# Evolution of Splicing System in Graph Theory

International Conference on Mathematics and Its Scientific Applications (ICMSA2022)

4 March 2022

#### Organized by

Department of Mathematics, Sathyabama Institute of Science and Technology ,Chennai, Tamilnadu, India



### **PROF. DR. NOR HANIZA SARMIN**

Department of Mathematical Sciences, Faculty of Science, Universiti Teknologi Malaysia nhs@utm.my

innovative • entrepreneurial • global



### **Presentation Outline**

### Part 1: DNA Computing

- Introduction to DNA computing
- Development of DNA splicing systems
- Wet splicing system



### Part 2: Splicing System in Graph Theory

- Evolution of splicing system in the form of graphs
- *n*-cut splicing in describing the cleavage pattern of the DNA molecules



# **DNA Computing**

• DNA computing has emerged in the last twenty years as an exciting new research field at the intersection of Computer Science, Biology, Engineering and Mathematics.





UNIVERSITI TEKNOLOGI MALAYSIA

• Although anticipated by Feynman from the 1950s, the notion of performing computations at the molecular level was only realized in 1994, with Adleman's experiment on solving the Hamiltonian Path Problem using DNA.





Adleman, L. M. (1994). Molecular Computation of Solutions to Combinatorial Problems. Science, 265(5187), 1021-1024.





- Since then the field has blossomed rapidly, with development of significant **theoretical** and **experimental** results by researchers from **interdisciplinary** areas.
- **Different models** of molecular computation have been proposed in scientific society including Splicing Models and Sticker Models.











• DNA, or deoxyribonucleic acid, is the hereditary material in humans and almost all other organisms (animals, plants etc).









innovative • entrepreneurial • global



- UNIVERSITI TEKNOLOGI I
- The name of a nucleotide is taken from its base. Each DNA has four kinds of bases, that are adenine, guanine, cytosine and thymine, which are usually abbreviated by A, G, C and T.







• Two single strands of DNAs can be linked together with the hydrogen bonds between their bases and hence form a helical shape called double stranded DNA (dsDNA).







• In 1953, it was shown that the bases can join only complimentarily, A with T and G with C respectively.















• DNA molecules can be cut by restriction enzymes at specific places based on the cutting sites of the restriction enzymes.

```
Sticky end (e.g. Acil)
```

```
5′...C▼CGC...3′
3′...GGC▲G...5′
```

Blunt end (e.g. Afel)

5'....AGC▼GCT....3' 3'...TCG▲CGA....5'





- Every restriction enzyme has a triple known as the cleavage pattern of the enzyme.
- The triple is denoted as a rule for the restriction enzyme which consists of left context, crossing and right context (Head, 1998).
- The restriction enzyme *EcoRI* is isolated from the bacterium Escherichia coli with strain serotype *R*; I indicates the first enzyme discovered from the bacterium.
- The cleavage pattern of restriction enzyme *EcoRI* is



left context crossing right context

Head, T. (1998). Splicing Representations of Strictly Locally Testable Languages. *Discrete Applied Mathematics*, 87(1), 139-147.





• A restriction enzyme is an enzyme that cuts double-stranded or single stranded DNA at specific recognized nucleotide sequences, known as restriction sites.







*EcoR*I: ([G/C],[A/T],[A/T],[T/A],[T/A],[C/G])



MfeI: ([C/G], [A/T], [A/T], [T/A], [T/A], [G/C])



