SRM TRP ENGINEERING COLLEGE
Affiliated to ANNA UNIVERSITY
TIRUCHIRAPPALLI

Department of Mathematics

Organizes

International Faculty Development Programme (FDP)

On

APPLIED MATHEMATICS IN ENGINEERING AND TECHNOLOGY

27.03.2024 10.30 AM -12.30 PM

DAY 07

Mode : Online

Resource Person

Dr NOR HANIZA SARMIN

Professor of Mathematics,
Faculty of Science,
Universiti Teknologi Malaysia Johor, Bahru Malaysia.

Applications of DNA Computation in Industrial Technology

Convenor
Dr. S. Radhakrishnan ,
AssistantProfessor/Mathematics,

Coordinator
Dr.K. Iyappan,
Associate Professor/Mathematics,

Organizing Secretary
Dr.S.Sridevi,
AssistantProfessor/ Mathematics,

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“Applications of DNA Computation in Industrial Technology”

International Faculty Development Program on
Applied Mathematics in Engineering and Technology

Organized by
Department of Mathematics,
SRM TRP Engineering College,
Tiruchirappalli, India

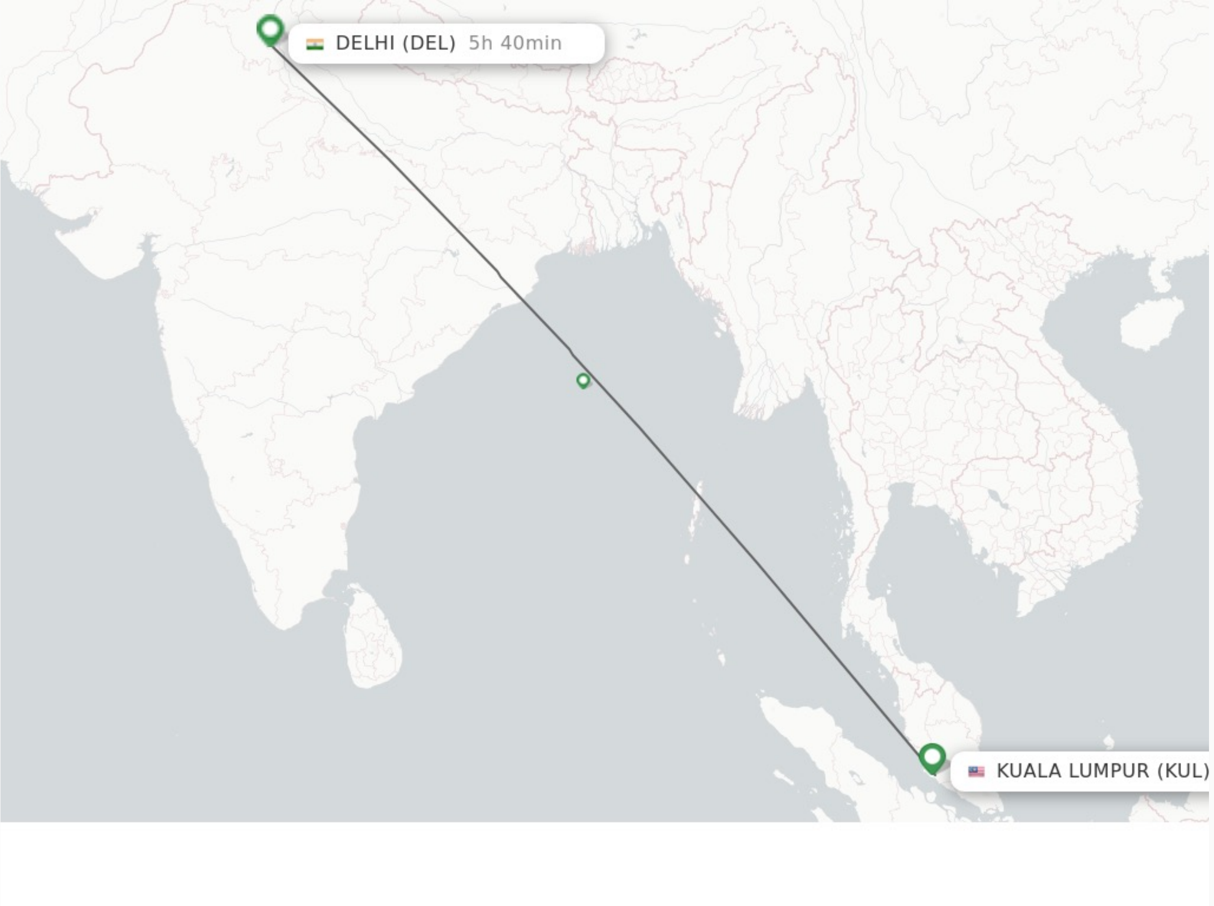
27 March 2024

PROF DR NOR HANIZA SARMIN
Department of Mathematical Sciences,
Faculty of Science, Universiti Teknologi Malaysia
nhs@utm.my

Innovating Solutions

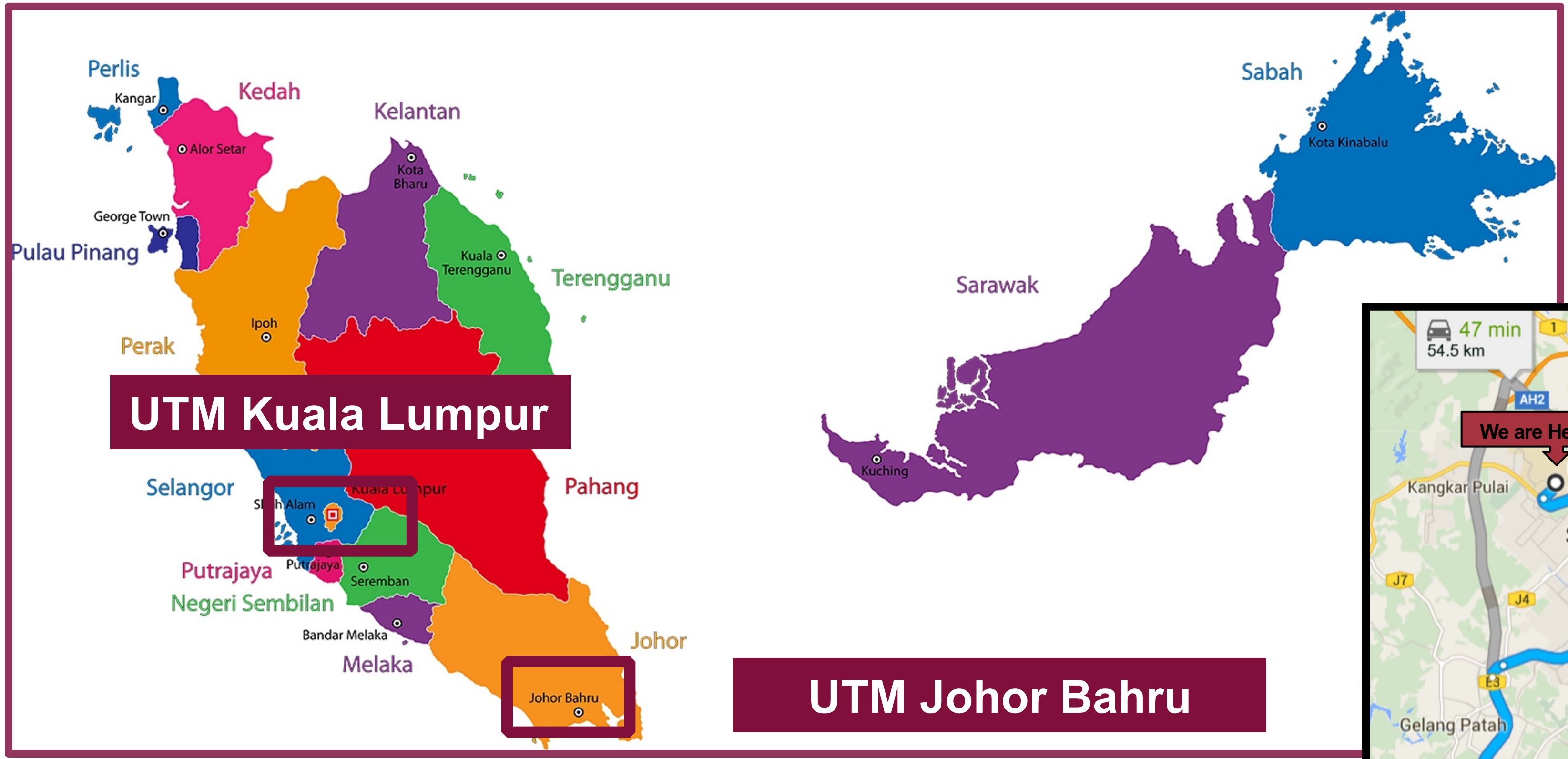
Malaysia in the World Map

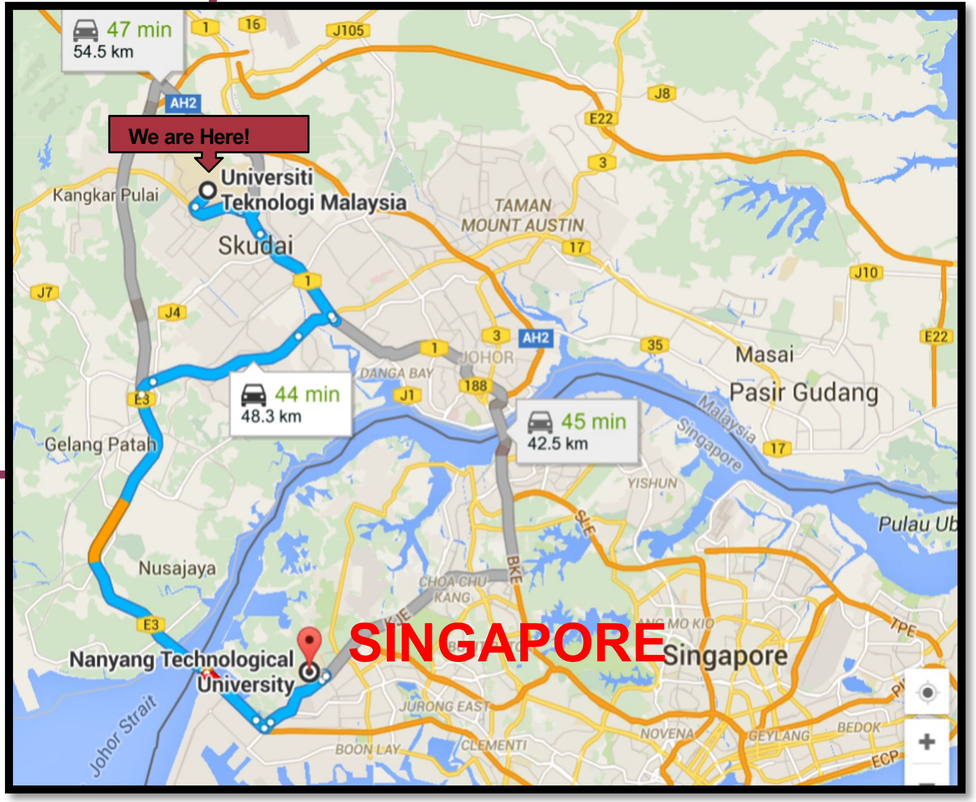
From India to Malaysia



- The distance between India and Malaysia is estimated at 4,218 km or 2621 miles.
- A typical flight would have a flying time of about 4 – 5 hours.
- Time difference between India and Malaysia is 2:30 hours.

