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Multifractal and joint analysis of soil arthropod diversity in the Brazilian Savanna

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ABSTRACT: Soil fauna organisms participate in a series of processes that benefit the physical and chemical soil properties; however, little is known about their spatial variability and scale. This study aimed to characterize the spatial variability of soil fauna from multifractal and joint multifractal analysis in Brazilian Savanna areas. Pitfall traps collected soil fauna in two Savanna formations (dense Savanna and typical Savanna) in two transects with 128 points. Organisms were identified and classified into functional groups (Microphages, Pollinators, Predators and Social), and then Ind trap^{-1} day^{-1} (number of individuals per day in the sample) and Richness were determined. Data were analyzed using multifractal and joint multifractal analysis, and the scale indexes *f(α,β)* were generated for the singularity indexes of *α(q,t)* and *β(q,t)*, considering Ind trap^{-1} day^{-1} and Richness as predictive variables. A total of 3456 and 1629 individuals were collected from T1 (dense Savanna) and T2 (typical Savanna), respectively. The singularity spectrum for soil fauna showed the greatest difference in dimensions D_{-10}–D_{10} for the functional group Pollinator (D_{-10}–D_{10} = 0.936) in T1 and for Social (D_{-10}–D_{10} = 0.620) in T2, reflecting more heterogeneous systems. The joint multifractal dimension showed a high correlation between Ind trap^{-1} day^{-1} and the functional groups (Pollinators, Predators, and Social) in T1, demonstrating how phytophysiognomy of this experimental plot (dense Savanna) favors the presence of these organisms and reflects the spatial correspondence of the measurement values along the geometric support. Abundance of organisms (Ind trap^{-1} day^{-1}) and Richness were promising variables to represent the set of relationships with the functional groups of soil invertebrate fauna. In general, multifractal analysis using abundance and Richness can assist in decision-making focused on conserving Savanna areas.

Keywords: multifractal dimension, joint multifractal dimension, soil arthropod, spatial variability scales, Oxisols.

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INTRODUCTION

In Brazil, Savanna areas cover 22 % of the national territory (Eiten, 1977; IBGE, 2012), corresponding to an area of 2,036,448 km^2 (MMA, 2020). Brazilian Savanna comprises different ecotones, including forest formations, typical Savannas, and Savanna fields (Ribeiro and Walter, 2008), representing an important hotspot of biological diversity (Araujo et al., 2021). In recent years, the Brazilian Savanna has suffered exceptional habitat loss (MMA, 2020) due to the expansion of agricultural frontiers in this region.

Around 56 % of Brazil's Savanna areas have already been converted to agricultural use, impacting soil biota organisms (Pompermaier et al., 2020). Soil fauna comprises a diversity of organisms that occupy different trophic levels (Roy et al., 2018) and are responsible for decomposition (Aubert et al., 2003; Bernardes et al., 2020), nutrient cycling (Martins et al., 2018; Silva et al., 2019), and soil structure (Bernardes et al., 2020). Soil organisms can be grouped as follows: according to their functionality (Siqueira et al., 2022); into organisms related to the process of decomposition and fragmentation of biological material in the soil–litter system (Aubert et al., 2003; Maggiotto et al., 2019); organisms closely linked to plant interactions, using them to obtain resources and making resources available for other interactions (Roy et al., 2018); organisms that regulate populations through prey–predator dynamics, occupying higher trophic levels (Siqueira et al., 2022); and organisms with aggregate behavior, which actively act in soil aggregation (Bernardes et al., 2020).

Given the importance of soil organisms, the decrease of soil biota affects the multifunctionality of ecosystems (Wagg et al., 2014), presenting greater spatial variability in the landscape (Gholami et al., 2017), and is positively or negatively affected by the use and coverage of soil (Silva et al., 2019; Bernardes et al., 2020). Soil fauna organisms should be studied on different spatial scales, allowing for the description and understanding of organisms communities functionality and dynamics that make up the soil system.

Variability is composed of variations and fluctuations in measures in the landscape (Goovaerts, 1998). Intrinsic variability of a variable depends on the observation scale and that the variations; and fluctuations of measures increase with the increase in the observation scale (Logsdon et al., 2008). Soil properties intrinsic variability depends on spacing, number of samples, sample size, and whether the measure being evaluated on a horizontal or vertical scale. For this reason, it is necessary to determine the variability of measurement values on different scales.

Fractal theory (Zeleke and Si, 2005, 2006; Caniego et al., 2006; Biswas et al., 2012; Siqueira et al., 2018; Silva et al., 2021; Siqueira et al., 2022) is an important tool for quantifying and characterizing spatial variability on different scales, allowing for an understanding of spatial heterogeneity (Biswas et al., 2012), regardless of the observation scale (Saravia et al., 2012). However, the multifractal methodology considers heterogeneity on multiple scales (Vidal-Vázquez et al., 2010; Biswas et al., 2012; Dafonte et al., 2015), characterizing the spatial distribution of a variable at different times of a statistical order (Peitgen et al., 1992; Caniego et al., 2006) and thus provides information about the heterogeneity of the variable on successive scales (Halsey et al., 1986; Biswas et al., 2012; Vidal-Vázquez et al., 2013; Silva et al., 2021).

Multifractal methodology has been used in soil science mainly to understand the spatial and scale variability of physical (Paz-Ferreiro et al., 2010; Vidal-Vázquez et al., 2010; Bertol et al., 2017; Siqueira et al., 2022) and chemical properties (Caniego et al., 2006; Biswas et al., 2012; Dafonte et al., 2015; Paz-Ferreiro et al., 2018; Siqueira et al., 2018). However, there is a knowledge gap regarding the scale variability for soil biological properties. Evaluating the multifractality of biological communities in a meadow, Yakimov et al. (2014) found species richness of natural pastures had different degrees of scale heterogeneity, which was influenced by the sample size. Studying species richness using multifractal

models, Yakimov et al. (2018) and Siqueira et al. (2022) found systems were influenced by the diversity and abundance of the species, describing differences in the degrees of heterogeneity or multifractality of the systems. Characterizing the invertebrate fauna in different systems of land-use and occupation, Silva and Siqueira (2020) and Siqueira et al. (2022) studied soil fauna and found the degree of heterogeneity or multifractality of the systems was influenced by a decrease in species richness in systems with greater use and management of the soil. In this sense, more studies involving multifractal methodology, including joint multifractal analysis, are needed to elucidate the diversity and spatial variability of soil invertebrate fauna on different scales.

Joint multifractal analysis allows for the joint characterization of different variables (Zeleke and Si, 2006; Banerjee et al., 2011; Biswas et al., 2012; Bertol et al., 2017; Siqueira et al., 2018, 2022). This is possible because joint multifractal analysis provides information about the association of measurement values of two variables in a geometric support, considering the spatial or temporal scale (Siqueira et al., 2018, 2022), in which $\alpha(q,t)$ and $\beta(q,t)$ singularity indices are generated for the measured values (Banerjee et al., 2011; Biswas et al., 2012). Joint multifractal distribution has already been used to characterize patterns of spatial variability in the physical and chemical soil properties (Zeleke and Si, 2005, 2006; Bertol et al., 2017; Siqueira et al., 2018) and for parameters related to crop yield (Kravchenko et al., 2000; Banerjee et al., 2011).

In general, it is necessary to understand soil fauna in multiple spheres and interactions and the parameters used to characterize it. Species richness is the most common metric for measuring diversity in a community or area of interest, as it directly quantifies the groups in the sample, providing a measured value to the database (Magurran, 2019), not attributing entropy to the system (Salat et al., 2017), and considering with equal importance the set of abundant and rare species present in the community (Magurran, 2019). Coupled with species richness, organisms abundance constitutes, in principle, the first inference about a biological community, in which it is possible to characterize the various organisms in terms of composition and distribution in a community (Silva et al., 2013). Furthermore, soil fauna can be characterized into functional categories through group functionality, interactions exercised in the environment, and services provided (Roy et al., 2018; Maggiotto et al., 2019). In addition to the intrinsic variability of soil invertebrate fauna, other processes interfere with these metric patterns, such as anthropic interference, use, management, and soil occupation (Siqueira et al., 2014; Martins et al., 2018; Silva et al., 2018; Bernardes et al., 2020).

Many studies have been concerned with understanding soil fauna interactions, mainly through richness and abundance (Gholami et al., 2017; Martins et al., 2018; Silva et al., 2018, 2019; Bernardes et al., 2020); however, little has been said about the determination of soil fauna spatial variability using multifractal methods. Thus, we tried to answer the following hypotheses: (1) the distribution and association of the richness and abundance of soil invertebrates can be determined using multifractal and joint multifractal analyses; and (2) the complexity of the functional groups of the soil fauna can present different degrees of multifractality. This study aimed to characterize the spatial variability of soil invertebrate fauna in Brazilian Savanna areas through the richness, abundance, and functionality of the soil fauna using multifractal and joint multifractal tools.

MATERIALS AND METHODS

Area of study

The study area covers 107.92 ha and is located in the municipality of Chapadinha (state of Maranhão, Brazil), whose geographic coordinates are 3° 73’ 34.68” S and 43° 32’ 03.12” W (Figure 1). The vegetation in the area is characterized as Savanna, and in Brazil, it comprises different phytophysiognomies known as the Cerrado (IBGE, 2012). These

phytophysiognomies comprise formations such as Savanna forests, typical Savanna, and Savanna fields (Ribeiro and Walter, 2008).