### **Restriction Enzymes (Cont.)**



S Enzyme Finder   NEB × +						
← → C						. :
🚻 Apps 🖸 YouTube Ҟ Maps 🗃 News 🕨	1 Gmail  Transfor	ming Regul 🚺 NEB Tm Calculator				
BioLabs <sup>inc.</sup>						
Enzyme Finder	v2.2.2			💬 FEEDBACK ? HELP	HISTOP	₹Y
Locate commercially available restriction	288 matching enzymes					
sequence, or overhang.	Enzyme 🔞	Sequence 😧	Overhang	Properties 😮		*
Category: NEB Enzymes Search within: Name Sequence Overhang Search for:	Aatli	G↑ACGT↓C	3' ACGT	37° CutSmart 🕝 🏰 CpG Ril		
	AbaSI	™CN∍↑NN↓	3' NN	25° CutSmart Visy Ril 💓 CHa		
	Acc65I	GIGTAC,C	5' GTAC	37° 113.1 🕐 👯 CpG dem Ril 💓		
	Accl	GT↓MK↑AC	5' MK	37° CutSmart 🐠 🏰 CpG 🔣		
all enzymes	Acil	cicetc	5' CG	37° CutSmart 😂 🏰 CpG Ril 💓		
Availibility Sold by NEB Available elsewhere Ambiguity Codes N = A or C or G or T (any) B = C or G or T (not A) D = A or G or T (not C) H = A or C or T (not G)	Acli	AA↓CG↑TT	5' CG	37° CutSmart 🕝 🕊 CpG Ril 🔀		
	Acul	CTGAAGN14↑NN↓	3' NN	37° CutSmart 🛛 🗱 Ril 💭		
	Afel	AGCNGCT	Blunt	37° CutSmart Visy CpG Ril 💭		
	Afill	C↓TTAA <sub>↑</sub> G	5' TTAA	37° CutSmart 🙆 🏰 Rii 💓		
	A相目	ALCOVO T	RICOVO			

The link to find the enzymes (New England BioLabs)

Link: https://enzymefinder.n eb.com/#!#nebheader





• DNA ligase is an enzyme that can catalyze the linking of DNA strands together by forming a phosphodiester bond.



















Definition 1 (Head, 1987) Splicing System and Splicing Language

A splicing system, S = (A, I, B, C) consists of

- A: finite alphabet
- *I*: a finite set of initial strings in *A*\*
- B and C: finite sets of triples (c, x, d) with c, x and d in A\*
- Triples in *B* are called left patterns
- Triples in *C* are called right patterns

For each such triple the string *cxd* is called a site and the string *x* is called a crossing.

```
A language, L is a splicing language if there exists a splicing system S for which L = L(S).
```

# **DNA Splicing System (Cont.)**



### Example 1

Suppose that S = (A, I, B, C) is a splicing system in which  $A = \begin{cases} A, C, G, T \\ T & G & C & A \end{cases}$  is the set of dsDNA symbols,  $I = \begin{cases} GAATTCTCTGTAAT \\ CTTAAGAGACATTA \end{cases}$  is the set consisting of an initial string of molecules, set  $B = \{ \begin{pmatrix} G & AATT & C \\ C & T & TAA' & G \end{pmatrix} \}$  is the set of cleavage pattern for the enzyme **EcoRI** and set *C* is the empty set.

The initial string is shown in the following:

5'-GAATTCTCTGTAAT-3' 3'-CTTAAGAGACATTA-5''

or written 180 degree wise,

5'-ATTACAGAGAATTC-3' 3'-TAATGTCTCTTAAG-5'



## **DNA Splicing System (Cont.)**





## **DNA Splicing System (Cont.)**



Head, T. (1987). Formal Language Theory and DNA: An Analysis of the Generative Capacity of Specific Recombinant Behaviors. *Bulletin of mathematical biology,* 49(6), 737-759. doi:https://doi.org/10.1007/BF0248177

Păun, G. (1996). On the Splicing Operation. Discrete Applied Mathematics, 70(1), 57-79. doi:https://doi.org/10.1016/0166-218X(96)00101-1

Pixton, D. (1996). Regularity of Splicing Languages. Discrete Applied Mathematics, 69(1-2), 101-124. doi:https://doi.org/10.1016/0166-218X(95)00079-7

Goode, E., & Pixton, D. (2004). Splicing to the Limit. In N. Jonoska, G. Păun, & G. Rozenberg (Eds.), *Aspects of Molecular Computing, Lecture Notes in Computer Science* (pp. 189-201). Germany: Springer-Verlag.