UTM Location





Faculties in UTM

12
Faculties

Civil Engineering

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

Mechanical Engineering

- Applied Mechanics & Design
- Thermo Fluids
- Aeronautics, Automotive & Ocean Engineering
- Materials, Manufacturing & Industrial Engineering

Chemical & Energy Engineering

- Chemical Engineering
- Petroleum Engineering
- Bioprocess & Polymer
- Energy Engineering

Petroleum Engineering **#44 & 2 in MAS**

Electrical Engineering

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

Computing

- Computer Science
- Applied Computing
- Software Engineering

Built Environment & Surveying

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

Architecture/ Built Environment **TOP 100 & #3 in MAS**

Management

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

Science

Environmental Sciences **TOP 200 & #3 in MAS**

- Biosciences
- Physics
- Chemistry
- Mathematical Sciences

Social Sciences & Humanities

Education **TOP 200 & #3 in MAS**

- 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

Faculty of Artificial Intelligence

- Engineering & Technology
- Science, Management & Design
- Advanced Informatics
- Perdana Centre

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

DEPARTMENT OF MATHEMATICAL SCIENCES
FACULTY OF SCIENCE
UNIVERSITI TEKNOLOGI MALAYSIA
https://science.utm.my/mathematics/

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

DEPARTMENT OF MATHEMATICAL SCIENCES
FACULTY OF SCIENCE
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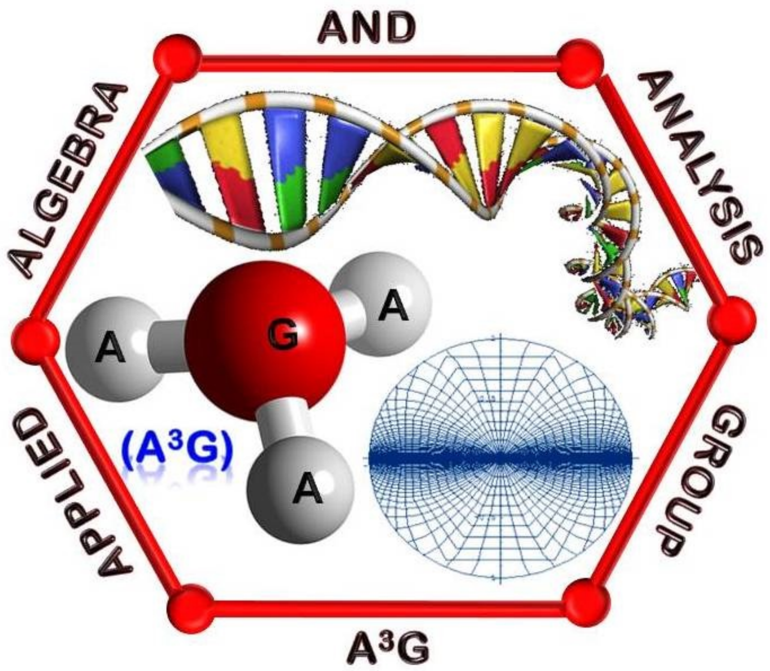
The department is divided into 5 broad research areas/**academic panels**:

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	1989 - 1990	1995 - 1998
B.Sc (Hons) Mathematics (Minor in Economics)	**MA Mathematics**	**PhD Mathematics**

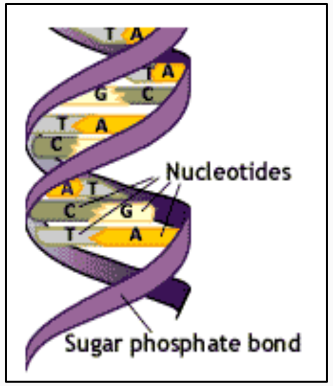
"Applications of DNA Computation in Industrial Technology"

Abstract

The diversity of mathematical applications in various scientific concepts has led to significant advancements in understanding complex biological processes. One area where this interdisciplinary collaboration thrives is DNA Computing, specifically DNA Splicing, a basic biological process in manipulating genetic information and simulated by the technique of recombinant DNA molecules that relies on restriction enzymes. This presentation explores the idea of DNA splicing in various concepts. Firstly, the fundamental mathematical framework behind DNA splicing is presented. Also, the interplay between mathematical models and wet lab experiments is shared to validate the theoretical findings. The emergence of DNA splicing in industrial technology, particularly in computer science where some computational models such as graphical user interface (GUI) are discussed. Finally, the graphical approach in mathematics to studying DNA splicing is presented to emphasize the role of visual representation in comprehending complex biological processes.

DNA Structure

Structure of DNA



DNA – Deoxyribonucleic Acid

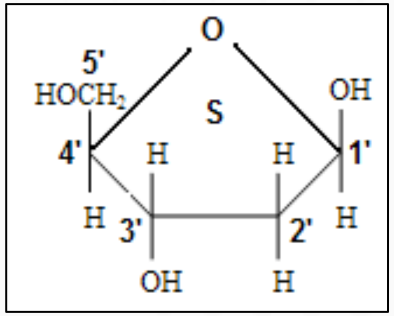
made up of

Nucleotides

Phosphate group

Base

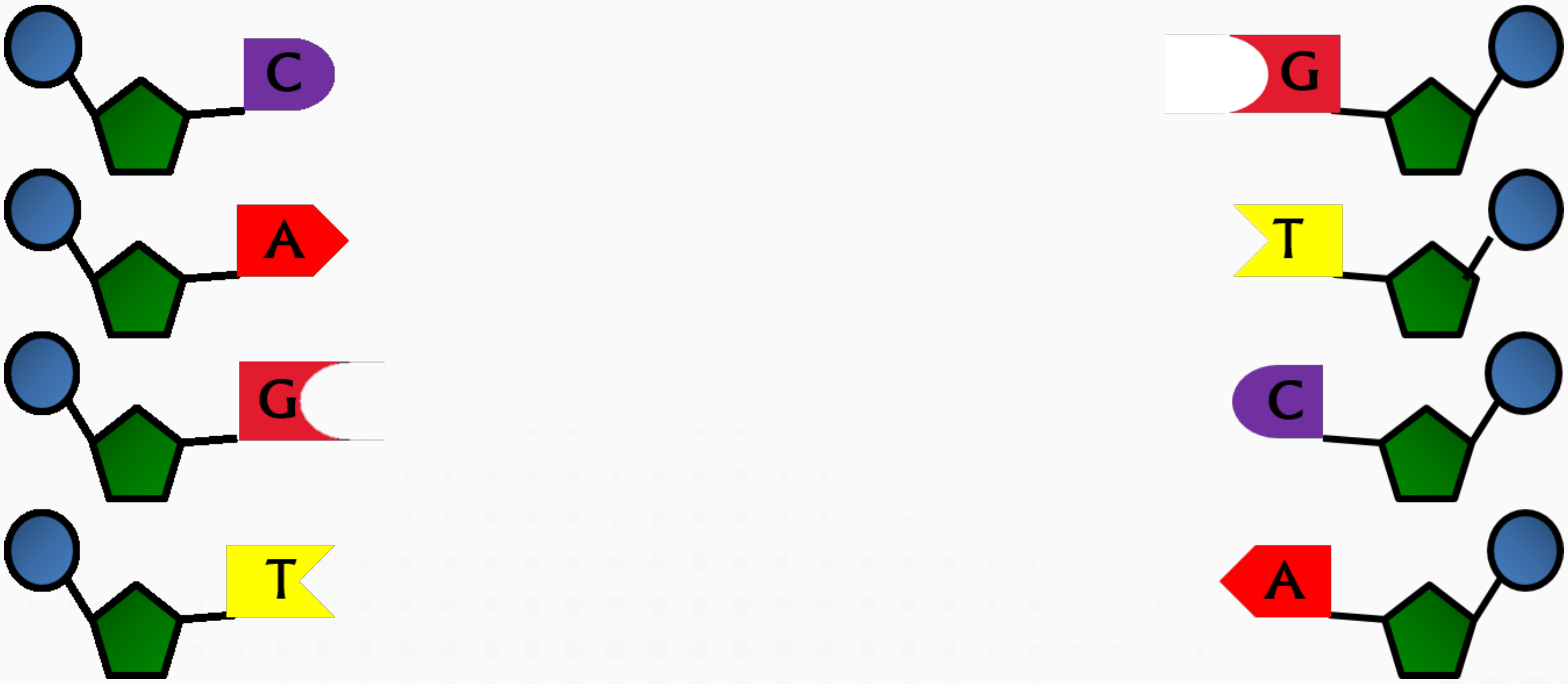
Pentose (a 5-carbon sugar)



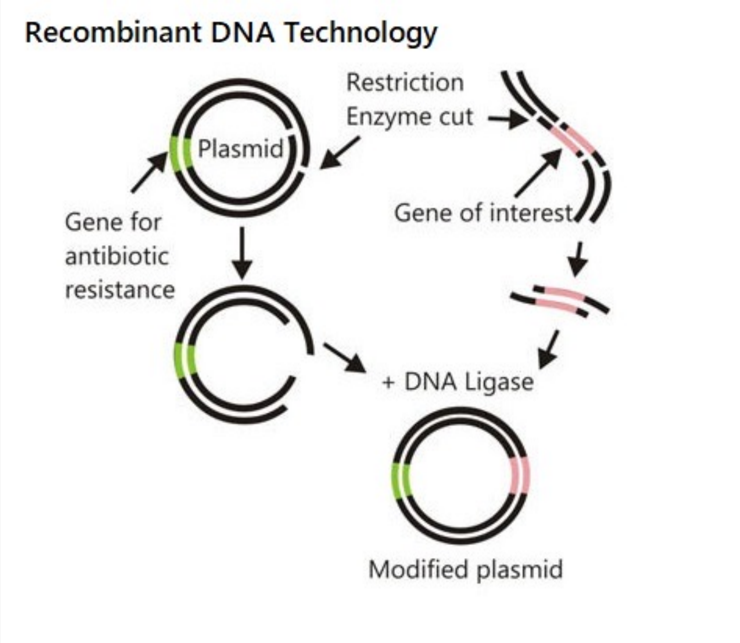
Adenine (A)
Cytosine (C)
Guanine (G)
Thymine (T)

Structure of DNA (Cont.)

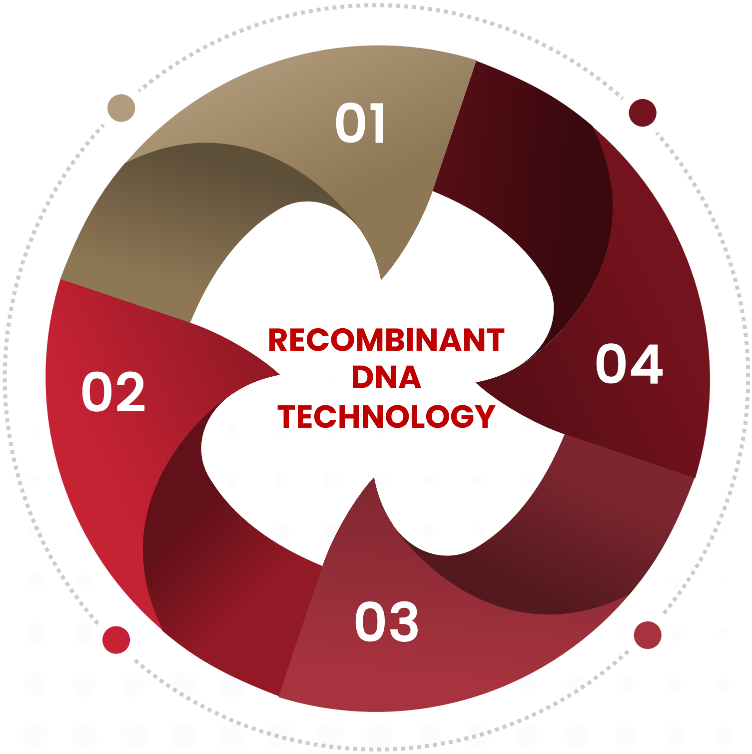
Watson-Crick Complementary



Recombinant DNA



VARIOUS APPLICATIONS OF RECOMBINANT DNA TECHNOLOGY



1. GENETICALLY MODIFIED PRODUCTS
Fruits
Vegetables
Crops
Microbs
Animals

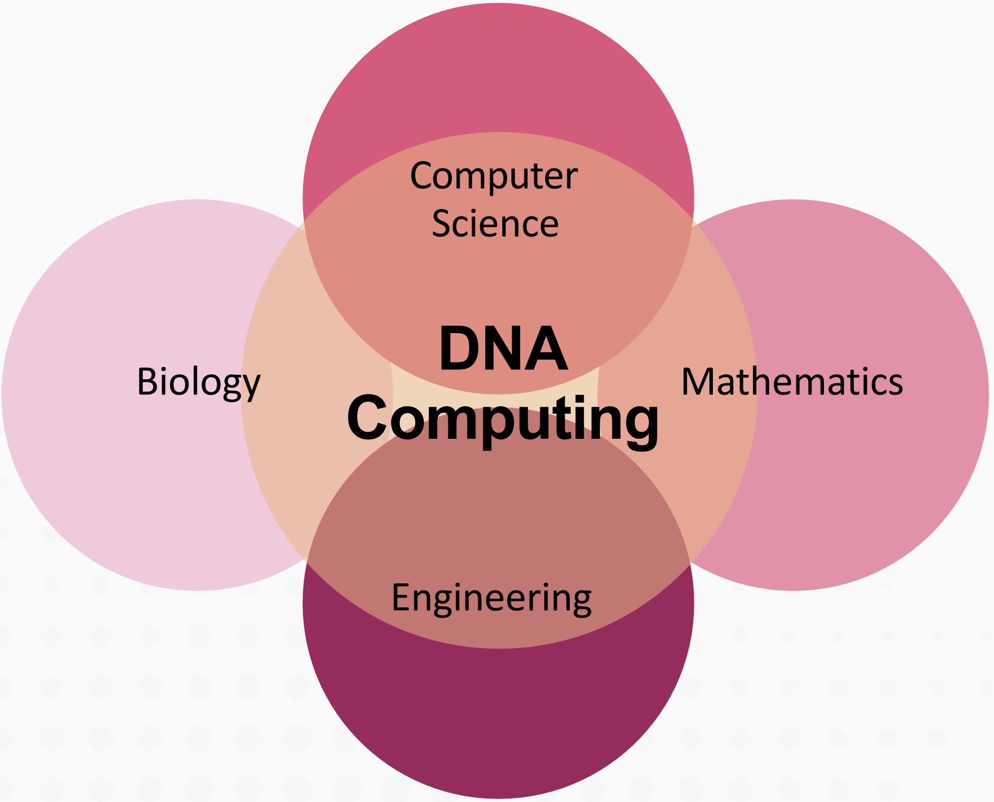
2. THERAPEUTIC PRODUCTS
Vaccines
Growth hormones
Antibodies
Anticancer drugs
Recombinant protein

