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# Critique of Genetic Mutation Rates in Evolving Populations: A Biomathematical Approach

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**ABSTRACT**

To better understand the dynamic mechanisms influencing genetic diversity, this work uses a biomathematical technique to examine genetic mutation rates in changing populations. Research uses a particular approach to investigate complex interactions between mutation rates, natural selection, and population dynamics. Research reveals that key discoveries provide insight into the complex interactions between genetic mutations and evolutionary paths. A quantitative framework for evaluating how mutations affect population-level outcomes is made possible by the use of mathematical modelling. Even if the study offers insightful information about the significance of genetic mutation rates, it is essential to consider several limitations. For determine the research used SPSS software and generate mathematical models related to the evolving populations. These limitations draw attention to areas where further research might improve methods and broaden the field of study. research study has ramifications that go beyond the local setting and provide insights into broader applications or consequences. research study adds to the larger conversation on evolutionary biology by clarifying the variables affecting genetic mutation rates and lays the groundwork for future research. To sum up, this biomathematical investigation of genetic mutation rates provides a thorough understanding of the fundamental processes of evolutionary change. Overall study founded significant link between them. Research study understanding of population genetics is expanded by the combination of mathematical modelling and empirical data, opening the door for further study to build upon these foundations.

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## 1. Introduction

The process of evolution has always been considered a complex process involving multifactor components that alter to proceed with the changes. A genetic mutation is always necessary for the ultimate evolution process. To study these mutational changes and evolution processes, it is important to learn the features up to radical reductions, and this can be done by introducing the concept of biomathematics. A biomathematical approach is defined as the analysis of mutation processes under a mathematical modelling technique that helps study the impact of mutations on the diversity of the population (Schuster, 2011). Although individual concepts of evolution in the field of biology were developed already in the eighteenth century, the idea of evolution on the population level was introduced by Charles Darwin. Later on, Gregor Mendel invented the laws of inheritance.

After almost sixty years, the work of both scientists was united by the mathematicians and population geneticists of that time. After that, it took a little while for other mathematicians to introduce laws and models for relating genetic mutations and the evolution of a population (Ravikumar et al., 2018). In 1908, Hardy Weinberg's law described the constancy of gene frequency along time variation by assuming no alteration in genetic drift and mutational changes. One of the other famous mathematicians of that time was Ronald Fisher, who introduced the biomathematical concept in history. He used various differential equations to deduce the results, however, differential equations in population genetics can only carry out specific features related to population dynamics (Etheridge, 2011).

Many different types of models have been proposed in a biomathematical way to show the effect of gene mutation on evolution. Selection of these models depends upon the pressure selection, drift in genetics, size of the population, and rate of mutation. One of these types of models are 'rate models of mutation'. Using these models allows different mutation rate constants that are eventually different for different species and genomic sequences. The Wright Fischer Model is

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another mathematical model that helps relate evolution to different populations. This model deals with the genetic drift and changes in allele frequency of the non-overlapping evolutionary generations. This model specifically works for small populations because they can drastically affect evolution by just a minor genetic drift. Submerging of coalescent theory with such models has also been done which helps in determining common ancestral allele pairs and can allow the drawing of common variation in the evolution of a population (Ibrahim et al., 2016).

A model called Muller's Rachet has also been put forward, which not only helps determine a population's evolutionary changes but also introduces the 'Rachet effect'. According to this effect, the number of deleterious mutations increases with the increase in evolution, most importantly in asexual populations based on a small number. In this case, the class that undergoes the minimum mutation showcases a ratchet kind of effect. Hence, the name rachet effect has been used in this model (Jiang et al., 2010). Another model has been named Kimora's model, based on the name of the scientist Motoo Kimura. In this model, molecular evolution was described on behalf of neutral theory and helped in describing the mutation rate of amino acid-based mutations. Similarly, the dynamics of populations can be studied by analyzing these mathematical models to determine the effect of these mutations on the size of the population and genetic pool.

The effect can either be positive or negative, as mutations do lead toward evolution, but too many mutations can also cause unusual deletion of genes (Vikhar, 2016). Therefore, this model helps find the appropriate balance between required beneficial mutations and non-required, unhealthy deleterious mutations emerging in a population. In this way, mathematical models can help in deriving information on the overall fitness of the population, after an evolution has taken place (Loewe & Hill, 2010).

