



EVOLUTION ALGEBRAS AND ITS SUBSTANTIAL SIGNIFICANCE IN THE DOMAIN OF GENETICS AND BIO-INFORMATICS

Manan Roy Choudhury, Government College of Engineering and Textile Technology, India
(mananroychoudhury@gmail.com)

Anurag Dutta, Government College of Engineering and Textile Technology, India (anuragdutta@gmail.com)

Ishan Banerjee, Chennai Mathematical Institute, India (ishanbanerjee.314@gmail.com)

Krishan Kundu, Government College Engineering and Textile Technology, India. (kk.cse81@gmail.com)

ABSTRACT

Evolution algebra has emerged as the leading branch of study with many scopes of development and further research. These notions lead to hierarchical structures for evolution algebras. A hierarchical structure of evolution algebra is stated by an inherited sequence of semidirect-sum decompositions and fractals which dynamically fabricate a well-ordered hierarchical structure that displays directions and indicates the induced algebraical transiency that engenders the rise of evolution algebra. This article will dive deep into numerous applications and solicitations of evolution algebra, which plays a significant role in the algebraic formulation of Non-Mendelian Genetics and its indispensable role in plant pathology. In this paper, we intend to draw the reader's attention to some of the basic principles behind evolution algebra and how they are related to Non-Mendelian Genetics and its application in plant pathology. Following that, we dive into a comparative study of *P.infestans* populations.

Keywords: Allele, Mendelian and Non-Mendelian Genetics, Plant Pathology, Commutative, Progeny, Chromosome, Genotype.

1. INTRODUCTION

Evolution algebra (Alsarayreh et al., 2017) is a type of algebra that is motivated by such evolution laws of genetics. Allele, is any one of two or more genes that occur at a particular site (locus) of the chromosome, affecting the expression of a particular trait. For example, the alleles I^A , I^B and I^O control our blood type. Apart from this, genotype (A. Adrian Albert, 1943) refers to the complete genetic makeup of an organism, in other words, its complete set of genes.

Evolution Algebra, a groundbreaking mathematical concept, represents a significant advancement in the field of algebraic structures. Developed through extensive research and analysis, this algebraic framework provides a comprehensive understanding of dynamic systems and their evolution over time. What sets Evolution Algebra apart is its ability to capture the intricate interplay between mathematical operations and temporal transformations, offering a powerful tool for modeling and analyzing complex phenomena in various domains, including physics, biology, and computer science.

At its core, Evolution Algebra is designed to study and describe dynamic processes. It takes inspiration from traditional algebraic structures, such as groups, rings, and fields, but introduces novel elements to account for the temporal aspect. In traditional algebra, operations and transformations are static, with little consideration for time-dependent changes. In contrast, Evolution Algebra incorporates the notion of time and provides a framework to analyze how systems evolve and transform over time.

One of the key features of Evolution Algebra is its treatment of evolution operators. These operators represent the transformations or changes that occur in a system over successive time steps. They capture the dynamic behavior of the system and allow for the study of temporal patterns, growth rates, and other aspects of system evolution. By incorporating these operators into algebraic structures, Evolution Algebra enables a deeper understanding of dynamic phenomena, facilitating the development of predictive models and the analysis of complex systems.

Furthermore, Evolution Algebra provides a versatile language to describe and analyze various dynamic systems. Whether it is the behavior of physical systems, the evolution of biological populations, or the dynamics of computational algorithms, Evolution Algebra offers a unified framework to model and study these processes. It allows researchers to represent and manipulate the complex relationships and interactions within dynamic systems, unlocking insights into their behavior and enabling predictions about future states.

The development and exploration of Evolution Algebra have already led to numerous applications and advancements across multiple fields. In physics, it has been used to model the behavior of quantum systems, studying the evolution of particles, wave functions, and probabilities over time. In biology, Evolution Algebra has provided a mathematical foundation for analyzing the growth and adaptation of populations, contributing to our understanding of evolutionary dynamics. In computer science, it has found applications in the analysis of algorithms and the study of computational processes, allowing for a deeper understanding of their time-dependent behavior.

Importantly, in the pursuit of knowledge, it is essential to emphasize that the discussion of Evolution Algebra is rooted in original research and ideas. It is critical to acknowledge and respect the intellectual contributions of researchers who have paved the way in this field. By properly attributing and acknowledging previous work, researchers can build upon existing knowledge, fostering genuine innovation and advancing scientific understanding.

In conclusion, Evolution Algebra stands as a transformative mathematical concept, offering a comprehensive framework to study and understand dynamic systems. Its incorporation of time-dependent transformations and evolution operators provides a powerful tool for modeling, analyzing, and predicting the behavior of complex phenomena. As researchers continue to explore its applications and delve deeper into its theoretical foundations, Evolution Algebra promises to unlock new insights and drive innovation across a range of scientific disciplines.

On the other hand, we say that an algebra \mathbf{A} is generated by a set $\mathbf{B} \subseteq \mathbf{A}$, if we can use the elements of \mathbf{B} and all available operations available on those elements, to get elements of \mathbf{A} . In evolution algebra (Bateson, 2009) we will be using the alleles as the generators and define the product of two simultaneous alleles G_i and G_j s the following

$$G_i \cdot G_j = \begin{cases} 0 & ; i \neq j \\ \sum_k a_{ik} G_k & ; i = j \end{cases}$$

Here $G_i \cdot G_i$ is considered as “self-reproduction” (Abrams et al., 2016) and is represented as $\sum_j a_{ij} G_j$ over all the generators. Later in the article, we will come back to the a_{ij} . We note here that this algebra is non-associative but commutative (Groups Geom., 2002)

NOTE: The multiplication here represents the reproduction
 Numerous mathematicians have tried to understand the algebra behind Mendelian Genetics (Paniello, 2021). Evolution algebra helps us to deal with the non-Mendelian genetics.

2. GENESIS OF EVOLUTION ALGEBRA

2.1 Asexual propagation

Prokaryotes usually are non-sexual reproductive unicellular organisms. In other words, they require a single parent to produce off-springs. Unlike the eukaryotes, their genetic based materials are majorly concentrated and packed up in the region called as nucleoid. They undergo binary fission for reproduction and don't have anything to do with mitosis or meiosis (Qaralleh & Mukhamedov, 2019).

