



**UTM**  
UNIVERSITI TEKNOLOGI MALAYSIA

**Kampus Merdeka**  
INDONESIA JAYA

# Guest LECTURE



**SPEAKER**

**PROFESSOR DR NOR HANIZA SARMIN**

**"Beyond the Double Helix: A Journey from DNA Recombination to Unravelling Its Computational Tapestry"**

**July, 16th 2024 at 13.00 WITA  
at Gedung Seminar Balingkang, Undiksha**



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# “Beyond the Double Helix: A Journey from DNA Recombination to Unravelling Its Computational Tapestry”

Guest Lecture

**Organized by**

Department of Mathematics and Natural Sciences,  
Universitas Pendidikan Ganesha,  
Bali, Indonesia

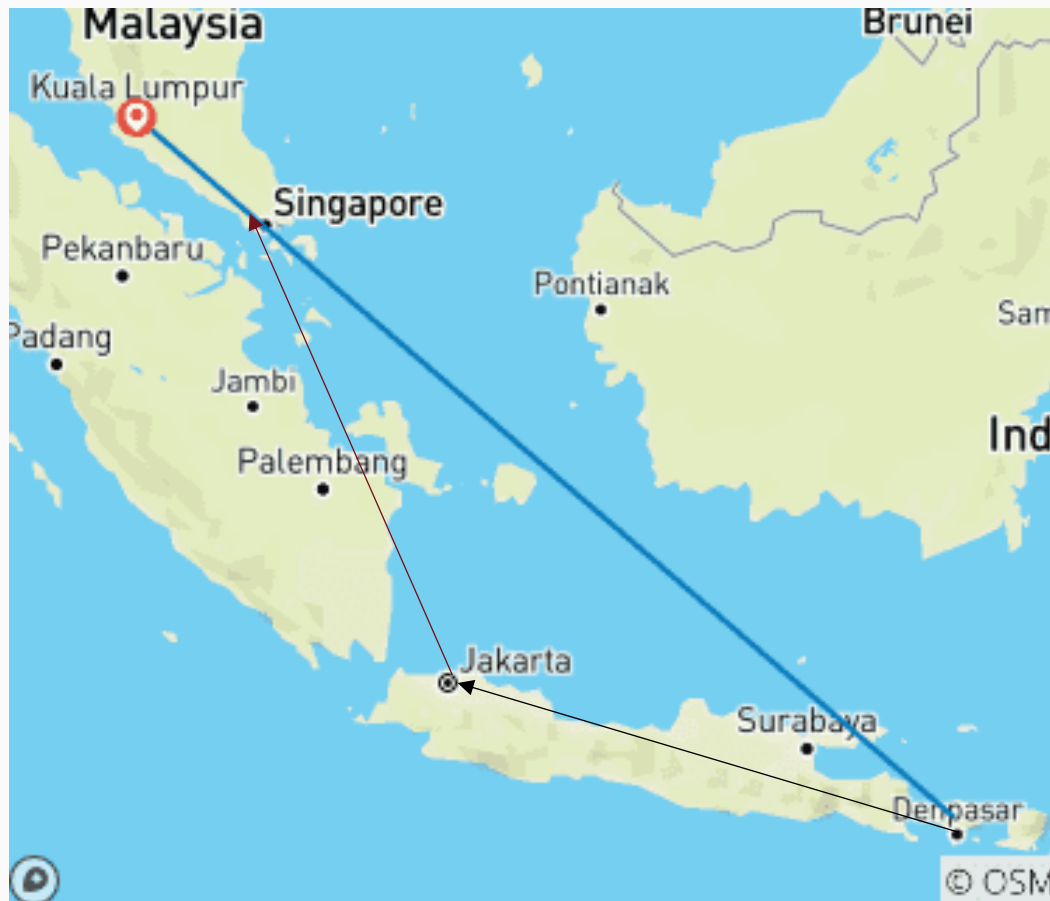
**16 July 2024**



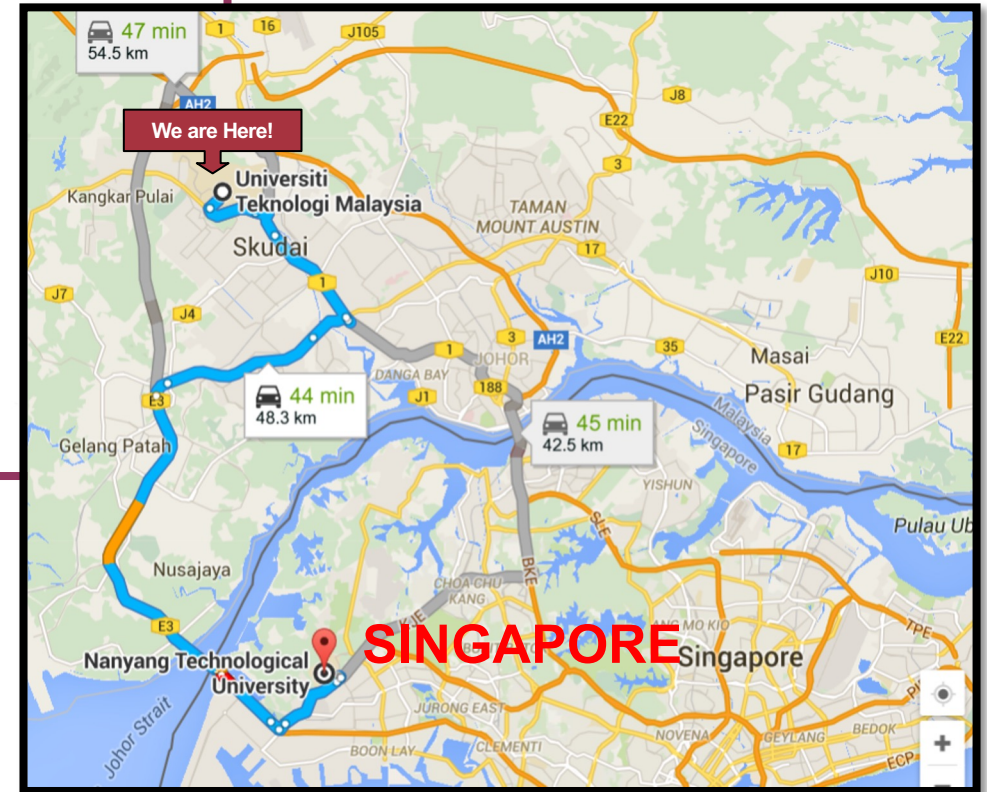
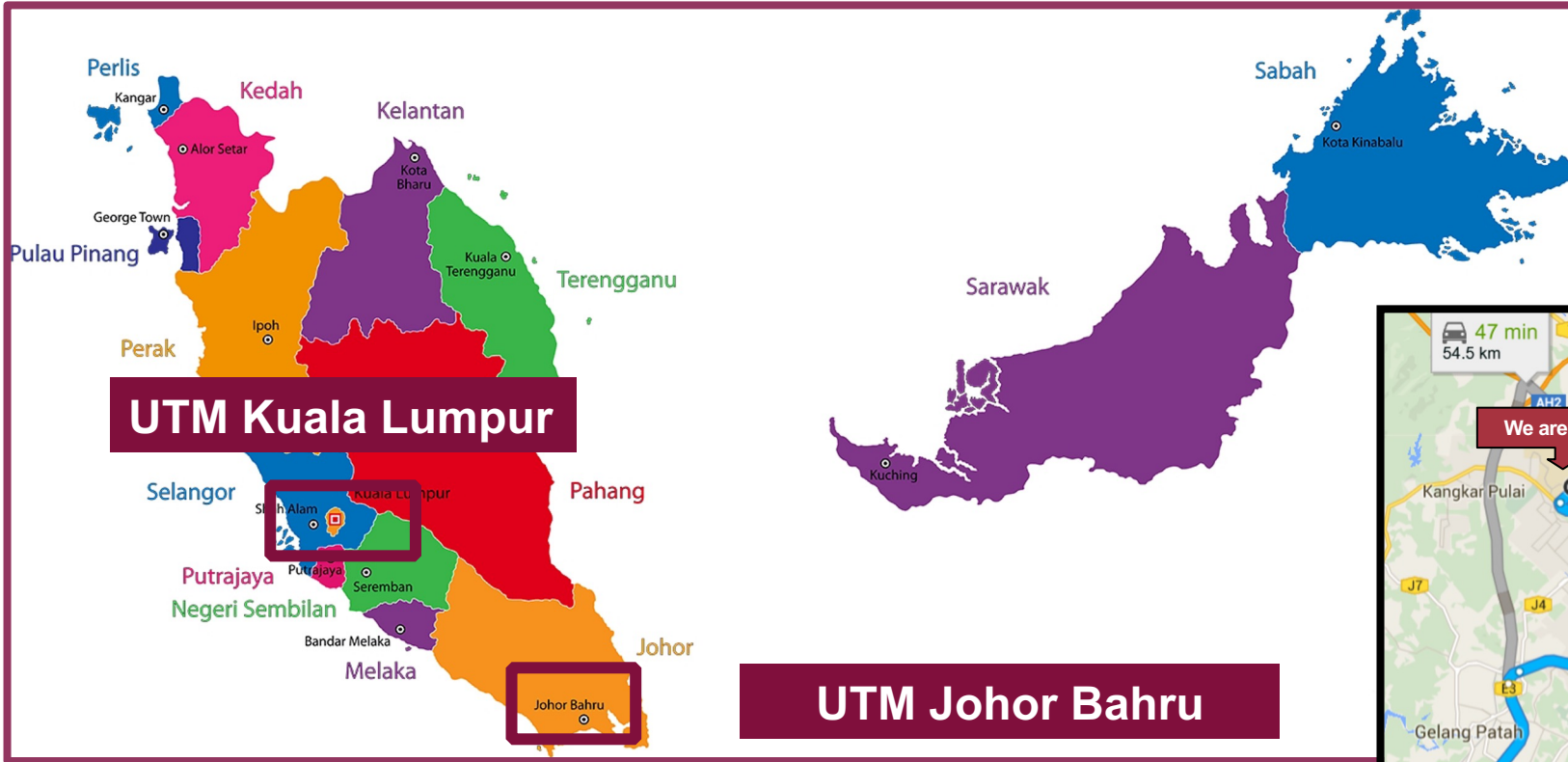
**PROF DR NOR HANIZA SARMIN**

Department of Mathematical Sciences,  
Faculty of Science, Universiti Teknologi Malaysia  
[nhs@utm.my](mailto:nhs@utm.my)

# From Bali to Malaysia



- The distance between Bali and Malaysia is estimated at 1,972.47 km or 1,225.64 miles.
- A typical flight would have an average flying time of about 3 hours.



12

Faculties

# Faculties in UTM

**Civil Engineering**

- Structure Materials
- Geotechnics and Transportation
- Water and Environmental Engineering

Civil & Structural  
TOP 100 & #1 in MAS

**Mechanical Engineering**

- Applied Mechanics & Design
- Thermo Fluids
- Aeronautics, Automotive & Ocean Engineering
- #2 in MAS Materials, Manufacturing & Industrial Engineering

Mechanical, Aeronautical & Manufacturing  
TOP 200

**Chemical & Energy Engineering**

- #2 in MAS Chemical Engineering
- Bioprocess & Polymer
- #2 in MAS Petroleum Engineering
- Energy Engineering

Chemical & Petroleum Engineering  
TOP 100

**Electrical Engineering**

- Communication Engineering
- Electronic and Computing Engineering
- Electrical Power Engineering
- Control and Mechatronics Engineering

Electrical and Electronics  
TOP 100

**Computing**

- Computer Science
- Applied Computing
- Software Engineering

Computer Science  
TOP 200

**Built Environment & Surveying**

- Architecture
- Quantity Surveying
- Urban and Regional Planning
- Landscape Architecture
- Geoinformation
- Real Estate

Architecture/  
Built Environment  
TOP 100 & #1 in MAS

**Management**

- Management
- Accounting
- Marketing
- Technology Management
- Information Technology
- Information Systems

**Science**

- #2 in MAS Physics
- Biosciences
- #3 in MAS Chemistry
- #2 in MAS Mathematical Sciences

Mathematics & Environmental Sciences  
TOP 200

**Social Sciences & Humanities**

- School of Education
- School of Human Resource Development & Psychology
- Academy of Islamic Civilisation
- Language Academy
- Centre for Advanced Studies on Islam, Science, and Civilisation
- FSSH KL

Education  
TOP 200

**Faculty of Artificial Intelligence**

- Intelligence Informatics
- Smart Engineering and Advanced Technology
- Business Intelligence, Humanities and Governance
- Creative Artificial Intelligence

**Azman Hashim International Business School**

- Business Administration
- Accounting and Finance
- Information System

Accounting & Finance  
TOP 250 & #7 in MAS

**Malaysia-Japan International Institute of Technology**

- Electronic System Engineering
- Mechanical Precision Engineering
- Chemical and Environmental Engineering
- Management of Technology
- Software Engineering

**54**

**ACADEMIC STAFF**

**456**

**UG STUDENTS**

**195**

**PG STUDENTS**

**8**

**RESEARCH CENTRE &  
GROUPS**

## POSTGRADUATE PROGRAMMES

We offer Masters and Doctoral Programmes in Mathematics.

## UNDERGRADUATE PROGRAMS

Bachelor of Science  
(Mathematics) with Honours

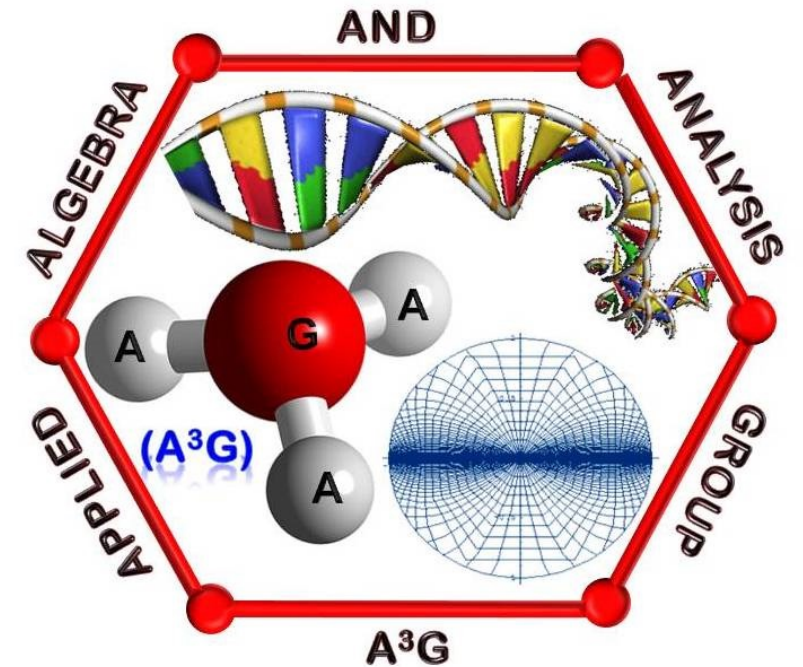
Bachelor of Science (Industrial  
Mathematics) with Honours

The department is divided into 5 broad research areas/**academic panels**:

1. Algebra & Analysis
2. Applied Mathematics
3. Numerical & Computational
4. Operations Research
5. Statistics

**Members** belong to specific **research groups** focused on diverse studies.

**Joined Department of Mathematics,  
Faculty of Science, UTM on  
2 May 1991**



# MY BACKGROUND



State University of New York at Binghamton  
(now known as Binghamton University), New York, USA