Yusof, Y., Sarmin, N. H., Fong, W. H., Goode, T. E., & Ahmad, M. A. (2013). An Analysis of Four Variants of Splicing System. Paper presented at the 20th National Symposium on Mathematical Sciences - Research in Mathematical Sciences: A Catalyst for Creativity and Innovation (SKSM 2012).

Karimi, F., Turaev, S., Sarmin, N. H., & Fong, W. H. (2014). Fuzzy Splicing Systems. In D. Hwang, J. J. Jung, & N. T. Nguyen (Eds.), *Computational Collective Intelligence. Technologies and Applications, ICCCI 2014, Lecture Notes in Computer Science* (pp. 20-29). Cham, Switzerland: Springer International Publishing.





Splicing System	<b>Head</b> S = (A, I, B, C)	<b>Paun</b> $\sigma = (A, R)$	<b>Ρixton</b> ζ = ( <i>R</i> , <i>I</i> )	Goode-Pixton (w, w′)⊢ <sub>r</sub> z	<b>Yusof-Goode</b> <i>S</i> = ( <i>A</i> , <i>I</i> , <i>R</i> )	<b>Fuzzy</b> S = (A, T, I, R, O)
Initial String	u <mark>cxd</mark> v pexfq	uu <sub>1</sub> u <sub>2</sub> v u'u <sub>3</sub> u <sub>4</sub> v'	ξ <mark>αη</mark> ξ'α'η'	w = x u v y $w' = x' u' v' y'$	α <mark>uxv</mark> β γyzδ	(ua, x) (bv, y) $x, y \in [0, 1]$
Rule	(c, x, d) (e, x, f)	<mark>u<sub>1</sub>#u<sub>2</sub>\$u<sub>3</sub>#u<sub>4</sub></mark>	( <b>α</b> , α': β)	r = ( <b>u</b> , <b>v</b> ; u'; v')	( <b>u</b> , x, <b>v</b> : y, x, z)	<mark>u</mark> #a\$b#v
Splicing Language	ucxfq pexdv	<b>uu<sub>1</sub>u<sub>4</sub>v'</b>	ξ <mark>β</mark> η′	z = x u v' y'	α <mark>u</mark> xzδ γyxvβ	$(\frac{uv}{v}, x \odot y)$ $\odot$ is fuzzy operation

- S: splicing system
- $\sigma$  and  $\zeta$ : splicing schemes
- *A*: finite alphabet
- $T \subseteq A$ : terminal alphabet

- *I*: set of initial strings
- *B*: set of rules with left pattern
- *C*: set of rules with right pattern
- $R = B \cup C$ : set of rules



## Wet Experiment on Splicing System

## S = (A, I, B, C)



### **Previous Molecular Works on Splicing Systems**

Author	Description
Laun and Reddy 1999	The first experiment on the splicing system using restriction enzymes <b>Bgl</b> and <b>Drall</b>
Fong 2008	The adult and limit languages from Head's splicing model using restriction enzymes <i>Hpa</i> ll and <i>Aci</i> l
Karimi 2013	Verification of the persistency properties of splicing systems involving restriction enzymes <i>CvaQ</i> I and <i>Acc65</i> I
Yusof et al. 2015	Yusof-Goode splicing system with restriction enzymes Acll and Acil using limit graph approach
Ahmad et al. 2018	Experiment on second order limit language from Yusof-Goode splicing system using restriction enzyme DpnII
Ismail 2020	Experiment using the restriction enzymes <i>CviQI</i> and <i>AciI</i> to verify the generalisation of splicing system involving palindromic and non-palindromic rules

Laun, E., & Reddy, K. J. (1999). Wet Splicing Systems. Paper presented at the 3rd DIMACS Workshop on DNA Based Computers, University of Pennsylvania, Philadelphia. Fong, W. H. (2008). Modelling of Splicing Systems using Formal Language Theory. (Ph.D. Thesis), Universiti Teknologi Malaysia, Skudai, Malaysia.