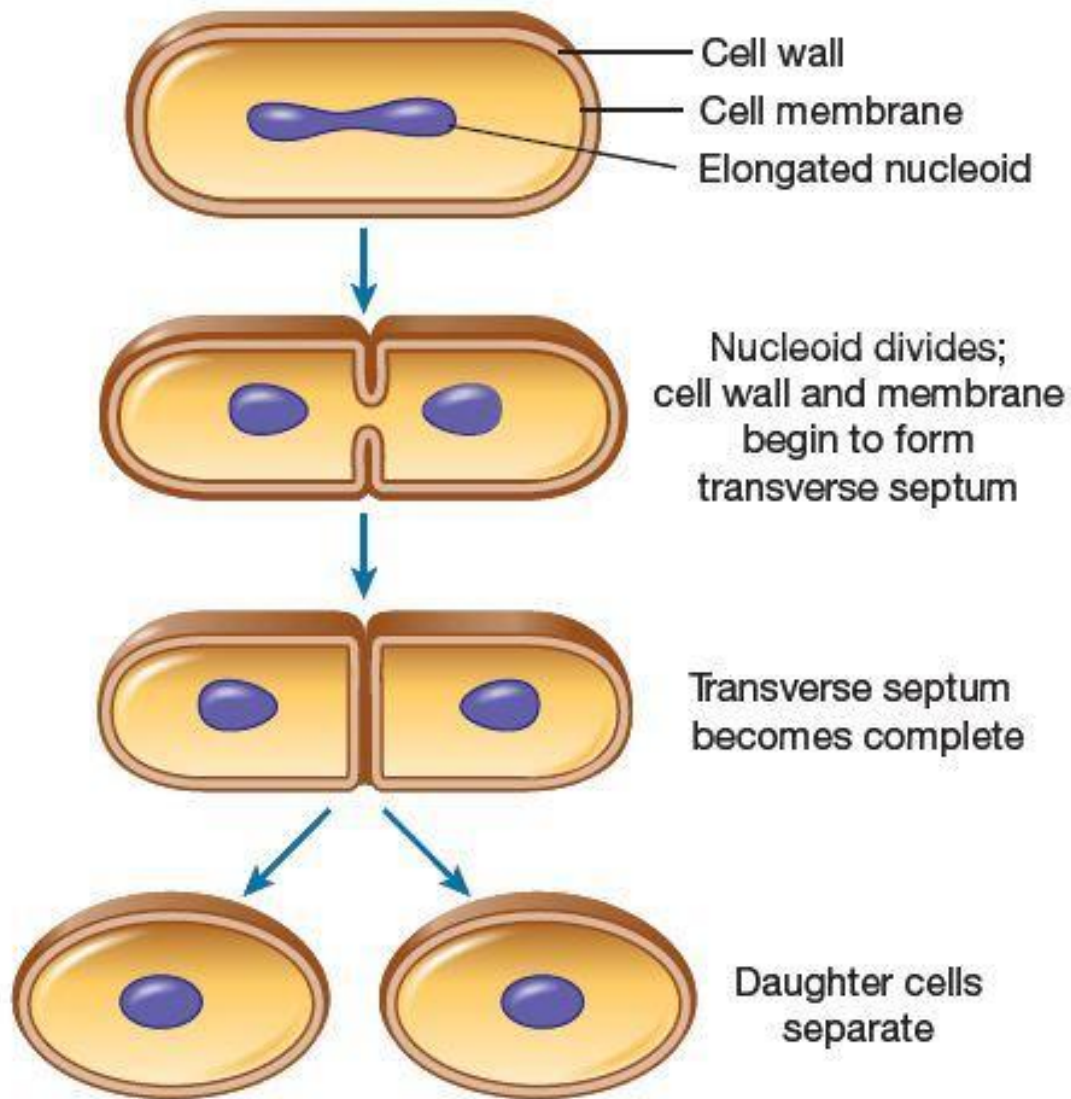


Figure 1: (Tian, 2008) Detailed diagrammatic representation of cell division and flow of genetic materials.

The genetic information transferred from the parent to the daughter cells must be conserved. However, there can be several external factors that can induce changes in the genetic material. In that case, the inheritance is no more Mendelian (Bayara et al., 2011).

Now let us represent reproduction mathematically. Assume that there are n genetically distinct prokaryotes $\{p_1, p_2, \dots, p_n\}$. We will also assume that the same environmental factors and terms are well maintained throughout. We now look at the new frequencies over the two generations (either from a population or individual's perspective) and make the following relations. $\{p_i \cdot p_i = \sum_{k=1}^n \alpha_{ik} p_k \cdot p_j = 0 ; i \neq j$

2.2 COMMENCING PROPERTIES OF EVOLUTION ALGEBRA

Considering the universal generator set as $\{e_1, e_2, \dots, e_n\}$

Non-associative: A binary operation $*$ on a set S is associative if it satisfies

$$(x * y) * z = x * (y * z) \text{ for } x, y, z \in S$$

Proof:

For some index i , we have $e_i \cdot e_i = \sum_j a_{ij}e_j$, there is $j \neq i$ such that $a_{ij} \neq 0$. Therefore, we have the following $(e_i \cdot e_i) \cdot e_j \neq 0$. But we see that, $e_i \cdot (e_i \cdot e_j) = e_i \cdot 0 = 0$ (As $e_i \cdot e_j = 0$). Therefore $(e_i \cdot e_i) \cdot e_j \neq e_i \cdot (e_i \cdot e_j)$. Hence Evolution algebra is non-associative.

Commutative: A binary operation on a set S is associative if it satisfies

$$x * y = y * x \text{ for } x, y \in S$$

Proof:

Consider any two elements of the algebra $x = \sum_j a_j e_j$ and $y = \sum_j b_j e_j$.

Now we will have

$$x \cdot y = \left(\sum_j a_j e_j \right) \cdot \left(\sum_j b_j e_j \right) = \left(\sum_{i,j} a_i e_i b_j e_j \right) = \left(\sum_i a_i b_i \right) e_i^2 = \left(\sum_{i,j} b_j e_j a_i e_i \right) = y \cdot x$$

Therefore, Evolution algebra is commutative (Tian, 2008).

“The direct sum of evolution algebras is also an evolution algebra.” (Tian, 2008).

Let us consider A_1 and A_2 be two evolution algebras having the generator sets $\{\xi_i \mid i \in A_1\}$ and $\{\varsigma_i \mid i \in A_2\}$ respectively. Thus, $A_1 \oplus A_2$ is having a generator set $\{\xi_i, \varsigma_j \mid i \in A_1, j \in A_2\}$. Now, we need to prove this property.

$$\begin{aligned} \xi_i \cdot \xi_i &= \sum_k a_{ik} \xi_k \\ \xi_i \cdot \xi_j &= 0, \quad i \neq j \\ \varsigma_i \cdot \varsigma_i &= \sum_k b_{ik} \varsigma_k \\ \varsigma_i \cdot \varsigma_j &= 0, \quad i \neq j \\ \xi_i \cdot \varsigma_j &= (\xi_i, 0) \cdot (0, \varsigma_j) = 0 \end{aligned}$$

Therefore, we get that $A_1 \oplus A_2$ is an evolution algebra too. So, our above statement was correct and is proved accordingly.

3. INTRODUCTORY NOTIONS ABOUT NON-MENDELIAN GENETICS

Mendel's rules are largely satisfied by the inheritance of nuclear genes, however they are not followed by organelles (such as the cell's organs). Learn about non-Mendelian genetics first before moving on to the algebraic formulation (Dmitri Piontkovski & Fouad Zitan, 2023). Erwin Baur demonstrated that *Pelargonium* chloroplast genes break four of Mendel's five laws in 1909.

During asexual reproduction, nuclear gene alleles remain unchanged and do not separate into different combinations. Offspring arising from heterozygous parent cells also maintain heterozygosity. On the other hand, in heteroplasmic cells, homoplasmic cells are produced when organelle gene alleles segregate twice, occurring between mitosis and meiosis. This process results in random segregation of alleles, and some copies of the organelle genome might replicate more frequently than others due to chance, selective pressures, or inherent advantages. Unlike "Mendel's first Law" of independent assortment for nuclear genes, organelle alleles may or may not segregate during meiosis.

Nuclear gene inheritance is characterized by biparental transmission, meaning these genes are inherited from both parents. However, in contrast, organelle genes, such as those found in mitochondria or chloroplasts, often originate from a single parent. This phenomenon deviates from Mendel's second law, as organelle genes are typically located on a single chromosome, leading to uniparental inheritance and preventing recombination through the fusion and exchange of genomes.

