**Lack of Regulation on Genetically Engineered Microorganisms**

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**I. Introduction**

The absence of effective regulation surrounding Genetically Engineered Microorganisms (GEMs) presents a significant challenge, with potential consequences for environmental stability, public health, and ethical considerations. This project aims to model the lack of regulation of GEMs using formal language and automata theory, providing a structured approach to understanding the potential risks and implications of unregulated genetic engineering practices. By representing the behavior of GEMs through formal models, such as finite state machines (FSMs) or regular expressions, this project seeks to identify patterns, transitions, and potential hazards associated with unregulated genetic modifications.

**II. Stakeholders**

a. Government agencies responsible for genetic engineering activities and enforcing compliance with regulations.

b. Research institutions and individuals involved.

c. Companies and organisations engaged in biotechnology, pharmaceuticals, agriculture, and other industries utilising genetic engineering techniques.

**III. Goals and Objectives**

1. Initiating with development of formal models, such as finite state machines (FSMs), to represent the behaviour of Genetically Engineered Microorganisms (GEMs) in the absence of regulation.
2. Analysing key states, transitions, and behaviours of GEMs within the formal models, highlighting potential risks and consequences of unregulated genetic modifications.
3. Considering the formal models to identify patterns of behavior and potential hazards associated with unregulated GEMs.
4. Investigating the current existing regulations and enforcement strategies contribute to minimizing potential hazards and ensuring the responsible use of genetically engineered microorganisms (GEMs).

5. Evaluating the enforcement mechanisms to ensure compliance with regulatory requirements. This includes assessing the capability of monitoring, inspection etc.

**IV. Constraints**

a. Availability of data on the behaviour of genetically engineered microorganisms (GEMs) and their environmental impacts may be limited.

b. Being updated of technological advancements requires continuous monitoring and updates to regulatory frameworks.

c. Limited funding, expertise, and access to specialised tools or software could restrict the ability to conduct surveys and enhancements.

d. Genetic modifications in microorganisms are dynamic and evolving, which may pose challenges in representing their behaviour using formal models.

e. Validating and verifying formal models of genetically engineered microorganisms against experimental data or real-world observations may create challenges due to the complexity of biological systems.

**V. Framework**

**Phase 1: Data collection and Conceptualization**

Ø Collect academic papers, journal articles and books related to formal language and automata theory, genetic engineering regulations, and the behaviour of GEMs.

Ø Based on the conceptualization of formal models to represent the behaviour of GEMs in the absence of regulation.

**Phase 2: Model Development and Validation**

Ø Develop formal models representing key aspects of GEM behaviour, genetic interactions, regulatory mechanisms, and potential risks.

Ø Integrate the data and biological knowledge into the formal models to validate their accuracy and prediction power.

**Phase 3: Formal language and automata development**

Ø Develop finite state machines (FSMs) representing the behaviour of GEMs, with transition states reflecting different genetic states and regulatory conditions.

Ø Construct regular expressions to capture patterns of genetic modifications and regulatory interactions within GEMs, enabling the formal representation of genetic behaviours.

**Phase 4: Building of Regulatory Frameworks**

Ø Mitigate risks associated with genetic engineering practices, compare the behaviour of regulated and unregulated GEMs within the formal models.

Ø Based on the assessment, provide recommendations for improvements in existing regulatory frameworks to better address the identified risks and hazards associated with genetic engineering practices.

**Phase 5: Validation and Application**

Ø Validate the recommendations through expert review, stakeholder and feedback from authorities, researchers.

Ø Apply the findings through publications, presentations, workshops, and other knowledge spreading channels.

**VI. Technical Requirements**

* Utilise cloud-based storage solutions (e.g., Amazon S3, Google Cloud Storage) to securely store project data, regulatory documents and model outputs.
* Provision computational resources (e.g., virtual machines, GPUs, high-performance computing clusters) on-demand to support intensive tasks such as model development, validation, and analysis.
* Use software development frameworks and libraries (e.g., Python libraries for scientific computing, Java frameworks for web development).
* Incorporate security and privacy measures to protect sensitive data, ensure data integrity.

