

A COMPREHENSIVE REVIEW OF THE EXISTING LITERATURE ON RESTRICTED STICKER SYSTEMS

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ABSTRACT

Using the Systematic Literature Review (SLR) approach and according to the recommended reporting items for systematic reviews and meta-analyses (PRISMA) standards, this systematic literature review explores the topic of restricted sticker systems via the perspective of 15 chosen studies. The study focuses on three major themes: the goal of the studies, the methodology used, and the restrictions imposed. The review provides a complete overview of restricted sticker systems by analysing these topics, synthesising research ideas and contributing to the existing body of knowledge. The results not only improve comprehension of the aims, methodology, and computational advancements in restricted sticker systems, but they also give direction for future research paths and prospective applications. The study highlights the significance of multidisciplinary collaboration and actual implementations in order to develop the area of restricted sticker systems. This extensive literature review is a vital resource for scholars, encouraging further study and supporting improvements in this field.

Keywords: Sticker systems, Sticker model, Restricted sticker systems, DNA computing.

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1. Introduction

All The goals of this study are to evaluate, analyse, and categorise the available literature on restricted sticker systems. This SLR explores research patterns and discovers studies with similar purposes, problems, and restrictions. Themes of this study are shown in Table 1.

Table 1: Themes of the study

No.	Themes of the study
1.	Purpose of the study
2.	Methodology
3.	Restriction used

Sticker systems were suggested in the spot study (Adleman, 1994) as language producing devices that replicate the adhering activity found in DNA computing, which is equivalent to the annealing process.



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The sticker systems described create languages built of double-stranded sequences comparable to DNA molecules, with complementarity between the symbols in the two strands, matching the Watson-Crick pairing of DNA nucleotides. Starting with a limited number of axioms, new sequences are constructed by expanding the current ones on the right by adhering single-stranded sequences to either the upper or lower strands, resulting in full double-stranded sequences. The paper investigates several versions of sticker systems and their generating capacity by comparing them to language families from the Chomsky hierarchy. This work, among other things, presents characterizations of regular and recursively enumerable languages, revealing the expressive capabilities of sticker systems.

DNA sequences in Adleman's work were represented as double-stranded structures made up of four nucleotides: A (adenine), C (cytosine), G (guanine), and T (thymine). Based on the Watson-Crick complementarity principle, these nucleotides formed pairs—A with T and C with G. When a single-stranded sequence of A, C, G, and T nucleotides is linked with its corresponding single-stranded sequence, the two sequences form hydrogen bonds and form a double-stranded DNA sequence.

2. Literature review

The sticker systems discussed in this context are computational models that generate languages through the use of sticker operations. These operations are inspired by the techniques employed by L. Adleman in his notable DNA computing experiment, where he computed a Hamiltonian path in a graph using DNA (Adleman, 1994). In DNA, sequences are composed of double-stranded, helical structures made up of four nucleotides: A (adenine), C (cytosine), G (guanine), and T (thymine). These nucleotides pair together based on the Watson-Crick complementarity, where A pairs with T and C pairs with G. By combining a single-stranded sequence containing A, C, G, T nucleotides with a complementary single-stranded sequence, the two sequences can be combined together through hydrogen bonding, resulting in a double-stranded DNA sequence (Kari et al., 1998).

Head introduced splicing systems as an early theoretical foundation for DNA-based computing in 1987 (Head, 1987). Splicing systems manipulate DNA sequences through the splicing process, which involves the cutting and recombination of DNA molecules. This method revealed information on DNA's potential computing capabilities. Sticker systems are another mathematical paradigm that has evolved in the realm of DNA computing. Adleman used the sticker system model to solve the Hamiltonian route problem in a graph using DNA molecules in his pioneering experiment (Adleman, 1994). Sticker systems make use of stickers, which are small DNA sequences that may be affixed to a larger DNA strand to enable specialised interactions and activities.

