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Research Article

Biomathematical Integration of the Functional Coexistence Between Macrofauna and Microorganisms in Nicaraguan Agroecosystems: Tau Index (τ)

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Abstract

Agroecology as a science and Biomathematics provide elements that support precision in agroecological designs. The present study was conducted in 10 agroecosystems in Nicaragua located in five departments (Chinandega, Carazo, Matagalpa, Estelí and Boaco). These sites present diversified systems with crops (corn, rice, beans, coffee), forest and cattle. 250 samples of microorganisms and 250 samples of macrofauna were collected and taken to the Laboratories of the National Agrarian University of Nicaragua. The results obtained describe an abundance of 2084 and a richness of 123 families in macrofauna in interaction with 19 genera of microorganisms. The design of 3D pyramidal graphs represented the functional biological interaction on the x, y, z axes between macrofauna families and genera of microorganisms. The design of the Tau index (τ) equation and the obtained values allow us to elucidate the coexistence between organisms. The 20 most significant macrofauna families with their respective positive Tau indices were: Lumbricidae (3.864), Rhinotermitidae (2.486), Acanthodrilidae (0.706), Agelenidae (0.265), Styloniscidae (0.247), Armadillidae (0.208), Porcellionidae (0.19), Polydesmidae (0.178), Histeridae (0.173) and Mycetophilidae (0.168). The families with negative Tau index were: Formicidae (-1.953), Scarabaeidae (-1.438), Chrysomelidae (-0.173), Ixodidae (-0.166), Elateridae (-0.125), Noctuidae (-0.125), Gryllidae (-0.105), Tettigoniidae (-0.74), Culicidae (-0.71) and Cicadidae (-0.05). The genera of microorganisms were: Aspergillus sp., Aureobasidium sp., Bacillus sp., Candida sp., Fusarium sp., Gliocladium sp., Macrophomina sp., Mucor sp., Paecilomyces sp., Penicillium sp., Pseudomonas sp., Pythium sp., Rhizoctonia sp., Rhizopus sp., Sarcina sp., Streptomyces sp., Torula sp., Trichoderma sp. and Verticillium sp. The Lumbricidae family reached the highest interaction in the 3D graphs and the best values of the Tau index. The functional biological diversity of species is irreplaceable by synthetic means. Synergistic actions should be promoted to increase populations of macrofauna that guarantee the coexistence of beneficial microorganisms for the design of agroecosystems with precise biological interactions.

Keywords

Agroecology, Mathematical Models, Biostatistics, Interactions, Soil, Biodiversity, Agroecosystems, Crops

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1. Introduction

Agroecology as a science seeks to explain the behavior of organized and managed species under anthropogenic stimuli, these processes taking place within dynamic agroecosystems. Specifying the mathematical axioms that determine biological behavior beyond classical statistics presents a challenge for researchers who choose this biomathematical path towards the sciences of complexity.

A new intellectual and scientific organon is being configured, whose tools such as network theory and dynamic models with differential equations have allowed the representation of system interactions and the discovery of the evolution induced in the system by those interactions [2]. Theoretical ecology and population dynamics seek to describe and explain how the growth or decline of species populations is affected by the environment or by their interactions; to achieve this, the use of mathematical models is required [1].

Soil fauna, as a fundamental fraction of terrestrial biodiversity, provides multiple ecosystem services for human well-being and health. Soil or ecosystem engineers promote alterations in the micromorphological and physical attributes of the soil [9]. It is stated that the soil biota, which intervenes in soil processes, affects community composition [39]. The soil food web is organized into different levels and is fundamentally based on the relationships between microorganisms, invertebrates, and plants.

The diverse uses and management practices of soil by humans have led ecosystems to undergo both positive and negative changes, in which soil organisms play a significant role in determining soil quality [20]).

Results obtained by Cairo & Díaz demonstrated that a progressive alfalfa cover allowed the establishment of macrofauna and symbiotic microorganisms (*Rhizobium meliloti*), forming nodules on the roots, which led to favorable alfalfa development and evident structural regeneration [5].

Soil biodiversity was analyzed (macrofauna, mesofauna, and microfauna) in agricultural units in Sucre, Colombia. The study indicated higher biodiversity in macrofauna. Pearson correlation analysis showed a significant statistical relationship between soil mesofauna and organic matter. In microfauna, heterotrophic bacteria and actinomycetes were the most abundant nitrogen-fixing organisms [8].

Food chains are typically depicted using pyramids where each trophic level is stacked above the previous one. Macrofauna, due to their feeding habits, consume materials containing microorganisms; these are neither above nor below macrofauna, but rather at the same level, as both are required for coexistence. This study will use biomathematics to provide a more accurate understanding of these concepts within integrated agroecosystems.

2. Materials and Methods

2.1. Location and Description of Agroecosystems

The research was conducted in ten agricultural ecosystems across five Nicaraguan sites (Chinandega, Carazo, Matagalpa, Estelí and Boaco) over the period 2018-2023.

Two agricultural ecosystems were sampled per site. The study began at the lowest altitude site, Santa Rosa (12°39'10.30" N, 87°8'4.00" W) in Chinandega at point "A" (Figure 1), which is 80 meters above sea level. This site served as the starting point for establishing straight lines to higher altitude ecosystems located towards the center of the country. Point A is 126 km from Estelí "B", 145 km from Matagalpa "C", 167 km from Boaco "D", and 133 km from Carazo "E" (Figure 1).

Nicaragua has a tropical climate with little seasonal temperature variation, ranging between 21 and 27 °C. The country experiences two distinct rainy seasons: a wet season (May to October) and a dry season (November to April) [37].

The selection of these agroecosystems was based on their strategic locations within diverse agroecological zones, allowing for the evaluation of multi-environmental conditions. The agroecosystems ranged from low-altitude to high- altitude sites, creating distinct agroecological zones with variations in key parameters such as temperature and precipitation (Table 1). The area enclosed by points A, B, C, D, and E is 14,995 km² with a perimeter of 481.73 km.

Altitude profiles showed irregular topographic features along all analyzed routes (A-B, A-C, A-D, A-E). Maximum slopes ranged from 2.6% to 37.7%, with an average variability of 1.9% to 7.1%. Precipitation across the five sites ranged from 826 to 1166 mm (Table 1).

An altitude profile is a side-view visualization tool that displays altitude data along a line (Figure 1). Data can be either 2D or 3D [25].

Natural barriers evident in the altitude profiles were analyzed to understand whether they isolate or not the population behavior of organisms. It is possible that these barriers did not create a geospatial impediment for different organisms to migrate indifferently to higher or lower sites. This allows coexistence with others, creating interactions within each agroecosystem.

