



ICAAMM 2018

**Proceedings of the
7th International Conference on Applied Analysis
and Mathematical Modeling**

**Editors
Mustafa Bayram
Aydin Secer**

Istanbul Gelisim University, Istanbul, Turkey

PROCEEDINGS OF THE 7th INTERNATIONAL CONFERENCE ON
APPLIED ANALYSIS

and

MATHEMATICAL MODELING, ICAAMM2018

June 20-24, 2018, Istanbul-Turkey

Editors

Mustafa Bayram
Istanbul Gelisim University

Aydin Secer
Yildiz Technical University

TABLE OF CONTENTS

MESSAGE FROM CHAIRMAN	iv
Chairs	v
Co-Chairs	v
Coordinator-Secretaries	v
Members of Organizing Committee	v
Scientific Committee	vi
Local Committee	vii
Plenary Speakers	vii
Management and valorization of urban solid waste in landfills: case of the TEC of the city of Batna	1
Haddad Louiza and Aouachria Zeroual	1
Galerkin vector solution of Kelvin problem for a mixture of two linear elastic solids	9
Emre Kurt and M. Salih Dokuz	9
A new machine learning approach to house price estimation	19
Changchun Wang and Hui Wu	19
On twisted sums of Schreier spaces and James- Schreier spaces	27
Haifa Bin Jebreen	27
Covariance matrix estimation of an elliptically symmetric distribution in high dimensional setting	35
Anis M. Haddouche, Fatiha Mezoued and Dominique Fourdrinier	35
Global existence results for semilinear perturbed fractional differential equations with infinite delay	41
Sara Litimein and Atika Matallah	41
Three-point value problem for a class of Hadamard fractional differential equations	59
F. Berhoun and Z. Malki	59
Spectrum of cayley graphs of dihedral groups and their energy	65
Amira Fadina Ahmad Fadzil, Nor Haniza Sarmin and Ahmad Erfanian	65

Closure properties of static Watson-Crick regular grammars	71
Aqilahfarhana Abdul Rahman, Wan Heng Fong, Nor Haniza Sarmin, Sherzod Turaev and Nurul Liyana Mohamad Zulkufli	71
The topological indices of non-commuting graph for quasidihedral group	77
Nur Idayu Alimon, Nor Haniza Sarmin, and Ahmad Erfanian	77
Common fixed point theorems for generalized fuzzy homotopic mappings in Q-fuzzy metric space	85
Seema Mehra	85
Solar cell parameter estimation using Hybrid Nelder-Mead and Big Bang Big Crunch optimization algorithms	95
Omer Gonul and Osman Kaan Erol	95
Study of turbulent flow through a thrust reverser	101
Rayane Dellali and Mahfoud Kadja	101
A combined semi-supervised classification approach for text categorization: A case study for movie reviews	113
Nur Uylas Sati	113
Generalisations of DNA splicing languages with one restriction enzyme using automata	119
Wan Heng Fong, Nurul Izzaty Ismail and Nor Haniza Sarmin	119
The mathematical modelling of DNA splicing system with Palindromic and Non-Palindromic restriction enzymes	127
Nurul Izzaty Ismail, Wan Heng Fong, Nor Haniza Sarmin	127
Existence of solutions for elliptic Kirchhoff equations in R^N	139
Atika Matallah and Sara Litimein	139
Existence of solutions for a nonhomogeneous p-Laplacian elliptic equation with critical Hardy-Sobolev exponent	143
Atika Matallah and Sara Litimein	143
Development of early warning system of dengue fever disease endemic: a computer sim- ulation model	153
Paian Sianturi	153
Controllability results for fractional integro-differential inclusions with infinite state de- pendent delay	165
Sara Litimein and Atika Matallah	165
Numerical study of coupled natural convection with surface radiation in a cylindrical annular enclosure	175
Belkacem Ould Said, Mohamed Amine Medebber, Nouredine Retiel, Aissa Abderrahmane and Mohammed El Ganaoui	175
Vibrational analysis and electronic proprieties of zwitterionic D-phenylalanine	185
A. Boukaoud, D. Sebbar, N. Guessabi, S. Aissou	185
Modeling Land Use Simulation of Istanbul for 2023 with Logistic Regression	195
Cemre Fazilet Aldogan, Ömer Akin, Ahmet Eroglu and Hande Demirel	195

On the Analytical Solution for Stochastic Differential Equations with Lie Symmetry Analysis	201
Tugcem Partal, Zuhale Kucukarslan Yuzbasi and Ebru Cavlak Aslan	201
The local and global dynamics of a cancer tumor growth with multiphase structure and treatment model	205
Veli Shakhmurov, A. Maharramov and Bunyad Shahmurzada	205

The mathematical modelling of DNA splicing system with Palindromic and Non-Palindromic restriction enzymes

Nurul Izzaty Ismail*, Wan Heng Fong, Nor Haniza Sarmin

*Department of Mathematical Sciences, Faculty of Science, Universiti Teknologi Malaysia, 81310 UTM
Johor Bahru, Johor, Malaysia*

E-mail: *Corresponding author: nurulizzaty1112@gmail.com

Abstract: The mathematical modelling of DNA splicing system is introduced by Head where restriction enzymes and a ligase cleave and recombine DNA molecules in particular ways based on the cleavage pattern of restriction enzymes. The set of molecules resulting from the splicing system is called a splicing language, which can be analysed using formal language theory. The restriction enzymes are also known as restriction endonucleases which made up of three sites namely the crossing, left and right context. Palindrome is a sequence of string that reads the same forwards and backwards. The restriction enzymes also recognize palindromic and non-palindromic sequences. In this research, DNA splicing systems with one cutting site each of palindromic and non-palindromic restriction enzymes are modelled via Head's splicing system. The splicing languages from the splicing systems for same and different crossings are generalized and presented as theorems, which are proved using induction and direct methods respectively. Some examples of DNA splicing systems with palindromic and non-palindromic restriction enzymes are also provided to obtain the corresponding splicing languages using these theorems.

Keywords: DNA, splicing system, splicing language, palindromic, restriction enzyme.

1 Introduction

In 1987, DNA splicing system is introduced by Head [1] and mathematically modelled from a relation between formal language theory and molecular biology. The splicing system is also known as Head's Splicing System. In splicing systems, deoxyribonucleic acid (DNA) molecules are cut and recombined when react with a ligase and restriction enzymes which are biologically called as endodeoxyribonucleases [2].