The sticker operation, as outlined in the subsequent section, serves as the formal model for this operation. It can be utilized in the construction of a generative or computing device by initiating the process with a given set of incomplete double-stranded sequences (axioms) along with two sets of single-stranded complementary sequences (Kari et al., 1998). Through iterative right prolongation using elements from these complementary sets, the paper generate "computations" of potentially variable lengths. The process concludes when a complete double-stranded sequence is achieved, indicating the absence of any remaining "sticky ends." Thus, a language is formed through this iterative procedure.

This study explores the generative capabilities of various versions of these mechanisms. The unrestricted scenario corresponds to the Adleman experiment and has been proven, with a weak coding modification, to characterize regular languages. Interestingly, when an additional constraint is imposed, specifically requiring the use of the same sequence of complementary strings from the initial sets, a characterization of recursively enumerable languages is obtained.

In a research conducted in 2011, the sticker model, which is recognized as one of the prominent models in DNA computing, was employed to propose three DNA algorithms for solving three distinct NP-complete graph-based problems (Razzazi & Roayaei, 2011). Notably, this study marked the first instance of using the sticker model to address the domatic partition, kernel, and induced path problems. Additionally, simulations were performed to validate the accuracy and effectiveness of these algorithms. A comparable study was conducted in 2001, where researchers tackled two NP-complete problems, namely Subset-sum and Knapsack, using a sticker-based model for DNA computations (-Jiménez & Sancho-Caparrini, 2001). To accomplish this, they employed a finite set sorting subroutine and provided a procedure for formally verifying the designed programs. This verification process involved labelling test tubes using inductive techniques.

Sticker systems with limited sets of axioms and sticker rules are known to create just regular languages without any further constraints (Xu et al., 2004). Researchers have linked sticker systems with monoids (Sebry et al., 2014) and permutation groups (Hamzah et al., 2014) to improve language-generation capabilities beyond ordinary languages. A modified variant of the sticker system known as the probabilistic sticker system was introduced in 2014 (Selvarajoo et al., 2014). Probabilities expressed as real values ranging from 0 to 1 are connected with the axioms in this probabilistic framework. The probability of creating a string z from two strings x and y is indicated as $p(z)$, and it is determined using the multiplication procedure outlined for probabilities. It is mathematically stated as $p(z) = p(x) * p(y)$. A probabilistic sticker system's language is composed of all strings created by the sticker system, whose associated probabilities fulfil specific pre-determined cut-points that can be larger than, less than, or equal to previously defined values.

A different study released a paper in 2016 that introduced a form of sticker systems known as the simple one-sided sticker system (Selvarajoo et al., 2016). The form of the attachment sequence is constrained in this variation. The study goes on to look at incorporating probability into the basic one-sided sticker system, resulting to the creation of the probabilistic simple one-sided sticker system. The use of probability provides a probabilistic aspect to the language production process, improving computing capabilities and broadening the spectrum of languages that the sticker system can create.

The Systematic Literature Review (SLR) is a rigorous research process that entails meticulously analysing prior studies using clear criteria to answer particular research questions. It is distinguished by the systematic identification, assessment, and interpretation of important material in order to build a thorough knowledge of the current body of literature (Akhigbe et al., 2017). Researchers frequently use standardised frameworks such as the Preferred Reporting Item for Systematic Reviews and Meta-analysis (PRISMA) (Moher et al., 2009) to guarantee a systematic and trustworthy approach. PRISMA gives guidance for developing specific research questions, choosing acceptable studies, and assessing their quality.

With the growing number of systematic reviews (SRs) being undertaken in a variety of sectors, it is not uncommon to see many SRs on a single topic (Aromataris & Pearson, 2014; Hoffmann et al., 2021; Ioannidis, 2016; Page, 2016). While most SRs are concerned with efficacy, their significance resides in presenting scientists, medics, and policymakers with a summary of current research. To ensure the relevance and trustworthiness of SRs, excellent methodological quality and proper reporting are required (Moher et al., 2007). However, investigations have revealed that many SRs still have space for improvement (Vivante et al., 2011). To address this issue, guidelines such as the recommended reporting items for systematic reviews and meta-analyses (PRISMA) have been created to improve reporting standards and overall SR article quality (Moher et al., 2009).