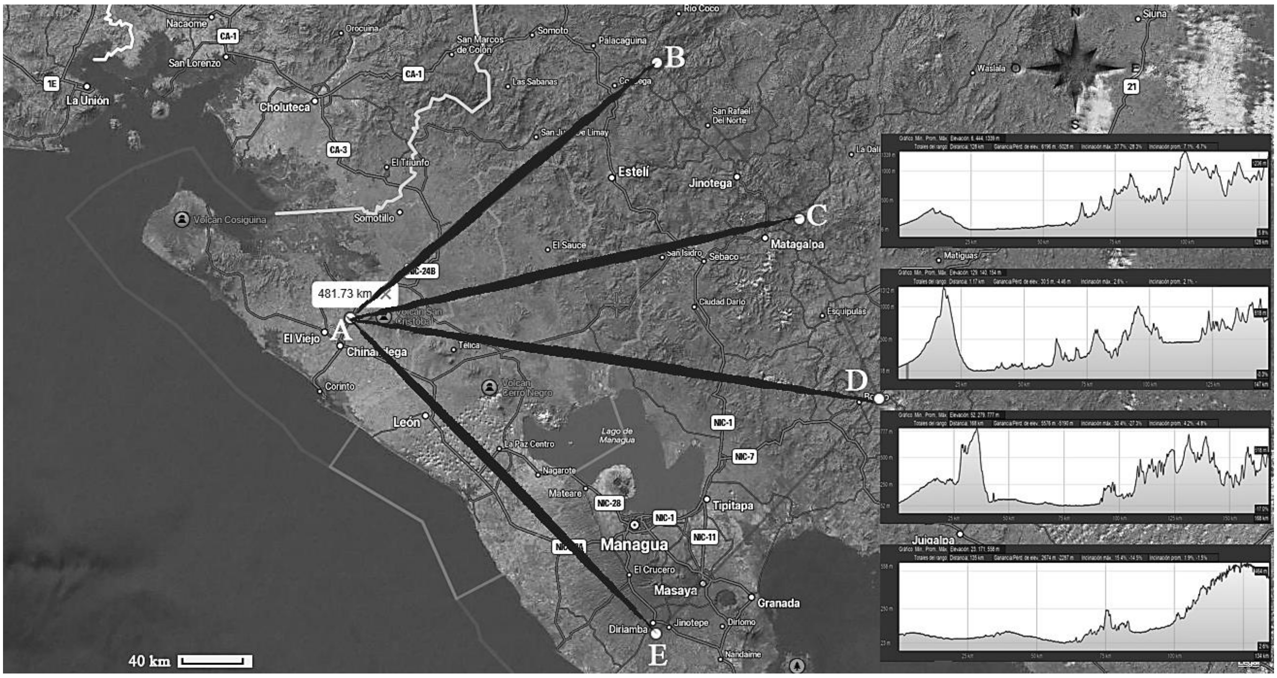

Figure 1. *Location of agricultural ecosystems per site A (Chinandega: Santa Rosa and Santa María), B (Estelí El Milagro de Dios and Linda Vista), C (Matagalpa: La Vecina and La Espadilla), D (Boaco: San Juan and Buena Vista), E (Carazo: El Manantial and El Chipote) and altitude profiles, 2018-2023.*

Table 1. *Location of agroecosystems and altitude profile from Chinandega, west-east orientation, Nicaragua, 2023.*

Site	Length O	Latitude N	Distance from "A" (km)	Altitude (masl)	Variation in altitude (m)	Maximum inclination (%)	Average inclination (%)	T (℃)	P (mm)
Chinandega	12°39'10.30"	87°8'4.00"	0	80	0	N/A	N/A	33	826
Estelí	13°23'58.20"	86°14'42.54"	126	1253	1173	37.7	7.1	29	1165
Matagalpa	12°58'19.16"	85°49'45.37"	145	818	738	2.6	2.1	27	1003
Boaco	12°28'15.53"	85°36'38.48"	167	519	439	30.4	4.2	29	873
Carazo	11°49'20.50"	86°14'22.00"	133	469	389	15.4	1.9	31	1166

T: Temperature; P: Precipitation, "A": Chinandega; masl: meters above sea level.

2.2. Management of Agroecosystems

In the five study agroecosystems, agroecological practices and technologies were implemented (green manure, agroecological fertilization, crop diversification, crop rotation, living barriers), while the remaining five agroecosystems employed conventional techniques (synthetic fertilizers, pesticides, nematicides, herbicides, monoculture). The main crops in Chinandega and Carazo were basic grains (rice, corn, and beans); in Estelí and Matagalpa, coffee; and in Boaco, livestock.

According to FAO, agroecology is a holistic and integrated approach that simultaneously applies ecological and social concepts and principles to the design and management of sustainable agricultural and food systems. It aims to optimize interactions among plants, animals, and the environment [12].

This study analyzed the coexistence of microorganism genera and macrofauna families identified in the 10 agroecosystems. A biological coexistence index was developed to assess this, considering agroecological functionality as a fundamental part of the differential calculation. This analysis contributed to understanding how one organism positively or negatively affected the existence of another, evidencing its population influence on the agroecosystem's entropy.

2.3. Sampling of Microorganisms and Macrofauna

The two types of organisms selected for the analysis were microorganisms and macrofauna, considered the variables to be evaluated. Microorganisms were sampled at a depth of 0.2 m in the soil. Five subsamples were analyzed per agroecosystem, with five samples per subsample, totaling 250 samples for all 10 agroecosystems under study. These samples were taken to the microbiology laboratory at the National Agrarian University of Nicaragua and genera of fungi, bacteria, and actinomycetes were identified, and their respective Colony Forming Units per gram of soil (CFU g^{-1}) were quantified. The respective culture media were: Potato Dextrose Agar, Nutrient Agar, and Oat Agar [28].

The macrofauna sampling method is described by Rodriguez & Salazar [29]. The sampling points are the same as those used for the microorganism sampling, thus ensuring that the coexistence between macrofauna families is determined by geospatial conditions of presence, with a direct or inversely proportional influence on the presence of microorganism genera. The abundance of each macrofauna family identified in each monolith was quantified. All counts were used to create databases that were analyzed using different fitting equations.

2.4. Need for a Coexistence Index

Agroecology emerged as a science in response to the limited capacity of conventional disciplines to understand the reality of a system that functions as an organized totality, which is complex and can only be analyzed from a transdisciplinary perspective [7].

The complexity of agroecosystems hinders the implementation of specialized actions to manage populations of macrofauna and microorganism organisms under planned abundance and diversity. It is a fact that interactions between organisms maximize or slow down the mutual behavior of their populations, and their coexistence has not been calculated from a biomathematical perspective under agroecological conditions.

There is a concept known as an umbrella species, which attempts to attribute the assurance of biodiversity to certain species. It is argued that a single umbrella species cannot ensure the conservation of all coexisting species, providing evidence that umbrella species of a higher taxon do not necessarily confer protection to sets of other taxa [27].

This study aims to answer the following questions: Which macrofauna family increases the number of microorganisms in the soil? Which macrofauna family increases the diversity of microorganisms in the soil? In what proportion, calculated using an index, can we affirm that they coexist and promote microbial populations? Is it possible to observe a negative coexistence with a functional role in an agroecosystem? All these questions were analyzed from a biomathematical perspective to obtain the following index.

2.5. Tau Index of Functional Biological Coexistence Between Macrofauna Families and Microorganism Genera

$$\tau = b\left[\frac{\sqrt{x^2-y^2}}{m(m^2-1)}\right] \tag{1}$$

If b=$\{-1 \text{ or } 1\}$ (Table 2)

Where:

x: Total number of individuals belonging to a macrofauna family in coexistence (abundance).

y: Accumulated absolute frequency of the presence of microorganisms. It is the sum of times that different genera of microorganisms associated with a macrofauna family were identified in different samplings. In this case, if the same type of microorganism is repeated,

m: Absolute frequency of observed microorganisms. It is the total number of different organisms observed in coexistence with a type of macrofauna. In this case, if the microorganism is observed in different samplings, it will only be added once.

b: Agroecological functionality of macrofauna

$\tau = Tau\ index\ (functional\ biological\ coexistence)$

2.6. Agroecological Functionality Values of Macrofauna

Microflora, as well as macrofauna, positively influence the main processes that develop in the soil ecosystem [32].

Macrofauna, due to its behavior determined by its feeding and reproductive habits, can become an ally during agroecological production or a negative agent when its activity within the agroecosystem becomes favorable to the destruction of crops and harvests.