The set of molecules resulting from a DNA splicing system is called as a splicing language which is simulated using formal language theory. A formal language consists of a set of strings of symbols from an alphabet [3]. Some notations in formal language theory, namely λ , $+$, \bar{u} and $*$ which denote the empty string, union, concatenation and star-closure respectively, are used in this research [3]. By using the concepts in formal language theory, the splicing language from a splicing system is associated with three sets. The first set is the set of double stranded DNA (dsDNA) symbols from nitrogenous base pairings: adenine (A) pairs with thymine (T), while cytosine (C) pairs with guanine (G) [4]. The second set consists of initial DNA molecules taken from the sub sequences or pattern in protein or nucleotide chains [5]. Lastly, the third set consists of the cleavage pattern of restriction enzymes. The rule for the cleavage pattern of restriction enzymes is made up of three sites namely the crossing, left and right context [6]. The symbols \downarrow and \uparrow indicate the upper and lower cutting sites of the restriction enzymes respectively.

Throughout the years, notations in Head's splicing system had been extended and variant of splicing models had been developed namely Paun [7], Pixton [8], Goode-Pixton [9] and Yusof-Goode [10] splicing systems. The variant of splicing systems resulted in many types of splicing languages.

The splicing languages from different model of splicing system can be obtained based on the specific sequences of restriction enzymes. This research focuses on palindromic and non-palindromic sequences of restriction enzyme. Palindrome is a sequence of strings that reads the same forwards and backwards [11]. Previously, Fong [12] had studied the modelling of DNA splicing system with palindromic restriction enzyme. Research on DNA splicing system with non-palindromic restriction enzymes had also been done in [13].

In this paper, the generalisations of splicing languages from DNA splicing system with one cutting site of each palindromic and non-palindromic restriction enzymes for same and different crossings are presented.

In the next section, some preliminaries related to this research are given.

2 Preliminaries

In this research, DNA splicing systems with palindromic and non-palindromic restriction enzymes are modelled using Head's splicing system. The definitions of Head's splicing system and splicing language are stated in the following.

Definition 2.1 (1). **Splicing System and Splicing Language** A splicing system $S = (A, I, B, C)$ consists of a finite alphabet A , a finite set I of initial strings in A^* , and finite sets B and C of triples (c, x, d) with c, x and d in A^* . Each such triple in B or C is called a pattern. For each such triple the string $cx d$ is called a site and the string x is called a crossing. Patterns in B are called left patterns and patterns in C are called right patterns. The language $L = L(S)$ generated by S consists of the strings in I and all strings that can be obtained by adjoining to $ucxfq$ and $perdv$ whenever $ucxdv$ and $perfq$ are in L and (c, x, d) and (e, x, f) are patterns of the same hand. A language, L is a splicing language if there exists a splicing system S for which $L = L(S)$.

Next, the definition of a palindromic string is stated.

Definition 2.2 (14). **Palindromic String** A string I of a dsDNA is said to be palindromic if the sequence from the left to the right side of the upper single strand is equal to the sequence from the right to the left side of the lower single strand.

In this paper, generalisations of splicing languages from DNA splicing system involving palindromic and non-palindromic sequences for restriction enzymes are done. For example, the enzyme $BfaI$
 $5' - \text{CTAG} - 3'$
 $3' - \text{GATC} - 5'$ is a palindromic restriction enzyme since the upper single strand of enzyme $BfaI$ matches

with the lower single strand when read from backwards; while the enzyme $BbvCI$
 $5' - \text{CCTCAGC} - 3'$
 $3' - \text{GGAGTCG} - 5'$ is a non-palindromic restriction enzyme since the upper single strand of enzyme $BbvCI$ does not match with the lower single strand when read from backwards.

3 Results and findings

In this research, the splicing languages from DNA splicing systems involving one cutting site each of palindromic and non-palindromic restriction enzymes are generalised and given as theorems. These theorems are mathematically proved. Some examples of DNA splicing systems with one cutting site each of palindromic and non-palindromic restriction enzymes are provided to determine the corresponding splicing languages by using these theorems. The generalisation of splicing languages from DNA splicing system with one cutting site each of palindromic and non-palindromic restriction enzymes and same crossing is presented in Theorem 1.

Theorem 3.1. Given $S = (A, I, B, C)$ is a DNA splicing system in which $A = \begin{matrix} A & C & G & T \\ T & G & C & A \end{matrix}$

is the set of dsDNA symbols, $I = \left\{ \begin{matrix} N_1 N_1' \dots N_1 X_1 Y X_2 M M \dots M W_1 Y W_2 N_2 N_2' \dots N_2 \\ N_1' N_1' \dots N_1' X_1' Y' X_2' M' M' \dots M' W_1' Y' W_2' N_2' N_2' \dots N_2' \end{matrix} \right\}$ is the set consisting of an initial string with one cutting site each of palindromic and non-palindromic restriction enzymes $\begin{matrix} X_1 Y X_2 \\ X_1' Y' X_2' \end{matrix}$ and $\begin{matrix} W_1 Y W_2 \\ W_1' Y' W_2' \end{matrix}$ respectively, set

$B = \left\{ \left(\begin{matrix} X_1 & Y & X_2 \\ X_1' & Y' & X_2' \end{matrix} \right), \left(\begin{matrix} W_1 & Y & W_2 \\ W_1' & Y' & W_2' \end{matrix} \right) \right\}$ is the set of cleavage pattern for the restriction enzymes and set C is the empty set, the resulting splicing language consists of strings of the form

$$\left(\begin{matrix} N_1 N_1' \dots N_1 & N_2' N_2' \dots N_2' W_2' Y W_1' M' M' \dots M' \\ N_1' N_1' \dots N_1' & N_2 N_2 \dots N_2 W_2 Y W_1 M M \dots M \end{matrix} \right) X_1 \left(\begin{matrix} Y X_2 & M M \dots M & W_1 \\ Y X_2' & M' M' \dots M' & W_1' \end{matrix} \right)^{n-1} Y \left(\begin{matrix} W_2 & N_2 N_2' \dots N_2' & X_2 N_1' N_1' \dots N_1' \\ W_2' & N_2' N_2' \dots N_2' & X_2 N_1 N_1 \dots N_1 \end{matrix} \right) \quad (3.1)$$

where $n \in \mathbb{Z}^+$, $\begin{matrix} N_1 & X_1 & Y & X_2 & M & W_1 & W_2 \\ N_1' & X_1' & Y' & X_2' & M' & W_1' & W_2' \end{matrix}$ and $\begin{matrix} N_2 \\ N_2' \end{matrix}$ denote arbitrary dsDNA symbol(s), N_1' , X_1' , Y' , X_2' , M' , W_1' , W_2' and N_2' are complementarities for N_1 , X_1 , Y , X_2 , M , W_1 , W_2 , and N_2 respectively, $\begin{matrix} Y \\ Y' \end{matrix}$ is the crossing, and

$$\left\{ \begin{matrix} X_1 Y X_2 & W_1 Y W_2 & W_2' Y' W_1' \\ X_1' Y' X_2' & W_1' Y' W_2' & W_2 Y W_1 \end{matrix} \right\} \notin \left\{ \begin{matrix} N_1 N_1' \dots N_1 & M M \dots M & N_2 N_2' \dots N_2 \\ N_1' N_1' \dots N_1' & M' M' \dots M' & N_2' N_2' \dots N_2' \end{matrix} \right\}.$$

