Splicing System: from Biology to Computer Science & Mathematics

UTM
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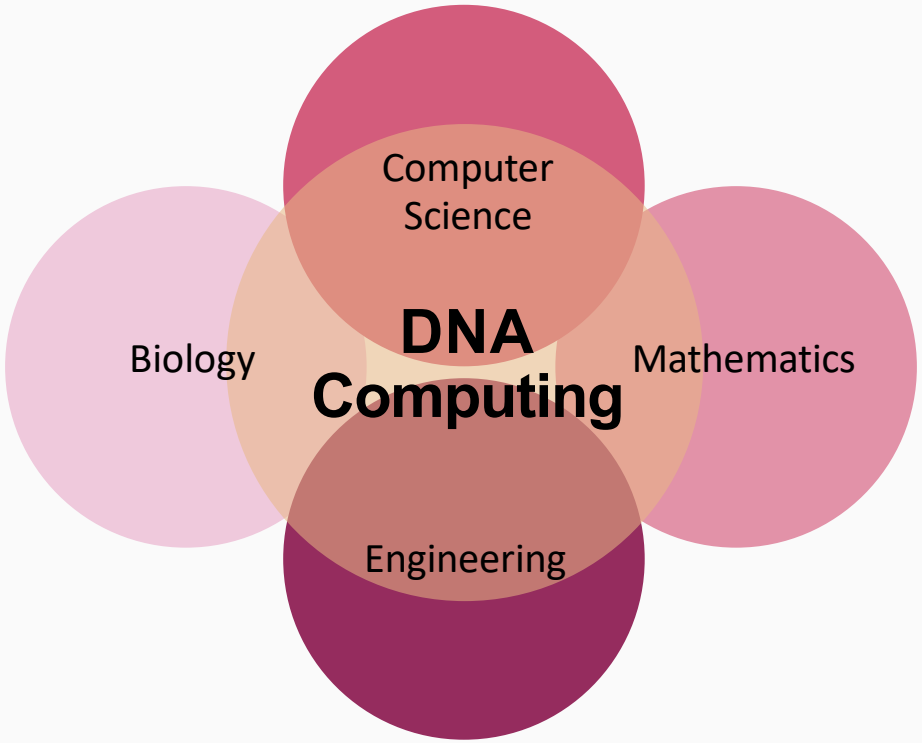
DNA Computing

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



DNA Computing (Cont.)

- The field has blossomed rapidly, with development of significant **theoretical** and **experimental** results by researchers from **interdisciplinary** areas.

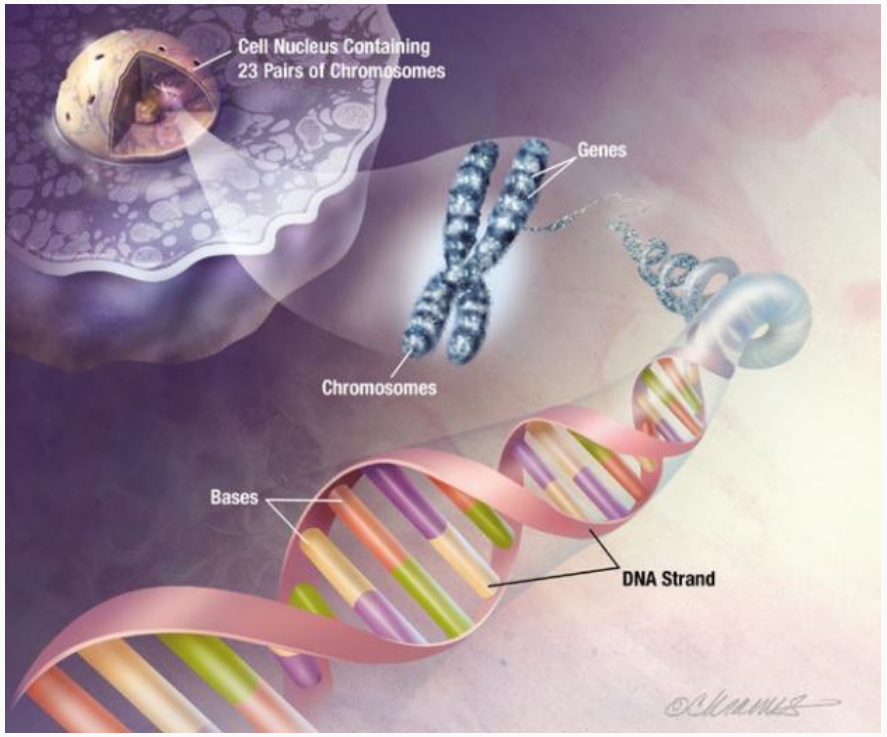
- **Different models** of molecular computation have been proposed in scientific society including Splicing Models and Sticker Models.

DNA Splicing System

1. Structure of DNA
2. Restriction Enzymes
3. DNA Ligase

Structure of DNA

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

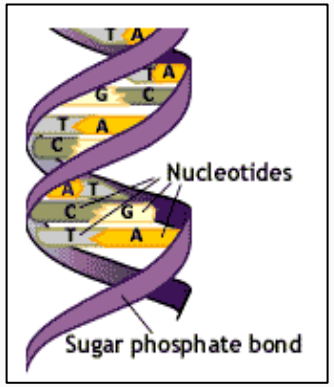


Structure of DNA (Cont.)

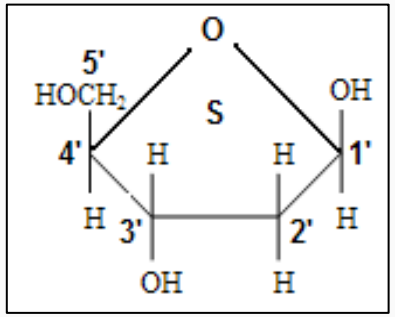
DNA – Deoxyribonucleic Acid

made up of

Nucleotides



Phosphate group



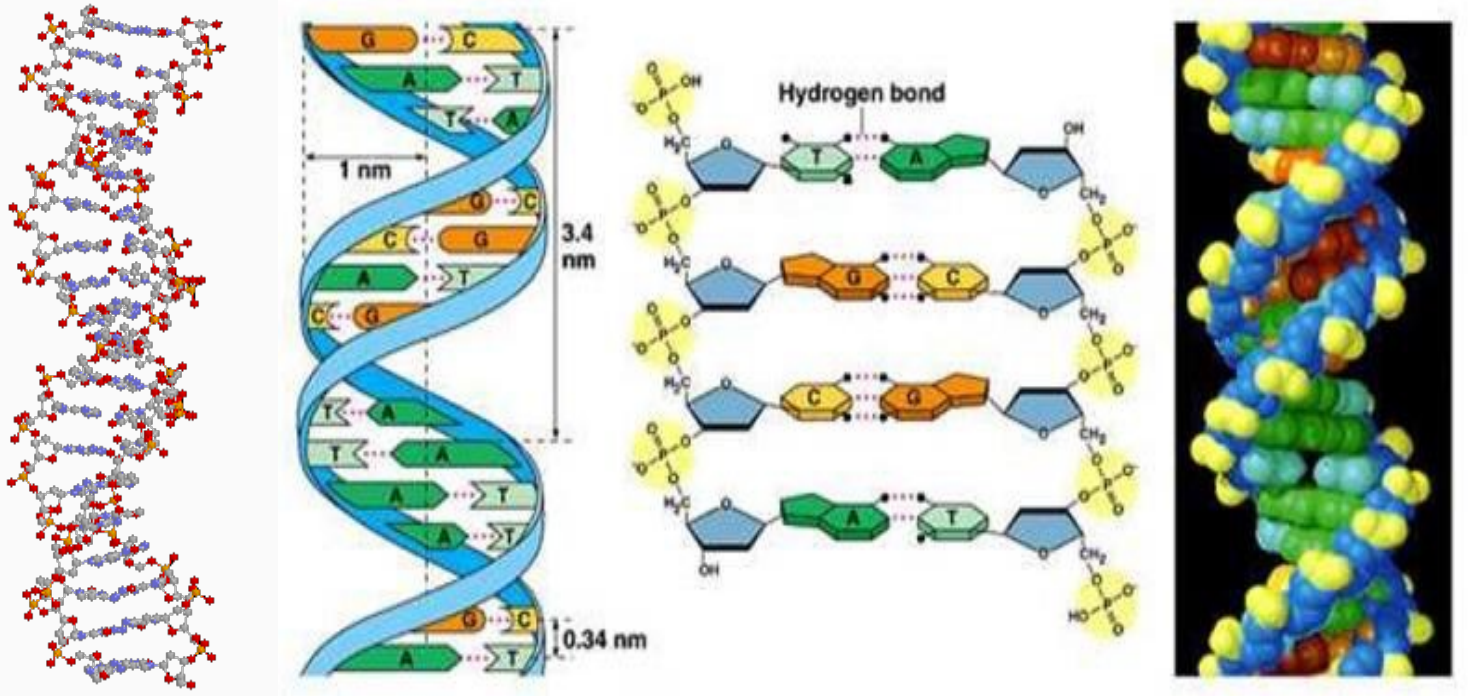
Base

Adenine (A)
Cytosine (C)
Guanine (G)
Thymine (T)

Pentose (a 5-carbon sugar)

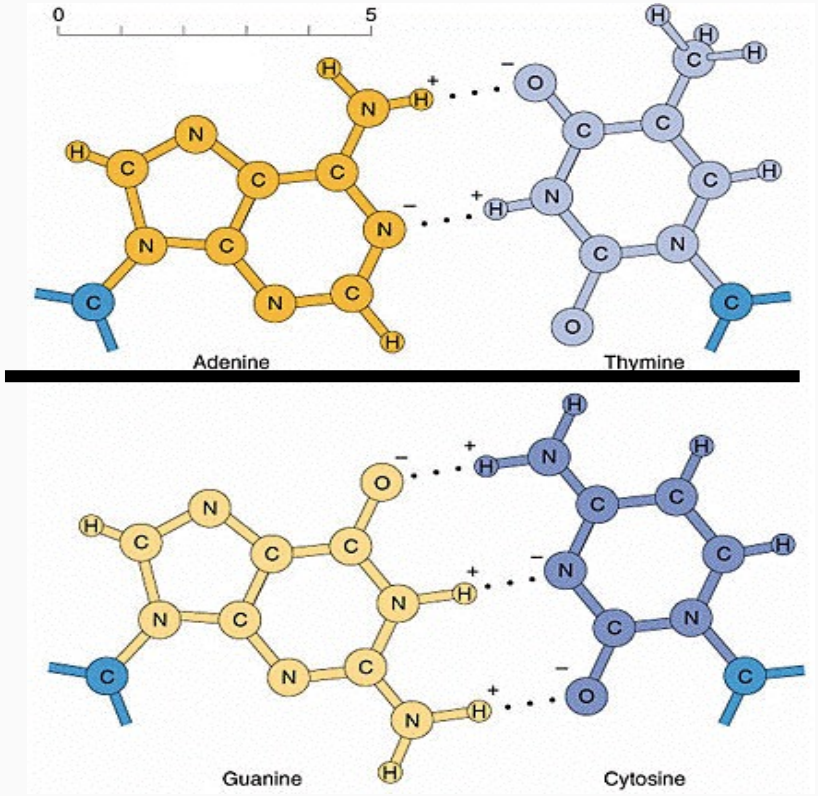
Structure of DNA (Cont.)

- 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).



Structure of DNA (Cont.)