Table 2. *Macrofauna functionality and assigned values required for the Tau index, Nicaragua, 2018-2023.*

Functionality coefficient (b)	Allocation criteria based on habits
-1	Phytophages, pests, diseases, omnivorous, hematophagous, defoliator, parasites
1	Predators, detritivores, saprophagous, sarcosaprophages, coprophagous, pollinator, microvivore

2.7. Integration and Mathematical Verification of the Index to Determine the Functional Biological Coexistence

$$\int \tau = \int b\left[\frac{\sqrt{x^2-y^2}}{m(m^2-1)}\right]dx$$

Get the constant:

$$= \frac{1}{(-1+m^2)m} b \int \sqrt{-y^2+x^2}\, dx$$

$$= \frac{b}{m(-1+m^2)} \int \sqrt{-y^2+x^2}\, dx$$

Integration by trigonometric substitution:

$$= \frac{b}{m(-1+m^2)} \int y^2\, tan^2(u)\sec(u)\, du$$

Constant:

$$= \frac{b}{m(-1+m^2)}\, y^2 \int tan^2(u)\sec(u)\, du$$

Use of trigonometric identities:

$$= \frac{b}{m(-1+m^2)}\, y^2 \int [-1+sec^2(u)]\sec(u)\, du$$

$$= \frac{b}{m(-1+m^2)}\, y^2 \int -\sec(u)+sec^3(u)du$$

$$= \frac{b}{m(-1+m^2)}\, y^2[-\int \sec(u)du+\int sec^3(u)\, du]$$

If:

$$\int \sec(u)du = ln|\tan(u)+\sec(u)|$$

$$\int sec^3(u)du = \frac{1}{2}\sec(u)\tan(u)+\frac{1}{2}\ln|\tan(u)+\sec(u)|$$

The development is:

$$= \frac{b}{m(-1+m^2)}\, y^2\left[-ln|\tan(u)+\sec(u)|+\frac{1}{2}\sec(u)\tan(u)+\frac{1}{2}ln|\tan(u)+\sec(u)|\right]$$

Replace: $u = arcsec\left(\frac{1}{y}x\right)$

$$= \frac{b}{m(-1+m^2)}\, y^2$$

$$\left[-ln\left|\tan\left(arcsec\left(\frac{1}{y}x\right)\right)+\sec\left(arcsec\left(\frac{1}{y}x\right)\right)\right|+\frac{1}{2}\sec\left(arcsec\left(\frac{1}{y}x\right)\right)\tan\left(arcsec\left(\frac{1}{y}x\right)\right)+\frac{1}{2}ln\left|\tan\left(arcsec\left(\frac{1}{y}x\right)\right)+\sec\left(arcsec\left(\frac{1}{y}x\right)\right)\right|\right]$$

Simplified:

$$= \frac{b}{2m(-1+m^2)}\left[x\sqrt{x^2-y^2}-y^2 ln\left(\frac{\left|x+\sqrt{x^2-y^2}\right|}{|y|}\right)\right]+\mathrm{c}$$

2.8. Interpretation of the Index

A mathematical model consists in the observation of certain properties, from which definitions and axioms are constructed, and the study of variables to establish the formulation of relationships between them considering the constructed definitions [13].

The Tau index (τ) determines with which numerical magnitude the functional coexistence of a macrofauna family is valued in close relation to all microorganisms present in a defined space-time.

The value of the index can be positive or negative depending on the agroecological function identified according to the principles established in the study by Rodriguez &Salazar [30].

The magnitude is independent of the functionality. A high positive index value indicates that the macrofauna family under analysis promotes the population growth of microbial genera and provides a positive synergistic functionality for the agroecosystem.

A macrofauna family with a high negative index value demonstrates a synergy to condition microbial growth with negative consequences for the productivity of agroecosystems with an agroecological approach.

An index value of zero indicates neutrality of the macrofauna family on the coexistence of microorganisms. In this case, the macrofauna promotes microbial life but not at levels considered significant by the index. These organisms can be considered essential for achieving a precise energy balance and guiding the agroecosystem towards balanced entropy states.

Systemic entropy is achieved with magnitudes in both positive and negative directions. The existence of all organisms is necessary to reach an ideal energy balance. To ensure continuous productivity, it is necessary to promote macrofauna families with higher index magnitudes and a positive sign, as they generate a purposeful chaos inherent to agroecosystem productivity.

Macrofauna families that are closer to the three-dimensional zero in graphs and index are those that, with positive or negative magnitudes, do not significantly influence soil microbial CFU g^{-1} in the agroecosystem. If the Tau index yields an absolute zero, it demonstrates a balanced biological functional entropy.

The Tau index should be applied to all macrofauna families under study observed in environmental interaction with present microorganisms. In this context, a community action of multiple macrofauna families coexisting in a specific space-time will promote microbial coexistence. This reality will not depend on a single taxon but on the joint action of several taxa in favor of microbial coexistence.

2.9. Designing the Graphics

Agroecology requires biomathematical knowledge to accurately specify actions to be taken within agroecosystems. The results presented correspond to data plotted in a three-dimensional space. Each point represents a position of influence in interaction, and complete information was gathered for each macrofauna family in contrast with all observed microorganisms.

The study of biodiversity is of interest to many biologists, but the mathematical tools they apply to measure it are not always correct for making inferences about changes in biological diversity [17].

The diversified organic matter present largely defines the in situ feeding of macrofauna and microorganisms, creating ideal conditions for multiple interactions and exponential coexistence among families.

Leaf litter mosaics and a better distribution of resources originate the coexistence of a very heterogeneous and numerous soil community, at the same time that it reduces competitive pressure among soil macroinvertebrates [4].

The 3D graphs present the axes "x", "y", "z". The "y" axis represents the accumulated absolute frequency of the presence of microorganisms. The "x" and "z" axes represent the abundance (magnitude) of macrofauna found and the functional sign (direction), respectively. Each pyramid is the fusion between the macrofauna family and the genera of microorganisms, and it presents five points, four at the base and one elevation. The elevations can be positive or negative depending on the agroecological function of the macrofauna family.

To illustrate the construction of a population representation of interacting macrofauna and microorganisms, data from the Actinopodidae family of spiders were analyzed. Sixteen individuals were found, and 16 corresponding soil samples were analyzed for microbial colony-forming units (CFU g^{-1}). The spatial configuration of data points follows a standardized pattern for all cases, with basal points C (0, 0, 0), L (x, 0, 0), K (x, y, 0), and N (0, y, 0), for elevation.

$$M\ \left(\frac{x}{2}, \frac{y}{2}, x\right) \quad (2)$$

For Actinopodidae x= 16; y=16. The spatial configuration of data points is as follows: C (0, 0, 0), L (16, 0, 0), K (16, 16, 0), and N (0, 16, 0), with the apex at M (8, 8, 16). The pyramid extends along the positive "z" axis to represent the beneficial predatory habits of the macrofauna family (Figure 2).