Proof Suppose the restriction enzyme $\begin{matrix} X_1 Y X_2 \\ X_1' Y' X_2' \end{matrix}$ is palindromic, so the base sequence of enzyme reads the same backwards and forwards:

$$\begin{matrix} X_1 Y X_2 \\ X_1' Y' X_2' \end{matrix} = \begin{matrix} X_2' Y' X_1' \\ X_2 Y X_1 \end{matrix}.$$

Since the restriction enzyme $\begin{matrix} W_1 Y W_2 \\ W_1' Y' W_2' \end{matrix}$ is not palindromic, so the base sequence of enzyme is not the same backwards and forwards:

$$\begin{matrix} W_1 Y W_2 \\ W_1' Y' W_2' \end{matrix} \neq \begin{matrix} W_2' Y' W_1' \\ W_2 Y W_1 \end{matrix}.$$

Then $\begin{matrix} X_1 \\ X'_1 \end{matrix} = \begin{matrix} X'_2 \\ X_2 \end{matrix}$, $\begin{matrix} Y \\ Y' \end{matrix} = \begin{matrix} Y' \\ Y \end{matrix}$, $\begin{matrix} X_2 \\ X'_2 \end{matrix} = \begin{matrix} X'_1 \\ X_1 \end{matrix}$, $\begin{matrix} W_1 \\ W'_1 \end{matrix} \neq \begin{matrix} W'_2 \\ W_2 \end{matrix}$ and $\begin{matrix} W_2 \\ W'_2 \end{matrix} \neq \begin{matrix} W'_1 \\ W_1 \end{matrix}$. Then, the initial string $N_1N_1 \dots N_1X_1YX_2M \dots MW_1YW_2N_2N_2 \dots N_2$ with the cutting site of the enzymes $N'_1N'_1 \dots N'_1X'_1Y'X'_2M'M' \dots M'W'_1Y'W'_2N'_2N'_2 \dots N'_2$ is shown respectively in the following:

$$\begin{matrix} N_1N_1 \dots N_1X_1 \\ N'_1N'_1 \dots N'_1X'_1 \end{matrix} \downarrow \begin{matrix} Y \\ Y' \end{matrix} \uparrow \begin{matrix} X_2M \dots MW_1 \\ X'_2M'M' \dots M'W'_1 \end{matrix} \begin{matrix} Y \\ Y' \end{matrix} \begin{matrix} W_2N_2N_2 \dots N_2 \\ W'_2N'_2N'_2 \dots N'_2 \end{matrix} \quad (3.2)$$

for the first cutting site and

$$\begin{matrix} N_1N_1 \dots N_1X_1 \\ N'_1N'_1 \dots N'_1X'_1 \end{matrix} \begin{matrix} Y \\ Y' \end{matrix} \begin{matrix} X_2M \dots MW_1 \\ X'_2M'M' \dots M'W'_1 \end{matrix} \downarrow \begin{matrix} Y \\ Y' \end{matrix} \uparrow \begin{matrix} W_2N_2N_2 \dots N_2 \\ W'_2N'_2N'_2 \dots N'_2 \end{matrix} \quad (3.3)$$

for the second cutting site.

The initial string can be written 180 degree wise as

$$\begin{matrix} N'_2N'_2 \dots N'_2W'_2Y'W'_1M'M' \dots M'X'_2Y'X'_1N'_1N'_1 \dots N'_1 \\ N_2N_2 \dots N_2W_2Y \ W_1M \ M \dots MX_2Y \ X_1N_1N_1 \dots N_1 \end{matrix} \quad (3.4)$$

Since $\begin{matrix} X_1 \\ X'_1 \end{matrix} = \begin{matrix} X'_2 \\ X_2 \end{matrix}$, $\begin{matrix} Y \\ Y' \end{matrix} = \begin{matrix} Y' \\ Y \end{matrix}$, $\begin{matrix} X_2 \\ X'_2 \end{matrix} = \begin{matrix} X'_1 \\ X_1 \end{matrix}$, string (3.4) can be written as

$$\begin{matrix} N'_2N'_2 \dots N'_2W'_2Y'W'_1M'M' \dots M'X_1 \\ N_2N_2 \dots N_2W_2Y' \ W_1M \ M \dots MX'_1 \end{matrix} \downarrow \begin{matrix} Y \\ Y' \end{matrix} \uparrow \begin{matrix} X_2N'_1N'_1 \dots N'_1 \\ X'_2N_1N_1 \dots N_1 \end{matrix} \quad (3.5)$$

When the enzymes $\begin{matrix} X_1YX_2 \\ X'_1Y'X'_2 \end{matrix}$ and $\begin{matrix} W_1YW_2 \\ W'_1Y'W'_2 \end{matrix}$ are added to the initial string, (3.2) combines with (3.3) which gives

$$\begin{matrix} N_1N_1 \dots N_1X_1YW_2N_2N_2 \dots N_2 \\ N'_1N'_1 \dots N'_1X'_1Y'W'_2N'_2N'_2 \dots N'_2 \end{matrix} \quad (3.6)$$

and

$$\begin{matrix} N_1N_1 \dots N_1X_1 \\ N'_1N'_1 \dots N'_1X'_1 \end{matrix} \begin{matrix} Y \\ Y' \end{matrix} \begin{matrix} X_2M \dots MW_1 \\ X'_2M'M' \dots M'W'_1 \end{matrix} \begin{matrix} Y \\ Y' \end{matrix} \begin{matrix} X_2M \dots MW_1 \\ X'_2M'M' \dots M'W'_1 \end{matrix} \begin{matrix} Y \\ Y' \end{matrix} \begin{matrix} W_2N_2N_2 \dots N_2 \\ W'_2N'_2N'_2 \dots N'_2 \end{matrix} \quad .$$

The results of the combination of strings (3.2) and (3.5) are

$$\begin{matrix} N_1N_1 \dots N_1X_1 \\ N'_1N'_1 \dots N'_1X'_1 \end{matrix} \begin{matrix} Y \\ Y' \end{matrix} \begin{matrix} X_2N'_1N'_1 \dots N'_1 \\ X'_2N_1N_1 \dots N_1 \end{matrix} \quad (3.7)$$

and

$$\begin{array}{c} N_2' N_2' \dots N_2' W_2' Y W_1' M' M' \dots M' X_1 \quad Y \quad X_2 M M \dots M W_1 \quad Y \quad W_2 N_2 N_2 \dots N_2 \\ N_2 N_2 \dots N_2 W_2 Y' W_1 M M \dots M X_1' \quad Y' \quad X_2' M' M' \dots M' W_1' \quad Y' \quad W_2' N_2' N_2' \dots N_2' \end{array} \downarrow \uparrow \quad (3.8)$$