3. Research methodology

The Systematic Literature Review (SLR) technique was used in this study, which followed the PRISMA principles, to assess the body of literature on restricted sticker systems. Identifying relevant articles, filtering them for eligibility, and analysing their substance were all part of the SLR process. A total of 15 publications were chosen for intensive research, resulting in a thorough comprehension of the area.

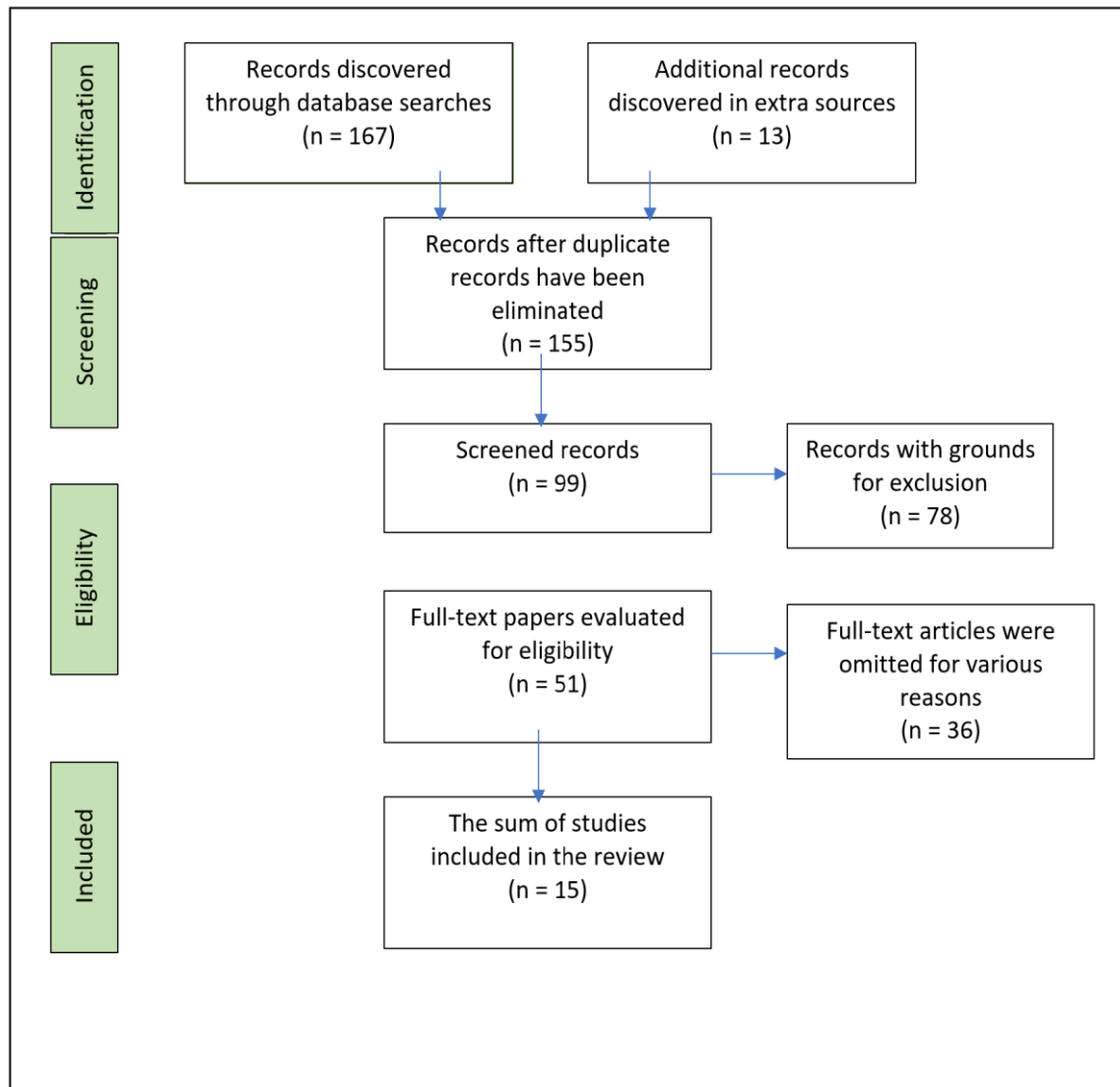


Figure 1. Flow of research data search and selection

Table 2: Identify the articles to be analyzed further.

No	Article Title	Year	Author's Name	Journal Name
1	Sticker Systems	1998	Paun, Rozenberg	Theoretical Computer Science
2	Computational Power of Probabilistic Simple One-Sided Sticker Language	2016	Selvarajoo, Fong, Sarmin, Turaev	Journal of Mathematical and Computational Science
3	The Generative Power of Weighted One-Sided and Regular Sticker Systems	2014	Siang, Fong, Sarmin, Turaev	AIP Conference Proceedings
4	Sticker systems over Monoids	2012	Sebry, Hamzah, Sarmin, Fong, Turaev	Malaysian Journal of Fundamental & Applied Sciences
5	Bidirectional Sticker Systems	1998	Freund, Paun, Rozenberg, Salomaa	Third Annual Pacific Conf. on Biocomputing, Hawaii
6	DNA computing, sticker systems, and universality	1998	Kari, Paun, Rozenberg, Salomaa, Yu	Acta Informatica 35, 401-420
7	Solving Knapsack Problems in a Sticker Based Model	2002	Perez-Jimenez, Sancho-Caparrini	DNA Computing: 7 th International Workshop on DNA-Based Computers
8	Exploring the Feasibility of DNA Computer: Design of an ALU using Sticker Based DNA Model	2017	Sarkar, Ghosal, Mohanty	IEEE Transactions on Nanobioscience
9	Computing by Observing Bio-Systems: the Case of Sticker Systems	2005	Alhazov, Cavaliere	DNA Computing: 10 th International Workshop on DNA Computing