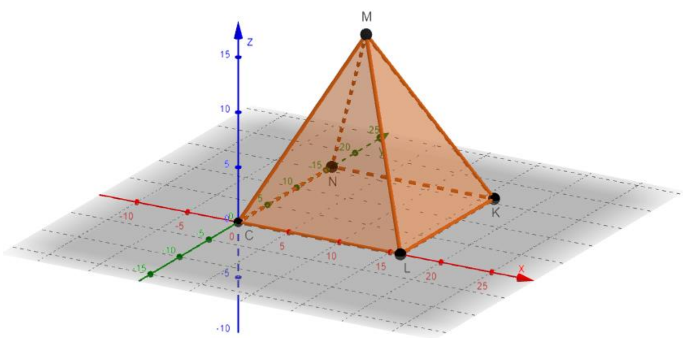

Figure. 2. *Pyramid of coexistence between the Actinopodidae family and microorganisms present, Nicaragua 2018-2023.*

3. Results

Agroecology drives the investigation of biotic interactions within diverse agroecosystems. This study focused on both positive and negative interactions in complex agroecosystems, assessing the ecosystem services provided by macrofauna families to support microbial coexistence.

The coexistence of species is not a random event, it depends on interactions between communities that share food resources and that generate actions that enhance population increase at exponential levels; This is the case of microorganisms. Macrofauna is intrinsically related to microorganisms; It is a bidirectional relationship that is intended to create optimal conditions for healthy soils ideal for agroecological environments of integrated production.

Macrofauna families exhibit varying degrees of contribution to microbial coexistence. The Actinopodidae family will be placed in a new figure, this family was used to explain in materials and methods the procedure developed to index its data and the data of the observed microorganisms, thus generating the 3D coordinates. This same procedure is executed for two additional families and placed next to Actinopodidae, thus visualizing their coexistence.

The Actinopodidae family (pyramid C, L, K, N, M) interacts with the smaller Amaurobiidae family (pyramid S, T, C, U, V) within the Arachnida class. The Histeridae family (pyramid BA, BC, C, BD, BE), belonging to the Coleoptera order, is an intermediate-sized polyphagous group that feeds on larvae, manure, and animal matter. Pyramid volume is proportional to family abundance, with Actinopodidae being the most abundant.

The observable interactions between pyramids denote moments of crossing between actions developed by one or another family in the sampling site where all these organisms coexist in the same line of time and space (*Figure 3*).

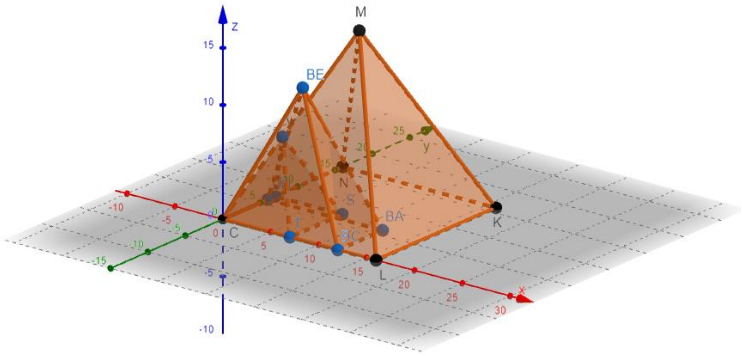

Figure 3. *Pyramids of macrofauna families Amaurobiidae (S, T, C, U, V), Histeridae (BA, BC, C, BD, BE), and Actinopodidae (C, L, K, N, M) in coexistence with microorganisms, Nicaragua 2018-2023.*

Greater pyramid volume does not guarantee effective synergistic microbial coexistence. The Tau index for Amaurobiidae (smallest pyramid) and Actinopodidae (largest pyramid) is 0, indicating neutrality and functional entropy. Histeridae (intermediate pyramid) has a Tau index of 0.173, suggesting strong positive interactions promoting microbial coexistence and growth.

The Tau index can be used to identify the macrofauna family that most effectively promotes microbial populations within the agroecosystem, providing a more nuanced understanding beyond functional entropy.

The three macrofauna families were examined under a magnified scale. Introducing the Acrididae family (inverted pyramid ABCED), a leaf-cutting pest, revealed a slight but significant negative Tau index (-0.020) suggesting limited promotion of microbial coexistence despite its negative impact on agroecosystem productivity. However, this family did not surpass the economic injury level in this study (Figure 4).

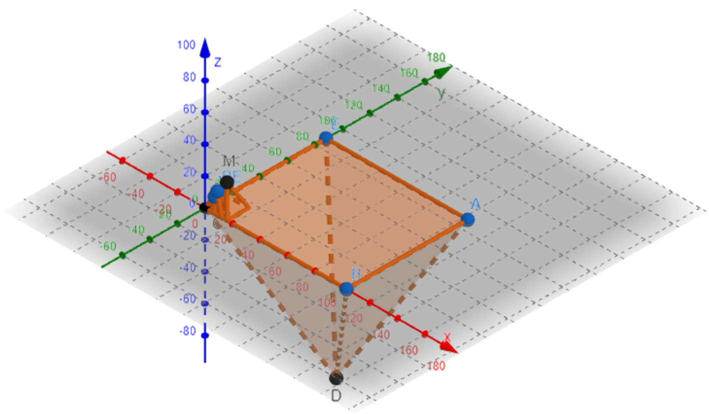

Figure 4. *3D pyramids for positive z-axis families Amaurobiidae, Histeridae, Actinopodidae and negative z-axis family Acrididae, Nicaragua 2018-2023.*

The relative importance of each macrofauna family was evaluated, the volumes of their pyramids were compared. Actinopodidae has a volume of 1,365.33 u^3, while Acrididae, with a negative z-axis value, has a much larger volume of 311,197.33 u^3. The small volume of Actinopodidae indicates minimal presence above the dominant Acrididae. Microorganisms rely on organic matter residues to initiate decomposition processes and nutrient cycling for plants. The leaf-cutting activities of Acrididae effectively promote microbial coexistence and are justified as long as population levels remain below the economic injury level.

The Chrysomelidae family (order Coleoptera), with a pyramid volume of 53,817,637.33 u^3 (negative z-axis), exceeded the economic injury level in all studied agroecosystems. In comparison, the Acrididae family (pyramid ABCED) had a smaller volume on the z-axis (Figure 5).

The abundant presence of Chrysomelidae, phytophagous pests, with a Tau index of -0.173 and a large pyramid volume (53,817,637.33 u^3), negatively impacts agroecosystem productivity but positively influences microbial activity. Acrididae (ABCED) has a smaller pyramid volume and is found beneath Chrysomelidae (Figure 5).

The taxonomic order Crassiclitellata includes two significant families in this study: Acanthodrilidae and Lumbricidae. Acanthodrilidae exhibited a higher Tau index of 0.706 and a volume of 38,357,077.33 u^3. Despite a smaller volume compared to Chrysomelidae, Acanthodrilidae demonstrated a stronger capacity to promote microbial coexistence. This highlights that the number of individuals alone does not determine microbial coexistence; rather, it depends on the specific interactions of each macrofauna family. The Tau index effectively quantifies this aspect, assigning higher values to families that facilitate microbial coexistence in the soil (Figure 6).

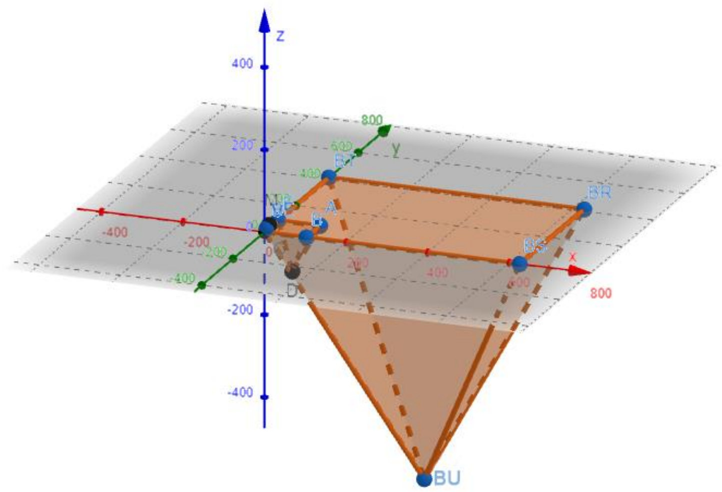

Figure 5. Chrysomelidae family in its inverted pyramidal form (BT, BR, BS, C, BU) and Acrididae family in 3D pyramid (A, B, C, E, D) Nicaragua 2018-2023.