The crucial aspect of Mendel's law applicable to organelle genes and gametes is the randomness of fertilization concerning genotype. This random fertilization process is the only relevant factor from Mendel's principles when considering organelle genes and their inheritance within gametes.

4. ALGEBRAIC FORMULATION OF NON-MENDELIAN GENETICS

Let us consider a population of organelles in a cell or a cell clone and we assume that there are n different genotypes which we will denote as g_1, g_2, \dots, g_n . According to point (3) of section 3, the crossing of genotypes (breeding of two individuals, resulting in offspring that carry genetic materials from each parent) is impossible as it is uniparental inheritance. We will represent the fact mathematically as

$$g_i \cdot g_j = 0 \quad (i \neq j)$$

Based on point (2) in section 3, the alleles of organelle genes may or may not separate during the process of meiosis. As a consequence, the frequency of each gene in the succeeding generation can fluctuate or vary. From point (4), intermolecular and intramolecular recombination within a lineage (A lineage can be considered as a line of descent among organisms with ancestral relations), we get to see that one organelle genotype (María Teresa Ceballos et al., 2020) is capable of giving rise to different genotypes. This can be mathematically represented as

$$g_i^2 = \sum_{j=1}^n \alpha_{ij} g_j$$

Here α_{ij} is considered as the rate of genotype g_j produced by g_i . Now here we have an algebra defined by the generators g_1, g_2, \dots, g_n . Despite, this being a general idea, it contains all the phenomena of Non-Mendelian Genetics (Inez et al., 2018).

5. SIGNIFICANCE OF EVOLUTION ALGEBRA IN PLANT PATHOLOGY

In the realm of genetics, non-Mendelian inheritance falls under the same overarching category as Mendelian genetics. Our particular focus lies on two genetic phenomena where evolution algebras have relevance. The first pertains to the population genetics of organelles, while the second deals with the population genetics of *Phytophthora infestans*. The process of transforming a heteroplasmic cell population into a homoplasmic one is referred to as inheritance and represents a perplexing trait of organelles. Within this context, cell divisions give way to cell population dynamics. Notably, the concepts of algebraic transiency and algebraic persistency embody the fundamental aspects of biological instability and transitory nature, respectively.

Evolution algebras offer a useful tool to illustrate this characteristic. They allow us to model algebraic triplasmy using a range of mutants as generators. Analyzing samples from patients with sporadic mitochondrial abnormalities appears straightforward. In the case of *Phytophthora infestans*, we observe a distinct form of uniparental inheritance.

By constructing relevant evolution algebras for the progeny populations of *Phytophthora infestans*, we can discern various genetically dynamic patterns within the complexity of the progenies. This leads to the projection that intermediate transients exist, and regular biological stable race reproduction takes place. Consequently, we can recommend timely intervention to halt the spread of the late blight disease in practical scenarios.

In theory, plant pathologists can leverage our algebraic models to gain insights into *Phytophthora infestans* reproduction and make informed decisions in real-life scenarios. The study of the patterns underlying plant disease is significantly impacted by evolution algebra (Boudi et al., 2022). The following are a few of them:

1. The assumption that intermediate transient races exist. Simply put, the biologically unstable genotypes will eventually become extinct by giving rise to new genotypes (GANIKHODJAEV et al., 2014). Diseases like late blight disease can be stopped from spreading by capturing and killing those races.
2. The predictable periodicity of stable race reproduction (those genotypes which will not go extinct). This can aid in our ability to forecast the spread of disease.
3. Evolution algebra is crucial for decomplicating the progeny population structure's complexity.

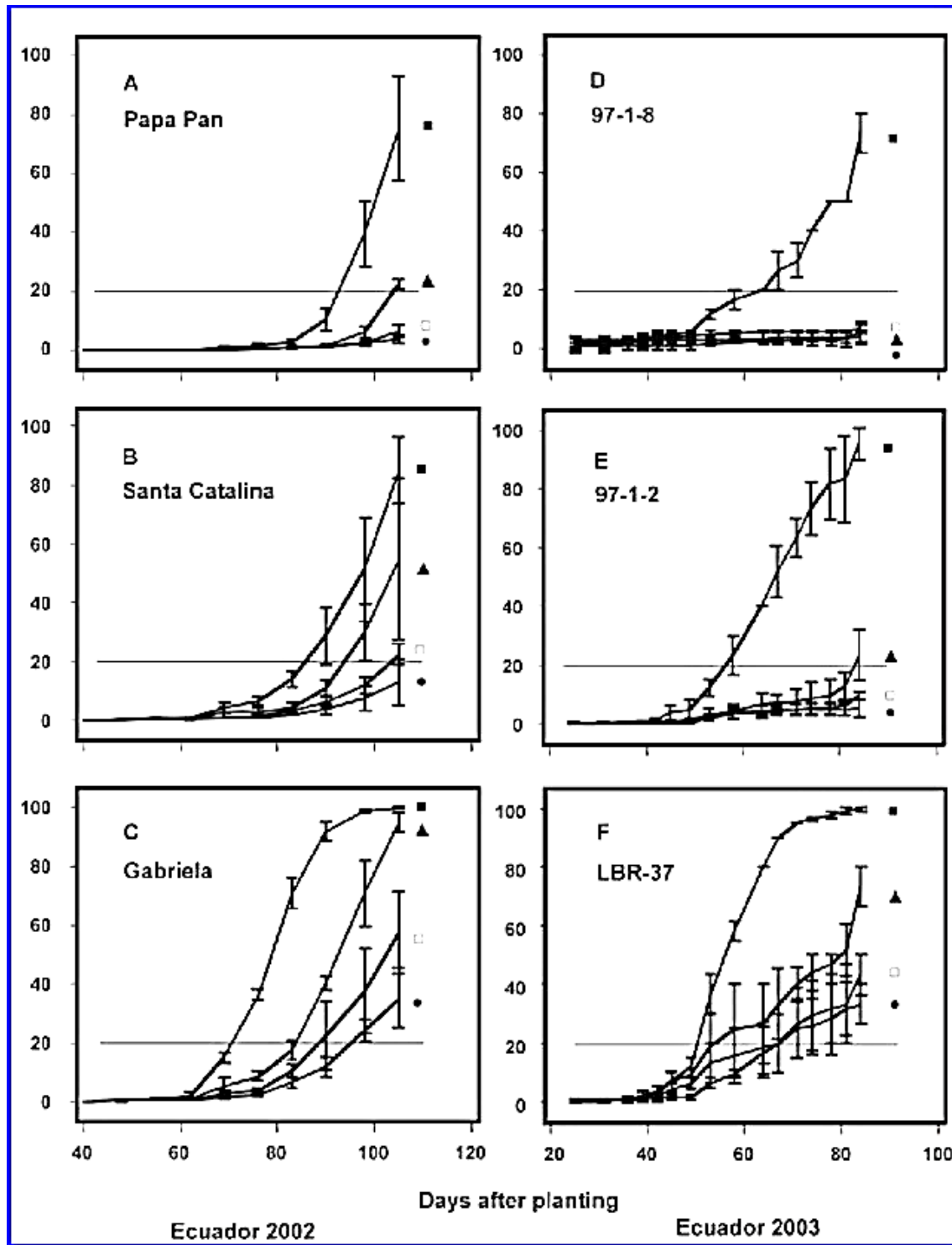


Figure 2. (Tian, 2008) Potato late blight (*Phytophthora Infestans*) disease progress curves for epidemics in selected potato genotypes in experiments in Ecuador.