Next, when string (3.3) combines with string (3.5), the other new strings arise:

$$\begin{array}{c} N_1 N_1 \dots N_1 X_1 \quad Y \quad X_2 M M \dots M W_1 \quad Y \quad X_2 N_1' N_1' \dots N_1' \\ N_1' N_1' \dots N_1' X_1' \quad Y' \quad X_2' M' M' \dots M' W_1' \quad Y' \quad X_2' N_1 N_1 \dots N_1 \end{array} ,$$

and

$$\begin{array}{c} N_2' N_2' \dots N_2' W_2' Y W_1' M' M' \dots M' X_1 \quad Y \quad W_2 N_2 N_2 \dots N_2 \\ N_2 N_2 \dots N_2 W_2 Y' W_1 M M \dots M X_1' \quad Y' \quad W_2' N_2' N_2' \dots N_2' \end{array} . \quad (3.9)$$

By using induction, this theorem can be proved. For $n = 1$, the string (3.1) is stated in (3.4), (3.6), (3.7) and (3.9). Next, let $n = k \in \mathbb{Z}^+$, string (3.1) becomes:

$$\left(\begin{array}{c} N_1 N_1 \dots N_1 \quad N_2' N_2' \dots N_2' W_2' Y W_1' M' M' \dots M' \\ N_1' N_1' \dots N_1' \quad N_2 N_2 \dots N_2 W_2 Y W_1 M M \dots M \end{array} \right) \begin{array}{c} X_1 \left(Y X_2 \quad M M \dots M \quad W_1 \right)^{k-1} Y \\ X_1' \left(Y' X_2' \quad M' M' \dots M' \quad W_1' \right)^{k-1} Y' \end{array} \begin{array}{c} W_2 \quad N_2 N_2 \dots N_2 \quad X_2 N_1' N_1' \dots N_1' \\ W_2' \quad N_2' N_2' \dots N_2' \quad X_2' N_1 N_1 \dots N_1 \end{array} \quad (3.10)$$

The following strings are among the strings in (3.10):

$$\begin{array}{c} N_1 N_1 \dots N_1 \quad X_1 \left(Y X_2 \quad M M \dots M \quad W_1 \right)^{k-1} Y \quad W_2 \quad N_2 N_2 \dots N_2 \\ N_1' N_1' \dots N_1' \quad X_1' \left(Y' X_2' \quad M' M' \dots M' \quad W_1' \right)^{k-1} Y' \quad W_2' \quad N_2' N_2' \dots N_2' \end{array} , \quad (3.11)$$

$$\begin{array}{c} N_1 N_1 \dots N_1 \quad X_1 \left(Y X_2 \quad M M \dots M \quad W_1 \right)^{k-1} Y \quad X_2 N_1' N_1' \dots N_1' \\ N_1' N_1' \dots N_1' \quad X_1' \left(Y' X_2' \quad M' M' \dots M' \quad W_1' \right)^{k-1} Y' \quad X_2' N_1 N_1 \dots N_1 \end{array} , \quad (3.12)$$

$$\begin{array}{c} N_2' N_2' \dots N_2' W_2' Y W_1' M' M' \dots M' X_1 \quad \left(Y X_2 \quad M M \dots M \quad W_1 \right)^{k-1} Y \quad W_2 \quad N_2 N_2 \dots N_2 \\ N_2 N_2 \dots N_2 W_2 Y' W_1 M M \dots M X_1' \quad \left(Y' X_2' \quad M' M' \dots M' \quad W_1' \right)^{k-1} Y' \quad W_2' \quad N_2' N_2' \dots N_2' \end{array} , \quad (3.13)$$

and

$$\begin{array}{c} N_2' N_2' \dots N_2' W_2' Y W_1' M' M' \dots M' X_1 \quad \left(Y X_2 \quad M M \dots M \quad W_1 \right)^{k-1} Y \quad X_2 N_1' N_1' \dots N_1' \\ N_2 N_2 \dots N_2 W_2 Y' W_1 M M \dots M X_1' \quad \left(Y' X_2' \quad M' M' \dots M' \quad W_1' \right)^{k-1} Y' \quad X_2' N_1 N_1 \dots N_1 \end{array} . \quad (3.14)$$

By expanding strings (3.11), (3.12), (3.13) and (3.14), the string can be written respectively as:

$$\begin{array}{c} N_1 N_1 \dots N_1 \quad X_1 \quad Y \quad X_2 \quad M M \dots M \quad W_1 \quad \left(Y X_2 \quad M M \dots M \quad W_1 \right)^{k-2} Y \quad W_2 \quad N_2 N_2 \dots N_2 \\ N_1' N_1' \dots N_1' \quad X_1' \quad Y' \quad X_2' \quad M' M' \dots M' \quad W_1' \quad \left(Y' X_2' \quad M' M' \dots M' \quad W_1' \right)^{k-2} Y' \quad W_2' \quad N_2' N_2' \dots N_2' \end{array} , \quad (3.15)$$

$$\begin{array}{c} N_1 N_1 \dots N_1 \quad X_1 \quad Y \quad X_2 \quad M M \dots M \quad W_1 \quad \left(Y X_2 \quad M M \dots M \quad W_1 \right)^{k-2} Y \quad X_2 N_1' N_1' \dots N_1' \\ N_1' N_1' \dots N_1' \quad X_1' \quad Y' \quad X_2' \quad M' M' \dots M' \quad W_1' \quad \left(Y' X_2' \quad M' M' \dots M' \quad W_1' \right)^{k-2} Y' \quad X_2' N_1 N_1 \dots N_1 \end{array} , \quad (3.16)$$

$$\begin{array}{l} N_2'N_2'\dots N_2'W_2'Y'W_1'M'M'\dots M'X_1 \\ N_2N_2'\dots N_2W_2Y'W_1MM'\dots MX_1' \end{array} \downarrow \begin{array}{l} Y \\ Y' \end{array} \uparrow \begin{array}{l} X_2 \\ X_2' \end{array} \begin{array}{l} MM'\dots M \\ M'M'\dots M' \end{array} W_1 \left(\begin{array}{l} YX_2 \\ Y'X_2' \end{array} \begin{array}{l} MM'\dots M \\ M'M'\dots M' \end{array} W_1 \right)^{k-2} \begin{array}{l} Y \\ Y' \end{array} \begin{array}{l} W_2 \\ W_2' \end{array} \begin{array}{l} N_2N_2'\dots N_2 \\ N_2'N_2'\dots N_2' \end{array}, \quad (3.17)$$

and

$$\begin{array}{l} N_2'N_2'\dots N_2'W_2'Y'W_1'M'M'\dots M'X_1 \\ N_2N_2'\dots N_2W_2Y'W_1MM'\dots MX_1' \end{array} \downarrow \begin{array}{l} Y \\ Y' \end{array} \uparrow \begin{array}{l} X_2 \\ X_2' \end{array} \begin{array}{l} MM'\dots M \\ M'M'\dots M' \end{array} W_1 \left(\begin{array}{l} YX_2 \\ Y'X_2' \end{array} \begin{array}{l} MM'\dots M \\ M'M'\dots M' \end{array} W_1 \right)^{k-2} \begin{array}{l} Y \\ Y' \end{array} \begin{array}{l} X_2N_1'N_1'\dots N_1' \\ X_2'N_1N_1'\dots N_1 \end{array}. \quad (3.18)$$