1986 – 1989

**B.Sc (Hons) Mathematics**  
(Minor in Economics)

1989 – 1990

**MA Mathematics**

1995 – 1998

**PhD Mathematics**



# “Beyond the Double Helix: A Journey from DNA Recombination to Unravelling Its Computational Tapestry”

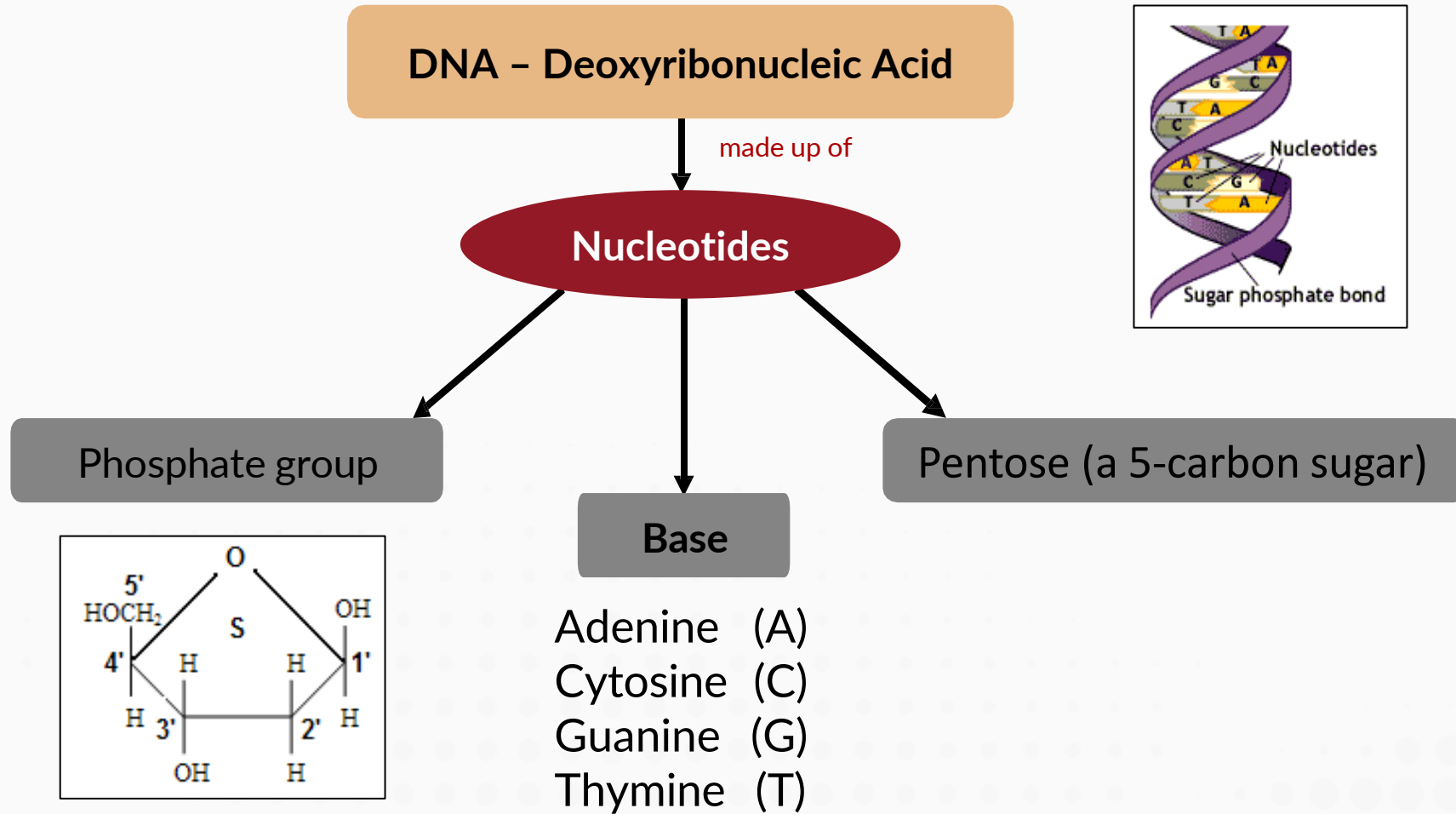
## Abstract

The groundbreaking work of the DNA splicing system introduced by Head in 1987 simulates the process of **cutting and pasting of DNA molecules** using **restriction enzymes** and **ligases**. By formal language theory, a relationship between splicing systems and molecular biology is explored. In this presentation, the mutual connections between **formal language theory**, **biomolecular science**, and the design of automated enzymatic processes and implementation within splicing systems, revealing their deterministic **finite automaton** structure will be shared. Additionally, **experimental validation** techniques are done, ensuring the theoretical results align with real-world observations.

# DNA Structure

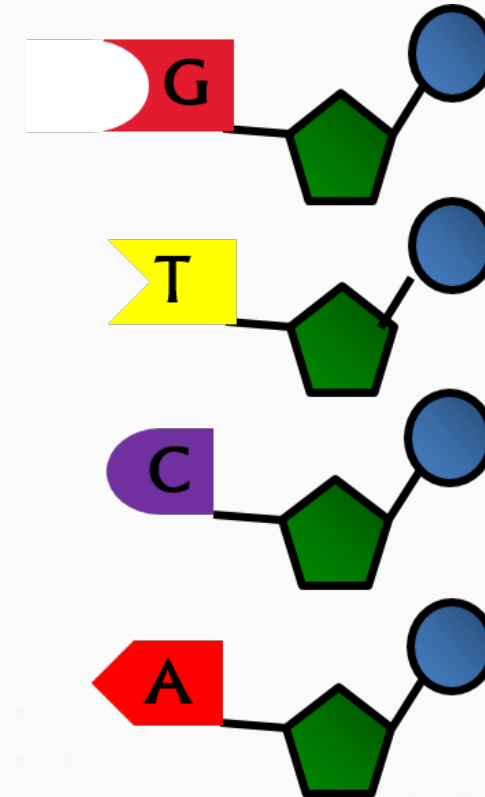
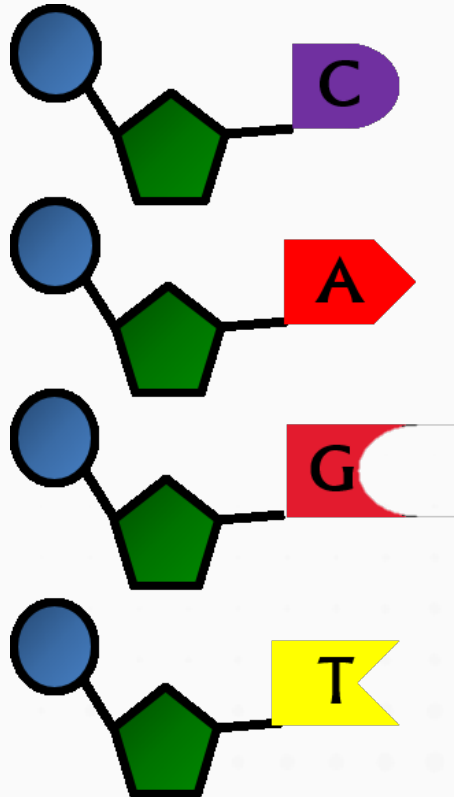


# Structure of DNA

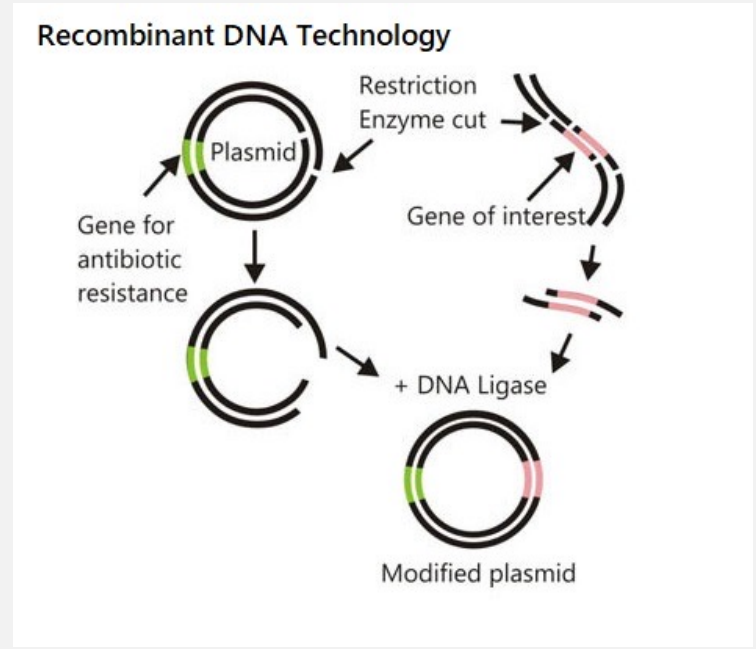


# Structure of DNA (Cont.)

## Watson-Crick Complementary



# Recombinant DNA



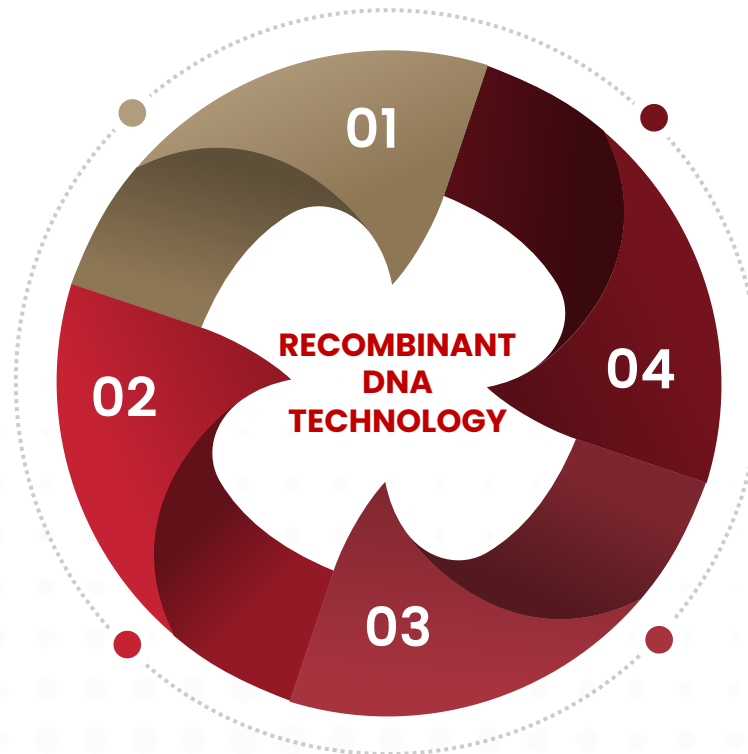
# VARIOUS APPLICATIONS OF RECOMBINANT DNA TECHNOLOGY

## 2. THERAPEUTIC PRODUCTS

- Vaccines
- Growth hormones
- Antibodies
- Anticancer drugs
- Recombinant protein

## 3. DIAGNOSIS

- Gene therapy
- Monitoring device
- Therapeutic strategies
- CRISPR



## 1. GENETICALLY MODIFIED PRODUCTS

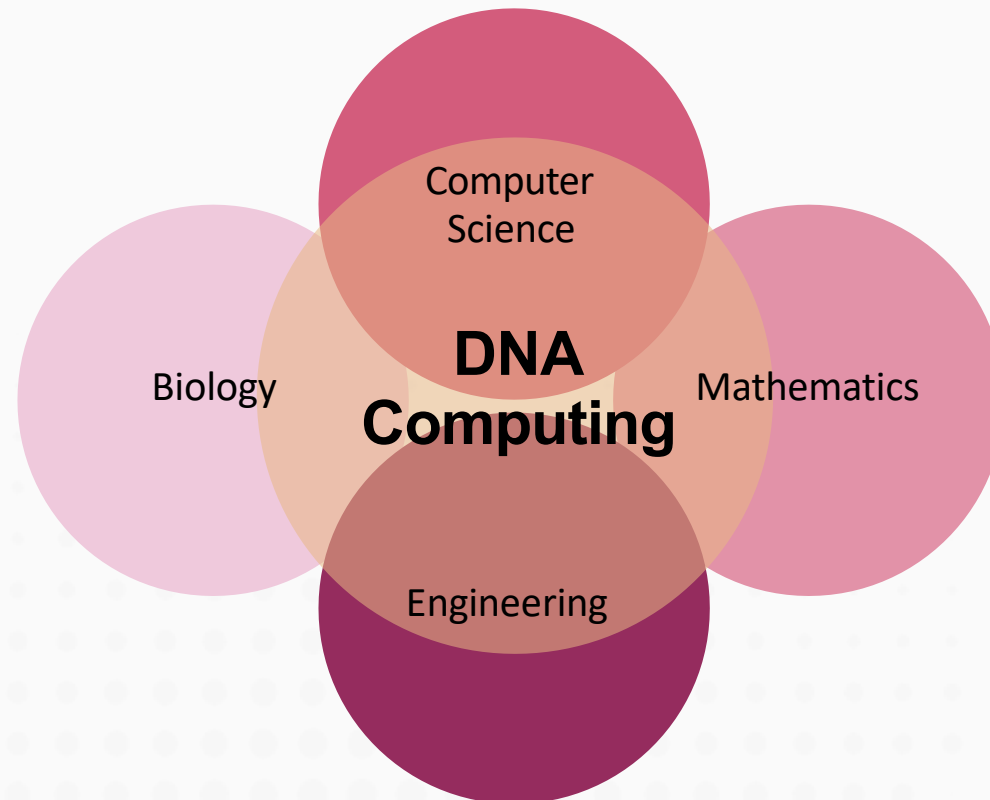
- Fruits
- Vegetables
- Crops
- Microbs
- Animals

## 4. ENERGY APPLICATIONS

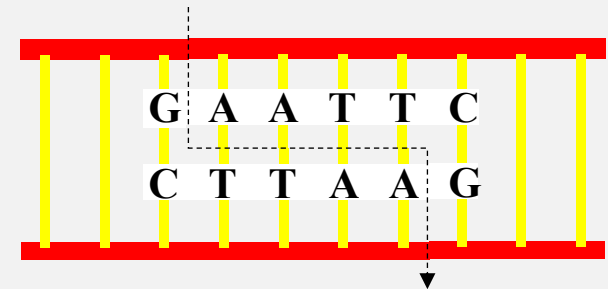
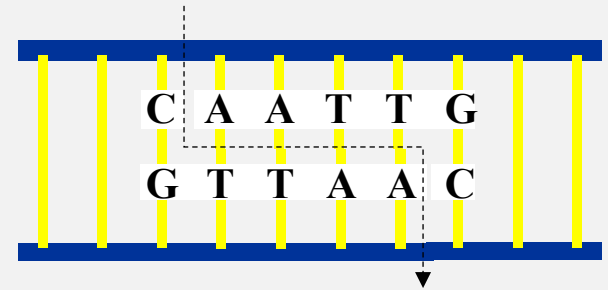
- Biohydrogen
- Bioethanol
- Biomethanol
- Biobutanol

# 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 Splicing System



...



# Mathematics and DNA Splicing System



- The mathematical modelling of splicing system was first defined by **Tom Head** in 1987.
- It was introduced as a **mathematical model** of the generative capacity of a **biological system** containing **DNA molecules** in the presence of appropriate **enzymes**.