3. DIAGNOSIS
Gene therapy
Monitoring device
Therapeutic strategies
CRISPR

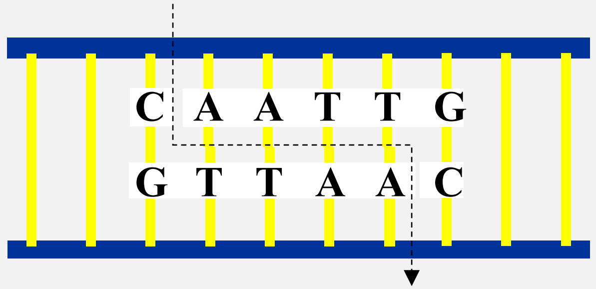
4. ENERGY APPLICATIONS
Biohydrogen
Bioethanol
Biomethanol
Biobutanol

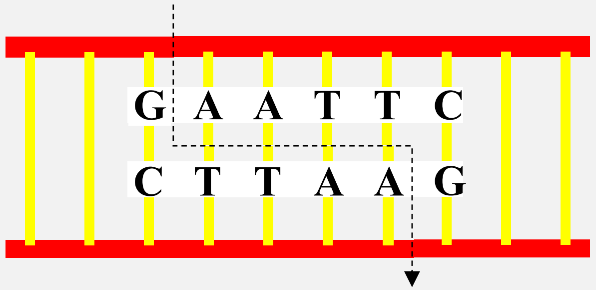
DNA Computing

- 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

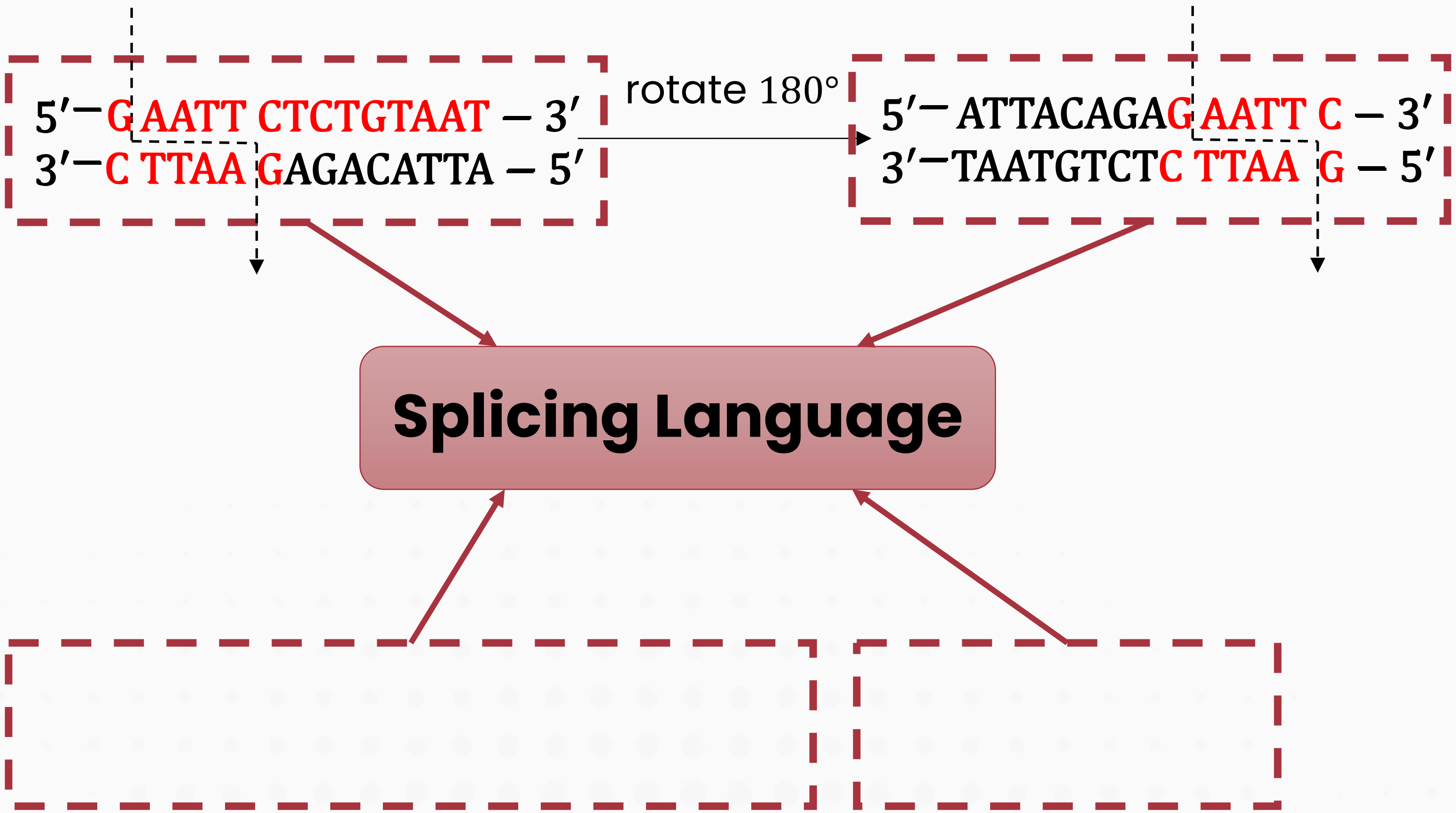
Mathematical Modelling of DNA Splicing System

How do we model it?

Mathematics and Formal Language	
Alphabets	$h, n, i, z, a, s, m, r, o$
Strings	nor & $haniza$ & $sarmin$
Grammar	$Nor + Haniza$ $Haniza + Sarmin$
Language	$Nor\ Haniza$ $Haniza\ Sarmin$

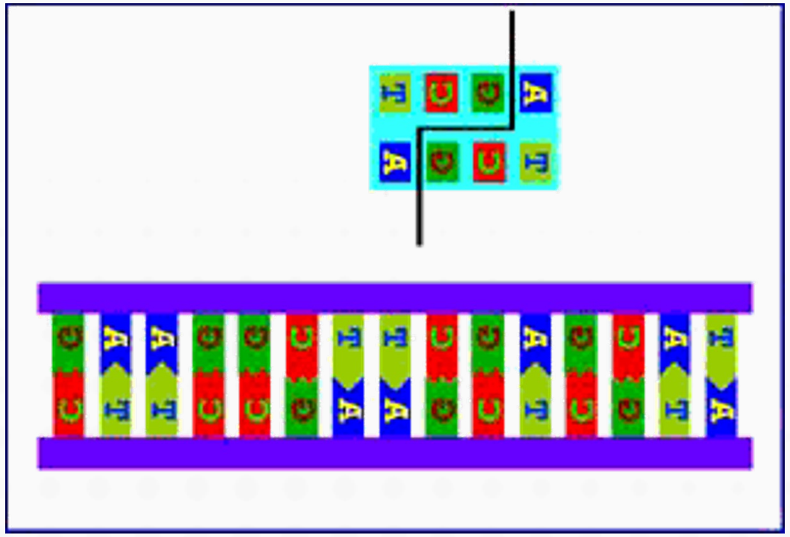
DNA in Mathematical Model	
DNA bases	a, c, g, t
DNA Sequence	$acgttgat$ & $gcgttga$
DNA Splicing	$acgt-$ $-tgat$ & $gcgt-$ $-tga$
Grammar	Watson-Crick
Language	$acgttga$ & $gcgttgat$

Mathematical Modelling of DNA Splicing System (Cont.)



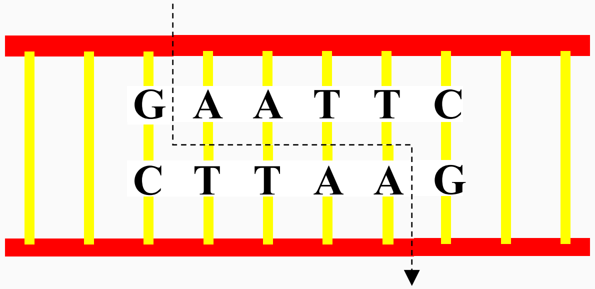
Restriction Enzymes

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

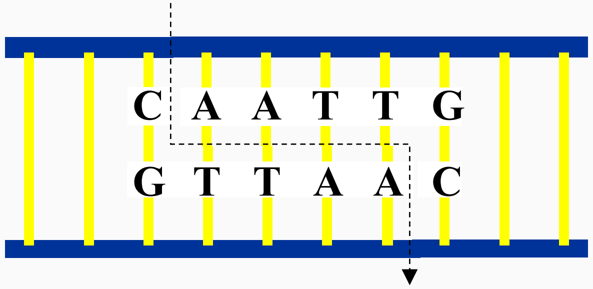


Restriction Enzymes (Cont.)

*Eco*RI: ([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])



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

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.

Types of DNA Splicing Systems (Cont.)

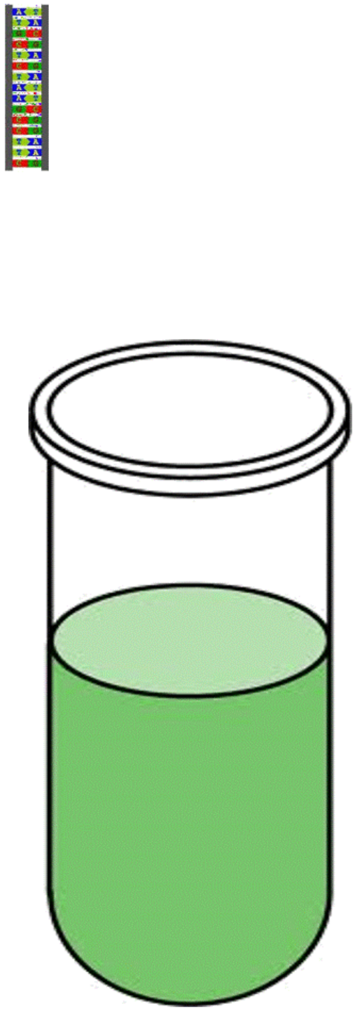
Splicing System	Head $S = (A, I, B, C)$	Paun $\sigma = (A, R)$	Pixton $\zeta = (R, I)$	Goode-Pixton $(w, w') \vdash_r z$	Yusof-Goode $S = (A, I, R)$	Fuzzy $S = (A, T, I, R, \odot)$
Initial String	$ucxdv$ $pexfq$	uu_1u_2v $u'u_3u_4v'$	$\xi\alpha\eta$ $\xi'\alpha'\eta'$	$w = xuvy$ $w' = x'u'v'y'$	$\alpha uxv\beta$ $\gamma yz\delta$	(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	$ucxfq$ $pexdv$	uu_1u_4v'	$\xi\beta\eta'$	$z = xuv'y'$	$\alpha uxz\delta$ $\gamma yxv\beta$	$(uv, x \odot y)$ $\odot$ is fuzzy operation

- S: splicing system
- σ and ζ: 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 *Aci*I

- 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 *Aci*I where the genome locations for the cutting sites are found at 42992-42995 and 43036-43039 respectively.
- Five sticky ends of molecules α, β, γ, $\alpha-\beta$ 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: $\alpha \overline{\text{ CviQI site }} \beta \overline{\text{ AciI site }} \gamma$

$|\alpha|$ = 35 bp

$|\beta|$ = 44 bp

$|\gamma|$ = 81 bp

$|\alpha-\beta|$ = 79 bp

$|\beta-\gamma|$ = 125 bp

Theoretical vs Lab Results (Cont.)
Wet Splicing System involving *Cvi*QI and *Aci*I

- 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 *Aci*I (non-palindromic)

5′…C▼CGC…3′

3′…CGC▲C…5′

Theoretical vs Lab Results (Cont.)