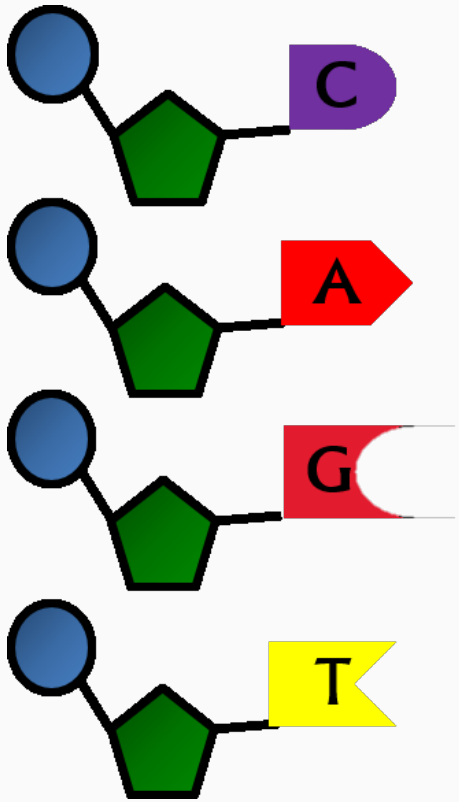
- In 1953, it was shown that the bases can join only complimentarily, A with T and G with C respectively.

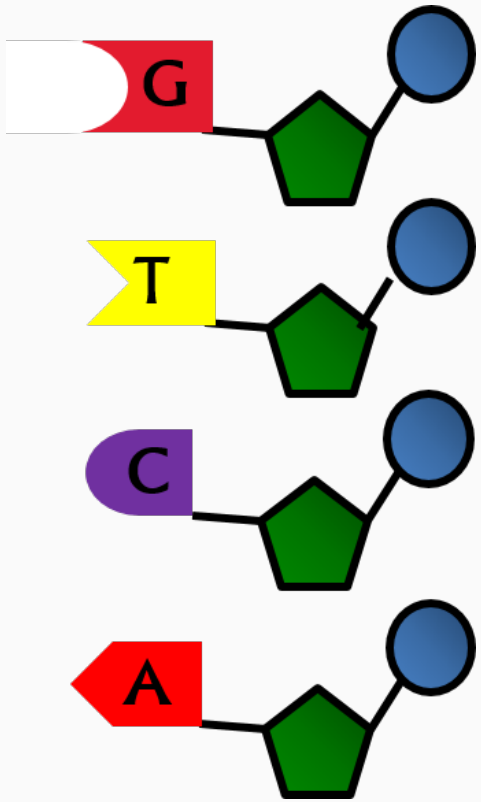


A - T

G - C

Structure of DNA (Cont.)





Restriction Enzymes

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

Sticky end (e.g. *Aci*I)

5’…C▼CGC…3’

3’…GGC▲G…5’

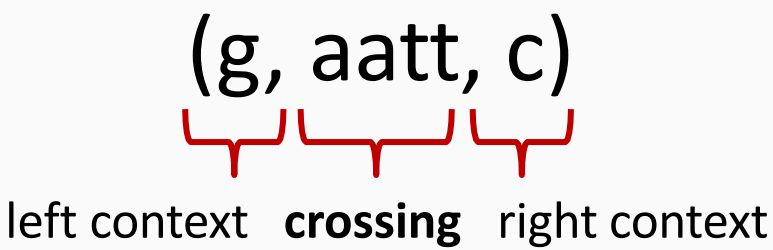
Blunt end (e.g. *Afe*I)

5’…AGC▼GCT…3’

3’…TCG▲CGA…5’

Restriction Enzymes (Cont.)

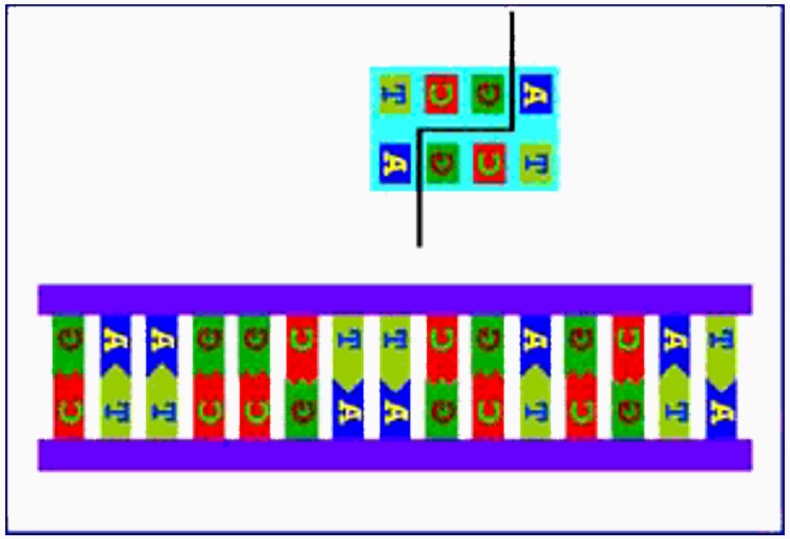
- Every restriction enzyme has a triple known as the cleavage pattern of the enzyme.
- The triple is denoted as a rule for the restriction enzyme which consists of left context, crossing and right context (Head, 1998).
- The restriction enzyme ***EcoR*I** is isolated from the bacterium Escherichia coli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



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

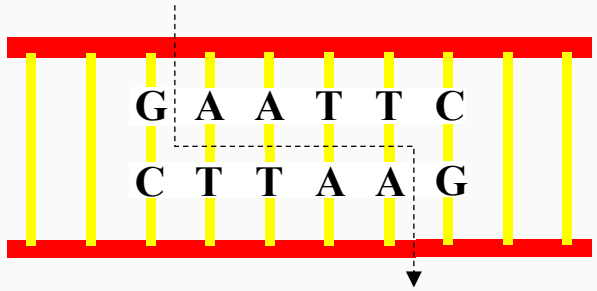
Restriction Enzymes (Cont.)

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

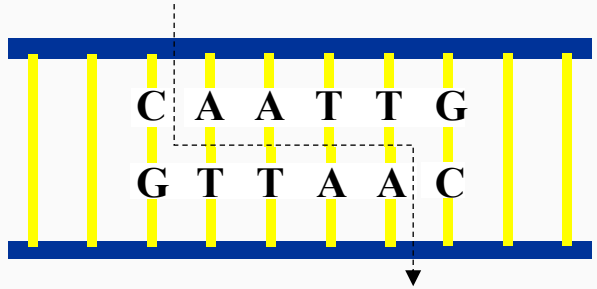


Restriction Enzymes (Cont.)

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

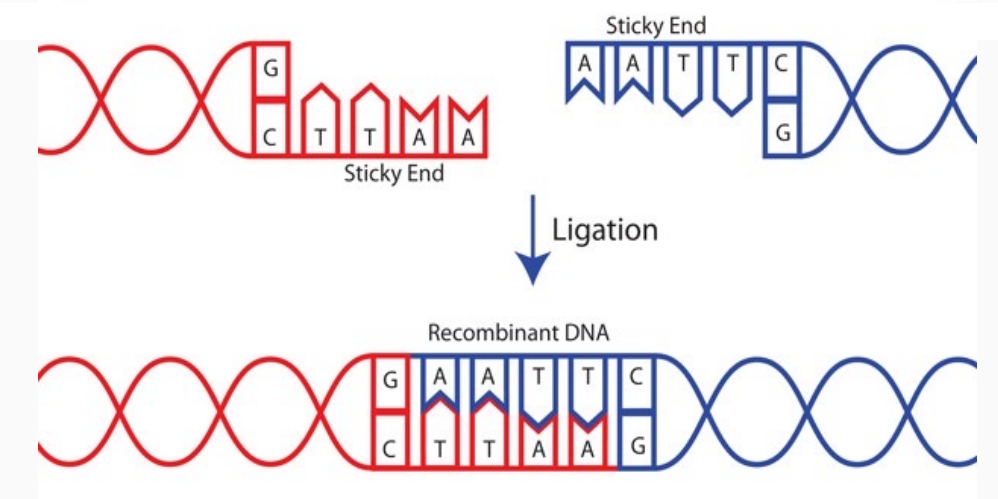


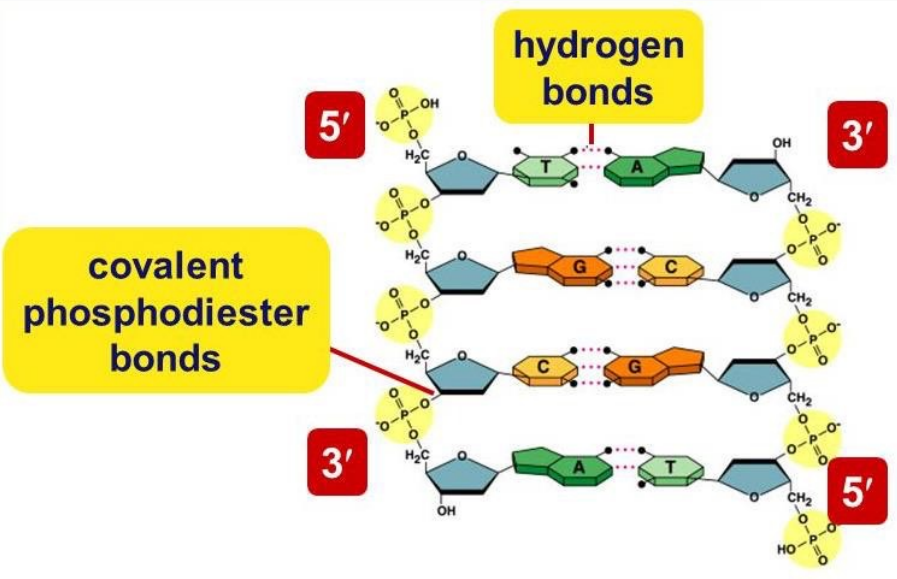
*Mfe*I: ([C/G],[A/T],[A/T],[T/A],[T/A],[G/C])



DNA Ligase

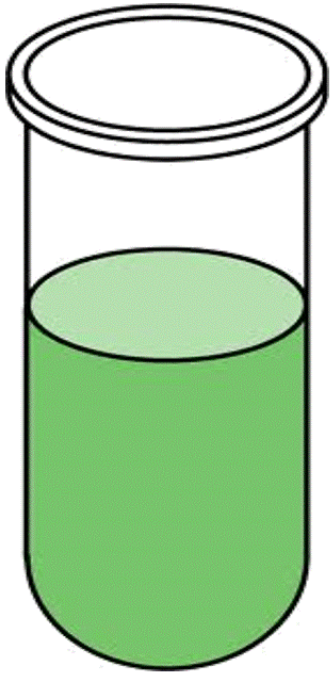
- DNA ligase is an enzyme that can catalyze the linking of DNA strands together by forming a phosphodiester bond.





Wet Experiment on Splicing System

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



Wet Experiment on Splicing System (Cont.)

Previous Molecular Works on Splicing Systems

Author	Description
Laun and Reddy 1999	The first experiment on the splicing system using restriction enzymes *Bgl*I and *Dra*III
Fong 2008	The adult and limit languages from Head's splicing model using restriction enzymes *Hpa*II and *Aci*I
Karimi 2013	Verification of the persistency properties of splicing systems involving restriction enzymes *CvaQ*I and *Acc65*I
Yusof et al. 2015	Yusof-Goode splicing system with restriction enzymes *Acl*I and *Aci*I using limit graph approach
Ahmad et al. 2018	Experiment on second order limit language from Yusof-Goode splicing system using restriction enzyme *Dpn*II
Ismail 2020	Experiment using the restriction enzymes *Cvi*QI and *Aci*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.

Wet Experiment on Splicing System (Cont.)

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

Wet Experiment on Splicing System (Cont.)

Universiti Teknologi Malaysia, 2007

Wet Experiment on Splicing System (Cont.)

Universiti Teknologi Malaysia, 2012

Wet Experiment on Splicing System (Cont.)

Universiti Teknologi Malaysia, 2015

Wet Experiment on Splicing System (Cont.)

