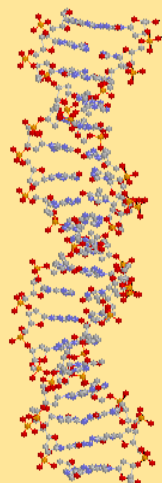
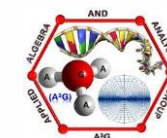




UTM
UNIVERSITI TEKNOLOGI MALAYSIA

**International Conference
on Advanced Research in
Mathematical Sciences
(ICARMS)**

24 February 2021

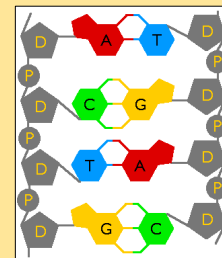


DNA Splicing System - From Birth to Present

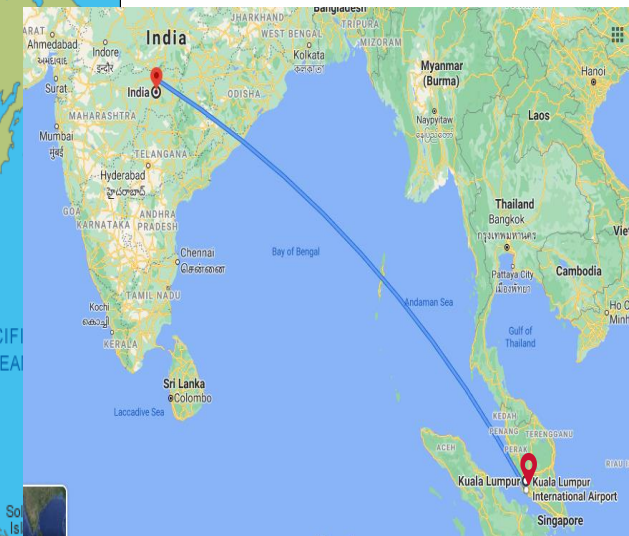
Prof. Dr. Nor Haniza Sarmin

Department of Mathematical Sciences, Faculty of Science,
Universiti Teknologi Malaysia, Johor, Malaysia.

Email: nhs@utm.my



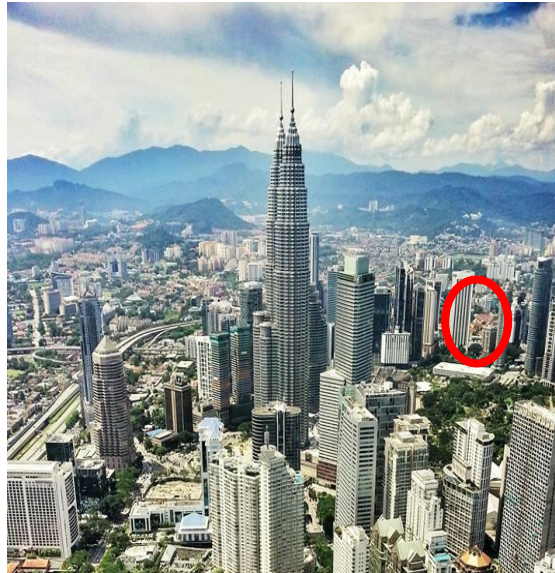
INDIA - MALAYSIA



3,081 km
Distance from India to Malaysia



UTM Johor Bahru
(1145 hectares) – main campus



UTM Kuala Lumpur Campus –
branch (19 hectares)



UTM Campus – Pagoh
Innovation Centre in Agritechology
for Advanced Bioprocessing (ICA)

Faculties in UTM

7
Faculties

200
PG
programs

55
Bachelor
programs

Engineering

- School of Chemical & Energy Eng.
- School of Electrical Eng.
- School of Civil Eng
- School of Mechanical Eng
- School of Biomedical Eng & Health Sciences
- School of Computing

Social Sciences & Humanities

- School of Education
- School of Human Resource Dev. & Psychology
- Islamic Civilization Academy
- Language Academy
- Raja Zarith Sofiah Center for Advanced Studies on Islam, Science and Civilization

Built Environment & Surveying

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

Science

- Physics
- Chemistry
- **Mathematical Sciences**
- Biosciences

Azman Hashim International Business School

- Business Administration
- Accounting and Finance
- Information System
- School of Computing

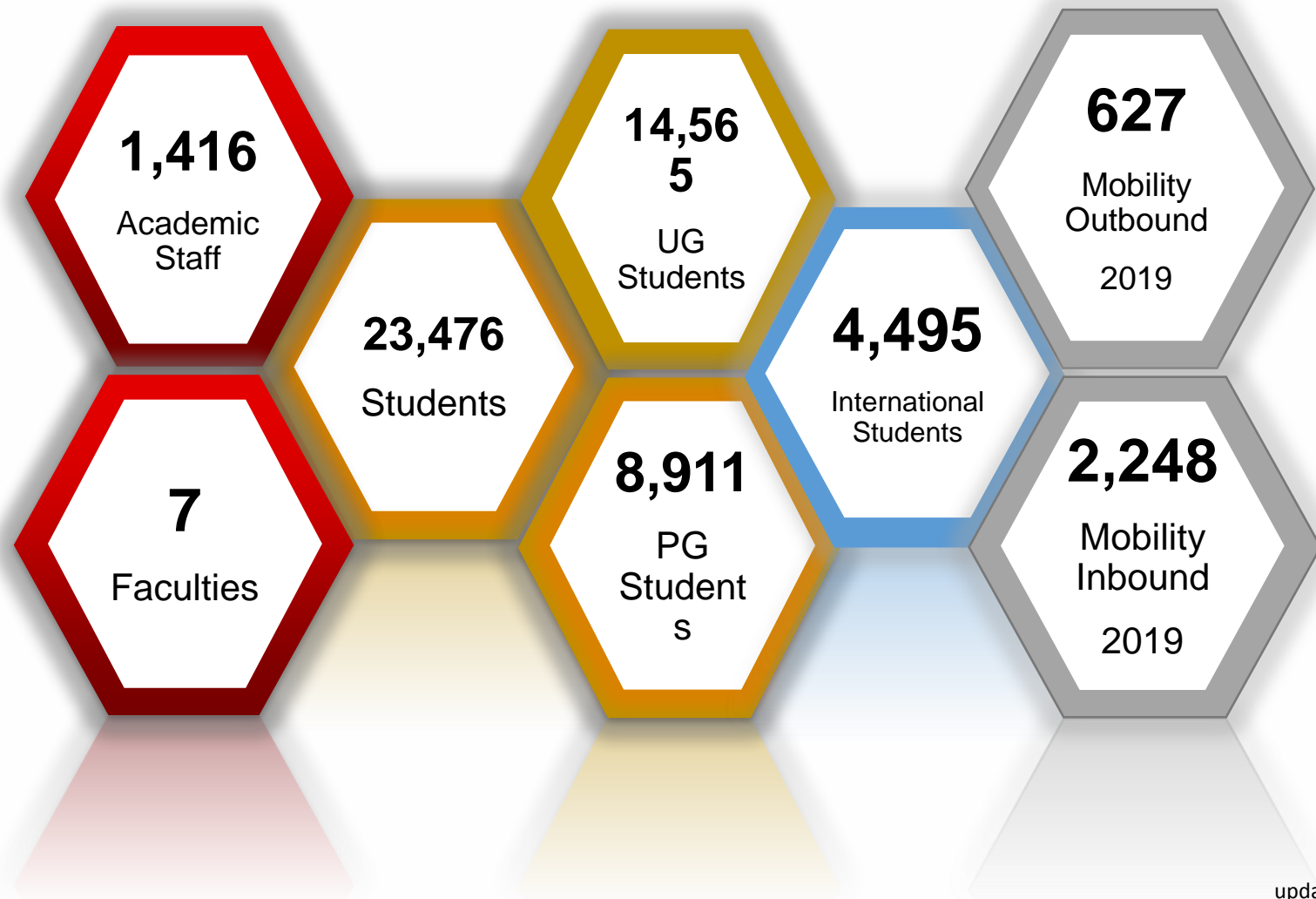
Razak Technology & Informatics

- Engineering & Technology
- Science Management and Design
- Advanced Informatics
- Perdana Center

Malaysia-Japan International Institute of Technology

- Electronic Systems Engineering
- Mechanical Precision Engineering
- Chemical Process Eng. & Sustainable Systems
- Technology & Innovation Management
- Disaster Risk Management
- Sustainability and Environmental Sciences

UTM Quick Facts and Figures



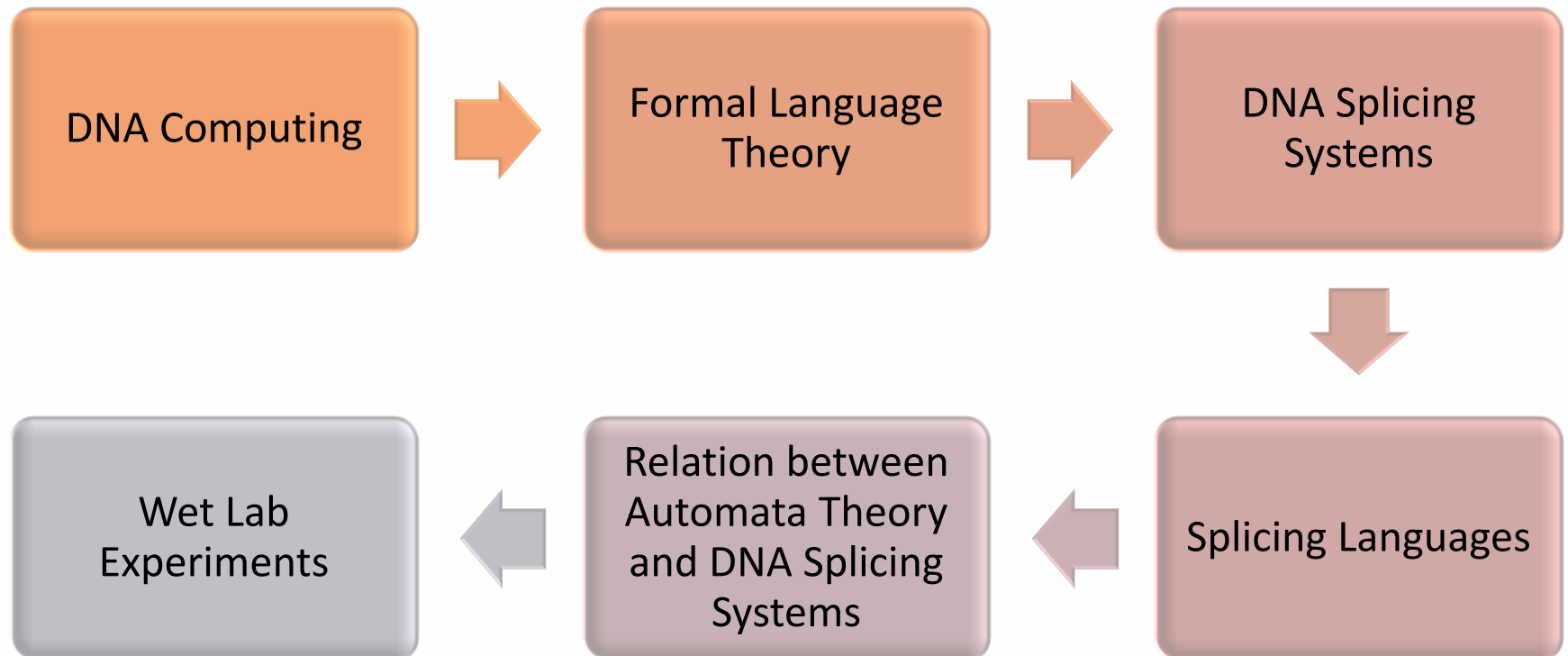
updated June 2020

DNA Splicing System - From Birth to Present

ABSTRACT

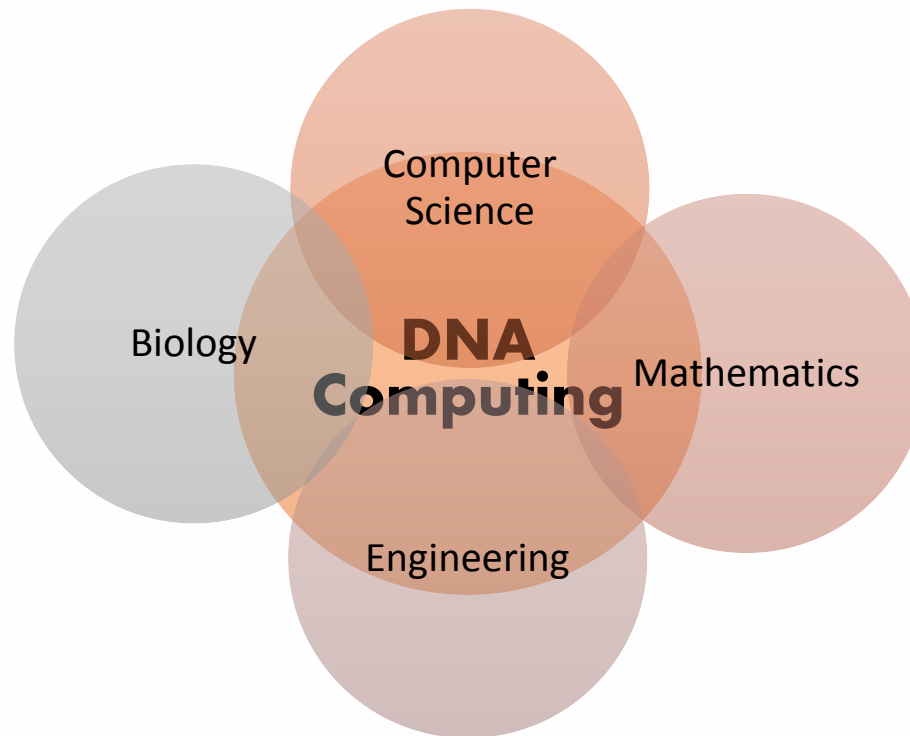
The mathematical modelling of **DNA splicing system** has first been introduced by Tom Head in 1987 which is simulated by the technique of **recombinant DNA molecules** that relies on **restriction enzymes** in the study of **formal language theory**. In this talk, **variants of splicing models** that have been developed over the years will be presented. Furthermore, the splicing systems will be shown as **graphically represented** using the concepts of **automata**. Lastly, **molecular works** for splicing systems which are conducted through **wet-lab experiments** will be shared to validate the existence of splicing languages.