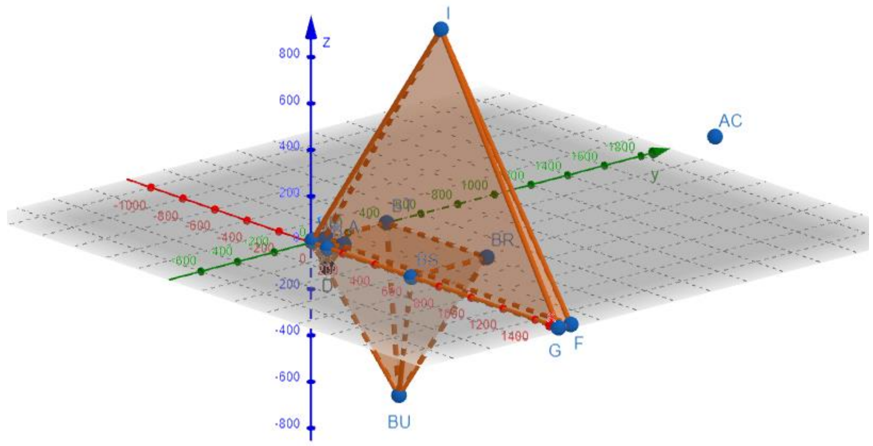

Figure 6. Family Acanthodrilidae pyramid (F, G, C, J, I) in positive z axis and Family Chrysomelidae in its inverted pyramidal form (BT, BR, BS, C, BU) negative z axis, 3D interaction graphs, Nicaragua 2018-2023.

The Scarabaeidae family, specifically the genus Phyllophaga sp., has an exceptionally large pyramid volume of 39,810,466,804.33 u^3, significantly surpassing Chrysomelidae. As a soil-dwelling pest targeting the root systems of both perennial and annual crops, Phyllophaga occupies the lowest negative region of the z-axis with a Tau index of -1.438. This indicates that while promoting microbial coexistence, Phyllophaga has a detrimental impact on agroecosystem productivity (Figure 7).

The Lumbricidae family exhibited the largest pyramid volume (266,407,474,809 u^3), highlighting its pivotal role in biodiverse agroecosystems. As a cornerstone of soil nutrient cycling and microbial coexistence, Lumbricidae achieved the highest Tau index of 3.864 among the ten studied agroecosystems (Figure 7).

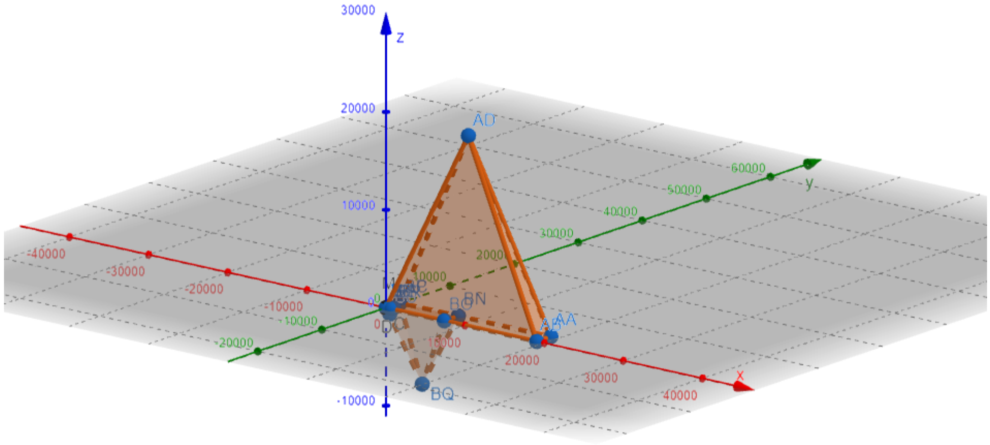

Figure 7*. Population pyramids of functional coexistence for the Lumbricidae (AA, AB, C, AC, AD) and Scarabaeidae (BN, BO, C, BP, BQ) families in 10 agroecosystems of Nicaragua, 2018-2023.*

The study involved the observation of 2084 individuals and the analysis of 123 macrofauna families: Acanthodrilidae, Acrididae, Actinopodidae, Agelenidae, Amaurobiidae, Ammotrechidae, Anthocoridae, Anyphaenidae, Aphrophoridae, Apidae, Araneidae, Argasidae, Argidae, Armadillidae, Blaberidae, Blattidae, Calliphoridae, Carabidae, Cephidae, Cerambycidae, Cercopidae, Chactidae, Chrysomelidae, Chrysopidae, Cicadellidae, Cicadidae, Clubionidae, Coccinellidae, Coreidae, Cosmetidae, Crabronidae, Ctenidae, Ctenizidae, Culicidae, Curculionidae, Cydnidae, Cynipidae, Dictynidae, Diguetidae, Dipluridae, Ectobiidae, Elateridae, Entomobryidae, Erebidae, Erotylidae, Eumastacidae, Forficulidae, Formicidae, Gelastocoridae, Gelechiidae, Geometridae, Geophilidae, Geotrupidae, Gnaphosidae, Gonyleptidae, Gryllacrididae, Gryllidae, Gryllotalpidae, Gyrinidae, Histeridae, Ichneumonidae, Ixodidae, Japygidae, Julidae, Laelapidae, Lampyridae, Linyphiidae, Liocranidae, Lithobiidae, Lumbricidae, Lycidae, Lycosidae, Lygaeidae, Machilidae, Mantidae, Mantispidae, Mecistocephalidae, Meloidae, Membracidae, Miridae, Muscidae, Mycetophilidae, Mydidae, Nabidae, Nitidulidae, Noctuidae, Nymphalidae, Oxyopidae, Papilionidae, Paradoxosomatidae, Paronellidae, Passalidae, Pentatomidae, Phasmatidae, Pholcidae, Pisauridae, Planorbidae, Polydesmidae, Pompilidae, Porcellionidae, Pteromalidae, Pulicidae, Pyralidae, Reduviidae, Rhinotermitidae, Salticidae, Scarabaeidae, Sclerosomatidae, Scolopendridae, Sicariidae, Sparassidae, Spirostreptidae, Spongiphoridae, Staphylinidae, Styloniscidae, Syrphidae, Tenebrionidae, Tetragnathidae, Tetrigidae, Tettigoniidae, Theridiidae, Thomisidae y Thyreocoridae.

Ranking in the top 10 with positive Tau values are: Lumbricidae (3.864), Rhinotermitidae (2.486), Acanthodrilidae (0.706), Agelenidae (0.265), Styloniscidae (0.247), Armadillidae (0.208), Porcellionidae (0.19), Polydesmidae (0.178), Histeridae (0.173) y Mycetophilidae (0.168). The top 10 taxa with negative Tau indices were: Formicidae (-1.953), Scarabaeidae (-1.438), Chrysomelidae (-0.173), Ixodidae (-0.166), Elateridae (-0.125), Noctuidae (-0.122), Gryllidae (-0.105), Tettigoniidae (-0.74), Culicidae (-0.71) y Cicadidae (-0.05).