Wet Splicing System involving *CviQ*I and *Aci*I

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

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

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

$$\alpha\,\underline{gtac}\left(\beta\,\underline{ccgg}\,\beta'\,\underline{gtac}\right)^{n-1}\alpha',$$

$$\alpha\,\underline{gtac}\left(\beta\,\underline{ccgg}\,\beta'\,\underline{gtac}\right)^{n-1}\beta\,\underline{ccgc}\,\gamma,$$

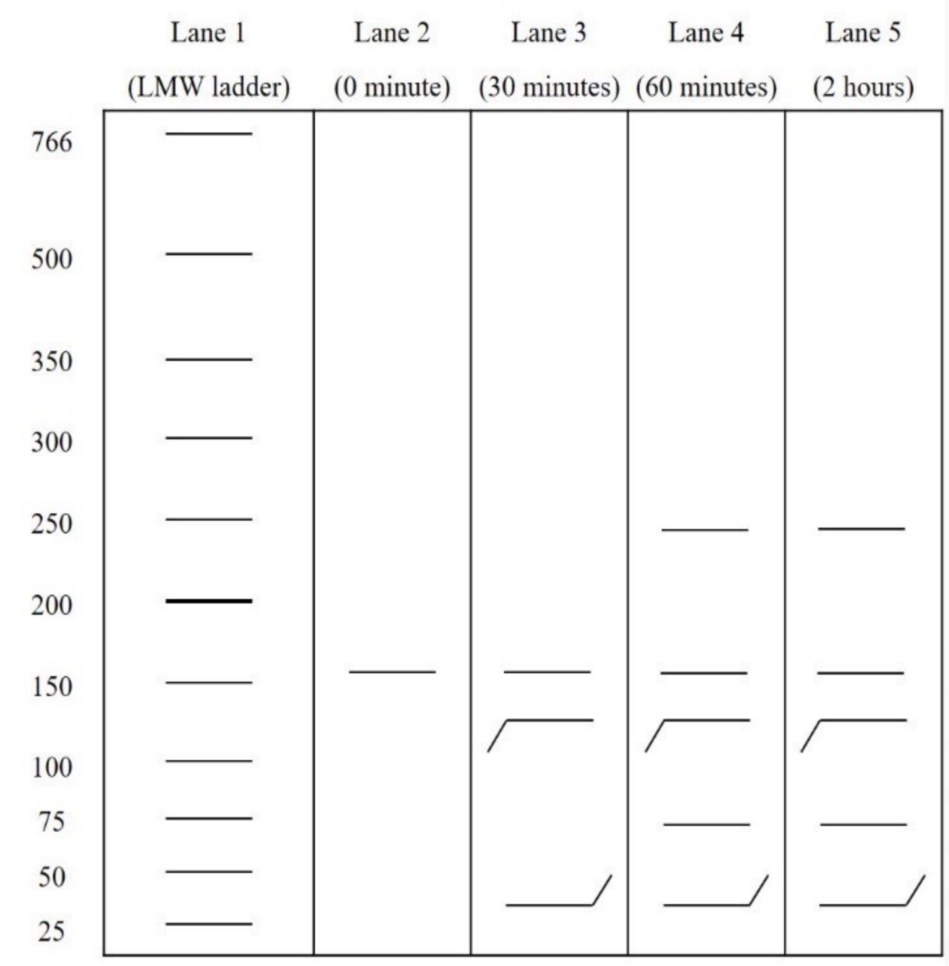
$$\gamma'\,\underline{gcg}\left(\underline{g}\,\beta'\,\underline{gtac}\,\beta\,\underline{ccg}\right)^{n-1}\underline{c}\,\gamma \text{ and}$$

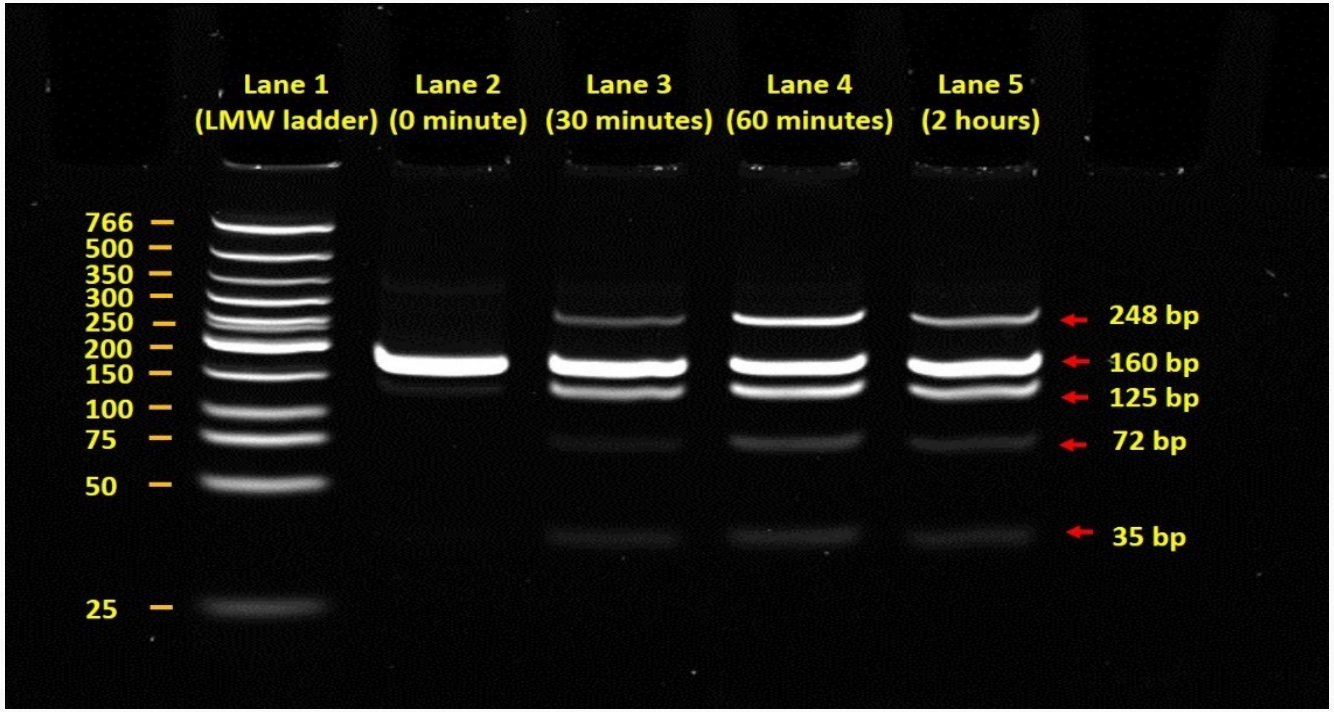
$$\gamma'\,\underline{gcg}\left(\underline{g}\,\beta'\,\underline{gtac}\,\beta\,\underline{ccg}\right)^{n-1}\underline{g}\,\beta'\,\underline{gtac}\,\alpha'$$

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

Theoretical vs Lab Results (Cont.)

Wet Splicing System involving *CviQI*

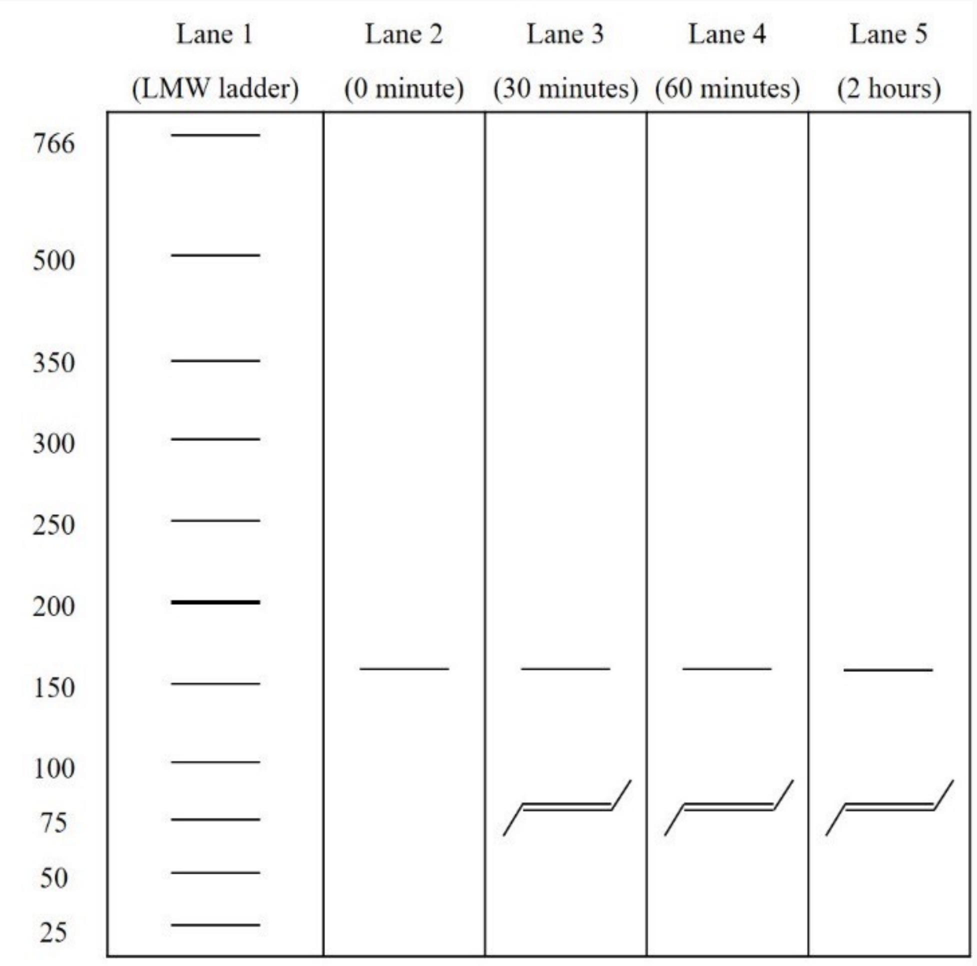


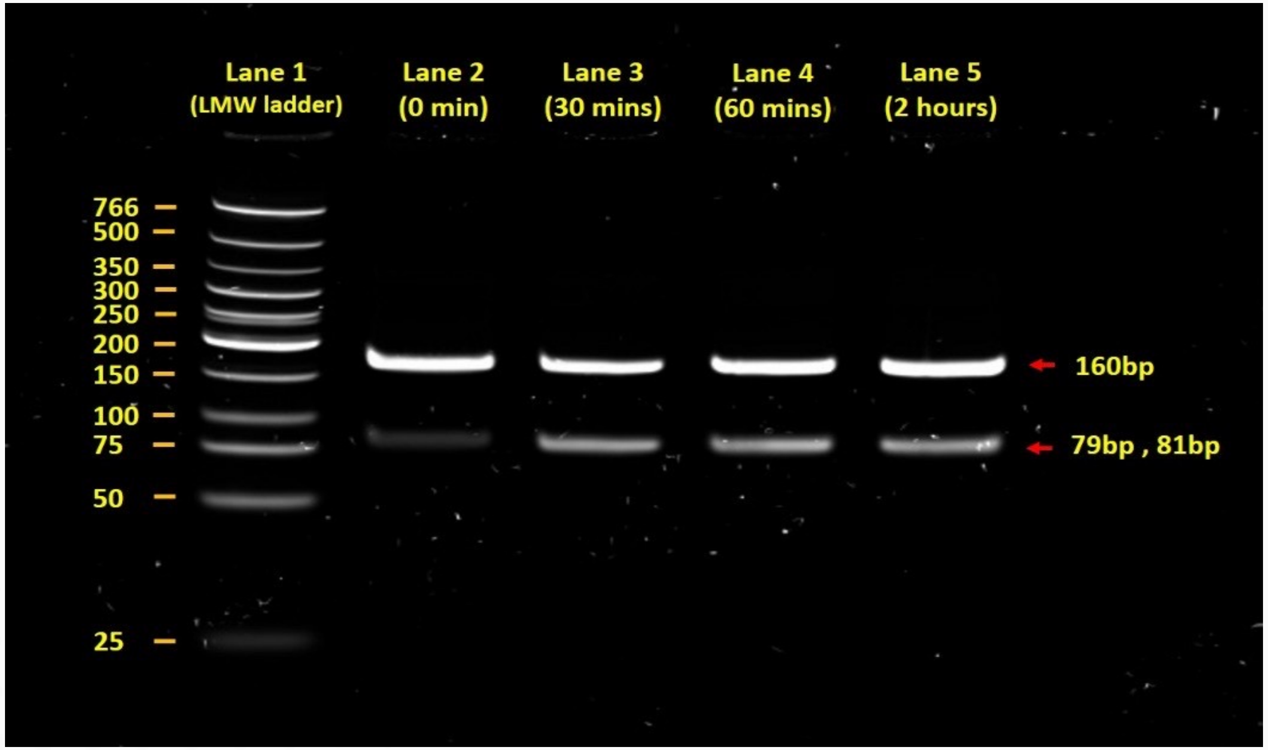


- Lane 1: LMW ladder
- Lane 2 (0 minute): 160 bp
- Lane 3 (30 minutes): 35 bp, 72 bp, 125 bp, 160 bp and 248 bp
- Lane 4 (60 minutes): 35 bp, 72 bp, 125 bp, 160 bp and 248 bp
- Lane 5 (2 hours): 35 bp, 72 bp, 125 bp, 160 bp and 248 bp

Theoretical vs Lab Results (Cont.)