There are major advantages to implementing a biomathematical approach in studying evolutionary changes due to mutational genetics. First, it allows the researchers to quantify the data and get the numbers and figures regarding genetic alterations, frequencies, mutations, and pressure selections. This approach aids in understanding the evolutionary processes more efficiently (Hassanat et al., 2019). Moreover, it allows the scientists to estimate a change in evolution under different circumstances and variable factors like mutation rates and evolution pace, etc. Using the mathematical models can allow the formulation of a hypothesis and relation of its authenticity with the empirical data of the model presented. This helps in the validation and prediction of an outcome as a result of genetic drift or mutation. Some models also allow the understanding of different evolutionary forces by drawing comparisons among them, i.e., comparisons between the theory of selection and mutation (Sniegowski et al., 2000). Also, the biomathematical assessment provides researchers and educators with visual models that can better convey the ideas related to genetic mutations and population evolutions, making further studies possible. The long-term assessment of periodic trends in genetic evolution can also be studied using the biomathematical approach as it helps draw comparisons from the past variations and accumulation of mutational changes over time in a specific set of population (Frenoy & Bonhoeffer, 2018).

The main components or drivers of genetic changes can also be identified easily by incorporating a required model over an essential set of evolutionary data and can aid researchers in finding out about the influence of certain factors related to population genetics. Besides, these models can integrate the data with empirical information, making them fit for a comprehensive look into the real-world circumstances (Goldstein & Pollock, 1997). Within the subject of evolutionary biology, genetic mutation rates in evolving populations are fundamental, impacting species dynamics and the trajectory of diversification across time. Scientists attempting to solve the puzzles surrounding the evolutionary history of life have long been enthralled with the complex interactions that occur between genetic mutations, natural selection, and population dynamics.

In light of this, the current work uses a biomathematical method to explore the intricacies of genetic mutation rates to offer a sophisticated comprehension of their influence on the evolution of populations. Genetic mutation rates are being studied for reasons other than academic curiosity; they include evolutionary biology, medicine, and conservation. Mutation is a continuous process affecting the genetic blueprint of an organism's DNA. This phenomenon provides the building blocks for evolution. Deciphering the mechanisms that drive speciation, adaptation, and ultimately the diversity of life on Earth requires understanding the rates at which these mutations arise and their effects on populations. Genetic mutation rates have historically been studied using various methods, from complex mathematical models to actual observations in wild populations.

Each method has its advantages and disadvantages, but the combination of empirical data and mathematical modelling has shown to be a potent tool for deciphering the intricate workings of evolutionary processes. By integrating biomathematics, researchers may investigate the effects of genetic changes on a population scale using a quantitative framework that extends beyond simple observation.

On the other hand, these systems have some shortcomings as well. Mathematical information received from these models can be limited and sometimes doesn't allow the involvement of biological factors, which makes systems unrealistic and non-reliable. The biomathematical information is also based on assumptions, and minor misunderstanding of these assumptions can lead to false assessment of population genetics. Also, the genetic systems are very complex and require tough assessment to estimate parameters related to population mutational changes. Similarly, some models may not be

available for full spectrum providence of genetic variations and can limit the advantages (Aleti & Moser, 2016).

## 2. Relevance of the Research:

Numerous academic fields recognize the importance of examining genetic mutation rates in dynamic populations. In medicine, knowing mutation rates is essential for deciphering the genetic causes of illnesses, forecasting how they will progress, and creating specialized treatment plans. Furthermore, understanding mutation rates is essential to conservation biology because it helps evaluate how adaptively prospective endangered species could respond to changing environmental conditions. The results of this study may also have ramifications for agriculture, as genetic mutation rates determine how quickly crops evolve and adapt to shifting environmental conditions.

Furthermore, the study's results might clarify how antibiotic resistance develops and how infectious illnesses work within the framework of microbial evolution. This work adds to the continuing efforts in science to improve and broaden the theoretical frameworks that support our comprehension of evolutionary biology. Using a biomathematical method, the study hopes to drive greater investigation into the mechanisms controlling genetic mutation rates in evolving populations and to create a more solid base for future research endeavours.