The climate is tropical hot and humid (Aw), with two well-defined seasons, a rainy season from December to May and a dry season from June to November, with an average temperature ranging from 27 to 30 °C and an average annual precipitation of 1600 mm (Silva et al., 2019). The relief of the region is smooth undulating, with an average altitude of 100 m, and the soil is classified as *Latossolo* (Santos et al., 2018), which corresponds to an Oxisol (Soil Survey Staff, 2014). Soil physical and chemical properties were determined according to Teixeira et al. (2017) and are shown in table 1.

Biological diversity

Biological diversity was sampled over two transects in an area with a Brazilian Savanna (Figure 1). Transect 1 (T1) was installed in an area with dense Savanna vegetation, with 1.605 trees ha^{-1}, and abundant bush/undergrowth; transect 2 (T2) represented the typical Savanna, with a predominance of undergrowth and sparse trees (0.467 trees ha^{-1}).

Soil invertebrate fauna sampling was carried out on 11/14/2014, in the transition period between the dry and rainy seasons. A total of 128 pitfall traps were installed in each of the two experimental plots (T1 and T2; total of 256 points), with a 3 m spacing between traps and a total transect length of 381 m. Each trap remained in the field for seven days and contained 4 % formaldehyde solution for the conservation of organisms (Aquino, 2001; Siqueira et al., 2014; Silva et al., 2018). In a laboratory, soil arthropods

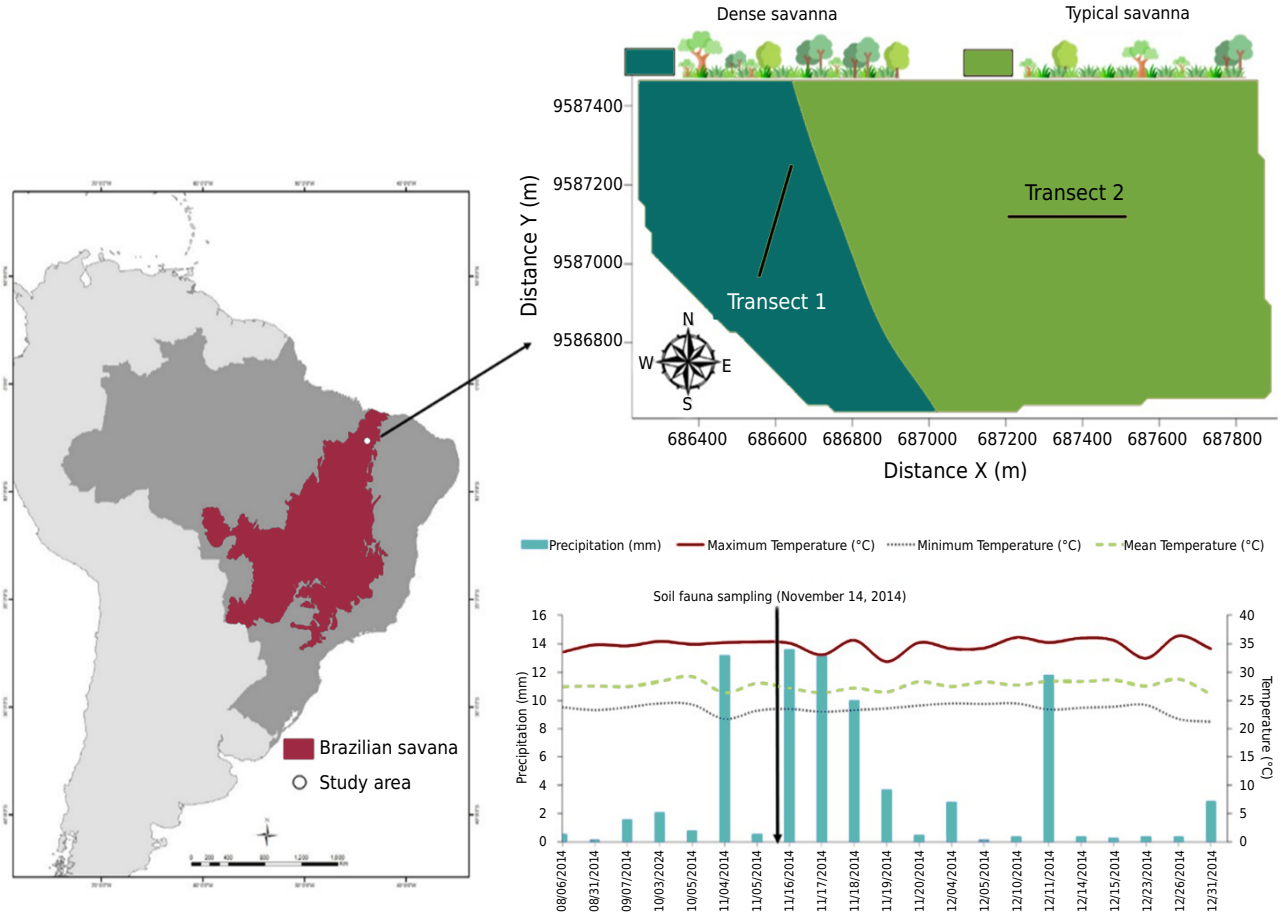

Figure 1. Map of the study area, vegetation formations (dense Savanna and typical Savanna) for transects 1 and 2, and meteorological parameters during the sampling period.

Table 1. Physical and chemical characterization of the superficial soil layer (0.00-0.20 m) in the experimental plots located in the municipality of Chapadinha (Maranhão, Brazil)

Experimental plots	Clay	Silt	Sand	OC	pH($CaCl_2$)	P	K^+	Ca^{2+}	Mg^{2+}	SB	CEC	V%
	%			g dm^{-3}		mg dm^{-3}	$mmol_c$ dm^{-3}					
Transect 1 (T1)	8	6	86	20	4.3	2	2.1	9	7	21.8	52.0	42.0
Transect 2 (T2)	16	6	78	12	4.3	5	3.7	6	4	19.8	48.4	40.9

OC: organic carbon; P: phosphorus; K: potassium; Ca: calcium; Mg: magnesium; SB: sum of bases; CEC: cation exchange capacity; V%: base saturation.

were screened and identified at the level of order, suborder, family, subfamily, and immature organism–larvae (Aquino, 2001; Rafael et al., 2012; Roy et al., 2018). Formicidae family was removed from the order Hymenoptera due to the ecological relationships established by ants in the environment, such as aggregate behavior and the diversity of trophic guilds. For T1, there was no capture of organisms for points 27 and 64; for T2, there was no capture of organisms for points 8, 14, 15, 62, 126, and 127.

Using invertebrate soil fauna data, we determined organisms abundance for the period in which the traps remained in the field (Ind $trap^{-1}$ day^{-1}) and the richness of taxonomic groups present at each of the sample points (Richness). Relative abundance was calculated as the number of organisms at each point divided by the total number of individuals in the transect sample.

Soil organisms were also grouped according to their functionality in the environment, following the methodology of Silva et al. (2013) and Maggiotto et al. (2019): Microphages (Acari, Archaeognatta, Aucheonorrhyncha, Blattodea, Dermaptera, Diplopoda, Entomobryomorpha, Gastropoda, Coleoptera larva, Formicidae larva, Trichoptera, and Zygentoma); Pollinators (Hymenoptera and Lepidoptera); Predators (Araneae, Coleoptera, Diplura, Diptera, Diptera Larva, Neuroptera, Opillionida, Orthroptera, and Scorpionida); Social (Formicidae and Isoptera); and Others (Heteroptera, Sternorrhyncha and Thysanoptera). Functional groups were classified according to the dataset for each transect and represented the real values of individuals at the sample points.

Descriptive statistics

The main statistical moments determined for the data under study were the mean, coefficient of variation (CV, %), asymmetry, kurtosis, and the maximum deviation in relation to the normal distribution (D-KS) using the Kolmogorov–Smirnov test, at an error probability of 0.01. Although it is important to characterize the frequency distribution of organisms along the transects to determine the normality of the data, this is not a requirement for multifractal analysis; multifractal analysis only requires that the data present values distribution in successive segments and that they obey a power law, as reported by Mandelbrot (1982).

Multifractal analysis

The number of samples along the transect was defined considering that the geometric support (L = 381 m) represented successive segments of size 2^k, thus allowing the geometric support to be divided into segments with known size, and that each segment was filled by samples decomposed from the total number of sample points at k = 0 to k = 7 (Halsey et al., 1986; Peitgen et al., 1992; Vidal Vázquez et al., 2013). In this way, successive partition functions generated for the segments in stages (k = 1, 2, 3 ...), were considered on a scale δ, to a segment of number, $N(\delta) = 2^k$ of characteristic length for $\delta = L \times 2^{-k}$.

Multifractal properties of the soil fauna attributes were converted into a mass distribution for the segments, considering the values for the biological attributes at the sampling points as representative, within a radius of 3 m around the sampling point. The normalized

mass function $p_i(\delta)$ ou $\mu_i(\delta)$, is a variable that describes the contribution of a segment or subintervals of size δ to the total mass (Equation 1).

$$p_i(\delta) = \varphi_i(\delta) / \sum_{i=1}^{n(\delta)} \varphi_i(\delta) \quad \text{Eq. 1}$$

in which: φ_i corresponds to the value of the measurement in the i-th scale segment δ; $n(\delta)$ corresponds to the number of segments with size δ, which covers the sample space; and $\sum_i^{n(\delta)} \varphi_i(\delta)$ represents the total mass of the entire transect under study.