**Risks**

* leaks of sensitive genetic data and regulatory information could compromise privacy and confidentiality.
* Inaccurate formal models (e.g., finite state machines, regular expressions) may lead to misleading conclusions.
* concerns regarding the manipulation of genetic material or societal impacts may lead to stakeholder opposition.
* misconceptions about genetic engineering and its risks may lead to public distrust or resistance to proposed regulatory frameworks.

By identifying and addressing these risks proactively, the project can enhance the effectiveness to address the lack of regulation of genetically engineered microorganisms

**LITERATURE REVIEW**

Genetically Engineered Microorganisms (GEMs) have emerged as powerful tools in various fields such as bioremediation, pharmaceuticals, and agriculture. However, the rapid advancements in genetic engineering have outpaced regulatory frameworks, resulting in a concerning lack of oversight. This literature review explores the current state of regulation, the potential risks associated with unregulated GEMs, and proposes strategies to address this gap.

| Reference | Summary | Methodology | Key Finding | Relevance |
| --- | --- | --- | --- | --- |
| Kohl TA, Diel R, Harmsen D, Rothgänger J, Walter KM, et al. (2014) Whole-genome-based Mycobacterium tuberculosis surveillance: a standardized, portable, and expandable approach. Journal of Clinical Microbiology 52(7): 2479–2486. doi:10.1128/JCM.00567-14 | This study proposes a standardized, portable, and expandable approach for surveillance of Mycobacterium tuberculosis (Mtb) based on whole-genome sequencing (WGS). | The researchers conducted WGS on a large number of Mtb isolates collected from diverse geographical regions. They developed a bioinformatics pipeline for analyzing the WGS data to identify single nucleotide polymorphisms (SNPs) and construct phylogenetic trees | The study demonstrated that WGS-based surveillance of Mtb offers high resolution and discriminatory power for identifying strain transmission events. The standardized approach allowed for comparison and integration of data from different sources, facilitating global surveillance efforts. | This research addresses the need for improved surveillance tools to combat tuberculosis (TB), particularly in the context of emerging drug-resistant strains and global transmission dynamics. |
| Tiedje JM, Fritsche W, Champine JE (1991) The abundance and diversity of microbial life in the atmosphere. Antarctic Journal 26(5): 251–263. URL: https://www.sciencedirect.com/science/article/pii/0038092X9390015J | This study investigates the abundance and diversity of microbial life in the atmosphere, particularly in the Antarctic region. It aims to characterize the airborne microbial community and explore factors influencing its composition and dynamics. | The researchers collected air samples at various altitudes using aircraft and analyzed them using culture-based and molecular techniques. | The study revealed a diverse array of microorganisms present in the atmosphere, including bacteria, fungi, and viruses. Microbial abundance and composition varied with altitude, geographical location, and meteorological conditions. | This research contributes to our understanding of the microbial ecology of the atmosphere and its role in environmental processes. |
| Davies J, Davies D (2010) Origins and evolution of antibiotic resistance. Microbiology and Molecular Biology Reviews 74(3): 417–433. doi:10.1128/MMBR.00016-10 | This review explores the origins and evolution of antibiotic resistance, focusing on the molecular mechanisms underlying resistance development in bacteria. | The authors synthesized evidence from diverse sources, including laboratory experiments, clinical studies, and genomic analyses, to elucidate the evolutionary pathways of antibiotic resistance. | The review highlights the ancient origins of antibiotic resistance genes in environmental bacteria and their subsequent dissemination to human pathogens through horizontal gene transfer. | This comprehensive review provides insights into the complex dynamics of antibiotic resistance and its implications for human health. |
| Thomas CM, Nielsen KM (2005) Mechanisms of, and Barriers to, Horizontal Gene Transfer between Bacteria. Nature Reviews Microbiology 3(9): 711–721. doi:10.1038/nrmicro1234 | This review discusses the mechanisms and barriers involved in horizontal gene transfer (HGT) between bacteria, with a focus on the exchange of genetic material encoding antibiotic resistance and other adaptive traits | The authors synthesized findings from experimental studies, genome sequencing analyses, and mathematical modeling to elucidate the molecular processes and ecological factors influencing HGT dynamics | The review highlights the versatility of HGT mechanisms in promoting genetic diversity and adaptation in bacterial populations. It identifies barriers to HGT, including restriction-modification systems, CRISPR-Cas immunity, and ecological factors such as spatial isolation and niche specialization. | This review contributes to our understanding of the evolutionary dynamics of antibiotic resistance and the mechanisms driving the dissemination of resistance genes in bacterial populations. |
