Spatial variability of edaphic attributes on Coleoptera (Insecta) in land use systems

Variabilidade espacial dos atributos edáficos sobre Coleoptera (Insecta) em sistemas de uso do solo

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ABSTRACT

The alteration of the natural landscape structure affects abiotic conditions and promotes a biological response in the local community. The diversity of edaphic organisms is related to the diversity of other taxa and abiotic characteristics, which represent potential bioindicators of the ecosystem. The objective of this study was to identify which soil attributes explain the beetle community and explore their effects through spatial modeling. The study was conducted in three landscapes in western Santa Catarina (Brazil), located in Chapecó, Pinhalzinho, and São Miguel do Oeste. The land use and cover systems identified were: no-till farming, native forest, pasture, eucalyptus planting, crop-livestock integration, and shrub vegetation. Soil, plant litter, and Coleoptera samples were collected. The variables were selected through the Threshold Indicator Taxa Analysis and spatial modeling by Geostatistics. Higher values of soil penetration resistance, associated with the no-till system, resulted in a lower abundance of Staphylinidae beetles, conditioned by total soil porosity. Lower volumetric moisture values, identified in the no-till system near native vegetation fragments, led to increased abundance of Nitidulidae family beetles, due to the family's adaptability to dry environments. The trend of higher microbial carbon concentration in native vegetation areas explained the greater abundance of Chrysomelidae family beetles in these areas, due to the phytophagous habits of the species in this family. Thus, the Coleoptera community has the potential to serve as bioindicators of soil quality, and their relationships with soil physics, chemical, and microbial attributes can be spatially modeled through Geostatistics.

Keywords: bioindicators; subtropical landscape; Geostatistics.

RESUMO

A alteração na estrutura natural da paisagem afeta condições abióticas e promove uma resposta biológica da comunidade local. A diversidade de organismos edáficos está relacionada com a diversidade de outros táxons e características abióticas, representando potenciais bioindicadores do ecossistema. O objetivo deste trabalho foi identificar quais atributos do solo explicam a comunidade de coleópteros e explorar seus efeitos por meio da modelagem espacial. O estudo foi desenvolvido em três paisagens do oeste de Santa Catarina (Brasil) localizadas em: Chapecó, Pinhalzinho e São Miguel do Oeste. Os sistemas de uso e cobertura do solo identificados foram: plantio direto, floresta nativa, pastagem, plantio de eucalipto, integração lavoura-pecuária e capoeira. Foram realizadas coletas de solo, liteira e coleópteros. A seleção das variáveis foi realizada pela Análise de Táxons Indicadores de Limiares e a modelagem espacial pela Geoestatística. Maiores valores de resistência a penetração associados ao sistema de plantio direto promoveram menor abundância de coleópteros da família Staphylinidae, condicionadas pela porosidade total do solo. Menores valores de umidade volumétrica, identificados em sistema plantio direto próximo de fragmentos de vegetação nativa, promoveram maior abundância da família Nitidulidae, em razão da adaptabilidade da família ao ambiente seco. A tendência de maior concentração de carbono microbiano em áreas de vegetação nativa explicou a maior abundância da família Chrysomelidae nessas áreas, em decorrência dos hábitos fitófagos das espécies dessa família. Dessa forma, a comunidade de coleópteros possui potencial como bioindicador da qualidade do solo e suas relações com os atributos físicos — químicos e microbiológicos — do solo podem ser modeladas espacialmente por meio da Geoestatística.

Palavras-chave: bioindicadores; paisagem subtropical; geoestatística.

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Introduction

Changes in the landscape´s natural structure affect abiotic conditions (Ezcurra, 2016; Salomão et al., 2018) and, consequently, promote a biological response from the local community (Martin, 2018). Some species are able to adapt to new conditions and can increase their populations, while others may disappear (Salomão et al., 2018). This means that species indicate different patterns in the environment, and some of them are better bioindicators than others.

Soil fauna can be affected directly or indirectly by soil management systems (Kumar et al., 2018). In the first case, the impacts are caused by mechanical action processes and the application of chemical compounds such as fertilizers and pesticides (Kraft et al., 2021). In the second case, these processes promote modification of the substrate structure, altering species habitat (Correia and Oliveira, 2000). Such conditions result in the loss of ecosystem services and interfere with the populations' ability to expand within existing habitat fragments or get established in new locations (Lander et al., 2019), causing the loss of these organisms in biodiversity (Nascimento et al., 2019; Salomão et al., 2018, 2019).

Soil biodiversity is responsible for essential ecosystem services, such as nutrient cycling, pest and disease control, carbon storage, and the release and maintenance of biological diversity. Through its trophic relationships, it contributes to the fragmentation of organic matter and nutrient cycle dynamics, and affects primary production indirectly (FAO et al., 2020; Velazco et al., 2022). Due to the ease of sampling, sensitivity, and rapid response of the community to environmental changes, the order Coleoptera (beetles) of the phylum Arthropoda and class Insecta has been highlighted in its role as an indicator of environmental pollution (Parikh et al., 2021) as well as changes in forest and agricultural habitats (Pompeo et al., 2023).

