \in A^{-1}[\boldsymbol{t}]$ for$1 \leq k \leq \frac{n^2-3n}{3}$. (Definition 6)
Let $g \in H$

If $g = e \Rightarrow E_n\boldsymbol{x}_i = E_n\boldsymbol{x}_j + \sum_{k=1}^{\frac{n^2-3n}{3}} \varepsilon_k E_n\boldsymbol{z}_k, E_n\boldsymbol{x}_j + \sum_{k=1}^{\frac{n^2-3n}{3}} \varepsilon_k E_n\boldsymbol{z}_k \in H(A^{-1}[\boldsymbol{t}])$
for$1 \leq k \leq \frac{n^2-3n}{3}$.

If$g = r^{\frac{n}{3}}$then we write $r^{\frac{n}{3}}$as a $n \times n$ permutation matrix, i.e. $r^{\frac{n}{3}} = T_{(1\ \frac{n}{3}+1\ \frac{2n}{3}+1)(2\ \frac{n}{3}+2\ \frac{2n}{3}+2)\dots(\frac{n}{3}\frac{2n}{3}\ n)}$, then

$$T_{(1\ \frac{n}{3}+1\ \frac{2n}{3}+1)(2\ \frac{n}{3}+2\ \frac{2n}{3}+2)\dots(\frac{n}{3}\frac{2n}{3}\ n)}\boldsymbol{x}_i = T_{(1\ \frac{n}{3}+1\ \frac{2n}{3}+1)(2\ \frac{n}{3}+2\ \frac{2n}{3}+2)\dots(\frac{n}{3}\frac{2n}{3}\ n)}\boldsymbol{x}_j + \sum_{k=1}^{\frac{n^2-3n}{3}} \varepsilon_k\, T_{(1\ \frac{n}{3}+1\ \frac{2n}{3}+1)(2\ \frac{n}{3}+2\ \frac{2n}{3}+2)\dots(\frac{n}{3}\frac{2n}{3}\ n)}\boldsymbol{z}_{k,}T_{(1\ \frac{n}{3}+1\ \frac{2n}{3}+1)(2\ \frac{n}{3}+2\ \frac{2n}{3}+2)\dots(\frac{n}{3}\frac{2n}{3}\ n)}\boldsymbol{x}_j + \sum_{k=1}^{\frac{n^2-3n}{3}} \varepsilon_k\, T_{(1\ \frac{n}{3}+1\ \frac{2n}{3}+1)(2\ \frac{n}{3}+2\ \frac{2n}{3}+2)\dots(\frac{n}{3}\frac{2n}{3}\ n)}\boldsymbol{z}_k$$

$\in H(A^{-1}[\boldsymbol{t}])$ for$1 \le k \le \dfrac{n^2-3n}{3}$.

If$g = r^{\frac{2n}{3}}$, then $r^{\frac{2n}{3}} = T_{(1\ \frac{2n}{3}+1\ \frac{n}{3}+1)(2\ \frac{2n}{3}+2\ \frac{n}{3}+2)\dots(\frac{n}{3}\ n\ \frac{2n}{3})}$,

$$T_{(1\ \frac{2n}{3}+1\ \frac{n}{3}+1)(2\ \frac{2n}{3}+2\ \frac{n}{3}+2)\dots(\frac{n}{3}\ n\ \frac{2n}{3})}\boldsymbol{x}_i = T_{(1\ \frac{2n}{3}+1\ \frac{n}{3}+1)(2\ \frac{2n}{3}+2\ \frac{n}{3}+2)\dots(\frac{n}{3}\ n\ \frac{2n}{3})}\boldsymbol{x}_j + \sum_{k=1}^{\frac{n^2-3n}{3}} \varepsilon_k\, T_{(1\ \frac{2n}{3}+1\ \frac{n}{3}+1)(2\ \frac{2n}{3}+2\ \frac{n}{3}+2)\dots(\frac{n}{3}\ n\ \frac{2n}{3})}\boldsymbol{z}_{k,}T_{(1\ \frac{2n}{3}+1\ \frac{n}{3}+1)(2\ \frac{2n}{3}+2\ \frac{n}{3}+2)\dots(\frac{n}{3}\ n\ \frac{2n}{3})}\boldsymbol{x}_j + \sum_{k=1}^{\frac{n^2-3n}{3}} \varepsilon_k\, T_{(1\ \frac{2n}{3}+1\ \frac{n}{3}+1)(2\ \frac{2n}{3}+2\ \frac{n}{3}+2)\dots(\frac{n}{3}\ n\ \frac{2n}{3})}\boldsymbol{z}_k$$

$\in H(A^{-1}[\boldsymbol{t}])$ for$1 \le k \le \frac{n^2-3n}{3}$.

If$g = sr$, then $sr = T_{(1\ n)(2\ n-1)\dots(\frac{n-1}{2}\frac{n+3}{2})}$,

$$T_{(1\ n)(2\ n-1)\dots(\frac{n-1}{2}\frac{n+3}{2})}\boldsymbol{x}_i = T_{(1\ n)(2\ n-1)\dots(\frac{n-1}{2}\frac{n+3}{2})}\boldsymbol{x}_j + \sum_{k=1}^{\frac{n^2-3n}{3}} \varepsilon_k\, T_{(1\ n)(2\ n-1)\dots(\frac{n-1}{2}\frac{n+3}{2})}\boldsymbol{z}_{k,}$$

$$T_{(1\ n)(2\ n-1)\dots(\frac{n-1}{2}\frac{n+3}{2})}\boldsymbol{x}_j + \sum_{k=1}^{\frac{n^2-3n}{3}} \varepsilon_k\, T_{(1\ n)(2\ n-1)\dots(\frac{n-1}{2}\frac{n+3}{2})}\boldsymbol{z}_k \in H(A^{-1}[\boldsymbol{t}]) \text{ for} 1 \le k \le \frac{n^2-3n}{3}.$$

If$g = sr^{\frac{n}{3}+1}$, then $sr^{\frac{n}{3}+1} = T_{(1\ \frac{2n}{3})(2\ \frac{2n}{3}-1)\dots(\frac{n}{3}\frac{n}{3}+1)(\frac{2n}{3}+1\ n)(\frac{2n}{3}+2\ n-1)\ \dots(\frac{5n-3}{6}\frac{5n+9}{6})}$,

$$T_{(1\ \frac{2n}{3})(2\ \frac{2n}{3}-1)\dots(\frac{n}{3}\frac{n}{3}+1)(\frac{2n}{3}+1\ n)(\frac{2n}{3}+2\ n-1)\dots(\frac{5n-3}{6}\frac{5n+9}{6})}\boldsymbol{x}_i =$$

$$T_{(1\ \frac{2n}{3})(2\ \frac{2n}{3}-1)\dots(\frac{n}{3}\frac{n}{3}+1)(\frac{2n}{3}+1\ n)(\frac{2n}{3}+2\ n-1)\dots(\frac{5n-3}{6}\frac{5n+9}{6})}\boldsymbol{x}_i + \sum_{k=1}^{\frac{n^2-3n}{3}} \varepsilon_k\, T_{(1\ \frac{2n}{3})(2\ \frac{2n}{3}-1)\dots(\frac{n}{3}\frac{n}{3}+1)(\frac{2n}{3}+1\ n)(\frac{2n}{3}+2\ n-1)\dots(\frac{5n-3}{6}\frac{5n+9}{6})}\boldsymbol{z}_k.$$

$$T_{(1\ \frac{2n}{3})(2\ \frac{2n}{3}-1)\dots(\frac{n}{3}\frac{n}{3}+1)(\frac{2n}{3}+1\ n)(\frac{2n}{3}+2\ n-1)\dots(\frac{5n-3}{6}\frac{5n+9}{6})}\boldsymbol{x}_j + \sum_{k=1}^{\frac{n^2-3n}{3}} \varepsilon_k\, T_{(1\ \frac{2n}{3})(2\ \frac{2n}{3}-1)\dots(\frac{n}{3}\frac{n}{3}+1)(\frac{2n}{3}+1\ n)(\frac{2n}{3}+2\ n-1)\dots(\frac{5n-3}{6}\frac{5n+9}{6})}\boldsymbol{z}_k \in H(A^{-1}[\boldsymbol{t}]) \text{ for} 1 \le k \le \frac{n^2-3n}{3}.$$

If $g = sr^{\frac{2n}{3}+1}$, then $sr^{\frac{2n}{3}+1} = T_{(1\ \frac{n}{3})(2\ \frac{n}{3}-1)\cdots(\frac{n}{3}+1\ n)(\frac{n}{3}+2\ n-1)\cdots(\frac{2n}{3}\frac{2n}{3}+1)}$,

$T_{(1\ \frac{n}{3})(2\ \frac{n}{3}-1)\cdots(\frac{n}{3}+1\ n)(\frac{n}{3}+2\ n-1)\cdots(\frac{2n}{3}\frac{2n}{3}+1)}\boldsymbol{x}_i$

$$= T_{(1\ \frac{n}{3})(2\ \frac{n}{3}-1)\cdots(\frac{n}{3}+1\ n)(\frac{n}{3}+2\ n-1)\cdots(\frac{2n}{3}\frac{2n}{3}+1)}\boldsymbol{x}_j + \sum_{k=1}^{\frac{n^2-3n}{3}} \varepsilon_k T_{(1\ \frac{n}{3})(2\ \frac{n}{3}-1)\cdots(\frac{n}{3}+1\ n)(\frac{n}{3}+2\ n-1)\cdots(\frac{2n}{3}\frac{2n}{3}+1)}\boldsymbol{z}_k,$$

$$T_{(1\ \frac{n}{3})(2\ \frac{n}{3}-1)\cdots(\frac{n}{3}+1\ n)(\frac{n}{3}+2\ n-1)\cdots(\frac{2n}{3}\frac{2n}{3}+1)}\boldsymbol{x}_j + \sum_{k=1}^{\frac{n^2-3n}{3}} \varepsilon_k T_{(1\ \frac{n}{3})(2\ \frac{n}{3}-1)\cdots(\frac{n}{3}+1\ n)(\frac{n}{3}+2\ n-1)\cdots(\frac{2n}{3}\frac{2n}{3}+1)}\boldsymbol{z}_k \in H(A^{-1}[\boldsymbol{t}]) \text{ for } 1 \le k \le \frac{n^2-3n}{3}.$$

Therefore $T_g\boldsymbol{x}_i$ accessible from $T_g\boldsymbol{x}_j$ by $H(\mathbf{B})$.