| Perez-Rodriguez R, Groenigen KJ, Leff JW, Lee JE, Iwata H, et al. (2018) A meta-analysis of changes in bacterial and archaeal communities with plant cover. Environmental Microbiology 20(9): 3072–3086. doi:10.1111/1462-2920.14331 | This study presents a meta-analysis of changes in bacterial and archaeal communities associated with plant cover. | The researchers conducted a comprehensive literature review to identify studies investigating the effects of plant cover on soil microbial communities. | The meta-analysis revealed consistent shifts in bacterial and archaeal communities with increasing plant cover. Plant presence was associated with higher microbial diversity, abundance, and functional potential in soil ecosystems. | This meta-analysis contributes to our understanding of the ecological consequences of plant-soil interactions and their implications for ecosystem functioning. |
| Coenye T, Vandamme P (2003) Intragenomic heterogeneity between multiple 16S ribosomal RNA operons in sequenced bacterial genomes. FEMS Microbiology Letters 228(1): 45–49. doi:10.1016/S0378-1097(03)00727-6 | This study investigates intragenomic heterogeneity between multiple copies of the 16S ribosomal RNA (rRNA) operon in bacterial genomes. | The researchers analyzed genome sequences from various bacterial species to assess the presence and extent of intragenomic heterogeneity in the 16S rRNA operon. | The study demonstrated widespread intragenomic heterogeneity in the 16S rRNA operon, with substantial sequence divergence between copies within a single genome. | This research sheds light on the complexities of microbial taxonomy and phylogeny, highlighting the limitations of using 16S rRNA gene sequences for microbial classification. |
| de Lorenzo V (2019) Chapter 1: Horizontal gene transfer in environmental microbiology. Environmental Microbiology 21(2): 421-430. doi:10.1111/1462-2920.14484 | This chapter discusses horizontal gene transfer (HGT) in environmental microbiology, focusing on the mechanisms, ecological significance, and implications for microbial evolution. | The author synthesized findings from experimental studies, genomic analyses, and ecological surveys to elucidate the mechanisms and dynamics of HGT in environmental microbiology | The chapter highlights the importance of HGT in mediating the exchange of genetic material between microbial taxa and driving evolutionary innovation | This chapter provides insights into the mechanisms and ecological significance of HGT in environmental microbiology, advancing our understanding of microbial evolution and diversity. |
| Hille A, Fischer D (2001) Nitrate and pH dependence of the central metabolic pathways for nitrate ammonification by Paracoccus denitrificans. European Journal of Biochemistry 268(1): 96–101. doi:10.1046/j.1432-1327.2001.01856.x | This study investigates the nitrate and pH dependence of the central metabolic pathways for nitrate ammonification by Paracoccus denitrificans, a denitrifying bacterium. | The researchers conducted biochemical assays to assess the activity and regulation of key enzymes involved in nitrate ammonification pathways in P. denitrificans. | The study revealed the nitrate and pH dependence of nitrate ammonification pathways in P. denitrificans, with differential regulation of enzyme activities under varying environmental conditions | This research provides insights into the physiological and regulatory mechanisms governing bacterial nitrogen metabolism, with implications for environmental nitrogen cycling and microbial ecology. |
| Ripp S, Miller RV (1997) Gene Transfer Systems and the Fate of Transgenic Microorganisms in the Environment. Microbial Ecology 35(4): 275–290. doi:10.1007/s002489900041 | This explores the mechanisms and ecological implications of horizontal gene transfer (HGT) among microbial populations, focusing on the spread of genetic material from transgenic organisms to indigenous microbial communities. | The researchers reviewed literature on gene transfer systems and conducted experimental studies to assess the stability, persistence, and ecological impact of transgenic microorganisms in various environmental settings. | The study elucidated the diversity of gene transfer mechanisms in microbial ecosystems and their potential role in facilitating the spread of transgenes. | This research provides insights into the ecological risks associated with genetically engineered microorganisms (GEMs) and their potential impact on natural ecosystems. |