Universiti Teknologi Malaysia, 2020

DNA Splicing System

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 $A = \begin{Bmatrix} A, C, G, T \\ T\ G\ C\ A \end{Bmatrix}$ is the set of dsDNA symbols, $I = \left\{ \begin{matrix} GAATTCTCTGTAAT \\ CTTAAGAGACATTA \end{matrix} \right\}$ is the set consisting of an initial string of molecules, set $B = \left\{ \left(\begin{matrix} G \\ C \end{matrix}, \begin{matrix} AATT \\ TTAA \end{matrix}, \begin{matrix} C \\ G \end{matrix} \right) \right\}$ is the set of cleavage pattern for the enzyme ***EcoR*I** and set C is the empty set.

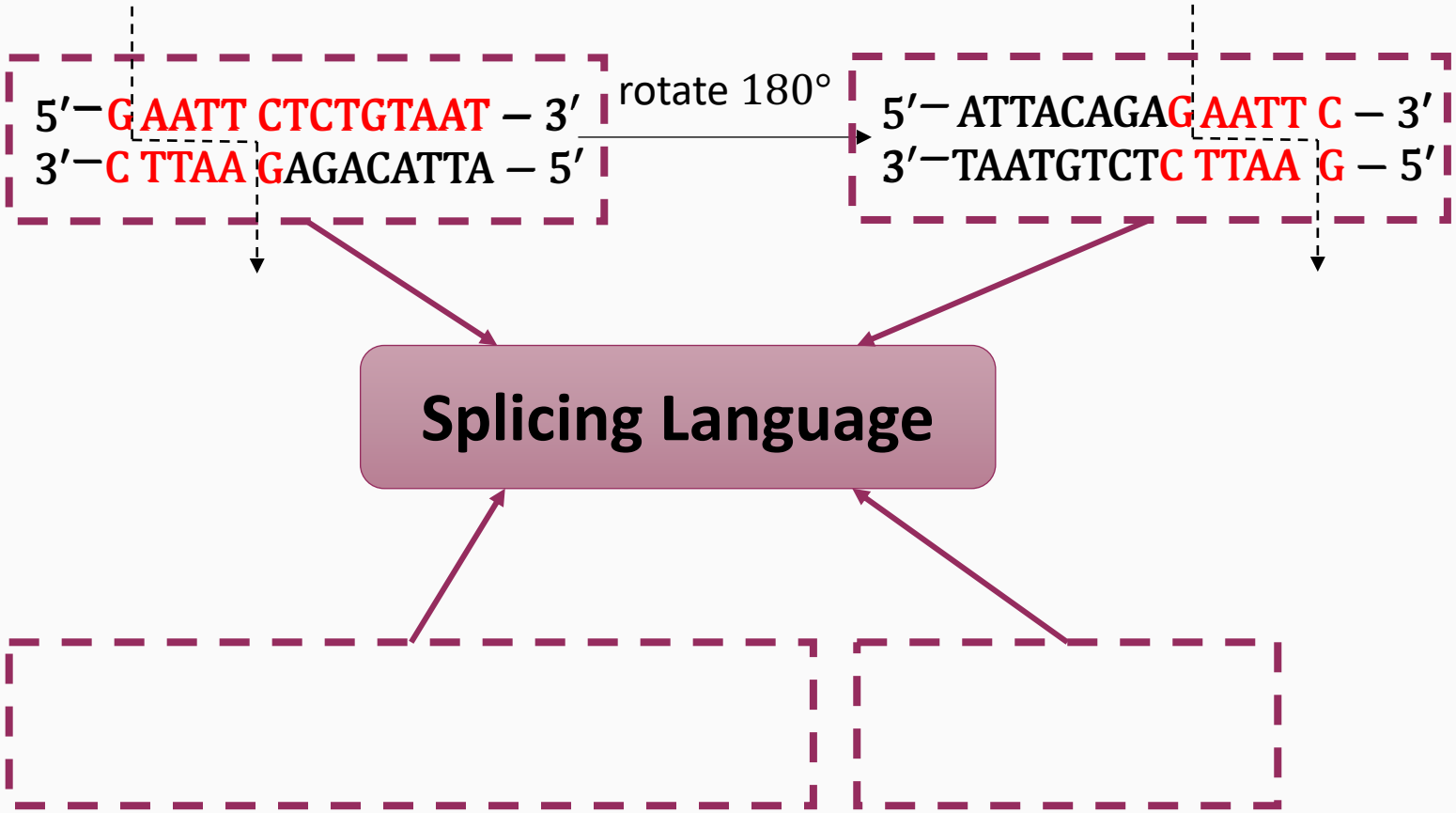
The initial string is shown in the following:

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

or written 180 degree wise,

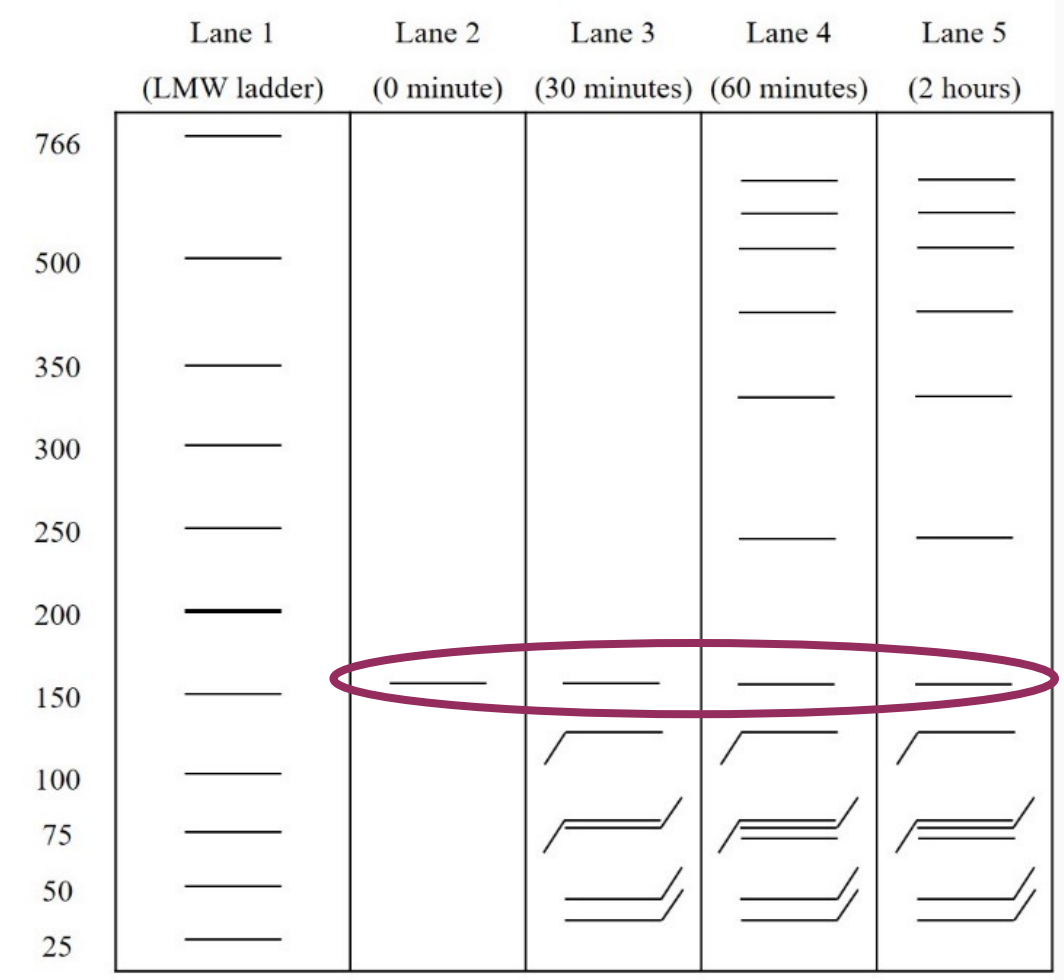
$$5'-ATTACAGAGAATTC-3'$$
$$3'-TAATGTCTCTTAAG-5'.$$

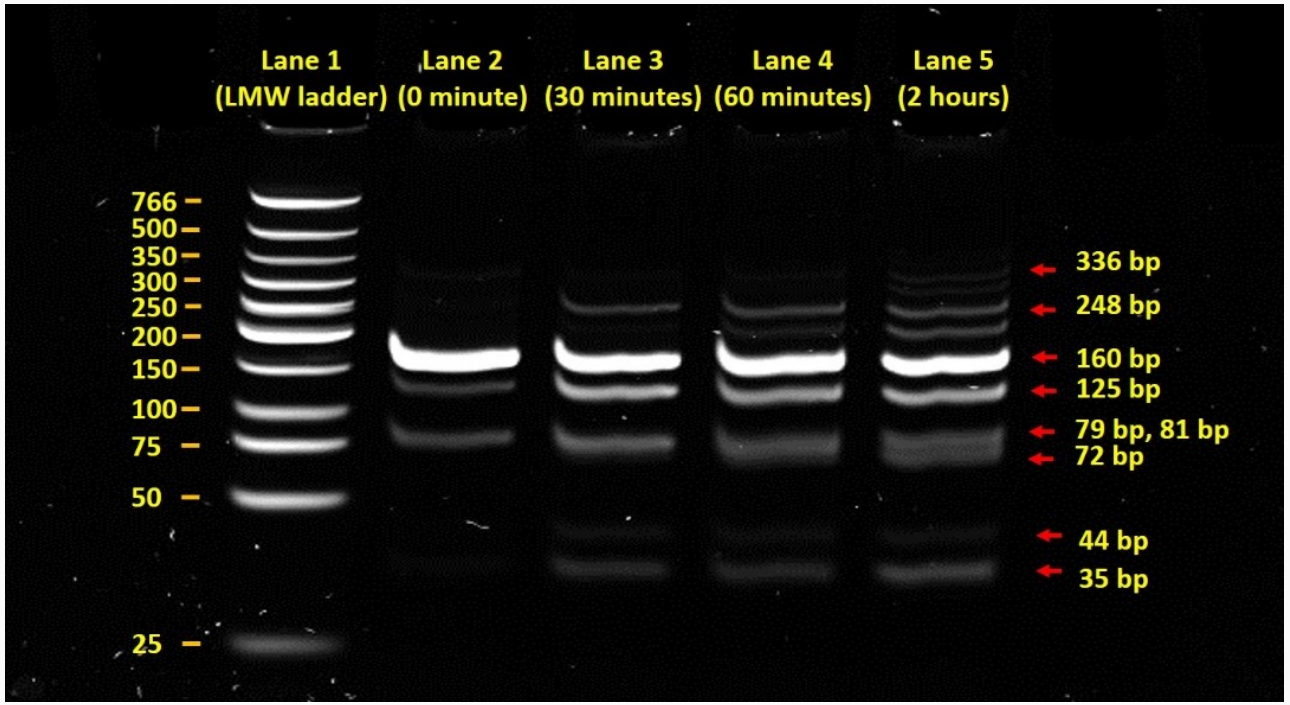
DNA Splicing System (Cont.)