Presentation Outlines



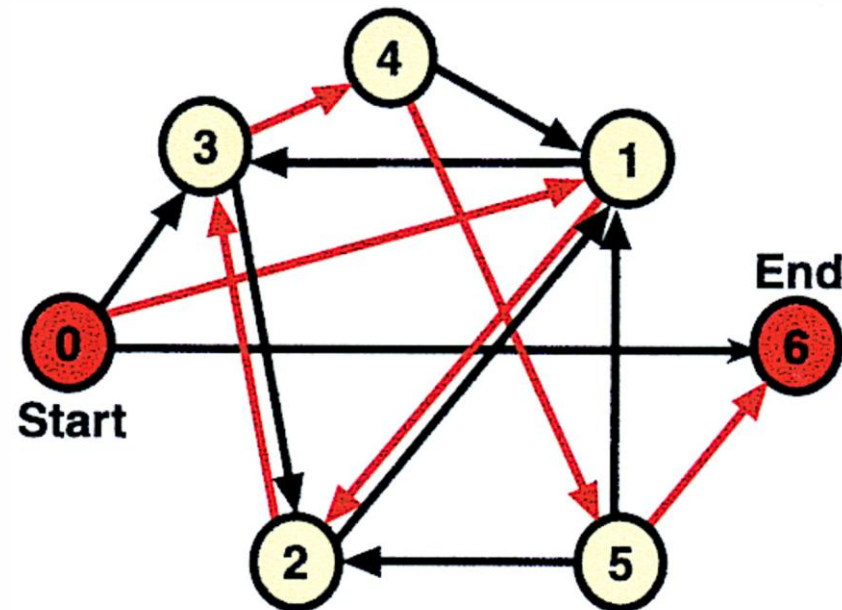
DNA Computing

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



DNA Computing (cont.)

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



DNA Computing (cont.)

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

Formal Language Theory

Splicing System

- Formal Language Theory
- Applied Discrete Mathematics
- Theoretical Computer Science

Formal Language Theory (cont.)

- Formal language theory is a study of **formal languages** which are defined with respect to an alphabet.
- The **alphabet** of language is a finite set of symbols or letters.
- The elements of the alphabet can be “ordinary” **letters** (A to Z, a to z), **digits** (0, 1, 2, ...) or any **symbols** (eg: #, \$, ...).
- A finite sequence that concatenate from symbols or letters is called a **string**.

Example

001 is a string over the alphabet {0, 1}

abba is a string over the alphabet {a, b}

Formal Language Theory (cont.)

- A **formal language** is a set of strings formed over an alphabet.
- Some notations and operations on languages are given in the following:-

Symbols	Description
A^*	A set of strings of symbols from an alphabet A
A^+	A set of strings of symbols from an alphabet A without the empty string
λ	Empty string
\cup	Union
\cdot	Concatenation
$*$	Star-closure
$\{ \}$ or $()$	Parentheses

Example

Let $A = \{a, b, c, \dots, y, z\}$. Then A^* is the set of all strings over the letters of Latin alphabet. In particular, the following are **formal languages**:

- the set of **strings** consisting of vowels only
 $\{a, e, i, o, u, aa, ii, oo, \dots\}$
- the set of **palindromes**: strings that read the same from right to left or from left to right
eg: $\{\text{level, madam, mom, } \dots\}$
- the set $\{\text{i, you, he, she, it, we, they}\}$
- the empty set.



**I graduated from State University of New York (SUNY) at Binghamton
(now known as Binghamton University), New York, USA
BSc (1989), MA (1990), PhD (1995-1998)**

DNA Splicing Systems

- The mathematical modelling of **splicing system** was first defined by **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**.



Tom Head's visit to UTM, 2004



Visit to SUNY Binghamton, USA, 2007



Visit and Research Seminar at SUNY Binghamton, 2007



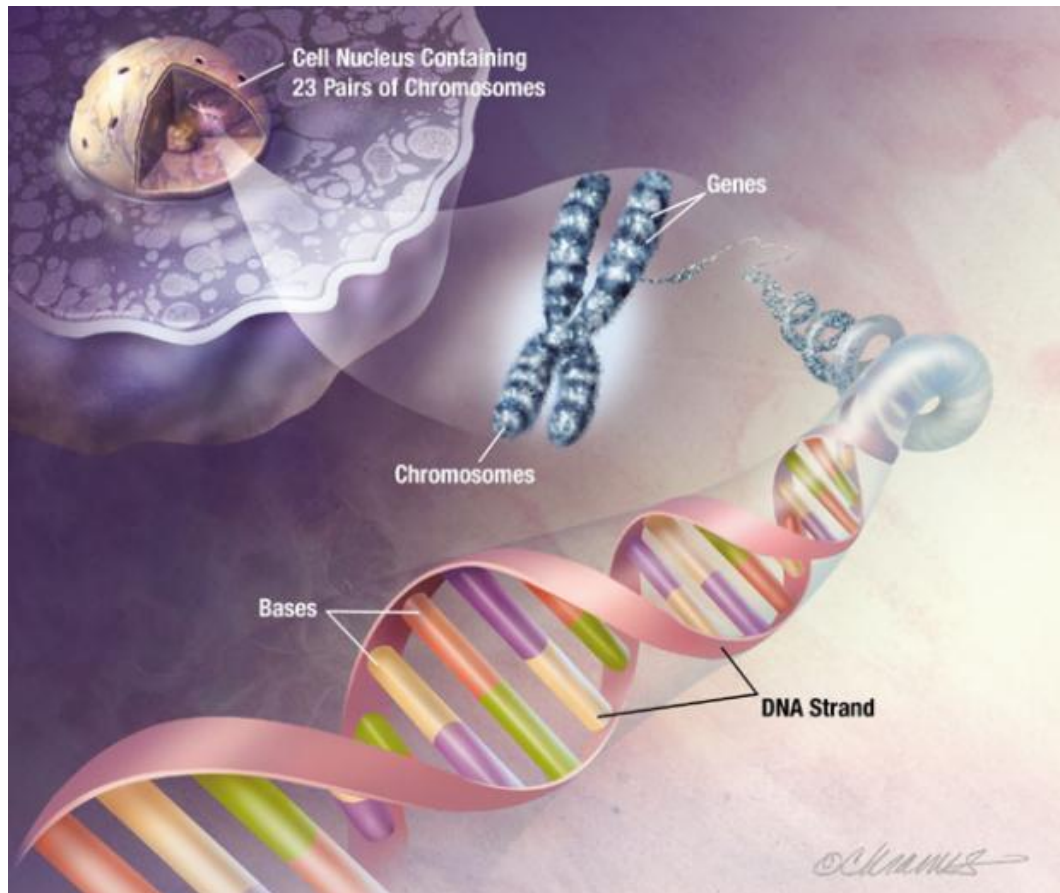
**Conference on Biomathematical Computing: Past, Present and Prospects,
 SUNY Binghamton, USA, 2008**

DNA Splicing Systems

- Structure of DNA
- Restriction Enzymes
- DNA Ligase

Structure of DNA

- **DNA**, or deoxyribonucleic acid, is the hereditary material in humans and almost all other organisms.



Structure of DNA (cont.)

DNA – DeoxyriboNucleic Acid

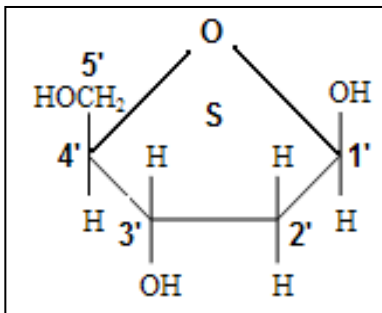
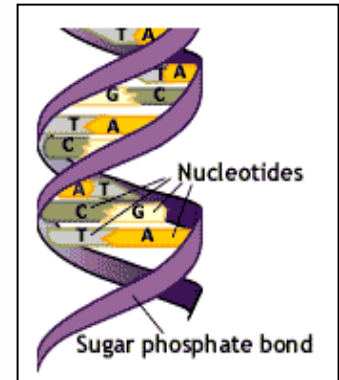
Made up of

Nucleotides

Phosphate group

Pentose (a 5-carbon sugar)