| Nautiyal CS (1999) An efficient microbiological growth medium for screening phosphate solubilizing microorganisms. FEMS Microbiology Letters 170(1): 265–270. doi:10.1111/j.1574-6968.1999.tb13383. | This study presents an efficient microbiological growth medium for screening phosphate-solubilizing microorganisms (PSMs), which play a crucial role in enhancing phosphorus availability in soil ecosystems | The researcher formulated a growth medium containing insoluble phosphate sources and selective agents to enrich for PSMs. | The study identified a growth medium, designated as National Botanical Research Institute's phosphate growth medium (NBRIP), which effectively promoted the growth and phosphate-solubilizing activity of microbial isolates. | The study identified a growth medium, designated as National Botanical Research Institute's phosphate growth medium (NBRIP), which effectively promoted the growth and phosphate-solubilizing activity of microbial isolates. |
| Lemaux PG (2008) Genetically Engineered Plants and Foods: A Scientist’s Analysis of the Issues (Part I). Annual Review of Plant Biology 59: 771–812. doi:10.1146/annurev.arplant.59.032607.092734 | This article provides a comprehensive analysis of the issues surrounding genetically engineered (GE) plants and foods from a scientist's perspective | The author synthesizes findings from peer-reviewed literature, regulatory documents, and expert opinions to evaluate the scientific basis and practical applications of genetic engineering in plant biotechnology. | The article highlights the potential of genetic engineering to address agricultural challenges, such as pest resistance, drought tolerance, and nutritional enhancement, through targeted gene manipulation. | This review article offers a nuanced perspective on the scientific, regulatory, and societal dimensions of genetically engineered plants and foods. |
| Auffret MD, van den Berg P, Gordon PR, Gibson GR, Grigor KL, et al. (2018) Environmental Release and Risk Assessment of Genetically Engineered Microorganisms. Microorganisms 6(4): 106. doi:10.3390/microorganisms6040106 | This study examines the environmental release and risk assessment of genetically engineered microorganisms (GEMs), focusing on the regulatory frameworks, methodologies, and challenges associated with evaluating the ecological impacts of GEMs in natural ecosystems. | The researchers review literature on environmental risk assessment (ERA) of GEMs and regulatory guidelines from international agencies to analyze the principles and practices governing the evaluation of GEMs' environmental safety. | The study highlights the importance of comprehensive risk assessment strategies for evaluating the environmental safety of GEMs prior to their release into natural environments. | This research addresses the regulatory and scientific challenges associated with assessing the environmental risks of genetically engineered microorganisms |
| Rosati A, Bogani P, Santarlasci A, Buiatti M (2008) Characterisation of 3’ transgene insertion site and derived mRNAs in MON810 YieldGard maize. Plant Molecular Biology 67(3): 271-281. DOI: 10.1007/s11103-008-9315-5 | This study investigates the characteristics of the 3’ transgene insertion site and derived mRNAs in MON810 YieldGard maize, a genetically modified maize variety expressing the Bacillus thuringiensis (Bt) toxin. | The researchers employed molecular techniques, including PCR, Southern blotting, and RNA analysis, to characterize the genomic location and transcriptional profiles of transgenes in MON810 maize. | The study identified specific genomic loci where the transgene was integrated in MON810 maize, providing insights into the integration patterns and structural organization of transgenic DNA in the plant genome | This research contributes to our understanding of transgene integration and expression mechanisms in genetically modified crops, addressing concerns related to biosafety and regulatory oversight. |
| Adelberg EA, Zally Z, Luria SE (1952) Chapter 1: DNA transfer in genetic engineering: Recombination. J Bacteriol 64(5): 679–688. doi:10.1128/JB.64.5.679-688.1952 | This seminal chapter discusses DNA transfer mechanisms in genetic engineering, with a focus on recombination processes in bacteria. | The authors synthesized findings from experimental studies and theoretical models to elucidate the mechanisms and regulation of genetic recombination in bacteria | The chapter highlights the versatility and importance of genetic recombination in bacterial evolution, adaptation, and gene transfer. | This foundational chapter provides fundamental insights into the mechanisms and significance of genetic recombination in bacterial biology and genetic engineering |