## **Prof Head's visit to UTM, 2004**

# Mathematical Modelling of DNA Splicing System

## How do we model it?

Mathematics and Formal Language

DNA in Mathematical Model

Alphabets

*h, n, i, z, a, s, m, r, o*

Strings

*nor & haniza & sarmin*

Grammar

*Nor + Haniza  
Haniza + Sarmin*

Language

*Nor Haniza  
Haniza Sarmin*

DNA bases

*a, c, g, t*

DNA Sequence

*acgttgat & gcgttga*

DNA Splicing

*acgt- -tgat & gcgt- -tga*

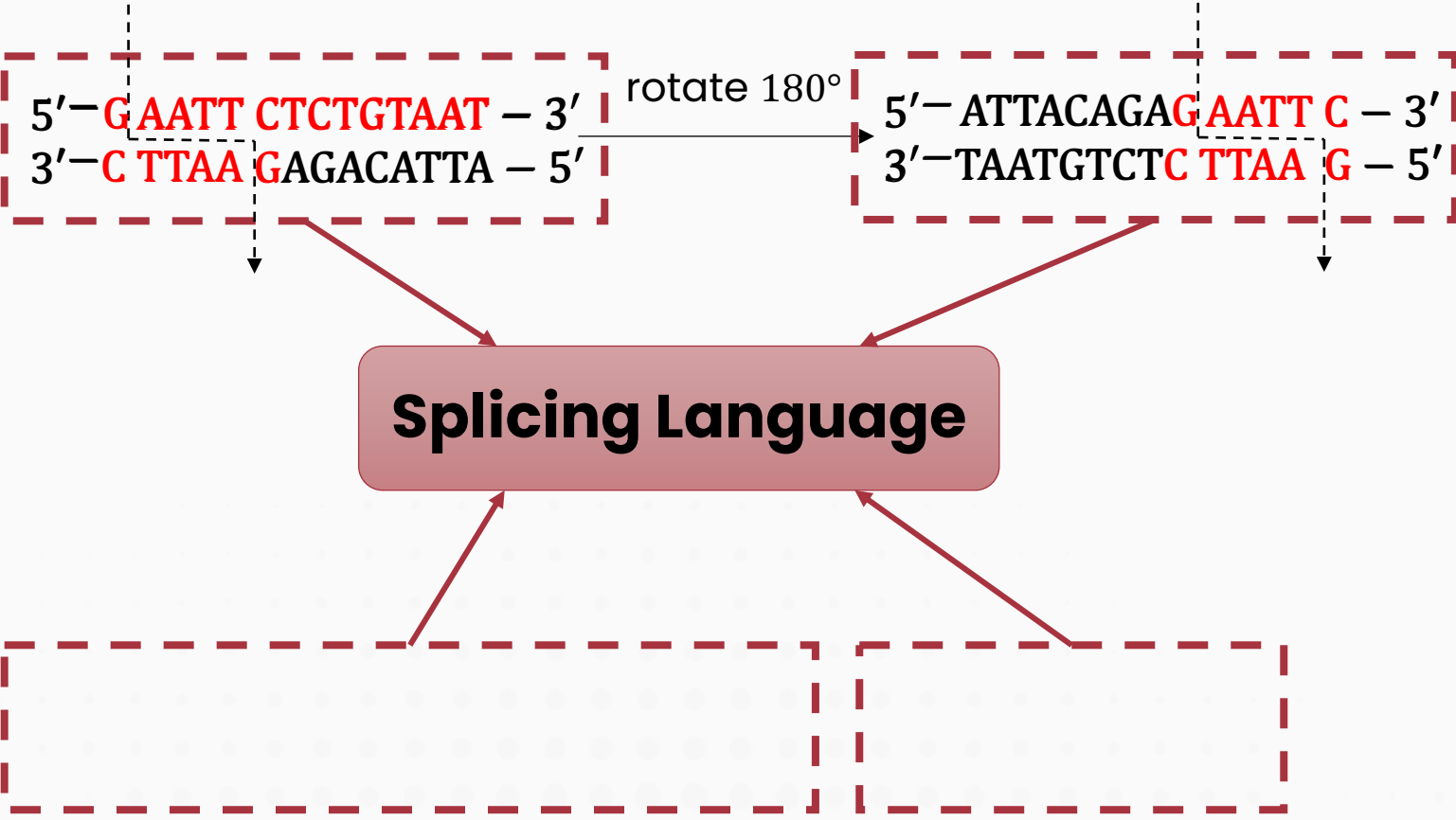
Grammar

Watson-Crick

Language

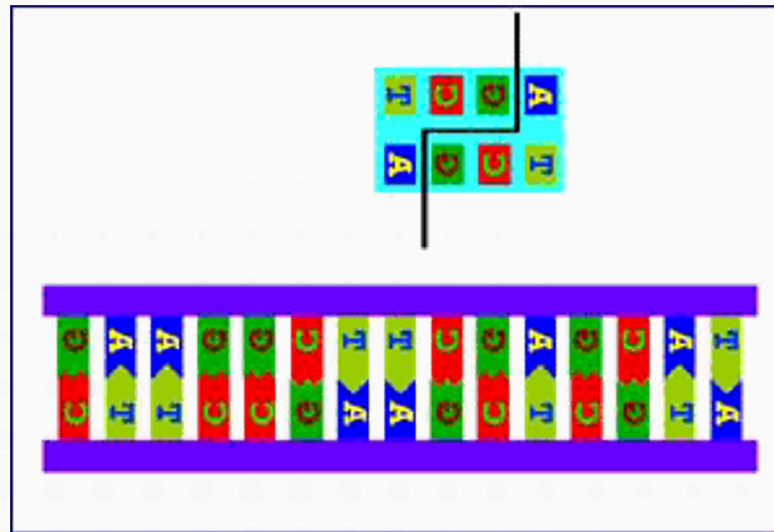
*acgttga & gcgttgat*

# Mathematical Modelling of DNA Splicing System (Cont.)



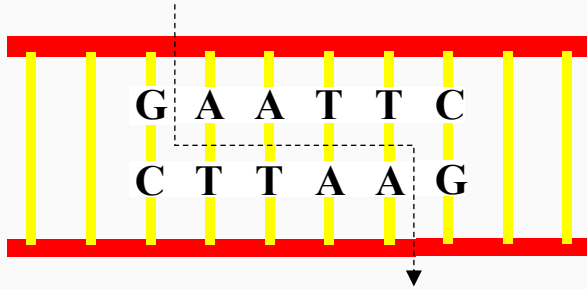
# Restriction Enzymes

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

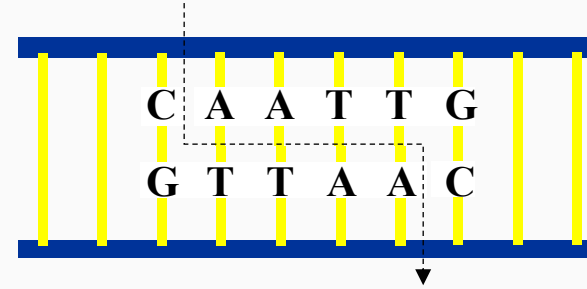


# Restriction Enzymes (Cont.)

*EcoRI*: ([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])



# Types of DNA Splicing Systems



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](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](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.

# Types of DNA Splicing Systems (Cont.)

Splicing System	Head $S = (A, I, B, C)$	Paun $\sigma = (A, R)$	Pixton $\zeta = (R, I)$	Goode-Pixton $(w, w') \vdash_r z$	Yusof-Goode $S = (A, I, R)$	Fuzzy $S = (A, T, I, R, \odot)$
Initial String	$ucxdv$ $pexfq$	$u u_1 u_2 v$ $u' u_3 u_4 v'$	$\xi \alpha \eta$ $\xi' \alpha' \eta'$	$w = x u v y$ $w' = x' u' v' y'$	$\alpha u x v \beta$ $\gamma y z \delta$	$(ua, x)$ $(bv, y)$ $x, y \in [0, 1]$
Rule	$(c, x, d)$ $(e, x, f)$	$u_1 \# u_2 \$ u_3 \# u_4$	$(\alpha, \alpha' : \beta)$	$r = (u, v; u'; v')$	$(u, x, v : y, x, z)$	$u \# a \$ b \# v$
Splicing Language	$ucxfq$ $pexdv$	$u u_1 u_4 v'$	$\xi \beta \eta'$	$z = x u v' y'$	$\alpha u x z \delta$ $\gamma y x v \beta$	$(uv, x \odot y)$ $\odot$ 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

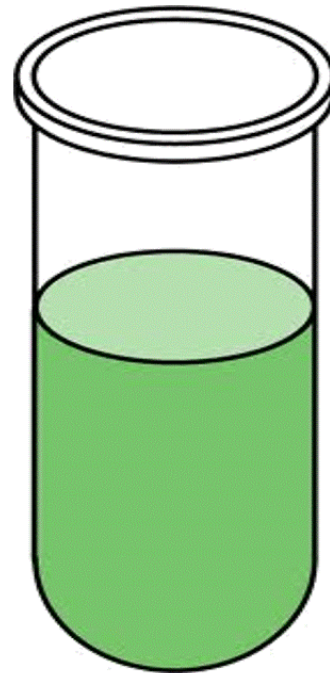


# Theoretical vs Wet Lab



# Wet Experiment on Splicing System

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



# Theoretical vs Lab Results

## Wet Splicing System involving *Cvi*QI and *Acil*

- An initial DNA molecule  $I$  used in this splicing model is a small segment taken from bacteriophage lambda between 42958 and 43117 with the length of 160 base pairs (bp).
- The initial molecule contains one cutting site each of the restriction enzymes *Cvi*QI and *Acil* where the genome locations for the cutting sites are found at 42992-42995 and 43036-43039 respectively.
- Five sticky ends of molecules  $\alpha$ ,  $\beta$ ,  $\gamma$ ,  $\alpha - \beta$  and  $\beta - \gamma$  are produced by the restriction enzymes when cutting the initial molecule. The lengths of fragments for the sticky ends are given in the following.

Fragment:  $\alpha$  *Cvi*QI site  $\beta$  *Acil* site  $\gamma$

$$|\alpha| = 35 \text{ bp}$$

$$|\beta| = 44 \text{ bp}$$

$$|\gamma| = 81 \text{ bp}$$

$$|\alpha - \beta| = 79 \text{ bp}$$

$$|\beta - \gamma| = 125 \text{ bp}$$

# Theoretical vs Lab Results (Cont.)

## Wet Splicing System involving *Cvi*QI and *Acil*

- Initial Molecule ( 42958 and 43117 from bacteriophage lambda)

*ggactatcgaagagtgcaaggcgatcaaggcagagtaccaacagaaactcaaagacctgcgaaatagcagaa  
gtgaggccgcatgacgttctcagtaaaaaccattccagacatgctcgttgaaacatacggaaatcagacagaagt  
agcacgcagactg* (160 bp)

- Enzyme *Cvi*QI (palindromic)

5'...G▼TAC...3'

3'...CAT▲G...5'

- Enzyme *Acil* (non-palindromic)

5'...C▼CGC...3'

3'...CGC▲C...5'

# Theoretical vs Lab Results (Cont.)

## Wet Splicing System involving CviQI and Acil

The splicing language from this splicing system  $S$  involving **one cutting site** each of **palindromic** restriction enzyme CviQI ( $g, ta, c$ ) and **non-palindromic** restriction enzyme Acil ( $c, cg, c$ ) with different palindromic crossings is shown in the following:

$$L(S) = \{\alpha \underline{gtac} (\beta \underline{ccgg} \beta' \underline{gtac})^{n-1} (\alpha' + \beta \underline{ccgc} \gamma)\} \\ + \{\gamma' \underline{gcg} (g \beta' \underline{gtac} \beta \underline{ccg})^{n-1} (c \gamma + g \beta' \underline{gtac} \alpha')\}.$$

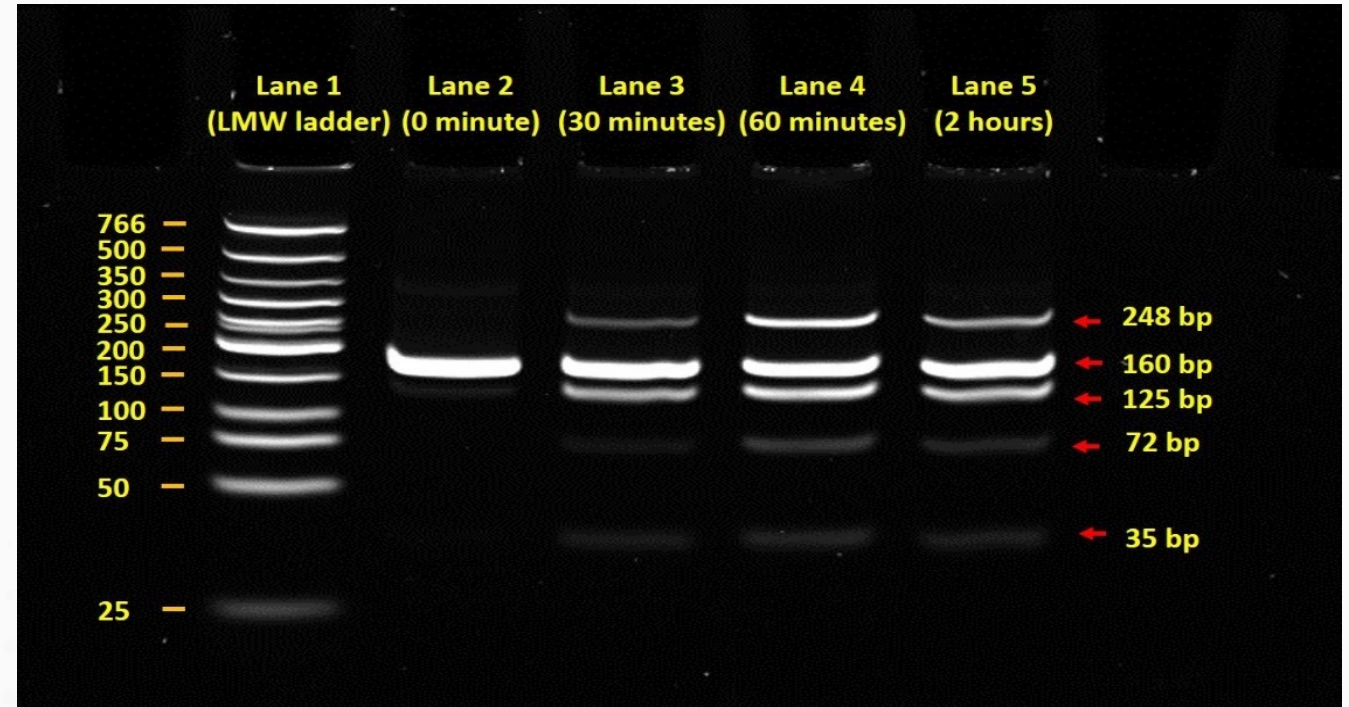
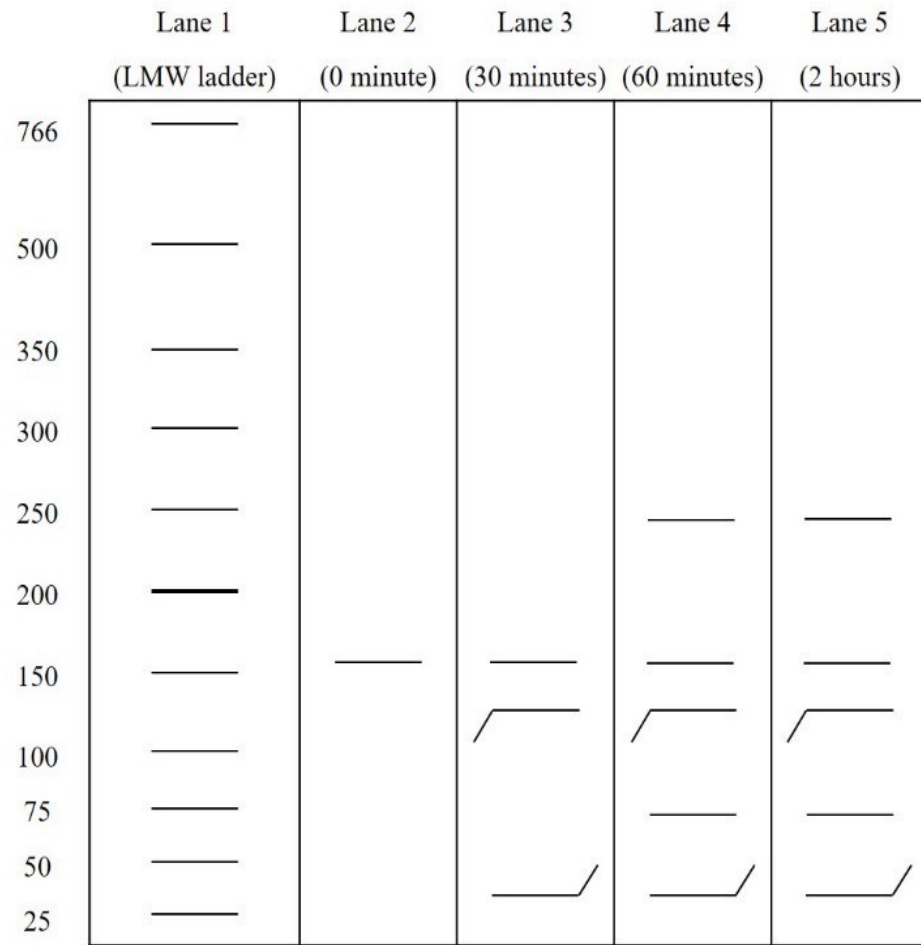
where  $n \in \mathbb{Z}^+$ . The fragments of DNA strings in the splicing language  $L(S)$  are stated as follows:

$$\alpha \underline{gtac} (\beta \underline{ccgg} \beta' \underline{gtac})^{n-1} \alpha', \\ \alpha \underline{gtac} (\beta \underline{ccgg} \beta' \underline{gtac})^{n-1} \beta \underline{ccgc} \gamma, \\ \gamma' \underline{gcg} (g \beta' \underline{gtac} \beta \underline{ccg})^{n-1} \underline{c} \gamma \text{ and} \\ \gamma' \underline{gcg} (g \beta' \underline{gtac} \beta \underline{ccg})^{n-1} \underline{g} \beta' \underline{gtac} \alpha'$$

where  $n \in \mathbb{Z}^+$  represents multiple copies of the specific strings.