6. COMPARATIVE ANALYSIS ON THE SEVEN P. INFESTANS POPULATION

In this section, we will be putting forward a comparison between the various populations of the Phytophthora Infestans, the water mould that causes the disease late blight in potatoes, on the basis of their Virulence Factor. We have excavated the dataset, that contained the virulent factors of the 7 species by studying their contingency on 20 genetically distinct samples of China (Uygun Jamilov et al., 2015) (GANIKHODZHAEV et al., 2011), from the famous scientific report submitted in Nature, and have used that to establish some relation between their virulent factors, making use of some statistical analysis moulded with Evolution Algebra.

Table 1: (Wu et al., 2016) Virulency of 11 variants of Phytophthora Infestans.

Virulence factor	Fuzhou	Gansu	Guangxi	Guizhou	Ningxia	Xiapu	Yunnan
avr1	0.15	0.6	0.05	0.55	0.5	0.25	0.6
avr2	0.05	0.4	0.15	0.6	0.5	0.35	0.3
avr3a	0.6	0.95	0.75	0.9	1	0.8	0.75
avr4	0.4	0.75	0.4	0.85	0.95	0.65	0.65
avr5	0	0.45	0.15	0.4	0.4	0.25	0.45
avr6	0.4	0.6	0.25	0.7	0.9	0.35	0.7
avr7	0.65	0.9	0.8	0.9	1	0.7	0.7
avr8	0.3	0.85	0.45	0.9	0.95	0.6	0.8
avr9	0.05	0.3	0.25	0.5	0.55	0.05	0.3
avr10	0.2	0.7	0.25	0.9	0.75	0.15	0.65
avr11	0	0.4	0.15	0.4	0.5	0.15	0.25

Virulence is an oomycete's genetic ability to overcome host resistance and cause disease. A gene-to-gene model can explain the P. infestans/plant host patosystem, which states that for each gene that determines the host's resistance, there is a specific gene that determines its pathogenicity or virulence.

The plant resistance gene is only effective if the pathogen has a corresponding a virulence gene The range of genes expressed by the isolate when inoculated in a differential series of genotypes with resistance genes is referred to as the virulence spectrum (Yolanda Cabrera Casado et al., 2019). Isolates that exhibit the same spectrum are referred to as physiological races, and they are considered very complex if they exhibit a broad spectrum of virulence (Wu et al., 2016).