The order Coleoptera has a strongly seasonal character and this is due to the range of abiotic tolerance the beetles have. Therefore, climatic elements directly influence the population dynamics of these communities (Johnson et al., 2015; Leivas et al., 2022). The preservation of evergreen vegetation areas, such as riparian forests, can minimize the seasonality effect of the community, seing that a better microclimatic condition is maintained when compared to areas with xerophilic vegetation (Guedes et al., 2020).

The Coleoptera community is also influenced by the intensity of land use and coverage, in which the maintenance of native vegetation promotes greater richness (Bernardes et al., 2020). Pasture areas present a strong decrease in the taxonomic diversity of Coleoptera (Cifuentes et al., 2017) as well as the maintenance of eucalyptus reforestation areas also promotes loss of diversity when compared to native vegetation (Pompeo et al., 2017, 2023).

The organization of edaphic characteristics respects a certain degree of ordering and continuity in space, which demonstrates the spatial dependence between points located in the same area (Dionisio et al., 2020). For this reason, mathematical analyses based on spatial statistics are viable in characterizing environmental responses. Thus, as Geostatistics responds to patterns of physical-chemical characteristics of the soil (Roveda et al., 2018), the tool has the potential to explain the community that responds ecologically to soil attributes and its different forms of use and management (Reay-Jones, 2017; Lovera et al., 2018; Pinchao and Muñoz, 2019; Dionisio et al., 2020; Santos et al., 2020). Based on the assumption that soil and plant attributes affect the abundance and richness of Coleoptera (I) and the hypothesis that the fragmentation of native vegetation and the reduction of habitats promote the loss of diversity of these organisms and can be modeled (II), with some families that can be used as indicators of these fragmentations (III), the objective of this work was to identify which soil attributes explain the Coleoptera community and explore their effects through spatial modeling.

Methodology

Samples were collected in the municipalities of Pinhalzinho (latitude 26°52'39.80" South, longitude 52°57'27.50" West, and altitude of 515 meters), São Miguel do Oeste (latitude 26°44'32.00" South, longitude 53°32'25.90" West, and altitude of 648 meters), and Chapecó (latitude 27°4'47.00" South, longitude 52°41'0.90" West, and altitude of 659 meters), located in western Santa Catarina in southern Brazil (Figures 1 and 2). The predominant climate in the three sample areas is type *Cfa* (humid subtropical climate) with warm summers (Alvares et al., 2014). The collections were carried out in the months of April (Period 1) and August (Period 2) of 2018, that is, at the beginning of autumn (warm and dry) and winter (cold and wet), as there are large climatic differences between these two seasons in the study region. In this sense, we sought a better representation of the conditions under which ground beetles were exposed in the landscape.
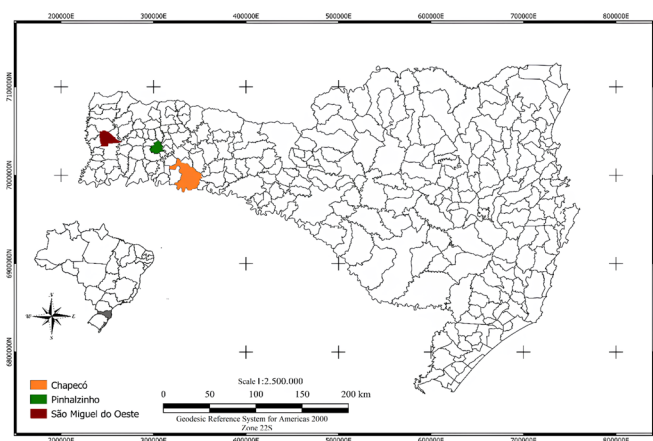