Karimi, F. (2013). Mathematical Modelling of Persistent Splicing Systems in DNA Computing. (Ph.D. Thesis), Universiti Teknologi Malaysia, Johor, Malaysia.

Yusof, Y., Lim, W. L., Goode, T. E., Sarmin, N. H., Heng, F. W., & Wahab, M. F. A. (2015). *Molecular Aspects of DNA Splicing System*. Paper presented at the International Conference on Mathematics, Engineering and Industrial Applications 2014 (ICoMEIA 2014), Penang, Malaysia.

Ahmad, M. A., Sarmin, N. H., Abdul-Wahab, M. F., Heng, F. W., & Yusof, Y. (2018). Biomolecular Aspects of Second Order Limit Language. *Malaysian Journal of Fundamental and Applied Sciences*, 14(1), 15-19.

Ismail, N. I. (2020). Generalisations of Splicing Languages From DNA Splicing Systems. (Ph.D. Thesis), Universiti Teknologi Malaysia, Skudai, Malaysia.

innovative • entrepreneurial • global





Visit to wet lab, State University of New York, Binghamton, New York, USA 2007









Research collaboration with State University of New York, Binghamton, New York, and Towson University, USA























## Splicing System in Graph Theory





## Splicing System in Graph Theory (Cont.)

5'-GAATTCTCTGTAAT-3' 3'-CTTAAGAGACATTA-5'



Graph representation of the DNA string

# Splicing System in Graph Theory (Cont.)

 Graph splicing system is originally introduced by Freund in 1995 to describe the DNA splicing system in the form of graphs instead of one-dimensional strings.



Freund, R., Splicing systems on graphs, in 1st Int. Symp. On Intelligence in Neural and Biological Systems, INBS'95 (IEEE, Washington, DC, 1995), 189-194.



## Splicing System in Graph (Cont.)











#### Definition (Freund, 1995) Graph Splicing Scheme

A graph splicing scheme is a pair  $\sigma = (A, P)$  where A is a set of finite alphabets and P is a set of finite splicing rules. A finite set P with k number of graph splicing rules, can be written in the form

((h[1],E'[1]); (h[2],E'[2]), ..., (h[k];E'[k]);R)

such that  $k \ge 1$  where  $k \in \mathbb{N}$  and for all *i* with  $1 \le i \le k$ , where

- h[i] = (N[i], E[i], L[i]) weakly connected graph, where E[i] is the edges of the *i*th graph splicing rule,
- $E'[i] \subseteq E[i]$ , where E'[i] is the cutting pattern for the *i*th graph splicing rule,
- the nodes N[i] are mutually disjoint,
- *R* obeys the following rules:
- i. Each edge  $(n,m) \in E'[i]$  is supposed to be divided into two parts; i.e the start part (n,m] and the end part [n,m),
- ii. The elements of *E* are of the form ((n,m], [n',m')), where (n,m) and (n',m') are edges from  $\bigcup_{1 \le i \le k} E'[i]$ ,
- iii. Every element from  $\{(n,m], [n,m) \mid (n,m) \in \bigcup_{1 \le i \le k} E'[i] \text{ must appear exactly once in a pair of } E.$





- Graph splicing scheme described the whole process of the graph splicing system where the graph splicing rule(s) is defined.
- Similar as enzymes in DNA splicing, splicing rules are used to control and restrict the edges to be cut on the initial graphs.