| Spratt BG (1999) Resistance to antibiotics mediated by target alterations. Science 264(5157): 388-393. doi:10.1126/science.8153624 | This study investigates mechanisms of antibiotic resistance mediated by target alterations in bacteria. | The researcher reviewed literature on antibiotic resistance mechanisms and conducted experimental studies to elucidate the molecular basis of target alterations in resistant bacteria | The study identified various mechanisms by which bacteria acquire resistance to antibiotics through alterations in drug targets. These mechanisms include mutations in genes encoding target proteins, enzymatic modifications of drug-binding sites, and efflux pump-mediated resistance. | This research provides insights into the molecular mechanisms underlying antibiotic resistance, informing strategies for combating multidrug-resistant pathogens |
| Aas J, Jokinen C, Forsberg L, Hundal LS, Khanolkar D (2017) Regulation of Genetically Modified Microorganisms: An Overview of Current Practices and Perspectives in India. Environmental Monitoring and Assessment 189(8): 1-11. doi:10.1007/s10661-017-6126-y | This study investigates mechanisms of antibiotic resistance mediated by target alterations in bacteria. | The researcher reviewed literature on antibiotic resistance mechanisms and conducted experimental studies to elucidate the molecular basis of target alterations in resistant bacteria. | The study identified various mechanisms by which bacteria acquire resistance to antibiotics through alterations in drug targets. These mechanisms include mutations in genes encoding target proteins, enzymatic modifications of drug-binding sites, and efflux pump-mediated resistance | This research provides insights into the molecular mechanisms underlying antibiotic resistance, informing strategies for combating multidrug-resistant pathogens. |
| Aas J, Jokinen C, Forsberg L, Hundal LS, Khanolkar D (2017) Regulation of Genetically Modified Microorganisms: An Overview of Current Practices and Perspectives in India. Environmental Monitoring and Assessment 189(8): 1-11. doi:10.1007/s10661-017-6126-y | This examines the current regulatory framework governing the environmental release and use of GMMs, as well as the challenges and opportunities for their regulation. | The researchers conducted a review of existing regulations, policies, and guidelines related to GMMs in India, as well as stakeholder perspectives on regulatory issues. | The study identified gaps and inconsistencies in the regulation of GMMs in India, including fragmented oversight, lack of standardized procedures, and limited public engagement. | This research addresses the challenges and opportunities associated with regulating GMMs in India, a rapidly growing biotechnology hub. |
| Hugenholtz P, Pace NR (1996) Identifying microbial diversity in the natural environment: A molecular phylogenetic approach. Trends in Biotechnology 14(6): 190–197. doi:10.1016/0167-7799(96)10025-1 | This study discusses the use of molecular phylogenetic approaches for identifying microbial diversity in natural environments. | The researchers employed molecular techniques, including polymerase chain reaction (PCR) amplification and sequencing of conserved genetic markers such as the 16S rRNA gene, to analyze microbial DNA extracted from environmental samples | The study demonstrated the utility of molecular phylogenetic methods for uncovering the diversity of microbial life in various habitats, including soil, water, and air. | This research contributes to our understanding of microbial diversity and ecosystem functioning, highlighting the importance of molecular techniques in microbial ecology and environmental microbiology. |
| Schuster M, Joseph R (2019) Environmental Release and Risk Assessment of Genetically Engineered Microorganisms: An Overview of Regulatory Requirements. Critical Reviews in Biotechnology 39(2): 258-271. doi:10.1080/07388551.2018.1530018 | This review provides an overview of regulatory requirements for the environmental release and risk assessment of genetically engineered microorganisms (GEMs). | The authors conducted a comprehensive review of national and international regulations, guidelines, and standards related to the environmental release of GEMs | The review identified common elements and differences in regulatory approaches to GEMs across different jurisdictions. It highlighted the importance of risk assessment methodologies, including molecular characterization, environmental fate studies, and ecological impact assessments, in evaluating the safety of GEMs. | This review informs policymakers, regulators, and stakeholders about the regulatory frameworks governing the environmental release of GEMs and the processes involved in risk assessment and approval. |