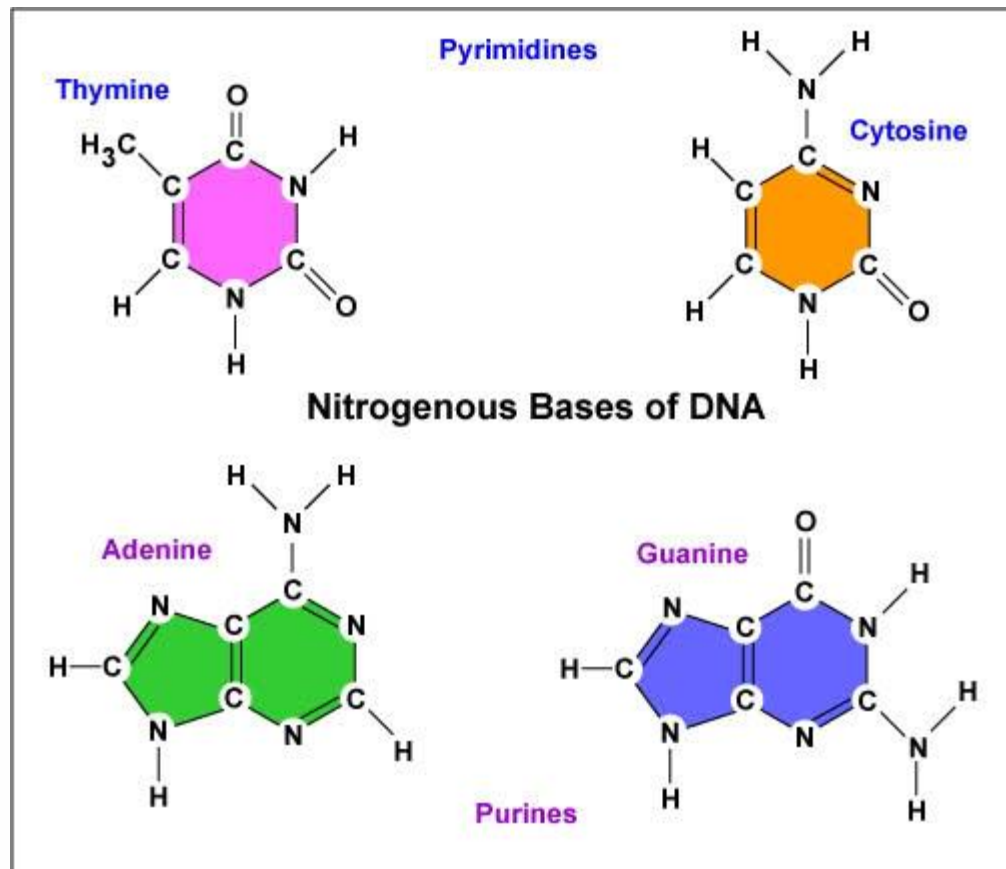
Base



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

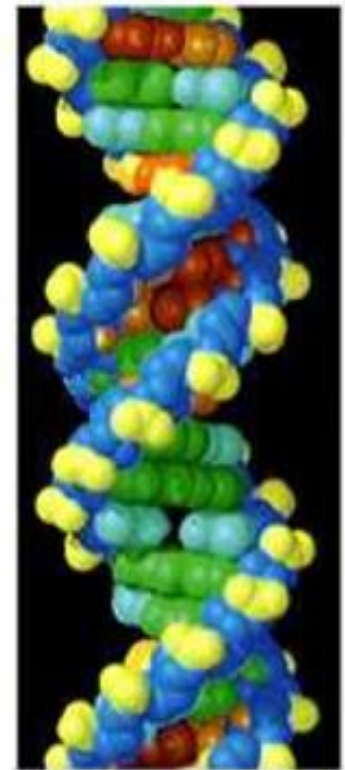
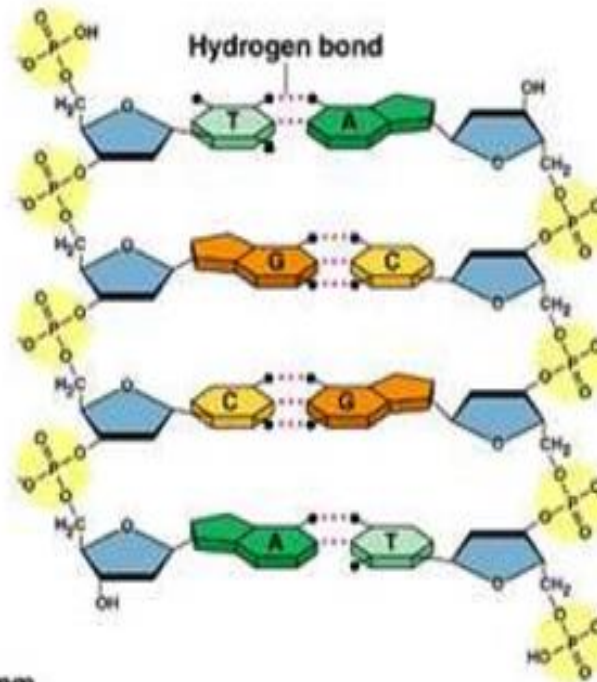
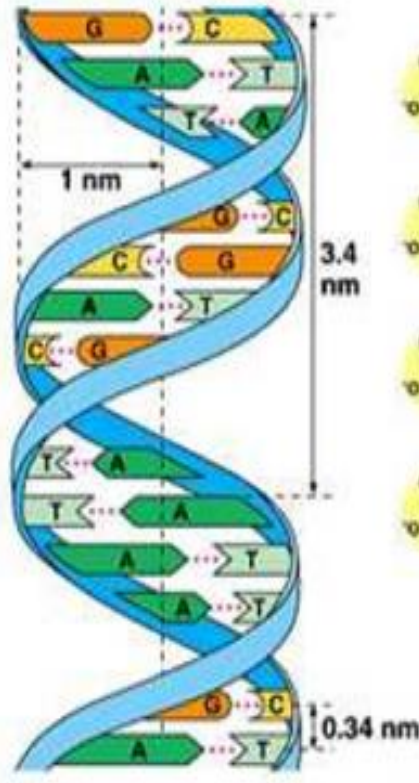
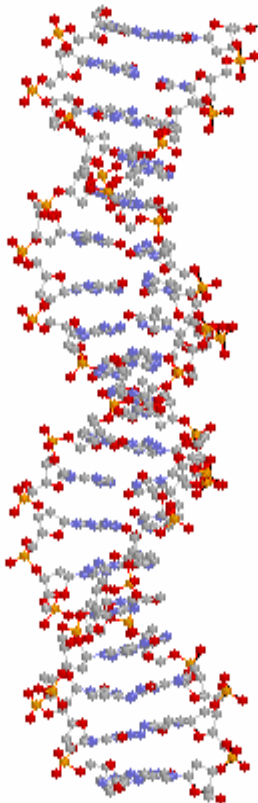
Structure of DNA (cont.)

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



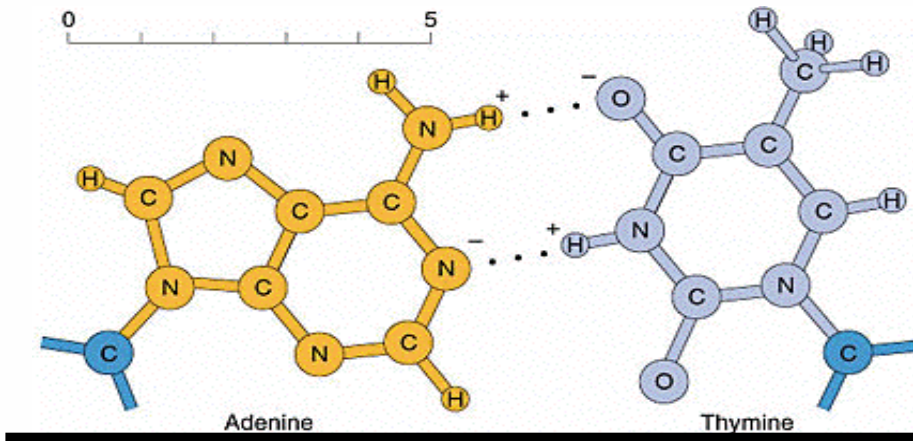
Structure of DNA (cont.)

- 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)**.

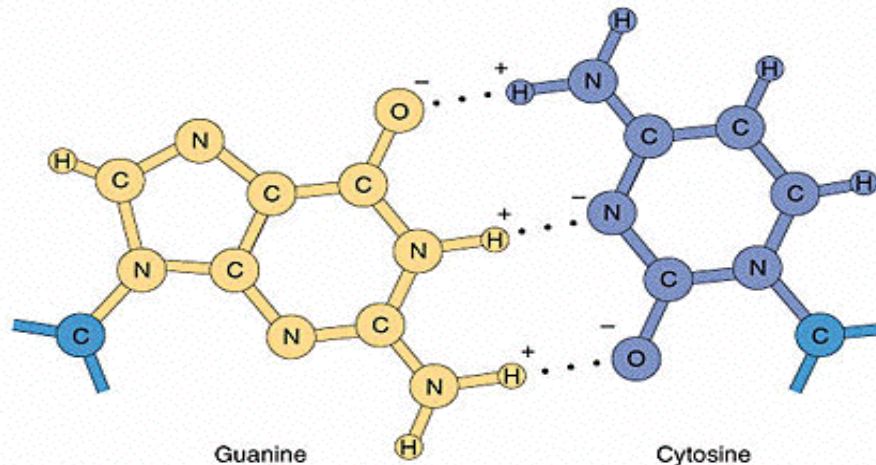


Structure of DNA (cont.)

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

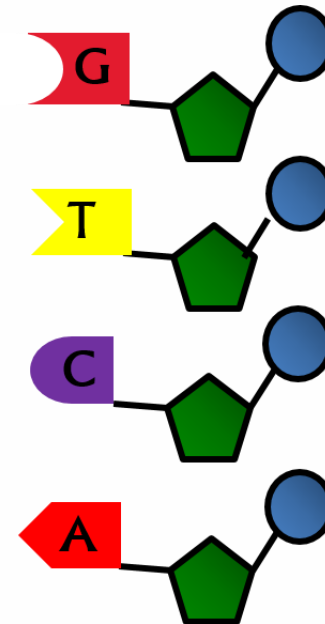
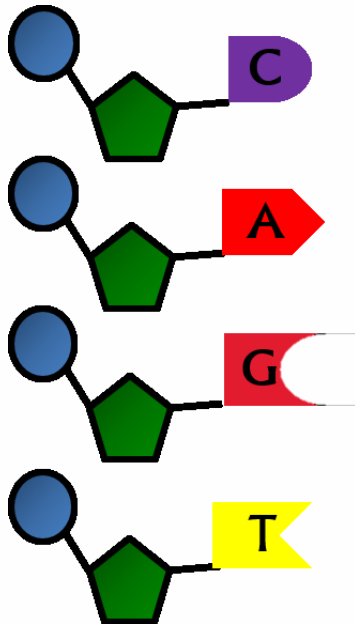


A – T



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. *Acil*)

5'...C▼CGC...3'

3'...GGC▲G...5'

Blunt end (e.g. *AfeI*)


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 *EcoRI* is isolated from the bacterium *Escherichia coli* with strain serotype *R*; I indicates the first enzyme discovered from the bacterium.
- The cleavage pattern of restriction enzyme *EcoRI* is

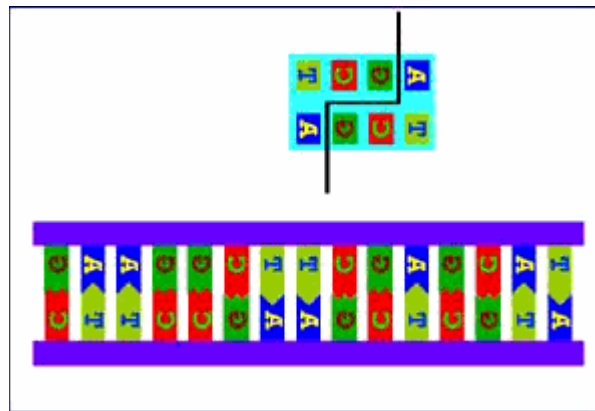
(g, aatt, c)



left context **crossing** right context

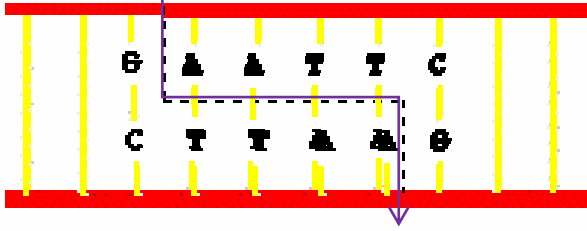
Restriction Enzymes (cont.)

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

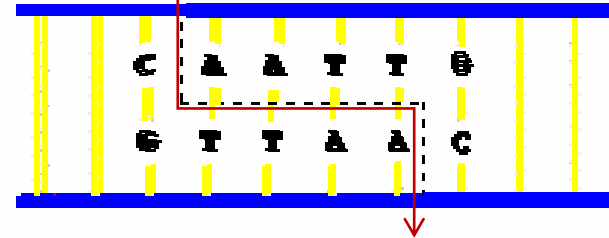


Restriction Enzymes (cont.)

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

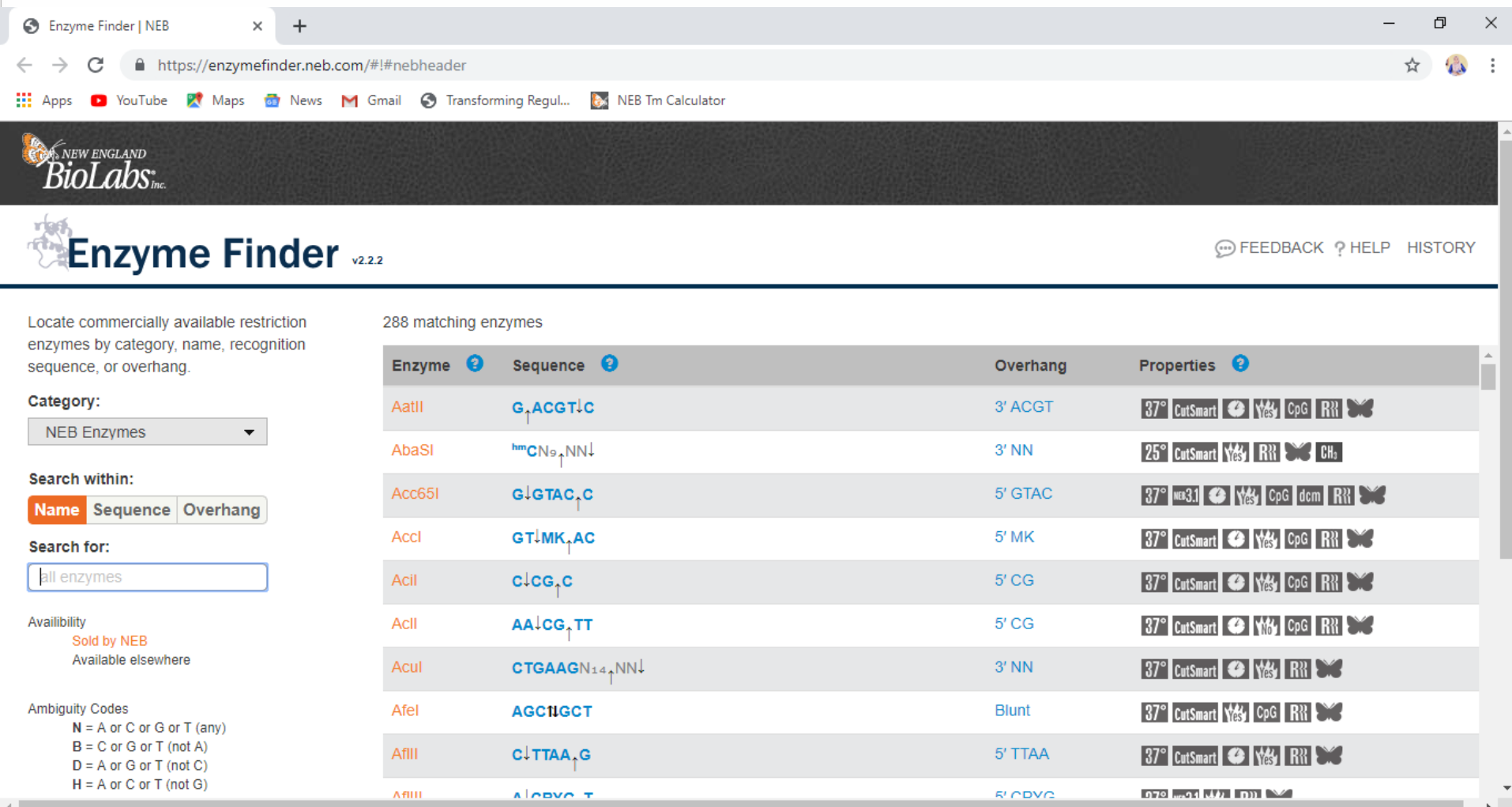


MfeI: ([C/G],[A/T][A/T][T/A][T/A],[G/C])



Restriction Enzyme (cont.)