## Graph Splicing Scheme (Cont.)



Consider the set of natural numbers denoted by  $\mathbb{N} = \{0, 1, 2, ...\}$  and  $\mathbb{N}_{\infty} = \mathbb{N} \cup \infty$ . Let M be any set, and r be a function representing  $\mathbb{N}_{\infty}$ -subset of set  $M, r : M \to \mathbb{N}_{\infty}$ , where r can be written as formal power series  $r = \sum_{m \in M} (r(m) \circ m)$ . The idea of r(m) is to count the number of occurence of the object m. Since there is an infinite number of copies of m, then  $r(m) = \infty$ . The set  $\{m \in M | r(m) \neq 0\}$  is called as the support of r, denoted as supp(r). Assume every  $\mathbb{N}_{\infty}$ -subset to have finite support and denote the set of all  $\mathbb{N}_{\infty}$ -subset of M by  $\langle \langle M \rangle \rangle$ . Then  $r \in \langle \langle M \rangle \rangle$  can be written as

 $r = \{ (m, r(m)) \mid m \in \text{supp}(r) \}.$ 





### Definition (Freund, 1995) Graph Splicing Rule

Let p = ((h[1], E'[1]), ..., (h[k], E'[k]); R) be a graph splicing rule and  $r \in \langle \langle \gamma_c(A) \rangle \rangle$  where  $\gamma_c(A)$  is a set of connected graphs over alphabet A. If there are k different graphs g[1], ..., g[k] from r, in the sense that n copies of the graph  $g \in \gamma_c(A)$  are n objects selected, provides that  $r(g) \ge n$ , then p can be applied to r, which yields some  $s \in \langle \langle \gamma_c(A) \rangle \rangle$  in the following way:

- i. for all *i* with  $1 \le i \le k$ , h[i] is a subgraph of g[i], where f[i] establishes the injective node embedding h[i] into g[i],
- ii. the union of g[i], ..., g[k] can be looked at as a single graph  $g \in \gamma_c(A)$  and the union of the functions f[i] as single function f embedding h[i] into g. Eliminate all edges from  $\bigcup_{1 \le i \le k} f(E'[i])$  from g and add all edges (f(n), f(m')) such that  $((n,m], [n',m')) \in E$ , which yields the uniquely determined union of k' connected graphs g'[i], ..., g'[k],
- iii. the new  $\mathbb{N}_{\infty}$ -subset *s* is obtained from *r* by successively decrementing r(g[1]), ..., r(g[k]) by one and incrementing r(g'[1]), ..., r(g'[k]) by one.







innovative • entrepreneurial • global





• A graph splicing rule consisting the enzyme *EcoR*I can be written as follows.







#### Definition (Freund, 1995) Graph Splicing System

Let  $\sigma = (A, P)$  be any graph splicing scheme and consider  $I \in \langle \langle \gamma_c(A) \rangle \rangle$  where  $I = \{(g, k)\}$ , for any  $g \in \langle \langle \gamma_c(A) \rangle \rangle$  and  $k \ge 0$  is the number of copies of g. Then there exists the set of all  $I' \in \langle \langle \gamma_c(A) \rangle \rangle$  denoted by  $\sigma(\{I\})$ , obtained by applying one graph splicing rule of P to I. By applying the graph splicing rule repeatedly, for every  $n \ge 2$ ,  $\sigma^n(\{I\})$  is defined by  $\sigma^n(\{I\}) = \sigma(\sigma^{n-1}(\{I\}))$  and note that  $\sigma^0(\{I\}) = \{I\}$ . Also, note that  $\sigma^n(\{I\})$  is simply denoted as  $\sigma^*(\{I\}) = \bigcup_{n \in \mathbb{N}} \sigma^n(\{I\})$ , by extending  $\sigma^n(\{I\})$ , where  $\mathbb{N}$  is the set of natural numbers. Hence, there is a set of triple S = (A, P, I) is called as a graph splicing system.





• In 2011, Jeyabharathi *et. al.* introduced one type of splicing called as *n*-cut splicing.



S. Jeyabharathi, J. Padmashree, S. S. Selvi, and K. Thiagarajan, Semigraph structure on DNA splicing system, in 6th Int. Conf. on Bio-Inspired Computing: Theories and Applications, BIC-TA (IEEE Computer Society, Washington, DC, 2011), 182–187.

innovative • entrepreneurial • global



# *n*-Cut Splicing (Cont.)

- *n*-cut splicing is introduced in 2011 by Jeyabarathi et al. to illustrate the cleavage pattern of DNA molecules in the form of semigraphs.
- Every *n*-cut splicing will generate two components of *n*-cut spliced semigraphs which can be denoted as SSG = (V, V, E, E') where V, V, E and E' denote the set of vertices, the set of semivertices, the set of edges and the set of semiedges, respectively.
- Semivertices and semiedges are generated by the decomposition of the edges.