The $\chi(q,\delta)$ partition function was estimated using the moment method (Evertsz and Mandelbrot, 1992), according to equation 2.

$$\chi(q,\delta) = \sum_{i=1}^{n(\delta)} [p_i(\delta)]^q \quad \text{Eq. 2}$$

in which: $n(\delta)$ corresponds to the number of segments with size δ, whose statistical moments q are defined for $-\infty < q < +\infty$. In this case, when shown graphically in relation to the size of the box, the partition function has the scale property expressed in equation 3.

$$\chi(q,\delta) \propto \delta^{-\tau(q)} \quad \text{Eq. 3}$$

in which: $\tau_{(q)}$ corresponds to a nonlinear function of q, known as a mass exponent function. The $\tau_{(q)}$ function is obtained from a graph $\chi(q,\delta)$ versus δ for the different values of q. When measurements are multifractal, non-linear function $\tau_{(q)}$ is adjusted, and for monofractal measurements, a linear function $\tau_{(q)}$ occur.

The generalized dimension Dq or Rényi dimension of the q order, Dq (Hentschel and Procaccia, 1983), was estimated by the moment method (Evertsz and Mandelbrot, 1992; Equation 4) for $q \neq 1$. When $q = 1$, D_1 becomes undetermined due to the denominator value being zero. For this particular case, when $q = 1$, Dq is obtained by the l'Hôpital rule according to equation 5.

$$D_q = \frac{1}{q-1} \lim_{\delta \to 0} \frac{\log[x(q,\delta)]}{\log \delta} = \frac{\tau(q)}{q-1}, \text{ when } q \neq 1 \quad \text{Eq. 4}$$

$$D_1 = \lim_{\delta \to 0} \frac{\sum_{i=1}^{n(\delta)} \mu_i(\delta) \log x(q,\delta)]}{\log \delta}, \text{ when } q \neq 1 \quad \text{Eq. 5}$$

Thus, for generalized dimensions, Dq for $q = 0$, $q = 1$, and $q = 2$ are named capacity dimension (D_0), Shannon entropy or entropy dimension (D_1), and correlation dimension (D_2), respectively.

For continuity, the scale functions were calculated using the Legendre transformation: $f(\alpha) = q(\alpha q) - \tau_{(q)}$ e $\alpha_q = d\tau_{(q)}/d_q$. In practice, the Legendre transformation has several disadvantages, such as higher error in the estimation of $f(\alpha)$ and α in negative moments. In this case, the direct method of Chhabra and Jensen (1989) is used more frequently. For the use of Chhabra and Jensen (1989), it is necessary to use the modified partition function χ (q, δ), in which the normalized generating function is obtained in $\mu_i(q, \delta)$ and defined by equation 6:

$$\mu_i(q,t) = \mu_i^q(\delta) / \sum_{i=1}^{n(\delta)} \mu_i^q(\delta) \quad \text{Eq. 6}$$

The singularity spectrum is represented by a graph of *f (α)* versus α, having a parable shape for multifractal (heterogeneous) systems. In a homogeneous monofractal system, the graphical representation of *f (α)* versus α has a spectrum reduced to a point (Siqueira et al., 2018). For multifractal spectra, the heterogeneity of the scale and the parable amplitude were estimated using equations 7 and 8.

$$\alpha(q) \propto \frac{\sum_{i=1}^{n(\delta)} \mu_i(q,\delta)\log[\mu_i(\delta)]}{\log(\delta)} \quad \text{Eq. 7}$$

$$f(\alpha(q)) = \propto \frac{\sum_{i=1}^{n(\delta)} \mu_i(q,\delta)\log[\mu_i(q,\delta)]}{\log(\delta)} \quad \text{Eq. 8}$$

For this study, the generalized dimension spectrum, *Dq,* was calculated for the statistical moments –10 ≤ q ≤ +10 at 2.0 lag increments, with determination coefficients R^2 ≥0.90.

Analysis of the joint partition functions was performed for the total length (L = 381 m), which was divided into boxes of size *δ,* in which the partitions were obtained (Bertol et al., 2017). Joint analysis is a tool used to characterize two variables at various scales of measurement in *p* and *r*, which are partitioned into *δ.* These variables (*p* and r) are defined as $p_i(\delta)$ and $r_i(\delta)$, and their exponents are related to *α* and *β*, maintaining the ratio of $p_i(\delta)$ and $r_i(\delta)$, with normalized partition function, $\mu_i(q,t,\delta)$. The joint distribution function, $p_i(\delta)$ and $r_i(\delta)$, was calculated according to equation 9.

$$\mu_i(q,t,\delta) = \frac{[p_i(\delta)]^q [r_i(\delta)]^t}{\sum_{i=1}^{n(\varepsilon)} [p_i(\delta)]^q [r_i(\delta)]^t} \quad \text{Eq. 9}$$

in which: *q* and *t* correspond to real numbers that represent the moment orders, and δ is the scale. Based on the contribution of intervals for each segment, the singularity indexes α *(q,t) and β (q,t)* were calculated in relation to the μi measure (Equations 10 and 11) (Zeleke and Si, 2006).

$$\alpha(q,t) = \lim_{\varepsilon \to 0} \frac{\sum_{i=1}^{n(\varepsilon)} [\mu_i(q,t,\delta) \cdot \log p_i(\delta)]}{\log \delta} \quad \text{Eq. 10}$$

$$\beta(q,t) = \lim_{\varepsilon \to 0} \frac{\sum_{i=1}^{n(\varepsilon)} [\mu_i(q,t,\delta) \cdot \log r_i(\delta)]}{\log \delta} \quad \text{Eq. 11}$$

Joint multifractal analysis

The dimension of the joint, *f* (α,β*)*, was determined for the set in which α (*q,t)* and β (*q,t)* represent the average of the measure's singularity under study (Biswas et al., 2012), following equation 12.

$$f(\alpha,\beta) = \lim_{\varepsilon \to 0} \frac{\sum_{i=1}^{n(\varepsilon)} [\mu_i(q,t,\varepsilon) \cdot \log(q,t,\varepsilon)]}{\log \varepsilon} \quad \text{Eq. 12}$$

Multifractal spectra graphs were constructed using the function *f*(*α*,*β*) in *α*(*q*,*t*) and *β*(*q*,*t*), which describe the intensity level distribution of a variable in contrast to another analyzed variable (Bertol et al., 2017).

Relationship between the biological variables under study was assessed by Pearson's linear correlation ($p<0.01$ and $p<0.05$). Pearson's linear correlation was also used to assess singularity indexes α(*q,t)* and β(*q,t)*, which were obtained through the joint multifractal analysis at a significance of $p<0.01$ and $p<0.05$ for the biological variables that from now on will be termed joint correlation.

Table 2. Taxonomic groups, relative abundance, number of points with occurrence of individuals (N), and rate of sample positivity (%) of soil fauna in Savanna transects

Taxonomic groups	Transect 1			Transect 2		
	Abundance	N	%	Abundance	N	%
PHYLUM MOLLUSCA						
Class Gastropoda	33	3 (2.34)	0.95	-	-	-
PHYLUM ARTHROPODA						
SUBPHYLUM MYRIAPODA						
Class Diplopoda	3	3 (2.34)	0.09	-	-	-
SUBPHYLUM CHELICERATA						
Class Arachnida						
Order Acari	14	14 (10.93)	0.41	4	4 (3.12)	0.25
Order Araneae	64	44 (34.37)	1.85	95	45 (35.15)	5.83
Order Opillionida	-	-	-	2	2 (1.56)	0.12
Order Scorpionida	-	-	-	5	3 (2.34)	0.31
SUBPHYLUM HEXAPODA						
Order Entomobryomorpha	1	1 (0.78)	0.03	-	-	-
Order Diplura	44	22 (17.18)	1.27	16	4 (3.12)	0.98
Class Insecta						
Order Archaeognatha	1	1 (0.78)	0.03	-	-	-
Order Zygentoma	9	6 (4.68)	0.26	-	-	-
Order Orthoptera	6	6 (4.68)	0.17	23	15 (11.71)	1.41
Order Dermaptera	4	4 (3.12)	0.12	-	-	-
Order Isoptera	97	9 (7.03)	2.81	7	5 (3.90)	0.43
Order Blattaria	4	4 (3.12)	0.12	1	1 (0.78)	0.06
Order Hemiptera						
Suborder Aucheonorrhyncha	8	7 (5.46)	0.23	-	-	-
Suborder Heteroptera	9	6 (4.68)	0.26	2	2 (1.56)	0.12
Suborder Sternorrhyncha	4	2 (1.56)	0.12	-	-	-
Order Thysanoptera	13	2 (1.56)	0.38	-	-	-
Order Coleoptera	69	37 (28.90)	2.00	239	53 (41.40)	14.67
Order Neuroptera	1	1 (0.78)	0.03	-	-	-
Order Hymenoptera	1517	116 (90.62)	43.89	605	108 (84.37)	37.14
Family Formicidae	1479	116 (90.62)	42.80	607	95 (74.21)	37.26
Order Trichoptera	6	4 (3.12)	0.17	-	-	-
Order Lepidoptera	1	1 (0.78)	0.03	-	-	-
Order Diptera	27	6 (4.68)	0.78	12	6 (4.68)	0.74
Immature organism						
Larva Coleoptera	2	2 (1.56)	0.06	1	1 (0.78)	0.06
Larva Diptera	32	5 (3.90)	0.93	-	-	-
Larva Formicidae	8	6 (4.68)	0.23	10	6 (4.68)	0.61
Functional groups						
Microphages	93	37 (28.90)	-	16	11 (8.59)	-
Pollinators	1518	116 (90.62)	-	605	110 (85.93)	-
Predators	243	85 (66.40)	-	392	89 (69.53)	-
Social	1576	121 (94.53)	-	614	109 (85.15)	-
Others	26	20 (15,62)		2	2 (1.57)	
Total	3,456	-	100 %	1,629	-	100 %
Richness	26	-	-	15	-	-
Number of points with individual	126*	-	-	122**	-	-

* In T1, no individuals were collected from points 27 or 64. In T2, no individuals were collected from points 8, 14, 15, 62, 126, or 127.