Theoretical vs Lab Results

Wet Splicing System involving *Cvi*QI and *Aci*I

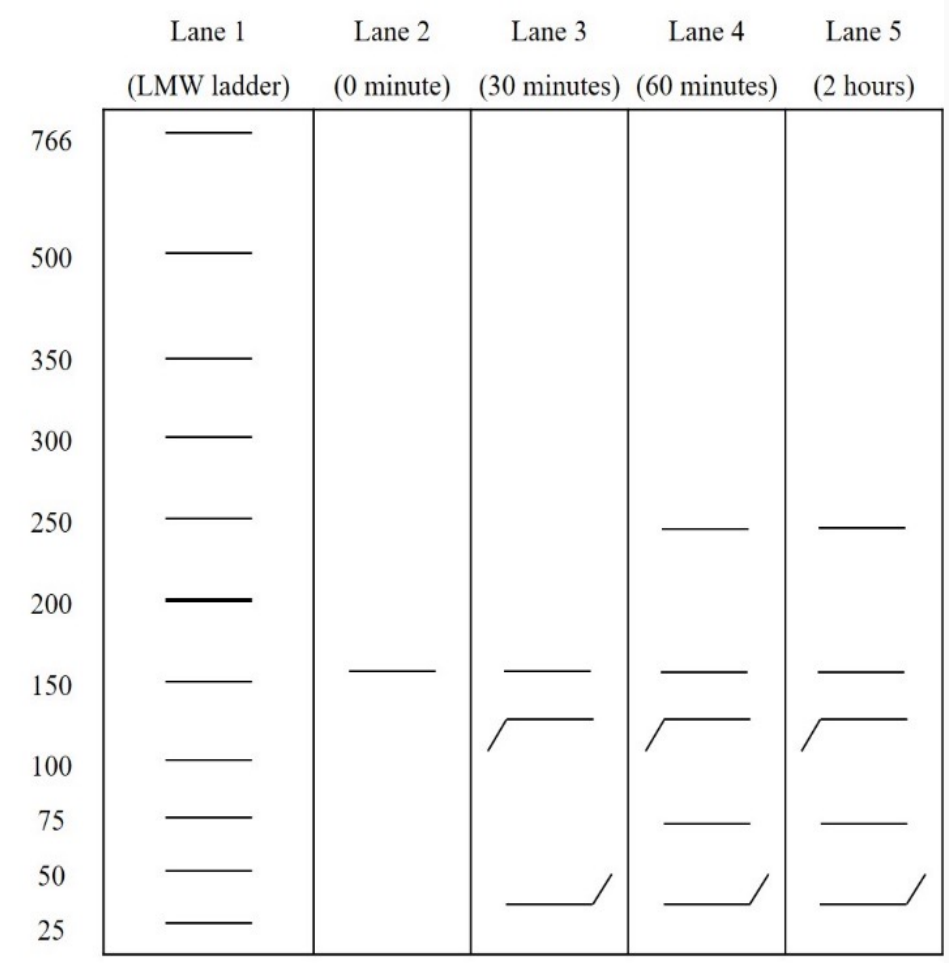


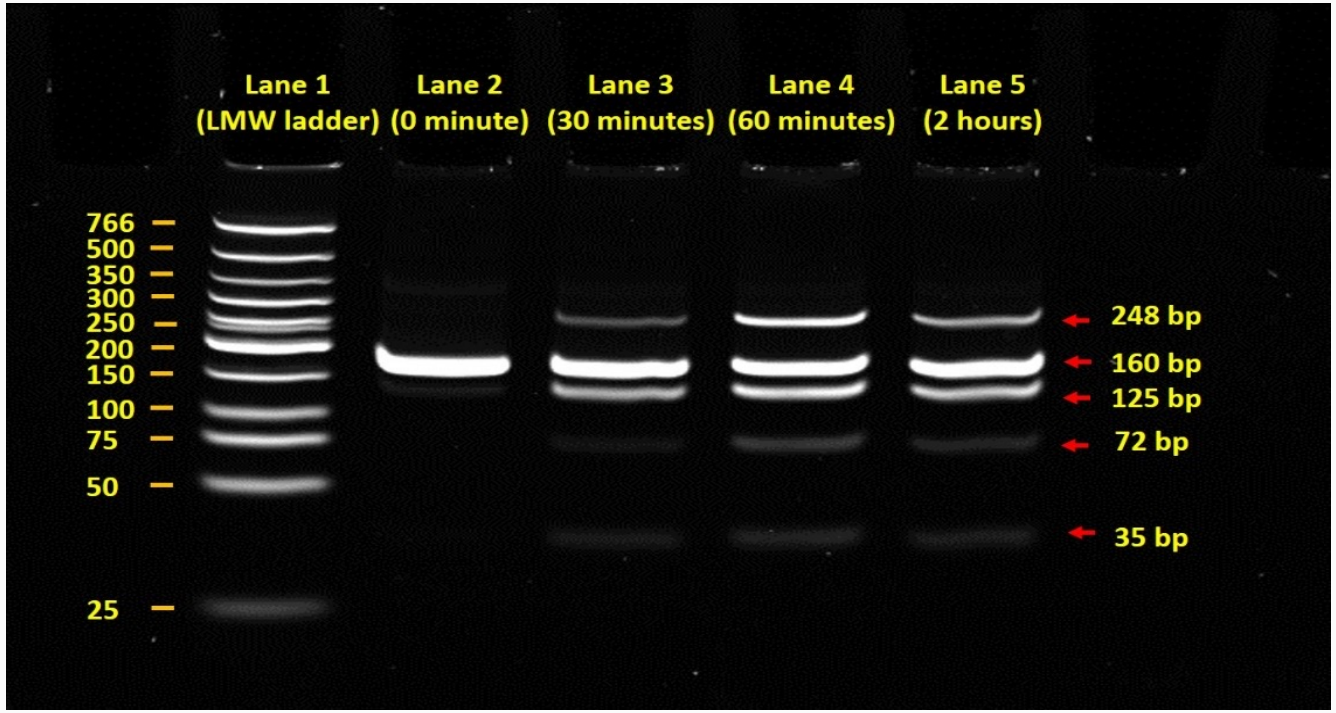


- Lane 1: LMW ladder
- Lane 2 (0 minute): 79 bp (or 81 bp), 125 bp and 160 bp
- Lane 3 (30 minutes): 35 bp, 44 bp, 79 bp, 81 bp, 125 bp, 160 bp, 248 bp
- Lane 4 (60 minutes): 35 bp, 44 bp, 79 bp, 81 bp, 125 bp, 160 bp, 248 bp
- Lane 5 (2 hours): 35 bp, 44 bp, 72 bp, 79 bp, 81 bp, 125 bp, 160 bp, 248 bp, 336 bp

Theoretical vs Lab Results

Wet Splicing System involving *Cvi*QI

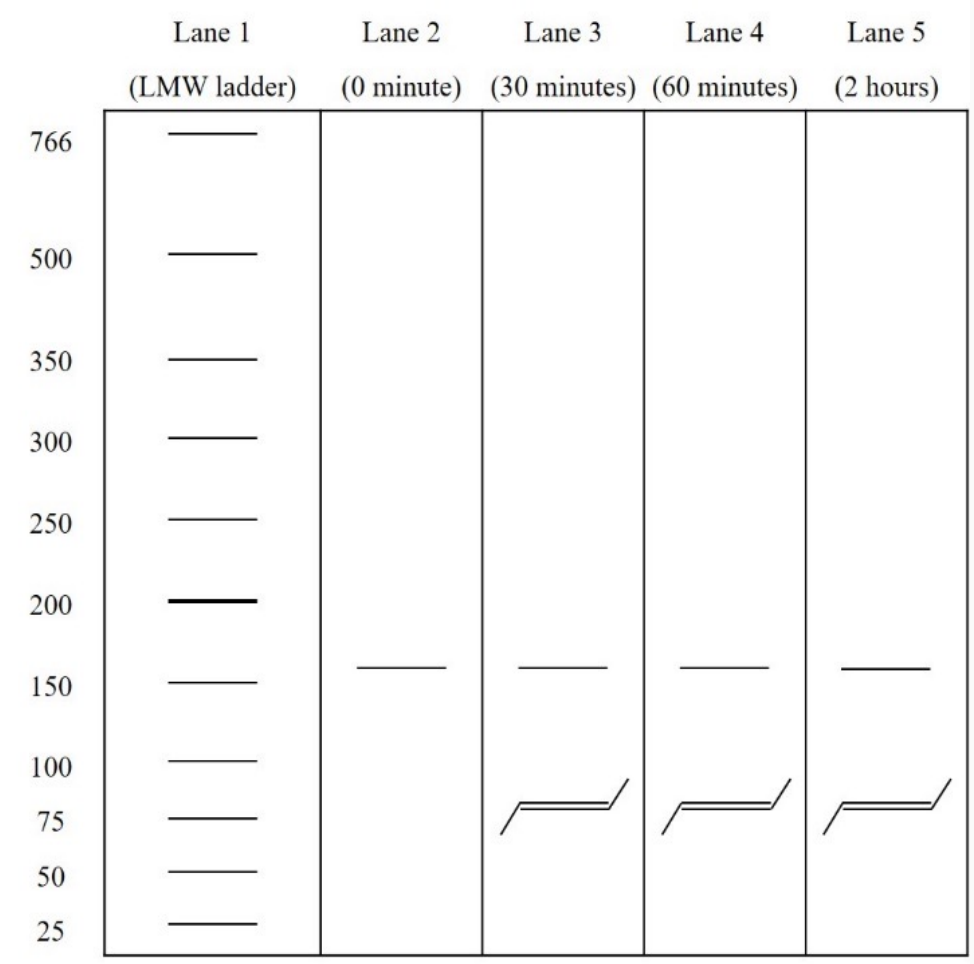


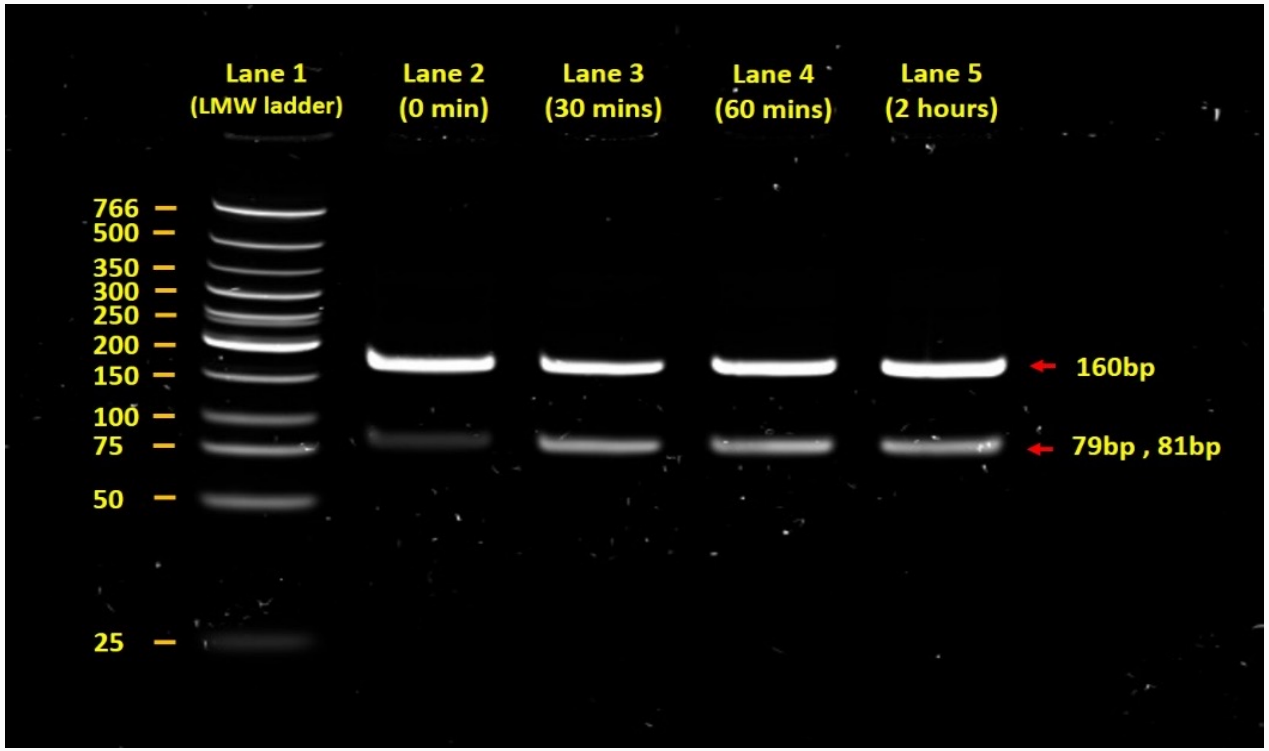


- Lane 1: LMW ladder
- Lane 2 (0 minute): 160 bp
- Lane 3 (30 minutes): 35 bp, 72 bp, 125 bp, 160 bp and 248 bp
- Lane 4 (60 minutes): 35 bp, 72 bp, 125 bp, 160 bp and 248 bp
- Lane 5 (2 hours): 35 bp, 72 bp, 125 bp, 160 bp and 248 bp