A total of 19 microbial genera were observed interacting with the macrofauna, including: Aspergillus sp., Aureobasidium, Bacillus sp., Candida sp., Fusarium sp., Gliocladium sp., Macrophomina sp., Mucor sp., Paecilomyces sp., Penicillium sp., Pseudomonas sp., Pythium sp., Rhizoctonia sp., Rhizopus sp., Sarcina sp., Streptomyces sp., Torula sp., Trichoderma sp. y Verticillium sp.

4. Discussion

The intensification of agricultural practices has underscored the imperative to integrate scientific principles and agroecological management models to harmonize agricultural production [33].

Model-based management necessitates fine-tuning to attain precise functional biology within agroecosystems. This study leverages agroecological principles to optimize functionality, as quantified by 3D visualizations and the Tau index of functional coexistence, while investigating dynamic processes.

Agroecology capitalizes on natural interactions within agroecosystems to minimize external inputs and optimize biological efficiency [34]. To enhance these interactions, the coexistence of organisms must be considered with each intervention, as illustrated in Figure 3, where three organisms generate quantifiable volumes concurrently.

The introduction of crops into agroforestry systems had varied impacts on soil macrofauna, driven by the heterogeneity of vegetation and land use [6]. These changes in macrofauna populations subsequently affected microbial communities, highlighting the complex interactions within agroecosystems (Figure 4).

A higher coefficient of positive interactions between plant species and natural enemies in more complex systems (63.1%) [18]. Conversely, less complex stations exhibited higher levels of negative interactions and lower arthropod diversity.

The Tau index of functional coexistence is used to measure the balance between antagonistic and synergistic interactions among organisms. By isolating interacting taxa, we can partially assess functional systemic entropy within agroecosystems. A Tau index value of zero represents perfect equilibrium (Figure 3).

Conventional agriculture has led to imbalances in agroecosystems. Agrobiodiversity seeks to address these issues by promoting the conservation and sustainable use of biodiversity within agricultural landscapes [19].

While many studies have examined the diversity, ecology, and conservation of vertebrate fauna, spiders have emerged as valuable ecological indicators for assessing ecosystem health [24]. However, due to methodological challenges associated with studying smaller organisms, the crucial roles of invertebrates like spiders in agroecosystems, particularly in biogeochemical cycles, are often overlooked. Agroecology offers a promising approach to enhance these cycles.

Cursorial spiders, particularly those belonging to the families Theraphosidae and Actinopodidae, have specialized habitat requirements and are sensitive to disturbances. These spiders need undisturbed areas within their habitat to thrive and serve as a food source [23]. Actinopodidae species, in particular, play a positive role in agroecosystems and can serve as valuable bioindicators of ecosystem health (Figure 7).

The low abundance of Amaurobiidae in the area may be attributed to their small size and cryptic habits, which reduce their detectability [26]. Despite their low visibility, this family has demonstrated positive contributions to agroecosystems (Figure 4).

Histerid beetles were found to be sensitive to habitat degradation, with diversity decreasing in areas with low plant complexity. These results suggest that Histeridae can serve as useful bioindicators of habitat quality [38]. Furthermore, Histeridae demonstrated a high level of functional coexistence within their communities (Figure 3).

Locusts (Orthoptera: Acrididae) are notorious agricultural pests that have caused widespread crop damage and famine throughout history [21]. The Acrididae family poses a significant threat to agroecosystems, especially when populations reach outbreak levels (Figure 4).

Macrofauna play a crucial role in maintaining ecosystem health by influencing soil microorganisms and improving soil conditions (Figure 6). This makes them valuable indicators of ecosystem response to socio-economic development, which often leads to changes in ecosystem functions, services, and biodiversity [36].

Leaf beetles (Coleoptera: Chrysomelidae) were assessed as bioindicators of habitat quality across various human-impacted landscapes and phytophisionomies [22]. The functional quality of multiple interacting families within agricultural landscapes will influence the overall quality of the agroecosystem and align with the goals of agroecological design (Figure 5).

Soil aggregates are formed through the interactions of biotic and abiotic factors, including roots, fungi, mesofauna, and bacteria [16]. These aggregates serve as structural units between individual soil particles. The family Acantodrilidae has a positive impact on soil quality (Figure 6).

It was found that earthworm species richness was higher in natural ecosystems, but that polycultures could mitigate the negative impacts of agricultural management on biodiversity [15]. The earthworms significantly enhance soil microbial activity, with microbial respiration increasing by nearly 90% in the first four weeks after soil passage through their guts [35]. Microbial biomass was highest in fresh casts and declined over time.

The pyramidal elevation of Lumbricidae populations is a strong indicator of soil fertility potential, suggesting that agroecosystems with abundant earthworms are more productive (Figure 7).

Phyllophaga larvae cause significant root damage between June and November, initiating their annual cycle with the emergence of adults from the soil [14]. Macrofauna families with detrimental effects on crops will exhibit inverted population pyramids (Figure 7)

The complex symbiotic relationship between worms and microorganisms must be highlighted [11]. Earthworms rely on microorganisms as a primary nutrient source and stimulate microbial activity in organic matter decomposition. Lumbricidae exhibited the highest coexistence Tau index (Figure 7).

The microbial community in soil plays a crucial role in transforming organic and inorganic matter, maintaining a delicate balance through self-regulation [3]. Arbuscular mycorrhizal fungi, key members of the soil microbiome, significantly influence crop growth and productivity through multiple mechanisms [10].

Aspergillus niger, a plant growth-promoting fungus, solubilizes soil phosphates by producing organic acids, reducing the need for chemical fertilizers [31].

Fungi, bacteria, and actinomycetes were evaluated alongside macrofauna in samples from ten agroecosystems. 3D visualizations and Tau index values revealed antagonistic, synergistic, and neutral interactions among these organisms. The presence of macrofauna significantly influenced the coexistence of microorganisms in all integrated agroecosystems.

5. Conclusions

The organic matter continuum, from crop residues to mineralized soil nutrients, serves as the primary interaction space for macrofauna and microorganisms. Collaborative activities between these organisms contribute to nutrient cycling and plant growth.

The Tau index can be used to quantify the functional coexistence between macrofauna and microorganisms.

Each taxonomic family can be conceptualized as a pyramid containing smaller pyramids of interacting organisms. These systems achieve coexistence through a balance of functional entropy.

3D graphs allow visualization of the volume calculated from biomathematics and represent the functional influence that each macrofauna family has within the agroecosystem. The z-axis will represent positive or negative actions depending on the macrofauna family. Families with positive functionality and their respective Tau indexes are: Lumbricidae (3.864), Rhinotermitidae (2.486), Acanthodrilidae (0.706), Agelenidae (0.265), Styloniscidae (0.247), Armadillidae (0.208), Porcellionidae (0.19), Polydesmidae (0.178), Histeridae (0.173) and Mycetophilidae (0.168). All those macrofauna families with pyramids below the z-axis should be analyzed in terms of population and functional. Families such as: Formicidae (-1.953), Scarabaeidae (-1.438), Chrysomelidae (-0.173), Ixodidae (-0.166), Elateridae (-0.125), Noctuidae (-0.122), Gryllidae (-0.105), Tettigoniidae (-0.74), Culicidae (-0.71) and Cicadidae (-0.05); if they present an economic damage threshold, they should be managed so that their population volume causes the least damage to the agroecosystem. It is observed that, even being negative in their Tau index, these families contribute to the coexistence of microorganisms, demonstrating a biomathematical agroecological analysis for decision making.