Next, string (3.3) combines with (3.15) and (3.16) which produces new strings

$$\begin{array}{l} N_1N_1'\dots N_1X_1Y \\ N_1'N_1'\dots N_1'X_1'Y' \end{array} \begin{array}{l} X_2MM'\dots MW_1 \\ X_2'M'M'\dots M'W_1' \end{array} \begin{array}{l} Y \\ Y' \end{array} \begin{array}{l} X_2 \\ X_2' \end{array} \begin{array}{l} MM'\dots M \\ M'M'\dots M' \end{array} W_1 \left(\begin{array}{l} YX_2 \\ Y'X_2' \end{array} \begin{array}{l} MM'\dots M \\ M'M'\dots M' \end{array} W_1 \right)^{k-2} \begin{array}{l} Y \\ Y' \end{array} \begin{array}{l} W_2 \\ W_2' \end{array} \begin{array}{l} N_2N_2'\dots N_2 \\ N_2'N_2'\dots N_2' \end{array} \quad (3.19)$$

and

$$\begin{array}{l} N_1N_1'\dots N_1X_1Y \\ N_1'N_1'\dots N_1'X_1'Y' \end{array} \begin{array}{l} X_2MM'\dots MW_1 \\ X_2'M'M'\dots M'W_1' \end{array} \begin{array}{l} Y \\ Y' \end{array} \begin{array}{l} X_2 \\ X_2' \end{array} \begin{array}{l} MM'\dots M \\ M'M'\dots M' \end{array} W_1 \left(\begin{array}{l} YX_2 \\ Y'X_2' \end{array} \begin{array}{l} MM'\dots M \\ M'M'\dots M' \end{array} W_1 \right)^{k-2} \begin{array}{l} Y \\ Y' \end{array} \begin{array}{l} X_2N_1'N_1'\dots N_1' \\ X_2'N_1N_1'\dots N_1 \end{array}. \quad (3.20)$$

Then, the other recombinations between string (3.8) with (3.17) and (3.18) can be shown as:

$$\begin{array}{l} N_2'N_2'\dots N_2'W_2'Y'W_1'M'M'\dots M'X_1 \\ N_2N_2'\dots N_2W_2Y'W_1MM'\dots MX_1' \end{array} \begin{array}{l} Y \\ Y' \end{array} \begin{array}{l} X_2MM'\dots MW_1 \\ X_2'M'M'\dots M'W_1' \end{array} \begin{array}{l} Y \\ Y' \end{array} \begin{array}{l} X_2 \\ X_2' \end{array} \begin{array}{l} MM'\dots M \\ M'M'\dots M' \end{array} W_1 \left(\begin{array}{l} YX_2 \\ Y'X_2' \end{array} \begin{array}{l} MM'\dots M \\ M'M'\dots M' \end{array} W_1 \right)^{k-1} \begin{array}{l} Y \\ Y' \end{array} \begin{array}{l} W_2 \\ W_2' \end{array} \begin{array}{l} N_2N_2'\dots N_2 \\ N_2'N_2'\dots N_2' \end{array}, \quad (3.21)$$

and

$$\begin{array}{l} N_2'N_2'\dots N_2'W_2'Y'W_1'M'M'\dots M'X_1 \\ N_2N_2'\dots N_2W_2Y'W_1MM'\dots MX_1' \end{array} \begin{array}{l} Y \\ Y' \end{array} \begin{array}{l} X_2MM'\dots MW_1 \\ X_2'M'M'\dots M'W_1' \end{array} \begin{array}{l} Y \\ Y' \end{array} \begin{array}{l} X_2 \\ X_2' \end{array} \begin{array}{l} MM'\dots M \\ M'M'\dots M' \end{array} W_1 \left(\begin{array}{l} YX_2 \\ Y'X_2' \end{array} \begin{array}{l} MM'\dots M \\ M'M'\dots M' \end{array} W_1 \right)^{k-1} \begin{array}{l} Y \\ Y' \end{array} \begin{array}{l} X_2N_1'N_1'\dots N_1' \\ X_2'N_1N_1'\dots N_1 \end{array}. \quad (3.22)$$

By simplifying strings (3.19), (3.20), (3.21) and (3.22), the resulting strings are:

$$\begin{array}{l} N_1N_1'\dots N_1X_1 \\ N_1'N_1'\dots N_1'X_1' \end{array} \left(\begin{array}{l} YX_2 \\ Y'X_2' \end{array} \begin{array}{l} MM'\dots M \\ M'M'\dots M' \end{array} W_1 \right)^{(k+1)-1} \begin{array}{l} Y \\ Y' \end{array} \begin{array}{l} W_2 \\ W_2' \end{array} \begin{array}{l} N_2N_2'\dots N_2 \\ N_2'N_2'\dots N_2' \end{array}, \quad (3.23)$$

$$\begin{array}{l} N_1N_1'\dots N_1X_1 \\ N_1'N_1'\dots N_1'X_1' \end{array} \left(\begin{array}{l} YX_2 \\ Y'X_2' \end{array} \begin{array}{l} MM'\dots M \\ M'M'\dots M' \end{array} W_1 \right)^{(k+1)-1} \begin{array}{l} Y \\ Y' \end{array} \begin{array}{l} X_2N_1'N_1'\dots N_1' \\ X_2'N_1N_1'\dots N_1 \end{array}, \quad (3.24)$$

$$\begin{array}{l} N_2'N_2'\dots N_2'W_2'Y'W_1'M'M'\dots M'X_1 \\ N_2N_2'\dots N_2W_2Y'W_1MM'\dots MX_1' \end{array} \left(\begin{array}{l} YX_2 \\ Y'X_2' \end{array} \begin{array}{l} MM'\dots M \\ M'M'\dots M' \end{array} W_1 \right)^{(k+1)-1} \begin{array}{l} Y \\ Y' \end{array} \begin{array}{l} W_2 \\ W_2' \end{array} \begin{array}{l} N_2N_2'\dots N_2 \\ N_2'N_2'\dots N_2' \end{array}, \quad (3.25)$$

and

$$\begin{array}{l} N_2'N_2'\dots N_2'W_2'Y'W_1'M'M'\dots M'X_1 \\ N_2N_2'\dots N_2W_2Y'W_1MM'\dots MX_1' \end{array} \left(\begin{array}{l} YX_2 \\ Y'X_2' \end{array} \begin{array}{l} MM'\dots M \\ M'M'\dots M' \end{array} W_1 \right)^{(k+1)-1} \begin{array}{l} Y \\ Y' \end{array} \begin{array}{l} X_2N_1'N_1'\dots N_1' \\ X_2'N_1N_1'\dots N_1 \end{array}. \quad (3.26)$$