## 3. Literature review:

Researchers reveal that clonal evolution is one of the reasons behind drug resistance in cancer patients. The resistance faced during the cancer therapy procedure is because of the clonal evolution. the resistance developed in cancer patients toward one drug also results in resistance toward other types of drugs. the cancer therapy works by destroying the cancer cells, but the resistant clone cells regenerate even after the therapy process(Acar et al., 2020). Studies suggest that technology-based algorithms are used for identifying genetic mutations. The complexity of the genetic problem is easily assessed using the GA.GA technology uses different operators to manage the working of the overall algorithmic system. The conceptual basis of genetics is dealt with using the GA algorithm(Alam et al., 2020).studies show that bacterial evolution is based on the HGT. the genomes of most bacterial species possess the HGT. In most cases, the HGT is specialized to alter the genetic makeup of bacteria, but in some cases, the HGT is beneficial (Arnold et al., 2022).Studies suggest that the problems related to the SRCPSP are solved using the HH-EGP methodology. This methodology helps improve the SRCPSP scheduling and predict the evolution process at a genetic level. Also, for effectively carrying out the decision-making process, the sequence voting system is employed in the SRCPSP scheduling (Chen et al., 2021).studies reveal that certain malignancies' are death-causing. PDAC is one of the malignancies that are considered death-causing malignancy.

The incidence of PDAC causes the majority of cancer-related deaths. PDAC is a carcinogenic disorder that results from genetic mutations (Connor & Gallinger, 2022).studies suggest that the treatment process against cancer has been slowed down because of the drug resistance phenomenon. the tumour progenesis in cancer patients is so strong that it resists the action of novel cancer therapies and novel drugs. Different biological disciplines have been developed to understand this drug resistance process in the last few years. Nanotechnology has been used in the medical field to assess the complexity behind the drug resistance mechanism in humans (Craig et al., 2020).Studies suggest that population models are used to study the impact of environmental adaptations on humans. The phylogenic traits are responsible for the adaptation of humans to different environments.

The genetic regulatory factors influence the (Fagny & Austerlitz, 2021).studies highlight that many advanced drugs are developed for treating different types of metastatic cancer. with time, the use of advanced drugs has declined due to the resistance shown by cancer patients to the drugs. the evolution of drug resistance with time has made the treatment procedure against cancer difficult (Gatenby & Brown, 2020).scholars explain that data related to the genomes is provided through whole genome sequencing. Whole genome sequencing is used in clinical practices to understand the genetic mutation patterns in different cancer patients.

To get information about the cause behind cancer in cancer patients, therapists use the mutational signature technique. The mutational signature process is specialized to identify the endogenous as well as exogenous characteristics responsible for cancer onset in patients (Koh et al., 2021).studies claim that there has been great advancement in the field of oncology in the last few decades, but all the advancements in the oncology field have failed to reduce the number of deaths caused by cancer. Modern treatment therapies are very advanced but show little treatment efficacy.

Modifying cancer therapies increases the chances of improvement in cancer-based treatment theory (Kuznetsov et al., 2021).studies explain that various models have been developed to understand the spread of three deadly infectious disorders. The first is COVID-19, the second infectious virus is SARS, and the third is MERS. the propagation model is established to comprehend the mechanism of initiating and inhibiting these three infections (Liang, 2020).studies reveal that the process of somatic mutation results as the cancer progresses.

The mathematical models explain that the fusion of somatic cells results in somatic evolution, resulting in the multiplication of tumor cells(Miroshnychenko et al., 2021).studies predict that gene diversification is a mechanism that influences the process of genetic evolution. the continuously directed gene evolution phenomenon provides more workable solutions than the traditional evolution methodologies. The continuous evolution method explains a large evolutionary trajectory related to the genetic process (Morrison et al., 2020).Scholars highlight that cancer is an evolutionary process as the human population evolves. The evolution of cancer with time has resulted in serious cancer-associated alternations. these alternations are so complicated that they are not treated through novel drugs or therapies. the most modern and evolved types of cancer cells are resistant to all types, so cancer therapies.

The cancer cells are studied at the single-cell level to develop effective and workable strategies to cope with the resistance offered by most cancer types. several technological approaches are used to determine the multi-domain nature of cancer cells (Nam et al., 2021).