The base width of a pyramid correlates with its interaction with microorganisms. However, the Tau index is necessary to quantify coexistence and proportional increases in microbial richness and diversity. Nested pyramids, where larger pyramids encompass smaller ones, exhibit higher Tau index values, indicating a greater influence on microbial communities.

The multiplication of macrofauna families such as Lumbricidae (τ = 3.864) and all those that obtain a higher Tau index should be promoted, because microbial coexistence should be diversified from several interacting taxa.

The design of precise biological interactions in agroecosystems requires the protection and promotion of functional biodiversity. Synergistic actions, such as increasing macrofauna populations, are essential for ensuring the coexistence of beneficial microorganisms.

In subsequent research, it is advisable to explore analyzes that involve a fourth dimension, placing time in parallel while meeting the parameters of the three dimensions demonstrated in this article. That would give rise to parallel pyramids that transcend time and space.

Abbreviations

τ	Tau Index
2D	Two Dimensions
3D	Three Dimensions
T	Temperature
P	Precipitation
Masl	Meters Above Sea Level
CFU g^{-1}	Colony Forming Units Per Gram of Soil
u^3	Cubic Units
sp.	Species

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Author Contributions

Hugo Rene Rodriguez Gonzalez: Conceptualization, Data curation, Formal Analysis, Investigation, Methodology, Software, Validation, Visualization, Writing – original draft, Writing – review & editing.

Dennis Jose Salazar Centeno: Funding acquisition, Investigation, Project administration, Resources, Supervision.

Hermann Alfred Jürgen Pohlan: Funding acquisition, Investigation, Project administration, Resources

Conflicts of Interest

The authors declare no conflicts of interest.

References

[1] Ávila Vales, E. (2000). Coexistence in a two-species competition system. Mathematical miscellany, 30, 17-25. Retrieved May 09, 2024, from https://miscelaneamatematica.org/welcome/default/download/tbl_articulos.pdf2.8c7ce34185a06ed1.4176696c612e706466.pdf

[2] Benítez, M., Rivera Núñez, T., & García Barrios, L. (2021). Agroecology and Complex Systems. México: SOCLA. Retrieved April 27, 2024, from https://copitarxives.fisica.unam.mx/TS0022ES/TS0022ES.html

[3] Borrero, C. A., & Silva H., M. R. (2005). Effects of Trichoderma (in vitro) on non-pathogenic microorganisms decomposing organic matter in a class IV Oxisol soil from the piedmont of the llanos. Orinoquía, 9(2), 6-14. Retrieved July 2, 2024, from https://www.redalyc.org/pdf/896/89690202.pdf

[4] Cabrera Dávila, G. d. (2018). Ecological characterization of soil macrofauna in two evergreen forest sites at El Salón, Sierra del Rosario, Cuba. Bosque, 3(39), 363-373. Retrieved April 05, 2024, from https://www.scielo.cl/pdf/bosque/v39n3/0717-9200-bosque-39-03-00363.pdf

[5] Cairo Cairo, P., & Díaz Martin, B. (2022). Effects of management and establishment of two plant species on the structure of a saline soil. Centro Agricola, 49(1), 167. Retrieved June 8, 2024, from https://openurl.ebsco.com/EPDB%3Agcd%3A9%3A17688137/detailv2?sid=ebsco%3Aplink%3Ascholar&id=ebsco%3Agcd%3A175448674&crl=c

[6] Castellanos González, L., González Pedraza, A. F., & Capacho Mogollón, A. E. (2019). Influence of agroforestry systems of the Plantar Project on soil macrofauna. BISTUA, 17(3), 105-116. https://doi.org/10.24054/bistua.vi.222

[7] Céspedes L., C., Vallejos Q., J., & Sánchez L., C. (2017). INIA Digital Library. (INIA, Ed.) Retrieved February 21, 2024, from Manejo agroecológico en sistemas latinoamericanos tradicionales: https://hdl.handle.net/20.500.14001/6618

[8] Chamorro Martínez, Y. P. (2022). Structure of soil macro-, meso- and microfauna and its relationship with soil quality parameters in agricultural units of northern Colombia: ecological implications. Barranquilla: University of the Coast Corporation. Retrieved June 8, 2024, from https://repositorio.cuc.edu.co/bitstream/handle/11323/9229/ESTRUCTU-RA%20DE%20LA%20MACRO%2c%20MESO%20Y%20MICROFAU-NA%20DEL%20SUELO.pdf?sequence=3&isAllowed=y

[9] Chavez Suarez, L., Rodríguez García, I., Estrada Prado, W., Magaly Herrera, V., & Medina Mesa, Y. (2021, November 08). Functional composition of the edaphic macrofauna in five grassland agroecosystems in the Granma province, Cuba. Pastos y Forrajes, 44, 1-12. Retrieved April 28, 2014, from http://scielo.sld.cu/pdf/pyf/v44/2078-8452-pyf-44-eE24.pdf

[10] Díaz Zorita, M., Correa, O., Fernández Canigia, M. V., & Lavado, R. S. (2013). Contributions of microbiology to crop production. Buenos Aires, Argentina: Universidad de Buenos Aires. Retrieved July 2, 2024, from https://www.researchgate.net/publication/306960003_LOS_MICROORGANIS-MOS_DEL_SUELO_Y_SU_ROL_INDISCUTIDO_EN_LA_NUTRICION_VEGETAL

[11] Edwards, C. A., & Arancón, N. Q. (2022, April 28). Interactions Between Earthworms, Microorganisms, and Other Invertebrates. Springer, 275-301. https://doi.org/10.1007/978-0-387-74943-3_9

[12] FAO. (2024, February 21). Agroecology Knowledge Center. Retrieved from ¿Qué es la agroecología?: https://www.fao.org/agroecology/overview/es/

[13] Fernández Bravo, J. A. (2010). Neurosciences and Mathematics Teaching. Ibero-American Journal of Education (51), 3-25. Retrieved April 05, 2024, from https://rieoei.org/historico/expe/3128FdezBravo.pdf

[14] FHIA. (2008). Advances in the study of the biology and habits of the blind hen (Phyllophaga obsoleta) in Honduras. San Pedro Sula, Honduras: FHIA. Retrieved April 26, 2024, from http://fhia.org.hn/dowloads/proteccion_veg_pdfs/hojatecnicaprotvegetal3fhia.pdf

[15] Huerta, E., Rodríguez Olan, J., Evia Castillo, I., Montejo Meneses, E., De la Cruz Mondragón, M., & García Hernández, R. (2005, Diciembre). The diversity of earthworms (annelida, oligochaeta) in the State of Tabasco, Mexico. University and Science, 21(42), 75-85. Retrieved April 27, 2024, from https://www.redalyc.org/pdf/154/15404203.pdf

[16] Jiménez Martínez, A. (2018). Formation of soil aggregates in the interaction of soil-root-endophytic microorganisms: micromorphology and image analysis. Tesis doctoral, Colegio de Posgraduados, Institución de Enseñanza e Investigación en Ciencias Agricolas, Montecillo. Retrieved April 27, 2024, from http://colposdigital.colpos.mx:8080/jspui/handle/10521/4146

[17] Lou, J., & González Oreja, J. A. (2012). Measuring biological diversity: beyond the Shannon index. Lilloana Zoological Act, 56(2), 3-14. Retrieved April 25, 2024, from https://www.lillo.org.ar/journals/index.php/acta-zoologica-lilloana/article/view/240

[18] Matienzo Brito, Y., Vázquez Moreno, L. L., & Simonetti, J. A. (2015). Complexity of the design and management of an urban agricultural production system and its relationship with the arthropod fauna. Veg Protection, 30, 171. Retrieved April 05, 2024, from http://scielo.sld.cu/pdf/rpv/v30s1/rpv148s15.pdf