Link: <https://enzyme finder.neb.com/#!/#nebheader>



The screenshot shows the NEB Enzyme Finder website. The browser address bar displays the URL <https://enzyme finder.neb.com/#!/#nebheader>. The website header includes the NEB logo and navigation links for FEEDBACK, HELP, and HISTORY. The main content area is titled "Enzyme Finder v2.2.2" and contains a search interface on the left and a list of 288 matching enzymes on the right.

Search Interface (Left):

- Category:** NEB Enzymes (dropdown menu)
- Search within:** Name (selected), Sequence, Overhang
- Search for:** all enzymes (input field)
- Availability:** Sold by NEB (selected), Available elsewhere
- Ambiguity Codes:**
 - N = A or C or G or T (any)
 - B = C or G or T (not A)
 - D = A or G or T (not C)
 - H = A or C or T (not G)

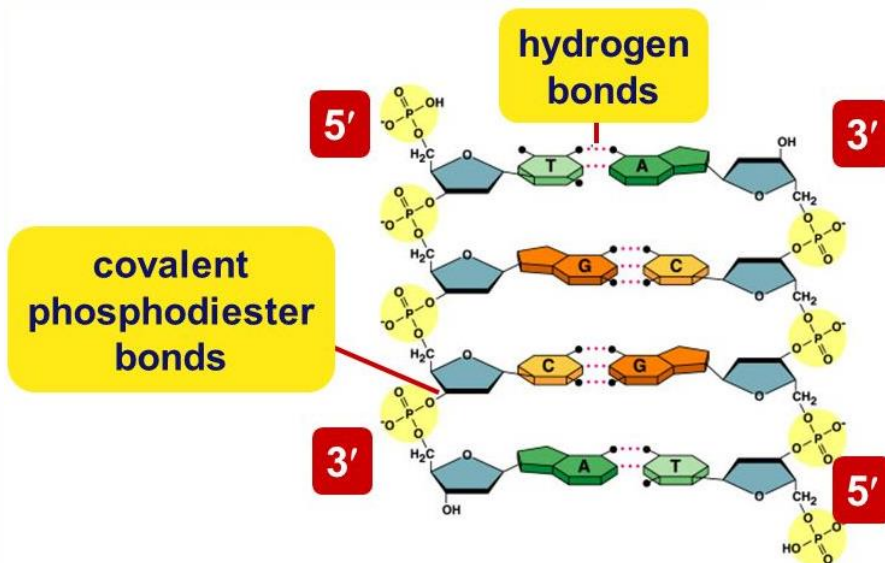
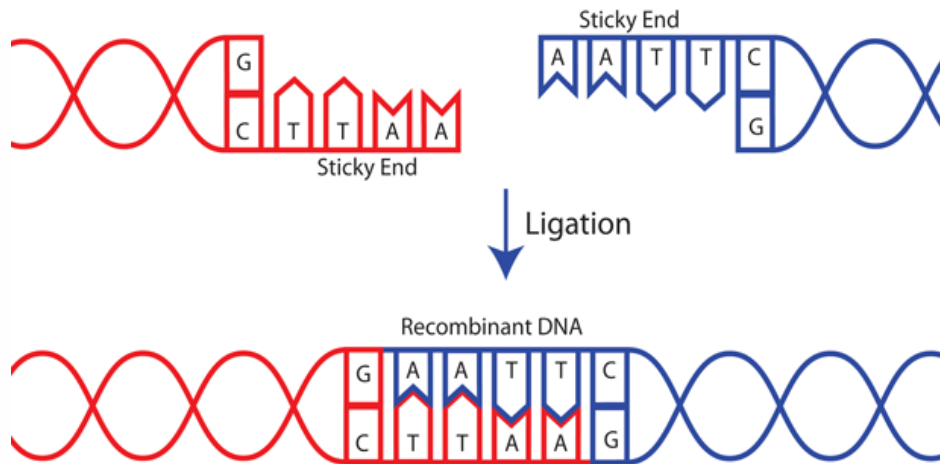
Enzyme List (Right):

288 matching enzymes

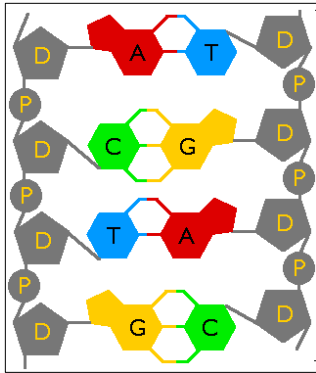
Enzyme	Sequence	Overhang	Properties
AatII	G↓ACGT↓C	3' ACGT	37° CutSmart Yes CpG RII
AbaSI	hmC↓NN↓	3' NN	25° CutSmart Yes RII CH ₃
Acc65I	G↓GTAC↓C	5' GTAC	37° Hae3.1 Yes CpG dcm RII
AccI	GT↓MK↓AC	5' MK	37° CutSmart Yes CpG RII
Acil	C↓CG↓C	5' CG	37° CutSmart Yes CpG RII
AcII	AA↓CG↓TT	5' CG	37° CutSmart No CpG RII
AcuI	CTGAAGN↓NN↓	3' NN	37° CutSmart Yes RII
AfeI	AGC↓IGCT	Blunt	37° CutSmart Yes CpG RII
AflII	C↓TTAA↓G	5' TTAA	37° CutSmart Yes RII
AflIII	A↓CGCG↓T	5' CGCG	37° Hae3.1 Yes RII

DNA Ligase

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



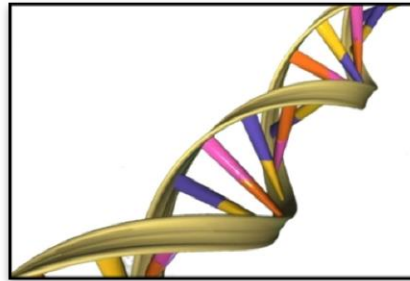
Modelling of DNA Splicing System



Nitrogenous base pairings



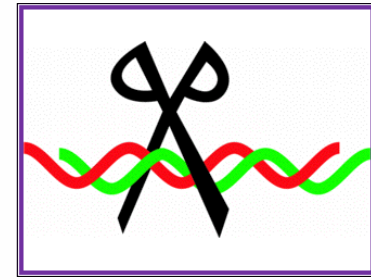
dsDNA



Nucleotide chains



DNA strings

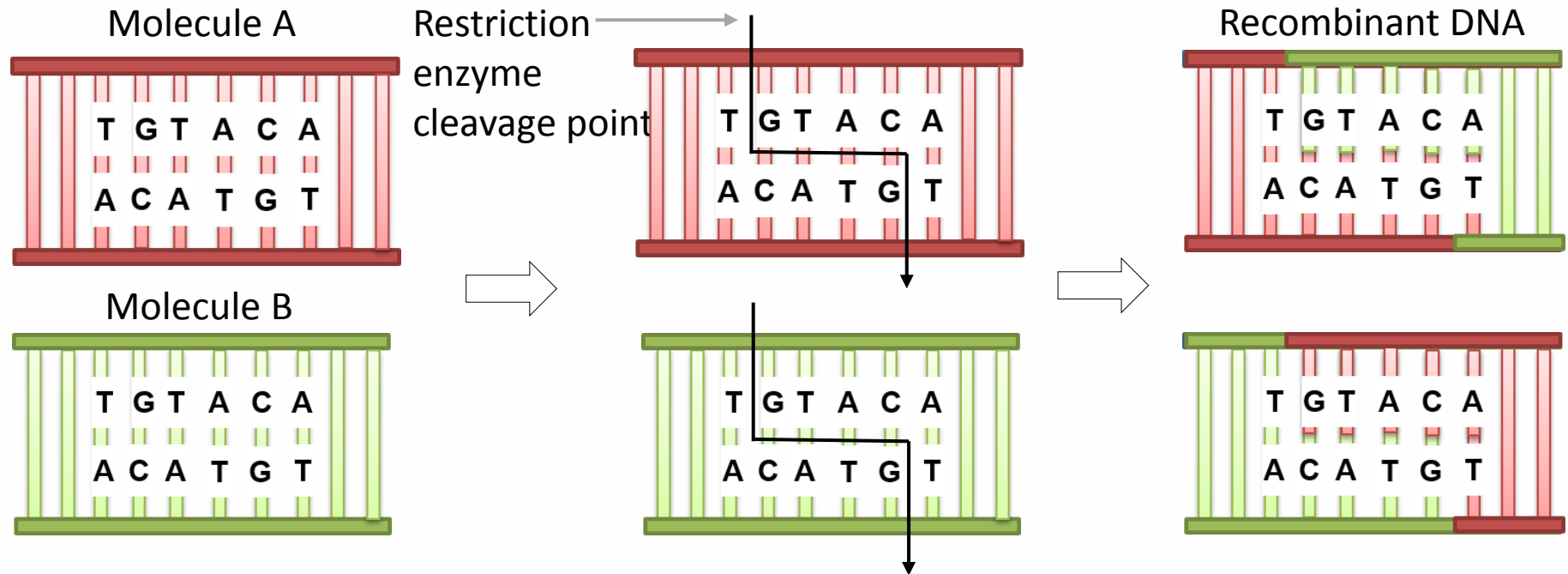


Restriction enzymes



rules

Modelling of DNA Splicing System (cont.)



G: Guanine A: Adenine C: Cytosine T: Thymine

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 $cx d$ 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

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, $I = \begin{Bmatrix} \text{GAATTC TCTGTAAT} \\ \text{CTTAAG AGACATTA} \end{Bmatrix}$ is the set consisting of an initial string of molecules, set $B = \left\{ \begin{pmatrix} G & AATT & C \\ C' & TTAA' & G \end{pmatrix} \right\}$ is the set of cleavage pattern for the enzyme **EcoRI** and set C is the empty set.

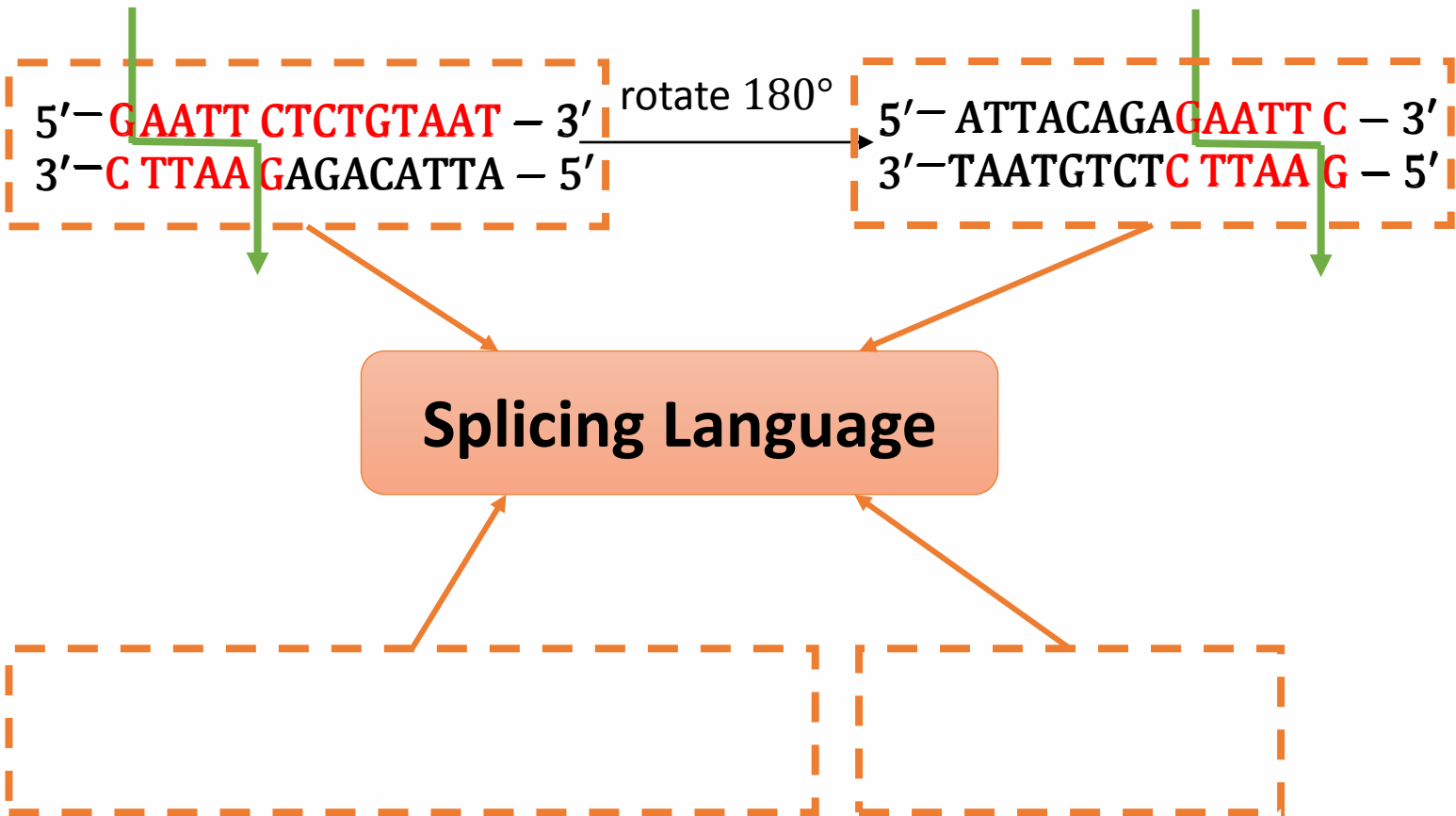
The initial string is shown in the following:



or written 180 degree wise,



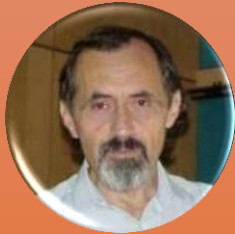
DNA Splicing System (cont.)