The analytic plot for the variant Fuzhou will be:-

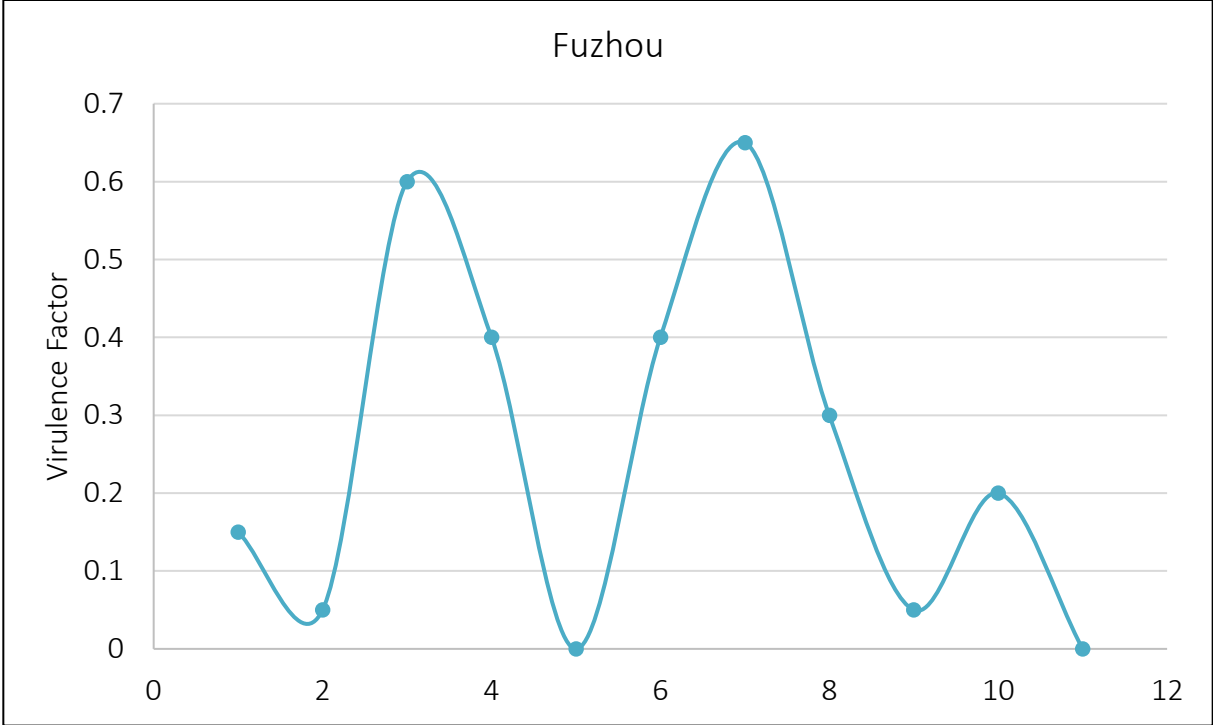


Figure 3: Virulence factor of Phytophthora Infestans in Fuzhou

The analytic plot for the variant Gansu will be:-

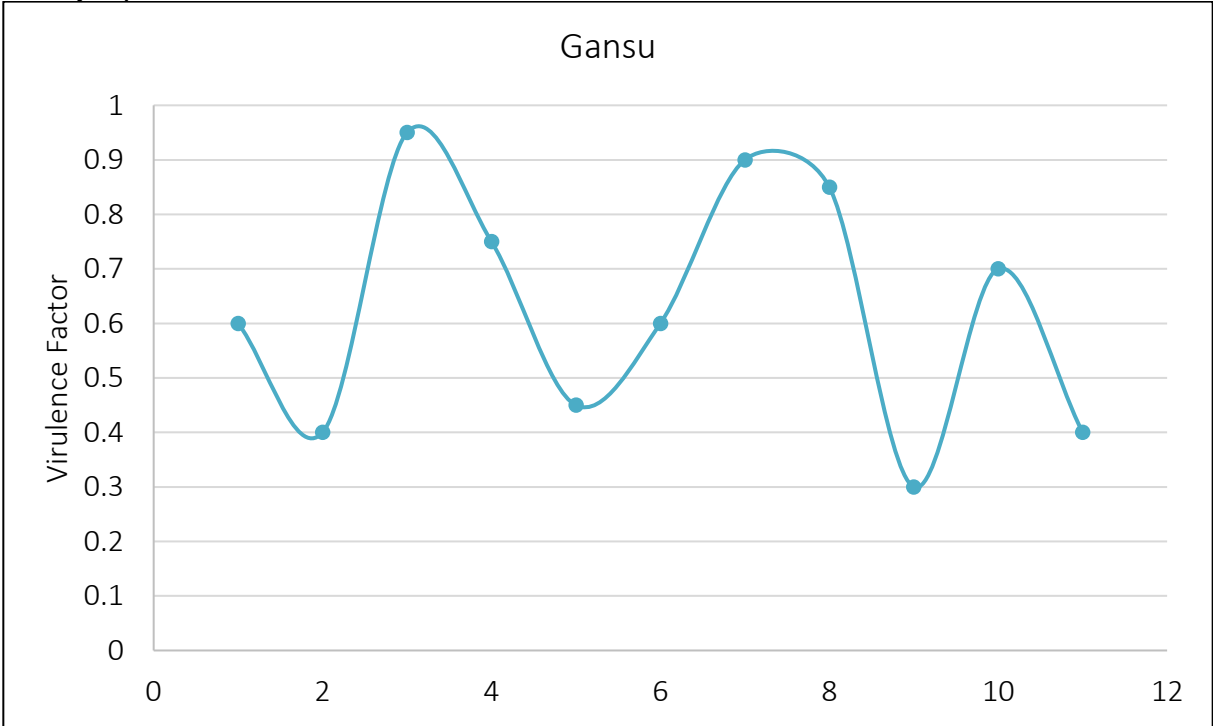


Figure 4. Virulence factor of Phytophthora Infestans of Gansu

The analytic plot for the variant Guangxi will be:-

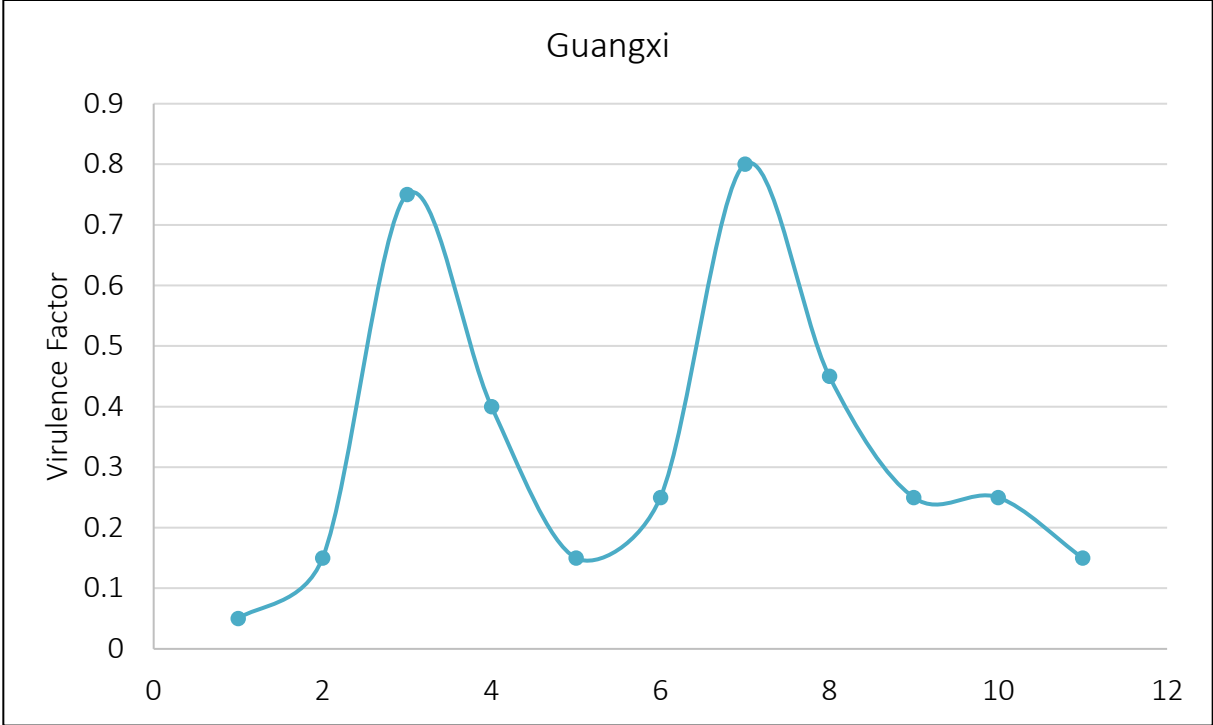


Figure 5. Virulence factor of Phytophthora Infestans of Guangxi

The analytic plot for the variant Guizhou will be:-

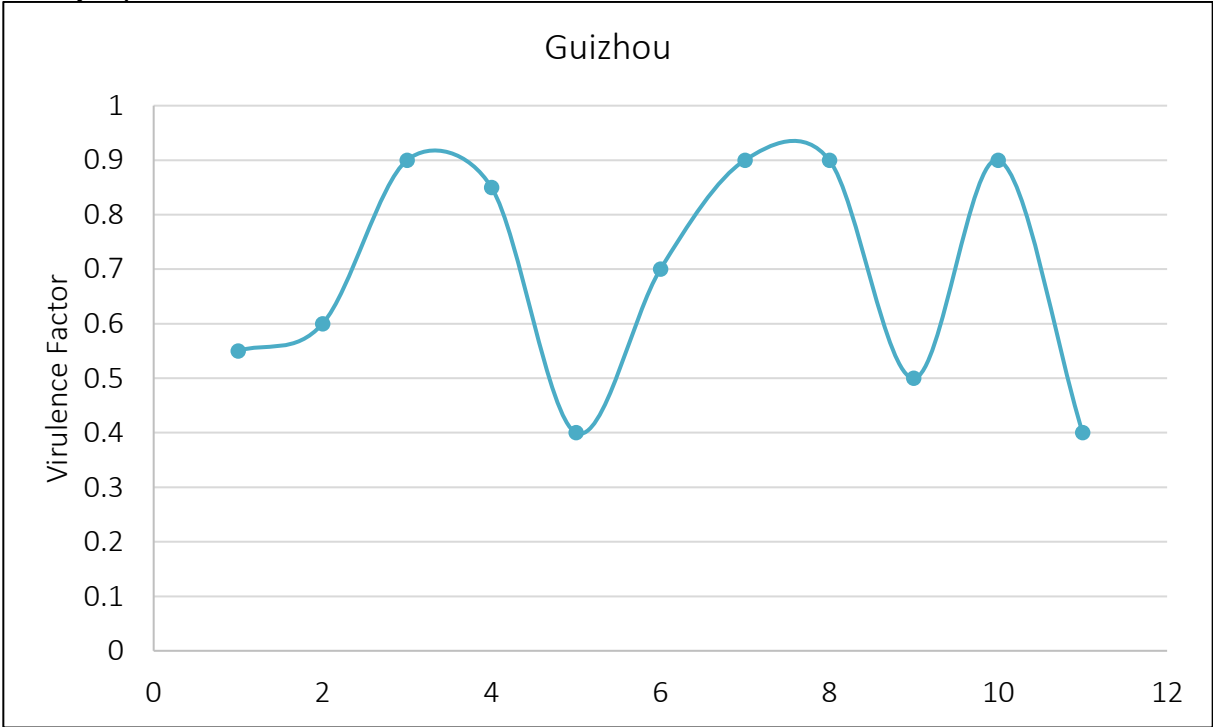


Figure 6. Virulence factor of Phytophthora Infestans of Guizhou

The analytic plot for the variant Ningxia will be:-

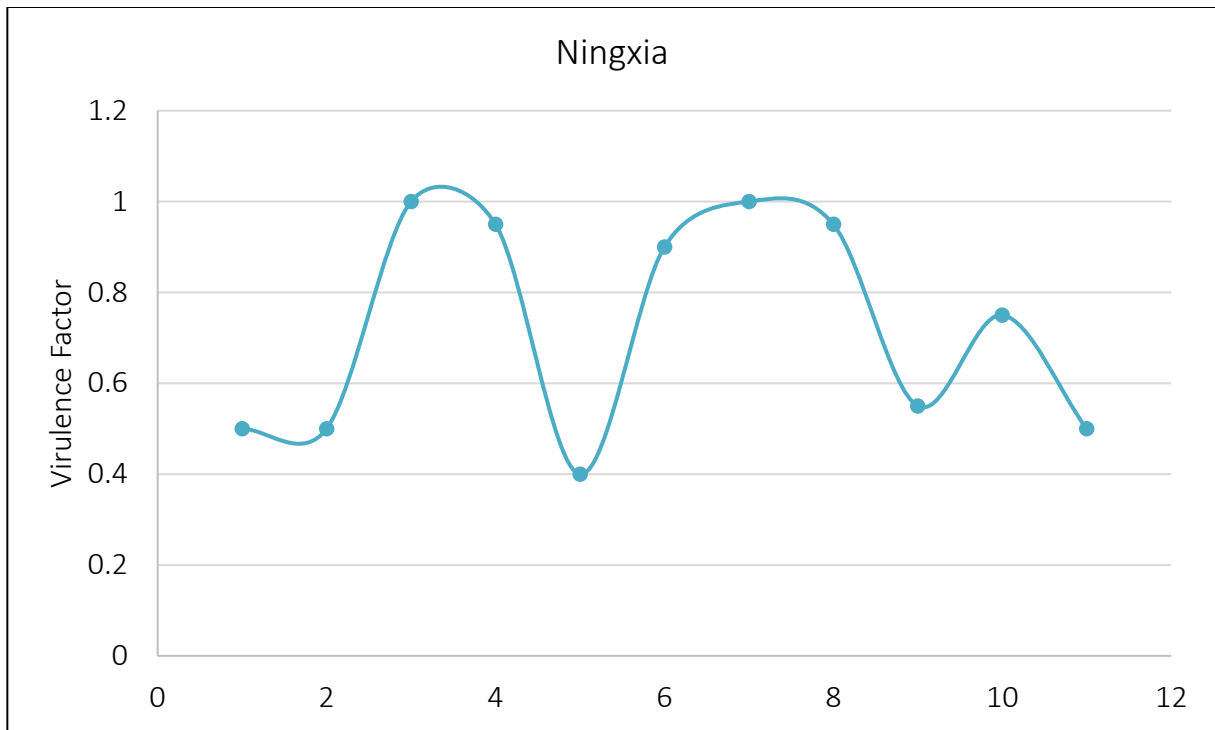


Figure 7. Virulence factor of *Phytophthora Infestans* of Ningxia

The analytic plot for the variant Xiapu will be:-

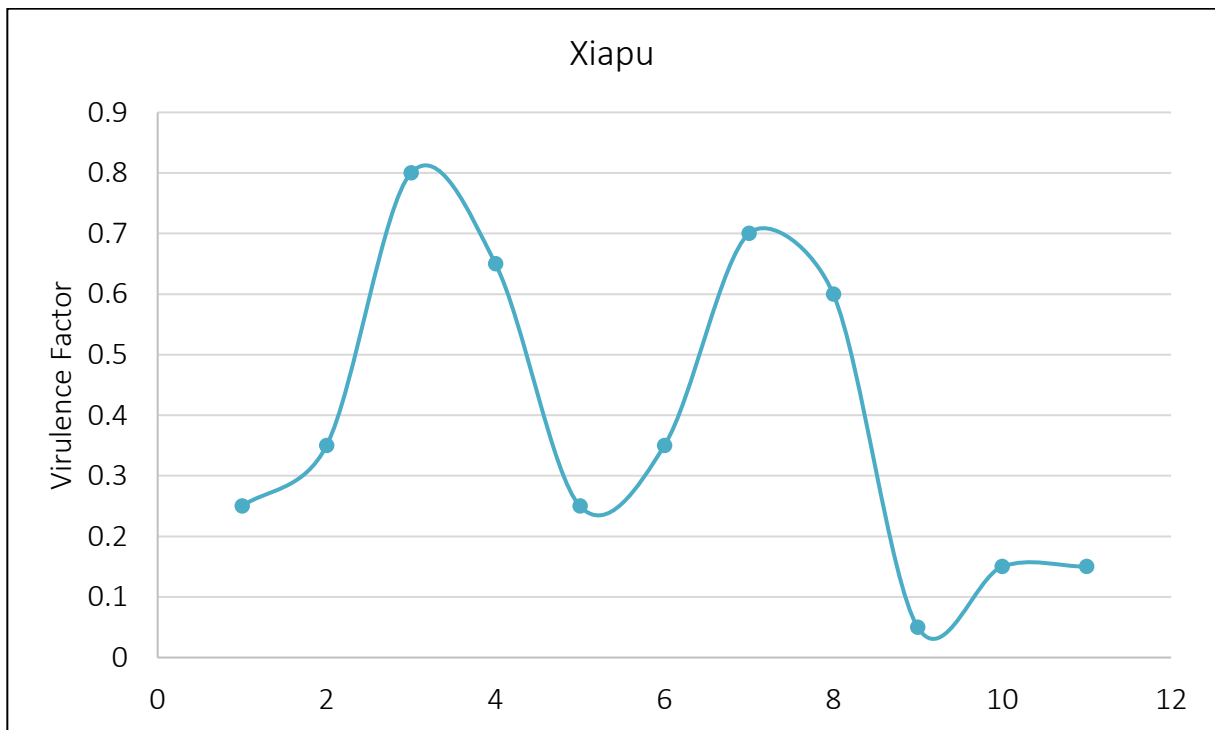


Figure 8. Virulence factor of *Phytophthora Infestans* of Xiapu

The analytic plot for the variant Yunnan will be:-

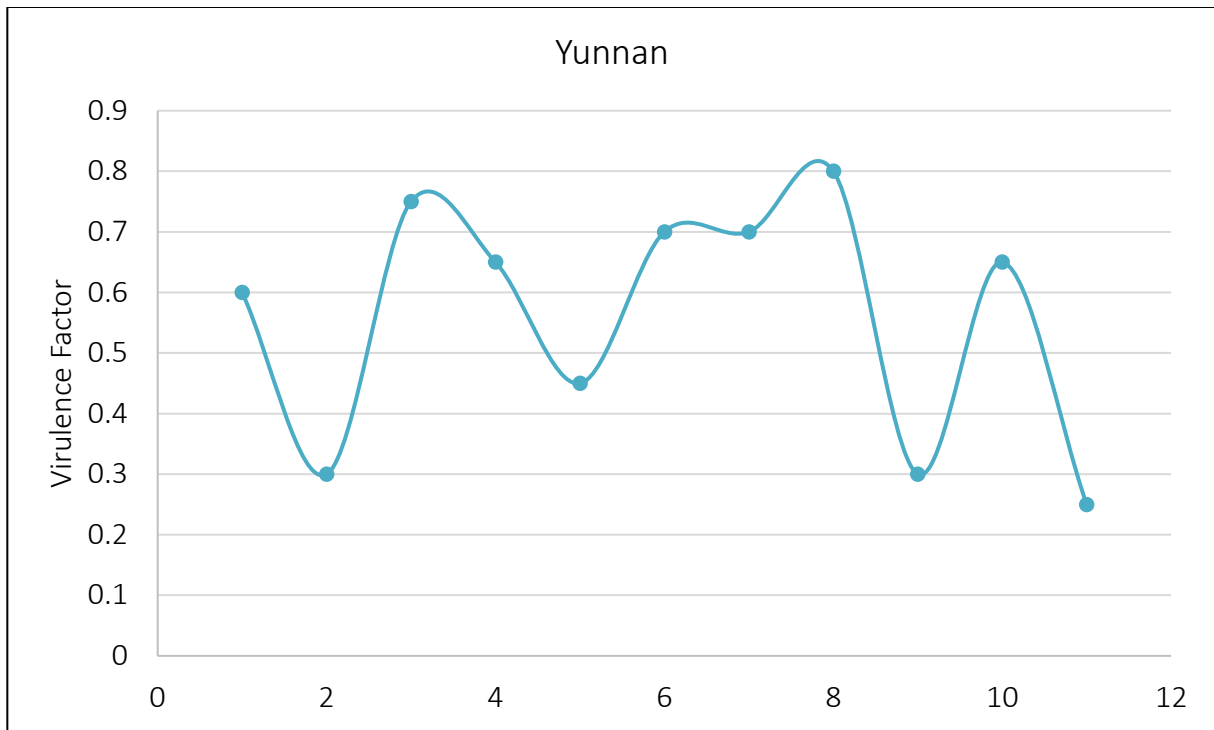


Figure 9. Virulence factor of *Phytophthora Infestans* of Yunnan

Combining all, we get the following plot

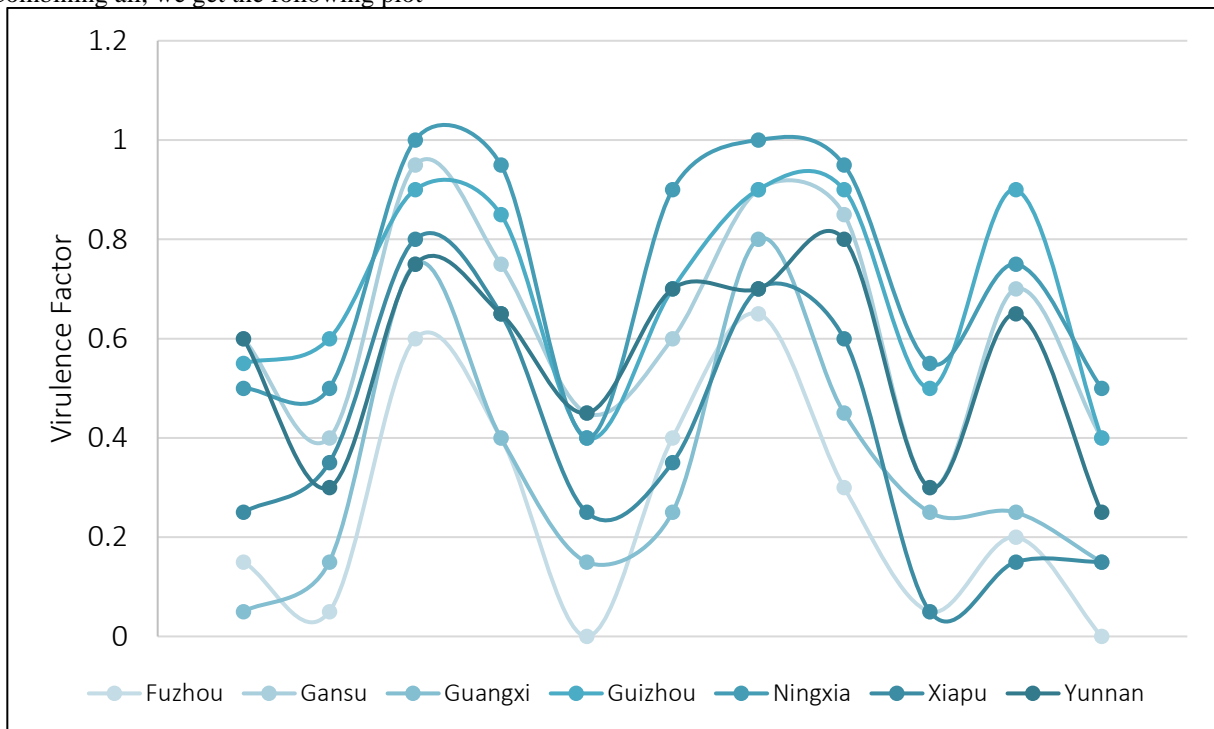