Table 3. Descriptive statistics of the diversity indexes of soil fauna in two transects in the Savanna biome

Parameters	Mean	CV	Skewness	Kurtosis	D-KS*
			%		
			T1		
Ind trap^{-1} day^{-1}	3.850	84.150	1.430	2.084	0.137n
Richness	5.990	38.510	0.710	1.490	0.202Ln
Microphages	0.727	298.017	5.848	39.161	0.368Ln
Pollinators	11.859	126.656	2.804	11.168	0.215Ln
Predators	1.898	151.281	2.609	7.079	0.286Ln
Social	12.313	95.745	2.254	8.125	0.173Ln
Others	0.203	328.00	5.988	39.256	0.369Ln
			T2		
Ind trap^{-1} day^{-1}	1.810	85.150	1.610	3.360	0.165Ln
Richness	5.630	46.510	0.110	0.500	0.167Ln
Microphages	0.125	155.032	3.441	15.174	0.259Ln
Pollinators	4.726	342.544	3.808	15.100	0.521Ln
Predators	3.062	95.060	2.164	5.255	0.247Ln
Social	4.796	109.636	2.393	7.296	0.228Ln
Others	0.015	399.200	4.200	7.540	0.332Ln

Ind trap^{-1} day^{-1}: Individuals trap^{-1} day^{-1}, CV%: Coefficient of variation; Ln: Lognormal; D-KS*: Kolmogorov–Smirnov normality test, 0.01%.

RESULTS

Taxonomic and functional groups

A total of 3,456 individuals were collected at T1 and distributed in 26 taxonomic groups, and 1,629 individuals were collected at T2 and distributed in 15 taxonomic groups (Table 2). Collected organisms were grouped according to their functionality in Microphages, Pollinators, Predators, Social, and Others (Table 2). Social functional groups (1,576 and 614 individuals in T1 and T2, respectively) and Pollinators (1518 and 605 individuals in T1 and T2, respectively) were the most abundant. Social organisms (Isoptera and Fomicidae) showed a positivity rate of 94.53 % for the organisms collected in T1 and 85.15 % in T2, where almost all organisms were represented by Formicidae.

Descriptive statistics

Mean values for Ind trap^{-1} day^{-1} and Richness indices were 3.850 and 5.990, respectively, in T1; and 1.810 and 5.630, respectively, in T2 (Table 3). Social organisms were the functional group with the highest average occurrence (12.313 in T1 and 4.796 in T2), followed by Pollinators (11.859 in T1 and 4.726 in T2), Predators (1.898 in T1 and 3.062 in T2), Microphages (0.727 in T1 and 0.125 in T2), and Others (0.203 in T1 and 0.015 in T2).

Kolmogorov–Smirnov test (D-KS, $p<0.01$) demonstrated all attributes under study had a lognormal frequency distribution (Ln), except Ind trap^{-1} day^{-1} in T1, which showed a normal frequency distribution.

Multifractal analysis

Multifractal analysis was carried out considering the total length of the transects (381 m), with a partition function, $\chi(q,\delta)$ (Figure 2), built for the successive segments of 2^k in $k = 0$ to $k = 7$ and moments of order $-10< q <10$ (Peitgen et al., 1992), with an interval for 2.0 scales. For both transects, seven variables were evaluated using multifractal analysis; however, in T1, five variables presented multifractality (Ind trap^{-1} day^{-1}, Richness, Pollinators, Predators, and Social), and for T2, three variables showed multifractality (Ind trap^{-1} day^{-1}, Richness, and Social). The partition functions with the highest coefficient of determination (R^2) (Figure 2) corresponded to the Richness in T1 and T2 ($R^2 = 0.999$) (Figures 2a and 2b).

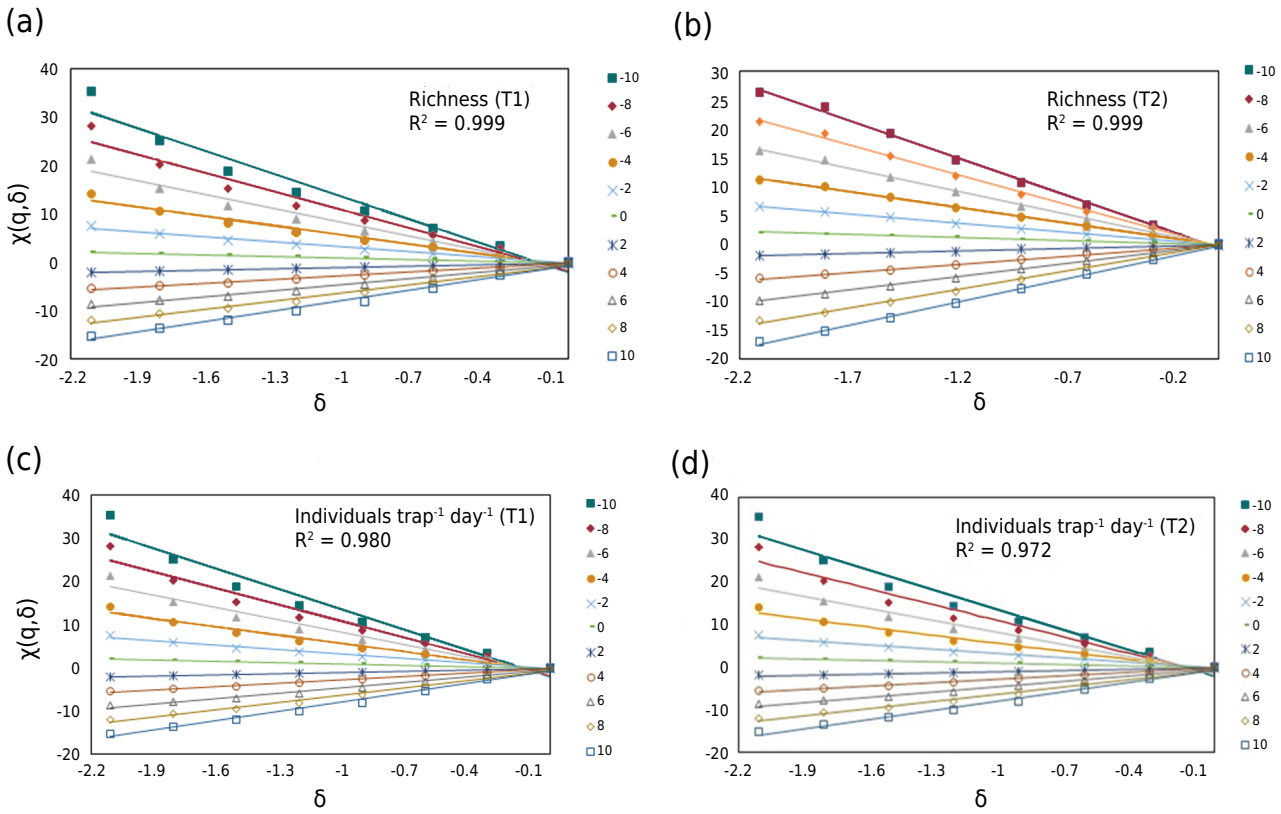

Figure 2. Partition function for the indexes of soil fauna. Richness in T1 (a) and T2 (b) individuals trap^{-1} day^{-1} in T1 (c) and T2 (d).

Generalized dimensions, *Dq* or Rényi dimension (Peitgen et al., 1992; Hentschel and Procaccia, 1983), are presented in table 4 and were estimated by the moment method, according to Evertsz and Mandelbrot (1992). The capacity dimension (D_0) provides global or average information about the system, indicating the segments have a mass value; that is, it represents the exponent of scale for the segments, computing the presence or absence of values through the sampling points. The lowest value of D_0 (Table 4) for the plots was described for the functional groups Predators (D_0 = 0.936 ± 0.024 in T1) and Social (D_0 = 0.976 ± 0.009 in T2), and the highest value was described for Ind trap^{-1} day^{-1} (D_0 = 0.997 ± 0.001 in T1 and D_0 = 0.991 ± 0.003 in T2), followed by Richness (D_0 = 0.996 ± 0.002 in T1 and D_0 = 0.990 ± 0.003 in T2).

The lowest value for the information dimension (D_1) was described for Predators (D_1 = 0.930 ± 0.020) at T1 and for Ind trap^{-1} day^{-1} (D_1 = 0.940 ± 0.014) at T1, and the highest values of D_1 was described for Richness in T1 and T2 (D_1 = 0.984 ± 0.004 and D_1 = 0.974 ± 0.005, respectively). Information of dimension (D_1) is related to Shannon's entropy information and quantifies the degree of disorder present in a distribution, and it must be in the range $0< D_1 <1$. In this way, when the D_1 value is close to 1, the system is uniformly distributed across all scales, while values lower than 1 describe a subset of scales with concentrated irregularities (Posadas et al., 2009; Vidal-Vázquez et al., 2013).