Theoretical vs Lab Results

Wet Splicing System involving *Acil*

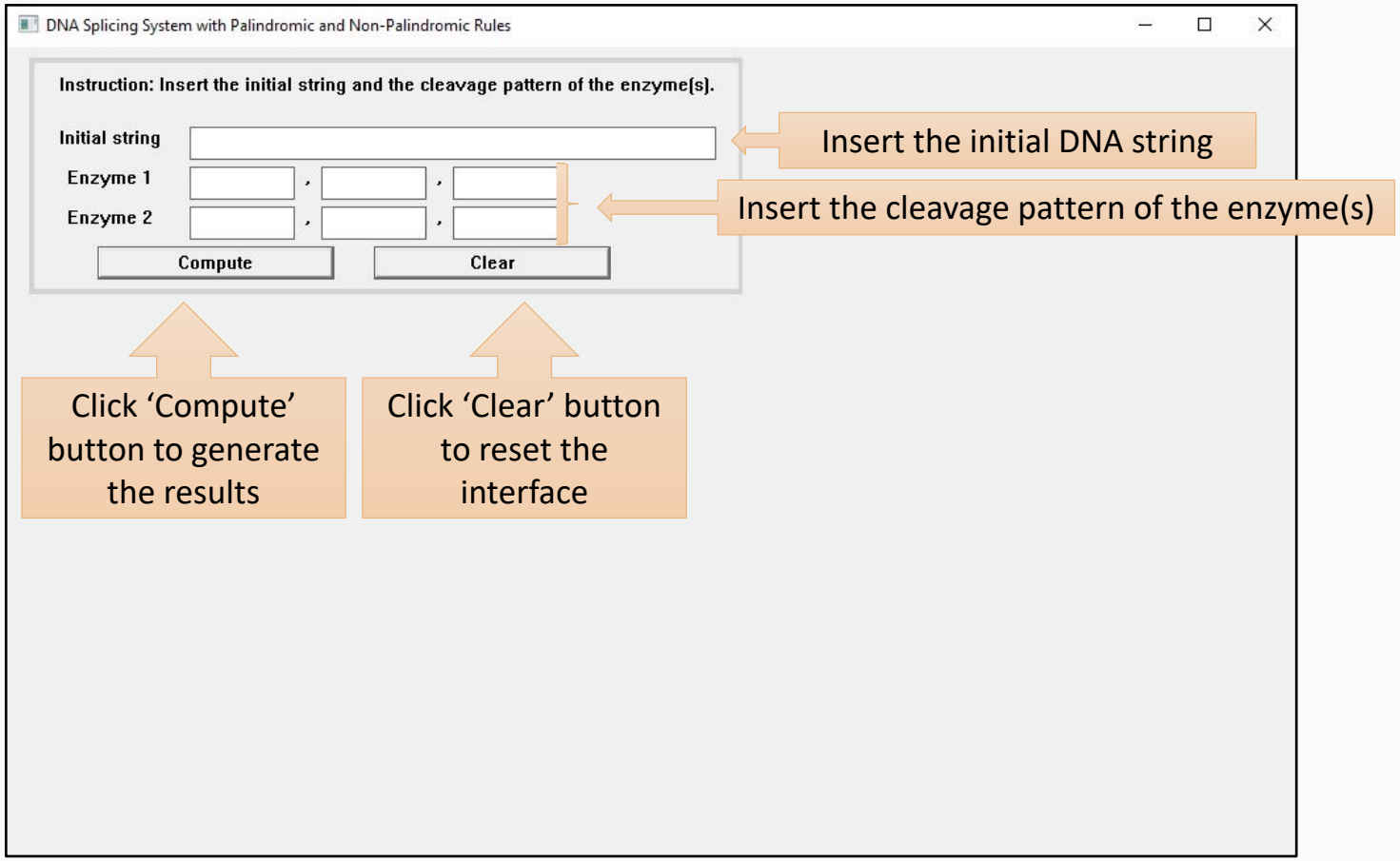




- Lane 1: LMW ladder
- Lane 2 (0 minute): 79 bp (or 81 bp) and 160 bp
- Lane 3 (30 minutes): 79 bp, 81 bp and 160 bp
- Lane 4 (60 minutes): 79 bp, 81 bp and 160 bp
- Lane 5 (2 hours): 79 bp, 81 bp and 160 bp

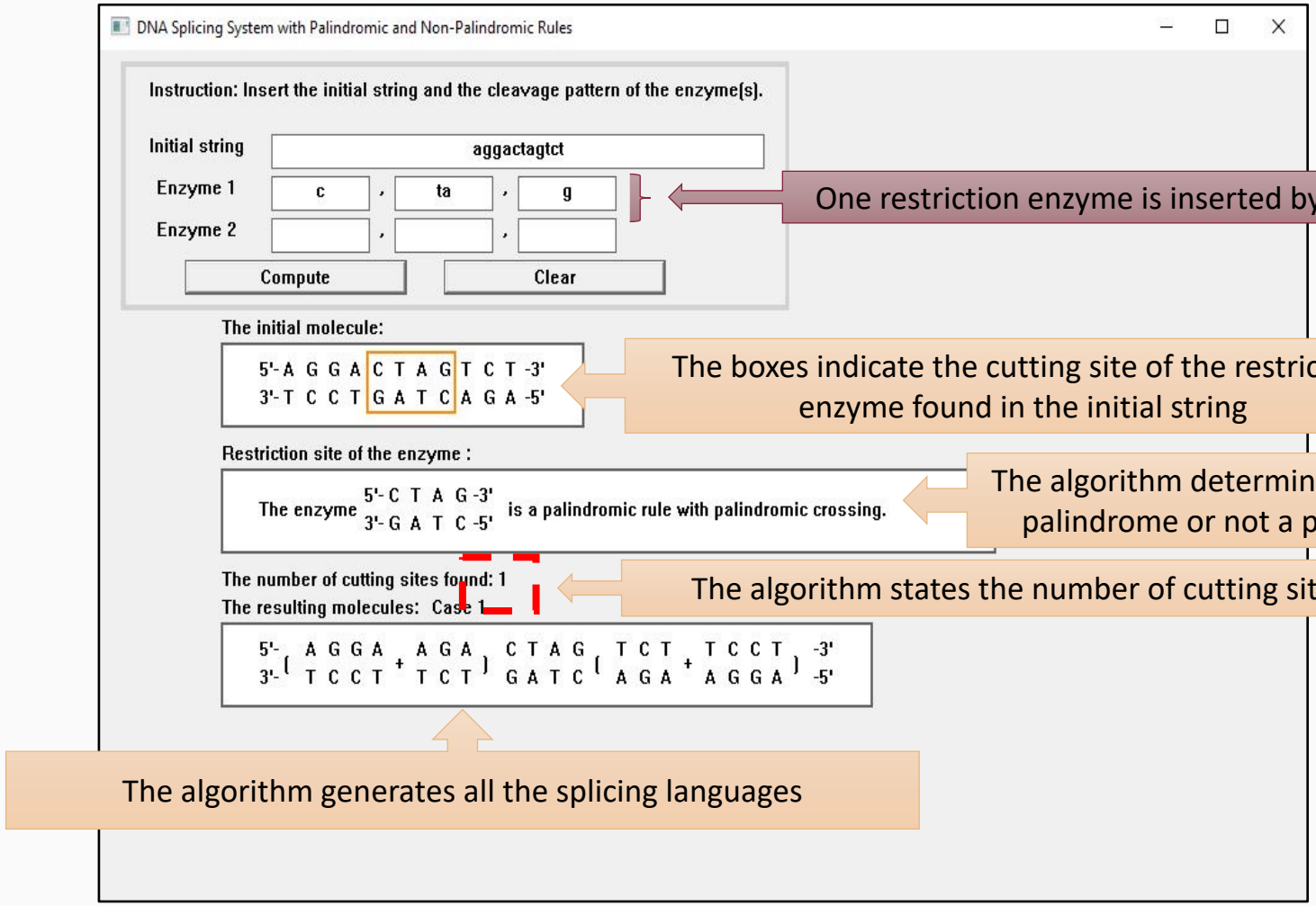
Programming Code

- A C++ program is created in **Microsoft Visual Studio** to **develop the GUI** for DNA splicing systems involving palindromic and non-palindromic rules.



Graphical User Interface (GUI)

Output of GUI for DNA Splicing System involving One Rule



One restriction enzyme is inserted by user

The boxes indicate the cutting site of the restriction enzyme found in the initial string

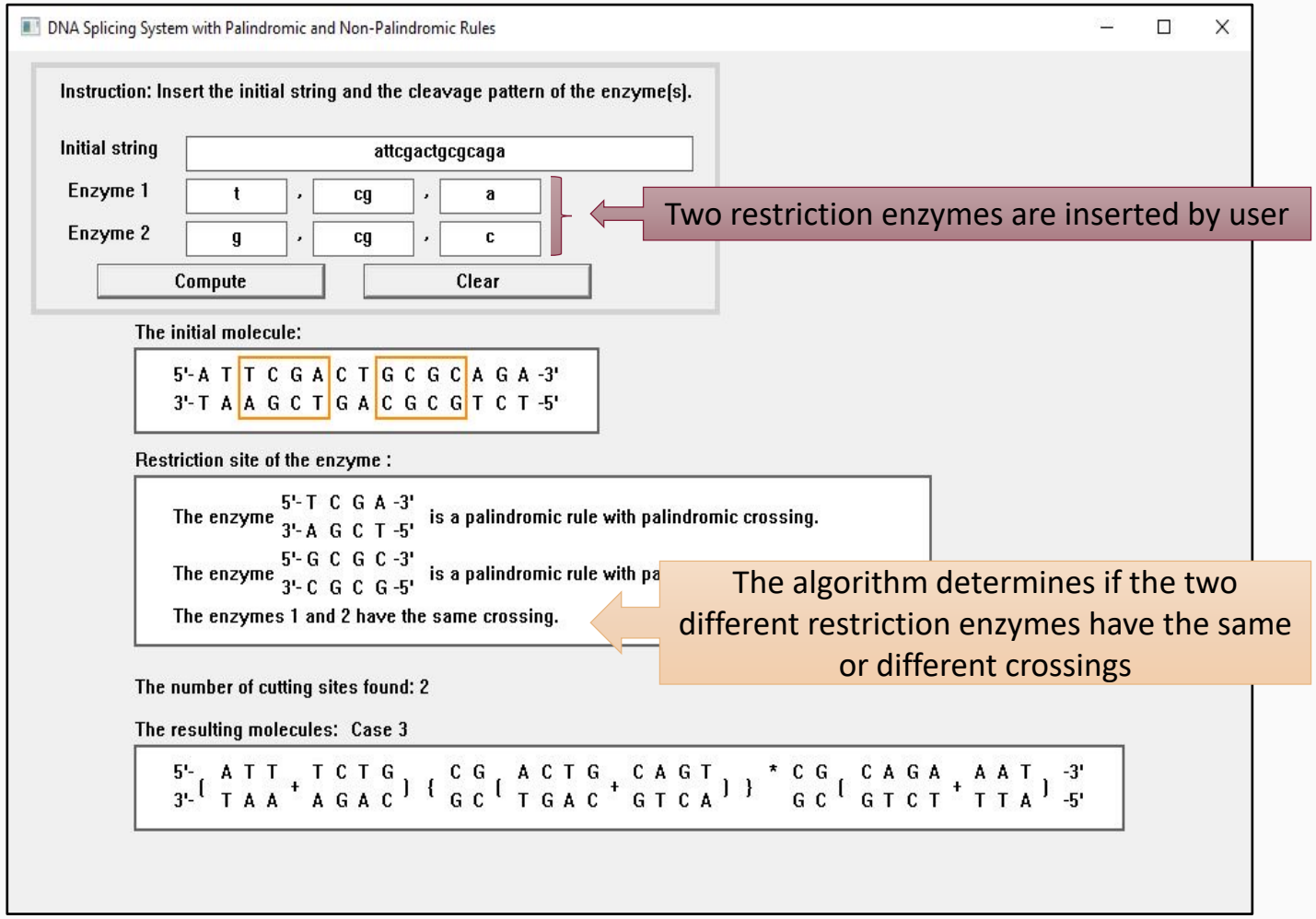
The algorithm determines if the restriction enzyme is a palindrome or not a palindrome including crossing

The algorithm states the number of cutting sites

The algorithm generates all the splicing languages

Graphical User Interface (GUI) (cont.)