10	The Properties of Probabilistic Simple Regular Sticker System	2015	Selvarajoo, Fong, Sarmin, Turaev	AIP Conference Proceedings
11	Computational Power of Probabilistic Bidirectional Sticker System in DNA Computing	2015	Selvarajoo, Fong, Sarmin, Turaev	International Journal of Applied Mathematics and Statistics
12	A DNA-Sticker Algorithm for Cryptanalysis LFSRs and NLFSRs Based Stream Cipher	2018	Sadkhan, Yaseen	International Conference on Advanced Science and Engineering (ICOASE)
13	Probabilistic Sticker Systems	2013	Selvarajoo, Fong, Haniza, Turaev	Malaysian Journal of Fundamental and Applied

				Sciences
14	Performing Mathematics using DNA: Complex Number Arithmetic using Sticker Model	2017	Sarkar, Ghosal	IEEE Computer Society Annual Symposium on VLSI
15	A Sticker Based Model for DNA Computation	1996	Roweis, Winfree, Burgoyne, Chelyapov, Goodman, Rothmund, Adleman	Journal of Computational Biology

4. Data collection and analysis

Data sources for this study were discovered using multiple online databases, including Google Scholar, Scopus, Research Gate, ERIC, and others. Some of the terminology used in data search include sticker systems, sticker model, restriction of sticker systems, and restricted sticker model. The papers chosen are from prestigious scientific journals. This study adds to the current knowledge on restricted sticker systems by synthesising the research findings (Freund et al., 1998; Sebry et al., 2014; Siang et al., 2014). The findings provide useful insights into the field's purpose, methods, and restrictions. Furthermore, the study acts as a roadmap for future research, indicating possible topics for examination and providing recommendations for further research.

Table 3. Data collected from the articles.