Therefore, from (3.23), (3.24), (3.25) and (3.26), the resulting splicing language can be summarized as

$$\left(\begin{array}{c} N_1 N_1 \dots N_1 \\ N_1' N_1' \dots N_1' \end{array} + \begin{array}{c} N_2' N_2' \dots N_2' W_2' Y W_1' M' \dots M' \\ N_2 N_2 \dots N_2 W_2 Y W_1 M \dots M \end{array} \right) X_1 \left(\begin{array}{c} Y X_2 \quad M M \dots M \quad W_1 \\ Y' X_2' \quad M' M' \dots M' \quad W_1' \end{array} \right)^{(k+1)-1} Y \left(\begin{array}{c} W_2 \quad N_2 N_2 \dots N_2 \quad X_2 N_1' N_1' \dots N_1' \\ W_2' \quad N_2' N_2' \dots N_2' \quad X_2' N_1 N_1 \dots N_1 \end{array} \right)$$

which depicts string (3.1) when $n = k + 1$. Hence, Theorem 1 is proved. ■

The splicing language from a DNA splicing system with one cutting site of each palindromic and non-palindromic restriction enzymes with same crossing is illustrated through Example 1.

Example 3.1. Given a DNA splicing system $S = (A, I, B, C)$ where $I = \left\{ \begin{array}{l} \text{ATCCGGGTCCGCGA} \\ \text{TAGGCCCCAGGCGCT} \end{array} \right\}$ is the set of initial string, set $B = \left(\begin{array}{cc} \text{C} & \text{CG, G} \\ \text{G} & \text{GC C} \end{array} \right), \left(\begin{array}{cc} \text{C} & \text{CG, C} \\ \text{G} & \text{GC G} \end{array} \right)$ is the set of cleavage pattern for the enzymes *HpaII* and *AciI* and set C is the empty set.

Solution 3.1. The enzyme *HpaII*, $\begin{array}{c} 5' - \text{CCGG} - 3' \\ 3' - \text{GGCC} - 5' \end{array}$ is palindromic since the base sequence of enzyme *HpaII* reads the same forwards and backwards; while *AciI*, $\begin{array}{c} 5' - \text{CCGC} - 3' \\ 5' - \text{GGCG} - 3' \end{array}$ is not palindromic since the base sequence of enzyme *AciI* does not read the same forwards and backwards. The enzymes *HpaII* and *AciI* also have the same crossing, $\begin{array}{c} 5' - \text{CG} - 3' \\ 3' - \text{GC} - 5' \end{array}$.

The initial string $\begin{array}{c} 5' - \text{ATC} \\ 3' - \text{TAG} \end{array} \downarrow \begin{array}{c} \text{CG} \\ \text{GC} \end{array} \uparrow \begin{array}{c} \text{GGTC} \\ \text{CCAG} \end{array} \downarrow \begin{array}{c} \text{CG} \\ \text{GC} \end{array} \uparrow \begin{array}{c} \text{CGA} - 3' \\ \text{GCT} - 5' \end{array}$ has one cutting site each of the enzymes *HpaII* and *AciI*. Thus, by using Theorem 1, the splicing language is

$$\begin{array}{c} 5' - \\ 3' - \end{array} \left(\begin{array}{c} \text{AT} \\ \text{TA} \end{array} + \begin{array}{c} \text{TCGCGGAC} \\ \text{AGCGCCTG} \end{array} \right) \begin{array}{c} \text{C} \\ \text{G} \end{array} \left(\begin{array}{c} \text{CCGGGTCCG} \\ \text{GGCCAGGC} \end{array} \right)^{n-1} \begin{array}{c} \text{CG} \\ \text{GC} \end{array} \left(\begin{array}{c} \text{CGA} + \text{GAT} \\ \text{GCT} + \text{CTA} \end{array} \right) \begin{array}{c} -3' \\ -5' \end{array}$$

where $n \in \mathbb{Z}^+$.

Next, the generalization of splicing languages from DNA splicing system with one cutting site each of two non-palindromic restriction enzymes and different crossings is presented in Theorem 3.2.

Theorem 3.2. Given $S = (A, I, B, C)$ is a DNA splicing system in which $A = \left\{ \begin{array}{cccc} \text{A} & \text{C} & \text{G} & \text{T} \\ \text{T} & \text{G} & \text{C} & \text{A} \end{array} \right\}$ is the set of dsDNA symbols, $I = \left\{ \begin{array}{l} N_1 N_1 \dots N_1 X_1 Y X_2 M M \dots M W_1 Z W_2 N_2 N_2 \dots N_2 \\ N_1' N_1' \dots N_1' X_1' Y' X_2' M' M' \dots M' W_1' Z' W_2' N_2' N_2' \dots N_2' \end{array} \right\}$ is the set consisting of an initial string with two non-overlapping cutting sites of one palindromic and non-

palindromic restriction enzymes $\frac{X_1 Y X_2}{X'_1 Y' X'_2}$ and $\frac{W_1 Z W_2}{W'_1 Z' W'_2}$ respectively, set

$$B = \left\{ \left(\begin{array}{ccc} X_1 & , Y & X_2 \\ X'_1 & Y' & X'_2 \end{array} \right), \left(\begin{array}{ccc} W_1 & , Z & W_2 \\ W'_1 & Z' & W'_2 \end{array} \right) \right\}$$

is the set of cleavage pattern for the restriction enzymes and set C is the empty set, the resulting splicing language consists of strings of the form

$$\left(\begin{array}{c} N_1 N_1 \dots N_1 \\ N'_1 N'_1 \dots N'_1 \end{array} + \begin{array}{c} N_2 N'_2 \dots N'_2 W'_2 Z' W'_1 M' M' \dots M' \\ N_2 N_2 \dots N_2 W_2 Z W_1 M M \dots M \end{array} \right) \frac{X_1 Y X_2}{X'_1 Y' X'_2} \left(\begin{array}{c} M M \dots M W_1 Z W_2 N_2 N_2 \dots N_2 \\ M' M' \dots M' W'_1 Z' W'_2 N'_2 N'_2 \dots N'_2 \end{array} + \begin{array}{c} N'_1 N'_1 \dots N'_1 \\ N_1 N_1 \dots N_1 \end{array} \right)$$