Output of GUI for DNA Splicing System involving Two Rules



Additional features:

- Certain messages are displayed on the interface if the number of cutting sites found exceeds two
- The interface prompts the users if the cutting sites of restriction enzyme overlap
- The users will be notified if the inputs are incorrect.

Splicing System in Graph Theory

A graph

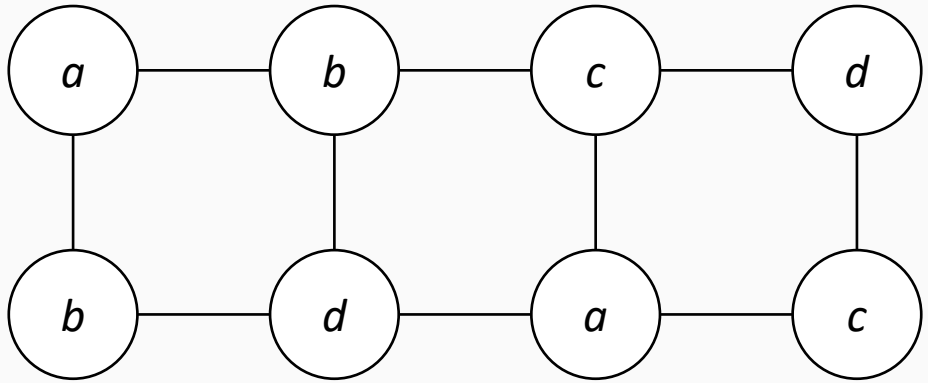
$G = (N, E, L)$

over

alphabet A

where

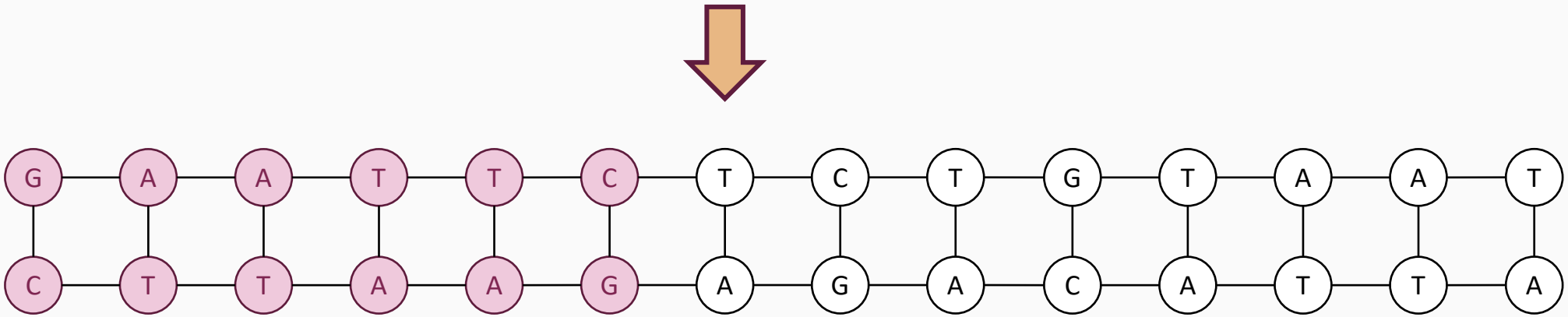
N : Nodes/Vertices
E : Edges
L : $N \rightarrow A$



$A = \{a, b, c, d\}$

Splicing System in Graph Theory (Cont.)

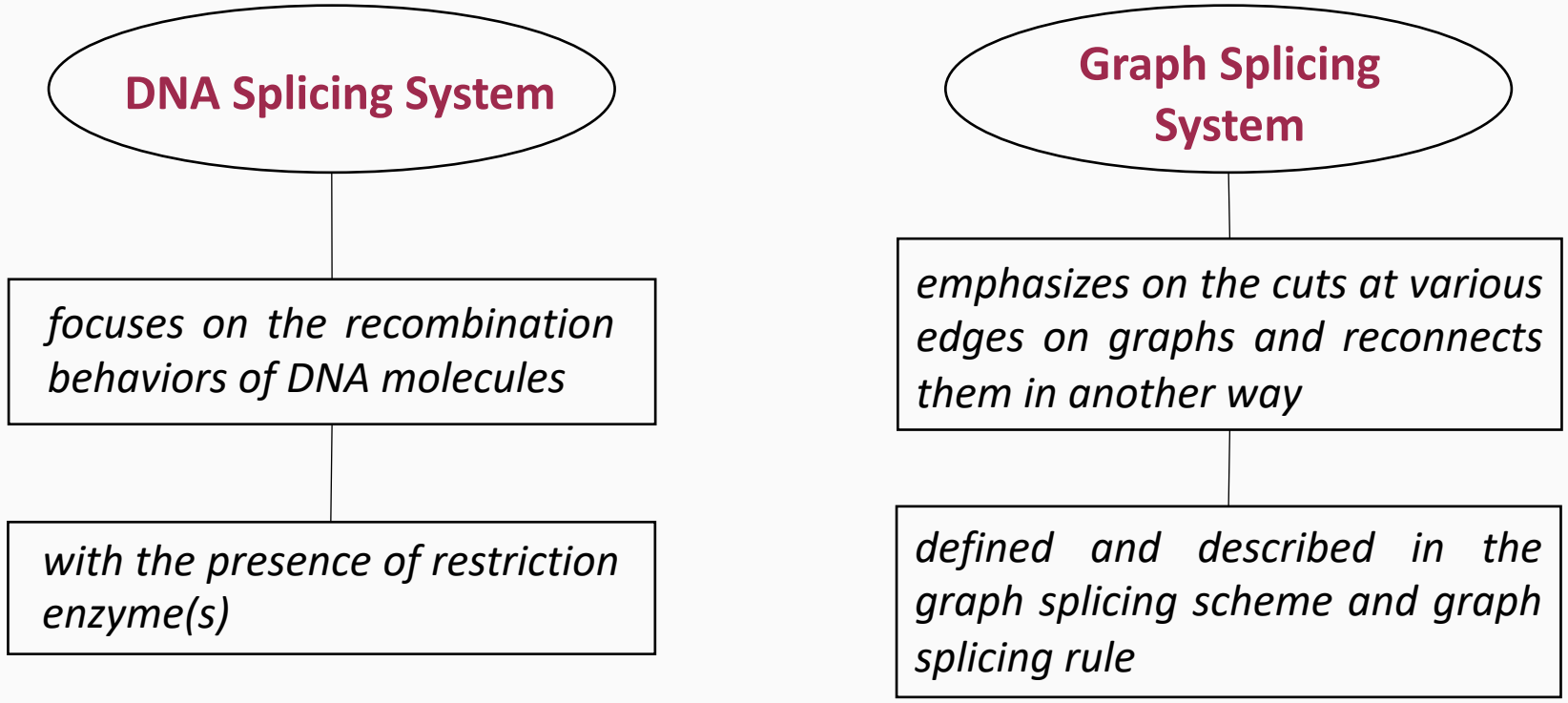
$5'$-GAATTCTCTGTAAT-$3'$
$3'$-CTTAAGAGACATTA-$5'$



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.

Graph Splicing System

Splicing Scheme

Splicing Rule

n-Cut Splicing

Graph Splicing Scheme

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

$$((h[1],E'[1]); (h[2],E'[2]), \ldots, (h[k];E'[k]);R)$$

such that $k \geq 1$ where $k \in \mathbb{N}$ and for all i with $1 \leq i \leq k$, where

- $h[i] = (N[i],E[i],L[i])$ weakly connected graph, where $E[i]$ is the edges of the ith graph splicing rule,
- $E'[i] \subseteq E[i]$, where $E'[i]$ is the cutting pattern for the ith 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 $\bigcup_{1 \leq i \leq k} E'[i]$,
iii. Every element from $\{(n,m], [n,m) \mid (n,m) \in \bigcup_{1 \leq i \leq k} E'[i]$ must appear exactly once in a pair of E.

Graph Splicing Scheme (Cont.)

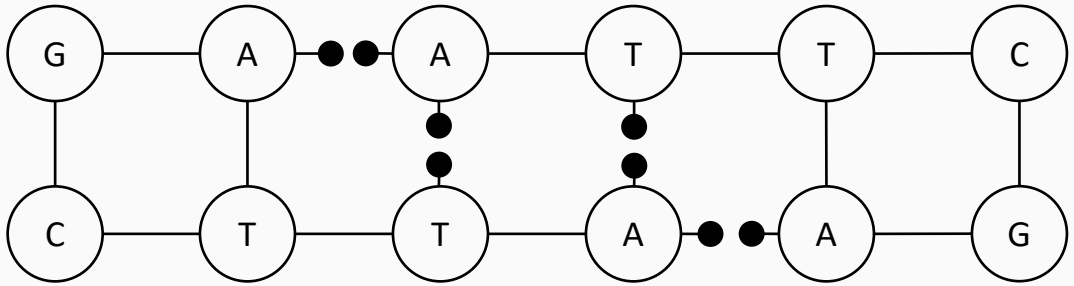
- Graph splicing scheme described the whole process of the graph splicing system where the graph splicing rule(s) is defined.

- Similar as enzymes in DNA splicing, splicing rules are used to control and restrict the edges to be cut on the initial graphs.

Cleavage pattern of restriction enzyme, *AclI*

$$\left\{\begin{matrix} AA\ CG\ TT \\ TT'\ GC'\ AA \end{matrix}\right\}$$

Graph representation of *AclI*



Graph Splicing Scheme (Cont.)

Consider the set of natural numbers denoted by $\mathbb{N} = \{0, 1, 2, \ldots\}$ 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 $\{m \in M \mid r(m) \neq 0\}$ 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