Wet Splicing System involving *Aci*I

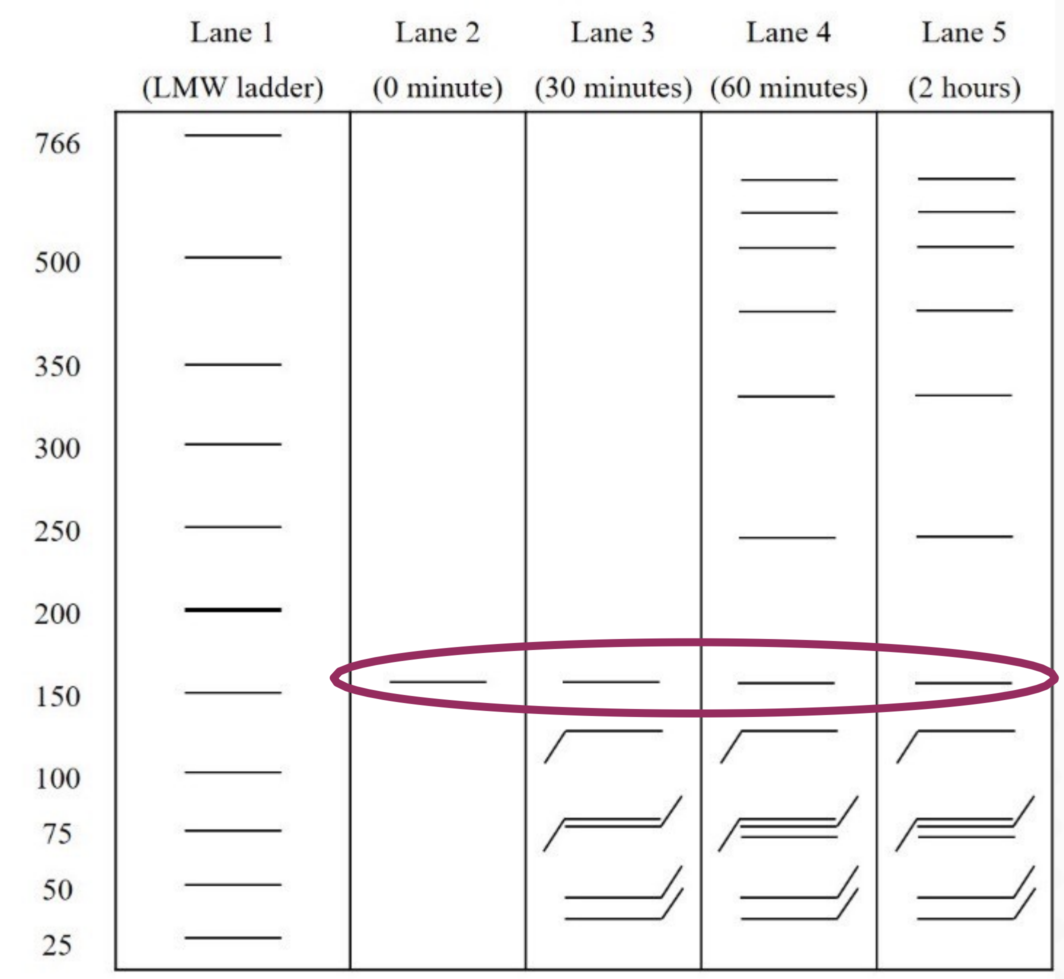


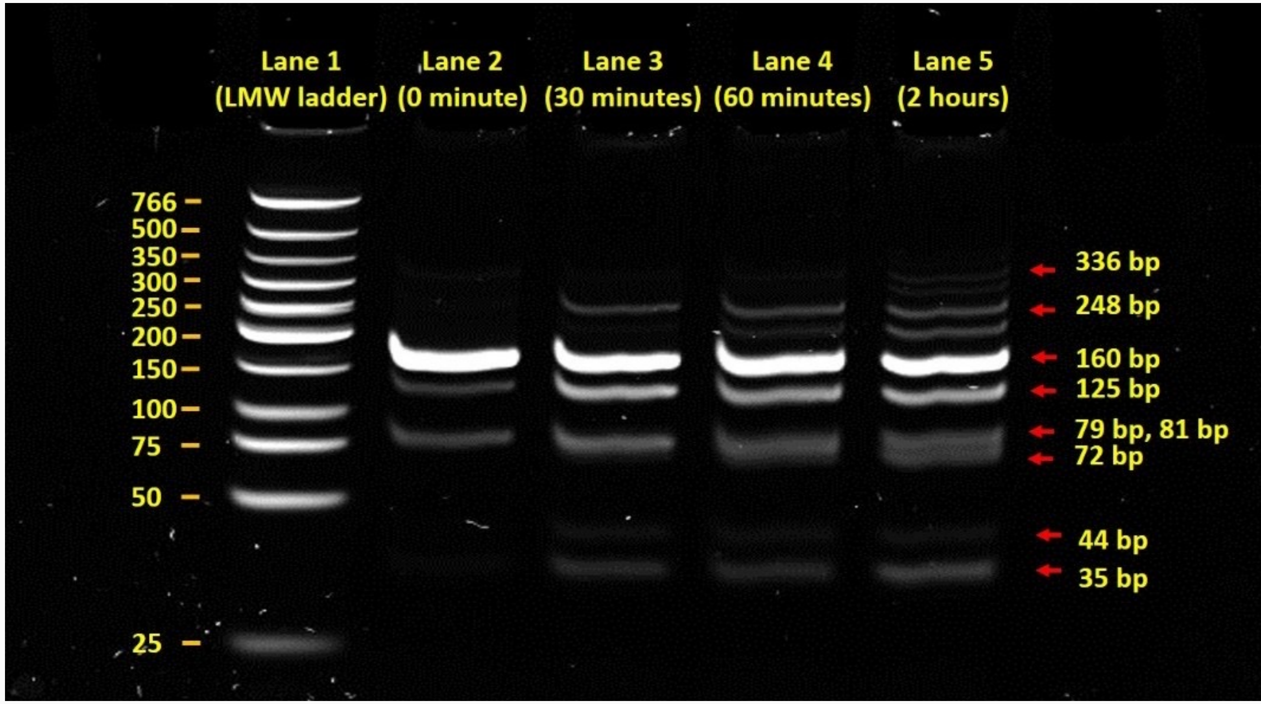


- Lane 1: LMW ladder
- Lane 2 (0 minute): 79 bp (or 81 bp) and 160 bp
- Lane 3 (30 minutes): 79 bp, 81 bp and 160 bp
- Lane 4 (60 minutes): 79 bp, 81 bp and 160 bp
- Lane 5 (2 hours): 79 bp, 81 bp and 160 bp

Theoretical vs Lab Results (Cont.)

Wet Splicing System involving *CviQ*I and *Aci*I



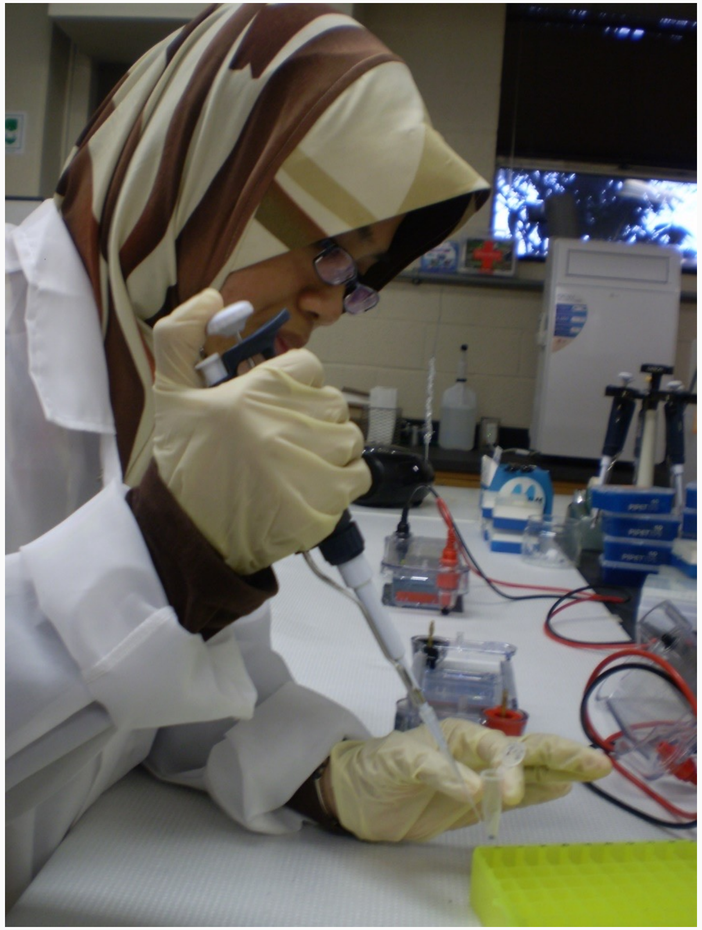


- Lane 1: LMW ladder
- Lane 2 (0 minute): 79 bp (or 81 bp), 125 bp and 160 bp
- Lane 3 (30 minutes): 35 bp, 44 bp, 79 bp, 81 bp, 125 bp, 160 bp, 248 bp
- Lane 4 (60 minutes): 35 bp, 44 bp, 79 bp, 81 bp, 125 bp, 160 bp, 248 bp
- Lane 5 (2 hours): 35 bp, 44 bp, 72 bp, 79 bp, 81 bp, 125 bp, 160 bp, 248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

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

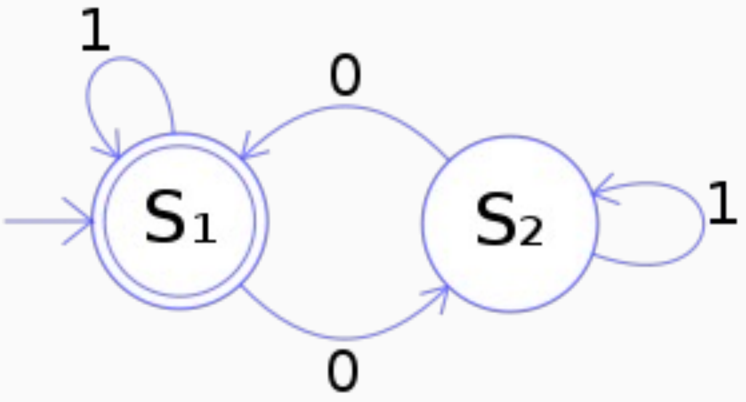
Wet-lab Experiment on Splicing System

Universiti Teknologi Malaysia, 2020

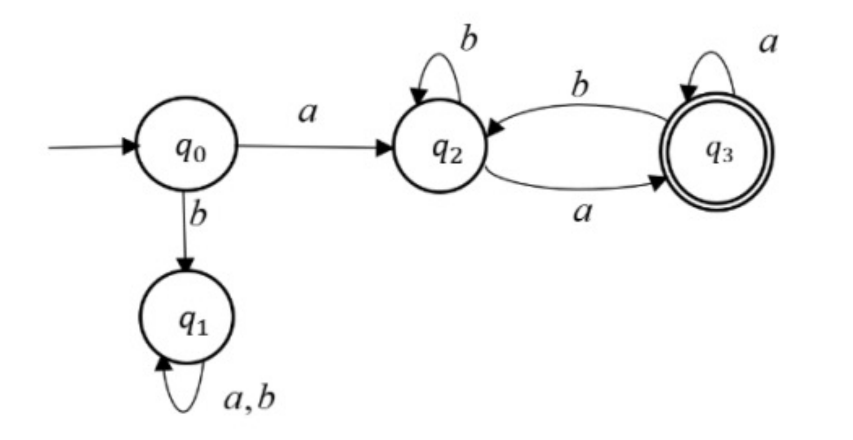
DNA Splicing in Computer Science

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.



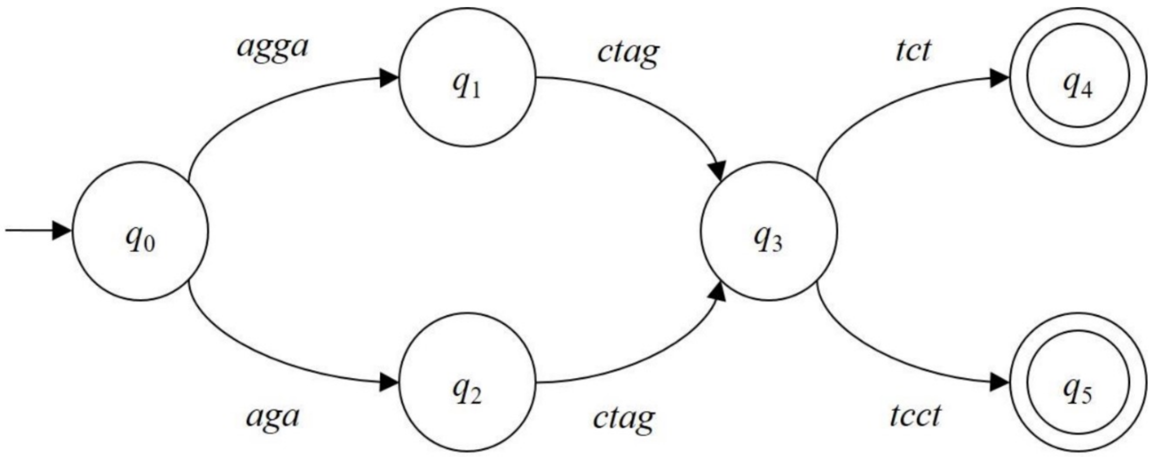
The automaton diagram for regular language

Example

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

The enzyme *Bfa*I, $\begin{matrix} 5' - \text{CTAG} - 3' \\ 3' - \text{GATC} - 5' \end{matrix}$ is a palindromic rule since the base sequence of enzyme *Bfa*I reads the same forwards and backwards.