Figure 1 – Geographic location map of the municipalities of Chapecó, Pinhalzinho, and São Miguel do Oeste, Santa Catarina, Brazil.
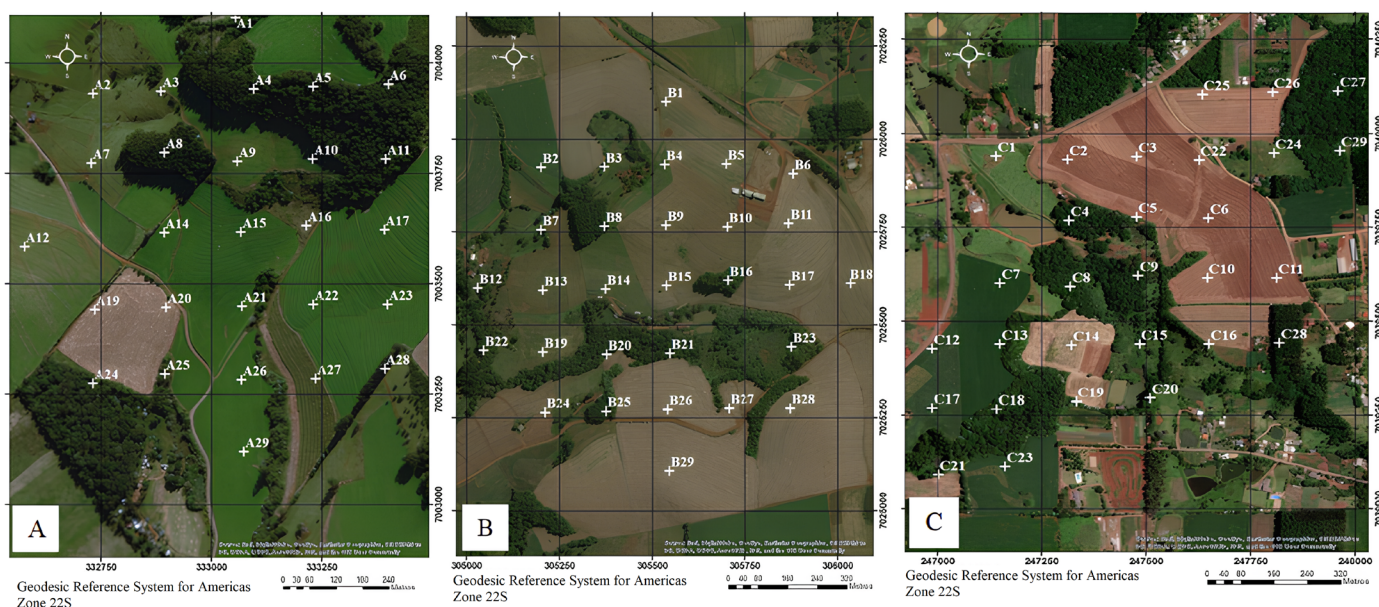Source: adapted from Pompeo (2020).

Figure 2 – Geographic distribution map of sampling points in the windows of Chapecó (A), Pinhalzinho (B), and São Miguel do Oeste (C), Santa Catarina, Brazil. Source: adapted from Pompeo (2020).

In each of the three municipalities, a landscape window was established (area where sampling was collected), presenting the different land use and cover systems described as follows. The no-tillage system (NT) was considered the central point of the landscape window and was chosen as the main use that makes up the area, along with the native forest (NF), as it is the predominant system in this region in the State of Santa Catarina. In addition, the windows also presented other land use and cover systems, including pasture (PA); eucalyptus plantation (EP); crop-livestock integration (CLI); and shrub vegetation (SV). Each window represented a diameter of 1 km and included a grid with 29 points spaced 167 m apart (a total of 87 points sampled per collection period) (Figure 1 in the Supplementary Material). We sought to select landscapes that covered all land uses, although the main focus of the present study was not limited to sampling by land use system.

As collection took place using a sampling grid in each landscape, the collection point could or could not fall within a certain land use. In this sense, the number of sampling points in each land use system was different. The following numbers of points were sampled per land use system and per collection period: NF (19 points), no-tillage (NT — 42), CLI (6), PA (14), EP (4), and SV (2). More information and a detailed history of the areas can be found in Pompeo (2020) and Pompeo et al. (2023) (Tables 1 and 2 of the Supplementary Material).

At each sampling point, Coleoptera collections were carried out using three different methods: i. Soil monolith (Tropical Soil Biology and Fertility — TSBF), which consists of collecting soil monoliths using a mold made of galvanized iron sheets with dimensions 25 × 25 × 10 cm (Anderson and Ingram, 1993); ii. Pitfall traps leveled with the ground and kept in the field for three days, composed of cylindrical containers of 8 cm in diameter, with a volumetric capacity of 500 mL, containing 200 mL of 0.5% (v/v) detergent (Baretta et al., 2014); and iii. Core method which consists of collecting soil samples with preserved structure, obtained with a 5 × 5 cm rigid PVC tube, according to ISO 2311-2 (2006). There were 29 monoliths, 29 traps, and 29 cores installed per landscape collected (a total of 87 samples for each method, per collection period) (Figure 1 in the Supplementary Material). Pupae and larvae were not evaluated.

The identification of taxonomic families was carried out using the identification keys and/or characterizations contained in the literature (Lima, 1952, 1953, 1955; Casari and Ide, 2012; Triplehorn and Johnson, 2015). The names and occurrences were verified in the Brazilian Fauna Taxonomic Catalog (Monné and Costa, 2020).