Variant of Splicing Models



Head's Splicing System
1987



Paun's Splicing System
1996



Pixton's Splicing System
1996



Goode-Pixton Splicing System
2004



Yusof-Goode Splicing System
2013



Fuzzy Splicing System
2014



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/BF02481771>

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).

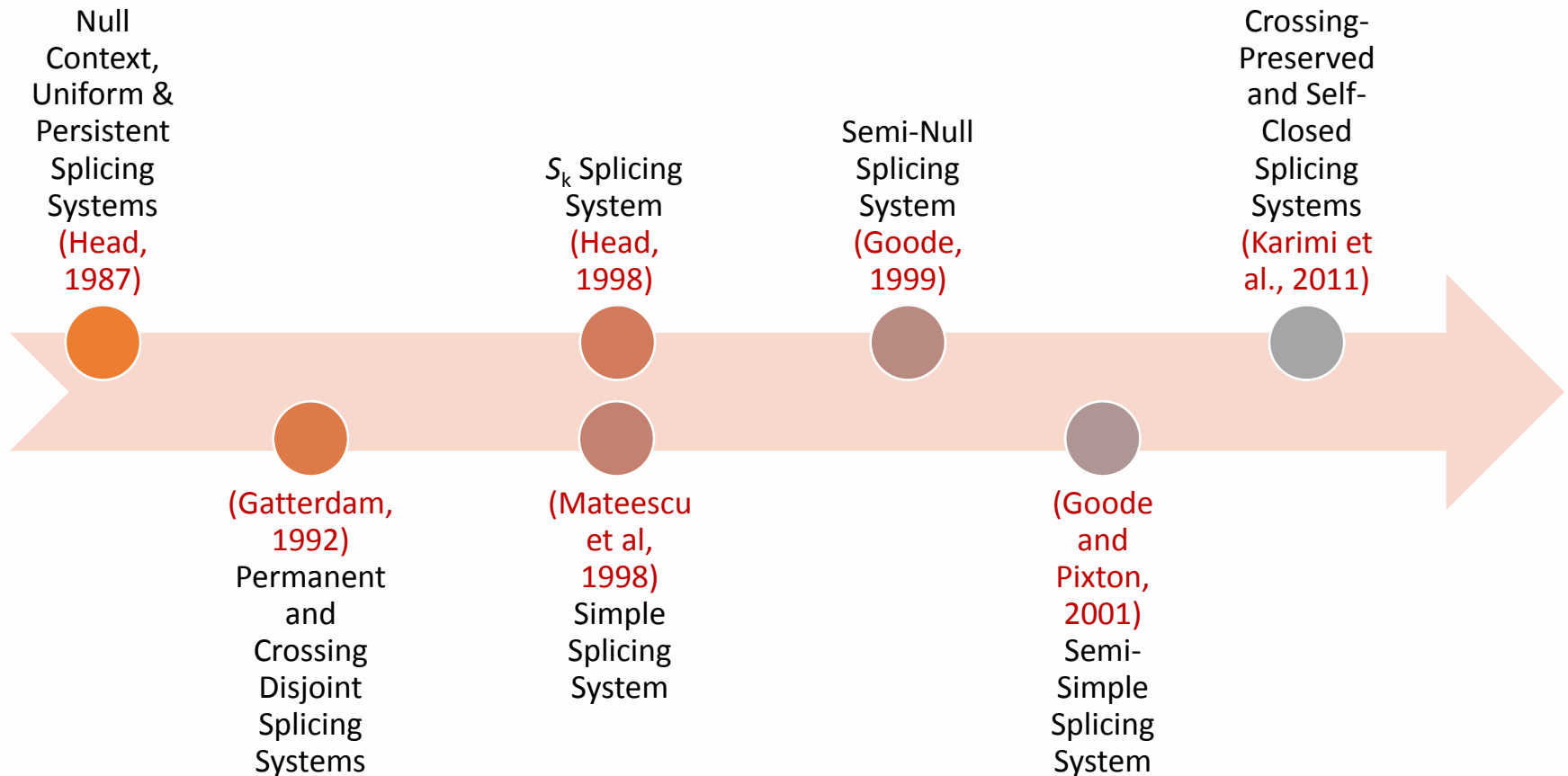
Karimi, F., Turaev, S., Sarmin, N. H., & Fong, W. H. (2014). Fuzzy Splicing Systems. In D. Hwang, J. J. Jung, & N. T. Nguyen (Eds.), *Computational Collective Intelligence. Technologies and Applications, ICCI 2014, Lecture Notes in Computer Science* (pp. 20-29). Cham, Switzerland: Springer International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

Notations of Splicing Systems

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 $S = (A, T, I, R, \Theta)$
Initial String	$ucxdv$ $pexfq$	uu_1u_2v $u'u_3u_4v'$	$\xi\alpha\eta$ $\xi'\alpha'\eta'$	$w = xuvy$ $w' = x'u'v'y'$	$\alpha u x v \beta$ $\gamma y z \delta$	(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	$ucxfq$ $pexdv$	uu_1u_4v'	$\xi\beta\eta'$	$z = xuv'y'$	$\alpha u x z \delta$ $\gamma y x v \beta$	$(uv, x \Theta y)$ Θ 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

Types of Splicing Systems



Types of Splicing Systems (cont.)

Definition 2 (Head, 1987) Null-Context Splicing System

A **null-context** splicing system is a splicing system $S = (A, I, B, C)$ for which each cleavage pattern in B and each in C has the form $(1, x, 1)$.

Definition 3 (Head, 1987) Uniform Splicing System

A **uniform** splicing system is a null context splicing system $S = (A, I, X, X)$ for which there is a positive integer P such that $X = A^P$. A language L is a uniform splicing language if there is a uniform splicing system S for which $L = L(S)$.

Definition 4 (Head, 1987) Persistent Splicing System

Let $S = (A, I, B, C)$ be a splicing system. Then S is **persistent** if for each pair of strings $ucxdv$ and $pexfq$, in A^* with (c, x, d) and (e, x, f) patterns of the same hand: If y is a subsegment of ucx (respectively xfq) that is the crossing of a site in $ucxdv$ (respectively $pexfq$) then this same subsegment y of $ucxfq$ **contains** an occurrence of the crossing of a site in $ucxfq$.

Types of Splicing Systems (cont.)

Definition 5 (Gatterdam, 1992) Permanent Splicing System

Let $S = (A, I, B, C)$ be a splicing system. Then S is **permanent** if for each pair of strings $ucxdv$, and $pexfq$, in A^* with (c, x, d) and (e, x, f) patterns of the same hand: If y is a subsegment of ucx (respectively xfq) that is the crossing of a site in $ucxdv$ (respectively $pexfq$) then this same subsegment y of $ucxfq$ **is** an occurrence of the crossing of a site in $ucxfq$.

Definition 6 (Gatterdam, 1992) Crossing Disjoint Splicing System

A splicing system $S = (A, I, B, C)$ is **crossing disjoint** if there **do not exist** patterns (a, x, b) in B and (c, x, d) in C with **the same crossing x** .

Types of Splicing Systems (cont.)

Definition 7 (Head, 1998) S_k Splicing System

Let k be an integer ≥ -1 . An S_k splicing system is a null-context splicing system $S = (A, I, B, C)$ for which, for each rule r in B or C , $\text{length } r < k$.

Definition 8 (Mateescu et al., 1998) Simple Splicing System

Let $S = (A, I, R)$ be a splicing system in which all rules in R have the form $(a, 1; a, 1)$ where $a \in A$. Then S is called a simple splicing system.

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

doi:[https://doi.org/10.1016/S0166-218X\(98\)00053-5](https://doi.org/10.1016/S0166-218X(98)00053-5)

Mateescu, A., Păun, G., Rozenberg, G., & Salomaa, A. (1998). Simple splicing systems. *Discrete Applied Mathematics*, 84(1-3), 145-163.

Types of Splicing Systems (cont.)

Definition 9 (Goode, 1999) Semi-Null Splicing System

Let (A, I, R) be a splicing system in which I and R are finite and every rule in R has the form $(u, 1; v, 1)$, where u, v are in A^+ . Thus $\sigma = (A, R)$ is called a semi-null splicing scheme, and (A, I, R) a **semi-null** splicing system.

Definition 10 (Goode and Pixton, 2001) Semi-Simple Splicing System

Let (A, I, R) be a splicing system in which I and R are finite and every rule in R has the form $(a, 1; b, 1)$, where a, b are in A . Thus $\sigma = (A, R)$ is called a semi-simple splicing scheme and (A, I, R) a **semi-simple** splicing system.

Laun, T. E. G. (1999). *Constants and Splicing Systems*. (Ph.D. Thesis), State University of New York, Binghamton.

Goode, E., & Pixton, D. (2001). Semi-Simple Splicing Systems. In C. Martín-Vide & V. Mitrana (Eds.), *Where Mathematics, Computer Science, Linguistics and Biology Meet* (pp. 343-352). Dordrecht: Springer.

Types of Splicing Systems (cont.)

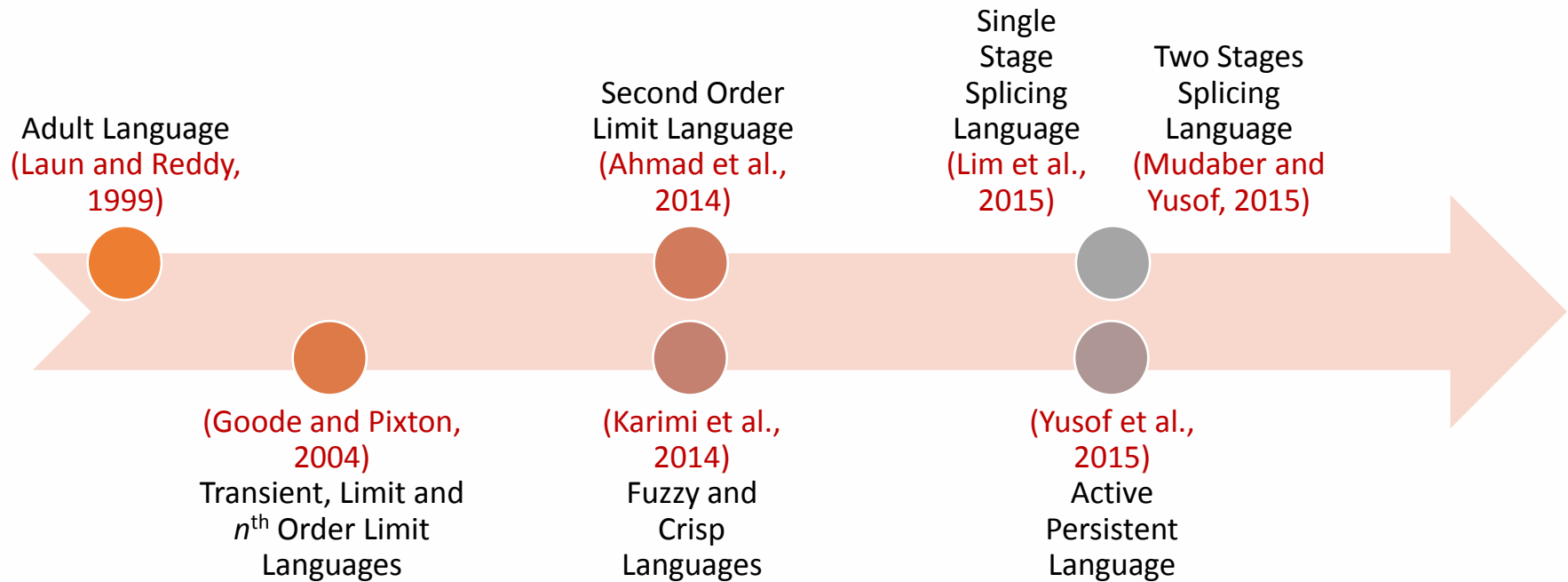
Definition 11 (Karimi et al., 2011) Self-Closed Splicing System

A set of splicing patterns B is called **self-closed** if the set of its sites is closed under its splicing rules. A splicing system is called **self-closed** if the sets of their patterns are self-closed .