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

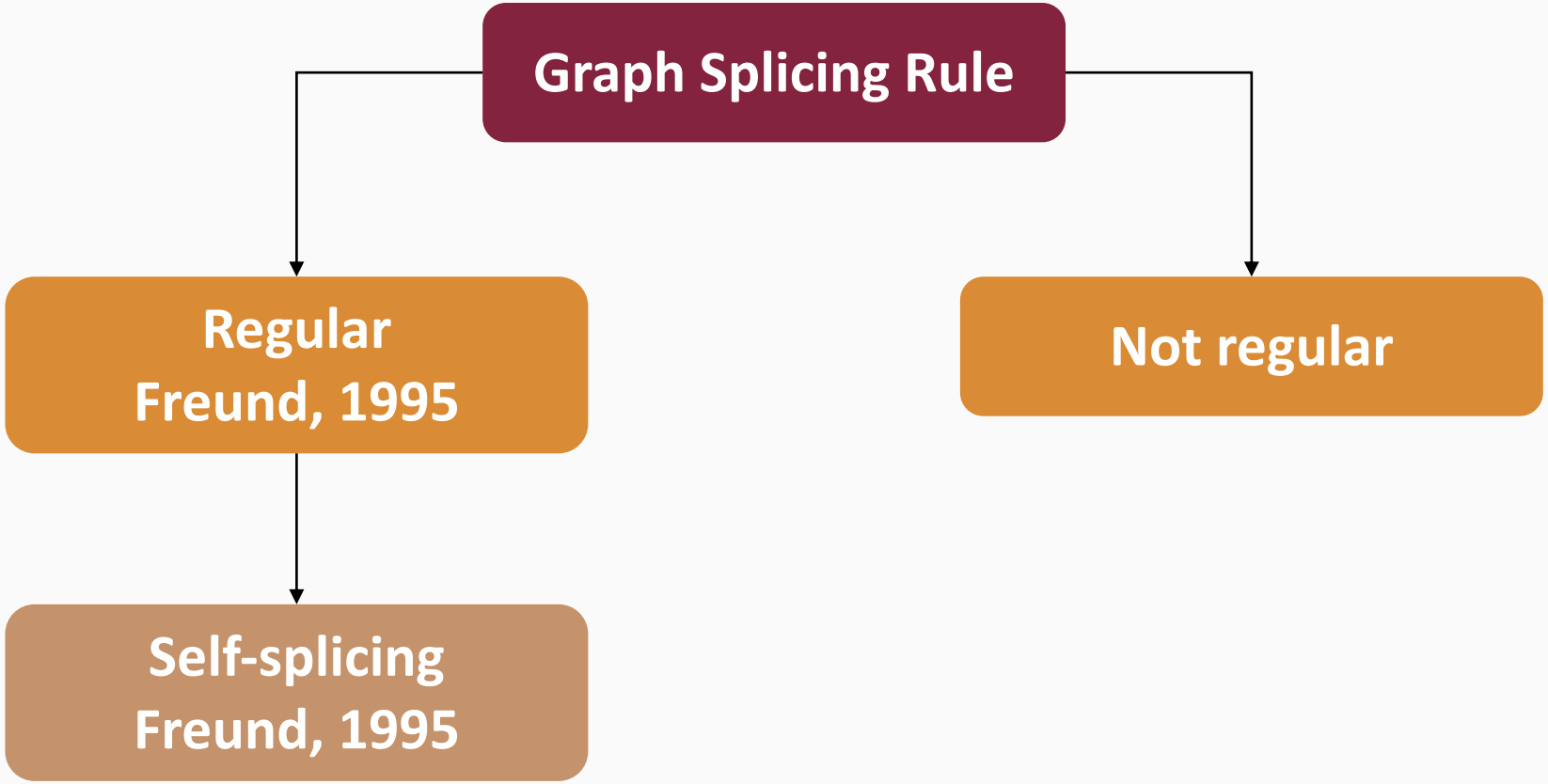
Graph Splicing Rule

Definition (Freund, 1995) Graph Splicing Rule

Let $p = ((h[1], E'[1]), \ldots, (h[k], E'[k]); R)$ 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 $g[1], \ldots, g[k]$ from r, in the sense that n copies of the graph $g \in \gamma_c(A)$ are n objects selected, provides that $r(g) \geq n$, 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 $1 \leq i \leq k$, $h[i]$ is a subgraph of $g[i]$, where $f[i]$ establishes the injective node embedding $h[i]$ into $g[i]$,
ii. the union of $g[i], \ldots, g[k]$ 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 $\bigcup_{1 \leq i \leq k} f(E'[i])$ 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 $g'[i], \ldots, g'[k]$,
iii. the new $\mathbb{N}_\infty$-subset s is obtained from r by successively decrementing $r(g[1]), \ldots, r(g[k])$ by one and incrementing $r(g'[1]), \ldots, r(g'[k])$ by one.

Graph Splicing Rule (Cont.)

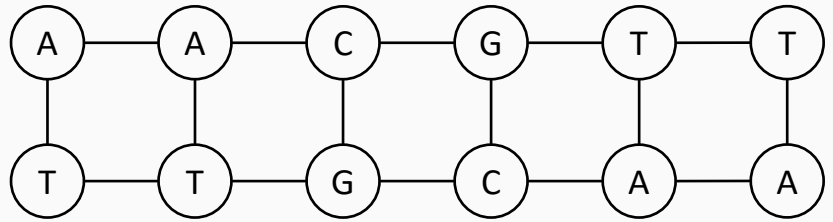


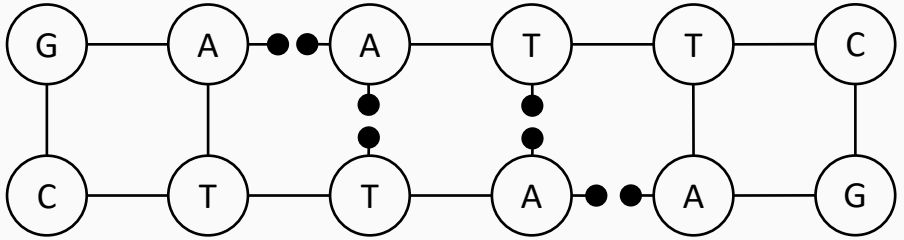
Graph Splicing Rule (Cont.)

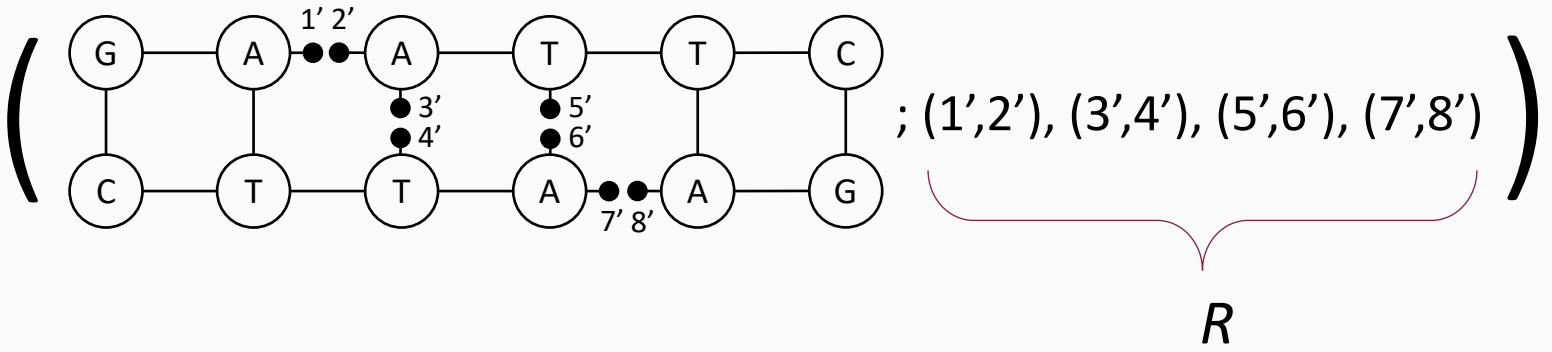
- A graph splicing rule consisting the enzyme *Acl*I can be written as follows.

$$p = ((h, E'); R)$$

*EcoR*I: $\begin{Bmatrix} \text{AA} & \text{CG} & \text{TT} \\ \text{TT'} & \text{GC'} & \text{AA} \end{Bmatrix}$

$h =$ 

$(h, E') =$ 

$p =$ 

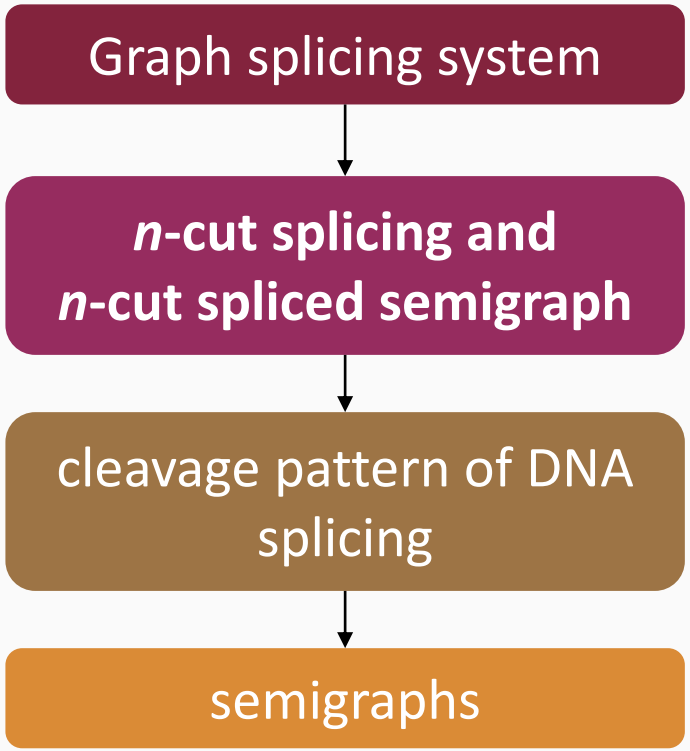
Graph Splicing System

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 $k \geq 0$ 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 $n \geq 2$, $\sigma^n(\{I\})$ 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.

n-Cut Splicing

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



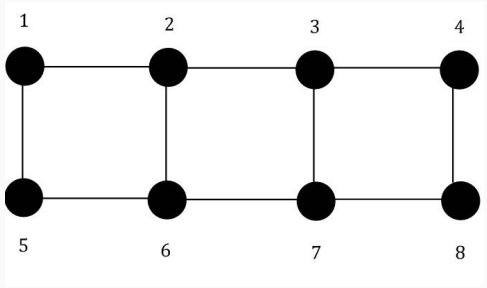
S. Jeyabharathi, J. Padmashree, S. S. Selvi, and K. Thiagarajan, *Semigraph structure on DNA splicing system*, in *6th Int. Conf. on Bio-Inspired Computing: Theories and Applications, BIC-TA* (IEEE Computer Society, Washington, DC, 2011), 182–187.

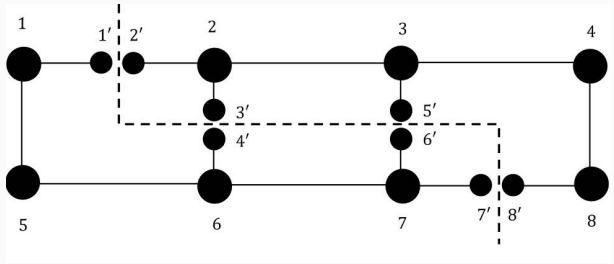
n-Cut Splicing (Cont.)

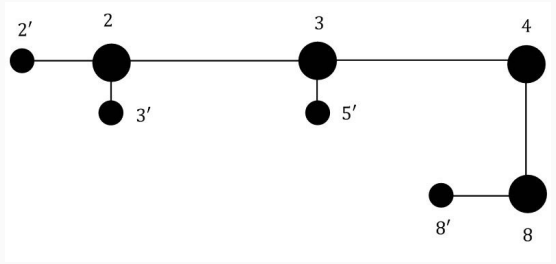
Semigraph representation of DNA molecule

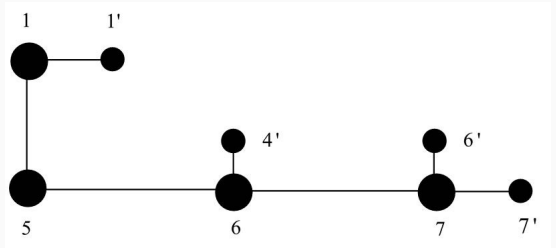
An *n*-cut splicing is applied

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



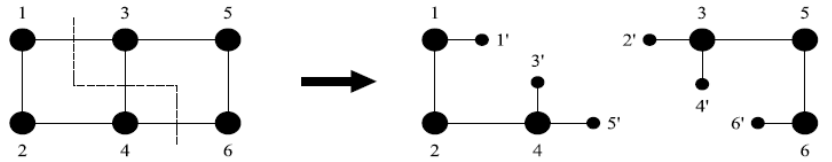
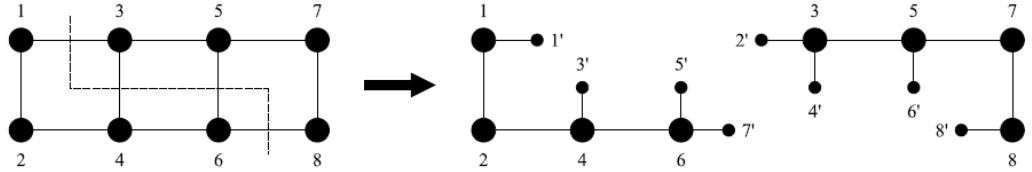
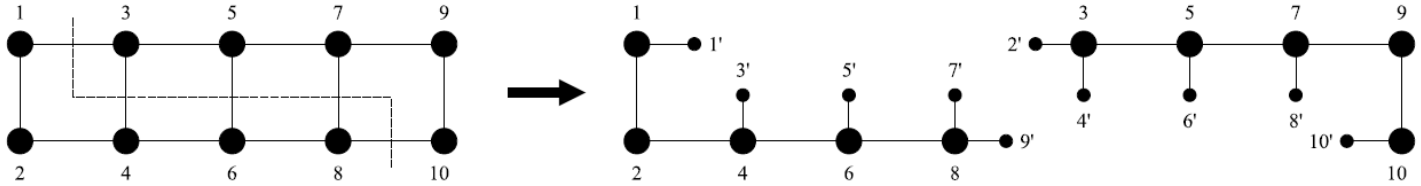