Scholars reveal that the population dynamics approach solves genetic problems associated with a large population. algebraic and probabilistic methodologies explain the genetic complexity associated with cancer evolution (Rozikov, 2020).studies elaborate that mutations caused in any body cell impact the health of humans. some mutations in body cells result in the onset of genetic disorders.to understand the mutations that occur at the cell level, next-generation technology-based techniques are used in research areas.

Moreover, sequencing tools are used to explain the single-cell mutations and assess the patients' DNA-related defects (Salk & Kennedy, 2020).scholars suggest that SARS-COV-2 results in mutations that increase the chances of neural alternations. The model made to understand the SARS-COV-2 prognosis predicts that the mutations caused by this mutant cause vaccine resistance (Van Egeren et al., 2021).studies claim that the architecture of tissues is a key factor that determines the origin of cancer cells from normal cells (West et al., 2021). Studies suggest that in an evolving population, the process of spreading mutations is explained by DFE. Using the (dn/ds) system helps explain the mutations associated with somatic cells. also, the human tissue-related mutations are predicted using the (dn/ds) method (Williams et al., 2020).the somatic evolution process is involved in the progression of tumour cells.To understand the pathophysiology behind cancer types, researchers use a gene-centric model. Also, the evolution of tumour cells is an evolutionary dynamic process that keeps evolving with time (Zahir et al., 2020).

The term "Biomathematics" can be explained as "the study of living organisms related to processes of living organisms by using mathematical rules such as summation, integration, multiplication and others". Recently, scientists have made continuous and effective efforts to study genetic mutation in populations using a mathematical approach. It made understanding quite easy because of the involvement of mathematics so that data can be easily organized in the form of digits. There are the following main applications for using the Bio bio-mathematical Approach to study the rate of genetic mutation in any evolving population(Slatkin, 1985).

### 3.1 Study Goals:

The main goals of this research are to:

(1) use a biomathematical framework to quantify genetic mutation rates in evolving populations;

(2) investigate the relationship between mutation rates, natural selection, and population dynamics;

(3) evaluate the implications of these findings on our more comprehensive understanding of evolutionary processes. Through the pursuit of these goals, the research aims to make a significant contribution to the current corpus of evolutionary biology knowledge.

## 4. Methodology:

The research describes that biomathematical models related to the genetic mutations. For measuring the research study used questions related to dependent and independent indicators. the SPSS software used for determine the research its included regression model, the chi square analysis, the variance analysis also that explain the control chart related to them.

### 4.1 Effect of environmental factors on genetic mutation:

Using the Bio bio-mathematical Approach, it has become easy to understand the accurate effect of environmental factors that can cause genetic mutations. We know that mutation means any abnormal change in genetic material, which can be dangerous for a living body. A combination of genetic and environmental factors causes the mutation. The genetic factors may be inherited from parents or grandparents, such as DNA related to haemophilia or diabetes(Beaumont & Nichols, 1996). Medical studies explain that environmental factors can cause mutations in the body, such as exposure to ionizing radiations such as alpha and beta rays.

Now, the question arises of how the biometric approach helps to study these environmental factors' effect on genetic mutation. There is a safe dose of these radiations in the body, which does not cause mutation in genetic material. Still, when exposure to such radiation rises above this safe limit, it can cause genetic mutation in the body, which can harm the overall population. After studying it, it was concluded that people more exposed to ionizing radiation are more prone to getting genetic mutations in a short time(Beaumont & Nichols, 1996).

## 4.2 Human diversity and evolution of species

The term diversity can be explained as "the variety of characters among species and within species ". When we talk about human diversity, we mean to say that we are going to study variations in the population of human beings. Scientific studies prove that its genetic material causes variations in any living organism. When we study genetic material, we can get an idea about human diversity in any specific population or region(Bellomo & Carbonaro, 2011).

As the evolving population is undergoing genetic mutation, which can bring more diversity to the human population, the study of genetic mutation by using a mathematical approach is necessary these days. We all are well familiar with the term evolution.

This term is related to changes in living organisms over a long period. The basis of evolution is the genetic mutation in any population that leads to a new character in the next population. The study of genetic mutation in Evolving Populations using a mathematical approach can be proved effective for getting an idea of human diversity and species evolution even before that evolution(Birky Jr et al., 1983).