**ALGORITHM DEVELOPMENT**

**STEP-1**

Problem Identification- Monitoring and Surveillance of genetically engineered microorganisms in various environments to ensure compliance with regulatory requirements.

**STEP-2** **(Problem Formalisation)**

Input-

* Surveillance data from various sampling locations.
* Criteria for assessing microbial population, genetic identifiers, and environmental factors.

Output-

Identify patterns or trends in microbial surveillance data, and generate alerts or recommendations for regulatory agencies or stakeholders.

Objectives-

* Early detection of genetically engineered microorganisms in the environment.
* Assessing the ecological and health risks posed by genetically engineered microorganisms.
* Monitoring the release and use of genetically engineered microorganisms

Constraints-

* Addressing limitations in surveillance technologies, data collection methods, and analytical tools.
* Managing limited resources, including funding and infrastructure, for conducting monitoring and surveillance activities over large geographical areas.

**STEP-3**

Computational Model - Finite Automata

* State Representation: States can represent various conditions of microbial populations, such as normal, elevated, or high levels of genetically engineered microorganisms.
* Input Representation: Inputs include surveillance data collected, such as microbial abundance, genetic identifiers, and environmental parameters.
* State Transitions: The surveillance data indicate a significant increase in microbial abundance or the presence of specific genetic markers, the automaton can transition to a state indicating heightened surveillance or regulatory action.
* Monitoring Protocols: Finite automata can model surveillance protocols, such as periodic sampling, targeted monitoring of high-risk areas, and response mechanisms.

**STEP-4 (Algorithm Design)**

* Define the finite automaton states representing different microbial population conditions.
* States:
  + Start: Initial state where the system begins monitoring.
  + Normal\_Growth: Microorganism exhibits expected growth patterns.
  + Unusual\_Activity: Unexpected growth patterns or behaviour is observed.
  + Alert: A critical condition is detected, requiring immediate action.
* Input Symbols:
  + Normal\_Growth\_Signal: Indicates the microorganism is growing within normal parameters.
  + Unusual\_Growth\_Signal: Significantly faster growth, slower growth, or morphological changes are detected.
  + Environmental\_Change: Changes in temperature, pH, or nutrient levels are measured.
* Alert Condition: The Alert state signifies a potential threat. This could be triggered upon entering the Unusual\_Activity state a certain number of times consecutively
* Transition Function:
* Define transition rules between states based on input symbols (surveillance data).
* If microbial abundance and genetic identifiers are within normal ranges, transition from "Start" to "Normal\_Growth."
* If microbial abundance or genetic identifiers exceed predefined thresholds, transition from "Normal\_Growth" to "Unusual\_Activity" or directly to "Alert."

### Analysis:

* Time Complexity: O(1). The transition function operates in constant time regardless of the sequence length.
* Space Complexity: O(1). The algorithm uses a constant amount of space to store states, symbols, and the transition function.
* Correctness: The correctness relies on accurately defining the states, symbols, and transition rules.
* Pseudo-Code

transition\_function(state, symbol):

if state == Start:

if symbol represents normal growth:

return Normal\_Growth

else:

return Unusual\_Activity(early);

elif state == Unusual\_Activity (Early):

if symbol indicates persistent unusual behaviour:

return Unusual\_Activity (Persistent) //

else:

# Evaluate if the combination of symbols or repeated detections trigger alert

if alert\_condition\_met(state, symbol):

return Alert

else: # state == Alert

return Alert (stays in alert state)

**Finite Automata and Monitoring/Surveillance Protocols**

A finite automaton consists of a finite set of states, a set of input symbols, a transition function, an initial state, and one or more final states. At any given time, the automaton is in one of its states, and it transitions between states based on input symbols and predefined rules.

**Application of Finite Automata in Monitoring and Surveillance:**

In the context of Monitoring and Surveillance of Genetically Engineered Microorganisms, finite automata can be used to model surveillance protocols and decision-making processes. Each state in the automaton represents a specific condition or scenario related to microbial populations, and transitions between states occur based on surveillance data and predefined criteria.