Coleoptera were identified and separated into morphospecies, which are visual assessments of individuals with different morphological characteristics. Initially, the morphospecies were characterized in spreadsheets and photographed with a camera attached to a stereoscopic microscope, using AxioVision 4.9© Image Software (Zeiss, 2017). The individuals, defined as identification references, were fixed in 99.5% absolute ethyl alcohol, in separate samples. The material was stored at the Soil Ecology Laboratory of the State University of Santa Catarina (UDESC-CAV), in Lages, Santa Catarina.

Litter was removed in four locations around each collection point with a 20 × 20 cm wooden sampler and then sieved through a 2 mm mesh to separate it from the soil. To separate fine particles from the soil, wet sieving was carried out using a 150 μm mesh.

Subsequently, the material was packed in paper bags and dried in an oven at 55°C, until constant weight. Soil collection for chemical and microbiological analyses was carried out at a depth of 0–10 cm with a Dutch auger, at 18 points around each collection point, to form a representative composite sample. For physical analysis, samples were removed using steel cylinders, 5 cm high and 6 cm in diameter (undeformed), and with a cutting shovel at a depth of 0–10 cm (Pompeo, 2020; Pompeo et al., 2023).

To analyze the different percentages of soil cover, the vegetation cover index was calculated (*VegCover index*) (Martins da Silva et al., 2017), according to the following Equation 1:

$$VegCover = [\%veg \, / \, \%Total \times (\%Total - \%Bare\ Soil)] \, / \, 100 \quad (1)$$

Where %Total refers to the sum of the percentages of vegetation and litter. The index varies from "1" (100% covered by vegetation) to "-1" (100% bare soil).

The following explanatory and environmental variables were used in the models: litter variables — plant litter dry weight (Ldw — g/m²), plant litter carbon (LC — %), plant litter nitrogen (LN — %); physical variables — micropores (Micro — m³/m³), macropores (Macro — m³/m³), biopores (Bio — m³/m³), saturated hydraulic conductivity (SHC — mm/h), total porosity (TP — m³/m³), bulk density (BD — g/m³), volumetric moisture (Moi — m³/m³), resistance to soil penetration carried out in the field — Penetrolog PLG1020 (penetration resistance, PRes — kPa); microbiological variables — microbial/basal respiration (BR — mg C-CO$_2$/kg of soil), microbial carbon (MC); chemical variables — soil carbon (SC — %), soil nitrogen (SNo — %), hydrogen potential in H$_2$O (pH), calcium (Ca — cmolc/dm³), magnesium (Mg — cmolc/dm³), aluminum (Al — cmolc/dm³), organic matter (OM — %), clay (Cl — %), phosphorus (P — mg/dm³), potassium (K — mg/dm³); and land cover variables — soil cover index (VegCover).

Statistical analysis

Variables were transformed by the standardization method using the *decostand* function, and the beetle families were transformed by the Hellinger standardization method. Multicollinearity between variables was tested by the variance inflation index (VIF), and the significance of the variables was obtained by canonical correlation/correspondence analysis (CCA). All analyzes were performed using the vegan package of R software version 4.1.3 (R Core Team, 2015). The analysis of the influence of variables on the Coleoptera community was tested by the Threshold Indicator Taxa Analysis (TITAN), which uses the Indicator Species Analysis (IndVal) with the TITAN2 package in the R software version 4.1.3 (R Core Team, 2015).

Geostatistical modeling was executed in Software ArcMap 10.8, with the complement Geostatistical Analyst – Geoestatistical Wizard

(ESRI, 2020). The type of kriging used was the ordinary considering the criteria $\left(\frac{standard\ deviation}{mean}\right) x\ 100 > 10$ (Andriotti, 2004). The semivariogram was optimized using the optimize model function, where the parameters of the semivariogram are optimized using cross-validation of the data. The models circular, spherical, tetraspherical, pentaspherical, exponential, Gaussian, and rational quadratic were tested. The selection of the model that best describes the spatial behavior of the data was selected using the parameter resulting from cross-validation as a criterion for choosing the models, as suggested by Vieira et al. (1983): RMSS (Root Mean Square Standardized) square root of the standardized squared error — the value must be closest to 1.

The behavior of the abundance data for each family in the different sampling windows was associated with sampling positions (sample points). To identify spatial dependence, the semivariance function was used, expressed by Equation 2:

$$Y(h) = \frac{1}{2}N(h)x \sum [Z(xi + h) - Z(xi)]^2 \quad (2)$$

Where:
Y(h) = semivariance;
N(h) = nº of observation pairs;
Z(xi); Z (xi+h) = point coordinates;
h = distance between observation pairs (x+h), x.

The selection criteria cited above were obtained from the main features of the omnidirectional semivariogram, in which: i. Nugget effect (C0): points where the semivariogram crosses the ordinate axis; ii. Range (a): corresponds to the spatial dependence zone of a sample; iii. Sill (C+C0): is the height at which the semivariogram stabilizes, reaching the total variability of sampled values (Andriotti, 2004).

Kriging interpolation maps were generated, except for cases in which the data presented a pure nugget effect, in which the variance was too small for data interpolation, and in families with abundances of less than three organisms.