Figure 10. Virulence factor of *Phytophthora Infestans* of the 7 population

The number of different kinds (such as species) present in a dataset (a community) is measured by a diversity index, which may also take into account the evolutionary relationships (such as richness, divergence, or evenness) among the individuals dispersed throughout those kinds. Although they can also represent genera, families, functional types, or haplotypes, the kinds of interest when applying Shannon indices in ecology are typically species. The things of interest are typically specific plants or animals, and a measure of abundance could, for instance, be the population size, biomass, or coverage. Humans are potential demographic entities, and different demographic groups may be the

subject of research. Characters or specific types of alphabetic letters might be considered entities in information science. The most popular diversity indices are straightforward transformations of the effective number of kinds (sometimes referred to as "real diversity").

Each Shannon index, however, can be taken into account separately as a measure that corresponds to certain real phenomenon (but a different one for each diversity index). Many indexes just assess the categorization diversity of subjects or things. Such indices, however, do not account for the overall diversity (diversity) that may exist across subjects or entities, which can only be quantified when both category and qualitative diversity are taken into consideration. The effective number of sorts, or true diversity, is the number of types that must be equally plentiful for the average proportionate abundance of the types to match that observed in the relevant dataset (where all types may not be equally abundant). We will now compare them using the Shannon index, which is frequently used to examine the diversifications of species in a dataset or, more specifically, in a community (Rasul Ganikhodzhaev, 1993)(Rozikov & Shamsiddinov, 2009).

Mathematically, it is the weighted GM of the diversities

$$\text{Index}_{\text{Shannon}} = - \sum_{\alpha=1}^{\rho} \xi_{\alpha} (\xi_{\alpha}) = - \left(\prod_{\alpha=1}^{\rho} (\xi_{\alpha} \xi_{\alpha}) \right)$$

where,

ξ_{α} is the population of the α 'th specie in community (Bateson, 2020).

α being the iterator

Population	Shannon Index
Fuzhou	0.91
Gansu	0.98
Guangxi	0.91
Guizhou	0.97
Ningxia	0.95
Xiapu	0.95
Yunnan	0.98