No	Article Title	Purpose of the studies	Methodology (Problems)	Restriction used
1	Sticker Systems	The purpose of this study is to analyse the generating power of many variations of sticker systems in which characterizations of regular, linear, and recursively enumerable languages are generated.	DNA Computing	None
2	Computational Power of Probabilistic Simple One-Sided Sticker Language	The computing capacity of probabilistic basic one-sided sticker systems is examined in this paper. The research demonstrates how imposing a probability constraint on a basic one-sided sticker system may boost the computing capacity of the languages generated.	DNA Computing	Simple one-sided sticker systems
3	The Generative	The generating power of weighted one-	DNA	Weighted

	Power of Weighted One-Sided and Regular Sticker Systems	sided sticker systems and weighted regular sticker systems is studied in this research.	Computing	sticker systems
4	Sticker systems over Monoids	The objective of the research is to introduce and investigate sticker systems over monoids where a component of a monoid is linked with each sticker operation and a complete double stranded order is regarded as effective if the computation of the associated elements of the monoid produces the neutral element.	DNA Computing	Valence sticker system
5	Bidirectional Sticker Systems	The article proposed two-sided sticker systems, which are a two-sided variant of a computability model introduced as an abstraction of Adleman's style of DNA computing. The systems are shown to have the same power as regular grammars, one variant is found to represent linear languages, and another is proven to be adept at indicate any recursively enumerable language.	DNA Computing	Bidirectional sticker systems
6	DNA computing, sticker systems, and universality	The study introduces sticker systems, a computability model that is an abstraction of computations implementing Watson-Crick complementarity, as shown in Adleman's DNA computing experiment.	DNA Computing	None
7	Solving Knapsack Problems in a Sticker Based Model	This paper's main purpose is to provide molecular solutions for two NP-complete problems, Subset-sum and Knapsack, in a sticker-based model for DNA computations.	NP-complete problems: Subset-sum and Knapsack	None
8	Exploring the Feasibility of DNA Computer: Design of an ALU	The creation of a full ALU utilising a Sticker-based DNA Model with experimental feasibility study is proposed in this work.	Arithmetic and Logic unit (ALU)	None

	using Sticker Based DNA Model			
9	Computing by Observing Bio-Systems: the Case of Sticker Systems	The study use finite automata (as observers) to observe the "evolution" of a sticker system and translate that "evolution" into comprehensible output.	Observer	None
10	The Properties of Probabilistic Simple Regular Sticker System	The goal of this research is to investigate the features of basic probabilistic regular sticker systems.	DNA Computing	Simple regular sticker systems
11	Computational Power of Probabilistic Bidirectional Sticker System in DNA Computing	Some features of a probabilistic bidirectional sticker system are examined in this research. The research demonstrates how a probabilistic bidirectional sticker system may boost the computing capacity of the created languages.	DNA Computing	Bidirectional sticker system
12	A DNA-Sticker Algorithm for Cryptanalysis LFSRs and NLFSRs Based Stream Cipher	The paper proposes a DNA sticker model-based algorithm, a computability model, that is a simulation of parallel computations using Molecular computing as in Adelman's DNA computing experiment, and it shows how to use a sticker-based model to design a simple DNA-based algorithm for attacking a linear and a non-linear feedback shift register (FSR)-based stream cipher.	Cryptanalysis LFSRs and NLFSRs Based steam cipher	None
13	Probabilistic Sticker Systems	The study introduces probabilistic sticker systems in which probabilities are initially associated with the axioms and the likelihood of the generated string is determined by multiplying the probabilities of all occurrences of the starting strings used in the string's computation by the probability of the created string.	DNA Computing	Probabilistic sticker systems

14	Performing Mathematics using DNA: Complex Number Arithmetic using Sticker Model	The main goal of this paper is to expand the capacity of DNA Computing to address such general-purpose issues. This work aims to do complex number arithmetic on two complex numbers, such as addition, subtraction, multiplication, and division.	Complex Number Arithmetic	None
15	A Sticker Based Model for DNA Computation	The article presents computing using the sticker model and explores physical implementation options for each operation. The research proposes a specific machine design for implementing the sticker model as a parallel robotic workstation controlled by a computer.	DNA Computing	None