Conversely,
if $T_g\boldsymbol{x}_i$ accessible from $T_g\boldsymbol{x}_j$ by $H(\mathbf{B})$, then there exists a sequence of moves $g\boldsymbol{z}_1, \dots, g\boldsymbol{z}_s \in H(\mathbf{B})$, $g \in H$, and $\varepsilon_k \in \{-1, 1\}$, $k = 1, \dots, \frac{n^2-3n}{3}$, such that

$$T_g\boldsymbol{x}_i = T_g\boldsymbol{x}_j + \sum_{k=1}^{\frac{n^2-3n}{3}} \varepsilon_k T_g\boldsymbol{z}_k,$$

$T_g\boldsymbol{x}_j + \sum_{k=1}^{\frac{n^2-3n}{3}} \varepsilon_k T_g\boldsymbol{z}_k \in H(A^{-1}[\boldsymbol{t}])$ for $1 \le k \le \frac{n^2-3n}{3}$. (Definition 6)

By multiplying the previous equations by T'_g, $g \in H$, we have

$$T'_g(T_g\boldsymbol{x}_i) = T'_g(T_g\boldsymbol{x}_j) + \sum_{k=1}^{\frac{n^2-3n}{3}} \varepsilon_k T'_g(T_g\boldsymbol{z}_k),$$

$$T'_g(T_g\boldsymbol{x}_j) + \sum_{k=1}^{\frac{n^2-3n}{3}} \varepsilon_k T'_g(T_g\boldsymbol{z}_k) \in H(A^{-1}[\boldsymbol{t}]) \text{ for } 1 \le k \le \frac{n^2-3n}{3}.$$

This implies, $(T'_gT_g)x_i = (T'_gT_g)x_j + \sum_{k=1}^{\frac{n^2-3n}{3}} \varepsilon_k(T'_gT)_g z_k$,

$$(T'_gT_g)\boldsymbol{x}_j + \sum_{k=1}^{\frac{n^2-3n}{3}} \varepsilon_k(T'_g T_g)\boldsymbol{z}_k \in \mathrm{H}(A^{-1}[\boldsymbol{t}]) \text{ for } 1 \le k \le \frac{n^2-3n}{3}.$$

Hence $E_n\boldsymbol{x}_i = E_n\boldsymbol{x}_j + \sum_{k=1}^{\frac{n^2-3n}{3}} \varepsilon_k E_n\boldsymbol{z}_k$,

$$E_n\boldsymbol{x}_j + \sum_{k=1}^{\frac{n^2-3n}{3}} \varepsilon_k E_n\boldsymbol{z}_k \in H(A^{-1}[\boldsymbol{t}]) \text{ for } 1 \le k \le \frac{n^2-3n}{3}.$$

Therefore, $\boldsymbol{x}_i = \boldsymbol{x}_j + \sum_{k=1}^{\frac{n^2-3n}{3}} \varepsilon_k \boldsymbol{z}_k$,

$\boldsymbol{x}_j + \sum_{k=1}^{\frac{n^2-3n}{3}} \varepsilon_k \boldsymbol{z}_k \in A^{-1}[\boldsymbol{t}]$ for $1 \le k \le \frac{n^2-3n}{3}$. [since $E_n\boldsymbol{x}_j = \boldsymbol{x}_j$ and $E_n\boldsymbol{z}_k = \boldsymbol{z}_k$]

Then $\boldsymbol{x}_i$ accessible from $\boldsymbol{x}_j$ by $\mathbf{B}$. □

Remark 21. Now, we will construct a connected graph by using the elements of $H(\mathbf{B})$. Let $g\boldsymbol{z}_k = T_g\boldsymbol{z}_k$ be an element of $H(\mathbf{B})$ for all $g \in H$ such that $g\,\boldsymbol{z}_k = g\boldsymbol{x}_k - g\boldsymbol{x}_{k-1} = T_g\boldsymbol{x}_k - T_g\boldsymbol{x}_{k-1}$, $k = 1, 2, \dots, \frac{n^2-3n}{3}$ is an edge connected $g\boldsymbol{x}_k = T_g\boldsymbol{x}_k$ and $g\boldsymbol{x}_{k-1} = T_g\boldsymbol{x}_{k-1}$ and, … , and $g\boldsymbol{z}_{\frac{n^2-3n}{3}} = g\boldsymbol{x}_0 - g\boldsymbol{x}_{\frac{n^2-3n}{3}-1} = T_g\boldsymbol{x}_0 - T_g\,\boldsymbol{x}_{\frac{n^2-3n}{3}-1}$ be an edge connected $T_g\boldsymbol{x}_0$ and $T_g\boldsymbol{x}_{\frac{n^2-3n}{3}-1}$, where$g\boldsymbol{x}_i \in A^{-1}[gt], g \in H$ $i = 0,1,2,\dots,\frac{n^2-3n}{3}-1$. Then we canconnect all $\frac{n^2-3n}{3} \times 3 \times \frac{n}{3}$ - contingency tables with fixed two dimensional marginals by $\frac{n^2-3n}{3}$ edges by applying moves from $H(\mathbf{B})$ to $T_g\,\boldsymbol{x}_0$ one by one and go from $T_g\,\boldsymbol{x}_0$ to $T_g\,\boldsymbol{x}_{\frac{n^2-3n}{3}-1}$ without causing negative cell frequencies on the way, and also from $T_g\,\boldsymbol{x}_{\frac{n^2-3n}{3}-1}$ to$T_g\boldsymbol{x}_0$. This forms undirected graph as shown in figure 2

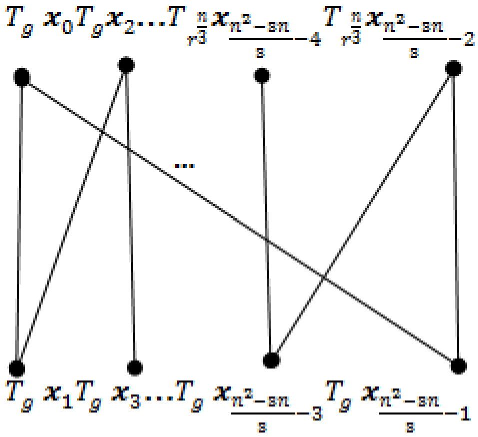


Figure2. The graph$T_g G = (T_g\,R, T_g\,W, H(\mathbf{B})) = A^{-1}[gt]_{H(\mathbf{B})} = A^{-1}[gt]_{\mathbf{B}}$, where the contingency tables interpreted as vertices and connecting moves are interpreted as edges of a graph, $T_g R = \{T_g\boldsymbol{x}_0, T_g\boldsymbol{x}_2, \dots, T_g\,\boldsymbol{x}_{\frac{n^2-3n}{3}-2}\}$ and $T_g W = \{T_g\boldsymbol{x}_1, T_g\boldsymbol{x}_3, \dots, T_g\,\boldsymbol{x}_{\frac{n^2-3n}{3}-1}\}$.

Theorem 22. The graphs $T_g G = (T_g\,R, T_g\,W, H(\mathbf{B}))$are connected bipartite graphs (up to graph isomorphism).

Proof :

Let $T_g\boldsymbol{x}_i, T_g\,\boldsymbol{x}_j \in A^{-1}[gt]$, if $0 \le i \le j \le \frac{n^2-3n}{3}-1, i \neq j$, by remark 21there exists a path $< T_g\boldsymbol{x}_i, T_g\boldsymbol{z}_{i+1}, T_g\boldsymbol{x}_{i+1}, T_g\boldsymbol{z}_{i+2}, \dots, T_{\frac{n}{r3}}\boldsymbol{x}_{j-1}, T_{\frac{n}{r3}}\boldsymbol{z}_j, T_{\frac{n}{r3}}\boldsymbol{x}_j >$, and if $0 \le j \le i \le \frac{n^2-3n}{3}-1, i \neq j$, by remark 21there exists a path $< T_g\boldsymbol{x}_j, T_g\boldsymbol{z}_{j+1}, T_g\boldsymbol{x}_{j+1}, T_g\boldsymbol{z}_{j+2}, \dots, T_g\boldsymbol{x}_{i-1}, T_g\boldsymbol{z}_i, T_g\boldsymbol{x}_i >$, and that implies there exists a path between every pair of distinct vertices $T_g\boldsymbol{x}_i, T_g\boldsymbol{x}_j \in A^{-1}[t]$of the graph, by (definition 3), G is a connected graph .