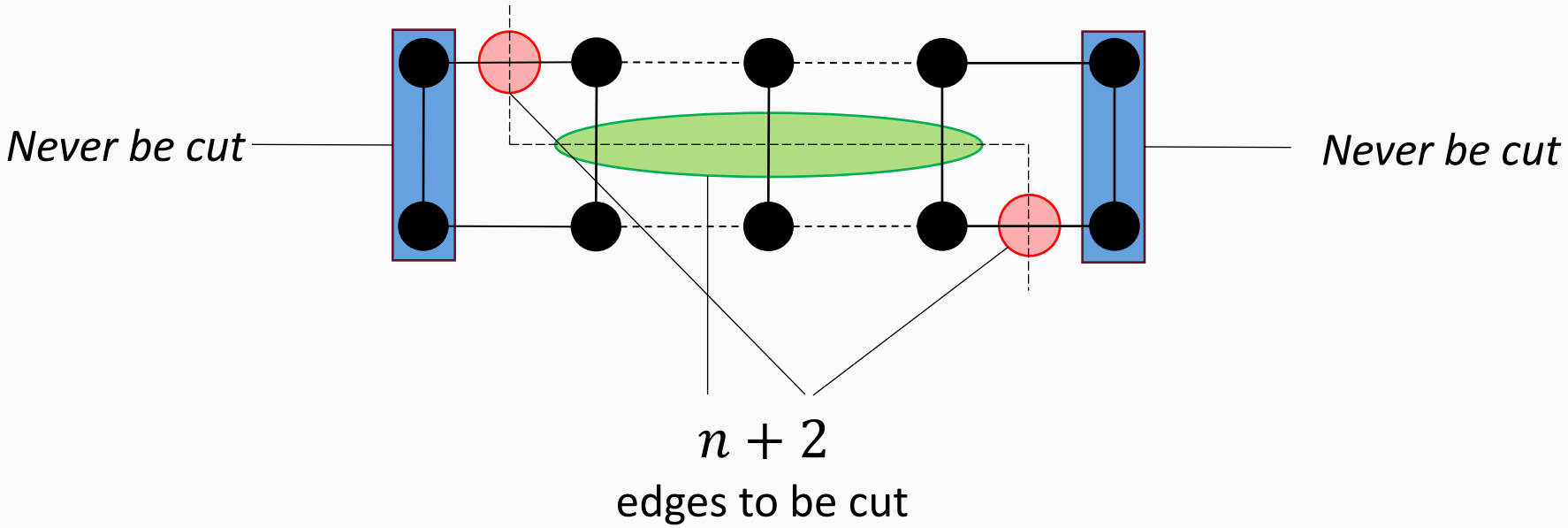
n-Cut Splicing (Cont.)

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

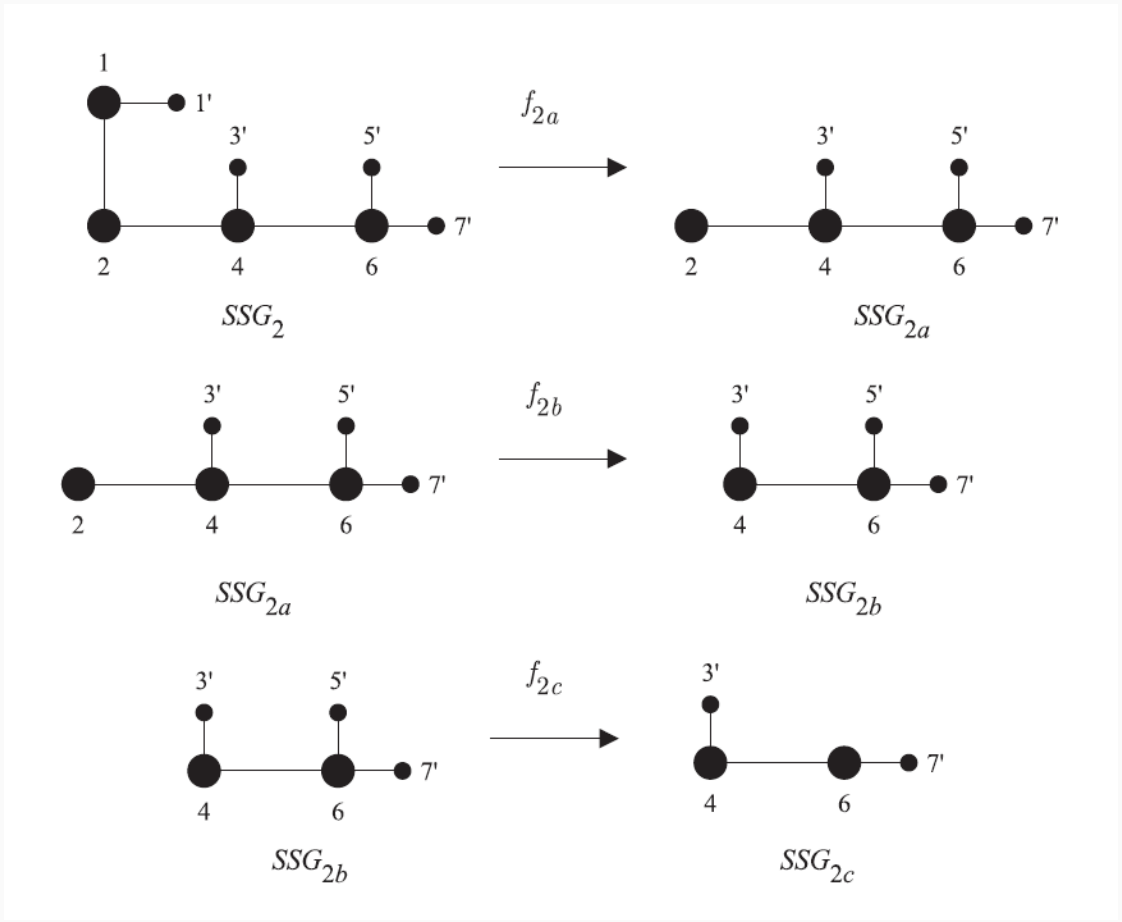
n	*n*-cut splicing
1	 1-cut splicing
2	 2-cut splicing
3	 3-cut splicing

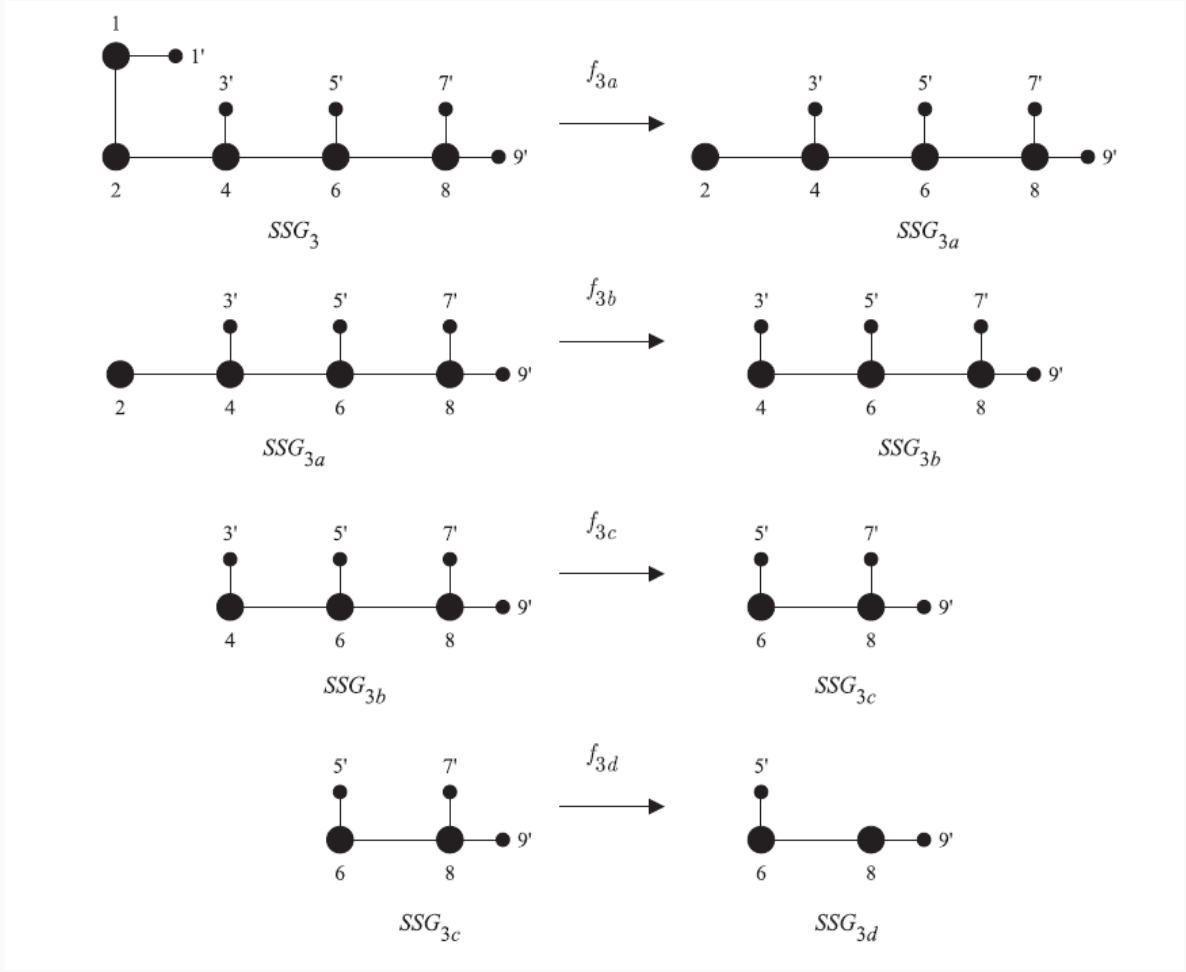
n-Cut Splicing (Cont.)

- 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.



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





Examples of *n*-cut spliced semigraphs folding

List of Publications

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

2010
Nor Haniza Sarmin, Yuhani Yusof and Fong Wan Heng, **Some Characterizations in Splicing Systems**, *International Conference on Mathematical Sciences (ICMS 2010)*, Abant Ỳzzet 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 6th 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 20th 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 20th 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 20th 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 *4th International Conference on Computational Collective Intelligence Technologies and Applications (ICCCI 2012)*, Ho Chi Minh city, Vietnam, 28-30 November 2012.

List of Publications (Cont.)

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

2014

Muhammad Azrin Ahmad, **Nor Haniza Sarmin,** Fong Wan Heng, Yuhani Yusof, **An Extension of First Order Limit Language,** *Proceedings of the 3rd 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 3rd 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 21st 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 22nd 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 22nd 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 23rd 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: https://people.utm.my/nizasarmin/

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 & 2021
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)

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THANK YOU

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Niza Sarmin

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In the Name of God for Mankind

w w w . u t m . m y

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Muhammad Nur Syiham
Abdul Razak