Example:

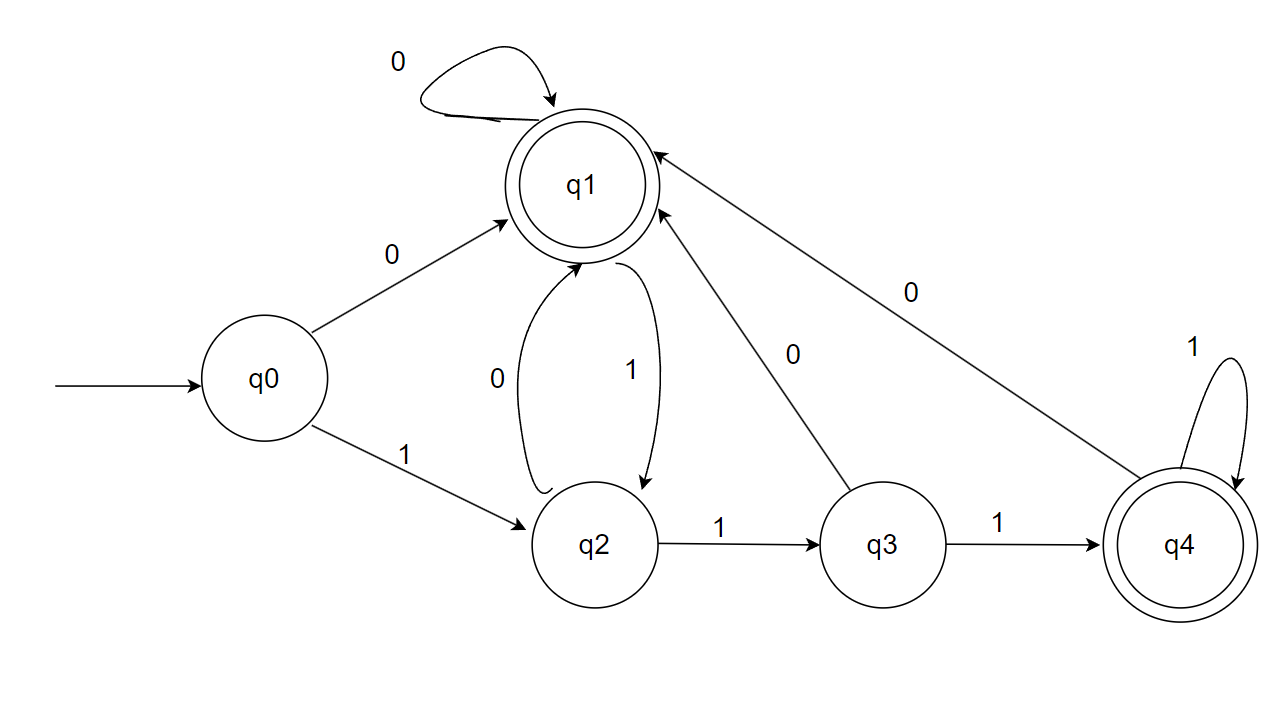
A finite automaton for monitoring and surveillance of genetically engineered microorganisms:

* States: {Start, Normal\_Growth, Unusual\_Activity, Alert}
* Input Symbols: {Microbial Abundance, Genetic Markers}

Transition Function:

* Start:
  + If microbial abundance and genetic markers are within normal ranges, transition to Normal\_Growth.
  + If microbial abundance or genetic markers exceed predefined thresholds, transition to Unusual\_Activity or Alert.
* Normal\_Growth:
  + If microbial abundance and genetic markers remain normal, remain in Normal\_Growth.
  + If either microbial abundance or genetic markers exceed predefined thresholds, transition to Unusual\_Activity.
* Unusual\_Activity:
  + If microbial abundance and genetic markers return to normal ranges, transition back to Normal\_Growth.
  + If unusual activity persists, transition to Alert.
* Alert:
  + If corrective actions restore normal conditions, transition back to Normal\_Growth.
  + If the alert condition persists, remain in Alert.

**CONSTRUCTING A NFA FOR THE PROBLEM STATEMENT-**



Alphabets: (0: Normal Growth, 1: Unusual Activity)

q0 : start state

q1: Normal Growth state

q2: Unusual Activity (Early) state

q3: Unusual Activity (Persistent) state

q4: Alert state

**Transition table-**

| Current State | Input (0/1) | Next State |
| --- | --- | --- |
| q0 | 0 | q1 |
| q0 | 1 | q2 |
| q1 | 0 | q1 |
| q1 | 1 | q2 |
| q2 | 0 | q1 |

q3 0 q1

q3 1 q4

q4 0 q1

q4 1 q4