# Theoretical vs Lab Results (Cont.)

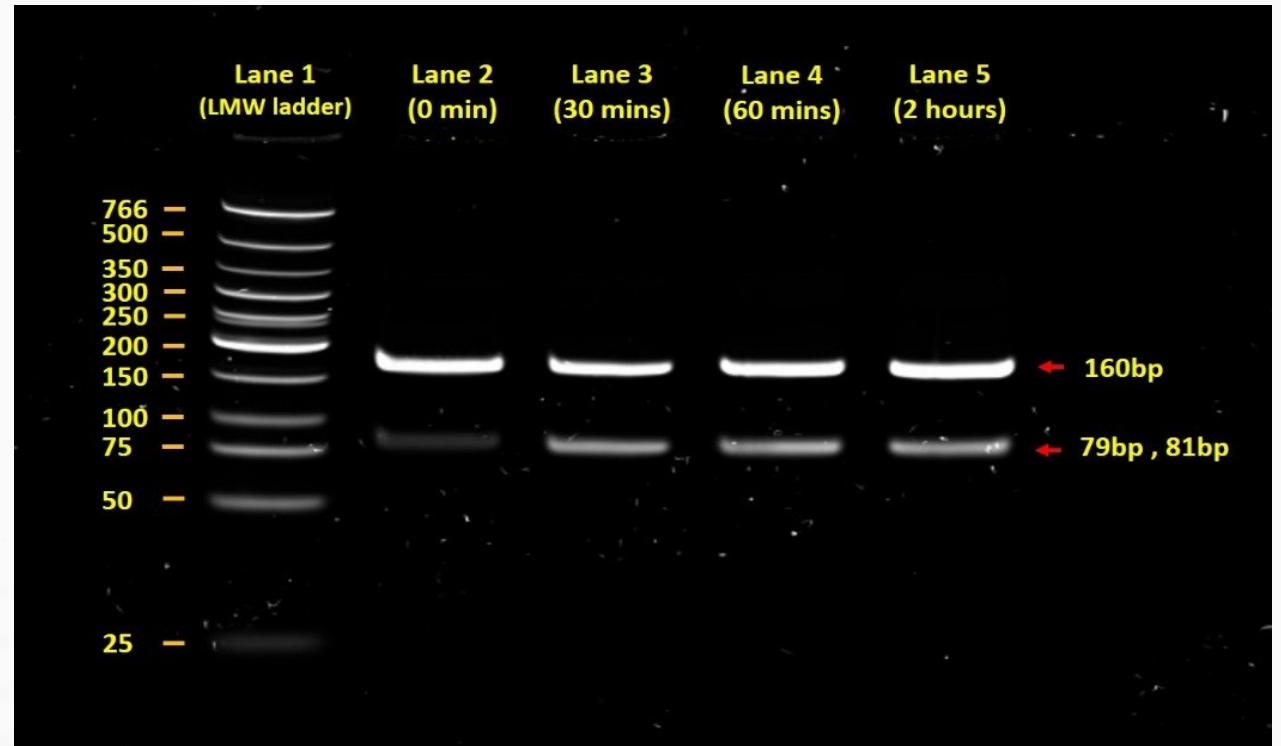
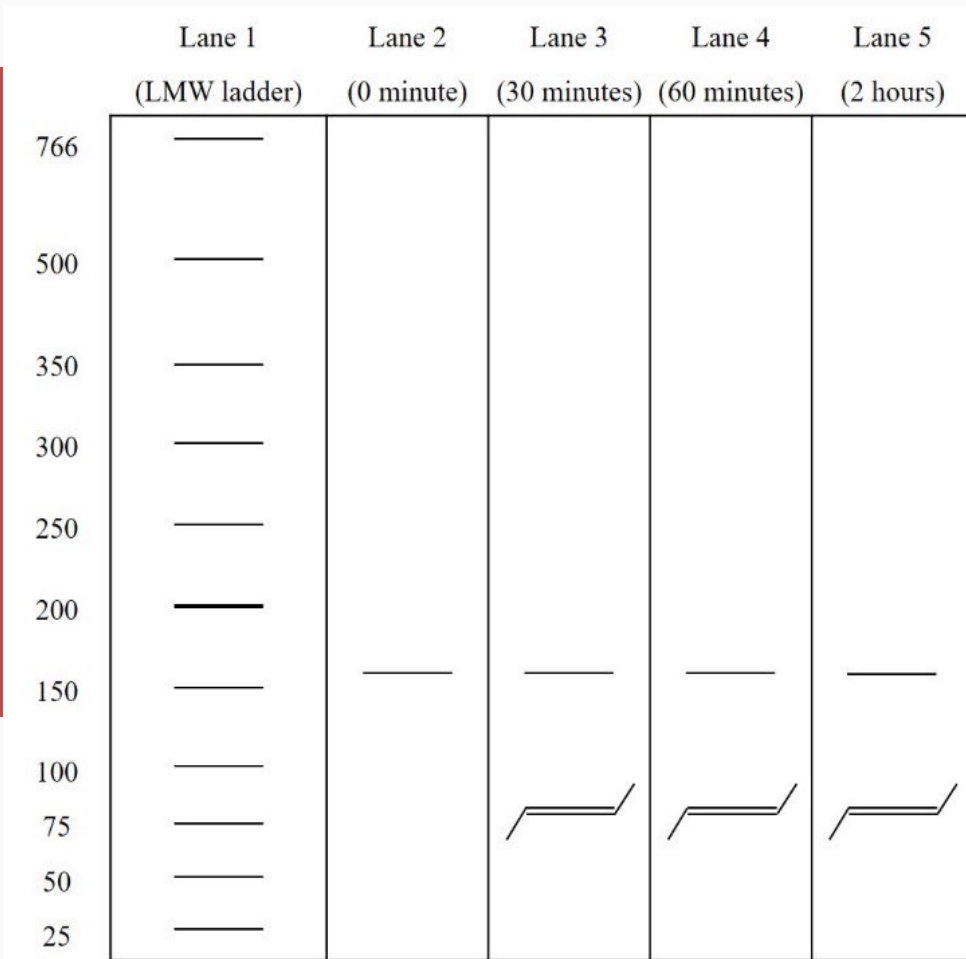
## Wet Splicing System involving CviQI



- 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 (Cont.)

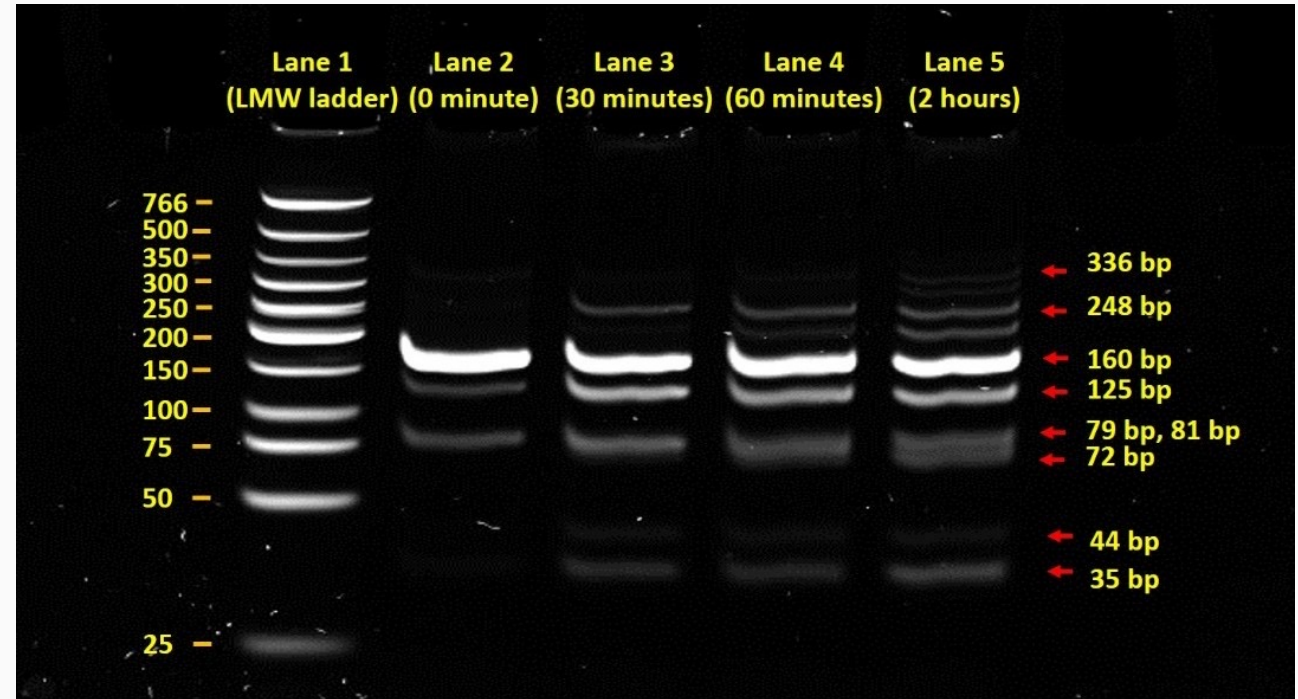
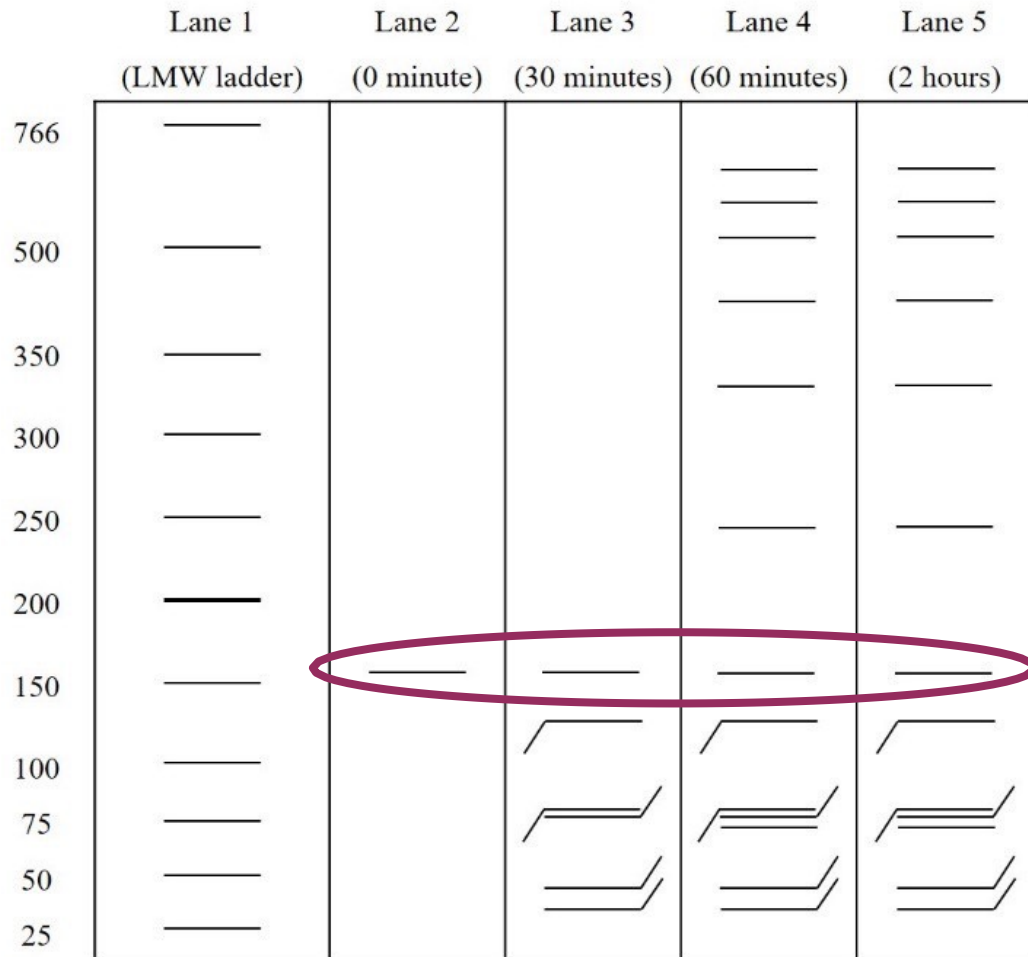
## Wet Splicing System involving *Acil*



- 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

# Theoretical vs Lab Results (Cont.)

## Wet Splicing System involving CviQ1 and Acil



- 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

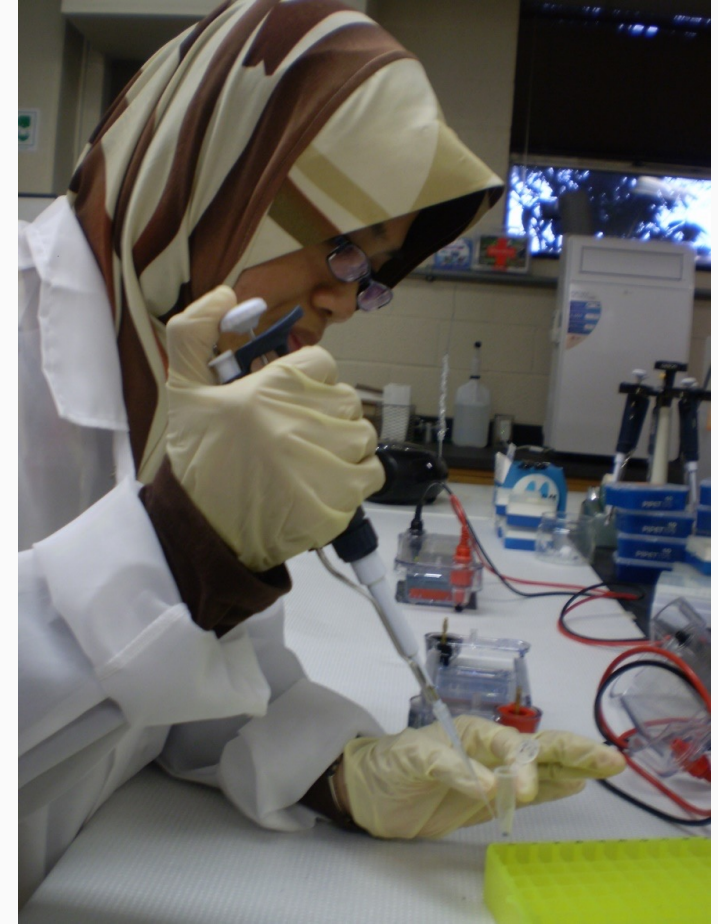


# Wet-lab Experiment on Splicing System



Universiti Teknologi Malaysia, 2007

## Wet-lab Experiment on Splicing System



State University of New York, Binghamton, New York, and Towson University, USA, 2010

# Wet-lab Experiment on Splicing System



Universiti Teknologi Malaysia, 2012

# Wet-lab Experiment on Splicing System



Universiti Teknologi Malaysia, 2015

# Wet-lab Experiment on Splicing System



Universiti Teknologi Malaysia, 2020

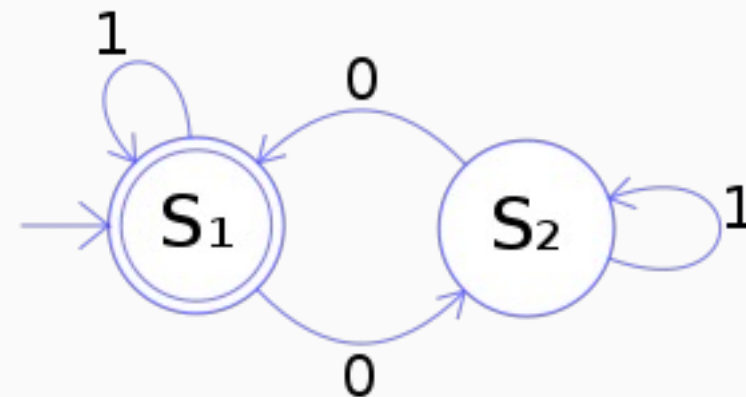
# DNA Splicing in Computer Science



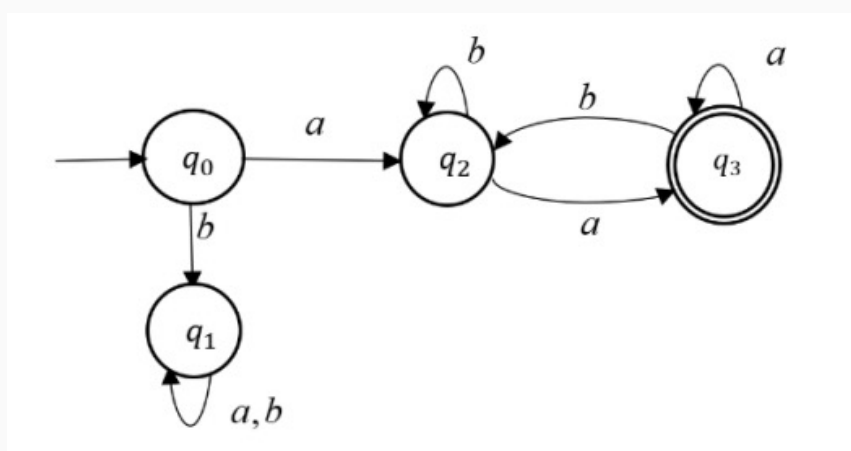


# Automata of Splicing System

**Automata theory** is the study of abstract machines, as well as the computational problems that can be solved using them. It is a theory in theoretical computer science.



The automaton described by this state diagram starts in state  $S_1$ , and changes states following the arrows marked 0 or 1 according to the input symbols as they arrive. The double circle marks  $S_1$  as an accepting state. Since all paths from  $S_1$  to itself contain an even number of arrows marked 0, this automaton accepts strings containing even numbers of 0s.



The automaton diagram for regular language

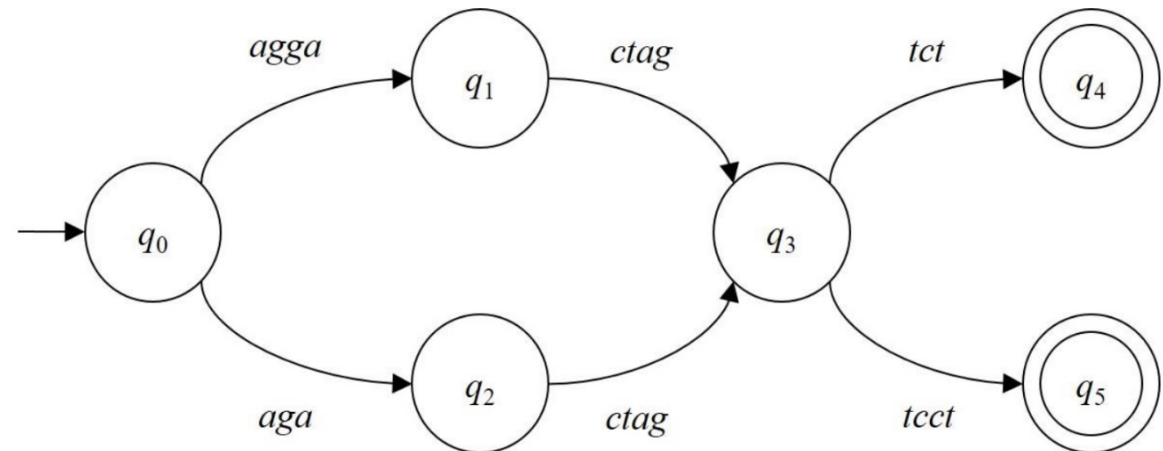


# Example

Given a splicing system  $S = (A, I, B, C)$  where  $I = \{AGGACTAGTCT\}$  is the set of initial string, set  $B = \left\{ \begin{pmatrix} C & TA & G \\ G' & AT' & C \end{pmatrix} \right\}$  is the set of cleavage pattern for the enzyme *BfaI*, and set  $C$  is the empty set.

The enzyme *BfaI*,  $5' - CTAG - 3'$  is a palindromic rule since the base sequence of enzyme *BfaI* reads the same forwards and backwards.