Now, we prove the graph $G = (T_g R, T_g W, H(\mathbf{B}))$ is a bipartite graph.

Let $T_g\boldsymbol{x}_i, T_g\,\boldsymbol{x}_{i+1}, \dots, T_g\boldsymbol{x}_{j-1}, T_g\boldsymbol{x}_j, T_g\boldsymbol{x}_{j+1} = T_g\boldsymbol{x}_i$be a cycle in G. Suppose$T_g\boldsymbol{x}_i \in T_g R$. Then $T_g\boldsymbol{x}_{i+1} \in T_g W$, since the edge$T_g\boldsymbol{z}_{i+1} = T_g\boldsymbol{x}_{i+1} - T_g\,\boldsymbol{x}_i \in H(\mathbf{B})$, then$T_g\,\boldsymbol{x}_{i+2} \in T_g R$, sincetheedge $T_g\boldsymbol{z}_{i+2} = T_g\boldsymbol{x}_{i+2} - T_g\boldsymbol{x}_{i+1} \in H(\mathbf{B})$. Continuing in this way, we see that if k is an odd, then$T_g\boldsymbol{x}_k \in T_g W$, and if k is even, then$T_g\boldsymbol{x}_k \in T_g R$. Since$T_g\boldsymbol{x}_{j+1} = T_g\boldsymbol{x}_i \in T_g R$, it implies that$j+1$ is even and thus the cycle is of even length. By theorem 5, then the graph $G = (T_g R, T_g W, H(\mathbf{B}))$ is a bipartite graph. □

4. Genomics and Phylogenetic

In this section, we describe some of the basic biological facts needed to understand phylogenetic models and then delve into the practical side of the algebraic statistics of these models. The basic genetic information of an organism is (almost always) carried in the form of DNA, a double helix consisting of two complementary B polymers bound together. The DNA molecules in a genome are typically represented as a number of frequencies of letters from the four letters alphabet= {A, C, G, T}. These letters correspond to the bases in the double helix that is the nucleotides Adenine, Cytosine, guanine and Thymine. The four nucleotides that form DNA come in two types: the purines (A and G) and the pyrimidine's (C and T). The two strands of the double helix are joined together via the base pairings A to T (via 2 hydrogen bonds) and C to G (via 3 hydrogen bonds). Since each cell typically contains a copy of the DNA of the organism, DNA copying occurs frequently. Several types of errors are possible during the replication of DNA. Single bases can mutate, or large pieces of DNA can separate and become reattached, possibly at another position, possibly in the opposite direction, these are just some of the events that occur over the course of evolution (C. Semple, M **[2]** and J. Felsenstein**[6])**.

5. A New Model of Genetic Algorithm Using the Action of Largest Subgroup of $D_n$for Invariance Markov Basis

In this section, we construct a new model of genetic algorithm that permutes the pieces of nucleotides in aligned DNA sequences using the actions of largest subgroup H of D_n for invariance Markov basis and toric ideals. Now, we describe our model in the following steps.

__**Step (1)**__:Suppose we have l-taxons of DNA sequences each taxion of length L such as

Taxon1: A G C T A A CG G T A T ⋯

Taxon2: C G A T C T G A C C T T ⋯

⋮⋮⋮⋮⋮⋮⋮⋮⋮⋮⋮⋮

Taxon$l$: A C G T C A C G T A G C ⋯

Now, we define a pattern $\boldsymbol{i} = i_1, i_2, \dots, i_m$to be the sequence of characters. We look at a single site (column) of our sequence data. In the sequences above, we can look at the first site in the sequences and see the pattern "AC . . .A". A pattern frequency $x_i$is that $\boldsymbol{i}$ appears in our set of sequence data , and we denote to the number of frequencies by n where $n = 3^m, m \in \mathbb{N}, m \ge 2$.

__**Step (2)**__:We can input pattern frequency x_i of above sequences in$3 \times \frac{n}{3}$ -contingency table as follows :

x_1	x_2	$\cdots$	$x_{\frac{n}{3}}$	$\sum_{i=1}^{\frac{n}{3}} x_i$
$x_{\frac{n}{3}+1}$	$x_{\frac{n}{3}+2}$	$\cdots$	$x_{\frac{2n}{3}}$	$\sum_{i=\frac{n}{3}+1}^{\frac{2n}{3}} x_i$
$x_{\frac{2n}{3}+1}$	$x_{\frac{2n}{3}+2}$	$\cdots$	x_n	$\sum_{i=\frac{2n}{3}+1}^{n} x_i$
$x_1 + x_{\frac{n}{3}+1} + x_{\frac{2n}{3}+1}$	$x_2 + x_{\frac{n}{3}+2} + x_{\frac{2n}{3}+2}$	$\cdots$	$x_{\frac{n}{3}} + x_{\frac{2n}{3}} + x_n$	$\lvert\boldsymbol{x}\rvert = \sum_{i\in I} x_i$

Where $\lvert\boldsymbol{x}\rvert = \sum_{i\in I} x_i = L$ is the length of sequences (the sample size), and

x_1 is the frequency of the first pattern .

Step(4): From remark 9,A is $\frac{n+9}{3} \times n$ matrix and

$$A=\begin{bmatrix} 1 & 1 & \cdots & 1 & 1 & 0 & 0 & \dots & 0 & 0 & 0 & 0 & \cdots & 0 & 0 \\ 0 & 0 & \cdots & 0 & 0 & 1 & 1 & \cdots & 1 & 1 & 0 & 0 & \cdots & 0 & 0 \\ 0 & 0 & \cdots & 0 & 0 & 0 & 0 & \cdots & 0 & 0 & 1 & 1 & \cdots & 1 & 1 \\ 1 & 0 & \cdots & 0 & 0 & 1 & 0 & \cdots & 0 & 0 & 1 & 0 & \cdots & 0 & 0 \\ 0 & 1 & \cdots & 0 & 0 & 0 & 1 & \cdots & 0 & 0 & 0 & 1 & \cdots & 0 & 0 \\ \vdots & \vdots & \cdots & \vdots & \vdots & \vdots & \vdots & \cdots & \vdots & \vdots & \vdots & \vdots & \cdots & \vdots & \vdots \\ 0 & 0 & \cdots & 0 & 1 & 0 & 0 & \cdots & 0 & 1 & 0 & 0 & \cdots & 0 & 1 \end{bmatrix}_{\frac{n+9}{3}\times n}$$

$A\boldsymbol{x} = \boldsymbol{t}$ $i.e$

$$\begin{bmatrix} 1 & 1 & \cdots & 1 & 1 & 0 & 0 & \dots & 0 & 0 & 0 & 0 & \cdots & 0 & 0 \\ 0 & 0 & \cdots & 0 & 0 & 1 & 1 & \cdots & 1 & 1 & 0 & 0 & \cdots & 0 & 0 \\ 0 & 0 & \cdots & 0 & 0 & 0 & 0 & \cdots & 0 & 0 & 1 & 1 & \cdots & 1 & 1 \\ 1 & 0 & \cdots & 0 & 0 & 1 & 0 & \cdots & 0 & 0 & 1 & 0 & \cdots & 0 & 0 \\ 0 & 1 & \cdots & 0 & 0 & 0 & 1 & \cdots & 0 & 0 & 0 & 1 & \cdots & 0 & 0 \\ \vdots & \vdots & \cdots & \vdots & \vdots & \vdots & \vdots & \cdots & \vdots & \vdots & \vdots & \vdots & \cdots & \vdots & \vdots \\ 0 & 0 & \cdots & 0 & 1 & 0 & 0 & \cdots & 0 & 1 & 0 & 0 & \cdots & 0 & 1 \end{bmatrix}_{\frac{n+9}{3}\times n} \begin{bmatrix} x_1 \\ x_2 \\ x_3 \\ x_4 \\ \vdots \\ x_n \end{bmatrix}$$

$$= \begin{bmatrix} t_1 \\ t_2 \\ t_3 \\ t_4 \\ \vdots \\ t_{\frac{n}{3}+3} \end{bmatrix}$$

Where the columns of the matrix A index by the elements of the column vector $\boldsymbol{x}$.

Step (5): We can find the Markov basis from remark 7.

Step (6): $A: Z^{3\times(n/3)} \to Z^{3+(n/3)}$ is a linear transformation, $\boldsymbol{t} \in \mathbb{Z}^{3+(n/3)}$, and $A^{-1}[\boldsymbol{t}]$ be the set of $\boldsymbol{t}$-fibers, and $\mathbf{B} \subset ker_Z(A)$. Use remark 13 to find the bipartite graph$G = (R, W, \mathbf{B}) = A^{-1}[\boldsymbol{t}]_{\mathbf{B}}$.

Step (7): We can find the toric ideals by using corollary 12 for each contingency tables.

Step (8): Find$T_g \mathbf{B} = \{T_g \boldsymbol{z}_1, T_g \boldsymbol{z}_2, \dots, T_g \boldsymbol{z}_{\frac{n^2-3n}{3}}\} = \mathbf{B}$ for all $g \in H$, where T_g is a permutation matrix of g.

Step (9): Find the set $\{T_g \boldsymbol{x}_0, T_g \boldsymbol{x}_1, \dots, T_g \boldsymbol{x}_{\frac{n^2-3n}{3}-1}\} \subseteq A^{-1}[g\boldsymbol{t}]$ ($g\boldsymbol{t}$-fibers) for all

x_2 is the frequency of the second pattern.