Results and Discussion

A total of 766 adult beetles were captured considering all sampling methods. The study evaluated a total of 485 Coleoptera order individuals in the sampling Period 1 and 281 individuals in sampling Period 2, distributed across 20 families (Table 3 in the Supplementary Material). From this total, the greatest abundance occurred in the municipality of Chapecó, followed by São Miguel do Oeste and Pinhalzinho, and the greatest richness occurred in Chapecó, followed by Pinhalzinho and São Miguel do Oeste.

From the set of variables studied regarding their response to the diversity of families found in the sampled municipalities, after removing the effect of multicollinearity, the variables tested for Period 1 were: Ldw, LC, LN, SHC, Moi, PRes, BR, MC, SC, Sno, and VegCover (Table 4 in

the Supplementary Material). From these variables, the following were significant for the biological data matrix: SHC (R^2=0.5821, p=0.001), MC (R^2=0.4769, p=0.001), PRes (R^2=0.4365, p=0.001), SNo (R^2=0.3227, p=0.001), VegCover (R^2=0.2258, p=0.002), Moi (R^2=0.1947, p=0.002), BR (R^2=0.1714, p=0.003), SC (R^2=0.1453, p=0.008), LN (R^2=0.1216, p=0.014) (Table 5 in the Supplementary Material).

The study shows the bioindicator potential of some Coleoptera families, and their geospatial distribution in different land use systems associated with the studied variables, and demonstrates that plant and soil attributes (physical, chemical, and biological), affect the abundance and richness of these organisms throughout the landscapes, confirming hypothesis I of the present study; as well as it allows modeling, confirming hypothesis II. The TITAN in collection Period 1 identified three indicator families of the 17 analyzed with a significant Indval score (p<0.050). The Staphylinidae family (purity 1.00; reliability 1.00) was selected as an indicator under the influence of the PRes variable, the Nitidulidae family (purity 1.00; reliability 1.00) under the influence of the Moi variable, and the family Chrysomelidae (purity 1.00; reliability 0.90) as an indicator under the influence of the MC variable (Figure 3). The semivariogram calibration criteria for Period 1 are presented in Table 6 of the Supplementary Material and the spatial modeling is presented in Figure 3.

In Period 1 for the municipality of Chapecó, Staphylinidae abundance values varied between 0–41 (B), and PRes values varied between 536–3,621 kPa (A). Higher PRes values were associated with lower Staphylinidae abundance values, linked to NT and CLI. For the Moi data and abundance of the Nitidulidae family, kriging maps were not presented once the abundance of the family varied between values lower than three individuals.
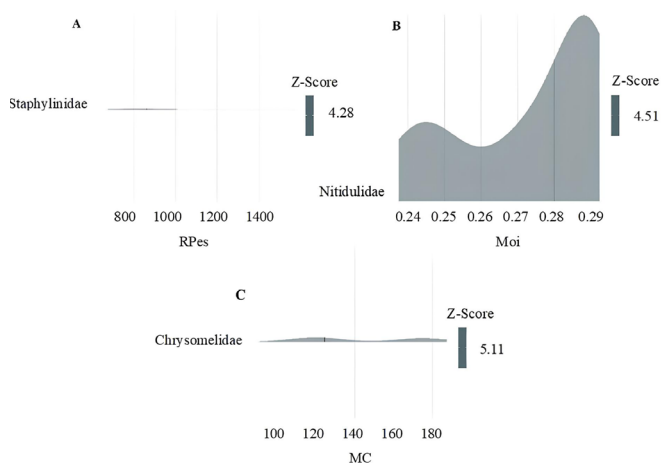

Figure 3 – Result of the Threshold Indicator Taxa Analysis (TITAN) for variables selected in collection Period 1. Threshold Indicator Taxa Analysis (A) for family Staphylinidae and penetration resistance (PRes); (B) for the Nitidulidae and moisture (Moi) variables; and (C) for the Chrysomelidae family and microbial carbon (MC).

For the municipality of Pinhalzinho, Staphylinidae abundance values varied between 0–5 (D), and PRes, between 235–2,317 kPa (C). Nitidulidae abundance values varied between 0–6 (F) and Moi values, between 0.200–0.452 m³/m³ (E). The greater abundance of Nitidulidae was associated with lower Moi values in an NT close to fragments of native vegetation. Chrysomelidae abundance values varied between 0–3 (H), and MC values varied between 82.9–261.7 (G). The greater abundance of Chrysomelidae was associated with lower MC in fragments of native vegetation.

For Period 1 in the municipality of São Miguel do Oeste, the Staphylinidae, Nitidulidae, and Chrysomelidae families were not subjected to interpolation by kriging, due to the pure nugget effect, therefore, spatial distribution maps of the explanatory variables were not generated.