Difference between D_{-10} and D_{10} was lower for Richness in T1 and T2 (D_{-10}–D_{10} = 0.204 and D_{-10}–D_{10} = 0.276), and the highest values of D_{-10}–D_{10} were described for Pollinators in T1 (D_{-10}–D_{10} = 0.936) and for the Social group in T2 (D_{-10}–D_{10} = 0.620).

Singularity spectra (α_0, α_{-10}, α_{10}, $\Delta_{\alpha L}$, $\Delta_{\alpha R}$) (Table 4 and Figure 3) demonstrated the scale properties of the data represented multifractal systems. System asymmetry was evaluated by considering $\Delta_{\alpha L}$ (α_0–α_{10}) and $\Delta_{\alpha R}$ (α_0–α_{-10}). Hölder exponent (α_0) is a parameter that quantifies the average degree of mass density of the measure obtained from the statistical distribution of the singularity spectrum (Paz-Ferreiro et al., 2010), while α_{-10} describes the minimum value for function *f(α)* versus function α of the singularity spectrum, and

Table 4. Multifractal parameters obtained for the partition function, generalized dimension (D_{10}, D_0, D_1, D_2, and D_{-10}), and singularity spectrum (q_+, q_-, α_0, α_{min}, and α_{max}) of soil fauna

Variables		D_{-10}	D_0	D_1	D_2	D_{10}	D_{-10}-D_{10}	q_+	q_-	α_0	α_{-10}	α_{10}	$\Delta\alpha_L$	$\Delta\alpha_R$
T1	Ind trap^{-1} day^{-1}	1.489± 0.086	0.997± 0.001	0.940± 0.012	0.898± 0.019	0.758± 0.032	0.731	6	−2	1.066± 0.026	1.460± 0.183	0.724± 0.072	0.342	−0.394
	Richness	1.106± 0.025	0.996± 0.002	0.984± 0.004	0.973± 0.006	0.902± 0.016	0.204	10	0	1.007± 0.003	1.125± 0.058	0.864± 0.014	0.143	−0.118
	Pollinators	1.585± 0.101	0.985± 0.006	0.975± 0.005	0.826± 0.032	0.649± 0.052	0.936	2	0	1.110± 0.021	1.111± 0.021	0.771± 0.084	0.339	−0.001
	Predators	1.174± 0.089	0.936± 0.024	0.930± 0.020	0.754± 0.018	0.610± 0.019	0.564	4	−2	1.024± 0.064	1.171± 0.145	0.599± 0.040	0.425	−0.147
	Social	1.496± 0.084	0.990± 0.003	0.980± 0.002	0.876± 0.024	0.709± 0.053	0.787	2	0	1.071± 0.023	1.172± 0.023	0.830± 0.065	0.342	−0.101
T2	Ind trap^{-1} day^{-1}	1.378± 0.077	0.991± 0.003	0.940± 0.014	0.902± 0.021	0.787± 0.041	0.591	8	−10	1.052± 0.020	1.409± 0.178	0.772± 0.088	0.280	−0.347
	Richness	1.180± 0.027	0.990± 0.003	0.974± 0.005	0.961± 0.006	0.904± 0.017	0.276	10	−4	1.008± 0.007	1.213± 0.068	0.875± 0.046	0.133	−0.205
	Social	1.328± 0.056	0.976± 0.009	0.960± 0.003	0.854± 0.029	0.708± 0.048	0.620	2	−2	1.046± 0.012	1.319± 0.109	0.804± 0.074	0.515	−0.273

Ind trap^{-1} day^{-1}: Individuals trap^{-1} day^{-1}.

α_{10} represents the maximum value of *f(α)* versus α for the singularity spectrum. The functional groups Predator and Social showed a singularity spectrum with an elongated branch to the left ($\Delta_{\alpha L}$ = 0.425 and $\Delta_{\alpha L}$ = 0.515 in T1 and T2, respectively), and the abundance of organisms (Ind trap^{-1} day^{-1}) presented a spectrum of singularity with an elongated branch to the right ($\Delta_{\alpha R}$) in T1 ($\Delta_{\alpha R}$ = −0.394) and T2 ($\Delta_{\alpha R}$ = −0.347).

Joint multifractal analysis

Graphs for the joint multifractal distribution (Figures 4 and 5) were obtained from the joint dimensions of *f*(α,β), in which the singularity indexes α(*q,t)* and β(*q,t)* are presented on the horizontal and vertical axes, respectively. Scale indexes [α(*q,t*) and β(*q,t*)] for the biological attributes under study were evaluated considering the linear (simple) correlation and the joint correlations by Pearson's correlation with significance considered at p<0.01 and p<0.05. Joint multifractal analysis was performed considering Ind trap^{-1} day^{-1} and Richness as fixed variables on the [*α(q,t)*] axis to assess the association with the functional groups of soil fauna on [*β(q,t)*].

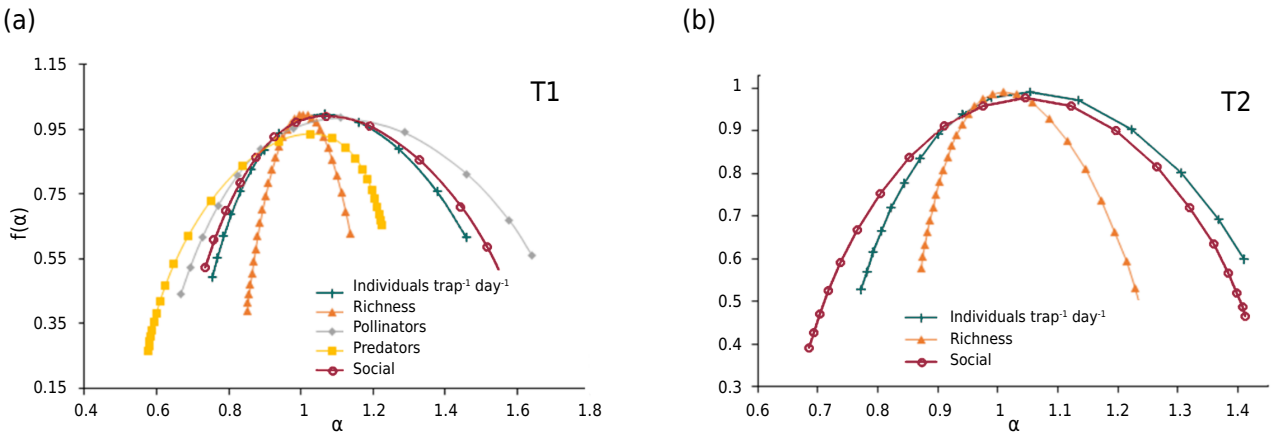

Figure 3. Spectrum of the singularity of soil fauna. Individuals trap^{-1} day^{-1}, Richness, Pollinators, Predators, and Social in T1 (a) and Individuals trap^{-1} day^{-1}, Richness, and Social in T2 (b).

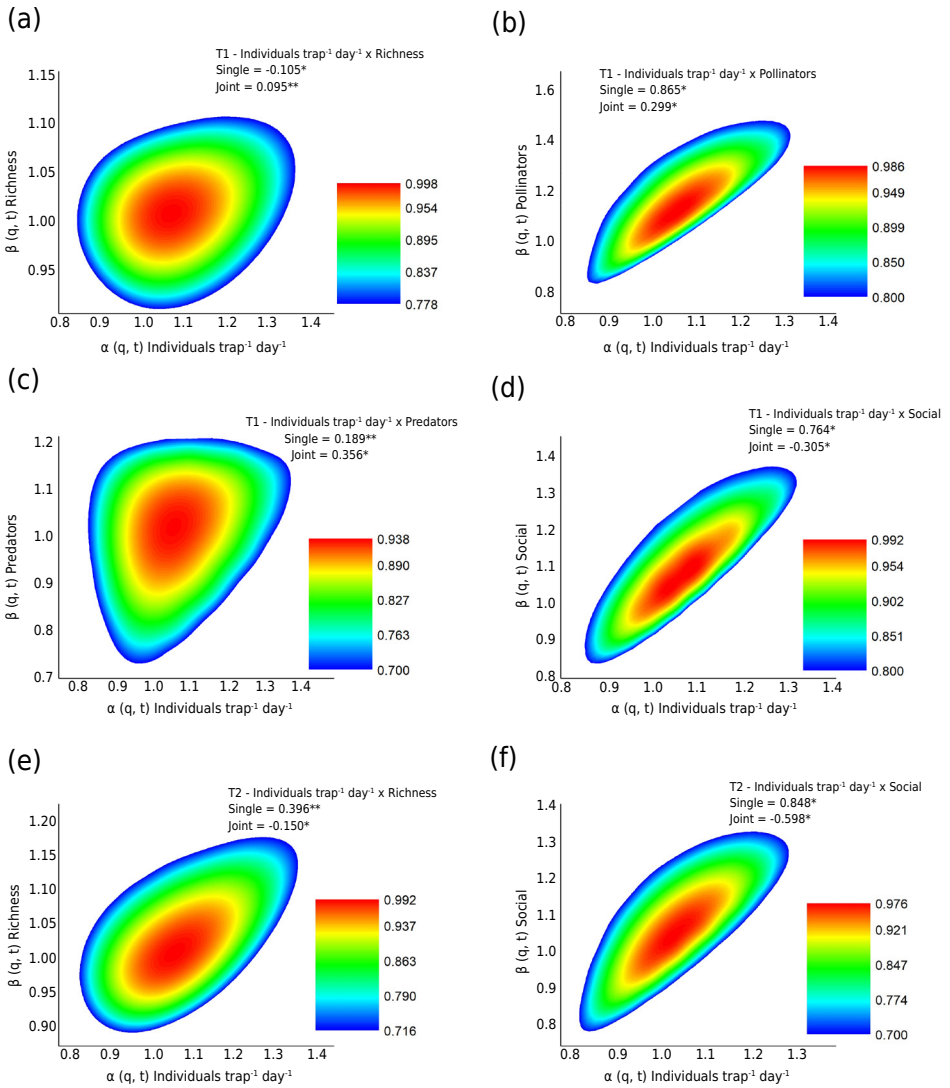

Figure 4. Joint multifractal distribution in T1 for Individuals trap^{-1} day^{-1} (horizontal axis) versus taxonomic groups (vertical axis): Richness (a), Pollinators (b), Predators (c), and Social (d) in T1; and Social (f) in T2, with Pearson's correlation coefficient on a joint scale of *α(q,t)* and *β(q,t)* and simple scale. * significance at p<0.01 and ** significance at p<0.05.