Definition 12 (Karimi et al., 2011) Crossing-Preserved Splicing System

A set of splicing patterns B is called **crossing-preserved** if for every pattern (c, x, d) that its crossing x contains a substring x_1 that is crossing of another site, then the pattern (cu, x_1, vd) is also in B where $x = ux_1v$. A splicing system is called **crossing-preserved** if the sets of their patterns are crossing-preserved.

Types of Splicing Languages



Types of Splicing Languages (cont.)

Definition 13 (Laun and Reddy, 1999) Adult Language

Adult language in $L(S)$ is the set of strings in $L(S)$ which cannot be used for splicing in a splicing system.

Definition 14 (Goode and Pixton, 2004) Transient Language

A splicing language is called **transient** if a set of strings is eventually used up and disappears in a given system.

Definition 15 (Goode and Pixton, 2004) Limit language

A **limit language** is the set of words that are predicted to appear if some amount of each initial molecule is present, and sufficient time has passed for the reaction to reach its equilibrium state, regardless of the balance of the reactants in a particular experimental run of the reaction.

Laun, E., & Reddy, K. J. (1999). *Wet Splicing Systems*. Paper presented at the 3rd DIMACS Workshop on DNA Based Computers, University of Pennsylvania, Philadelphia.

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.

Types of Splicing Languages (cont.)

Definition 16 (Goode and Pixton, 2004) n^{th} Order Limit language

Let L_{n-1} be the set of second order limit words of L , the set L_n of n^{th} order limit words of L to be the set of first order limit word of L_{n-1} . We obtain L_n from L_{n-1} by deleting the words that are transient in L_{n-1} .

Definition 17 (Ahmad et al., 2014) Second Order Limit Language

Let L_1 be the set of second order limit words of L , the set L_2 of second order limit words of L to be the set of first order limits of L_1 . We obtain L_2 from L_1 by deleting words that are transient in L_1 .

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.

Ahmad, M. A., Sarmin, N. H., Heng, F. W., & Yusof, Y. (2014). *An Extension of First Order Limit Language*. Paper presented at the 3rd International Conference on Mathematical Sciences (ICMS3), Kuala Lumpur, Malaysia.

Definition 18 (Karimi et al., 2014) Fuzzy Language

The **fuzzy** language generated by a fuzzy splicing system $\gamma = (V, T, A, R, \mu, \Theta)$ is defined as $L_f(\gamma) = \{(z, \mu(z)) \in \sigma^* f(A) : z \in T^*\}$.

Definition 19 (Karimi et al., 2014) Crisp language

The **crisp** language generated by a fuzzy splicing system $\gamma = (V, T, A, R, \mu, \Theta)$ is defined as $L_c(\gamma) = \{z : (z, \mu(z)) \in L_f(\gamma)\}$.

Definition 20 (Lim et al., 2015) Single Stage Splicing Language

Single stage splicing language is defined as

$$[L_1 = L_1(S)] \cong \sum_{r=1}^n (Rr + I_r + l)$$

R_r = set of rules, $1 \leq r \leq n$

I_r = set of initial strings, $1 \leq r \leq n$

l = ligases

Let $S = (A, I, R)$ be the Y-G splicing system. The set of **single stage splicing language**, $L_1 = L_1(S)$, models the set of all molecule types which appear when all the restriction enzymes, double stranded deoxyribonucleic acid strings and ligases act simultaneously in a single buffer.

Types of Splicing Languages (cont.)

Definition 21 (Mudaber and Yusof, 2015) Two Stages Splicing Language

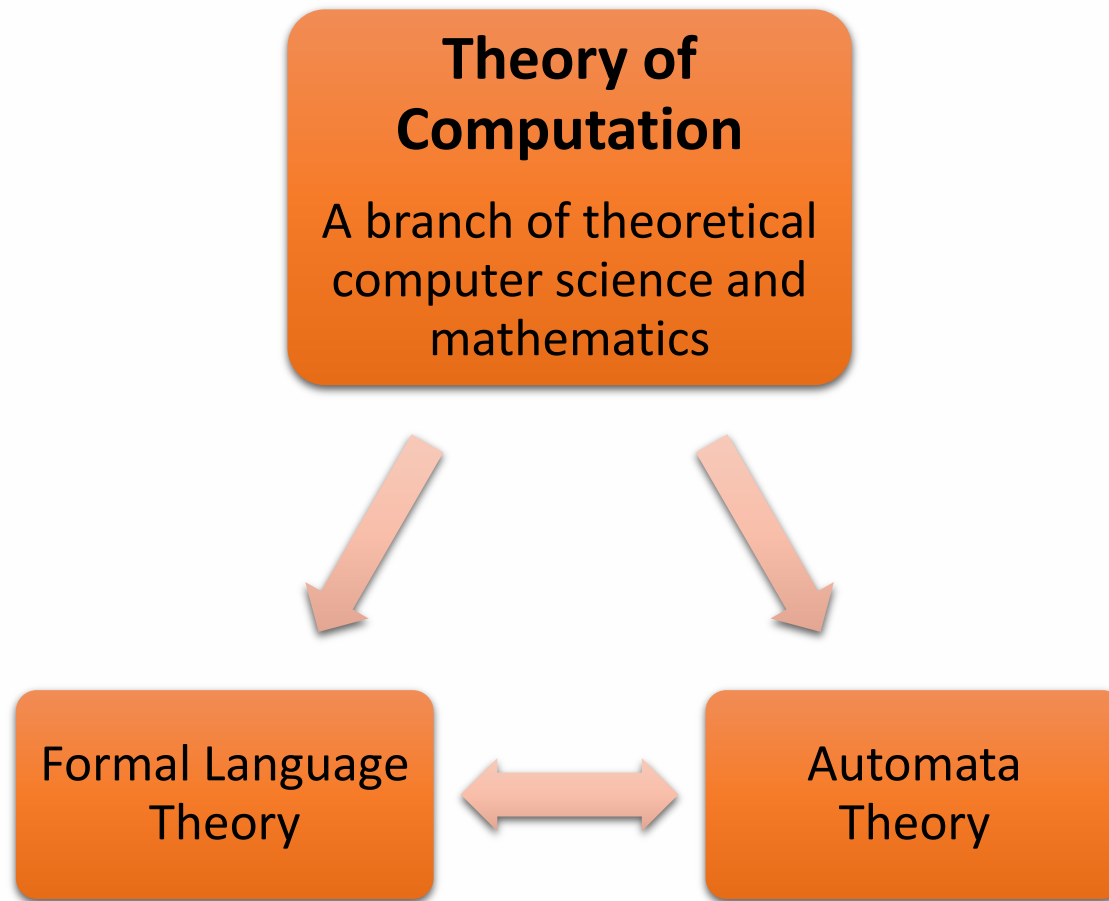
Let $S = (A, I, R)$ is a splicing system. Furthermore, let $L = L(S)$ is the set of stage one splicing languages produced by splicing system S and $L = L(S)$ is the set of stage two splicing languages produced by S that consists of $L' = L'(S)$ and all splicing languages that can be resulted by splicing L . Then, the **union of stage one and stage two splicing languages** are called two stages splicing languages.

Definition 22 (Yusof et al., 2015) Active Persistent Language

An **active persistent language** is a set of strings that participate in further splicing and is also contained in the limit language, L_∞ .

Mudaber, M. H., & Yusof, Y. (2015). *Two Stages Splicing System*. Paper presented at the International Conference on Mathematics, Engineering & Industrial Applications 2014 (ICoMEIA 2014), Penang, Malaysia.


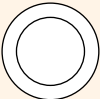

Yusof, Y., Lim, W. L., Goode, T. E., Sarmin, N. H., Heng, F. W., & Wahab, M. F. A. (2015). *Molecular Aspects of DNA Splicing System*. Paper presented at the International Conference on Mathematics, Engineering and Industrial Applications 2014 (ICoMEIA 2014), Penang, Malaysia.



An **automaton** is a finite representation of a formal language.

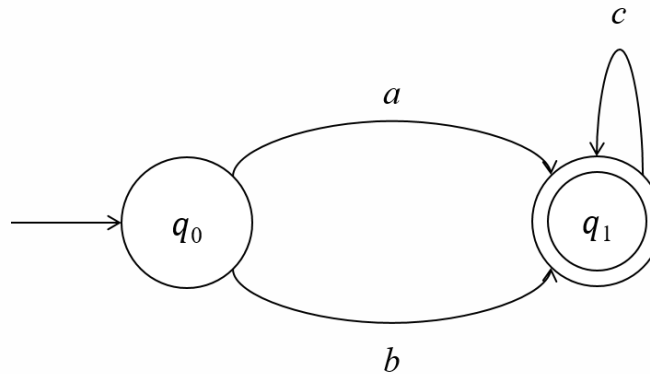
Automata Theory

- The theory of automata is a study of abstract machines or **automata** where the **computational problems** can be solved using the machines.
- Automaton is an abstract model of machine that performs computation on **inputs** by moving through a **series of states** according to the **transition** functions and stops moving at the **final states**.

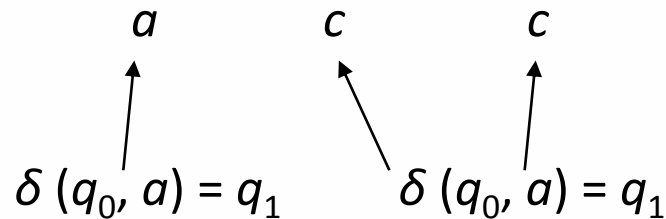
Symbols	Description
	State
	Final State
	Transition

Automata Theory (cont.)

- The automaton reads the symbols of input one after another and transitions from state to state until a string is formed.



- Derivation of a string *acc*:

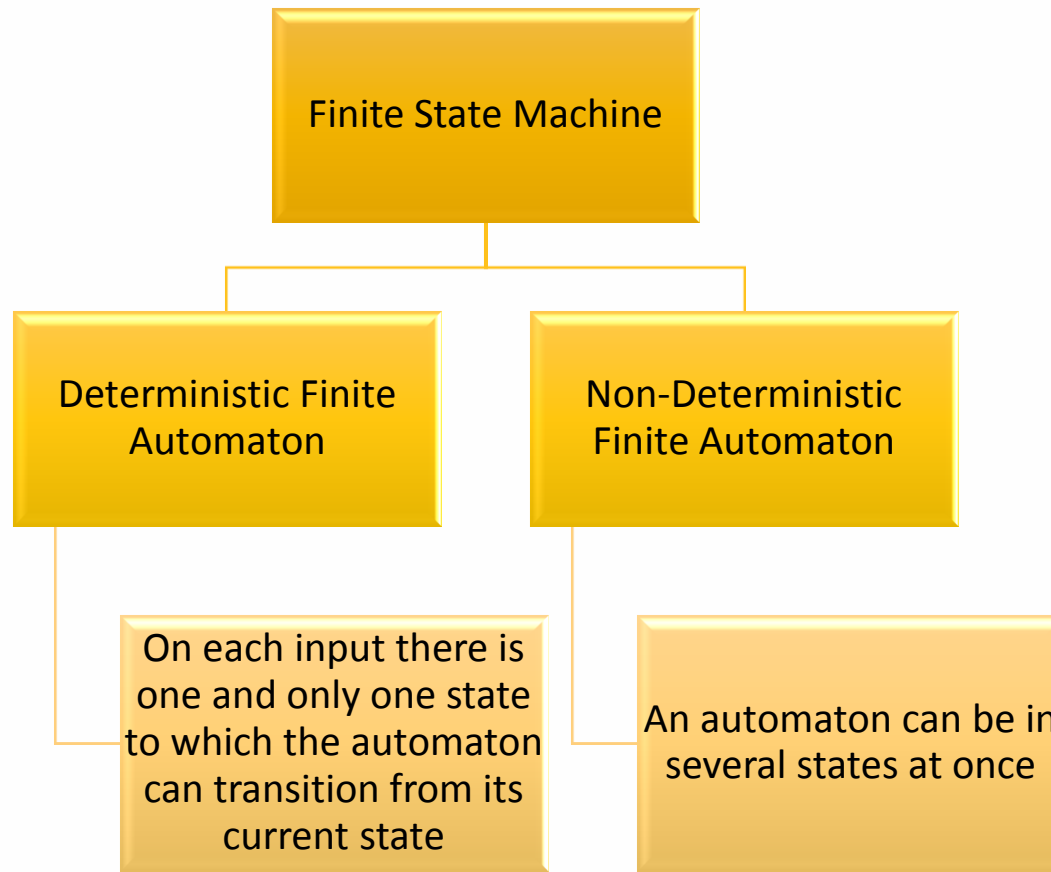


- The **language** L accepted by the automaton is the set of all strings formed by the automaton.

$$L = \{a, ac, acc, \dots, b, bc, bcc, \dots\}$$

Automata Theory (cont.)

- An automaton that contains only a finite number of states is called a **finite state machine**.



Automata Theory (cont.)

Definition 23 (Linz, 2006) Deterministic Finite Automaton

A **deterministic finite automaton** M is a 5-tuple, $(Q, \Sigma, \delta, q_0, F)$ consisting of a finite set of states Q , a finite set of input symbols called the alphabet Σ , a transition function $\delta : Q \times \Sigma \rightarrow Q$, an initial state $q_0 \in Q$ and a set of final states $F \subseteq Q$.