5. Results and Discussion

5.1 Purpose of the studies

The data analysis used in this study is content analysis in relation to this SLR. When using this approach to analyse data, three phases are taken: (a) purpose analysis, (b) issues analysis, and (c) restriction analysis. Table 3 shows that the objective of the selected articles is similar: to present the characteristics of the sticker systems. Some articles focus on specific applications and solutions, whereas the majority of papers discuss the computing capacity and producing capabilities of sticker systems. However, it can be stated that the computational potential of sticker systems is widely examined and frequently experimented with in order to boost the generating power and serve as a theoretical model for DNA-based computers (Chomsky, 1956). This outcome encourages more research on the models of sticker systems.

5.2 Methodology on Problems

Table 4. Problems used in the studies

Problems	Number of studies
DNA Computing	10
NP-Complete	1
Arithmetic and Logic Unit (ALU)	1
Observer	1
Cryptanalysis LFSRs and NLFSRs	1
Complex and Number Arithmetic	1

The table depicts the many problem areas. Problems vary depending on the study's goal. One paper represented np-complete, arithmetic and logic unit (ALU), observer, cryptanalysis LFSRs and NLFSRs, and complex number arithmetic among the 15 publications chosen. In 10 articles, sticker systems are used to tackle various computing challenges. Based on this information, we may conclude that sticker systems are commonly employed to tackle DNA computing challenges. The computational power of the sticker model, on the other hand, has yet to reach its peak (Kari et al., 2012). As a result, further publications on boosting the computational capacity of sticker systems in DNA computing should be published in the future.

5.3 Restriction used

Table 5. Restriction used in the studies

Simple one-sided	Weighted	Valence	Bidirectional	Simple regular	Probabilistic	None
1	1	1	2	1	1	8

Table 3 summarises the restrictions applied in the papers studied. Eight research appear to have used no restrictions at all, two studies applied bidirectional restriction, and one articles used a simple one-sided, weighted, valence, simple regular, and probabilistic restriction. The limitations of addressing DNA computing using sticker systems must be investigated in order to enhance computational capacity (Chomsky, 1959; Hameed, 2011). If DNA possesses the greatest RE language capacity in the Chomsky Hierarchy, the model may be utilised as a theoretical model for DNA-based computers. DNA-based computers have significant benefits over traditional silicon-based computers (El-Seoud et al., 2017). DNA-based computers may do calculations in massive parallel due to the inherent parallelism of DNA operations. A huge quantity of data may be encoded by each DNA strand, allowing for dense data storage. Since there have been no restrictions that have attained the utmost power, additional study employing restricted sticker systems in solving DNA computing should be developed.

6. Conclusion

This study is a systematic literature review (SLR) on restricted sticker systems. It analyses at 15 articles published in prominent worldwide journals between 1996 and 2018. These articles were chosen based on specified criteria to verify their relevancy and quality. The goal of this SLR is to offer a thorough knowledge of restricted sticker systems by analysing, categorising, and synthesising research data based on particular topics. The data analysis highlighted three major themes: the study's purpose, problems, and the restrictions that were imposed. The paper intends to provide insight on the numerous objectives pursued in restricted sticker systems research, the methodology used to evaluate them, and the various restricts used to boost their computing capabilities by studying these areas. This systematic analysis provides a better and more thorough overview of limited sticker systems, adding to the current body of knowledge in this topic. Furthermore, the selected applications and issue domains mentioned in this work have real-world implementation potential for restricted sticker systems. The findings have the potential to motivate researchers as well as practitioners to investigate and create fresh applications in fields such as finance, biology, optimisation, and artificial intelligence. New and novel solutions to complicated issues can be found by harnessing the computing power and flexibility of restricted sticker systems.

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9. Conflict of Interest

The authors have no conflicts of interest to declare.

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