The automata for the splicing system  $S$

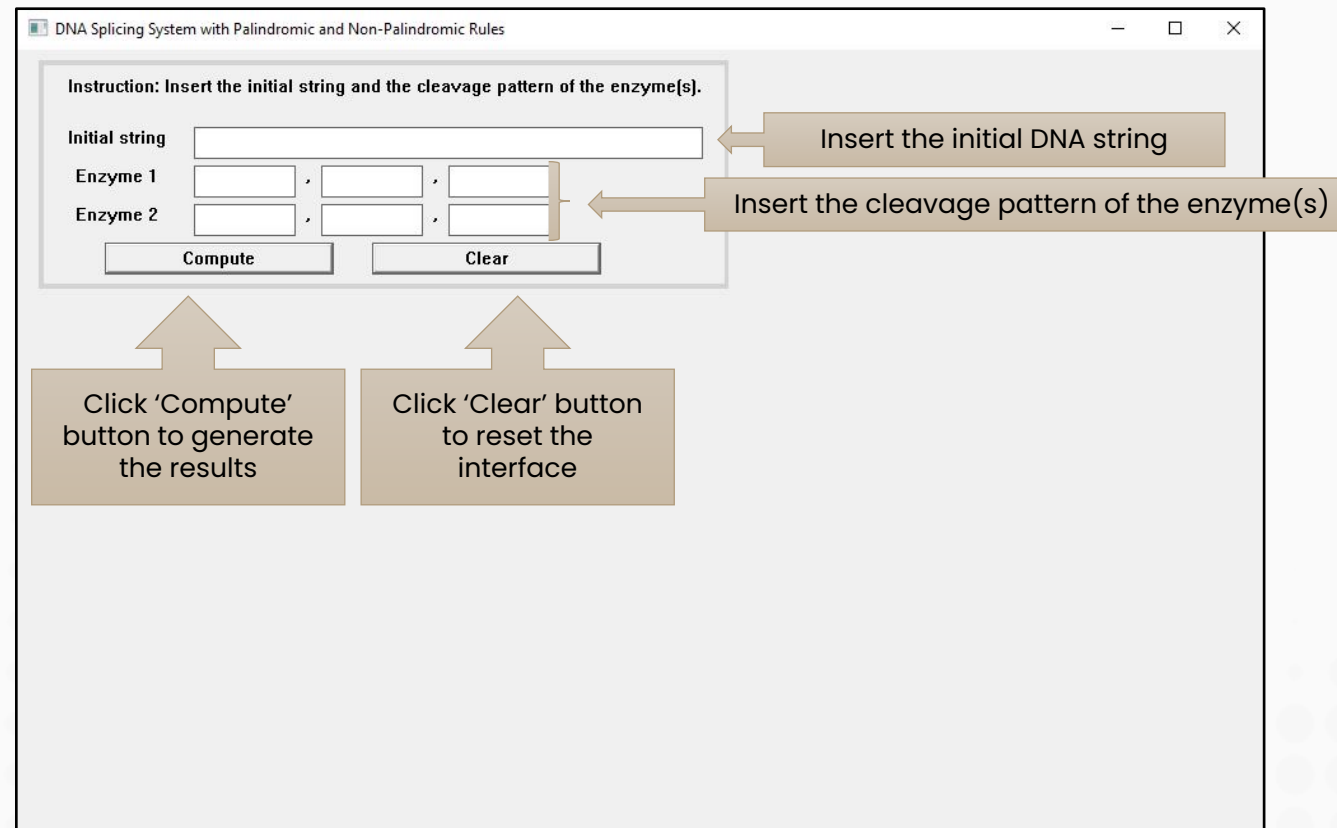




# Graphical User Interface (GUI) for DNA Splicing System

## DNA Splicing Language Generator (DNASpliceGen)

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



# DNA Splicing Language Generator (DNASpliceGen)

DNA Splicing System with Palindromic and Non-Palindromic Rules

Instruction: Insert the initial string and the cleavage pattern of the enzyme(s).

Initial string:

Enzyme 1:  ,  ,

Enzyme 2:  ,  ,

The initial molecule:

```

5'-A G G A C T A G T C T -3'
3'-T C C T G A T C A G A -5'
    
```

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

Restriction site of the enzyme :

```

The enzyme 5'-C T A G -3'
           3'-G A T C -5' is a palindromic rule with palindromic crossing.
    
```

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

The number of cutting sites found: 1

The resulting molecules: Case 1

```

5'- A G G A A G A C T A G T C T T C C T -3'
3'- ( T C C T + T C T ) G A T C ( A G A + A G G A ) -5'
    
```

The algorithm states the number of cutting sites

The algorithm generates all the splicing languages

# DNA Splicing Language Generator (DNASpliceGen)

## Output of GUI for DNA Splicing System involving Two Rules

The screenshot shows a GUI window titled "DNA Splicing System with Palindromic and Non-Palindromic Rules". The interface includes an instruction box, input fields for an initial string and two enzymes, and buttons for "Compute" and "Clear". Below the input fields, the initial DNA molecule is displayed with its two strands. The restriction sites for the two enzymes are shown, along with a message indicating that both enzymes have the same crossing. The number of cutting sites found is 2. Finally, the resulting DNA molecule is shown, which is a complex structure with multiple strands and cut sites.

Instruction: Insert the initial string and the cleavage pattern of the enzyme(s).

Initial string: attcgactgcgcaga

Enzyme 1: t, cg, a

Enzyme 2: g, cg, c

Buttons: Compute, Clear

The initial molecule:

```
5'-A T T C G A C T G C G C A G A -3'
3'-T A A G C T G A C G C G T C T -5'
```

Restriction site of the enzyme :

The enzyme 5'-T C G A -3' is a palindromic rule with palindromic crossing.  
3'-A G C T -5'

The enzyme 5'-G C G C -3' is a palindromic rule with palindromic crossing.  
3'-C G C G -5'

The enzymes 1 and 2 have the same crossing.

The number of cutting sites found: 2

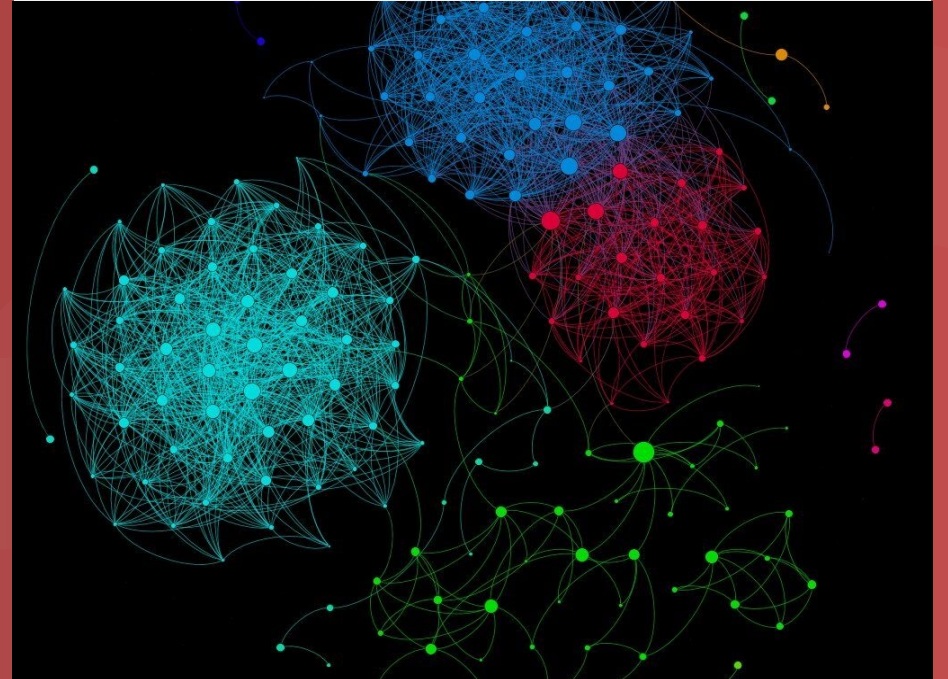
The resulting molecules: Case 3

```
5'- A T T T C T G ) { C G A C T G C A G T } * C G C A G A A A T -3'
3'- ( T A A + A G A C ) { G C ( T G A C + G T C A ) } G C ( G T C T + T T A ) -5'
```

### Additional features:

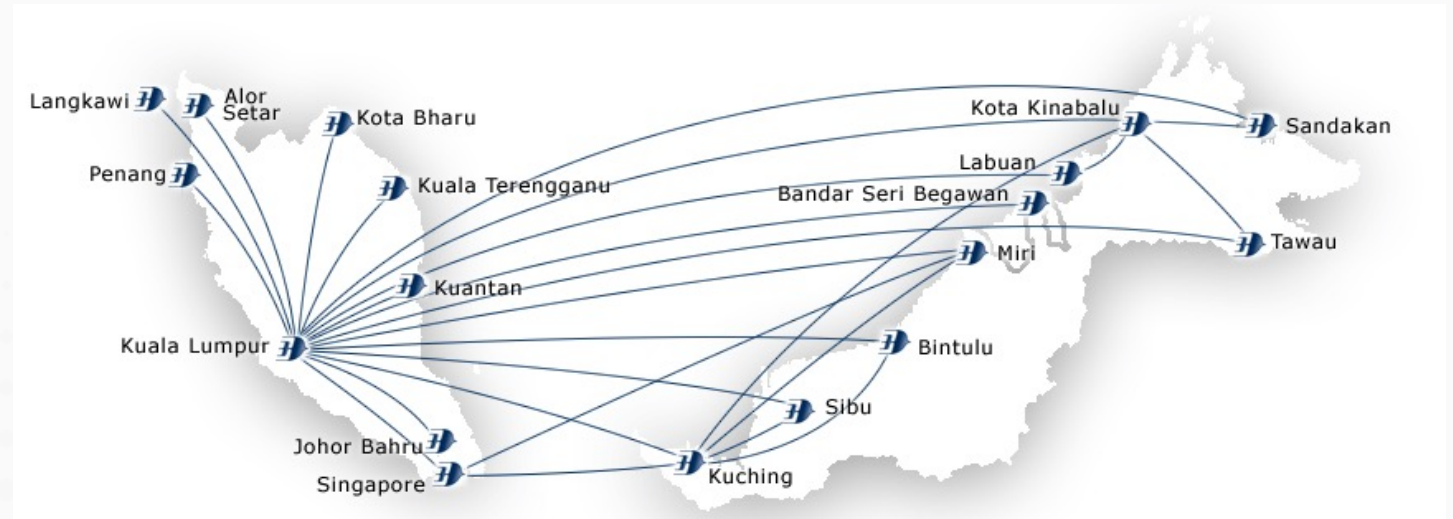
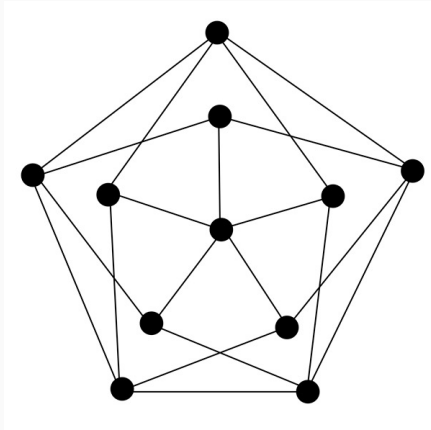
- Certain messages are displayed on the interface if the number of cutting sites found exceeds two
- The interface prompts the users if the cutting sites of restriction enzyme overlap
- The users will be notified if the inputs are incorrect.

# DNA Splicing in Graph Theory



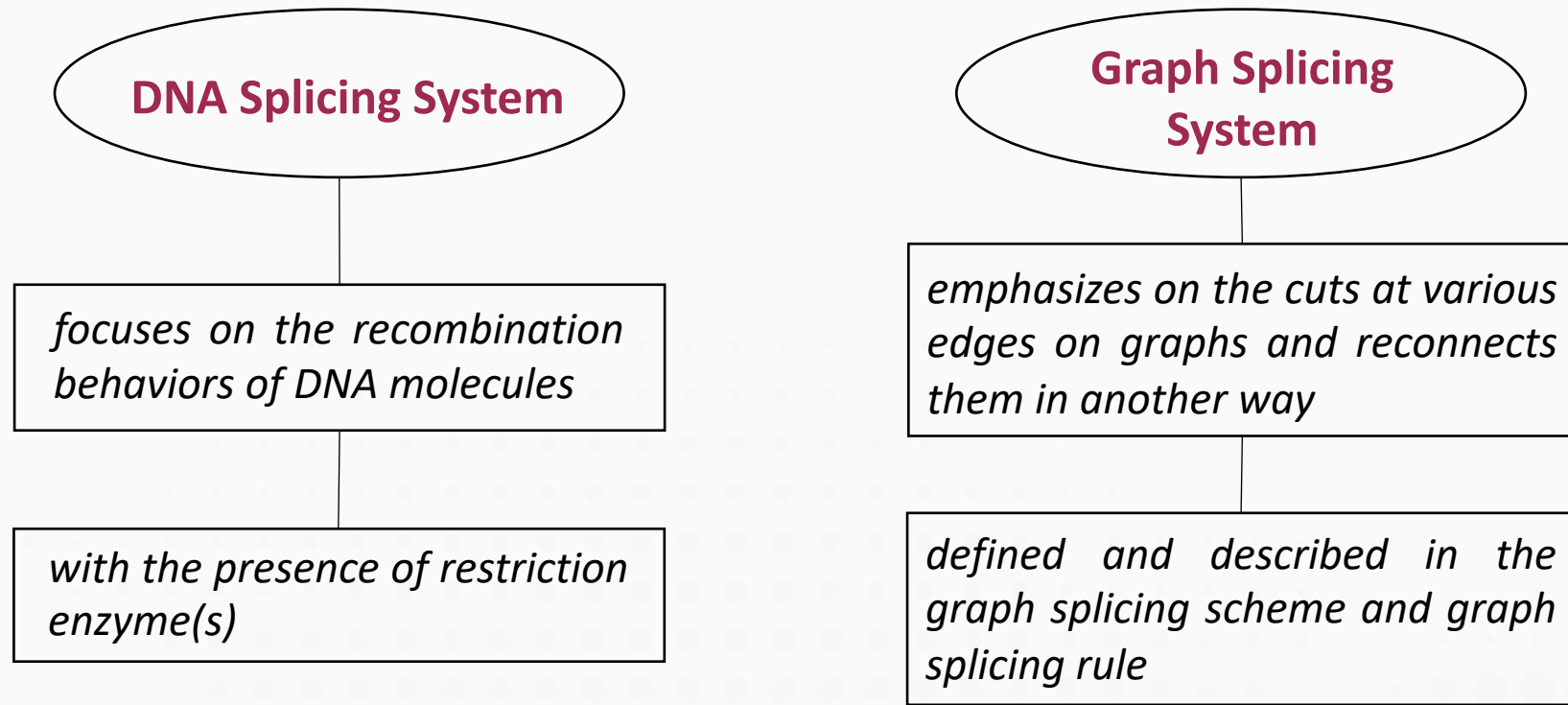
# Graph Theory

A graph is a **mathematical structure** consists of two finite sets called the set of **vertices,  $V$**  and **edges,  $E$** .



# Splicing System in Graph Theory

**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.



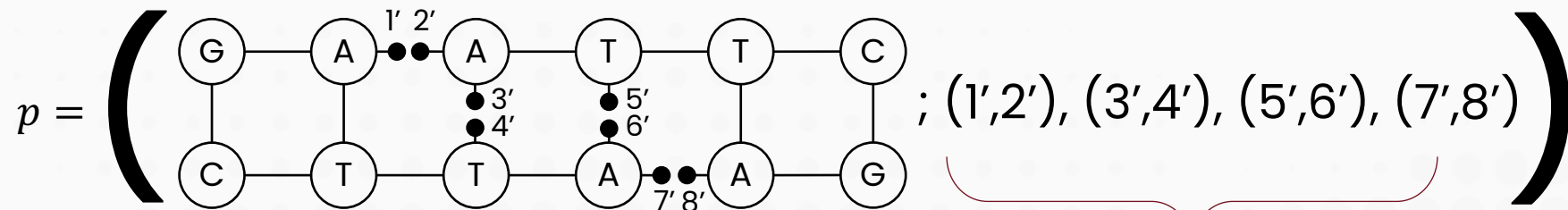
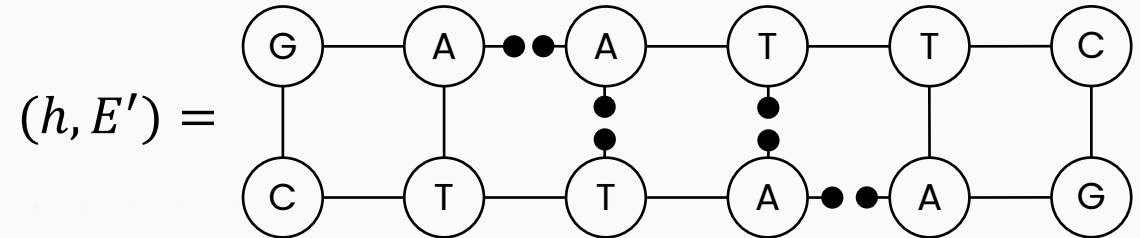
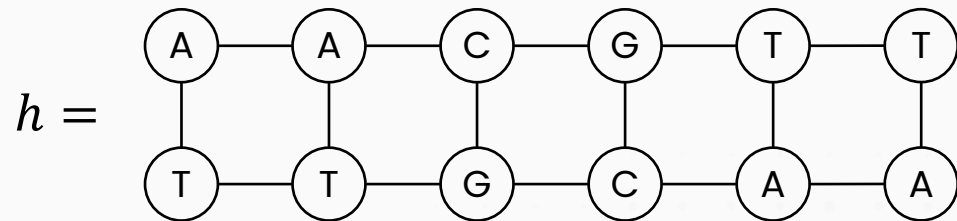
Freund, R. **Splicing systems on graphs**, in 1st Int. Symp. On Intelligence in Neural and Biological Systems, INBS'95 (IEEE, Washington, DC, 1995), 189-194.