Definition 24 (Linz, 2006) Non-Deterministic Finite Automaton

A **non-deterministic finite automaton** M is a 5-tuple, $(Q, \Sigma, \delta, q_0, F)$ consisting of a finite set of states Q , a finite set of input symbols called the alphabet Σ , a transition function $\delta : Q \times \Sigma \rightarrow P(Q)$ where $P(Q)$ denotes the power set of Q , an initial state $q_0 \in Q$ and a set of final states $F \subseteq Q$.

Automata for DNA Splicing Systems

- The concepts of **automata** theory can be applied in DNA splicing systems.

Author	Description
Gatterdam 1992	The associated automaton for crossing disjoint, reduced, permanent splicing system.
Bonizzoni et al. 1998	The properties of splicing systems and finite state automata
Fong et al. 2008	Non-deterministic finite automaton diagrams for simple splicing systems
Khairuddin et al. 2019	Deterministic finite Automaton and its application for splicing system
Ismail et al. 2020	The generalisations of splicing languages in deterministic finite automata

Gatterdam, R. W. (1992). Algorithms for Splicing Systems. *SIAM Journal on Computing*, 21(3), 507-520.

Bonizzoni, P., Ferretti, C., Mauri, G., & a di Milano-Bicocca, D.-U. (1998). Splicing Systems with Marked Rules. *Romanian Journal of Information Science and Technology*, 1(4), 295-306.

Fong, W. H., Sarmin, N. H., & Ibrahim, Z. (2008). Recognition of Simple Splicing Systems using SHAutomaton. *Malaysian Journal of Fundamental and Applied Sciences*, 4(2), 337-342.

Khairuddin, S., Ahmad, M., & Adzhar, N. (2019). *Splicing System in Automata Theory: A Review*. Paper presented at the 2nd International Conference on Applied & Industrial Mathematics and Statistics, Kuantan, Pahang, Malaysia.

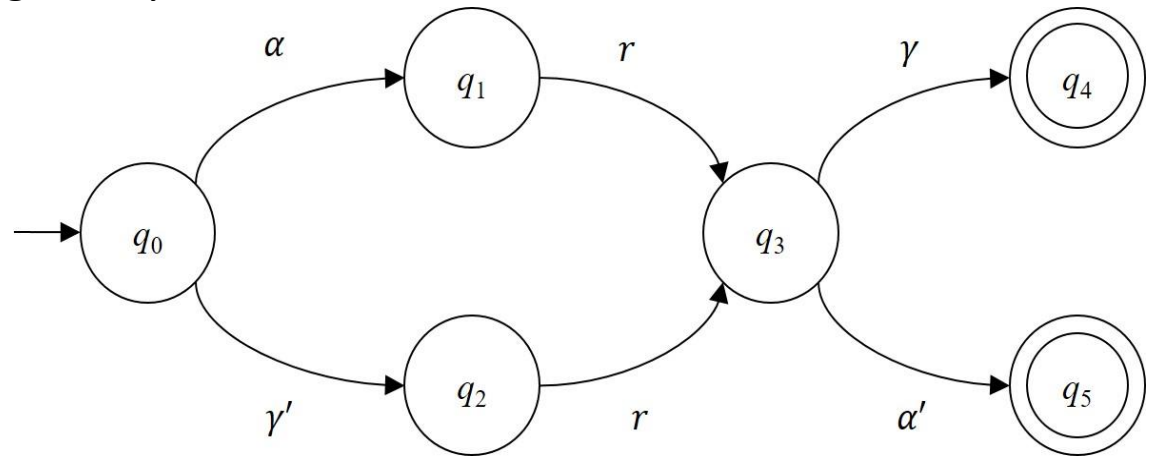
Ismail, N. I., Fong, W. H., & Sarmin, N. H. (2020). Automata for DNA Splicing Languages with Two Restriction Enzymes. *ASM Science Journal*, 13, 1-7.

Automaton for Simple Splicing System with One Cutting Site of a Palindromic Rule

Theorem 1

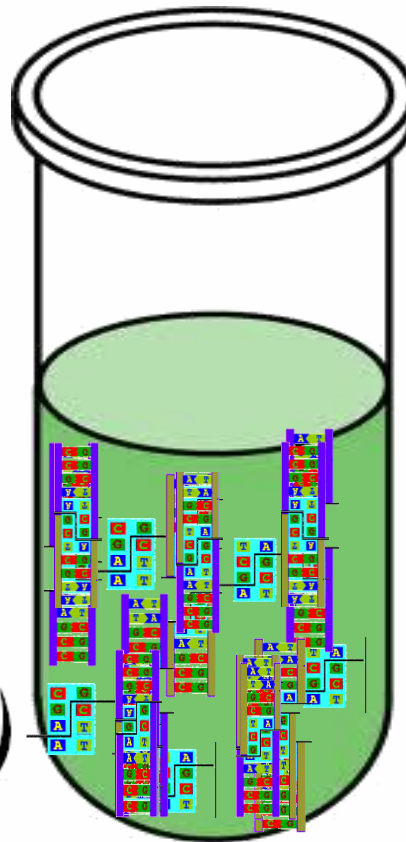
Given $S = (A, \alpha r \gamma, r)$ is a simple splicing system involving a cutting site of a palindromic rule r where $A = \{\alpha, r, \gamma\}$ are the set of variables used to denote any arbitrary dsDNA string, and α', r' and γ' are α, r and γ respectively after 180° rotation, $M = (Q, \Sigma, \delta, q_0, F)$ is a deterministic finite automaton for the splicing system that accepts the language $L(S)$, in which $Q = \{q_0, q_1, q_2, q_3, q_4, q_5\}$ is the set of states where q_0 is the initial state and $F = \{q_4, q_5\}$ is the set of final states, $\Sigma = \{\alpha, \alpha', r, \gamma, \gamma'\}$ is the set of inputs and δ is given by

$$\begin{aligned} \delta(q_0, \alpha) &= q_1, \\ \delta(q_0, \gamma') &= q_2, \\ \delta(q_1, r) &= q_3, \\ \delta(q_2, r) &= q_3, \\ \delta(q_3, \gamma) &= q_4 \text{ and} \\ \delta(q_3, \alpha') &= q_5. \end{aligned}$$



Wet Lab Experiment for DNA Splicing System

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



Previous Molecular Works on Splicing Systems

Author	Description
Laun and Reddy 1999	The first experiment on the splicing system using restriction enzymes <i>BglI</i> and <i>DraIII</i>
Fong 2008	The adult and limit languages from Head's splicing model using restriction enzymes <i>HpaII</i> and <i>AccI</i>
Karimi 2013	Verification of the persistency properties of splicing systems involving restriction enzymes <i>CvaQI</i> and <i>Acc65I</i>
Yusof et al. 2015	Yusof-Goode splicing system with restriction enzymes <i>AccI</i> and <i>AccI</i> using limit graph approach
Ahmad et al. 2018	Experiment on second order limit language from Yusof-Goode splicing system using restriction enzyme <i>DpnII</i>

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.

Wet Lab Experiment



Visit to wet lab, SUNY Binghamton, USA, 2007

Wet Lab Experiment (cont.)



Universiti Teknologi Malaysia, 2007



Wet Lab Experiment (cont.)



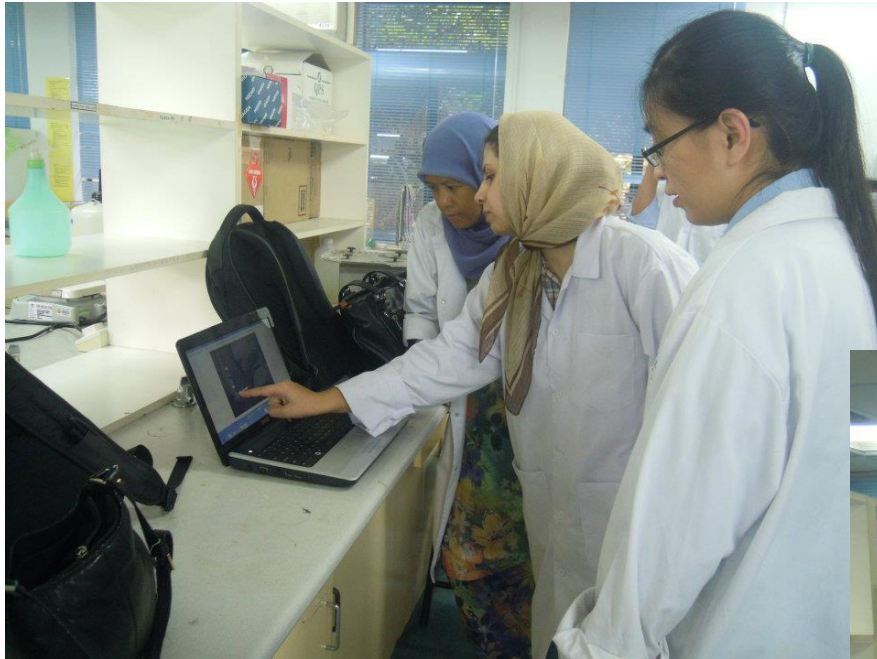
Towson University, USA, 2010

Wet Lab Experiment (cont.)



Research collaboration with Towson University, USA, 2010

Wet Lab Experiment (cont.)



Universiti Teknologi Malaysia, 2012



Wet Lab Experiment (cont.)

Universiti Teknologi Malaysia, 2015



Wet Lab Experiment (cont.)



Universiti Teknologi Malaysia, 2020



Laboratory Procedure

Polymerase chain reaction (PCR)

- To make several copies of a specific DNA segment

Process of Restriction Enzyme Digestion and Ligation

- The restriction enzymes recognize specific restriction sites in DNA molecules
- The restriction enzymes and ligase then cut and rejoin the molecules to generate further molecules

Polyacrylamide gel electrophoresis (PAGE)

- to separate proteins based on their molecular weight

Polymerase Chain Reaction (PCR)



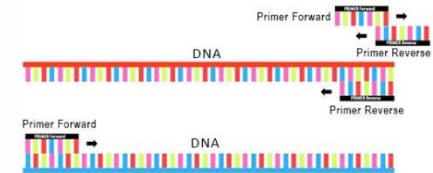
PCR machine



PCR tube



Lambda DNA



Primers



DNA Polymerase
(PCR reagent)