Graphs of contour lines of the joint dimensions of T1 and T2 for Richness *versus* Functional groups (Ind trap^{-1} day^{-1}, Pollinators, Predators, and Social) are shown in figure 5. In general, the graphs of the joint dimension using Richness as a predictor variable (Figure 5) showed slightly lower correlation values compared to the joint correlation values using Ind trap^{-1} day^{-1} as a predictor variable (Figure 4). This fact is justified since Richness has less variability along the geometric support and in the scales, while the abundance of organisms (Ind trap^{-1} day^{-1}) represents a system with greater heterogeneity.

The results of the joint multifractal analysis (Figures 4 and 5) showed attributes under study had different degrees of association between scale indexes α(*q,t)* and β(*q,t)* in T1 and T2. The graphs of the joint multifractal spectrum [*f*(α,β)] were represented by contour lines in relation to the distribution of high or low values, with the lower left part representing high values of α(*q,t*) and β(*q,t)*, and the upper right representing low values of α(*q,t)* and *β(q,t)* (Zeleke and Si, 2006). This represents a diagonal graph with ellipses and narrow/close lines, showing a strong correlation between values (Biswas et al., 2012). Circular contour lines indicated no association between the joint dimensions of scales, representing more rounded graphics (Figures 4 and 5).

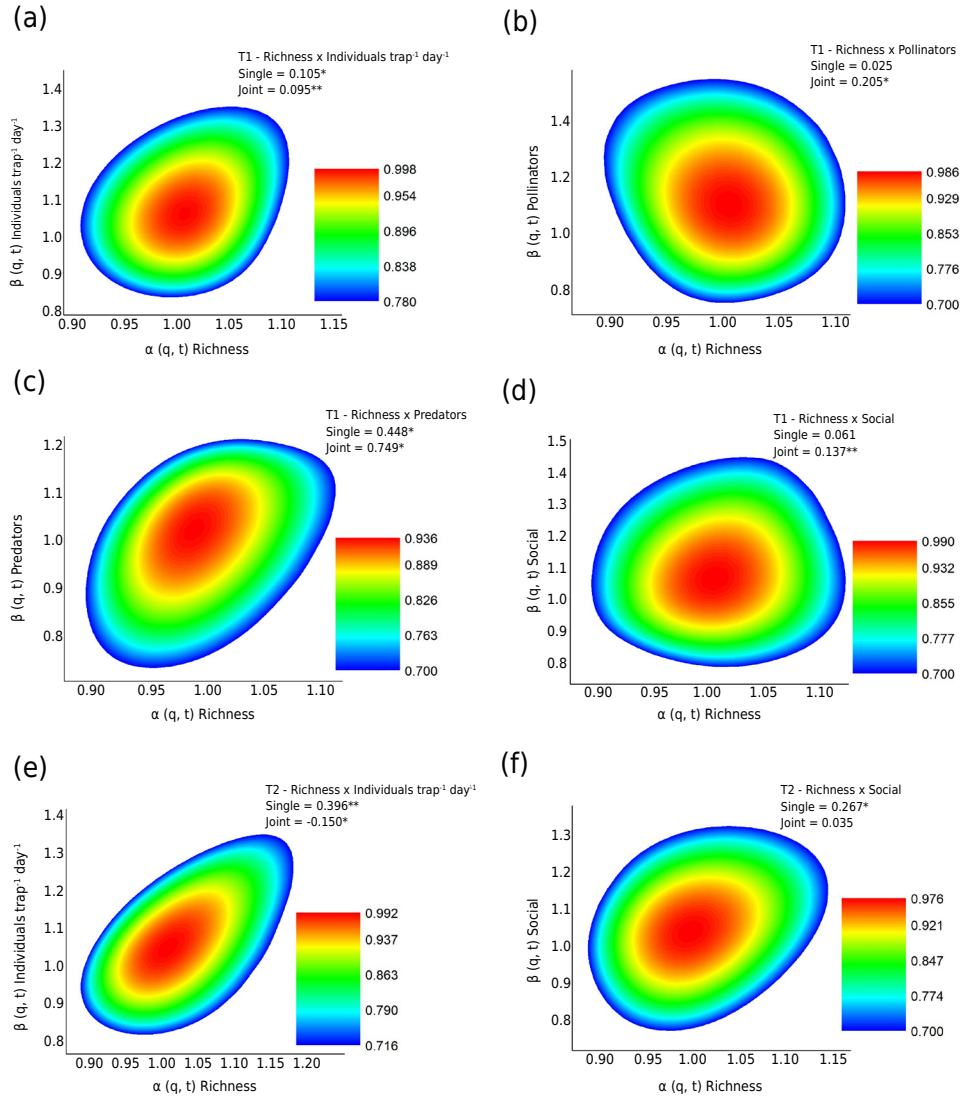

Figure 5. Joint multifractal distribution in T1 for Richness (horizontal axis) versus taxonomic groups (vertical axis): Individuals trap^{-1} day^{-1} (a) and Social (b) in T2, with Pearson's correlation coefficient on a joint scale of *α(q,t)* and *β(q,t)* and simple scale. * significance at p<0.01 and ** significance at p<0.05.

Contour plot of the joint dimension for Ind trap^{-1} day^{-1} *versus* Richness at T1 (Figure 4a) showed a single correlation of R = −0.105 (p<0.01) and a joint correlation of R = 0.095 (p<0.05). In general, the graph describes circular contour lines, indicating that the joint scales [*α(q,t)* and *β(q,t)*] do not have a well-defined correlation, especially for the high measurement values of *α(q,t)* and *β(q,t)*. The Ind trap^{-1} day^{-1} *versus* Richness in T2 (Figure 4e) described a single correlation of R = 0.396 (p<0.05) and a joint correlation of R = −0.150 (p<0.01). Results demonstrated that there was a strong correlation in the scales *α(q,t)* and *β(q,t)* for these variables. In this case, the contour lines had diagonal distribution and elliptical lines, indicating a high correlation in the joint scales (Biswas et al., 2012). The presence of a higher joint correlation for Ind trap^{-1} day^{-1} *versus* Richness in T2, compared to T1, was justified by the greater uniformity and symmetry of the singularity spectrum for these variables, according to the initial multifractal analysis (Table 4 and Figure 3). This demonstrates how vegetation type affects the scales of variability of the soil invertebrate fauna, which is in agreement with the results of Silva and Siqueira (2020).

Joint multifractal dimensions for Ind trap^{-1} day^{-1} *versus* Pollinators (Figure 4b) in T1, Ind trap^{-1} day^{-1} *versus* Social (Figure 4d) in T1, and Ind trap^{-1} day^{-1} *versus* Social

(Figure 4f) in T2 presented graphs with diagonal contour lines and in ellipses, describing a high relationship for the distribution of the scales of $\alpha(q,t)$ and $\beta(q,t)$, resulting in high values of joint correlation: Ind trap^{-1} day^{-1} *versus* Pollinators (R = 0.299, p<0.01) at T1, Ind trap^{-1} day^{-1} *versus* Social (R = −0.305, p<0.01) at T1, and Ind trap^{-1} day^{-1} *versus* Social in T2 (R = −0.598, p<0.01). The high correlation in the joint scales for the abundance of organisms (Ind trap^{-1} day^{-1}) and for the functional groups (Pollinators and Social) reflected the spatial correspondence for the measurement values of these variables along the geometric support; thus, there was a correlation in the single and joint scales. The abundance of organisms presented itself as a variable that could predict pollinating and social functional groups. However, abundance does not directly reflect biological diversity (Magurran, 2019).

Multifractal spectra of the joint distributions in T1 for Richness *versus* Ind trap^{-1} day^{-1} (Figure 5a) presented a weak correlation, presenting graphs with circular contour lines, with different values of joint correlation: 0.095 significant at p<0.05. Contour plots for the joint multifractal association of Richness *versus* Pollinators (Figure 5b; R = 0.205, p<0.01), Richness *versus* Social (Figure 5d; R = 0.137, p<0.05) in T1, and Richness versus Social in T2 (Figure 5f; R = 0.035, not significant) presented circular lines, confirming low correlation for the scales $\alpha(q,t)$ and $\beta(q,t)$. The presence of a low joint correlation for these pairs of variables was a direct result of the intrinsic variability of each system. Richness comprised a system with low heterogeneity for the values of measures along the transect, with 126 measures for T1 and 122 measures for T2, thus ensuring that all joint partitions were filled with values. However, the data from the functional groups Pollinators (T1) and Social (T1 and T2) had a high heterogeneity of measures, with variable partitions filling in the geometric support and related to the positivity rate of these groups (Table 2). In this sense, despite the low joint correlation values for these variables, there were associations on multiple scales (Biswas et al., 2012).