## 4.3 Adaptation of species

Adaptation means acclimatizing any species to its surrounding environment because of suitable characteristics in that particular species. When we study evolution, we know that most of the species of past eras have become extinct because of poor adaptation to the environment. The ability to adapt to any species is related to the genetic makeup of the species. When the genetic makeup is suitable in that particular environment, the chance of adaptation of species increases at that place. For example, in Africa, those people have such genetic makeup that they can bear hotter temperatures than Europeans(Drake & Holland, 1999).

In the same way, Europeans can endure colder temperatures than African people. This is because of their genetic makeup difference, which made them adapt to a particular place. All of this discussion gives us the idea that the biometric approach, when used in studying genetic mutation in evolving populations, can also help us understand the adaptation abilities of that species in that specific environment. This application of the Bio mathematical Approach can help us shortly in artificial breeding and making those species adapt to their environment(Roff, 1993).

## 4.4 To study disease susceptibility:

The term susceptibility can be enumerated as the risk of getting any disease at that particular time. For example, the disease susceptibility of older people is higher than that of young people. Disease susceptibility is related to the body's immune system, and the body's immune system is indirectly related to the body's genetic makeup. If there is any genetic mutation in any particular population, there would also be a change in the immune system. If this change is in negative terms, it will increase the chance of disease susceptibility(Orr, 2009).

When we study genetic mutations with the help of biomathematical approaches, we can understand the chance of disease susceptibility in any particular population. This idea of disease susceptibility before time will enable physicians to plan the type and time of treatment before the onset of disease in that population(Lange, 2002).

## 4.5 To study treatment outcomes:

Treating any mild or chronic disease is related to the body's positive response to that type of treatment. For example, if there is any disease because of bacteria, there will be a response in the body when antibiotics are taken. Sometimes, we see that treatment does not affect the patient. This is because of any genetic mutation in the Patient or genetic resistance character in that pathogen (Smith, 1978).

When we study genetic mutation in that person using the biomathematical approach, we can understand why treatment is not working. And we get an idea about any resistance to pathogens. In that case, we will have to develop different kinds of medicines that will be able to cope with the increasing risk of resistance to pathogens. Thus, the possible outcomes of treatment can be easily assessed and analyzed using the biomathematical approach to study genetic mutation in evolving populations (Bürger & Lynch, 1995).

**Table 1:** Result of Correlations

| Correlations | | | | | | | |
|---|---|---|---|---|---|---|---|
| | | Genetic Mutation Rates 1 | Genetic Mutation Rates 2 | Genetic Mutation Rates 3 | Evolving Population s 1 | Evolving Population s 2 | Evolving Population s 3 |
| Genetic Mutation Rates 1 | Pearson Correlation | 1 | -.076 | -.108 | .016 | -.206 | .178 |
| | Sig. (2-tailed) | | .581 | .435 | .908 | .131 | .194 |
| | N | 55 | 55 | 55 | 55 | 55 | 55 |
| Genetic Mutation Rates 2 | Pearson Correlation | -.076 | 1 | -.090 | -.236 | -.087 | .172 |
| | Sig. (2-tailed) | .581 | | .515 | .083 | .527 | .208 |
| | N | 55 | 55 | 55 | 55 | 55 | 55 |
| Genetic Mutation Rates 3 | Pearson Correlation | -.108 | -.090 | 1 | .080 | -.115 | -.219 |
| | Sig. (2-tailed) | .435 | .515 | | .563 | .402 | .109 |
| | N | 55 | 55 | 55 | 55 | 55 | 55 |
| Evolving Populations 1 | Pearson Correlation | .016 | -.236 | .080 | 1 | -.089 | .122 |
| | Sig. (2-tailed) | .908 | .083 | .563 | | .520 | .374 |
| | N | 55 | 55 | 55 | 55 | 55 | 55 |
| Evolving Populations 2 | Pearson Correlation | -.206 | -.087 | -.115 | -.089 | 1 | .012 |
| | Sig. (2-tailed) | .131 | .527 | .402 | .520 | | .933 |
| | N | 55 | 55 | 55 | 55 | 55 | 55 |
| Evolving Populations 3 | Pearson Correlation | .178 | .172 | -.219 | .122 | .012 | 1 |
| | Sig. (2-tailed) | .194 | .208 | .109 | .374 | .933 | |
| | N | 55 | 55 | 55 | 55 | 55 | 55 |