$\vdots$

$x_{\frac{n}{3}}$ is the frequency of the $\frac{n}{3}$ pattern.

$x_{\frac{n}{3}+1}$ is the frequency of the $\frac{n}{3}+1$ pattern.

$x_{\frac{n}{3}+2}$ is the frequency of the $\frac{n}{3}+2$ pattern.

$\vdots$

x_n is the frequency of the n pattern.

Step (3): Represent the contingency table $\boldsymbol{x} = \{x_i\}_{i\in I} \in \mathbb{N}^n$as a n- dimensional column vector of non-negative integers $\boldsymbol{x} = (x_1, x_2, \dots, x_n)'$, Where$'$ denotes the transpose of a vector or matrix , as in remark (1.4.2) then $\boldsymbol{x}$isa $\boldsymbol{t}$-fiber (i.e) $\boldsymbol{x} \in A^{-1}[\boldsymbol{t}]$where$A^{-1}[\boldsymbol{t}] = \{\boldsymbol{x} \in \mathbb{N}^n : A\boldsymbol{x} = \boldsymbol{t}\}$.

$g \in H$,where

$r^{\frac{n}{3}}\boldsymbol{t} = \left(t_3, t_1, t_2, t_4, \dots, t_{\frac{n}{3}+3}\right)'$, $r^{\frac{2n}{3}}\boldsymbol{t} = \left(t_2, t_3, t_1, t_4 \dots, t_{\frac{n}{3}+3}\right)$, $sr\boldsymbol{t} = \left(t_3, t_2, t_1, t_{\frac{n}{3}+3}, t_{\frac{n}{3}+2} \dots, t_4\right)$,

$sr^{\frac{n}{3}+1}\boldsymbol{t} = \left(t_2, t_1, t_3, t_{\frac{n}{3}+3}, t_{\frac{n}{3}+2} \dots, t_4\right)$ and

$sr^{\frac{2n}{3}+1}\boldsymbol{t} = \left(t_1, t_3, t_2, t_{\frac{n}{3}+3}, t_{\frac{n}{3}+2} \dots, t_4\right)$.

Step (10): Use remark 21 and theorem 22 to find the graphs $T_g G = A^{-1}[g\boldsymbol{t}]_{\mathbf{B}}$for all $g \in H$.

Step (11): Use corollary 19 to find the toric ideal $I_A = < P_{g(i+l)} P_{g(j+k)} - P_{g(j+l)} P_{g(i+k)} ;\ i,j = 1,2,\dots,\frac{n}{3}$ and $l,k = 0,\frac{n}{3},\frac{2n}{3}$, such that$i < j$ and $l < k >$ for all $g \in H$.

Step (12): Use the $\frac{n^2-3n}{3} \times 3 \times \frac{n}{3}$ -contingency tables ($\boldsymbol{t}$-fibers) in step (6), and $\frac{n^2-3n}{3} \times 3 \times \frac{n}{3}$ -contingency tables ($g\boldsymbol{t}$-fibers) in step (9) for all $g \in H$ to find the permutation of nucleotides in aligned DNA sequences.

Example (23): Suppose we have the following three aligned DNA sequences

Taxon 1: A G C T G A T T G G C C C G T T T T T G
Taxon 2: A G A T C T A T C G A A A C A A A T T C
Taxon3: A T T C A G A T C T T T T A A A A T T C

Step (1): There are three taxons of above DNA sequences with $|\boldsymbol{x}| = \sum_{i\in I} x_i = L = 20$ and nine patterns A A A, G G T, C A T, T T C, G C A, A T G, T A A, T T T, G C C with frequencies $1, 2, 4, 1, 2, 1, 4, 3$ and 2 respectively where $n = 9$.

Step (2): Now, we input the patterns frequency x_i of above sequences in 3×3-contingency table as follows :

1	2	4	7
1	2	1	4
4	3	2	9
6	7	7	20

Then the table of marginal and conditional probability is:

0.05	0.10	0.20	0.35
0.05	0.10	0.05	0.20
0.20	0.15	0.10	0.45

Step (3): Represent the contingency table $\boldsymbol{x} = \{x_i\}_{i\in I} \in \mathbb{N}^9$ as a 9- dimensional column vector of non- negative integers $\boldsymbol{x} = (1,2,4,1,2,1,4,3,2)'$, as in remark (1.5.2) then $\boldsymbol{x}$ is a $\boldsymbol{t}$-fiber

(i.e. $\boldsymbol{x} \in A^{-1}[\boldsymbol{t}]$, where

$$A^{-1}[\boldsymbol{t}] = \{\boldsymbol{x} \in \mathbb{N}^9 : A \begin{bmatrix} x_0 \\ x_1 \\ x_2 \\ x_3 \\ x_4 \\ x_5 \\ x_6 \\ x_7 \\ x_8 \end{bmatrix} = \begin{bmatrix} 7 \\ 4 \\ 9 \\ 6 \\ 7 \\ 7 \end{bmatrix}\}.)$$

Step(4): A is 6×9 matrix and

$$A = \begin{bmatrix} 1 & 1 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 1 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 1 & 1 \\ 1 & 0 & 0 & 1 & 0 & 0 & 1 & 0 & 0 \\ 0 & 1 & 0 & 0 & 1 & 0 & 0 & 1 & 0 \\ 0 & 0 & 1 & 0 & 0 & 1 & 0 & 0 & 1 \end{bmatrix}_{6\times 9}, \text{ and}$$

$A\boldsymbol{x} = \boldsymbol{t}$ *i.e*

$$\begin{bmatrix} 1 & 1 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 1 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 1 & 1 \\ 1 & 0 & 0 & 1 & 0 & 0 & 1 & 0 & 0 \\ 0 & 1 & 0 & 0 & 1 & 0 & 0 & 1 & 0 \\ 0 & 0 & 1 & 0 & 0 & 1 & 0 & 0 & 1 \end{bmatrix}_{6\times 9} \begin{bmatrix} 1 \\ 2 \\ 4 \\ 1 \\ 2 \\ 1 \\ 4 \\ 3 \\ 2 \end{bmatrix}_{9\times 1}$$

$$= \begin{bmatrix} 7 \\ 4 \\ 9 \\ 6 \\ 7 \\ 7 \end{bmatrix}_{6\times 1} = \begin{bmatrix} t_1 \\ t_2 \\ t_3 \\ t_4 \\ t_5 \\ t_6 \end{bmatrix}_{6\times 1}$$

Where the columns of the matrix A index by the elements of the column vector $\boldsymbol{x}$, and $t_1 = \sum_{i=1}^{3} x_i = 7, t_2 = \sum_{i=1}^{3} x_{i+3} = 4, t_3 = \sum_{i=1}^{3} x_{i+6} = 9,$ $t_4 = x_1 + x_4 + x_7 = 6,$ $t_5 = x_2 + x_5 + x_8 = 7,$ and $t_6 = x_3 + x_6 + x_9 = 7.$

Step (5): We can find the Markov basis from remark 7. Then the number of moves is $\frac{n^2-3n}{3} = \frac{9^2-3\times 9}{3} = 18$ elements in the set

$\mathbf{z}_1 =$

1	-1	0
-1	1	0
0	0	0

, , $\mathbf{z}_2 =$

0	0	0
1	-1	0
-1	1	0

, $\mathbf{z}_3 =$

1	0	-1
-1	0	1
0	0	0

$z_4 =$

0	0	0
1	0	-1
-1	0	1

, z_5 =

0	1	-1
0	-1	1
0	0	0

, z_6

0	1	-1
0	0	0
0	-1	1

$z_7 =$

0	0	0
0	1	-1
0	-1	1

, z_8 :

1	-1	0
0	0	0
-1	1	0

, $z_9 =$

1	0	-1
0	0	0
-1	0	1

z_{10} =

-1	1	0
1	-1	0
0	0	0

, z_{11} =

0	0	0
-1	1	0
1	-1	0

, z_{12} =

-1	0	1
1	0	-1
0	0	0

z_{13}

0	0	0
-1	0	1
1	0	-1

, $z_{14} =$

0	-1	1
0	1	-1
0	0	0

, $z_{15} =$

0	-1	1
0	0	0
0	1	1

z_{16} =

0	0	0
0	-1	1
0	1	-1

, z_{17} =

-1	1	0
0	0	0
1	-1	0

, $z_{18} =$

-1	0	1
0	0	0
1	0	-1

Step (6):The connected graph $A^{-1}[t]_B = G = (R, W, \mathbf{B})$ with $\frac{n^2-3n}{3} = 18$ (t- fibres) 3×3- contingency tables as vertices of it.