Process of Restriction Enzyme Digestion and Ligation



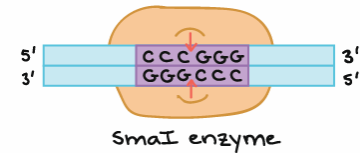
Thermomixer



Microcentrifuge Tube



PCR Product

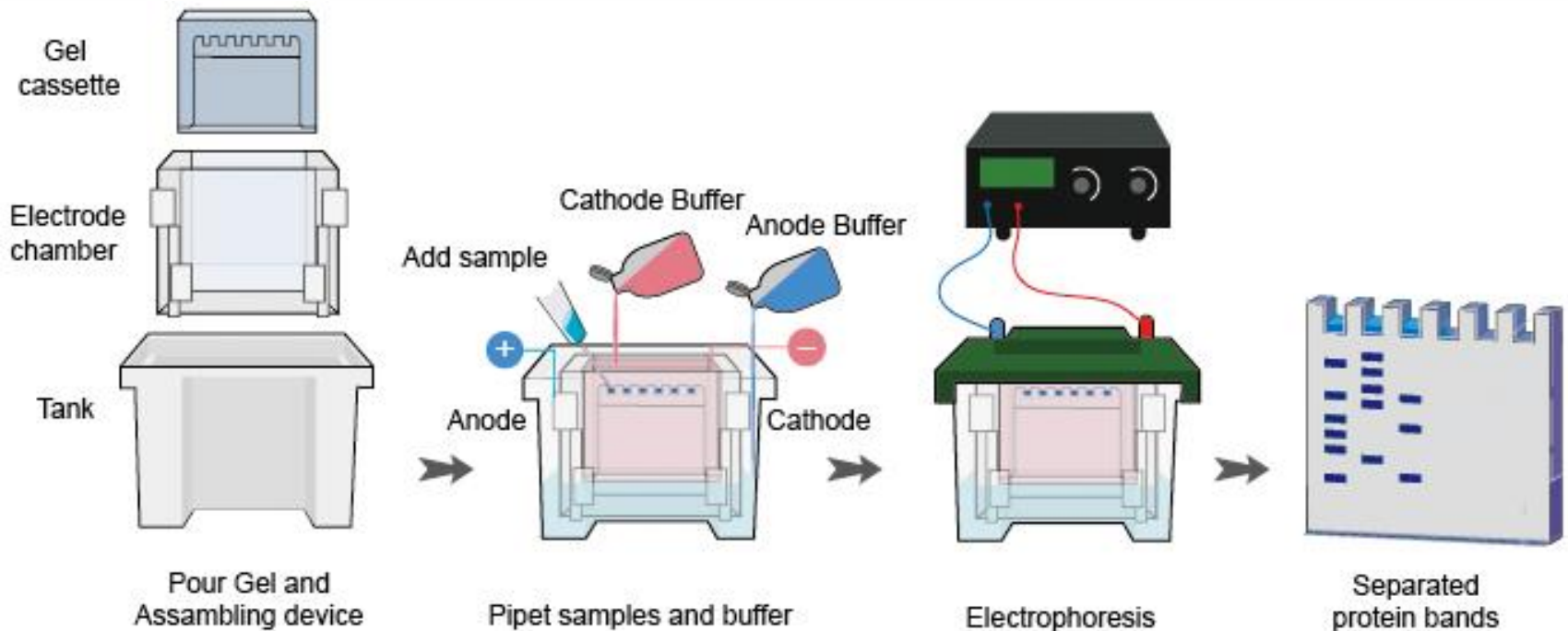


Restriction Enzyme

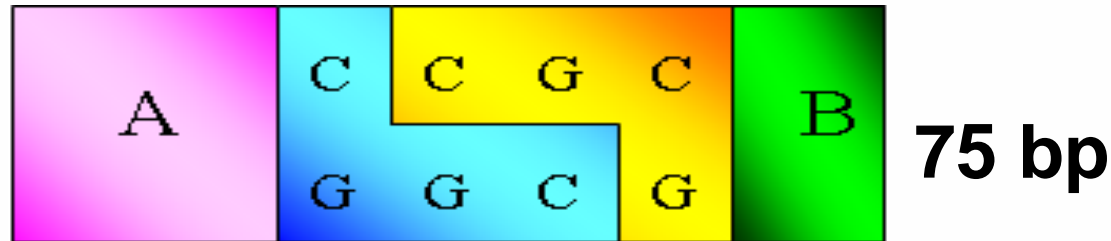


Ligase and Buffer

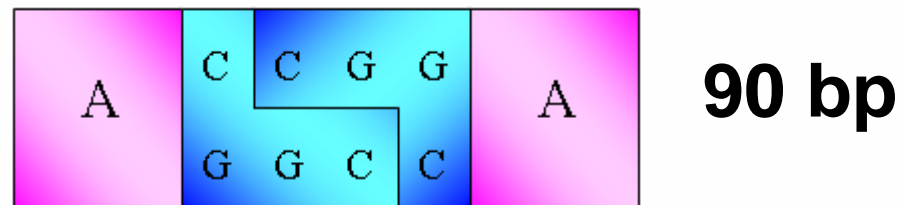
Polyacrylamide gel electrophoresis (PAGE)



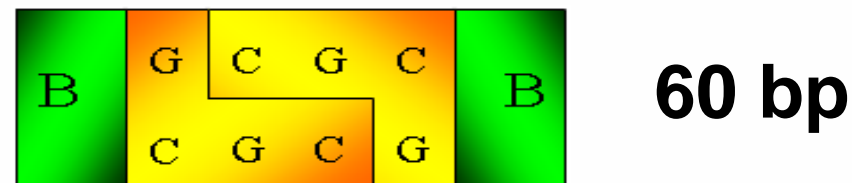
Example of a wet lab experiment



Limit Language

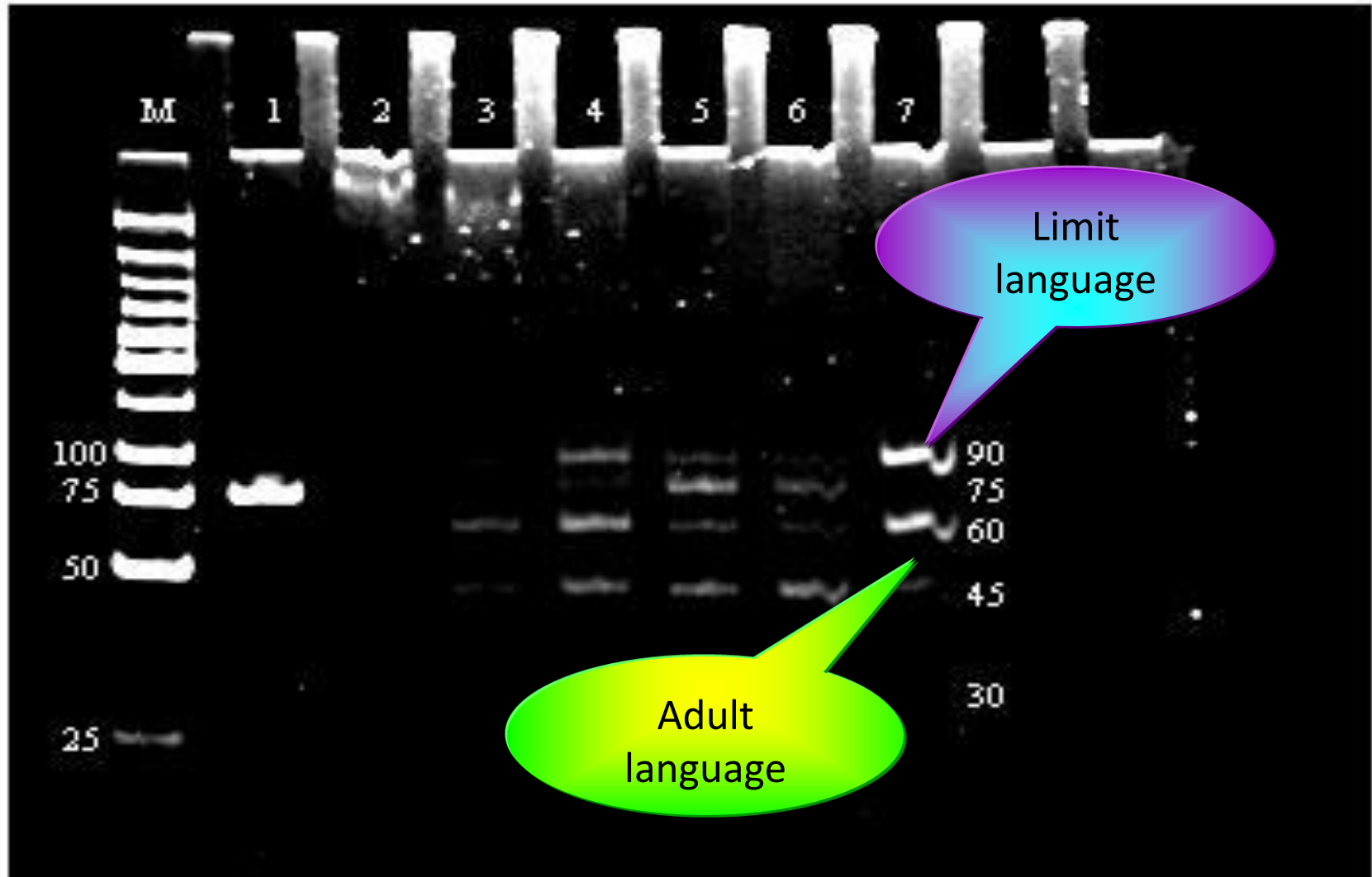


Adult Language



Example of a gel photo

LMW Uncut 0 5 10 20 45
Marker 75bp min min min min min overnight



Experimental Design for DNA Splicing System involving Enzymes *Cvi*QI and *Ac*II

- An **initial DNA molecule** / 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 *Ac*II 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: α *Cvi*QI site β *Ac*II site γ

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

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

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

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

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

Experimental Design for DNA Splicing System involving Enzymes *Cvi*QI and *Ac*II (cont.)

- Initial Molecule (42958 and 43117 from bacteriophage lambda)

*ggactatcgaagagtgcaaggcgatcaaggcaga**gtac**caacagaaactcaaagacctgcgaaatagcaga*
*agtgagg**ccgc**atgacgttctcagtaaaaaccattccagacatgctcgttgaaacatacggaatcagacagaa*
gtagcacgcagactg (160 bp)

- Enzyme *Cvi*QI (palindromic)

5'...G▼TAC...3'

3'...CAT▲G...5'

- Enzyme *Ac*II (non-palindromic)

5'...C▼CGC...3'

3'...GGC▲G...5'

DNA Splicing System involving *Cvi*QI and *Ac*II

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

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

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

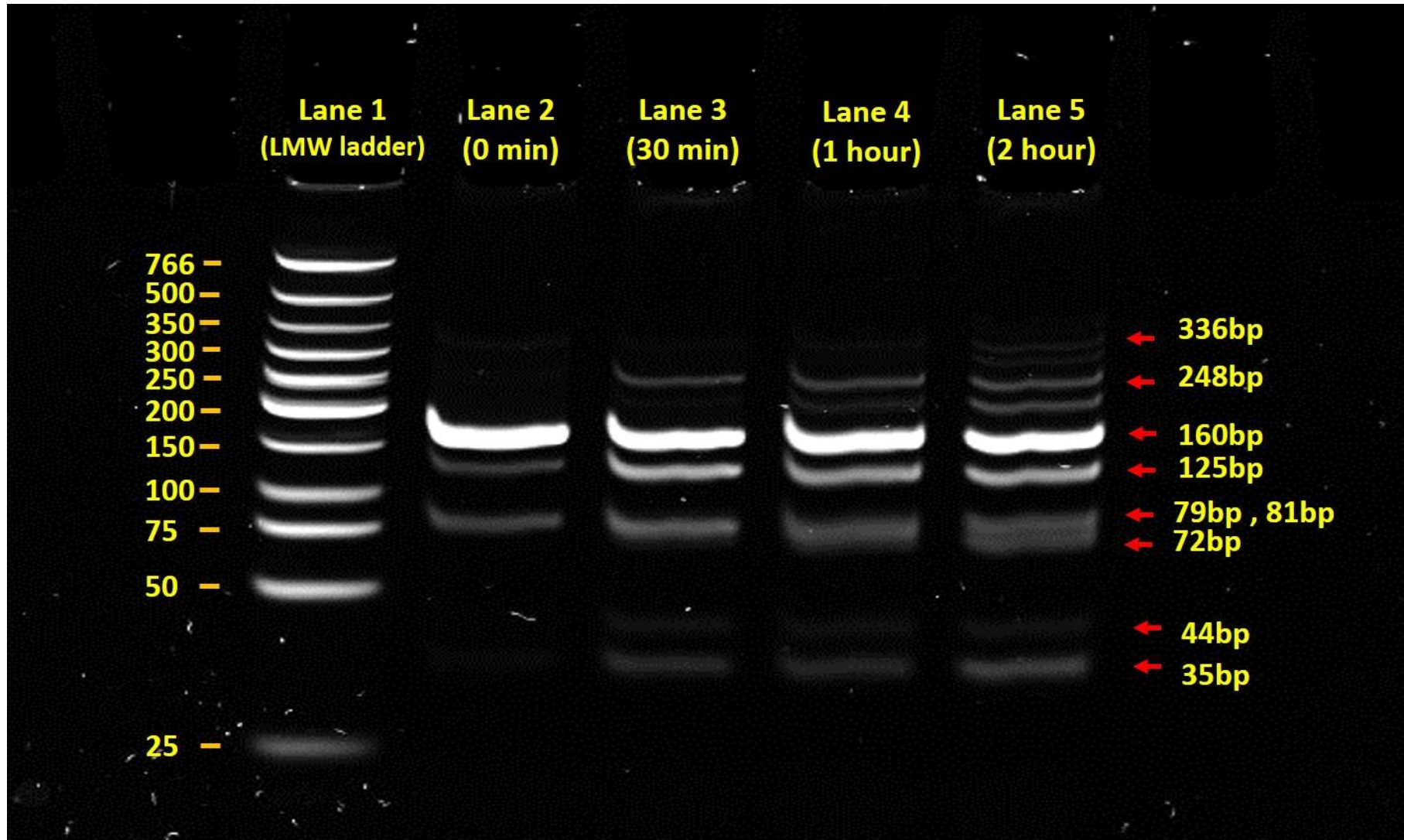
$$\alpha \underline{gtac} (\beta \underline{ccgg} \beta' \underline{gtac})^{n-1} \alpha', \\ \alpha \underline{gtac} (\beta \underline{ccgg} \beta' \underline{gtac})^{n-1} \beta \underline{ccgc} \gamma, \\ \gamma' \underline{gcb} (\underline{g} \beta' \underline{gtac} \beta \underline{ccg})^{n-1} \underline{c}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

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

DNA Splicing System involving *Cvi*QI and *Ac*II (cont.)

No.	Molecule	Size (bp)		Lane 1 (LMW ladder)	Lane 2 (0 min)	Lane 3 (30 min)	Lane 4 (1 hour)	Lane 5 (2 hour)
1.		35	766	—				
2.		44					—	—
3.		81	500	—			—	—
4.		37					—	—
5.		44	350	—				
6.		79	300	—				
7.		79	250	—			—	—
8.		125	200	—				
9.		160	150	—	—	—	—	—
10.		72, 160, 248, 336,	100	—		—	—	—
11.		160, 248, 336, 424,	75	—		—	—	—
12.		160, 248, 336, 424,	50	—		—	—	—
13.		160, 248, 336, 424,	25	—		—	—	—

DNA Splicing System involving *Cvi*QI and *Ac*I (cont.)



List of Publications

Link: <https://people.utm.my/nizararmin/>

2010

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).

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.

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.

List of Publications (cont.)

Link: <https://people.utm.my/nizararmin/>

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).

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)

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Thank You

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