The above result of table 1 represents that the correlation between dependent and independent variables result describes the Pearson correlation, significant values, and the number of observations related to the variables. The overall result presents some positive and some negative links between them. The evolving population is the main dependent variable. The result shows that its Pearson correlation value is 13%, 52%, and 40%, describing a 55% significant level between them. The result also describes that genetic mutation rates represent -0.108 and 10% negative but significant values between them.

## 5. Justification for the Study:

Using a biomathematical approach, this work provides a more thorough and quantitative examination, given the essential role that genetic mutation rates play in evolutionary processes. The researchers want to close the gap between theoretical predictions and practical findings by combining mathematical models with data from observation.

Incorporating biomathematics facilitates a more intricate investigation of the variables impacting genetic mutation rates, providing a more profound comprehension of how these rates contribute to the variability and adaptability of dynamic populations.

## 6. Chi-square analysis:

**Table 2:** Result of Test Statistics

| Test Statistics | | | | | | |
|---|---|---|---|---|---|---|
| | Genetic Mutation Rates 1 | Genetic Mutation Rates 2 | Genetic Mutation Rates 3 | Evolving Populations 1 | Evolving Populations 2 | Evolving Populations 3 |
| Chi-Square | 21.964[a] | 31.564[a] | 16.836[a] | 19.673[a] | 29.709[a] | 22.073[a] |
| df | 2 | 2 | 2 | 2 | 2 | 2 |
| Asymp. Sig. | .000 | .000 | .000 | .000 | .000 | .000 |
| a. 0 cells (0.0%) have expected frequencies less than 5. The minimum expected cell frequency is 18.3. | | | | | | |

The above result of table 2 describes that the chi-square values represent the chi-square values of genetic mutation rates 1,2, and 3, which are 21.964, 31.564 and 16.836, showing us positive chi-square values between them. The evolving populations 1, 2, and 3 show 19.673, 29.709, and 22.073 positive chi-square values, respectively. The result represents that the overall significant value is 0.000, showing a 100% significant level between them.

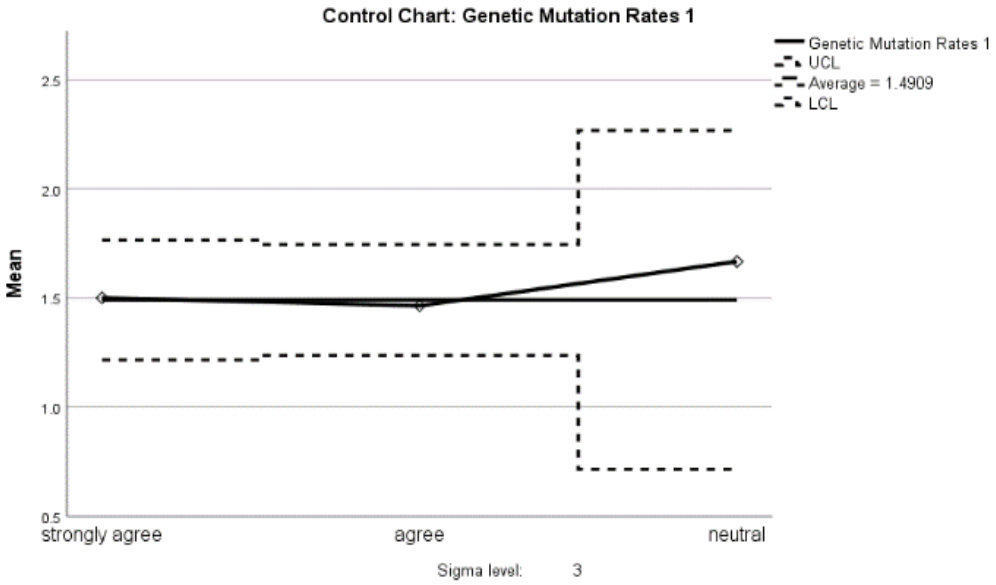


**Figure 1:** Control chart

The above graph of figure 1 shows that the control chart result shows that the average value is 1.4909 related to the indicator. The vertical side represents mean values starting from 0.5 and ending at 2.5. The horizontal side describes the strong agree, agree and neutral levels between them. The above lines present a control chart between them.