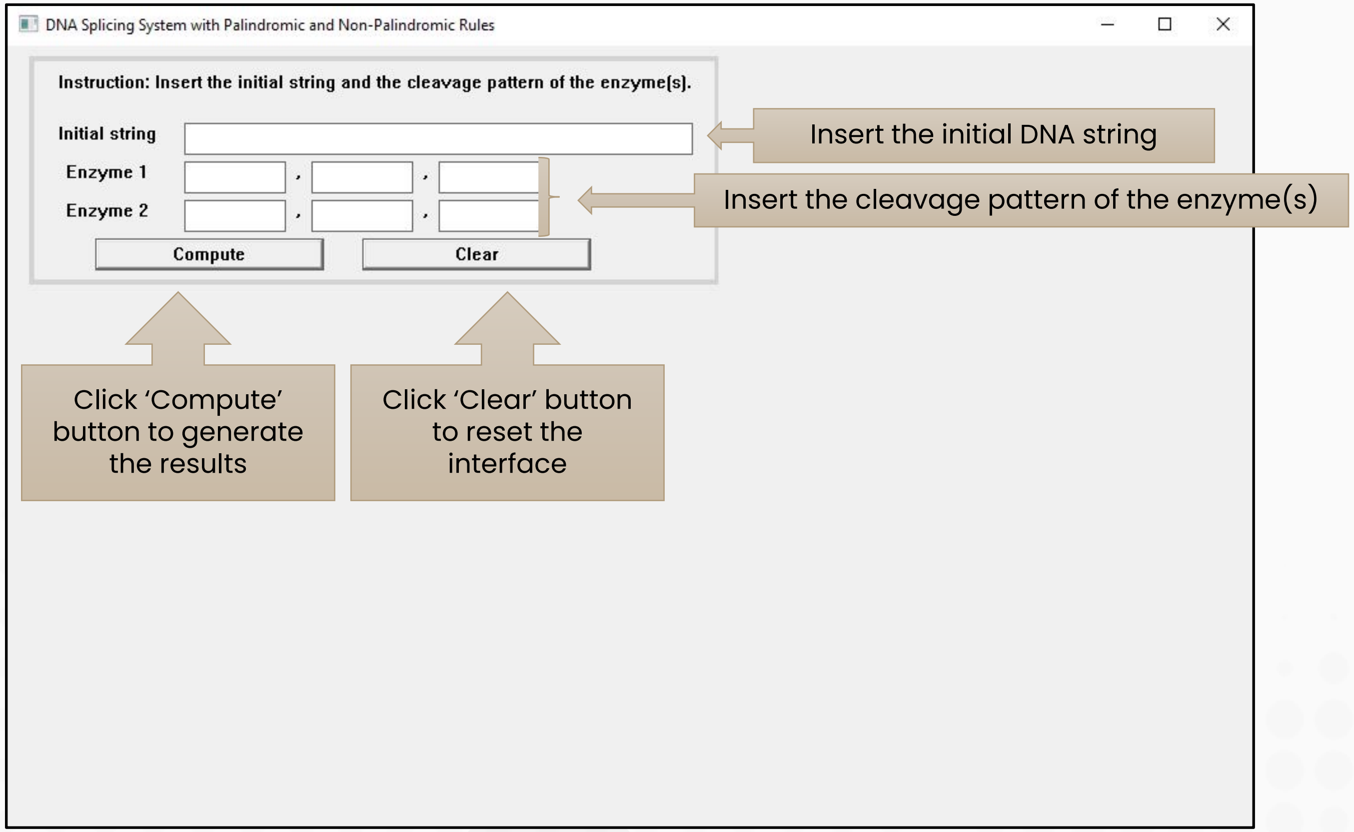
The automata for the splicing system S



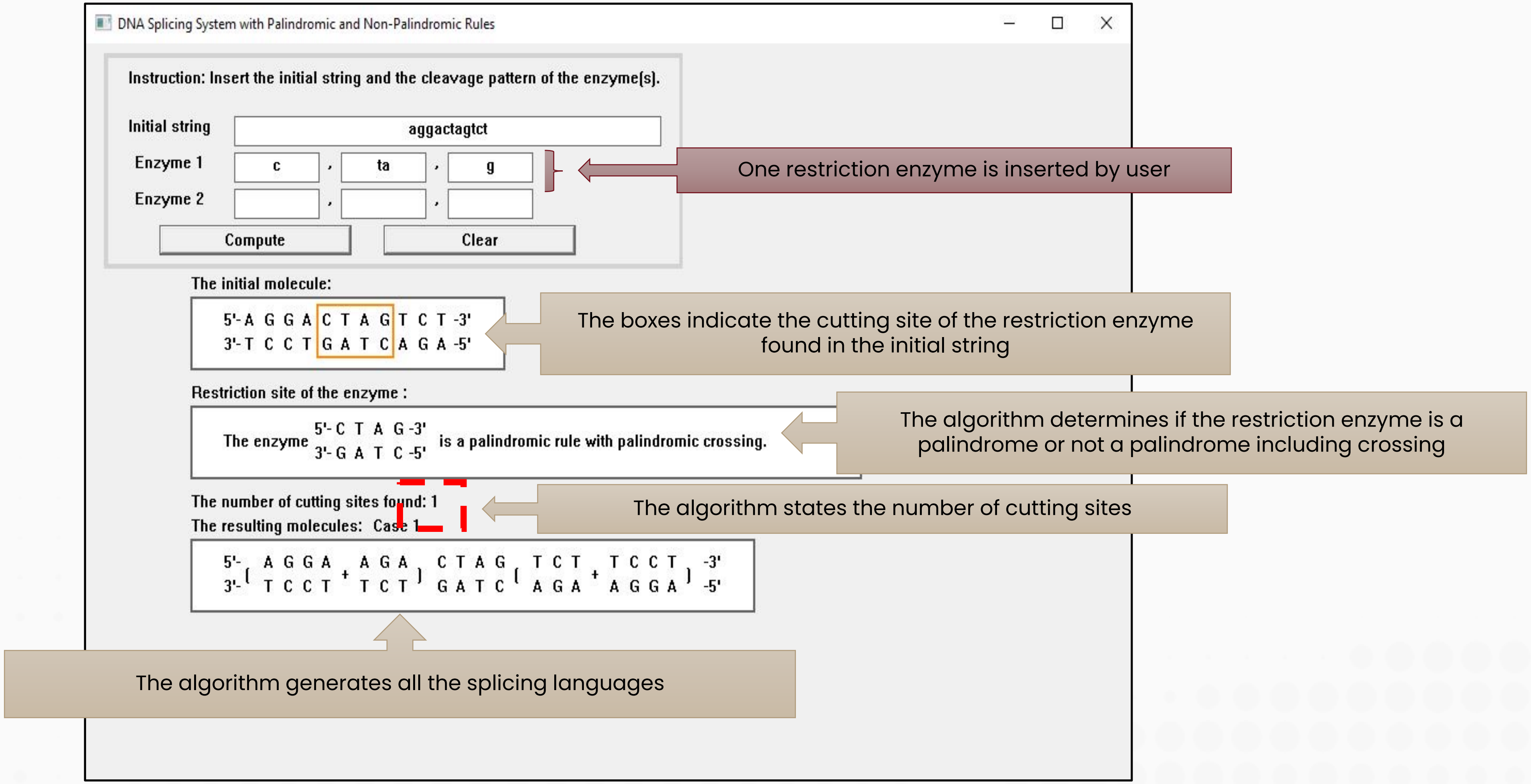
Graphical User Interface (GUI) for DNA Splicing System

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.

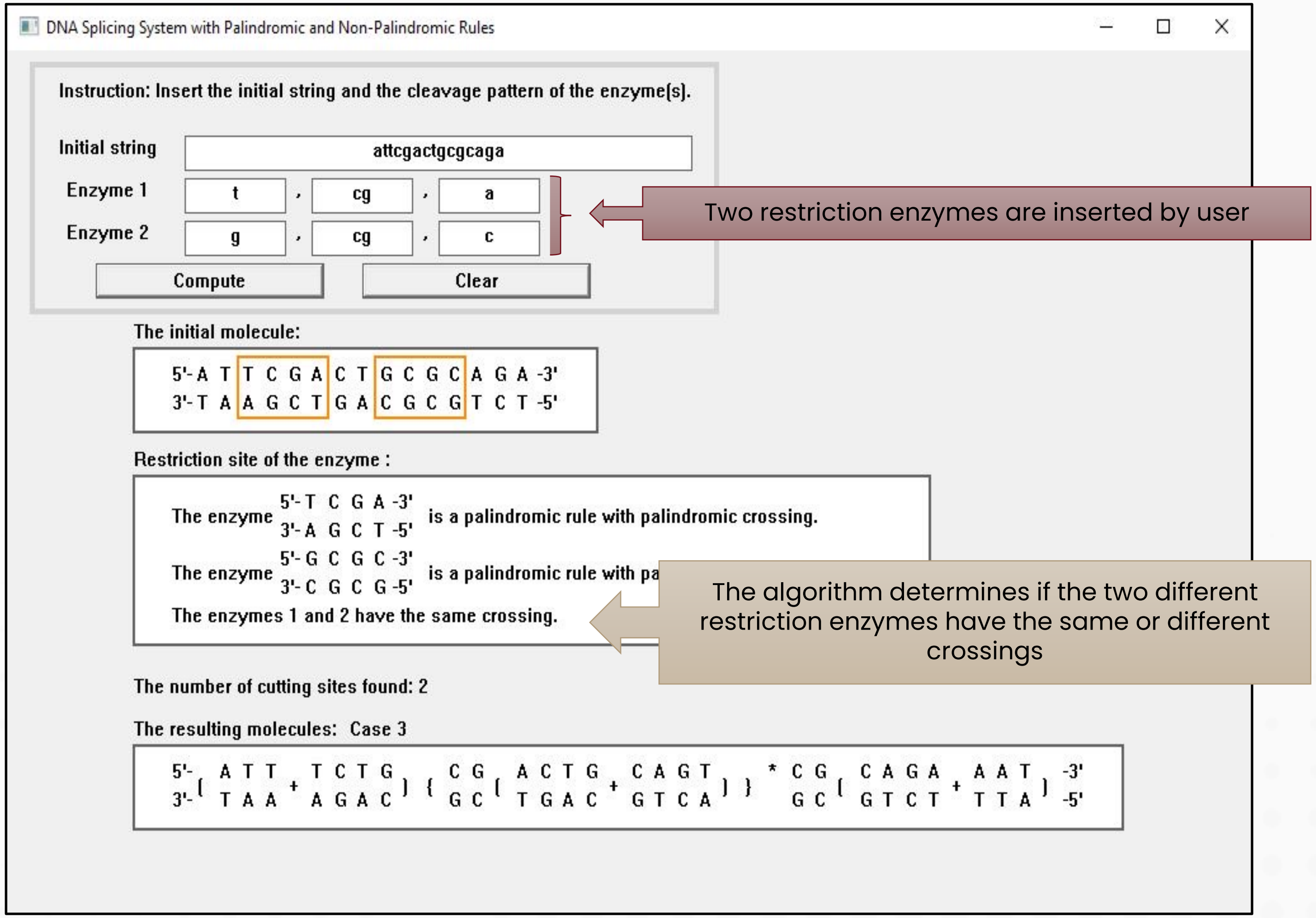


DNA Splicing Language Generator (DNASpliceGen)



DNA Splicing Language Generator (DNASpliceGen)