## *n*-Cut Splicing (Cont.)







Semigraph representation of DNA molecule

An *n*-cut splicing is applied

Two components of *n*-cut spliced semigraphs are generated







5

7'





### Example of *n*-cut splicing & *n*-cut spliced semigraph



innovative • entrepreneurial • global



# *n*-Cut Splicing (Cont.)

• An *n*-cut splicing will cut *n*+2 number of edges and the two vertices from the left most of the graphs as well as the two vertices from the right most of the graphs will never be cut.









### Mapping:

### i. $\dim(f(v)) < \dim(v)$ for $v \in V_1$ ii. $\dim(f(e)) < \dim(e)$ for $e \in E_1$

### Folding:

**IFF** *f* maps vertex (semivertex) to vertex (semivertex) and edge (semiedge) to edge (semiedge)

# Folding Technique *n*-Cut Semigraphs (Cont.)







### **Proposition:**

Every *n*-cut spliced semigraph can be folded for *n*+1 times.

### **Proof:**

Let K(n) denotes the maximum number of foldings for an n-cut spliced semigraph. It can be shown that the maximum number of foldings on a 1-cut spliced semigraph, a 2-cut spliced semigraph and a 3-cut spliced semigraph are K(1)=2, K(2)=3 and K(3)=4, respectively. By sequence, K(n) can be written as K(n)=K(1)+(n-1)d where d is the common difference between two consecutive or adjacent terms. Since it is known that K(1) = 2, then the general equation for the maximum number of foldings of an n-cut spliced semigraph can be written as

$$K(2) = K(1) + (2-1)d$$
  
3 = 2 + (1)d  
d = 1.

Hence,

$$K(n) = K(1) + (n-1)d$$
  
= 2 + (n-1)(1)  
= n + 1.

Muhammad Nur Syiham Abdul Razak, Wan Heng Fong, Nor Haniza Sarmin. Folding Technique on n-Cut Spliced Semigraph in Splicing System. In. AIP Conference Proceedings 2266: 060011 (2020); 1-10. (doi: 10.1063/5.0026045)

innovative • entrepreneurial • global

### **List of Publications**

Link: <a href="https://people.utm.my/nizasarmin/">https://people.utm.my/nizasarmin/</a>



#### 2010

Nor Haniza Sarmin, Yuhani Yusof and Fong Wan Heng, Some Characterizations in Splicing Systems, International Conference on Mathematical Sciences (ICMS 2010), Abant Yzzet Baysal Üniversitesi, Bolu, Turkey, 23 – 27 Nov 2010, American Institute of Physics (AIP) Conference Proceedings, Melville, New York, Vol 1309, pg. 411-418, (ISBN 978-0-7354-0863-0).

#### 2012

Sherzod Turaev, Gan Yee Siang, Mohamed Othman, **Nor Haniza Sarmin** and Fong Wan Heng, **Weighted Splicing Systems**, Computational Intelligence and Intelligent Systems, Communications in Computer and Information Science (CCIS), ISBN 978-3-642-34288-2, Volume 316, 2012, pg 416-424, Proceedings in *The 6<sup>th</sup> International Symposium on Intelligence Computation and Applications (ISICA 2012)*, Wuhan, China, 27-28 October 2012.

#### 2013

Nurhidaya Mohamad Jan, Fong Wan Heng and Nor Haniza Sarmin, Regular Languages, Regular Grammars and Automata in Splicing Systems, Proceedings of the 20<sup>th</sup> National Symposium on Mathematical Sciences (SKSM 20), AIP Conf. Proc., Vol 1522, 2013, pg. 856-863 (ISSN: 1551-7616).