# Graph Splicing Rule

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

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

$$EcoRI: \begin{cases} AA \ CG \ TT \\ TT' \ GC' \ AA \end{cases}$$



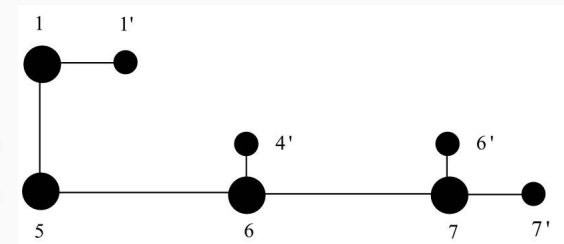
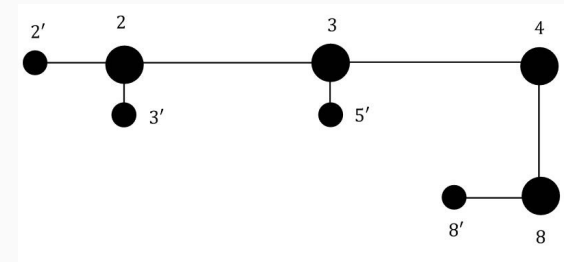
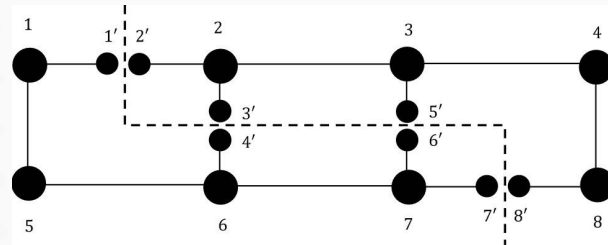
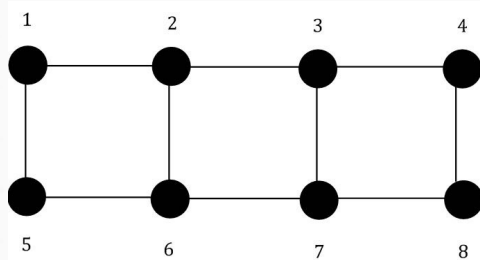
$R$

# $n$ -Cut Splicing (Cont.)

Semigraph representation of DNA molecule

An  $n$ -cut splicing is applied

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





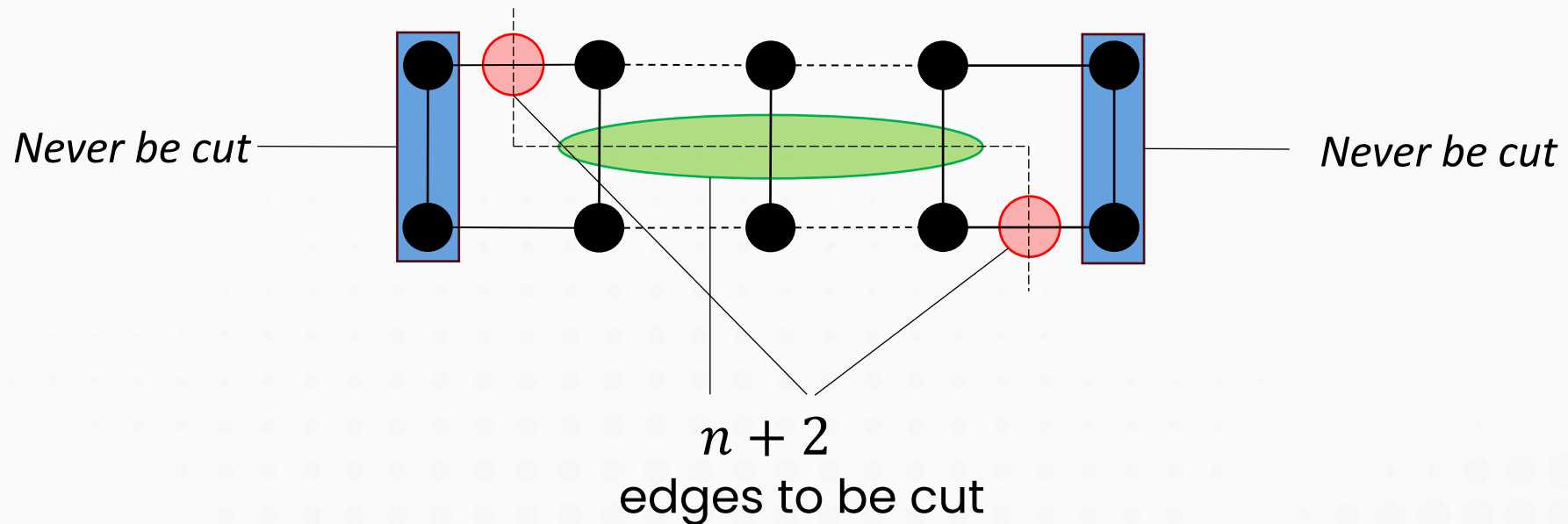
# $n$ -Cut Splicing (Cont.)

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

$n$	$n$ -cut splicing
1	<p>1-cut splicing</p>
2	<p>2-cut splicing</p>
3	<p>3-cut splicing</p>

# $n$ -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.



# Spectral Graph Partitioning

## *DNA sequence GTACCGCGTACA of length 12*

- The DNA sequence GTACCGCGTACA has the unit distance path graph as shown in Figure 4.1.

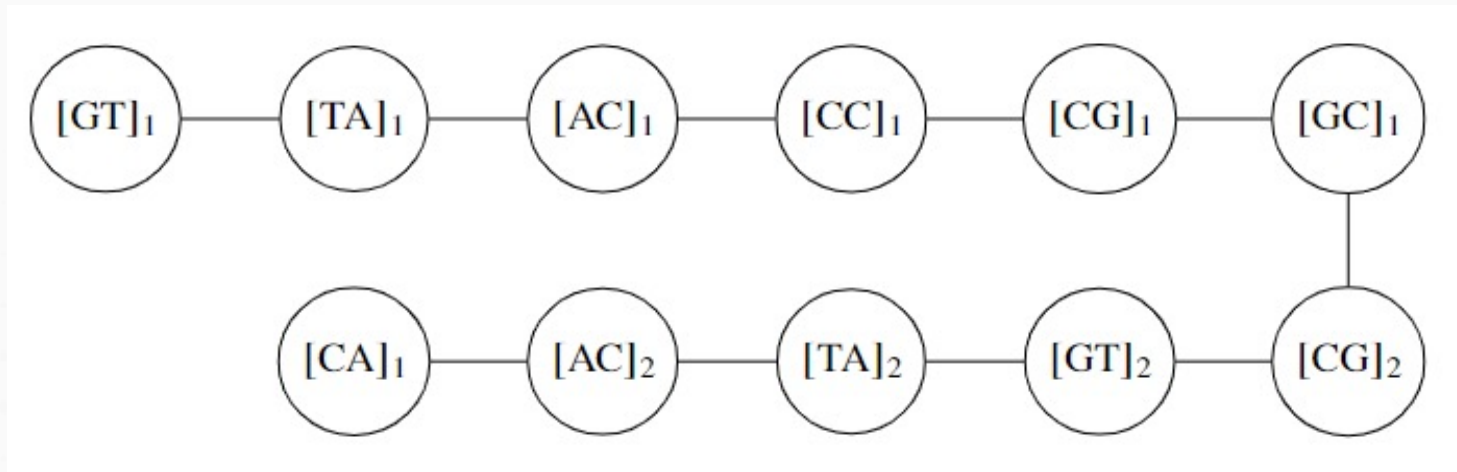


Figure 4.1: Unit distance path graph of DNA sequence GTACCGCGTACA.

# DNA sequence *GTACCGCGTACA* of length 12 (Cont.)

- The graph in Figure 4.1 is denoted as  $G_1$ , Laplacian matrix of the graph,  $L(G_1)$  is obtained.

$$L(G_1) = \begin{pmatrix} 1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ -1 & 2 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & -1 & 2 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & -1 & 2 & -1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -1 & 2 & -1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & -1 & 2 & -1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & -1 & 2 & -1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & -1 & 2 & -1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & -1 & 2 & -1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -1 & 2 & -1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -1 & 1 \end{pmatrix}.$$

# DNA sequence GTACCGCGTACA of length 12 (Cont.)

- The eigenvalues and eigenvectors of  $L(G_1)$  are computed, as shown below.

Table 4.1: Set of eigenvalues and eigenvectors of  $L(G_1)$ .

$i$	Eigenvalue, $\lambda_i$	Eigenvector, $v_i$
1	0	$(1 \ 1 \ 1 \ 1 \ 1 \ 1 \ 1 \ 1 \ 1 \ 1 \ 1 \ 1)^T$
2	0.0810	$(-1 \ -0.9190 \ -0.7635 \ -0.5462 \ -0.2846 \ 0 \ 0.2846 \ 0.5462 \ 0.7635 \ 0.9190 \ 1)^T$
3	0.6903	$(-1 \ 0.3097 \ 0.5944 \ 1.0822 \ 0.8308 \ 0 \ -0.8308 \ -1.0882 \ -0.5944 \ 0.3097 \ 1)^T$
4	1.7154	$(-1 \ 0.7154 \ 1.2036 \ -0.3728 \ -1.3097 \ 0 \ 1.3097 \ 0.3728 \ -1.2036 \ -0.7154 \ 1)^T$
5	2.8308	$(-1 \ 1.8308 \ -0.5211 \ -0.5211 \ -1.3979 \ 1.6825 \ 0 \ -1.6825 \ 1.3979 \ 0.5211 \ -1.8308 \ 1)^T$
6	0.3175	$(1 \ 0.6825 \ 0.1483 \ -0.4330 \ -0.8768 \ -1.0422 \ -0.4330 \ 0.1483 \ 0.6825 \ 1)^T$
7	3.6825	$(-1 \ 2.6825 \ -3.5133 \ 3.2287 \ -1.9190 \ 0 \ 1.9190 \ -3.2287 \ 3.5133 \ -2.6825 \ 1)^T$
8	1.1692	$(1 \ -0.1692 \ -1.1406 \ -0.7784 \ 0.4938 \ 1.1887 \ 0.4938 \ -0.7784 \ -1.1406 \ -0.1692 \ 1)^T$
9	2.2846	$(1 \ -1.2846 \ -0.6344 \ 1.4652 \ 0.2173 \ -1.5270 \ 0.2173 \ 1.4652 \ -0.6344 \ -1.2846 \ 1)^T$
10	3.3097	$(1 \ -2.3097 \ 2.0251 \ -0.3426 \ -1.5764 \ 2.4072 \ -1.5764 \ -0.3426 \ 2.0251 \ -2.3097 \ 1)^T$
11	3.9190	$(1 \ -2.9190 \ 4.6015 \ -5.9112 \ 6.7420 \ -7.0267 \ 6.7420 \ -5.9112 \ 4.6015 \ -2.9190 \ 1)^T$

# DNA sequence *GTACCGCGTACA* of length 12 (Cont.)

- From Table 4.1, the **Fiedler value** obtained is 0.0810.
- The **Fiedler vector** obtained is  
 $(-1 \quad -0.9190 \quad -0.7635 \quad -0.5462 \quad -0.2846 \quad 0 \quad 0.2846 \quad 0.5462 \quad 0.7635 \quad 0.9190 \quad 1)^T$ .
- For **bisection cut**, the splitting value  $s$  is the median of the entries of Fiedler vector, which is  $s = 0$  in this case. Hence, the partitions of DNA sequence *GTACCGCGTACA* obtained are **GTACCG** and **CGTACA** with **equal length of 6**.
- For **gap cut**, the splitting value  $s$  is the largest gap of the sorted entries of Fiedler vector, which is 0.2846 in this case. Hence, the partitions of DNA sequence *GTACCGCGTACA* are **GTACCGC (length 7)** and **GTACA (length 5)**, which are of **unequal lengths**.
- Therefore, bisection cut is the balanced cut for *GTACCGCGTACA*.

# Shortest Path Problem and Minimized DNA String

## Case of Initial Base A

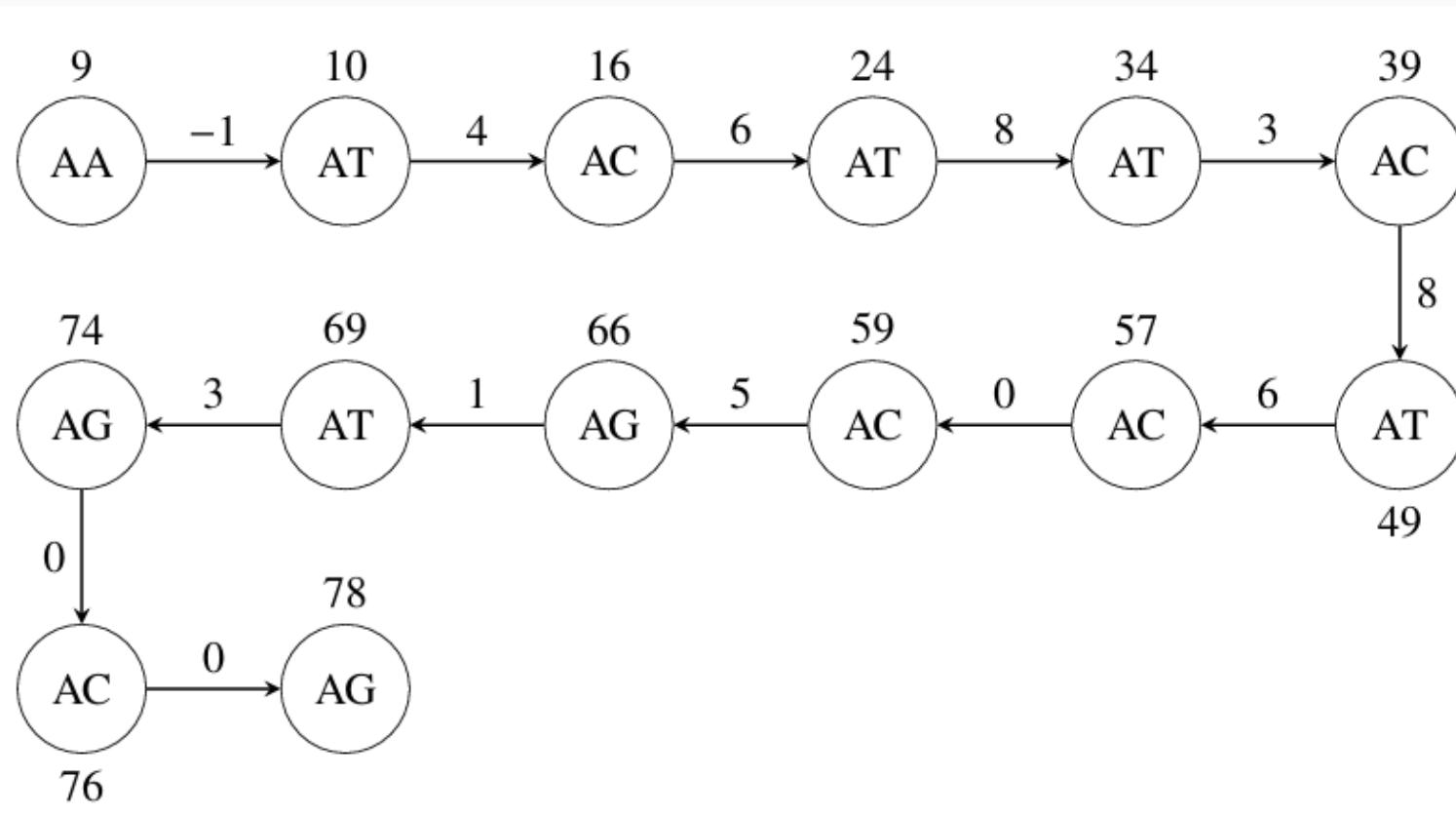
- The string taken is from the 12841 base to the 12920 base of Lambda.
- The string obtained is:  $\alpha =$  GCGTGGGGAA TCTTTACCGG CTGATGCGCG GCTATGCCAC CGGCGGTTAT GTCGGTACAC CGGGCAGCAT GGCAGACAGC.

```
>Lambda_NEB
GGGCGGCGACCTCGCGGGTTTTTCGCTATTTATGAAAATTTCCGGTTTAAGGCGTTTTCCGTTCTTCTTCG
TCATAACTTAATGTTTTTATTTAAAATACCCTCTGAAAAGAAAGGAAACGACAGGTGCTGAAAGCGAGGC
TTTTTGGCCTCTGTCGTTTCTTTCTGTTTTGTCCGTGGAATGAACAATGGAAGTCAACAAAAGCA
GCTGGCTGACATTTTGGTGCAGATATCCGTACCATTGAGAACTGCGAGGAAACAGGGAATGCCGTTCTG
CGAGGCGGTGGCAAGGTAATGAGGTGCTTTATGACTCTGCCGCGTCAAAAATGGTATGCCGAAAGGG
ATGCTGAAATTGAGAACGAAAAGCTGCGCCGGGAGGTTGAAGAAGTGCAGGAGCCAGCGAGGCGAGATCT
CCAGCCAGGAACTATTGAGTACGAACGCCATCGACTTACCGGTGCGCAGGCCGACGCACAGGAACTGAAG
AATGCCAGAGACTCCGCTGAAGTGGTGGAAACCGCATTCTGTACTTTCTGTGCTGTGCGGGATCGCAGGTG
AAATTGCCAGTATTCTCGACGGGCTCCCCTGTGCGGTGACGCGGTTTTCCGGAACGAAAACCGACA
TGTGATTTCTGAAAACGGGATATCATCAAAGCCATGAACAAAAGCAGCCGCGCTGGATGAACTGATACCG
GGGTTGCTGAGTGAATATATCGAACAGTCAAGTTAACAGGCTGCGGCATTTTGTCCGCGCCGGGCTTCGC
TCACTGTTCAAGCCGGAGCCACAGACCCGTTGAATGGGCGGATGCTAATTAATCTCCCGAAAGAAT
CCGCATACCAGGAAGGGCGCTGGGAAACTGCCCTTTACGCGGCCATCATGAATGCGATGGGCGAGCA
CTACATCCGTGAGGTGAATGTGGTGAAGTCTGCCCGTGTGCGTTATCCAAAATGCTGCTGGGTGTTTAT
GCCTACTTTATAGAGCATAAGCAGCGCAACACCCCTATCTGTTGCGGACGGATGGTATGCCGAGAAGT
TTATGAAAACCCACGTTGAGCCGACTATTCGTGATATCCGTGCTGCTGGCGCTGGCCCCGTTGGTATGG
CAAAAAGCACCGGATAACACGCTCACCATGAAGCGTTTCACTAATGGGCGTGGCTTCTGGTGCCTGGG
GGTAAAGCGGCAAAAACACTACCGTGAAGTCCGTTGGATGTGGCGGTTATGATGAACTTGTGCTTTTG
ATGATGATATTGAACAGGAAGGCTCTCCGACGTTCTGGGTGACAAGCGTATTGAAGGCTCGGTCTGGCC
AAAGTCCATCCGTGGCTCCACGCCAAAAGTGAGAGGCACCTGTGAGATTGAGCGTGCAGCCAGTGAATCC
CCGCATTTTATGCGTTTTATGTTGCTGCCCGATTGCGGGGAGGAGCAGTATCTTAAATTTGGCGACA
AAGAGACGCCGTTTGGCCTCAAATGGACGCCGGATGACCCTCCAGCGTGTATCTGCGAGCATAA
TGCCTGCGTATCCGCCAGCAGGAGCTGGACTTACTGATGCCCGTTATATCTGCGAAAAGACCGGGATC
TGGACCCGTGATGGCATTCTCTGTTTTGCTCATCCGGTGAAGAGATTGAGCCACCTGACAGTGTGACCT
```

```
CGCTTCAGGCAGAACTCCGGACGCTGGAGAAGCATGCCGGAGCAAATGAGAAAATCAGCCAGCAGCGCCG
GGATTTGTGGAAGGCGGAGAGTCACTTCGCGGTTACTGGAGGAGGCGGCGCAACGTGCGCCAGCTGTCTGCA
CAGGAGAAATCCCTGCTGGCGCATAAAGATGAGACGCTGGAGTACAAAACGCCAGCTGGCTGCACTTGGCG
ACAAGGTTACGTATCAGGAGCGCTGAACGCGCTGGCGCAGCAGGCGGATAAATTCGCACAGCAGCAACG
GGCAAAACGGGCCGCAATTGATGCGAAAAGCCGGGGGCTGACTGACCGGCAGGCAGAACGGGAAGCCAG
GAACAGCGCCTGAAGGAACAGTATGGCGATAATCCGCTGGCGCTGAATAACGTCATGTGAGAGCAGAAAA
AGACCTGGGCGGCTGAAGACCAGCTTCGCGGGAACGGATGGCAGGCTGAAGTCCGGCTGGAGTGAAGT
GGAAGAGAGCGCCACGGACAGTATGTGCGAGGTAAAAGTGCAGCCACGCAGACCTTTGATGGTATTGCA
CAGAATATGGCGGCGATGCTGACCGCAGTGAAGCAGAACTGGCGCAGCTTACCCGTTCCGTGCTGTCCA
TGATGACAGAAATCTGCTTAAGCAGGCAATGGTGGGATTGTGCGGAGTATCGGCAGCGCCATTGGCGG
GGCTGTTGGTGGCGGCGCATCCGCGTCAAGCGGTACAGCCATTGAGCCGCTGCGGCGAAATCCATTTT
GCAACCGGAGGATTTACGGGAACCGCGGCAAAATATGAGCCAGCGGGGATTGTTACCCGTGGTGAATTTG
TCTTACGAAGGAGGCAACAGCCGGATTGGCGTGGGGAATCTTTACCGGCTGATGCGCGGCTATGCCAC
CGGCGGTTATGTCGGTACACCGGGCAGCATGGCAGACAGCCGGTGCAGGCGTCCGGGACGTTTGAAGCAG
AATAACCATGTGGTGAATTAACAACGACGGCACGAAACGGGCGAGATAGGTCCGGCTGCTCTGAAGGCGGTG
ATGACATGGCCCCGAAGGGTGCCTGATGAAATCAGACACAGATGCGTGAAGTGGCCTGTTCTCCGG
```