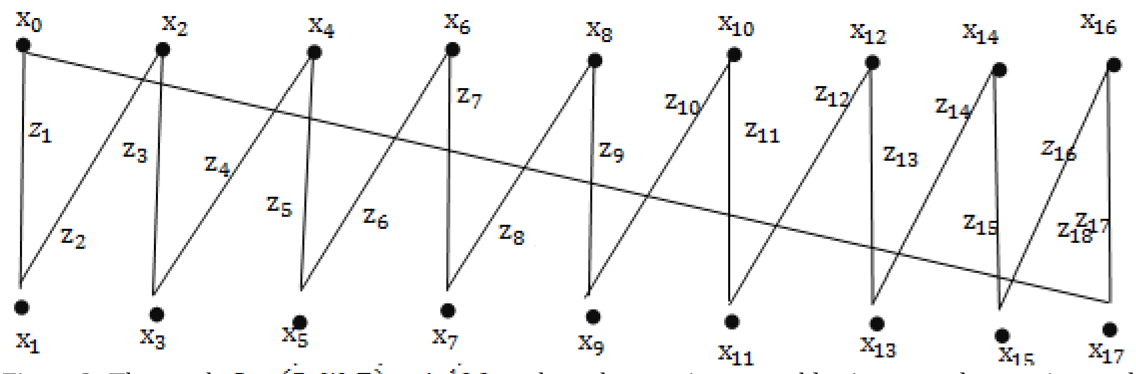


Figure 3: The graph $G = (R, W, \mathbf{B}) = A^{-1}[t]_B$, where the contingency tables interpreted as vertices and connecting Markov basis are interpreted as the edges of a graph,$R = \{x_0, x_2, x_4, x_6, x_8, x_{10}, x_{12}, x_{14}, x_{16}\}$ and $W = \{x_1, x_3, x_5, x_7, x_9, x_{11}, x_{13}, x_{15}, x_{17}\}$

Where

$\mathbf{x}_0$

1	2	4	7
1	2	1	4
4	3	2	9
6	7	7	20

, $\mathbf{x}_1 =$

2	1	4	7
0	3	1	4
4	3	2	9
6	7	7	20

, $\mathbf{x}_2$:

2	1	4	7
1	2	1	4
3	4	2	9
6	7	7	20

$\mathbf{x}_3$

3	1	3	7
0	2	2	4
3	4	2	9
6	7	7	20

, $\mathbf{x}_4$:

3	1	3	7
1	2	1	4
2	4	3	9
6	7	7	20

, $\mathbf{x}_5$

3	2	2	7
1	1	2	4
2	4	3	9
6	7	7	20

$\mathbf{x}_6 =$

3	3	1	7
1	1	2	4
2	3	4	9
6	7	7	20

, $\mathbf{x}_7 =$

3	3	1	7
1	2	1	4
2	2	5	9
6	7	7	20

, $\mathbf{x}_8$

4	2	1	7
1	2	1	4
1	3	5	9
6	7	7	20

$\mathbf{x}_9 =$

5	2	0	7
1	2	1	4
0	3	6	9
6	7	7	20

, $\mathbf{x}_{10} =$

4	3	0	7
2	1	1	4
0	3	6	9
6	7	7	20

, $\mathbf{x}_1$:

4	3	0	7
1	2	1	4
1	2	6	9
6	7	7	20

$\mathbf{x}_{12} =$

3	3	1	7
2	2	0	4
1	2	6	9
6	7	7	20

, $\mathbf{x}_{13}$

3	3	1	7
1	2	1	4
2	2	5	9
6	7	7	20

, $\mathbf{x}_{14}$

3	2	2	7
1	3	0	4
2	2	5	9
6	7	7	20

$\mathbf{x}_{15} =$

3	1	3	7
1	3	0	4
2	3	4	9
6	7	7	20

, $\mathbf{x}_{16} =$

3	1	3	7
1	2	1	4
2	4	3	9
6	7	7	20

, $\mathbf{x}_{17}$

2	2	3	7
1	2	1	4
3	3	3	9
6	7	7	20

Step (7): We can find the toric ideals by using corollary 12 for each contingency tables. Then the toric ideals that correspond the Markov basis that shown in the a previous figure is:

$I_A =< P_1P_5 - P_2P_4\ , P_4P_8 - P_5P_7\ ,\ P_1P_6 - P_3P_4\ ,\ P_4P_9 - P_6P_7\ ,\ P_2P_6 - P_3P_5\ ,\ P_2P_9 - P_3P_8\ ,\ P_5P_9 - P_6P_8\ ,\ P_1P_8 - P_2P_7\ ,\ P_1P_9 - P_3P_7 >$

$I_A =< 0.005 - 0.005\ ,0.0075 - 0.02\ , 0.0025\ - 0.01\ ,0.005 - 0.01\ ,$
$0.005\ - 0.02\ ,0.01\ - 0.03\ , 0.01 - 0.0075\ , 0.0075\ - 0.02\ \ , 0.005 - 0.04 >$

.

$\Rightarrow I_A =< 0.0025 >$

Step (8):we find the set$T_{\gamma^3}\mathbf{B} = \{T_{\gamma^3}\mathbf{z}_1, T_{\gamma^3}\mathbf{z}_2, T_{\gamma^3}\mathbf{z}_3, T_{\gamma^3}\mathbf{z}_4, T_{\gamma^3}\mathbf{z}_5, T_{\gamma^3}\mathbf{z}_6, T_{\gamma^3}\mathbf{z}_7,$
$T_{\gamma^3}\mathbf{z}_8, T_{\gamma^3}\mathbf{z}_9, T_{\gamma^3}\mathbf{z}_{10}, T_{\gamma^3}\mathbf{z}_{11}, T_{\gamma^3}\mathbf{z}_{12}, T_{\gamma^3}\mathbf{z}_{13}, T_{\gamma^3}\mathbf{z}_{14}, T_{\gamma^3}\mathbf{z}_{15}, T_{\gamma^3}\mathbf{z}_{16}, T_{\gamma^3}\mathbf{z}_{17}, T_{\gamma^3}\mathbf{z}_{18}\}.$
Such that

$T_{r^2}z_1$:

0	0	0
-1	1	0
1	-1	0

$T_{r^2}z_2$ =

-1	1	0
0	0	0
1	-1	0

, $T_{r^2}z_3$ =

0	0	0
1	0	-1
-1	0	1

$T_{r^2}z_4$ =

-1	0	1
0	0	0
1	0	-1

, $T_{r^2}z_5$ =

0	0	0
0	1	-1
0	-1	1

, $T_{r^2}z_5$ =

0	-1	1
0	1	-1
0	0	0

$T_{r^2}z_7$:

0	-1	1
0	0	0
0	1	-1

, $T_{r^2}z_8$ =

-1	1	0
1	-1	0
0	0	0

, $T_{r^2}z_9$ =

-1	0	1
1	0	-1
0	0	0

$T_{r^2}z_{10}$ =

0	0	0
-1	1	0
1	-1	0

, $T_{r^2}z_{11}$ =

1	-1	0
0	0	0
-1	1	0

, $T_{r^2}z_{12}$ =

0	0	0
-1	0	1
1	0	-1

$T_{r^2}z_{13}$

1	0	-1
0	0	0
-1	0	1

$T_{r^2}z_{14}$ =

0	0	0
0	-1	1
0	1	-1

, $T_{r^2}z_{15}$ =

0	1	-1
0	-1	1
0	0	0

$T_{r^2}z_{16}$ =

0	1	-1
0	0	0
0	-1	1

, $T_{r^2}z_{17}$ =

1	-1	0
-1	1	0
0	0	0

, $T_{r^2}z_{18}$ =

1	0	-1
-1	0	1
0	0	0

Step (9): We find the set $\{T_{r^3}x_0, T_{r^3}x_1, T_{r^3}x_2, T_{r^3}x_3, T_{r^3}x_4, T_{r^3}x_5, T_{r^3}x_6, T_{r^3}x_7, T_{r^3}x_8, T_{r^3}x_9, T_{r^3}x_{10}, T_{r^3}x_{11}, T_{r^3}x_{12}, T_{r^3}x_{13}, T_{r^3}x_{14}, T_{r^3}x_{15}, T_{r^3}x_{16}, T_{r^3}x_{17}\} \subseteq A^{-1}[r^3t]$ (r^3t-fibers) where $r^3t = (9,7,4,6,7,7)'$. We have.