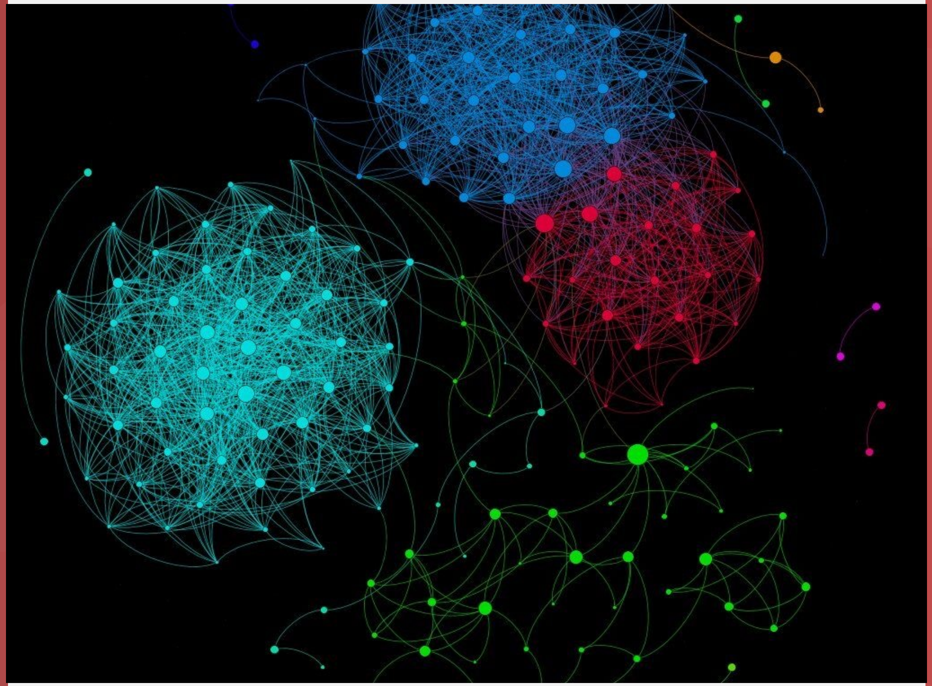
Output of GUI for DNA Splicing System involving Two Rules



Additional features:

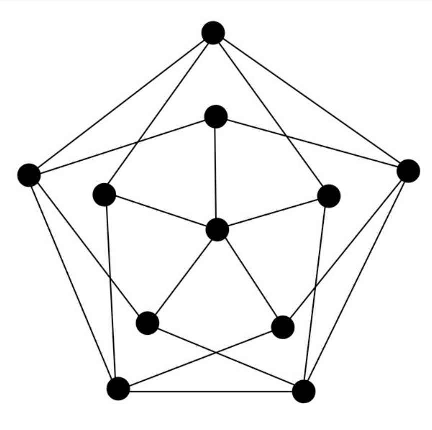
- Certain messages are displayed on the interface if the number of cutting sites found exceeds two
- The interface prompts the users if the cutting sites of restriction enzyme overlap
- The users will be notified if the inputs are incorrect.

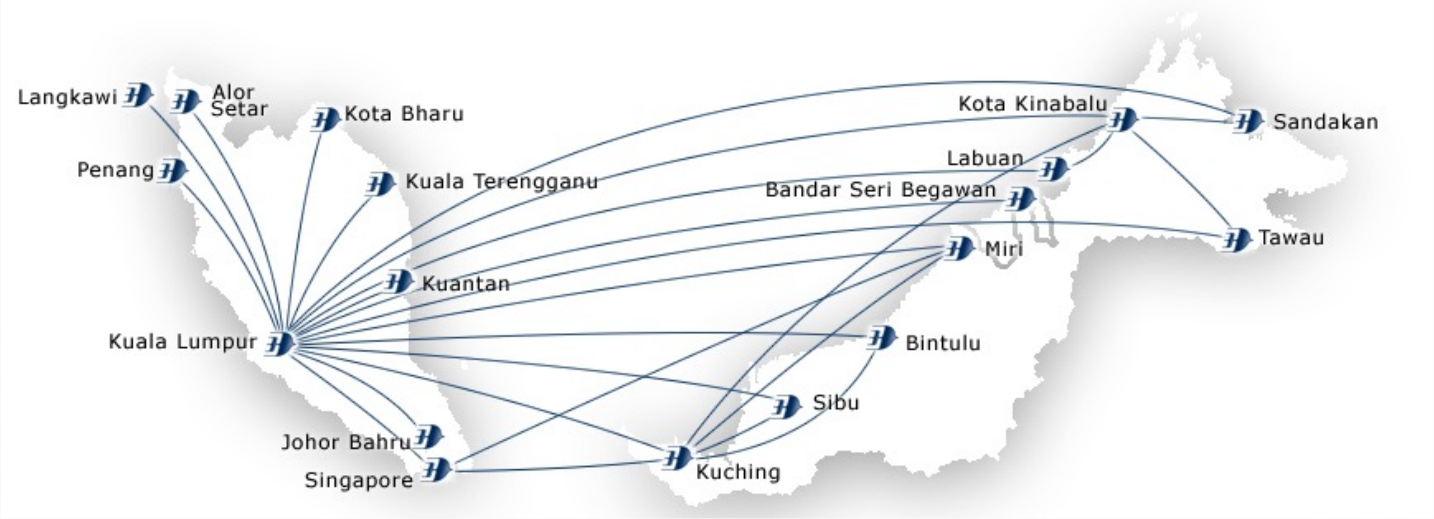
DNA Splicing on Graph Theory



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.

DNA Splicing System

focuses on the recombination behaviors of DNA molecules

with the presence of restriction enzyme(s)

Graph Splicing System

emphasizes on the cuts at various edges on graphs and reconnects them in another way

defined and described in the graph splicing scheme and graph splicing rule

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.

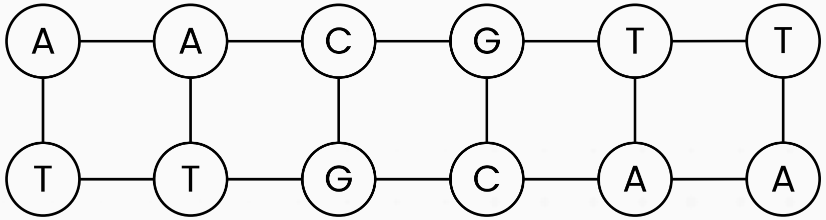
Graph Splicing Rule

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

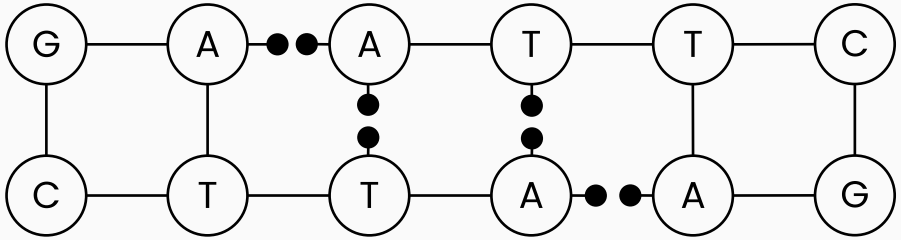
$$p = ((h, E'); R)$$

*EcoR*I: $\left\{\begin{matrix} AA & CG & TT \\ TT' & GC' & AA \end{matrix}\right\}$

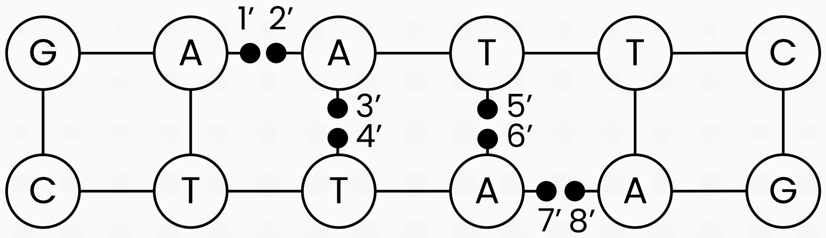
$h =$



$(h, E') =$



$p =$



; (1′,2′), (3′,4′), (5′,6′), (7′,8′)

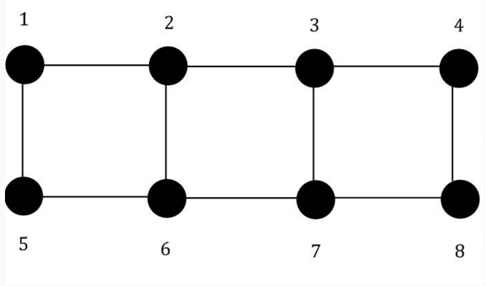
R

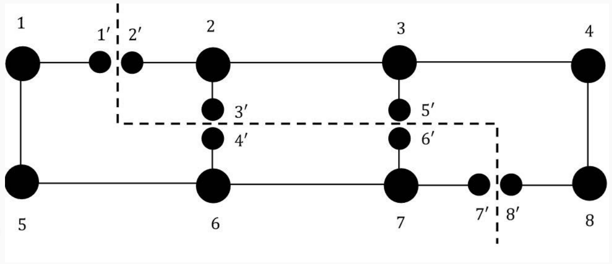
n-Cut Splicing (Cont.)

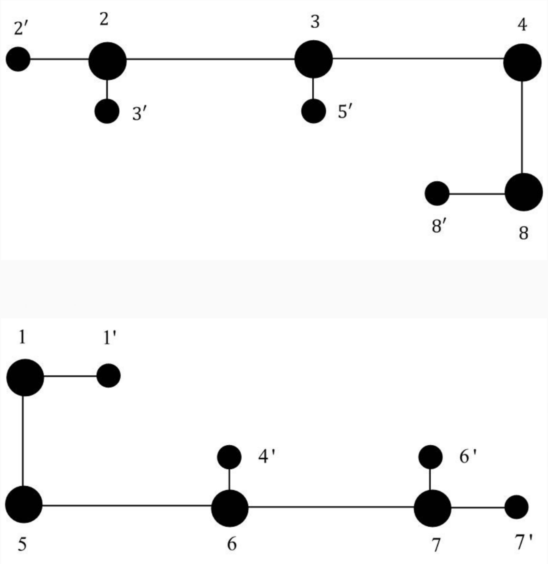
Semigraph representation of DNA molecule

An *n*-cut splicing is applied

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

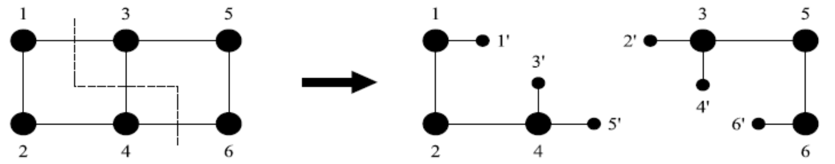
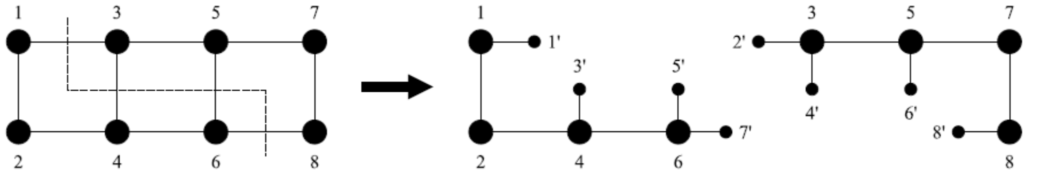
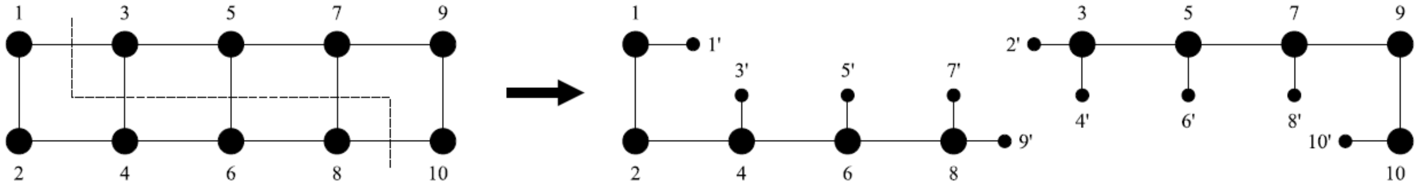






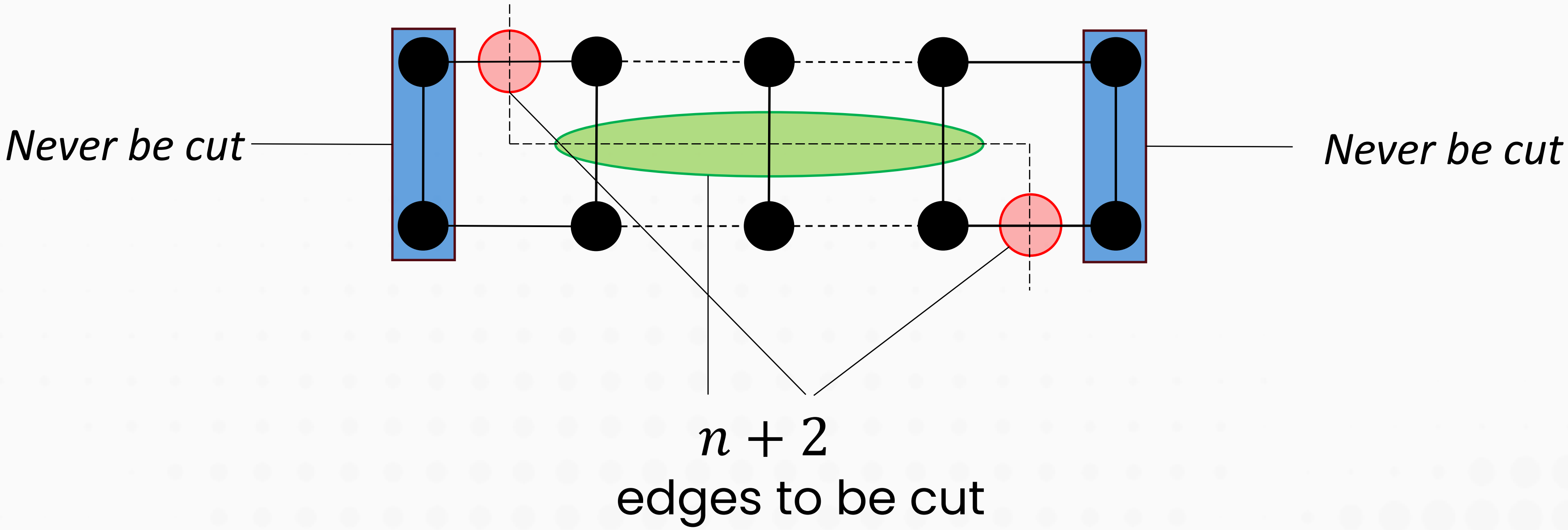
n-Cut Splicing (Cont.)