Removing the effects of multicollinearity, the variables tested for sampling Period 2 were Ldw, LC, LN, Macro, PRes, BR, MC, Mg, Al, Cl, P, K, and VegCover, whose descriptive analysis of the data is presented in Table 7 of the Supplementary Material. From these variables, the following were significant for the biological data matrix: VegCover (R^2=0.4460, p=0.001), MC (R^2=0.3584, p=0.001), LC (R^2=0.3322, p=0.001), Ldw (R^2=0.2208, p=0.001), PRes (R^2=0.1570, p=0.003), LN (R^2=0.1490, p=0.006), Mg (R^2=0.1304, p=0.009), P (R^2=0.1168, p=0.010), K (R^2=0.0883, p=0.043), and Cl (R^2=0.1061, p=0.020) (Table 8 in the Supplementary Material).

For collection Period 2, the TITAN identified two indicator families out of the 18 families analyzed with a significant Indval score (p<0.050). The Scarabaeidae (purity 1.00; reliability 0.98) and Salpingidae (purity 1.00; reliability 1.00) families were selected as indicators, influenced by the VegCover variable (Figure 4). Lower VegCover values were associated with greater abundance of organisms from the Scarabaeidae family, while higher values of this attribute were associated with greater abundance from the Salpingidae family.

In Period 2, the VegCover variable presented a pure nugget effect in the municipalities of Pinhalzinho and São Miguel do Oeste, making spatial modeling unfeasible. The Scarabaeidae family modeling was possible only in the municipality of São Miguel do Oeste, but presented abundance values varying between 0–3 organisms, which does not represent a significant ecological response. Such is the Salpingidae family, which was modeled only in the municipality of Chapecó, with abundances varying between 0–1 organism.

For sampling Period 1, regardless of the sampled municipality, within the different use systems, factors such as hydraulic conductivity and resistance to root penetration, as well as microbial biomass, showed the greatest relationship with the diversity of organisms in the landscape (Table 5 of the Supplementary Material). As in sampling Period 2, which relates to a high correspondence between vegetation characteristics (percentage of VegCover, C, and Ldw), microbiological attributes of the soil (microbial biomass) and PRes as Coleoptera families were determinants of plant diversity in the land use systems studied (Table 8 in the Supplementary Material).
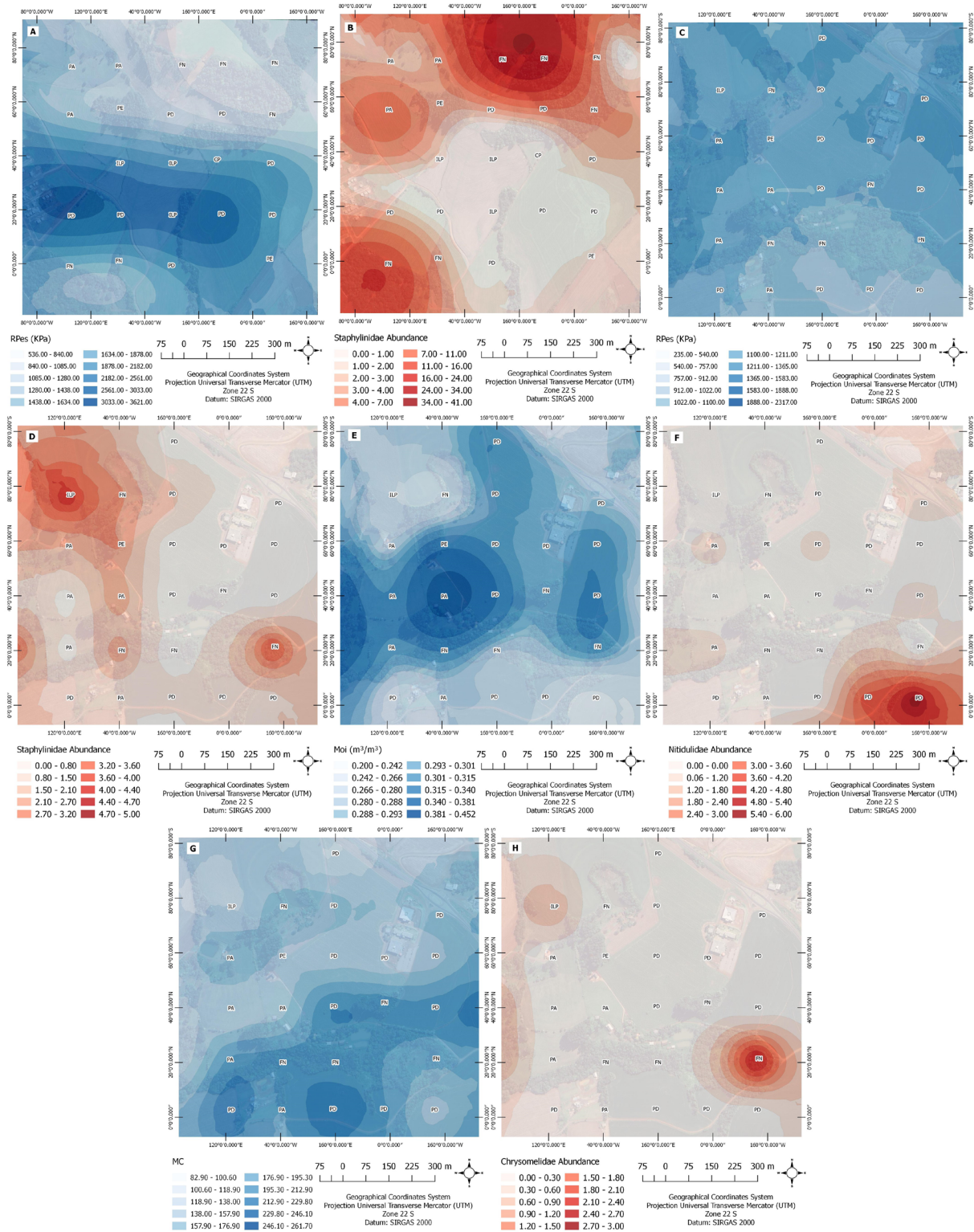
Figure 4 – Geostatistical modeling of soil use and cover system for Period 1 from penetration resistance (PRes — kPa) (A, C) data and family Staphylinidae (B, D) abundance for the municipality of Chapecó; Moi (m³/m³) (E) and abundance of the Nitidulidae (F) family; MC (G) and family Chrysomelidae (H) abundance in the municipality of Pinhalzinho.