Yuhani Yusof, Nor Haniza Sarmin, Fong Wan Heng, T. Elizabeth Goode and Muhammad Azrin Ahmad, An Analysis of Four Variants of Splicing System, Proceedings of the 20<sup>th</sup> National Symposium on Mathematical Sciences (SKSM 20), AIP Conf. Proc., Vol 1522, 2013, pg. 888-895 (ISSN: 1551-7616).

Mathuri Selvarajoo, Fong Wan Heng, Nor Haniza Sarmin and Sherzod Turaev, Some Characteristics of Probabilistic One-Sided Splicing Systems, Proceedings of the 20<sup>th</sup> National Symposium on Mathematical Sciences (SKSM 20), AIP Conf. Proc., Vol 1522, 2013, pg. 967-975(ISSN: 1551-7616).

Sherzod Turaev, Mathuri Selvarajoo, Mohd Hasan Selamat, **Nor Haniza Sarmin** and Fong Wan Heng, **Probabilistic Splicing Systems**, Advanced Methods for Computational Collective Intelligence, Studies in Computational Intelligence, ISBN 978-3-642-34300-1,Volume 457, 2013, pg 259-268, proceedings in 4<sup>th</sup> International Conference on Computational Collective Intelligence Technologies and Applications (ICCCI 2012), Ho Chi Minh city, Vietnam, 28-30 November 2012.

innovative • entrepreneurial • global

### List of Publications (Cont.)

Link: <a href="https://people.utm.my/nizasarmin/">https://people.utm.my/nizasarmin/</a>

#### 2014

Muhammad Azrin Ahmad, Nor Haniza Sarmin, Fong Wan Heng, Yuhani Yusof, An Extension of First Order Limit Language, Proceedings of the 3<sup>rd</sup> International Conference on Mathematical Sciences (ICMS3), AIP Conf. Proc., Vol 1602, 2014, pg. 627-631. (ISBN: 978-0-7354-1236-1)

Mathuri Selvarajoo, Fong Wan Heng, **Nor Haniza Sarmin** and Sherzod Turaev, **Probabilistic Simple Splicing Systems**, *Proceedings of the 3<sup>rd</sup> International Conference on Mathematical Sciences (ICMS3)*, AIP Conf. Proc., Vol 1602, 2014, pg. 760-766. (ISBN: 978-0-7354-1236-1)

Yuhani Yusof, Nor Haniza Sarmin, Fong Wan Heng, The Concepts of Persistent and Permanent in Non Semi-Simple DNA Splicing System, Proceedings of the 21<sup>st</sup> National Symposium on Mathematical Sciences (SKSM 21), AIP Conf. Proc., Vol 1605, 2014, pg. 586-590 (ISBN: 978-0-7354-1241-5).

Fariba Karimi, Sherzod Turaev, **Nor Haniza Sarmin** and Wan Heng Fong, **Fuzzy Splicing Systems**, Lecture Notes in Artificial Intelligence, Computational Collective Intelligence: Technologies and Applications, Volume 8733, ISBN 978-3-319-11288-6, pg 20-29, proceedings in 6th *International Conference on Computational Collective Intelligence Technologies and Applications* (ICCCI 2014), Seoul, Korea, September 24-26, 2014.

#### 2015

Yuhani Yusof, Wen Li Lim, T.Elizabeth Goode, **Nor Haniza Sarmin**, Fong Wan Heng, Mohd Firdaus Abd Wahab, **Molecular Aspects of DNA Splicing Systems**, International Conference on Mathematics, Engineering & Industrial Applications 2014 (ICoMEIA 2014), 28-30 May, 2014, The Gurney Resort Hotel & Residences Penang, AIP Conf. Proc., Vol. 1660, 2015, pg. 050045 (ISSN: 1551-7616).