DISCUSSION

The first hypothesis of this study is that the distribution and association of the richness and abundance of soil invertebrates could be determined using multifractal and joint multifractal analyses. To test our hypothesis, it was initially necessary to understand how the treatment environment (T1 – dense Savanna and T2 – typical Savanna) affected organisms richness (26 in T1 and 15 in T2) and abundance (3456 in T1 and 1629 in T2). In this particular case, our results corroborate those of other studies. Silva et al. (2019) studied the soil fauna in an area with preserved and anthropized Savanna and identified 2,384 and 1,777 individuals distributed in 15 and 11 taxonomic groups, respectively. Characterizing the soil macrofauna in agroforestry systems in a Savanna area, Martins et al. (2018) identified 1,993 specimens distributed in 27 taxonomic groups. Studying epigeal soil fauna in a Savanna area, Souza et al. (2017) identified 454 individuals distributed in 13 taxonomic groups.

High abundance of Formicidae in Savanna areas has been reported in previous studies (Martins et al., 2018; Silva et al., 2018, 2019; Vicente et al., 2018). Pollinating organisms are represented by the taxonomic groups Hymenoptera and Lepidoptera, with a positivity rate greater than 85.93 %. Hymenoptera order was the most abundant in T1 (1517 individuals), followed by the family Formicidae (1479 individuals), while in T2, the family Formicidae was the most abundant (607 individuals), followed by the order Hymenoptera, with 605 individuals (Table 2). The separation of the Formicidae family from the order Hymenoptera was carried out considering the aggregated behavior of ants (Vicente et al., 2018) and their diversified ecological habits (Costa-Milanez et al., 2014) in relation to the order Hymenoptera, which in most cases are winged.

Richness and abundance make up complex and heterogeneous systems, as demonstrated in the multifractal analysis (Figures 2 and 3 and Table 4). However, these variables show

correlation on multiple scales (joint multifractal analysis; Figures 4 and 5). To evaluate the multiple scales of the data, it is necessary to understand the dynamics of the functional groups, which will later be crossed with abundance and richness.

Predatory organisms (Araneae, Coleoptera, Diplura, Diptera, Diptera Larva, Neuroptera, Opillionida, Orthroptera, and Scorpionida) occurred in 66.40 % (T1) and 69.53 % (T2) of the traps. Their occurrence along the transect is related to different environmental factors and, above all, the availability of food resources, as described by Silva et al. (2013). The functional group Microphages (Acari, Archaeognatta, Aucheonorrhyncha, Blattodea, Dermaptera, Diplopoda, Entomobryomorpha, Gastropoda, Coleoptera larva, Formicidae larva, Trichoptera, and Zygentoma) were sampled in 8.59 % of the traps in T2 and 28.90 % of the traps in T1. The greater occurrence of Microphages in T1 is justified by the vegetation strata diversity in this plot compared to T2. Our results corroborate those of Silva et al. (2013) and Maggiotto et al. (2019), who also reported greater Microphage diversity related to environments with a greater quantity and diversity of food resources.

For the Coleoptera order, 239 individuals were identified, representing 14.67 % of the sample population in T2 and 69 individuals (2 %) in T1 (Table 2), demonstrating that the abundance of beetles is influenced by vegetation cover. In a study of soil fauna in a Savanna area, Martins et al. (2018) identified 350 organisms that represented 17.56 % of the total number of individuals. Bernardes et al. (2020) found 282 beetles distributed among 20 taxa in a Savanna area. Characterizing the soil fauna in Savanna transition areas, Santos et al. (2017) sampled 141 Coleoptera, representing 2.05 % of the collected individuals. Evaluating Coleoptera population fluctuation in the Savannah area, Gonçalves (2017) collected 2123 beetles, representing an average of 176.91 organisms per month.

For the Isoptera group, 97 individuals were identified in T1, and 7 individuals in T2 (Table 2). Oliveira et al. (2013) identified 115 individuals (Isoptera) in areas with typical Savanna formations and Savanna fields, indicating the presence of this group was associated with the presence of litter. Lower abundance of certain organisms, such as Archaeognatta, Entomobryomorpha, and Neuroptera, is related to the content of organic matter (Roy et al., 2018). This might also be related to the absence of predators, benefiting invertebrate fauna organisms such as Lepidoptera and Blattodea, which are active, winged, and synanthropic organisms (Rafael et al., 2012).

A total of 27 adult and 32 larval dipterans were collected in T1, and 12 adult dipterans were collected in T2. The presence of adult and larval dipterans in the present study is justified by the organic matter content (20 and 12 g dm^{-3} for T1 and T2, respectively; Table 1). According to Kaneda et al. (2013), these organisms benefit from decomposing organic matter. However, studying soil fauna and its relationship with physical and chemical soil properties, Moço et al. (2010) showed the clay content was one of the determining factors determining the richness of soil fauna and found an indirect negative effect of clay content for Predators (functional group).

Studying soil macrofauna in a riparian forest, Gholami et al. (2017) found an average abundance of 39.60 individuals m^{-2} and an average Richness of 1.40, indicating that invertebrate fauna organisms were associated with the type of vegetation cover. This corroborates the results of the present study, which showed vegetation type influenced the average abundance of individuals. Systems with greater vegetation cover favor the formation of microclimates and the supply of food resources for soil fauna (Marichal et al., 2014).

Evaluating organisms' richness and abundance through multifractal and joint multifractal analysis, we found that, in both situations, the multifractal analysis described high heterogeneity at scales. The spectrum of singularity for richness demonstrated that along the transect, there was a predominance of high-value scales of wealth measures for T1 and a predominance of low-measured values along the transect for T2. This factor

is important because it describes the complexity of the environment in terms of the heterogeneity of scales and allows the environment to determine the complexity of the environment.

The abundance described by the Ind trap^{-1} day^{-1} index in the two systems had similarities, with the measurement values in the scales revealing singularity spectra with sparser values, indicating that in the partitions, the heterogeneity is smaller compared to the richness of organisms and that in T1 and T2, the number of organisms that fell into each of the traps were similar in each of the treatments and in the partitions/scales. Therefore, regardless of the environment, the probability of capturing individuals from soil fauna was similar, demonstrating a pattern that could not be identified through classical spatial analysis methods.

The highest occurrence of social organisms, represented mainly by the family Formicidae, occurs due to a high variety of guilds, different ecological niches (Moreira et al., 2010), aggregate behavior (Vicente et al., 2018), and different eating habits (Costa-Milanez et al., 2014). Regarding pollinating organisms (Hymenoptera and Lepidoptera), their occurrence was not expected in the present study since these organisms are winged, and, according to Correia and Oliveira (2000), their occurrence in ground-level traps is justified by the use of formaldehyde, which, in addition to functioning as a preservative agent, also acts as an attractant for this group. It is important to highlight that, for the functional group Pollinators, the order Hymenoptera contributed the most to the rate of positivity (Table 2).

Predator organisms are represented in this study mainly by the Araneae group, and their main function is in biological regulation through prey–predator dynamics (Bedano et al., 2016). Microphages showed a higher mean in T1 than in T2, and, as previously discussed, such behavior is a direct result of the quantity and availability of organic carbon in these plots, corroborating the results of Silva et al. (2013) and Maggiotto et al. (2019). The Others group had the lowest mean value associated with T2 (Mean = 0.015), indicating this environment is less diverse than T1.

Soil invertebrate fauna had different degrees of heterogeneity in the experimental plots (Figure 2). The greater description of multifractal patterns for T1 is due to the greater spatial distribution of the measured values for these variables in the transect and the partitions. Studying the invertebrate fauna in different land-use and tillage methods, Silva and Siqueira (2020) described that the scale variability of the abundance and Richness of the organisms reflects the environment in terms of disturbance and conservation. In this way, the occurrence of greater multifractality for T1 in relation to T2 describes how the diversity of the environment in T1 benefits the arthropod fauna community in this plot, showing systems with greater complexity and spatial continuity in the measurement values.

Richness described the homogeneity of taxonomic groups through the transects, with no clear relationship with abundance, in agreement with the results of Saravia et al. (2012). However, the occurrence of lower values of R^2 for Ind trap^{-1} day^{-1} in T1 and T2 (T2: R^2 = 0.972, Figure 2d; and T1: R^2 = 0.980, Figure 2c) indicated that the internal structure of the system for the abundance of organisms was heterogeneous, as shown by the positivity rate (Table 2). In general terms, the partition function is indicative of the scale structure, which can be monofractal (single scale) or multifractal (multiple scale) (Zeleke and Si, 2006; Vidal-Vázquez et al., 2013; Bertol et al., 2017; Siqueira et al., 2018, 2022; Silva et al., 2021). Results found in this study demonstrated that the attributes under study were distributed to a greater or lesser degree of multifractality on multiple scales (Saravia et al., 2012; Salat et al., 2017; Silva and Siqueira, 2020).

A better fit for Richness in relation to Ind trap^{-1} day^{-1} occurred because the distribution values of Richness measures were uniformly distributed throughout the geometric support and in

the partitions, with low variability between the measured values, while for Ind trap^{-1} day^{-1}, there was a greater variation between the measured values, resulting in a partition function with less adjustment (T2: R^2 = 0.972 and T1: R^2 = 0.980, Figures 2d and 2c).