NT: direct planting system (no-tillage); NF: native forest, PA: pasture; EP: *Eucalyptus* plantation; CLI: crop-livestock integration; SV: shrubland (shrub vegetation); PRes: penetration resistance; Moi: soil moisture; MC: microbial carbon.

Soil conditions such as compaction and silt content have a negative influence on taxonomic metrics (Correa and Da Silva, 2022). Soil compaction is a limiting factor for the soil community, because compacted soil ends up promoting an anaerobic environment, with a decrease in air and water circulation (Pompeo et al., 2017), also affecting the occurrence of soil microorganisms (Pessotto et al., 2020). In comparison, soils in natural areas are generally more porous than in anthropic areas, mainly due to the greater predominance of Bio, which promotes the concentration of a greater number of Coleoptera families. since these pores can serve as shelter and space for movement of individuals (Pompeo et al., 2017, 2020).

The increase in PRes in areas of NT and/or CLI occurs due to external pressure applied to the soil, resulting from machinery, which promotes the accommodation of particles and a reduction in pore space (Valente et al., 2018), in addition to the action of animal trampling causing compaction in integration areas. Another factor that corroborates the data is the greater diversity of roots found in natural environments when compared to man-made environments, increasing the number of Bio due to root growth and biological activity, associated with lower values of PRes (Dos Santos et al., 2019) found in native areas.

Within the different land use systems, the study can select some bioindicator families at each sampling time, in addition to demonstrating that areas with greater fragmentation, as in the case of São Miguel do Oeste, presented lower biodiversity (Tables 1 and 2 of the Supplementary Material), which answers to hypothesis III.

The Staphylinidae family is generally associated with areas of native vegetation, conditioned by the total porosity of the soil (Pompeo et al., 2017), which determines its lower occurrence in areas with greater compaction and high resistance to root penetration. The Staphylinidae family is also sensitive to levels of soil OM, K, and Ca (Portilho et al., 2011), with a preference for more preserved areas, environments that offer moderate and favorable climatic conditions and with a high degree of litter (Fernandes et al., 2011). This explains the ecological attributes of beetles from the Staphylinidae family, such as their excavatory, phytophagous, and saprophagous habits, consequently leading to the movement of OM in the soil (Baretta et al., 2006). Furthermore, the family's lower abundance values associated with the CLI system may be related to this family's habitat preference on the soil surface, closer to the litter (epigeans) (Audino et al., 2007); as well as due to their predatory habit, the occurrence and abundance of these insects are also closely associated with the availability and characteristics of prey in the area (Paliy et al., 2020). In the present study, the Staphylinidae family showed greater response potential as an indicator of the native vegetation system.

The Nitidulidae family is characterized by detritivorous habits, performing the function of recycling plants and animal organic matter. Furthermore, some species in this family are considered grain pests (Boston et al., 2020). Food habits explain the greater abundance of this family in direct planting areas close to fragments of native vegetation, as these constitute a system with high litter deposition (Spera et al., 2019; Salomão et al., 2020). This family is more adapted to winter and dry environments (Patucci et al., 2018) due to the different feeding habits of the species and high adaptability (Audino et al., 2007).