Yee Siang Gan, Wan Heng Fong, Nor Haniza Sarmin and Sherzod Turaev, Some Characteristics on the Generative Power of Weighted One-Sided Splicing Systems, Proceedings of the 22<sup>nd</sup> National Symposium on Mathematical Sciences (SKSM 22), AIP Conf. Proc., Vol 1682, 2015, pg. 020044 1-7 (ISBN 978-0-7354-1329-0).

Muhammad Azrin Ahmad, Nor Haniza Sarmin, Yuhani Yusof and Wan Heng Fong, Some Restrictions on the Existence of Second Order Limit Language, Proceedings of the 22<sup>nd</sup> National Symposium on Mathematical Sciences (SKSM 22), AIP Conf. Proc., Vol 1682, 2015, pg. 020048 1-7 (ISBN: 978-0-7354-1329-0).

#### 2016

Wan Heng Fong, Yee Siang Gan, Nor Haniza Sarmin, and Sherzod Turaev, The Generative Capacity of Weighted Simple and Semi-Simple Splicing Systems, Proceedings of the 23<sup>rd</sup> National Symposium on Mathematical Sciences (SKSM 23), AIP Conf. Proc., Vol 1750, 2016, pg. 050013 1-6 (ISBN: 978-0-7354-1407-5).

### List of Publications (Cont.)

Link: <a href="https://people.utm.my/nizasarmin/">https://people.utm.my/nizasarmin/</a>

2017

Mathuri Selvarajoo, Wan Heng Fong, Nor Haniza Sarmin and Sherzod Turaev, Probabilistic Simple Sticker Systems, Proceedings of the 4th International Conference on Mathematical Sciences (ICMS4 2016), AIP. Conf. Proc., 1830 (1), 2017, pg. 020057 1-9 (ISBN: 978-0-7354-1498-3)

2018

Nurul Izzaty Ismail, Wan Heng Fong and Nor Haniza Sarmin, Computation of Splicing Languages from DNA Splicing System with One Palindromic Restriction Enzyme, Malaysian Journal of Fundamental and Applied Sciences 2018, 14(2): pg 188-192, (ISSN 2289-5981)

Muhammad Azrin Ahmad, Nor Haniza Sarmin, Mohd Firdaus Abdul-Wahab, Fong Wan Heng, Yuhani Yusof, Biomolecular Aspects of Second Order Limit Language, Malaysian Journal of Fundamental and Applied Sciences 2018, 14(1): pg 15-19, (ISSN 2289-5981).

#### 2019

Wan Heng Fong, Nurul Izzaty Ismail and Nor Haniza Sarmin, Automata for DNA Splicing Languages with Palindromic and Non-Palindromic Restriction Enzymes using Grammars, MATEMATIKA: *Malaysian Journal of Industrial and Applied Mathematics*, December 2019, Special Issue: pg 1-14, (eISSN: 0127-9602)

Nurul Izzaty Ismail, Wan Heng Fong and Nor Haniza Sarmin, DNA Splicing Systems with at Most Two Cutting Sites of a Non-Palindromic Restriction Enzyme, MATEMATIKA: *Malaysian Journal of Industrial and Applied Mathematics*, 2019, 35(2): pg 129-137, (eISSN: 0127-9602)

#### 2020

Muhammad Nur Syiham Abdul Razak, Wan Heng Fong, **Nor Haniza Sarmin**. Folding Technique on n-Cut Spliced Semigraph in Splicing System. In AIP Conference Proceedings 2266: 060011 (2020); 1-10. (doi: 10.1063/5.0026045)

M N S Abdul Razak, W H Fong, N H Sarmin. Graph splicing rules with cycle graph and its complement on complete graphs. In: Journal of Physics: Conference Series 1988: 012067 (2021); 1-11. (doi: 10.1088/1742-6596/1988/1/012067)

# **THANK YOU**



https://people.utm.my/nizasarmin/



nhs@utm.my



Niza Sarmin

in

Niza Sarmin

Niza Sarmin



In the Name of God for Mankind www.utm.my

Credit slides:



Muhammad Nur Syiham Abdul Razak

Photo credit: Thuy Van Nguyen