[19] Morales Alonso, S. I., & Zamora Aviles, N. (2023, Julio-Agosto). Importance of entomophagous insects and entomopathogenic microorganisms for the agroecological management of agricultural pests and diseases. UANL Science, 26(120). https://doi.org/10.29105/cienciauanl26.120-4

[20] Morel, A., & Ortiz Acosta, O. (2022, March 8). Soil quality in different uses and management through macrofauna as a biological indicator. Brazilian Journal of Animal and Environmental Research, V(1), 996-1006. https://doi.org/10.34188/bjaerv5n1-074

[21] OIRSA. (2019). Action plan for the management of the Central American lobster. San Salvador, El Salvador: OIRSA. Retrieved April 04, 2024, from https://www.oirsa.org/contenido/2020/(17%20marzo2020)%20Plan%20de%20accio%CC%81n%20y%20atencio%CC%81n%20de%20brotes%20corregido%202.pdf

[22] Pimienta, M., & De Marco, P. (2015). Leaf Beetle (Chrysomelidae: Coleoptera) Assemblages in a Mosaic of Natural and Altered Areas in the Brazilian Cerrado. Ecology, Behavior and Bionomics, 44(1), 242-255. https://doi.org/10.1007/s13744-015-0280-y

[23] Politi, N., & Rivera, L. (2019, February 5). Limitations and progress to achieve sustainable forest management in the Southern Yungas. Southern Ecology, 29(1), 138-145. Retrieved April 25, 2024, from http://www.scielo.org.ar/scielo.php?pid=S1667-782X2019000100015&script=sci_arttext

[24] Pompozzi, G., Copperi, S., Schwerdt, L., & Ferretti, N. (2014). Ecology of the cursorial spider Odo bruchi (Araneae: Zoridae) in a natural grassland reserve in central Argentina. Journal of Tropical Biology, 62(1), 11-117. Retrieved April 25, 2024, from https://www.scielo.sa.cr/scielo.php?pid=S0034-77442014000200009&script=sci_abstract&tlng=es

[25] QGIS. (2024, February 21). QGIS. Retrieved February 21, 2024, from Elevation profile view: https://docs.qgis.org/3.28/es/docs/user_manual/map_views/elevation_profile.html

[26] Quijano, L., & Martínez H., N. (2015, July). Temporal variation of the araneofauna (Arachnida: Araneae) in a fragment of Tropical Dry Forest (BST), in the department of Atlántico, Colombia. Scientific Bulletin Museum Center Museum of Natural History, 19(2), 381-396. https://doi.org/10.17151/bccm.2015.19.2.24

[27] Roberge, J. M., & Angelstam, P. (2004). Usefulness of the Umbrella Species Concept as a Conservation Tool. Conservation Biology, 18(1), 76-85. https://doi.org/10.1111/j.1523-1739.2004.00450.x

[28] Rodríguez González, H. R. (2014). Agronomic evaluation with an agroecological approach in a diversified system of guava (Psidium guajava L.), cactus pear (Opuntia ficus L.), pineapple (Ananas comosus L.) and papaya (Carica papaya L.) using vermicompost, Managua, Nicaragua, 2009- 2011. Managua: National Agrarian University. Retrieved January 26, 2024, from https://repositorio.una.edu.ni/2206/1/tnf04r696a.pdf

[29] Rodríguez González, H. R., & Salazar Centeno, D. J. (2021). Agroecological heuristics: Xi (Ξ) biomathematical models of alpha diversity and Lambda functional entropy index (λ) applied for macrofauna in diversified agroecosystems of Nicaragua. Journal of Agriculture and Rural Development, 122(2). https://doi.org/10.17170/kobra-202112035149

[30] Rodríguez González, H. R., Salazar Centeno, D. J., & Jurgen Pohlan, H. A. (2022). Gangia Index (ϒ) of Beta Diversity and Biomathematical Equations Applied to Quantify the Agroecological Multifunctional Entropy: Macrofauna Observed in Agroecosystems of Nicaragua. Canadian Journal of Agriculture and Crops, 7(2), 78-97. https://doi.org/10.55284/cjac.v7i2.684

[31] Rodríguez Rodríguez, J. E. (2023). Aspergillus niger as a phosphate solubilizer and plant growth promoter of Solanum lycopersicum and Capsicum annuum. Coahuila, México: Antonio Narro Autonomous Agrarian University. Retrieved July 2, 2024, from http://repositorio.uaaan.mx:8080/xmlui/handle/123456789/49007

[32] Sánchez, S., & Reinés, M. (2001). Role of edaphic macrofauna in livestock ecosystems. Pastures and Forages, 24(3), 191-202. Retrieved February 22, 2024, from https://www.uv.mx/personal/tcarmona/files/2010/08/Sanchez-y-Reines-2001.pdf

[33] Sans, F. X. (2007). The diversity of agroecosystems. Ecosystems, 16(1), 44-49. Retrieved April 25, 2024, from https://www.revistaecosistemas.net/index.php/ecosistemas/article/view/137/134

[34] Sarandón, S., & Flores, C. (2014). Theoretical bases for the design and management of sustainable agroecosystems (First ed.). La PLata, Argentina: UNLP. https://doi.org/10.35537/10915/37280

[35] Scheu, S. (1987). Microbial activity and nutrient dynamics in worm excrement (Lumbricidae). Biol Fert Suelos, 5(1), 230-234. https://doi.org/10.1007/BF00256906

[36] Tejeda Cruz, C., Mehltreter, K., & Sosa, V. J. (2008). Multi-taxonomic ecological indicators. In R. H. Manson, V. Hernandez Ortiz, S. Gallina, & K. Mehltreter, Coffee agroecosystems of Veracruz, Biodiversity, Management and Conservation (pp. 271-278). México. Retrieved April 26, 2024, from https://d1wqtxts1xzle7.cloudfront.net/36844652/agrosistemas_cafetaleros_de_veracruz-libre.pdf?1425415319=&response-content-disposition=inline%3B+filename%3DAgrosistemas_cafetaleros_de_veracruz.pdf&Expires=1714186170&Signature=DXjnBrgwtUgNe-t-EbbNuvpTOSTVi

[37] USAID. (2017). Nicaragua Climate Risk Profile. Managua: USAID. Retrieved February 21, 2024, from https://www.climatelinks.org/sites/default/files/asset/document/2017_USAID_ATLAS_Climate%20Risk%20Profile%20-%20Nicaragua_Spanish.pdf

[38] Vieira, L., Nascimento, P. K., & Leivas, F. W. (2018, September 20). Habitat Association Promotes Diversity of Histerid Beetles (Coleoptera: Histeridae) in Neotropical Ecosystems. The Coleopterists Bulletin, 72(3), 541-549. https://doi.org/10.1649/0010-065X-72.3.541

[39] Zerbino, M. S. (2011). Chapter VI. Soil macrofauna and its relationship with floristic heterogeneity. In A. Altesor, W. Ayala, & J. M. Paruelo, Ecological and technological bases for grassland management (pp. 97-111). Montevideo, Uruguay, Uruguay: INIA. Retrieved June 7, 2024, from https://www.researchgate.net/profile/Maria-Zerbino/publication/264044534_La_macrofauna_del_suelo_y_su_relacion_con_la_heterogeneidad_floristica/links/53f485d00cf2fceacc6e881e/La-macrofauna-del-suelo-y-su-relacion-con-la-heterogeneidad-floristica.pdf#page=

Research Fields

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