## 7. Regression model:

**Table 3:** Result of Coefficients

| Coefficients | | | | | | |
|---|---|---|---|---|---|---|
| Model | | Unstandardized Coefficients | | Standardized Coefficients | t | Sig. |
| | | B | Std. Error | Beta | | |
| 1 | (Constant) | 1.879 | .401 | | 4.686 | .000 |
| | Genetic Mutation Rates 1 | .005 | .134 | .005 | .035 | .972 |
| | Genetic Mutation Rates 2 | -.259 | .154 | -.230 | -1.683 | .098 |
| | Genetic Mutation Rates 3 | .056 | .130 | .060 | .434 | .666 |

a. Dependent Variable: Evolving Populations 1

The above result of table 3 describes that regression analysis results describe beta values, standard error values, the t-statistic value and the significant value of each independent variable. The genetic mutation rate 1 shows that the beta value is 0.005, the standard error rate is 0.134, the t-statistic value is 0.035, and the significant value is 0.972, showing that positive and 97% significant levels between them. Similarly, genetic mutation 2 shows that the t statistic value is -1.683, and the significant rate is 0.098, which offers a 9% significant level between them. The genetic mutation rate 3 shows 43% positive and 66% significant rates between them.

**Table 4:** Result of ANOVA

| ANOVA | | | | | | |
|---|---|---|---|---|---|---|
| Model | | Sum of Squares | df | Mean Square | F | Sig. |
| 1 | Regression | 1.124 | 3 | .375 | 1.070 | .370[b] |
| | Residual | 17.857 | 51 | .350 | | |
| | Total | 18.982 | 54 | | | |

a. Dependent Variable: Evolving Populations 1

b. Predictors: (Constant), Genetic Mutation Rates 3, Genetic Mutation Rates 2, Genetic Mutation Rates 1

The above result of table 4 describes the sum of square values, mean square values, F statistic and significant value of each model, including regression and residual total values. The sum of squares presents 1.124, 17.857 and 18.982 positive sums of square rates. The mean square values describe that 0.375 and 0.350 show 37% and 35% average square rates between the regression and residual values, respectively. The overall significant value is 0.370, which shows a 37%

significant level. The F statistic rate is 1.070, which shows positive rates between them.

## 8. Conclusion:

To sum up, the research on genetic mutation rates in evolving populations using a biomathematical method offers a number of important discoveries and advances in the subject. A thorough investigation was made possible by the application of which produced. Our knowledge of genetic dynamics within populations is deepened using mathematical modelling to analyses evolutionary processes. It is important to recognize certain limitations inherent in the research. There may be a degree of uncertainty in the outcomes due to the dependence on specific assumptions. Furthermore, they were overlooked in the study's scope, which might impact how broadly the findings can be applied to other groups or situations. This research has ramifications that go beyond its immediate conclusions. Understanding genetic mutation rates in changing populations is essential for related applications or areas, and our work significantly contributes to the current conversation.

The research based on primary data analysis for determine the research study used SPSS software and generate results included correlations, the chi squares analysis, the regression models, also that control chart present overall research. However, the limitations that have been found should be addressed in future research endeavours, and possible methodological improvements might further strengthen our understanding of this field. It is clear from the present research that genetic mutation rates are crucial in determining the course of evolution. The knowledge gathered from this research serves as a guide for future studies and encourages more research. Expanding on the groundwork our study established, we may work towards a more thorough comprehension of the complex interactions between genetic mutations and population dynamics.

The research concluded that direct and significant impact between dependent and independent indicators. In conclusion, examining the results with a critical lens is essential, even if this biomathematical technique provides insightful information on genetic mutation rates in changing populations. The field of evolutionary biology will surely continue to change if the restrictions are addressed and research in this area is encouraged. After discussing the main applications of biometric approaches for studying genetic mutation in evolving populations, we concluded that it is a positive step toward analyzing and treating genetic mutations that will help in the near future.

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