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

n	*n*-cut splicing
1	 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.



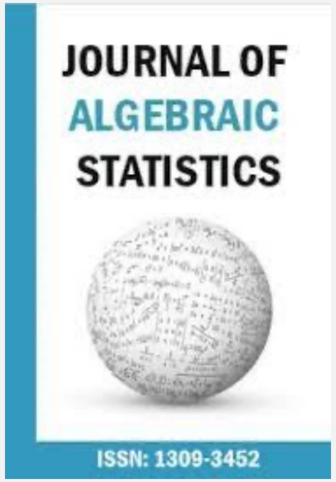
Ongoing Research

A Theoretical DNA Based Computer Model for Food Authentification 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 micro-organisms relevant to food like probiotics.

Publication

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



Watson-Crick Automata

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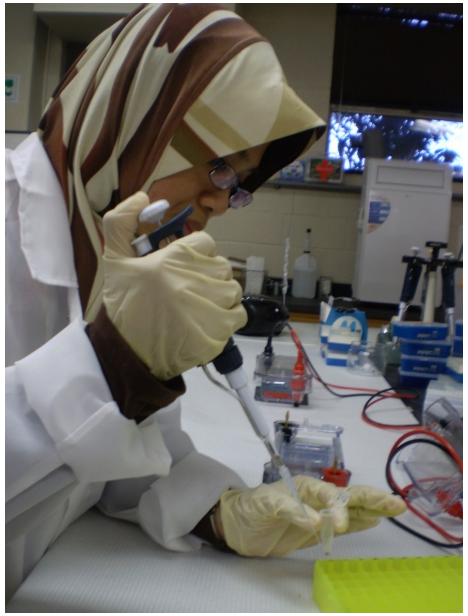
Types of Splicing System



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2. 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).
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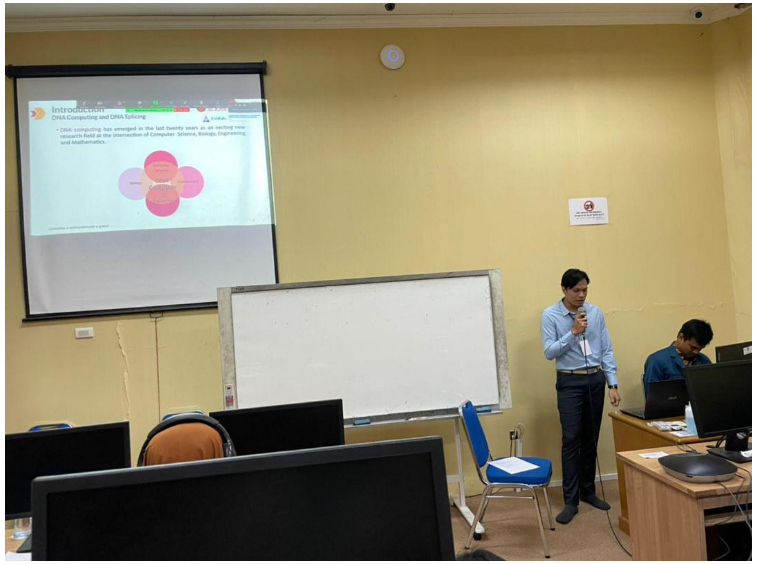
Graph Splicing Systems



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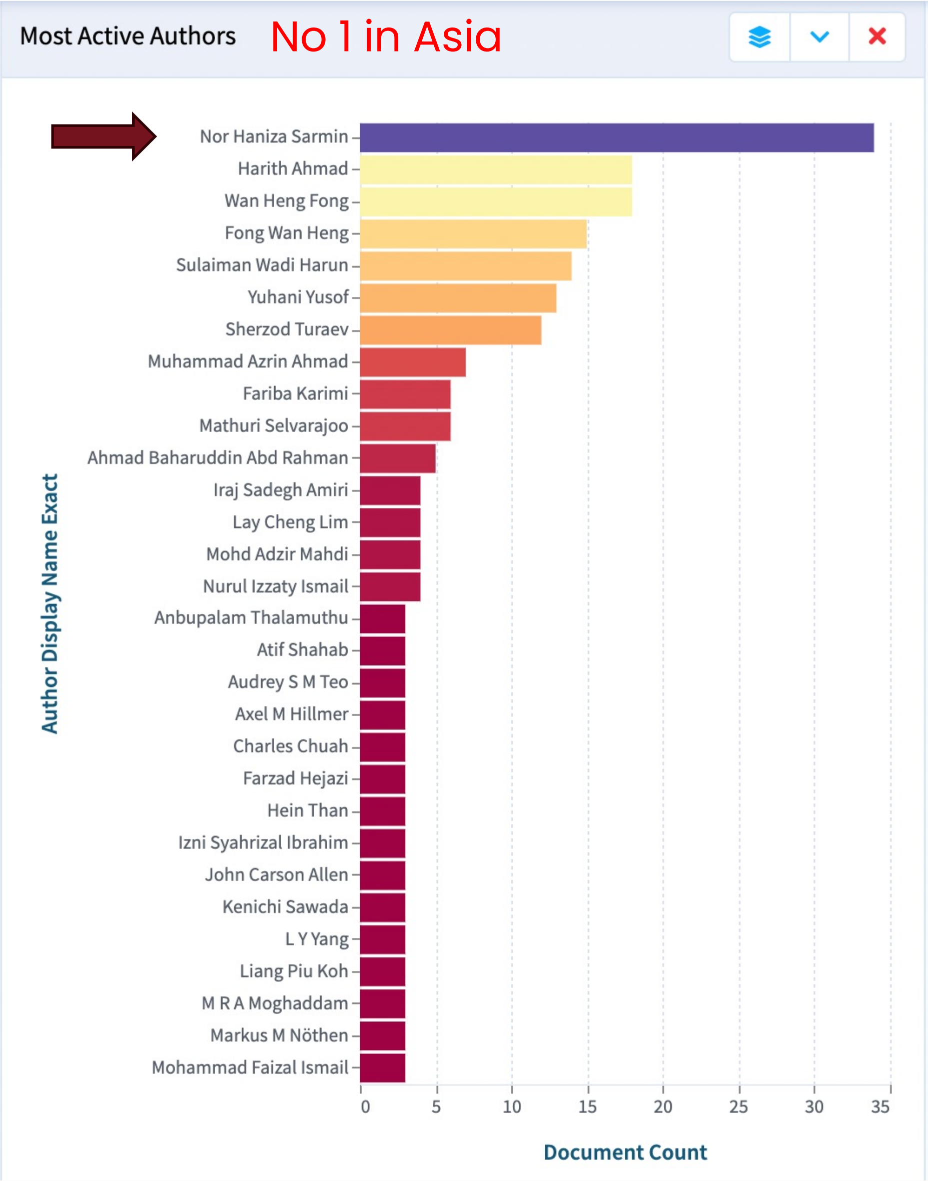
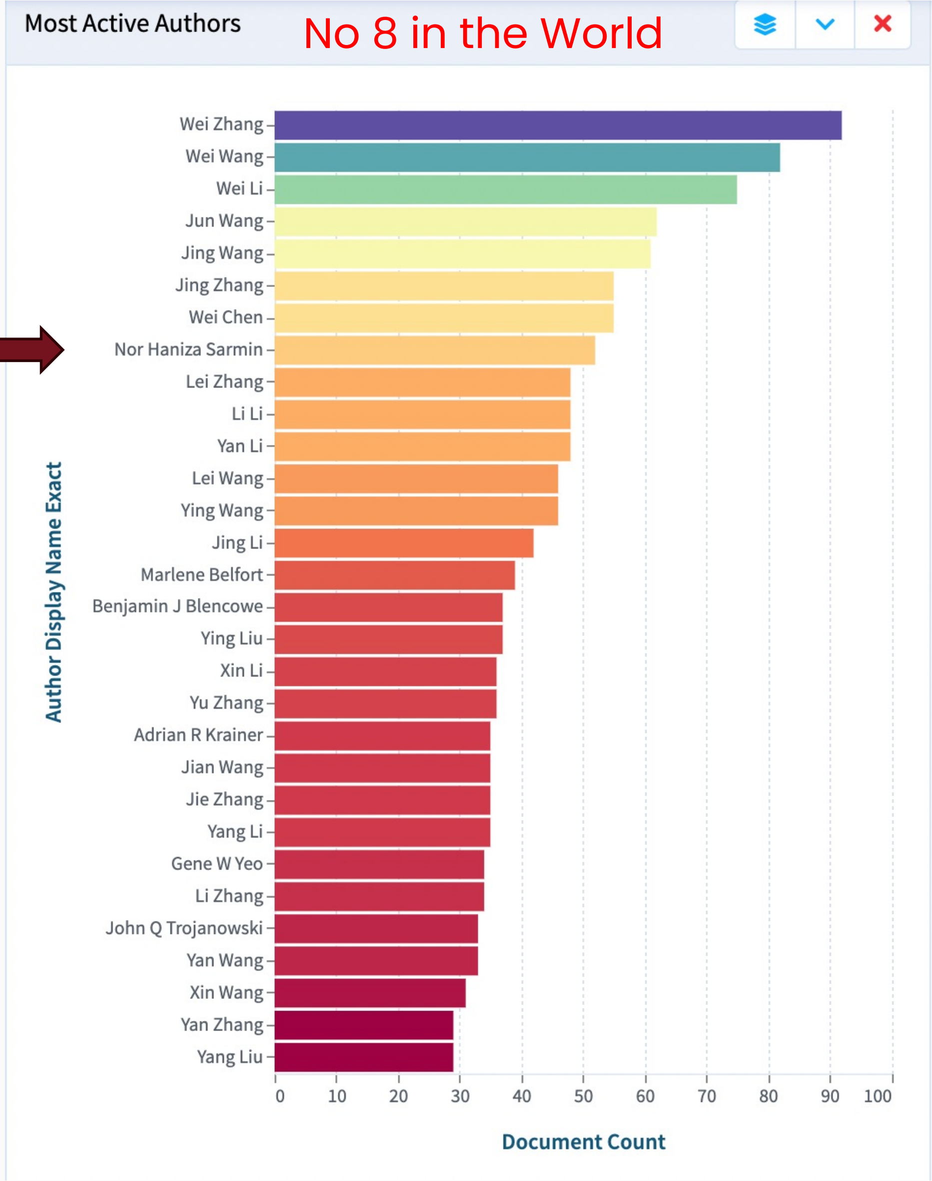
Ranking in Splicing Systems (Lens.org)





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

Dr. Alfi Yusrotis Zakiyyah

Lecturer in Mathematics and Statistics, School of Computer Science, Bina Nusantara University (BINUS), Jakarta, Indonesia

IndoMS Research Visit Program 2022 to UTM (18 – 30 November 2022)

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- Beuerle, James R
- Visscher, Matthew P

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- 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

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- Subramaniam, K. G

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- Mudaber, Hassan

United Arab Emirates
- Turaev, Sherzod

Qatar
- El-Sanfaz, Mustafa Anis

Libya
- Omer, Sanaa Mohamed Saled
- Awad, Emtinan

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

Nigeria
- Gambo, Ibrahim

South Africa
- Engelbrecht, Andries Petrus
- Russo, Francesco G

Italy
- Malinin, Dmitry A

India
- Suji, Suresh

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

South Korea
- Jun, Young Bae

Taiwan
- Gan, Yee Siang

Indonesia
- Herwindiati, Dyah
- Muchtadi, Intan
- Wijayanti, Indah Emilia
- Wardhana, Adhitya
- Alfi Yusrotis Zakiyyah
- Siti Zahidah

Brunei Darussalam
- Venkat, Ibrahim

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THANK YOU

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Niza Sarmin

Niza Sarmin

In the Name of God for Mankind