$T_{r^3}x_0$ =

4	3	2	9
1	2	4	7
1	2	1	4
6	7	7	20

, $T_{r^3}x_1$ =

4	3	2	9
2	1	4	7
0	3	1	4
6	7	7	20

, $T_{r^3}x_2$ =

3	4	2	9
2	1	4	7
1	2	1	4
6	7	7	20

$T_{r^3}x_3$ =

3	4	2	9
3	1	3	7
0	2	2	4
6	7	7	20

, $T_{r^3}x_4$ =

2	4	3	9
3	1	3	7
1	2	1	4
6	7	7	20

, $T_{r^3}x_5$ =

2	4	3	9
3	2	2	7
1	1	2	4
6	7	7	20

$T_{r^3}x_6$ =

2	3	4	9
3	3	1	7
1	1	2	4
6	7	7	20

, $T_{r^3}x_7$ =

2	2	5	9
3	3	1	7
1	2	1	4
6	7	7	20

, $T_{r^3}x_8$ =

1	3	5	9
4	2	1	7
1	2	1	4
6	7	7	20

Step (10): Use remark 21 and theorem 22 to find the graph

$T_{r^3}x_9$ =

0	3	6	9
5	2	0	7
1	2	1	4
6	7	7	20

, $T_{r^3}x_{10}$ =

0	3	6	9
4	3	0	7
2	1	1	4
6	7	7	20

, $T_{r^3}x_{11}$ =

1	2	6	9
4	3	0	7
1	2	1	4
6	7	7	20

$T_{r^3}x_{12}$ =

1	2	6	9
3	3	1	7
2	2	0	4
6	7	7	20

, $T_{r^3}x_{13}$ =

2	2	5	9
3	3	1	7
1	2	1	4
6	7	7	20

, $T_{r^3}x_{14}$ =

2	2	5	9
3	2	2	7
1	3	0	4
6	7	7	20

$T_{r^3}x_{15}$ =

2	3	4	9
3	1	3	7
1	3	0	4
6	7	7	20

, $T_{r^3}x_{16}$ =

2	4	3	9
3	1	3	7
1	2	1	4
6	7	7	20

, $T_{r^3}x_{17}$ =

3	3	3	9
2	2	3	7
1	2	1	4
6	7	7	20

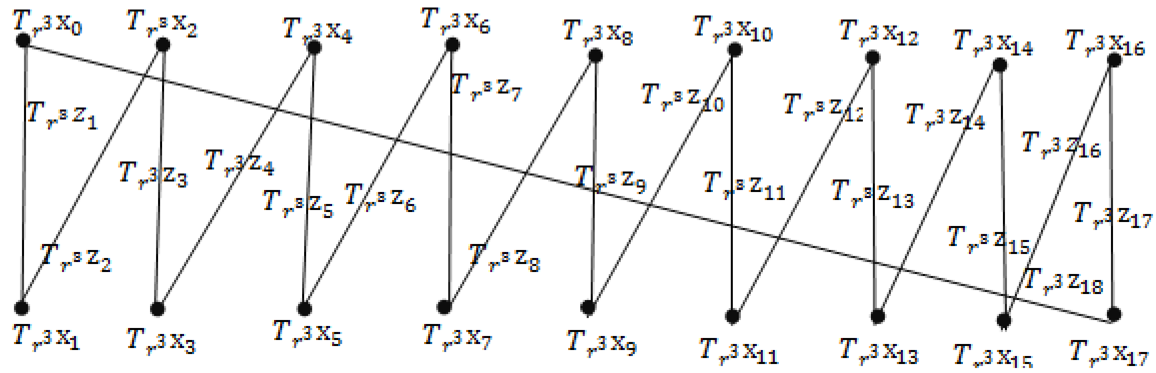


Figure 4: The graph $T_{r^3}G = \left(T_{r^3}R, T_{r^3}W, H(\mathbf{B})\right) = A^{-1}[r^3\boldsymbol{t}]_{H(\mathbf{B})} = A^{-1}[r^3\boldsymbol{t}]_{\mathbf{B}}$, where the contingency tables interpreted as vertices and connecting moves are interpreted as edges of a graph, $T_{r^3}R = \{r^3\boldsymbol{x}_0, r^3\boldsymbol{x}_2, r^3\boldsymbol{x}_4, r^3\boldsymbol{x}_6, r^3\boldsymbol{x}_8, r^3\boldsymbol{x}_{10}, r^3\boldsymbol{x}_{12}, r^3\boldsymbol{x}_{14}, r^3\boldsymbol{x}_{16}\}$ and $T_{r^3}W = \{r^3\boldsymbol{x}_1, r^3\boldsymbol{x}_3, r^3\boldsymbol{x}_5, r^3\boldsymbol{x}_7, r^3\boldsymbol{x}_9, r^3\boldsymbol{x}_{11}r^3, \boldsymbol{x}_{13}, r^3\boldsymbol{x}_{15}, r^3\boldsymbol{x}_{17}\}$.

Step (11):

Use corollary 19 to find the toric ideal $I_A =< P_{i+l}P_{j+k} - P_{j+l}P_{i+k} :\ i, j = 1, 2, \dots, \frac{n}{3}$ and $l, k = 0, \frac{n}{3}, \frac{2n}{3}$, such that $i < j$ and $l < k >=< P_1P_5 - P_2P_4\ , P_4P_8 - P_5P_7\ , P_1P_6 - P_3P_4\ , P_4P_9 - P_6P_7\ , P_2P_6 - P_3P_5\ , P_2P_9 - P_3P_8\ , P_5P_9 - P_6P_8\ , P_1P_8 - P_2P_7\ , P_1P_9 - P_3P_7 >$

.

If $g = sr$, then $T_{sr}\mathbf{B} = \{T_{sr}\mathbf{z}_1, T_{sr}\mathbf{z}_2, T_{sr}\mathbf{z}_3, T_{sr}\mathbf{z}_4, T_{sr}\mathbf{z}_5, T_{sr}\mathbf{z}_6, T_{sr}\mathbf{z}_7, T_{sr}\mathbf{z}_8, T_{sr}\mathbf{z}_9, T_{sr}\mathbf{z}_{10}, T_{sr}\mathbf{z}_{11}, T_{sr}\mathbf{z}_{12}, T_{sr}\mathbf{z}_{13}, T_{sr}\mathbf{z}_{14}, T_{sr}\mathbf{z}_{15}, T_{sr}\mathbf{z}_{16}, T_{sr}\mathbf{z}_{17}, T_{sr}\mathbf{z}_{18}\}$,

$T_{sr}\boldsymbol{z}_1 =$

0	0	0
0	1	-1
0	-1	1

, $T_{sr}\mathbf{z}_2 =$

0	1	-1
0	-1	1
0	0	0

, $T_{sr}\mathbf{z}_3 =$

0	0	0
1	0	-1
-1	0	1

$T_{sr}\boldsymbol{z}_4 =$

1	0	-1
-1	0	1
0	0	0

, $T_{sr}\mathbf{z}_5 =$

0	0	0
1	-1	0
-1	1	0

, $T_{sr}\mathbf{z}_5 =$

1	-1	0
0	0	0
-1	1	0

$T_{sr}\boldsymbol{z}_7 =$

1	-1	0
-1	1	0
0	0	0

, $T_{sr}\mathbf{z}_8 =$

0	1	-1
0	0	0
0	-1	1

, $T_{sr}\mathbf{z}_9 =$

1	0	1
0	0	0
-1	0	-1

$T_{sr}\boldsymbol{z}_{10} =$

0	0	0
0	-1	1
0	1	-1

, $T_{sr}\mathbf{z}_{11} =$

0	-1	1
0	1	-1
0	0	0

, $T_{sr}\mathbf{z}_{12} =$

0	0	0
-1	0	1
1	0	-1

$T_{sr}\boldsymbol{z}_{13}$:

-1	0	1
1	0	-1
0	0	0

$T_{sr}\mathbf{z}_{14} =$

0	0	0
-1	1	0
1	-1	0

, $T_{sr}\mathbf{z}_{15} =$

-1	1	0
0	0	0
1	-1	0

$T_{sr}\boldsymbol{z}_{16} =$

-1	1	0
1	-1	0
0	0	0

, $T_{sr}\mathbf{z}_{17} =$

0	-1	1
0	0	0
0	1	-1

, $T_{sr}\mathbf{z}_{18} =$

-1	0	1
0	0	0
1	0	-1

Also, we find the set $\{T_{sr}\ \boldsymbol{x}_0, T_{sr}\ \boldsymbol{x}_1, T_{sr}\ \boldsymbol{x}_2, T_{sr}\ \boldsymbol{x}_3, T_{sr}\ \boldsymbol{x}_4, T_{sr}\ \boldsymbol{x}_5, T_{sr}\ \boldsymbol{x}_6, T_{sr}\ \boldsymbol{x}_7, T_{sr}\ \boldsymbol{x}_8,$

$T_{sr}\ \boldsymbol{x}_9, T_{sr}\ \boldsymbol{x}_{10}, T_{sr}\ \boldsymbol{x}_{11}, T_{sr}\ \boldsymbol{x}_{12}, T_{sr}\ \boldsymbol{x}_{13}, T_{sr}\ \boldsymbol{x}_{14}, T_{sr}\ \boldsymbol{x}_{15}, T_{sr}\ \boldsymbol{x}_{16}, T_{sr}\ \boldsymbol{x}_{17}\} \subseteq A^{-1}[sr\boldsymbol{t}]$ ($sr\boldsymbol{t}$-fibers) where, $sr\boldsymbol{t} = (9, 4, 7, 7, 7, 6)'$, such that

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$T_{sr}\mathbf{x}_0 =$

2	3	4	9
1	2	1	4
4	2	1	7
7	7	6	20

, $T_{sr}\mathbf{x}_1 =$

2	3	4	9
1	3	0	4
4	1	2	7
7	7	6	20

, $T_{sr}\mathbf{x}_2 =$

2	4	3	9
1	2	1	4
4	1	2	7
7	7	6	20

$T_{sr}\mathbf{x}_3$

2	4	3	9
2	2	0	4
3	1	3	7
7	7	6	20

, $T_{sr}\mathbf{x}_4 =$

3	4	2	9
1	2	1	4
3	1	3	7
7	7	6	20

, $T_{sr}\mathbf{x}_5 =$

3	4	2	9
2	1	1	4
2	2	3	7
7	7	6	20

$T_{sr}\mathbf{x}_6 =$

4	3	2	9
2	1	1	4
1	3	3	7
7	7	6	20

, $T_{sr}\mathbf{x}_7 =$

5	2	2	9
1	2	1	4
1	3	3	7
7	7	6	20

, $T_{sr}\mathbf{x}_8 =$

5	3	1	9
1	2	1	4
1	2	4	7
7	7	6	20

$T_{sr}\mathbf{x}_9 =$

6	3	0	9
1	2	1	4
0	2	5	7
7	7	6	20

, $T_{sr}\mathbf{x}_{10} =$

6	3	0	9
1	1	2	4
0	3	4	7
7	7	6	20

, $T_{sr}\mathbf{x}_{11} =$

6	2	1	9
1	2	1	4
0	3	4	7
7	7	6	20

$T_{sr}\mathbf{x}_{12} =$

6	2	1	9
0	2	2	4
1	3	3	7
7	7	6	20

, $T_{sr}\mathbf{x}_{13} =$

5	2	2	9
1	2	1	4
1	3	3	7
7	7	6	20

, $T_{sr}\mathbf{x}_{14} =$

5	2	2	9
0	3	1	4
2	2	3	7
7	7	6	20

$T_{sr}\mathbf{x}_{15} =$

4	3	2	9
0	3	1	4
3	1	3	7
7	7	6	20

, $T_{sr}\mathbf{x}_{16} =$

3	4	2	9
1	2	1	4
3	1	3	7
7	7	6	20

, $T_{sr}\mathbf{x}_{17} =$

3	3	3	9
1	2	1	4
3	2	2	7
7	7	6	20

Now, use remark 21 and theorem 22 to find the graph $T_{sr}\ G = A^{-1}[srt]_{B}$.