According to Banerjee et al. (2011) and Vidal-Vázquez et al. (2013), a D_0 value equal to 1 indicates that all sample points are associated with a numerical value, whereas values <1 represent the absence of a numerical value at one or more points throughout the segment of the partition function. Therefore, the highest values of D_0 were for Ind trap^{-1} day^{-1}, followed by Richness, indicating there were few points without measurement values in the geometric support and, consequently, in the partitions. Occurrence of lower values of D_0 for the functional groups indicates the absence of measurement values in the geometric support, indicating the variability of functional groups in the geometric support is influenced by greater or lesser environmental complexity in T1 and T2. Generalized dimensions reflect the structural heterogeneity of the biological community, where the greatest differences are described by the abundance of organisms and richness of species that make up the sample (Gelashvily et al., 2008). In this sense, D_0 in T1 represents a system with greater structural heterogeneity, with a greater number of measurements along the geometric support (N = 126 points with measurement values), while T2 has a greater number of points without associated measurements (N = 122 points with measurement values).

The greater distribution of values uniformity in the scales for Richness describes systems uniformly distributed in T1 and T2, with partitions occupied by measurement values with low variation between the measurement values present in the partitions, while the less uniformity in the scales for Predators and Ind trap^{-1} day^{-1} reflects the heterogeneity of the measures of values in the partitions. Our results demonstrate that Richness is little influenced spatially by the heterogeneity of the abundance of organisms (Ind trap^{-1} day^{-1}), since Richness is the result of a series of environmental relationships (Gholami et al., 2017) and the complexity of the soil invertebrate fauna community (Roy et al., 2018).

Dimension D_2 is mathematically associated with the correlation function and computes the correlation of the measures contained between intervals (Posadas et al., 2009). It is a measure that describes how closely the segments are correlated and represents the complexity of the systems (Grassberger and Procaccia, 1983). Thus, we might infer the attributes under study represent complex systems, not necessarily stating they are multifractal systems, as there is a trend that can be confirmed if $D_0 > D_1 > D_2$, as described by Banerjee et al. (2011), Vidal-Vázquez et al. (2013), Dafonte al. (2015), and Siqueira et al. (2018, 2022). However, when the dimensions are represented by $D_0 = D_1 = D_2$, the system is characterized as monofractal; that is, the structure of the system is self-similar (Mandelbrot, 1982; Caniego et al., 2006). When the dimensions are represented by $D_0 \approx D_1 \approx D_2$, the systems have certain homogeneity.

The values of D_{-10}–D_{10} are often used to determine the degree of multifractality of the system scale (Caniego et al., 2006; Paz-Ferreiro et al., 2010; Dafonte et al., 2015). Thus, soil biological attributes under study differ in spatial distribution, representing different degrees of heterogeneity. It is necessary to consider the variability of soil fauna results from the interaction of factors in the environment, such as the interaction of climatic and edaphic factors (Silva and Siqueira, 2020), as well as from the interaction of physical and chemical factors (Bedano et al., 2016) and the occurrence of ecological niches (Wagg et al., 2014; Roy et al., 2018). Thus, the interference of these factors can contribute to a greater or lesser degree of heterogeneity in the soil community. In this sense, our results demonstrate the spatial distribution of Richness in the geometric support has low variability compared to the other parameters under study. We also emphasize that the high variability of the data for the functional groups in general reflects the data heterogeneity, especially with regard to the abundance of organisms (Ind trap^{-1} day^{-1}),

which in both transects had high variability (CV = 84.150 % in T1 and 85.154 % in T2, Table 3).

As previously discussed, the variability of Ind trap^{-1} day^{-1} had a direct association with soil fauna functional groups along the transect. In this case, the singularity spectrum for Ind trap^{-1} day^{-1} represented a system with a greater variety of high singularity exponent values, which were associated with low concentrations of measured values, thus justifying the reverse behavior for Social organisms (Table 4 and Figures 3a and 3b), having asymmetrical branches and elongated to the left, and the high measures of Ind trap^{-1} day^{-1} are associated.

The singularity spectrum for Richness showed a concentration of high singularity exponents in T1 and T2 (Figures 3a and 3b); however, there was asymmetry of the branches to the left in T1 and to the right in T2. Thus, the spectrum of uniqueness for Richness reflected the complexity of the environment, and the differentiation for the asymmetry of branches in T1 and T2 represented the characteristics of vegetation formation for each of the experimental plots. There was a greater diversity of vegetation strata in T1, thus influencing the composition and abundance of soil fauna in this treatment, corroborating studies by Aubert et al. (2003), Sereda et al. (2012), and Gholami et al. (2017).

The joint correlation for Ind trap^{-1} day^{-1} *versus* Predators (Figure 4c) and Richness *versus* Predators (Figure 5c) was 0.356 ($p>0.01$) and 0.749 ($p>0.01$) for T1. Richness *versus* Predators had a better association on multiple scales than Ind trap^{-1} day^{-1} *versus* Predators. This was expected since the Richness measures had less variation in geometric support and scales compared to Ind trap^{-1} day^{-1}, corroborating the second hypothesis of this study.

The joint multifractal analysis describing the attributes under study showed an association for scale indexes $\alpha(q,t)$ and $\beta(q,t)$ with greater or lesser values of joint correlation. The use of Ind trap^{-1} day^{-1} and Richness as predictor variables for functional groups (Pollinators, Predators, and Social) indicated that functional groups with greater abundance (Pollinators and Social) and greater distribution along the geometric support showed a better association with Ind trap^{-1} day^{-1}. Richness showed a high association with Predators related to T1, and predatory organisms did not show multifractality in T2. Thus, the portion with vegetation formation of the dense Savanna type (T1) presented greater multifractality for the variables under study related to the availability of food resources, corroborating the results of Silva et al. (2013), Costa-Milanez et al. (2014), Marichal et al. (2014), Gholami et al. (2017), and Martins et al. (2018). However, the presence of social organisms in T1 and T2, whose multifractality of data was evidenced in this study, confirms the capacity of these organisms to explore the environment, a direct result of the high diversity of guilds (Moreira et al., 2010) and their aggregate behavior (Vicente et al., 2018).

Richness and abundance (Ind trap^{-1} day^{-1}) represent the invertebrate fauna of the soil, thus describing the spatial variability of the different biological communities and their interactions. Studying the multifractality of Richness and abundance of small mammals, Gelashvily et al. (2008) showed that the study of these variables using multifractal analysis reflects the structural heterogeneity of a community, which in most studies is evaluated by different diversity indexes. Thus, the results demonstrated the invertebrate fauna of soil had differences in structural heterogeneity that mainly represent the degree of disturbance, availability of food resources (Costa-Milanez et al., 2014; Marichal et al., 2014), and the predominance and/or dominance of some groups (Magurran, 2019; Silva et al., 2019).

Our results corroborate the importance of studying and understanding the heterogeneity of the soil invertebrate fauna using multifractal analysis. In this sense, further studies are needed to ascertain how biological diversity is represented through multifractal parameters. Results showed the biological diversity of invertebrate fauna can be assessed using generalized multifractal dimensions, amplitude, and the asymmetry of the singularity

spectrum. In this sense, the methodological application of multifractal analysis for the knowledge and understanding of the structural heterogeneity of soil invertebrate fauna groups communities presented itself as a promising tool since it is possible to evaluate a set of biological–environment interactions, based on the Richness and abundance of organisms, according to joint multifractal analysis. However, the effective use of multifractal analysis to understand soil biological diversity requires a sampling effort, which is influenced by variations in the landscape, the size of the experimental plot, the spatial distribution of fragments with natural vegetation, and the degree of disturbance.

When evaluating biological data using multifractal tools, it is interesting to consider the intrinsic behavior of the variable under study; in this case, we chose variables that did not present entropy or added little entropy to the system (Salat et al., 2017) because depending on the variable, some parameters can be favored (Magurran, 2019). The present study made use of the Richness of organisms, as it understands that this evaluation includes both rare and abundant species; in turn, the use of abundance (Ind trap^{-1} day^{-1}) is also necessary, as this is an elementary parameter for biological characterization, providing the first information about the community, such as group dominance and inferences about the spatial distribution of organisms in the area. The study of the spatial variability of soil invertebrates allows decision-making, supporting conservationist actions, considering Richness and abundance, key parameters for assessing environments.

CONCLUSIONS

Soil invertebrate fauna presented different degrees of multifractality related to the complexity of Savanna type formation. Multifractal analysis showed vegetation composition for the formation of a typical Savanna (T2) presented less heterogeneity in the scale measures than the dense Savanna (T1). Experimental plot T1 presented better conditions for soil fauna, reflecting greater availability of food resources and greater dynamics among individuals in the soil community, resulting in greater abundance and Richness. The high scale ratio of Richness with functional group Predators in T1 demonstrated the variation in abundance of this functional group influenced the values of Richness, which were homogeneous throughout the landscape. The Ind trap^{-1} day^{-1}, as a predictor variable, best described the heterogeneity of value relationships in the joint multifractal distribution for the functional groups (Pollinators, Predators, and Social). Joint multifractal analysis proved to be an important tool for understanding the variability of soil invertebrate fauna and the associations of the variability scales for the variables under study.

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DATA AVAILABILITY

The datasets generated are available from the corresponding author on request.

AUTHOR CONTRIBUTIONS

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