Modifying the soil cover system promotes changes in the flow of nutrients in the ecosystem, impacting the dynamics of soil microbial biomass, with higher MC values being associated with natural systems (Primieri et al., 2017). The degradation of organic matter promoted by some species of Coleoptera has an effect on nutrient cycling, favoring the activity of microorganisms and the interaction between fauna organisms and soil microorganisms (Pereira et al., 2020). The greater abundance of Coleopterans of the Chrysomelidae family in areas of native vegetation can be explained by their phytophagous habits, feeding mainly on leaves (Audino et al., 2007).

The VegCover index takes into account factors such as the percentage of vegetation, the ratio of the percentage of vegetation to straw, and the percentage of bare soil. Pompeo et al. (2023) associated higher VegCover values with greater abundance of Coleoptera because greater Vegcover collaborates in the maintenance of the microclimate. Contrary to what was expected with the result for areas of native vegetation, the VegCover index represents an important alert to the relationship between anthropogenic soil uses and native vegetation in microlandscapes. That is, fragments of native vegetation in the Pinhalzinho microlandscape presents other types of use in its interiors, which compromises its environmental quality.

The Scarabaeidae family, popularly known as dung beetles, is associated to the system with the greatest anthropogenic disturbance and the lowest VegCover index, which is in line with the functional characteristics of many species in this family. Among these characteristics, the detritivorous habit of scarabeids stands out, acting in the cycling of OM and decomposition of some agricultural inputs, for example, the litter itself (Wang et al., 2017; Gruss et al., 2019). This explains the family's association (detritivorous habits) with PA areas. On the other hand, beetles from the Salpingidae family are mainly found under the bark of trees in deciduous and coniferous forests, feeding on fungi, OM, and other insects (Kakiopoulos and Demetriou, 2022), which explains the greater diversity of this associated family to the highest VegCover rates (Figure 5).

The use of spatial modeling, represented by semivariograms and kriging maps, made it possible to visualize the spatial distribution of the variables studied in the different municipalities, providing a more in-depth understanding of the relationships between Coleoptera and their environment. The results of the TITAN reinforce the importance of spatial analysis when identifying specific families as indicators in different regions. The association of these families with environmental variables, evidenced through maps and graphs, highlights the capacity of spatial analysis to reveal patterns of ecological response in different geographic contexts.
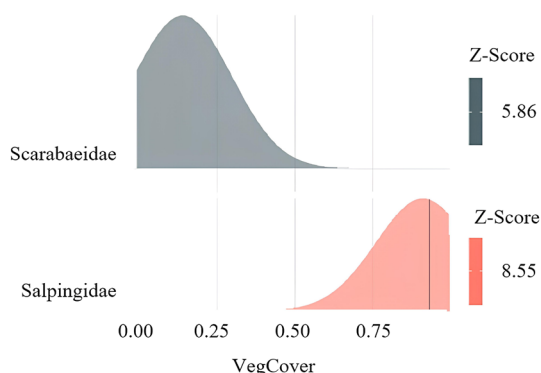
Figure 5 – Results from the Threshold Indicator Taxa Analysis (TITAN) for the selected variables in the Period 2 collection.

This spatial approach is crucial to understanding how local factors can influence the distribution of organisms, thus contributing to the development of more effective conservation and management strategies.

Regarding the modeling of organisms on a landscape scale, some authors prove the feasibility of using geostatistical models in predicting species of the Coleoptera order related to the phytosanitary control of species in cultivation systems (Reay-Jones, 2017; Pinchao and Muñoz, 2019; Dionisio et al., 2020) and productivity (Lovera et al., 2018). Thereby, the geospatial contribution, among other analyses, was considered a tool to evaluate the influence of soil attributes on other organisms, highlighting the importance of vegetation cover in maintaining soil characteristics and its relationship with edaphic organisms.

Conclusions

Physical and microbiological attributes as well as soil vegetation cover affect the abundance and richness of Coleoptera families.

Higher penetration resistance values promoted a lower abundance of Coleoptera from the Staphylinidae family, while lower moisture values promoted a higher abundance of the Nitidulidae family. The highest concentration of microbial carbon explained the greater abundance of the Chrysomelidae family.

The Staphylinidae, Nitidulidae, Crhysomelidae, Scarabaidae, and Salpingidae families have potential as soil bioindicators and are affected by the fragmentation of native vegetation and the reduction of habitats that promotes the loss of diversity of these organisms, and can be spatially modeled by Geostatistics.

The study shows that the geostatistical tool, commonly applied to study soil chemical characteristics, has the potential to graphically represent the occurrence and distribution of Coleoptera and other soil organisms in landscape studies.

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Authors' contributions

NARCISO, N.B.: conceptualization, data curation, writing – original draft. POMPEO, P.N.: acquisition, investigation, methodology. BARETTA, D.: Writing – review & editing. REZENDE, R.S.: software, validation. BARETTA, C.R.D.M.: conceptualization, project administration, supervision, validation, writing – review & editing.

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