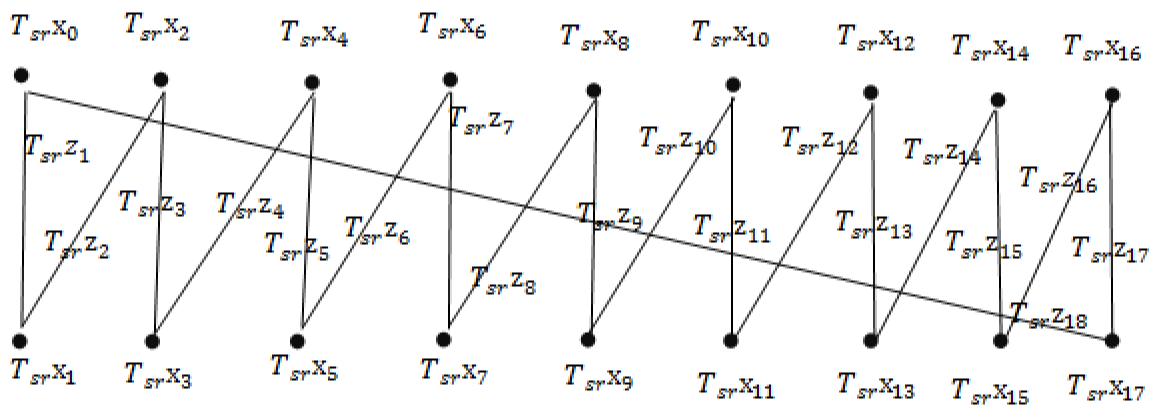

Figure 5: The graph $T_{sr}G = (T_{sr}R, T_{sr}W, H_2(\mathbf{B})) = A^{-1}[srt]_{H_2(\mathbf{B})} = A^{-1}[srt]_{\mathbf{B}}$, where the contingency tables interpreted as vertices and connecting moves are interpreted as edges of a graph, where $T_{sr}R = \{T_{sr}\boldsymbol{x}_0, T_{sr}\boldsymbol{x}_2, T_{sr}\boldsymbol{x}_4, T_{sr}\boldsymbol{x}_6, T_{sr}\boldsymbol{x}_8, T_{sr}\boldsymbol{x}_{10}, T_{sr}\boldsymbol{x}_{12}, T_{sr}\boldsymbol{x}_{14}, T_{sr}\boldsymbol{x}_{16}\}$ and $T_{sr}W = \{T_{sr}\boldsymbol{x}_1, T_{sr}\boldsymbol{x}_3, T_{sr}\boldsymbol{x}_5, T_{sr}\boldsymbol{x}_7, T_{sr}\boldsymbol{x}_9, T_{sr}\boldsymbol{x}_{11}, T_{sr}\boldsymbol{x}_{13}, T_{sr}\boldsymbol{x}_{15}, T_{sr}\boldsymbol{x}_{17}\}$.

Step(12): Use the $18 \times 3 \times 3$ -contingency tables ($\boldsymbol{t}$-fibers) in step (6), $18 \times 3 \times 3$ -contingency tables ($\boldsymbol{gt}$-fibers) in step (9) to find the permutation of nucleotides in aligned DNA sequences.

Then the change in the type of DNA sequences under the Markov basis.

Be as Figure 3 where

$x_0 =$
①②④①②①④③②
Taxon1: AGCTGA TTG G CCCG TTTTT G
Taxon2: AGA TC T AT C GA A ACAAA TT C
Taxon3: A T TCA GATCTTTTAAAA TTC

$x_1 =$
②①④⓿③①④③②
Taxon1: AGCGA TTG AC CCG G TTTTTG
Taxon2: A GAC T AT C AAA A C CA AATTC
Taxon3: A T TA GATC AT TT AAA AATTC

$x_2 =$
②①④①②①③④②
Taxon1: AGCTGA TTG ACCCG TTTTTG
Taxon2: AGA TC TAT C AA A ACAA TTTC
Taxon3: AT TCA G ATC ATTTAAA TTTC

$x_3 =$
③①③⓿②②③④②
Taxon1: AGCGATT G AACCG ATTTTT G
Taxon2: AGAC T AT C AAA ACTA ATTT C
Taxon3: A T TA GATC AATTA GA ATTTC

$x_4 =$
③①③①②①②④③
Taxon1: AGCTGA TTG AA CCGTTTT G G
Taxon2: AGA TC T AT C AA AACA TTT C C
Taxon3: A T TCA GATC AATT AA TTTC C

$x_5 =$
③②②①①②②④③
Taxon1: AGCTGA TTG A A G CATTTT G G
Taxon2: AGA TC T AT CAA GATA TTT C C
Taxon3: A T TCA GATCA A TTGA TTTC C

$x_6 =$
③③①①①②②③④
Taxon1: AGCTGA TTG A A GG ATTTG G G
Taxon2: AGA TC T AT CAAGGTA TTC C C
Taxon3: A T TCA GATCA ATTG A TTC C C

$x_7 =$
③③①①②①②②⑤
Taxon1: AGCTGA TTG A A GG G TTGG G G
Taxon2: AGA TC T AT CAAGGCA TCC C C
Taxon3: A T TCA GATCA ATTAA TCC C C

$x_8 =$
④②①①②①①③⑤
Taxon1: AGCTGA TTG A A A G G TTGG G G
Taxon2: AGA TC T AT CAAA GCTTCC C C
Taxon3: A T TCA GATCA AATATTCC C C

$x_9 =$
⑤②⓿①②①⓿③⑥
Taxon1: AGTGA TG A A A A G G TTGG G G G
Taxon2: AG TC T T CAAA A GCTTCC C C C
Taxon3: A T CA GTCA AA ATATTCC C C C

$x_{10} =$
④③⓿②①①⓿③⑥
Taxon1: AGTGA TG A A A GG TTTGG G G G
Taxon2: AG TC T T CAAA GGTTTCC C C C
Taxon3: A T CA GTCA AA TTCTTCC C C C

$x_{11} =$
④③⓿①②①①②⑥
Taxon1: AGTGATTG A A A GG G TGG G G G
Taxon2: AG TC TAT CAAA GGCTCC C C C
Taxon3: A T CA GATCA AA TTATCC C C C

$x_{12} =$
③③①②②⓿①②⑥
Taxon1: AGCTGTTG A A GGT G TGG G G G
Taxon2: AG ATC AT CAAGGTCTCC C C C
Taxon3: A TTCA ATCA ATTCATCC C C C

$x_{13} =$
③③①①②①②②⑤
Taxon1: AGCTGA TTG A A GG G TTGG G G
Taxon2: AGA TC T AT CAAGGCA TCC C C
Taxon3: A T TCA GATCA ATTAA TCC C C

$x_{14} =$
③②②①③⓿②②⑤
Taxon1: AGCTGTTG A A GC G G TTGG G G
Taxon2: AGA TC AT CAAGAC CA TCC C C
Taxon3: A T TCA ATCA ATTAAA TCC C C

$x_{15} =$
③①③①③⓿②③④
Taxon1: AGCTGTTG A A CC G G TTTG G G
Taxon2: AGA TC AT CAAA AC CA TTC C C
Taxon3: A T TCA ATCA ATTAAA TTC C C

$x_{16} =$
③①③①②①②④③
Taxon1: AGCTGA TTG AA CCGTTTT G G
Taxon2: AGA TC T AT C AA AACA TTT C C
Taxon3: A T TCA GATC AATT AA TTTC C

$x_{17} =$
②②③①②①③③③
Taxon1: AGCTGA TTG AGCCGTTTT G G
Taxon2: AGA TC T AT C AG AACA ATT C C
Taxon3: A T TCA GATC ATTT AA ATTC C

And the change in the type of DNA sequences under the action of r^3 on the set of Markov basis. Be as Figure 4 where

$T_{r^3} x_0 =$
④③②①②④①②①
Taxon1: AGCTGA TTG A A AGGCG A A AT
Taxon2: AGA TC T AT C A A AGG A CTTTT
Taxon3: A T TCA GATC A A ATTTAGGGT

$T_{r^3} x_1 =$
④③②②①④⓿③①
Taxon1: AGCTGA TG A A A GGCTA A ATT
Taxon2: A GA TC T T C AAA GG ATTTTTT
Taxon3: A T TCA GTC A A ATTTCGGGTT