where $\frac{N_1}{N'_1}, \frac{X_1}{X'_1}, \frac{Y}{Y'}, \frac{X_2}{X'_2}, \frac{M}{M'}, \frac{W_1}{W'_1}, \frac{Z}{Z'}, \frac{W_2}{W'_2}$ and $\frac{N_2}{N'_2}$, denote arbitrary dsDNA symbols, $N'_1, X'_1, Y', X'_2, M', W'_1, Z', W'_2$ and N'_2 are complementaries for $N_1, X_1, Y, X_2, M, W_1, Z, W_2$, and N_2 respectively, $\frac{Y}{Y'}$ and $\frac{Z}{Z'}$ are the different crossings, and

$$\left\{ \begin{array}{ccc} X_1 Y X_2 & W_1 Z W_2 & W'_2 Z' W'_1 \\ X'_1 Y' X'_2 & W'_1 Z' W'_2 & W_2 Z W_1 \end{array} \right\} \notin \left\{ \begin{array}{ccc} N_1 N_1 \dots N_1 & M M \dots M & N_2 N_2 \dots N_2 \\ N'_1 N'_1 \dots N'_1 & M' M' \dots M' & N'_2 N'_2 \dots N'_2 \end{array} \right\}.$$

Proof Suppose the restriction enzyme $\frac{X_1 Y X_2}{X'_1 Y' X'_2}$ is palindromic, so the base sequence of enzyme reads the same backwards and forwards:

$$\frac{X_1 Y X_2}{X'_1 Y' X'_2} = \frac{X'_2 Y' X'_1}{X_2 Y X_1}.$$

Since the restriction enzyme $\frac{W_1 Z W_2}{W'_1 Z' W'_2}$ is not palindromic, so the base sequence of enzyme is not the same backwards and forwards:

$$\frac{W_1 Z W_2}{W'_1 Z' W'_2} \neq \frac{W'_2 Z' W'_1}{W_2 Z W_1}.$$

Then $\frac{X_1}{X'_1} = \frac{X'_2}{X_2}, \frac{Y}{Y'} = \frac{Y'}{Y}, \frac{X_2}{X'_2} = \frac{X'_1}{X_1}, \frac{W_1}{W'_1} \neq \frac{W'_2}{W_2}, \frac{Z}{Z'} \neq \frac{Z'}{Z}$ and $\frac{W_2}{W'_2} \neq \frac{W'_1}{W_1}$.

The initial string, $\frac{N_1 N_1 \dots N_1 X_1 Y X_2 M M \dots M W_1 Z W_2 N_2 N_2 \dots N_2}{N'_1 N'_1 \dots N'_1 X'_1 Y' X'_2 M' M' \dots M' W'_1 Z' W'_2 N'_2 N'_2 \dots N'_2}$ with the cutting site of the enzymes $\frac{X_1 Y X_2}{X'_1 Y' X'_2}$ and $\frac{W_1 Z W_2}{W'_1 Z' W'_2}$ is shown respectively in the following:

$$\begin{array}{c} N_1 N_1 \dots N_1 X_1 \\ N'_1 N'_1 \dots N'_1 X'_1 \end{array} \downarrow \begin{array}{c} Y \\ Y' \end{array} \uparrow \begin{array}{c} X_2 M M \dots M W_1 Z W_2 N_2 N_2 \dots N_2 \\ X'_2 M' M' \dots M' W'_1 Z' W'_2 N'_2 N'_2 \dots N'_2 \end{array} \quad (3.27)$$

for the first cutting site and

$$\begin{array}{ccccccc} N_1 N_1 \dots N_1 X_1 & Y & X_2 M M \dots M W_1 & & Z & & W_2 N_2 N_2 \dots N_2 \\ N'_1 N'_1 \dots N'_1 X'_1 & Y' & X'_2 M' M' \dots M' W'_1 & \downarrow & Z' & \uparrow & W'_2 N'_2 N'_2 \dots N'_2 \end{array} \quad (3.28)$$

for the second cutting site.

The initial string can be written 180 degree wise as

$$\begin{array}{c} N'_2 N'_2 \dots N'_2 W'_2 Z' W'_1 M' M' \dots M' X'_2 Y' X'_1 N'_1 N'_1 \dots N'_1 \\ N_2 N_2 \dots N_2 W_2 Z W_1 M M \dots M X_2 Y X_1 N_1 N_1 \dots N_1 \end{array} \quad (3.29)$$

Since $\frac{X_1}{X'_1} = \frac{X'_2}{X_2}$, $\frac{Y}{Y'} = \frac{Y'}{Y}$, $\frac{X_2}{X'_2} = \frac{X'_1}{X_1}$, string (3.29) can be written as

$$\begin{array}{ccccccc} N'_2 N'_2 \dots N'_2 W'_2 Z' W'_1 M' M' \dots M' X_1 & & Y & & X_2 N'_1 N'_1 \dots N'_1 \\ N_2 N_2 \dots N_2 W_2 Z W_1 M M \dots M X'_1 & \downarrow & Y' & \uparrow & X'_2 N_1 N_1 \dots N_1 \end{array} \quad (3.30)$$

Since $\frac{W_1}{W'_1} \neq \frac{W'_2}{W_2}$, $\frac{Z}{Z'} \neq \frac{Z'}{Z}$, $\frac{W_2}{W'_2} \neq \frac{W'_1}{W_1}$ and the crossings $\frac{Y}{Y'} \neq \frac{Z}{Z'}$ are different, then there is no new resulting molecule to combine with string (3.28).