## Case of Initial Base A (Cont.)

- GCGTGGGGAA TCTTTACCGG CTGATGCGCG GCTATGCCAC  
CGGCGGTTAT GTCGGTACAC CGGGCAGCAT GGCAGACAGC.

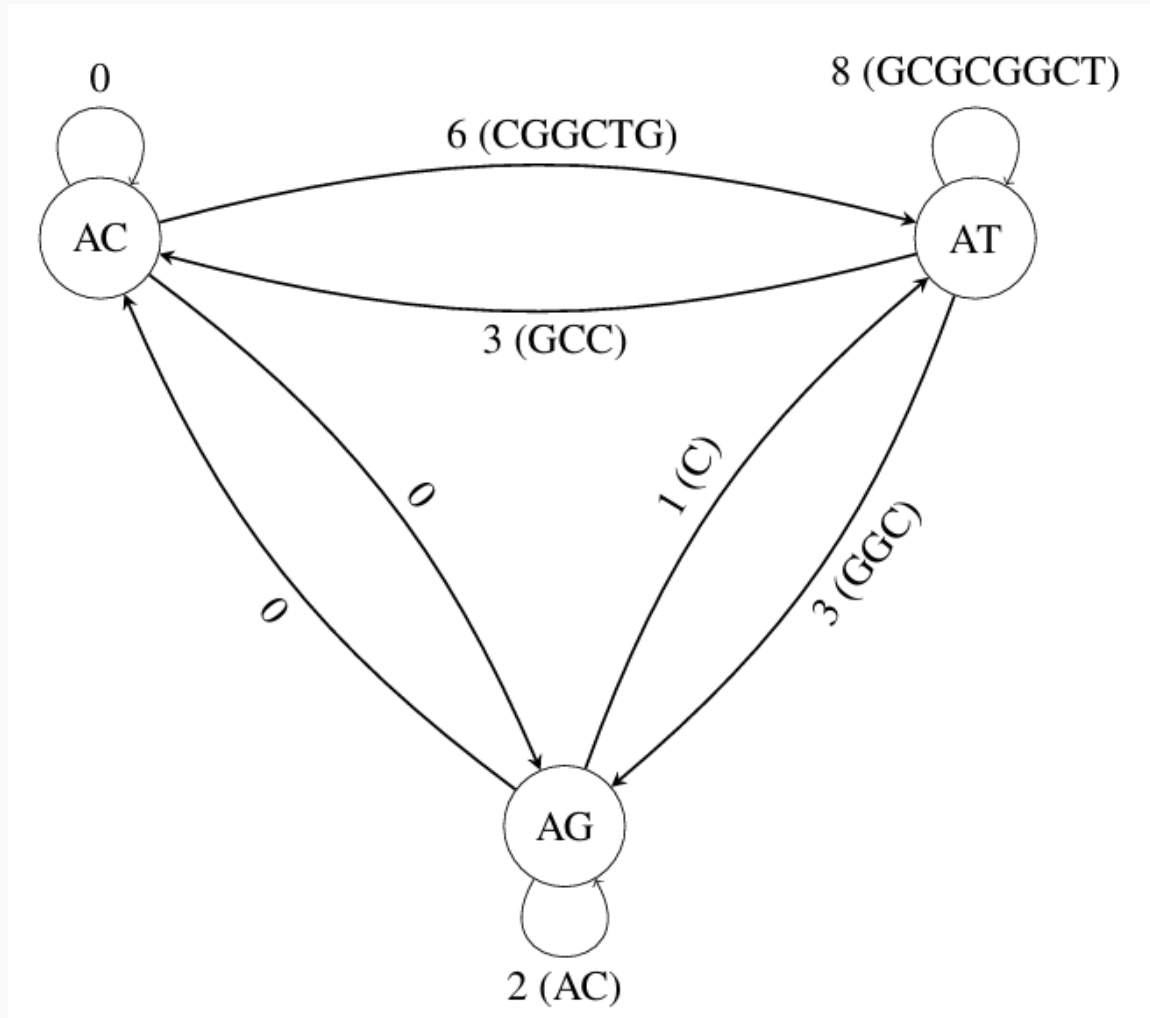




## Case of Initial Base A (Cont.)

Start vertex \ End vertex	Position	AA	AT	AC	AT	AT	AC	AT	AC	AC	AG	AT	AG	AC	AG
		9	10	16	24	34	39	49	57	59	66	69	74	76	78
AA	9	-	-1	5	13	23	28	38	46	48	55	58	63	65	67
AT	10	-	-	4	12	22	27	37	45	47	54	57	62	64	66
AC	16	-	-	-	6	16	21	31	39	41	48	51	56	58	60
AT	24	-	-	-	-	8	13	23	31	33	40	43	48	50	52
AT	34	-	-	-	-	-	3	13	21	23	30	33	38	40	42
AC	39	-	-	-	-	-	-	8	16	18	25	28	33	35	37
AT	49	-	-	-	-	-	-	-	6	8	15	19	23	25	27
AC	57	-	-	-	-	-	-	-	-	0	7	10	15	17	19
AC	59	-	-	-	-	-	-	-	-	-	5	8	13	15	17
AG	66	-	-	-	-	-	-	-	-	-	-	1	6	8	10
AT	69	-	-	-	-	-	-	-	-	-	-	-	3	5	7
AG	74	-	-	-	-	-	-	-	-	-	-	-	-	0	2
AC	76	-	-	-	-	-	-	-	-	-	-	-	-	-	0
AG	78	-	-	-	-	-	-	-	-	-	-	-	-	-	-

## Case of Initial Base A (Cont.)



- Reduced graph with vertex set  $V'_\alpha$  for  $\alpha$ .

## Case of Initial Base A (Cont.)

Start vertex	End vertex	Path taken	Path length
AC	AC	AC → AC	0
		AC → AG → AC	0 + 0 = 0
		AC → AG → AT → AC	0 + 1 + 3 = 4
		AC → AT → AC	6 + 3 = 9
		AC → AT → AG → AC	6 + 3 + 0 = 9
	AG	AC → AC → AG	0 + 0 = 0
		AC → AG	0
		AC → AT → AG	6 + 3 = 9
	AT	AC → AC → AT	0 + 6 = 6
		AC → AG → AT	0 + 1 = 1
		AC → AT	6
	AG	AC	AG → AC
AG → AG → AC			2 + 0 = 2
AG → AT → AC			1 + 3 = 4
AG		AG → AC → AG	0 + 0 = 0
		AG → AC → AT → AG	0 + 6 + 3 = 9
		AG → AG	2
		AG → AT → AG	1 + 3 = 4
AT		AG → AT → AC → AG	1 + 3 + 0 = 4
		AG → AC → AT	0 + 6 = 6
		AG → AG → AT	2 + 1 = 3
	AG → AT	1	

Start vertex	End vertex	Path taken	Path length
AT	AC	AT → AC	3
		AT → AG → AC	3 + 0 = 3
		AT → AT → AC	8 + 0 = 8
	AG	AT → AC → AG	3 + 0 = 3
		AT → AG	3
	AT	AT → AT → AG	8 + 3 = 11
		AT → AC → AT	3 + 6 = 9
		AT → AC → AG → AT	3 + 0 + 1 = 4
		AT → AG → AT	3 + 1 = 4
		AT → AG → AC → AT	3 + 0 + 6 = 9
		AT → AT	8

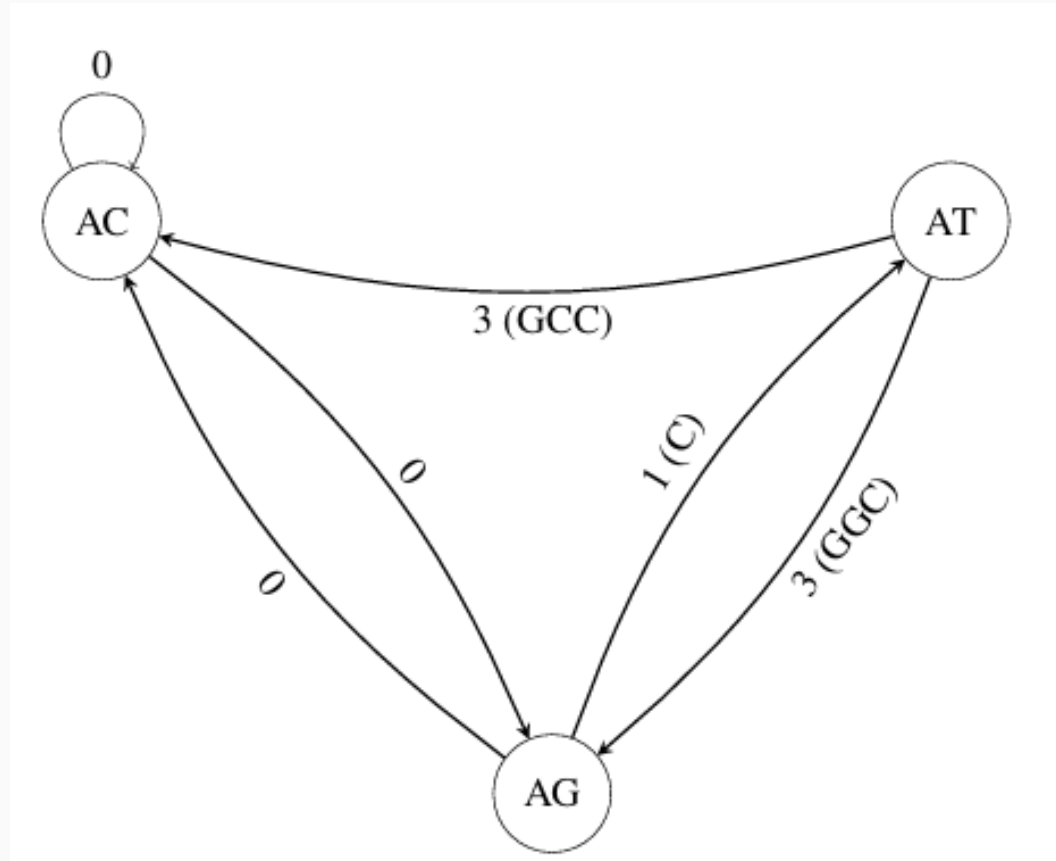
- Calculation of the shortest path

## Case of Initial Base A (Cont.)

- Shortest path and the minimized DNA string for each path

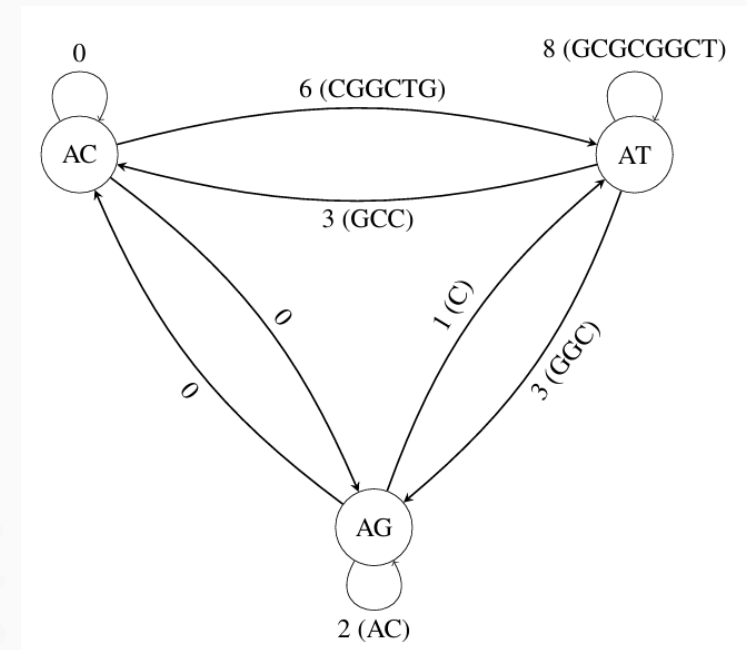
Start vertex	End vertex	Path taken	Path length	Minimized DNA string
AC	AC	AC → AC	0	ACAC
	AG	AC → AG	0	ACAG
	AT	AC → AG → AT	0 + 1 = 1	ACAGCAT
AG	AC	AG → AC	0	AGAC
	AG	AG → AC → AG	0 + 0 = 0	AGACAG
	AT	AG → AT	1	AGCAT
AT	AC	AT → AC	3	ATGCCAC
	AG	AT → AG	3	ATGGCAG
	AT	AT → AG → AT	3 + 1 = 4	ATGGCAGCAT

## Case of Initial Base A (Cont.)



- Simplified graph with vertex set  $V'_\alpha$  for  $\alpha$ .