$T_{r^3} x_2 =$
③④②②①④①②①
Taxon1: AGCTGA TTG A A GGG CTA A AT
Taxon2: AGA TC TAT C AA GGGATTTTT
Taxon3: AT TCA G ATC A ATTTTCGGGT

$T_{r^3} x_3 =$
③④②③①③⓿②②
Taxon1: AGCTGAT G AAGGG CTTAAT G
Taxon2: AGA TC T T C AAGGGATTTTT C
Taxon3: A T TCA GTC AATTTTC CGGTC

$T_{r^3} x_4 =$
②④③③①③①②①
Taxon1: AGCTGA TTG AGGGCCTTA AT
Taxon2: AGA TC T AT C AGGGAA TTTTT
Taxon3: A T TCA GATC ATTTTTC CGGT

$T_{r^3} x_5 =$
②④③③②②①①②
Taxon1: AGCTGA TTG AGGGCCTTGA G
Taxon2: AGA TC T AT CAGGGAA TTCT C
Taxon3: A T TCA GATCATTTTTC CAG C

$T_{r^3} x_6 =$
②③④③③①①①②
Taxon1: AGCTGA TTG AGGCCCTTGG G
Taxon2: AGA TC T AT CAGGAAA T TCC C
Taxon3: A T TCA GATCATTTTTC CAA C

$T_{r^3} x_7 =$
②②⑤③③①①②①
Taxon1: AGCTGA TTG AGCCCCTTGG T
Taxon2: AGA TC T AT CAGAAAA TTC C T
Taxon3: A T TCA GATCATTTTTC CA AT

$T_{r^3}x_8 =$ ①③⑤④②①①②①
Taxon1: AGCTGA TTG GGCCCCTTTG T
Taxon2: AGA TC T AT CGGAAAA TTT C T
Taxon3: A T TCA GATCTTTTTTC C CAT

$T_{r^3}x_9 =$ ⓿③⑥⑤②⓿①②①
Taxon1: GCTGTTG GGCCC CCTTTTG T
Taxon2: GA TC AT CGGAAAAA TTTT C T
Taxon3: T TCA ATCTTTTTTTCC C CAT

$T_{r^3}x_{10} =$ ⓿③⑥④③⓿②①①
Taxon1: GCTGTTG GGCCC CCTTTGG T
Taxon2: GA TC AT CGGAAAAA TTTC C A
Taxon3: T TCA ATCTTTTTTTCC C A AA

$T_{r^3}x_{11} =$ ①②⑥④③⓿①②①
Taxon1: AGCTGTTG GCCC CCTTTGG T
Taxon2: AGA TC AT CGAAAAA TTTC C T
Taxon3: A T TCA ATCTTTTTTTCC C A AT

$T_{r^3}x_{12} =$ ①②⑥③③①②②⓿
Taxon1: AGCTGA TTGCCC CCTTGG TT
Taxon2: AGA TC T ATGAAAAA TTC C A T
Taxon3: A T TCA GATTTTTTTC C A AA T

$T_{r^3}x_{13} =$ ②②⑤③③①①②①
Taxon1: AGCTGA TTG AGCCCCTTG G T
Taxon2: AGA TC T AT CAGAAAA TTC C T
Taxon3: A T TCA GATCATTTTTCCAAT

$T_{r^3}x_{14} =$ ②②⑤③②②①③⓿
Taxon1: AGCTGA TTAGCC CCTTGATT
Taxon2: AGA TC T ATAGAAAA TTC TTT
Taxon3: A T TCA GATATTTTTC C A GTT

$T_{r^3}x_{15} =$ ②③④③①③①③⓿
Taxon1: AGCTGA TTAGGC CCTTA ATT
Taxon2: AGA TC T ATAGGAAA TTTTTT
Taxon3: A T TCA GATATTTTTC C GGTT

$T_{r^3}x_{16} =$ ②④③③①③①②①
Taxon1: AGCTGA TTG AGGGCCTTA AT
Taxon2: AGA TC T AT CAGGGAA TTTTT
Taxon3: A T TCA GATCATTTTTC CGGT

$T_{r^3}x_{17} =$ ③③③②②③①②①
Taxon1: AGCTGA TTG AAGGCCTGA AT
Taxon2: AGA TC T AT CAAGGAA TCTTT
Taxon3: A T TCA GATCAATTTTC AGGT

And the change in the type of DNA sequences under the action of sr on the set of Markov basis. Be as Figure 5 where

$T_{sr}x_0 =$ ②③④①②①④②①
Taxon1: AGCTGA TTG AGGC CCGTTTT
Taxon2: AGA TC T AT C AGGAAACA AAT
Taxon3: A T TCA GATC ATTTTT AA AAT

$T_{sr}x_1 =$ ②③④①③⓿④①②
Taxon1: AGCTGTTG AGGC CCGGTTTG
Taxon2: AGA TC AT C AGGAAACCA AAC
Taxon3: A T TCA ATC ATTTTT AAA AAC

$T_{sr}x_2 =$ ②④③①②①④①②
Taxon1: AGCTGA TTG AGGGCCGTTTG
Taxon2: AGA TC TAT C AGGGA ACAAAC
Taxon3: AT TCA G ATC ATTTTTA AAAC

$T_{sr}x_3 =$ ②④③②②⓿③①③
Taxon1: AGCTGTT G AGGGCCTGTTG G
Taxon2: AGA TC AT C AGGGA ATCA AC C
Taxon3: A T TCA ATC ATTTTTCAA ACC

$T_{sr}x_4 =$ ③④②①②①③①③
Taxon1: AGCTGA TTG AA GGGCGTT G G
Taxon2: AGA TC T AT C AA GGGA CAA C C
Taxon3: A T TCA GATC AATTTTAAAC C

$T_{sr}x_5 =$ ③④②②①①②②③
Taxon1: AGCTGA TTG A A GGG CTT G G
Taxon2: AGA TC T AT CAA GGGATAT C C
Taxon3: A T TCA GATCA A TTTTCATC C

$T_{sr}x_6 =$ ④③②②①①①③③
Taxon1: AGCTGA TTG A A AGG CTTT G G
Taxon2: AGA TC T AT CAA AGGA TTT C C
Taxon3: A T TCA GATCA A ATTTCTT C C

$T_{sr}x_7 =$ ⑤②②①②①①③③
Taxon1: AGCTGA TTG A A AAG C GTT G G
Taxon2: AGA TC T AT CAA AAGACTT C C
Taxon3: A T TCA GATCA A A ATTATT C C

$T_{sr}x_8 =$ ⑤③①①②①①②④
Taxon1: AGCT GA TTG A A A A GG GTG G G
Taxon2: AGA T C T AT CAAA A GGCTC C C
Taxon3: A T TCA GATCA AAATTATC C C

$T_{sr}x_9 =$ ⑥③⓿①②①⓿②⑤
Taxon1: AGTGA TG A A A A A G G G TG G G G
Taxon2: AG TC T T CA AAA A G GCTC C C C
Taxon3: A T CA GTCA A AA ATTATC C C C

$T_{sr}x_{10} =$ ⑥③⓿①①②⓿③④
Taxon1: AGTGA TG A A A A A G G ATT G G G
Taxon2: AG TC T T CA AAA A G GTTT C C C
Taxon3: A T CA GTCA A AA ATTGTT C C C

$T_{sr}x_{11} =$ ⑥②①①②①⓿③④
Taxon1: AGCTGATG A A A A A G GTT G G G
Taxon2: AG ATC TT CAAA A A GCTT C C C
Taxon3: A TTCA GTCA AA A A TA TT C C C

$T_{sr}x_{12} =$ ⑥②①⓿②②①③③
Taxon1: AGCGA TTG A A A A AG GATT G G
Taxon2: AGAC T AT CAAA A AGCTTT C C
Taxon3: A T TA GATCA AAAATAGTT C C

$T_{sr}x_{13} =$
⑤②②①②①①③③
Taxon1: AGCTGA TTG A A A AG CGTT G G
Taxon2: AGA TC T AT CA A A AGA CTT C C
Taxon3: A T TCA GATCAAAATTATT C C

$T_{sr}x_{14} =$
⑤②②⓿③①②②③
Taxon1: AGCGA TTG A A A AG CG G TTGG
Taxon2: AGAC T AT CA A A AGA C CA TCC
Taxon3: A T TA GATCAAAATTAAA TCC

$T_{sr}x_{15} =$
④③②⓿③①③①③
Taxon1: AGCGA TTG A A A GG CG G TTGG
Taxon2: AGAC T AT CA A A GGA C CA ACC
Taxon3: A T TA GATCAAATTTAAA ACC

$T_{sr}x_{16} =$
③④②①②①③①③
Taxon1: AGCTGA TTG AA GGG CGTT G G
Taxon2: AGA TC T AT C AA GGGA CAA C C
Taxon3: A T TCA GATC AATTTTAAAC C

$T_{sr}x_{17} =$
③③③①②①③②②
Taxon1: AGCTGA TTG AA GGCCGTTT G
Taxon2: AGA TC T AT C AA GG AACA AT C
Taxon3: A T TCA GATC AATTTT AA AT C

Remark 24:

i. We refer to ①, ②, ③, ④, ⑤and⑥ inexample 23to the frequencies of thepatterns in DNA sequences.

ii. We refer⓿to the hidden in the pattern frequency of DNA sequences.

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