When the enzymes $\frac{X_1 Y X_2}{X'_1 Y' X'_2}$ is added to the initial string, string (3.27) combines with (3.30) which gives

$$\begin{array}{ccccc} N_1 N_1 \dots N_1 X_1 Y X_2 & N'_1 N'_1 \dots N'_1 \\ N'_1 N'_1 \dots N'_1 X'_1 Y' X'_2 & N_1 N_1 \dots N_1 \end{array} \quad (3.31)$$

and

$$\begin{array}{ccccccc} N'_2 N'_2 \dots N'_2 W'_2 Z' W'_1 M' M' \dots M' X_1 & Y & X_2 M M \dots M W_1 & Z & W_2 N_2 N_2 \dots N_2 \\ N_2 N_2 \dots N_2 W_2 Z W_1 M M \dots M X'_1 & Y' & X'_2 M' M' \dots M' W'_1 & Z' & W'_2 N'_2 N'_2 \dots N'_2 \end{array} \quad (3.32)$$

From (3.27), (3.30), (3.31) and (3.32), the resulting splicing language is simplified as

$$\left(\begin{array}{c} N_1 N_1 \dots N_1 \\ N'_1 N'_1 \dots N'_1 \end{array} + \begin{array}{c} N'_2 N'_2 \dots N'_2 W'_2 Z' W'_1 M' M' \dots M' \\ N_2 N_2 \dots N_2 W_2 Z W_1 M M \dots M \end{array} \right) \frac{X_1 Y X_2}{X'_1 Y' X'_2} \left(\begin{array}{c} M M \dots M W_1 \\ M' M' \dots M' W'_1 \end{array} \frac{Z}{Z'} \frac{W_2 N_2 N_2 \dots N_2}{W'_2 N'_2 N'_2 \dots N'_2} + \begin{array}{c} N'_1 N'_1 \dots N'_1 \\ N_1 N_1 \dots N_1 \end{array} \right).$$

Thus, Theorem 3.2 is proved. ■

Example 3.2 shows the splicing language from a DNA splicing system with one cutting site of each palindromic and non-palindromic restriction enzymes for different crossings.

Example 3.2. Given a DNA splicing system $S = (A, I, B, C)$ where $I = \begin{array}{c} \text{TGTACGGACCGCGC} \\ \text{ACATGCCTGGCGCG} \end{array}$ is

the set of initial string, set $B = \begin{pmatrix} G & TA & C \\ C & AT & G \end{pmatrix}, \begin{pmatrix} C & CG & C \\ G & GC & G \end{pmatrix}$ is the set of cleavage pattern for the enzymes CviAII and AciI and set C is the empty set.

Solution 3.2. The enzyme CviAII, $\begin{matrix} 5'-GTAC-3' \\ 3'-CATG-5' \end{matrix}$ is palindromic since the base sequence of enzyme

CviAII reads the same forwards and backwards; while AciI, $\begin{matrix} 5'-CCGC-3' \\ 3'-GGCG-5' \end{matrix}$ is not palindromic since the base sequence of enzyme AciI does not read the same forwards and backwards. The enzymes CviAII and AciI have different crossings where crossing sites CviAII and AciI are $\begin{matrix} 5'-TA-3' \\ 3'-AT-5' \end{matrix}$ and $\begin{matrix} 5'-CG-3' \\ 3'-GC-5' \end{matrix}$ respectively.

The initial string $\begin{matrix} 5'-TG & TA & CGGAC & CG & CGC-3' \\ 3'-AC & AT & GCCTG & GC & GCG-5' \end{matrix}$ has one cutting site each of the enzymes CviAII and AciI. Thus, by using Theorem 2, the splicing language is

$$\begin{matrix} 5'- \\ 3'- \end{matrix} \left(\begin{matrix} TG & GCGCGGTCC \\ AC & CCGGCCAGG \end{matrix} \right) \begin{matrix} GTAC \\ CATG \end{matrix} \left(\begin{matrix} GGACCGCGC & CGC \\ CCTGGCGCG & GCG \end{matrix} \right) \begin{matrix} -3' \\ -5' \end{matrix}$$

4 Conclusion

In this research, the generalizations of splicing languages from DNA splicing system with one cutting site of each palindromic and non-palindromic restriction enzymes for same and different crossings are presented as Theorem 1 and 2 respectively. The respective theorems are proved using induction and direct methods. By using these theorem, the splicing languages from different DNA splicing system are obtained when any initial string, palindromic and non-palindromic restriction enzymes are used.

Acknowledgement

The first author would like to express gratitude to UTM Zamalah Scholarship for supporting her study. The second and third authors would also like to thank the Ministry of Higher Education (MOHE) and Research Management Centre (RMC), Universiti Teknologi Malaysia (UTM) for the funding through Research University Grant Vote No. 13H18.

Competing interests

The authors declare that they have no competing interests.

Authors' contributions

All authors have contributed to all parts of the article. All authors read and approved the final manuscript.

References

- [1] Head, T. Formal Language Theory and DNA: An Analysis of the Generative Capacity of Specific Recombinant Behaviors. *Bulletin of Mathematical Biology*. 1987. 49(6): 737-759.
- [2] Kim, S. M. Computational Modeling for Genetic Splicing Systems. *SIAM Journal on Computing*. 1997. 26(5): 1284-1309.
- [3] Linz, P. An Introduction to Formal Languages and Automata. 4th. ed. USA: Jones and Bartlett Publisher. 2006.
- [4] Paun, G., Rozenberg, G., and Salomaa, A. DNA Computing: New Computing Paradigms. Germany: Springer -Verlag Berlin Heidelberg. 1998.
- [5] Brejová, B., DiMarco, C., Vinar, T., Hidalgo, S. R., Holguin, G., and Patten, C. Finding Patterns in Biological Sequences. Unpublished project report for CS798G, University of Waterloo, Fall. 2000.
- [6] Head, T. Splicing Representations of Strictly Locally Testable Languages. *Discrete Applied Mathematics*. 1998. 87(1): 139-147.
- [7] Păun, G. On the Splicing Operation. *Discrete Applied Mathematics*. 1996. 70(1): 57-79.
- [8] Pixton, D. Regularity of Splicing Languages. *Discrete Applied Mathematics*. 1996. 69(1-2): 101-124.
- [9] Goode, E. and Pixton, D. Splicing to the Limit, in: *Aspects of Molecular Computing*: Springer-Verlag. 189-201; 2004.
- [10] Yusof, Y., Sarmin, N. H., Fong, W. H., Goode, T. E., and Ahmad, M. A. An Analysis of Four Variants of Splicing System. *Proceeding of the 20th National Symposium on Mathematical Sciences - Research in Mathematical Sciences: A Catalyst for Creativity and Innovation (SKSM 2012)*. December 18-20, 2012. Melville, NY: AIP Conference Proceeding. 2013. 888-895.
- [11] Tomohiro, I., Inenaga, S., and Takeda, M. Palindrome Pattern Matching. *Theoretical Computer Science*. 2013. 483: 162-170.
- [12] Fong, W. H. and Ismail, N. I. Generalisations of DNA Splicing Systems with One Palindromic Restriction Enzyme. *Malaysian Journal of Industrial and Applied Mathematics*. Accepted.
- [13] Fong, W. H., Ismail, N. I., and Sarmin, N. H. The Modelling of DNASplicing Systems with Two Non-Palindromic Restriction Enzymes. 2nd Asia International Multidisciplinary Conference (AIMC 2018). Universiti Teknologi Malaysia, Johor Bahru, Malaysia, 12-13 May 2018, Presented.
- [14] Yusof, Y. DNA Splicing System Inspired by Bio Molecular Operations. Ph.D. Thesis. Universiti Teknologi Malaysia; 2012.