- The minimized DNA string is ATGCCACACAGCATGCCAGAC.



- Reduced graph form

# Ongoing Research

## ***A Theoretical DNA Based Computer Model for Food Authentication Process***

The **authentication of food** is an urgent concern owing to the increasing population and direct consequences of food on public health. **Food authentication using DNA and omics-based methods** is gaining ground due to critical advantages notably in the areas of food adulteration in plant and animal-based food and feed products and in determining the quality of food and food spoilage. Besides, there is greater demand for the detection of **genetically modified foods** (GMOs) and the detection of allergens, toxins, and carcinogens like tobacco in the food. Advanced DNA and omics-based methods (genomics, metabolomics, and proteomics) have been used in the **food industry** including DNA-based methods that rely on specific markers known as reference genes for food authentication. Novel methods like CRISPR-Cas have been recently introduced for the management of beneficial microorganisms relevant to food like probiotics.

# Publication

<https://people.utm.my/nizasarmin/journal-papers/>





# Watson-Crick Automata

1. Deborah Lim Shin Fei & Nor Haniza Sarmin, "**Watson-Crick Automata**", International Conference on Research and Education in Mathematics (ICREM 2), 27-29 May, 2006, Residence Hotel at UNITEN, Bangi, Selangor, Malaysia, pp 436-443.
2. Deborah Lim Shin Fei & Nor Haniza Sarmin, "**Watson-Crick Automata: Theoretical Computation Models in DNA Computing**", Menemui Matematik (Discovering Mathematics), Vol. 27, No. 2 (2006): 1-8.
3. Deborah Lim Shin Fei, Nor Haniza Sarmin & Wan Heng Fong, "**Three Variants of Splicing Systems – Head, Paun and Pixton**", 2007, LT/M BIL.04/2007.
4. Deborah Lim Shin Fei, Nor Haniza Sarmin & Wan Heng Fong, "**Adult and Limit Languages in Splicing Systems**", 2007, LT/M BIL.03/2007.





# Types of Splicing System

1. **Nor Haniza Sarmin**, Yuhani Yusof and Fong Wan Heng, **Some Characterizations in Splicing Systems**, *International Conference on Mathematical Sciences (ICMS 2010)*, Abant İzzet 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).
2. Fong Wan Heng, **Nor Haniza Sarmin** and Yuhani Yusof, **Some Analysis on Certain Types of Splicing Systems**, *The Fifth IEEE International Conference on Bio-Inspired Computing: Theories and Applications (BIC-TA 2010)*, Liverpool Hope University, Liverpool, United Kingdom, 8-10 September 2010, pg. 1319-1321. (IEEE Catalog Number: CFP1001F-CDR, ISBN: 978-1-4244-6439-5).
3. 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).
4. 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).



# Fuzzy Splicing Systems

1. 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.
2. Fariba Karimi, Nor Haniza Sarmin and Fong Wan Heng, "**Common-Crossing and Persistent Splicing Systems**" *International Journal of Applied Mathematics & Statistics (IJAMAS)*, Vol. 43, No. 13, 2013, pp. 293-296. (ISSN: 0973-7545).
3. Fariba Karimi, Nor Haniza Sarmin and Fong Wan Heng, "**The Characterizations of Different Splicing Systems**", *International Journal of Modern Physics: Conference Series*, 2012, Vol 9: pg 89-94. (ISSN: 2010-1945)



# Weighted Splicing System

1. 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.
2. 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).
3. 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).



# Probabilistic Splicing System

1. 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).
2. 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, Vol. 457, 2013
3. 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)
4. 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)
5. Mathuri Selvarajoo, Fong Wan Heng, **Nor Haniza Sarmin** and Sherzod Turaev, **The characteristics of simple splicing languages over permutation groups**, *AIP Conference Proceedings* 2266, 060004 (2020); (doi: 10.1063/5.0018731)
6. Mathuri Selvarajoo, Fong Wan Heng, **Nor Haniza Sarmin**, Sherzod Turaev. **The Properties of Semi-Simple Splicing System Over Alternating Group,  $A^3$** , *Journal of Physics Conference Series*, 1770(1): 012001.
7. Mathuri Selvarajoo, Fong Wan Heng, Nor Haniza Sarmin, and Sherzod Turaev. **"The properties of probabilistic simple regular sticker systems"**, *AIP Conference Proceedings* 1682, 020047 (2015). (doi: 10.1063/1.4932456).



# Limit Language in Splicing System

1. 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).
2. 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).
3. 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).
4. 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).



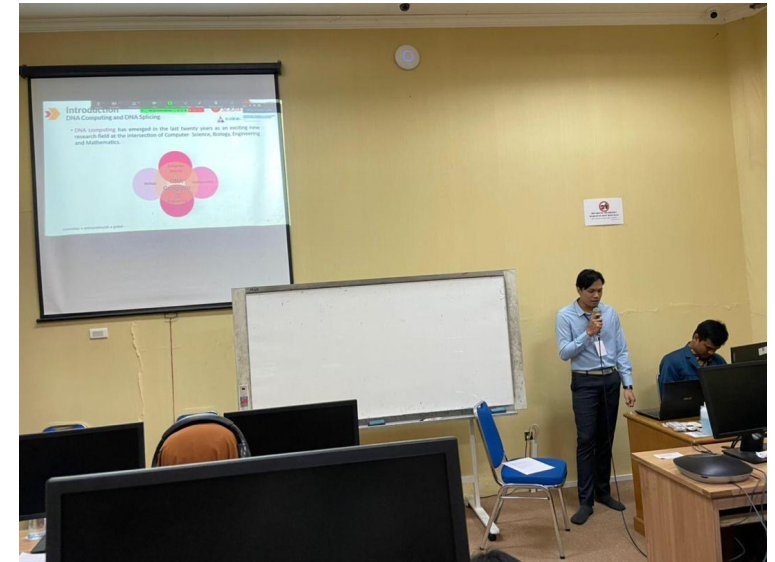
# Splicing Systems with Palindromic and Non-Palindromic Restriction Enzymes

1. 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)
2. 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)
3. 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)
4. Nurul Izzaty Ismail, Wan Heng Fong and Nor Haniza Sarmin, **Molecular aspects on generalisations of splicing languages**, AIP Conference Proceedings 2266, 060008 (2020); (doi: 10.1063/5.0018377)
5. Nurul Izzaty Ismail, Wan Heng Fong, Nor Haniza Sarmin, **Generalisations of Splicing Languages in DNA Splicing Systems Involving Two Palindromic Restriction Enzymes**, Malaysian Journal of Fundamental and Applied Sciences (MJFAS), 17(2), 128-138, 2021.



# Graph Splicing Systems

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)
2. Muhammad Nur Syiham Abdul Razak, Wan Heng Fong and Nor Haniza Sarmin, **Graph Splicing Rules with Cycle Graph and its Complement on Complete Graphs**, Journal of Physics: Conference Series, 1988: 012067, 2021.
3. Muhammad Nur Syiham Abdul Razak, Wan Heng Fong and Nor Haniza Sarmin, **Spliced Graphs of One Cutting Site in Graph Splicing Systems**. Proceedings of Science and Mathematics, Vol 7 (2022); 1-4
4. Wan Heng Fong, Muhammad Nur Syiham Abdul Razak and Nor Haniza Sarmin, **On  $n$ -Cut Splicing and Its Properties**, AIP Conference Proceedings 2465: 020016 (2022); (doi: 10.1063/5.0078670).



# Fuzzy Splicing Systems

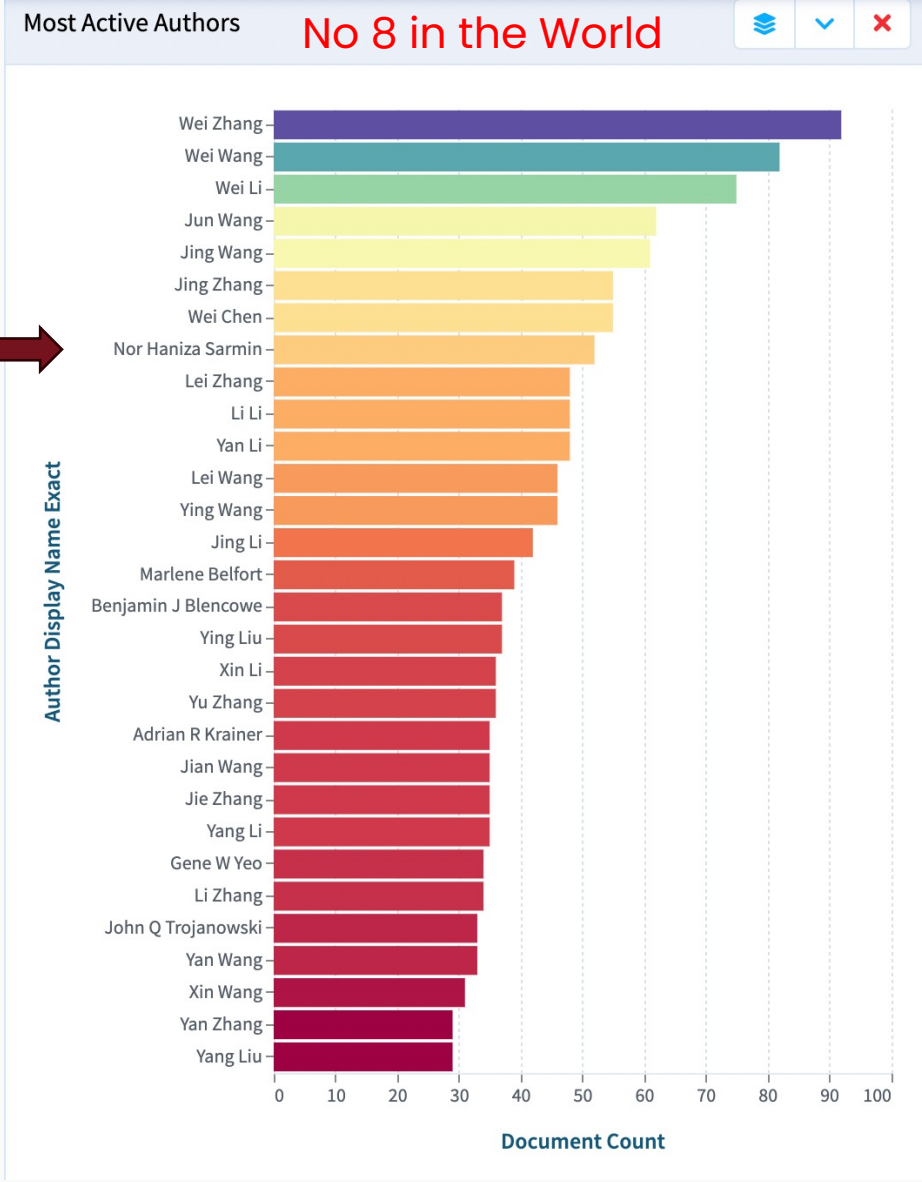
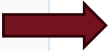
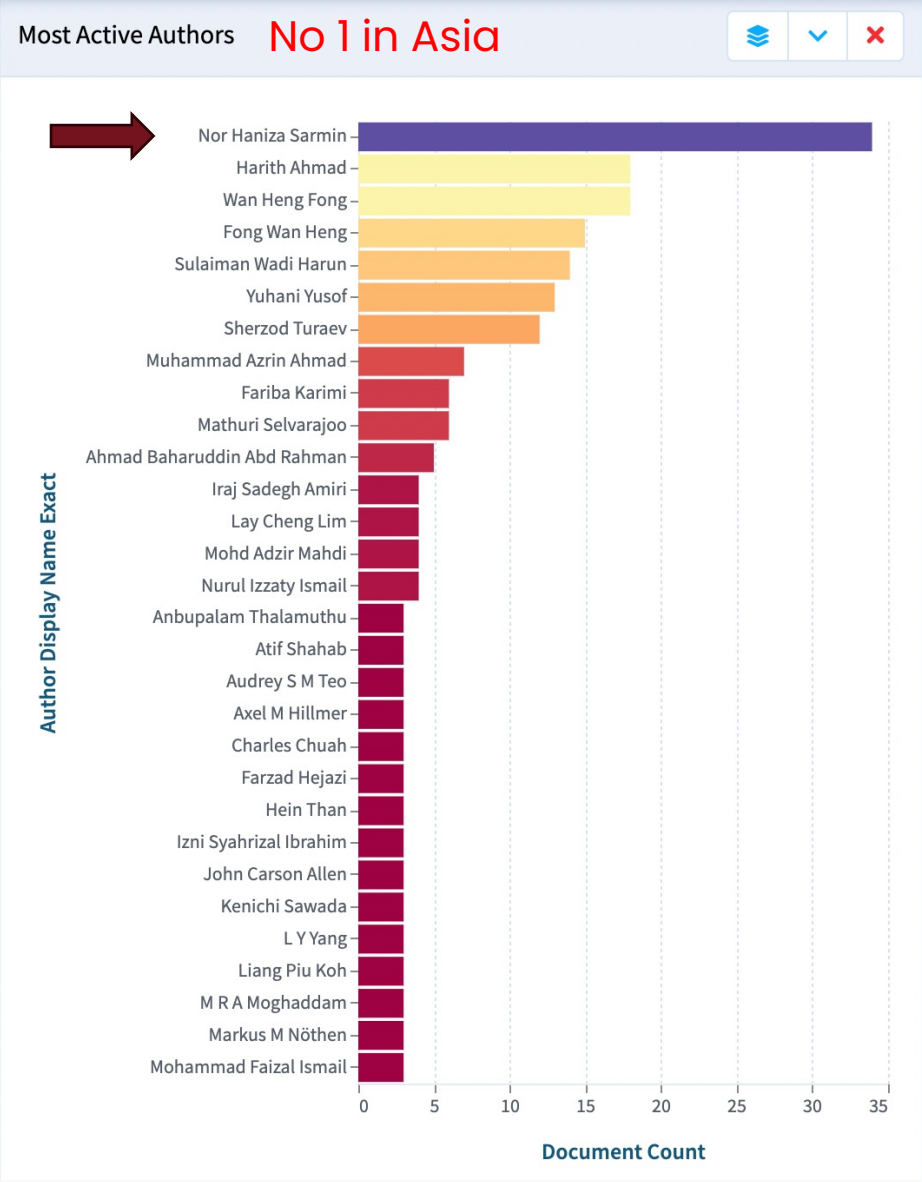
1. Mohd Pawiro Santono, Mathuri Selvarajoo, Wan Heng Fong, Nor Haniza Sarmin, **Some Properties of Bounded-Addition Fuzzy Splicing Systems**, International Journal of Mechanical Engineering, vol. 6, no. 3, pp. 2698–2705, 2021
2. Mohd Pawiro Santono, Mathuri Selvarajoo, Wan Heng Fong and Nor Haniza Sarmin, **Bounded-Addition Fuzzy Simple Splicing Systems**, Journal of Algebraic Statistics, vol. 13, no. 2, pp. 2079–2089, 2022.







# Ranking in Splicing Systems (Lens.org)



# Active Collaborator on DNA Splicing System



## Specialization:

1. Formal Languages and Automata
2. DNA Computing
3. Artificial Intelligence
4. Cryptography

**Ass. Prof. Dr. Sherzod Turaev**

College of Information Technology, United Arab Emirates University

Co-supervisor for some PhD students

# Active Collaborator on DNA Splicing System



## Specialization:

1. Spectral of Laplacian Hypergraph and Graph
2. Distance Matrices and Quadratic Embedding of Graphs
3. Machine Learning
4. DNA Sequencing

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# My Collaborators Around the World

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- Visscher, Matthew P

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- Darafsheh, Mohammad Reza
- Erfanian, Ahmad
- Molaei, Mohammad Reza
- Tolue, Behnaz
- Rashid, Samad
- Moradipour, Kayvan
- Karimi, Fariba A.Hediyeh
- Jahandideh, Mariam
- Barakat, Yasamin
- Ghouchan, M Farrokhi
- Jafarabadi, Hossein M

## Iraq

- Khasraw, Sanhan
- Samin, Nizar Majeed
- Mohialdeen, Vian Salah
- Abdulla, Chenar

## Afghanistan

- Mudaber, Hassan

## United Arab Emirates

- Turaev, Sherzod

## Qatar

- El-Sanfaz, Mustafa Anis

## Libya

- Omer, Sanaa Mohamed Saled
- Awad, Emtinan
- Saleh, Masaoud Omran
- Ramadan, Fatma

## Saudi Arabia

- Birkia, Rabiha
- Al-Rehali, Suad
- Alshammari, Maryam

## United Kingdom

- Subramaniam, K. G

## Nigeria

- Gambo, Ibrahim

## South Africa

- Engelbrecht, Andries Petrus
- Russo, Francesco G

## Italy

- Malinin, Dmitry A

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- A. Divya
- A. Manimaran

## Brunei Darussalam

- Venkat, Ibrahim

## Pakistan

- Khan, Asghar
- Khan, Faiz Muhammad
- Khan, Hidayatullah
- Ghafoor, Asad

## South Korea

- Jun, Young Bae

## Taiwan

- Gan, Yee Siang

## Indonesia

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- Muchtadi, Intan Alamsyah
- Wijayanti, Indah Emilia
- Wardhana, Adhitya
- Alfi Yusrotis Zakiyyah
- Siti Zahidah
- Maulana, Fariz
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In the Name of God for Mankind