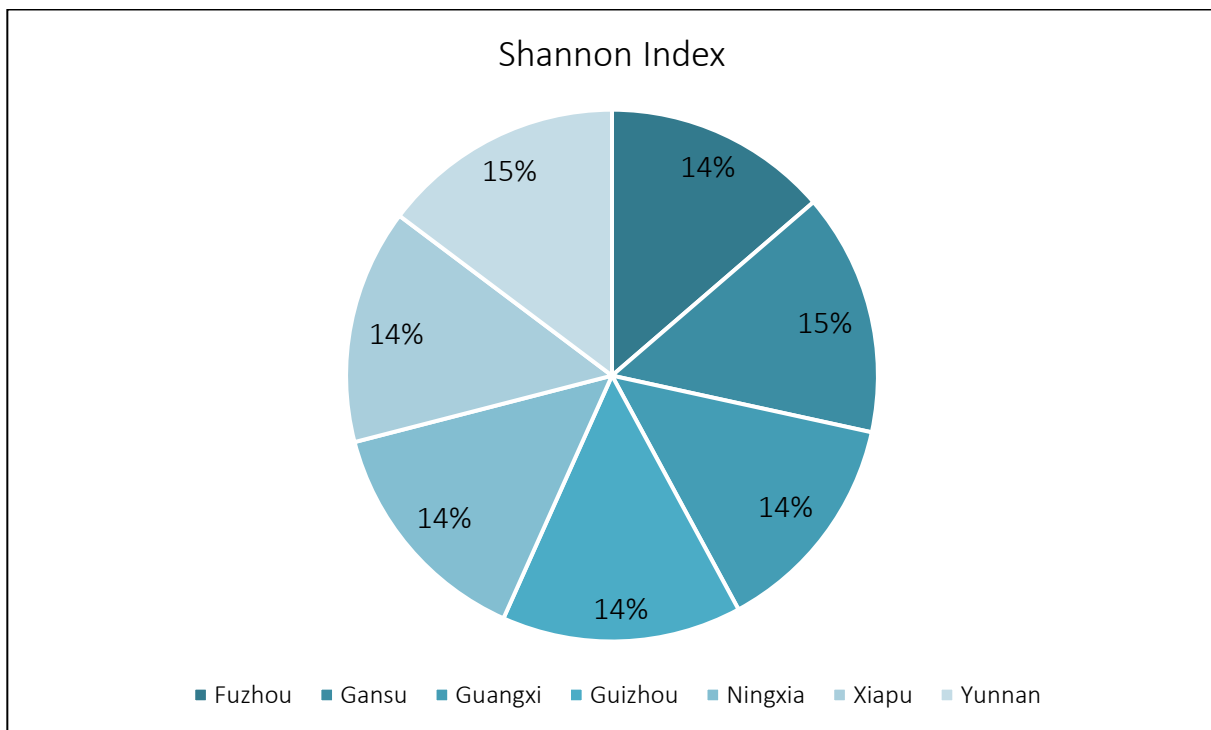


Figure 10: Index_{Shannon} of the 7 population

7. CONCLUSION

The idea of evolution algebra has solely been derived from the concepts behind genetics and Markov chains and has played a significant role in different fields, especially in the study of genetics, including the flow of heredity and the spread of diseases.

In this paper, we have verified the aptness of the sequel, which we have jot down in bullets in the body below, encapsulated within this section

- Evolution algebra is non-associative
- Evolution algebra is commutative

Further, we have worked on idiosyncrasies like:

- The difference between Mendelian and Non-Mendelian genetics.
- Algebraic formulation of non-Mendelian genetics.

Noting all these applications of evolution algebra on genetics we can suffice that in near future the genesis of evolution algebra will prove to be a boon for domains like Genetics and Bio- Informatics. Stepping forward, we have exhumed dataset of the disease Late Blight in 20 genetically distinct potato species from China, and have studied their behaviour, based on their virulent factors for the 7 different species of *Phytophthora Infestans*, the water mould. Also, we have obtained the result that the Shannon Index of all the species were nearly the same (14%), taken as a total of 100% in pie chart, which denotes the dataset, we have worked upon is chaotic enough to study its ambience.

REFERENCES

- Abrams, G., Ara, P., & Mercedes Siles Molina. (2017). Leavitt Path Algebras. <https://doi.org/10.1007/978-1-4471-7344-1>
- Adrian Albert. (1943). Quasigroups. I. 54(3), 507–519. <https://doi.org/10.1090/s0002-9947-1943-0009962-7>
- Alsarayreh, A. A., Izzat Qaralleh, & Ahmad, M. (2017). Derivation Of Three-Dimensional Evolution Algebra. 39(4), 425–444. <https://doi.org/10.17654/nt039040425>
- Bateson, B. (2009). William Bateson, Naturalist. <https://doi.org/10.1017/cbo9780511693946>
- Bateson, W., & Mendel, G. (2009). Mendel's Principles of Heredity. <https://doi.org/10.1017/cbo9780511694462>
- Bayara, J., Conseibo, A., Micali, A., & Ouattara, M. (2011). Derivations in power-associative algebras. *Discrete & Continuous Dynamical Systems - S*, 4(6), 1359–1370. <https://doi.org/10.3934/dcdss.2011.4.1359>
- Boudi, N., Cabrera Casado, Y., & Siles Molina, M. (2022). Natural families in evolution algebras. *Publicacions Matemàtiques*, 66, 159–181. <https://doi.org/10.5565/publmat6612206>
- Dmitri Piontkovski, & Fouad Zitan. (2023). Bernstein algebras that are algebraic and the Kurosh problem. 617, 275–316. <https://doi.org/10.1016/j.jalgebra.2022.11.009>
- Ganikhodjaev, N. N., Ganikhodjaev, R. N., & Jamilov, U. U. (2014). Quadratic stochastic operators and zero-sum game dynamics. *Ergodic Theory and Dynamical Systems*, 35(5), 1443–1473. <https://doi.org/10.1017/etds.2013.109>
- Ganikhodzhaev, R., Mukhamedov, F., & Rozikov, U. (2011). Quadratic Stochastic Operators And Processes: Results And Open Problems. *Infinite Dimensional Analysis, Quantum Probability and Related Topics*, 14(02), 279–335. <https://doi.org/10.1142/s0219025711004365>
- Inez, M., Gonçalves, D., Barquero, D. M., González, Cándido Martín, & Molina, M. S. (2018). Squares and associative representations of two dimensional evolution algebras. <https://doi.org/10.48550/arxiv.1807.02362>
- María Teresa Ceballos, Núñez, J., & Tenorio, Á. F. (2020). Finite dimensional evolution algebras and (pseudo)digraphs. 45(4), 2424–2442. <https://doi.org/10.1002/mma.6632>
- Paniello, I. (2021). Markov evolution algebras. 70(19), 4633–4653. <https://doi.org/10.1080/03081087.2021.1893636>
- Qaralleh, I., & Mukhamedov, F. (2019). Volterra evolution algebras and their graphs. *Linear and Multilinear Algebra*, 1–17. <https://doi.org/10.1080/03081087.2019.1664387>
- Rasul Ganikhodzhaev. (1993). Quadratic Stochastic Operators, Lyapunov Functions, And Tournaments. 76(2), 489–506. <https://doi.org/10.1070/sm1993v076n02abeh003423>
- Rozikov, U. A., & Shamsiddinov, N. B. (2009). On Non-Volterra Quadratic Stochastic Operators Generated by a Product Measure. *Stochastic Analysis and Applications*, 27(2), 353–362. <https://doi.org/10.1080/07362990802678994>

- Tian, J. (2008). Evolution Algebras and their Applications. <https://doi.org/10.1007/978-3-540-74284-5>
- Uygun Jamilov, Scheutzow, M., & Maite Wilke-Berenguer. (2015). On the random dynamics of Volterra quadratic operators. 37(1), 228–243. <https://doi.org/10.1017/etds.2015.30>
- Wu, E-Jiao., Yang, L.-N., Zhu, W., Chen, X.-M., Shang, L.-P., & Zhan, J. (2016). Diverse mechanisms shape the evolution of virulence factors in the potato late blight pathogen *Phytophthora infestans* sampled from China. *Scientific Reports*, 6(1). <https://doi.org/10.1038/srep26182>
- Yolanda Cabrera Casado, Müge Kanuni, & Mercedes Siles Molina. (2019). Basic ideals in evolution algebras. 570, 148–180. <https://doi.org/10.1016/j.laa.2019.01.010>