

SPATIAL MODEL FOR PREDICTING COMMUNITIES OF PREDATORY MITES (MESOSTIGMATA) OF LEAF LITTER

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Abstract: The importance of the predatory mites Mesostigmata of the litter lies in its function of population regulation to maintain the balance of soil organisms. Leaf litter is one of the main habitats of these organisms, however, the effect of its properties on the spatial distribution of mites is still unknown. The objective of this research was to know the effect of physical and chemical properties of litter on the abundance of mites. Litter from coniferous, deciduous, and mixed forests was sampled, these forests were located 90 km northwest of Peace River, Alberta, Canada. The generalized additive model (GAM) with the negative binomial distribution modeled the overdispersion of the mite frequency, with an explained deviance of 71.8%. Second degree non-linear relationships were significant between the total abundance of Mesostigmata mites and the variables of Elevation, depth, temperature, humidity and pH. The relationship between abundance and geographic coordinates was fifth order, indicating that the greater abundance of mites was the result of geographic variability. The optimal conditions for the production of Mesostigmata mites are: Elevation below 700 meters above sea level, depth greater than 12 cm, temperature between 11 to 12 degrees centigrade and acidic pH. The least favorable percentage of humidity is between 60 to 90%. The number of mites in the coniferous forest (CD) was statistically equal to that in the deciduous forest (DD), but different from the mixed forest (MX) with $p < 0.05$, the latter having a higher abundance of mites. It is concluded that GAM models are useful to estimate the abundance of mites and predict them in adjacent areas that have not been sampled.

Keywords: predatory mites, Mesostigma, boreal forest, generalized additive model, geospatial, GAM.

INTRODUCTION

Mites constitute the most diverse group of arachnids with a cosmopolitan distribution, they inhabit terrestrial and aquatic environments, they present a great variety of feeding habits and establish different relationships with practically all living beings (Pérez, et al., 2014). In particular, the boreal forest has a large amount of soil fauna within which the Mesostigmata mites are identified, which affect various soil processes (Díaz et al., 2013). These processes produce distinctive biochemical and physical characteristics that are closely related to the development of deciduous, coniferous and mixed forest stands. Under the premise that forest soil communities are closely associated with physical and chemical soil characteristics, it is essential to identify the optimal conditions for the production of predatory mites (Mesostigmata), which are essential to maintain the balance of soil organisms. These soil organisms have been the subject of study to produce them as biocontrollers for commercial agricultural products such as onions (Rivest and Kharouba, 2021). Chaires-Grijalva, et al. (2015) have studied them for their importance as biological control agents for bark beetles.

Regarding statistical modeling, Mineriro et al. (2009) have studied the distribution of mites in the soil, using the Shannon diversity index. Minor and Cianciolo (2007) applied bootstrap resampling to study the effect of various types of land use on the abundance of various Mesostigmata mite species, while Manu et al. (2022) applied multivariate analysis to find a relationship between communities of soil mites (Acari: Mesostigmata) with some environmental variables in experimental grasslands of the Bucegi mountains in Romania. Although the literature review reports classic statistical methods to evaluate strictly linear relationships between the

abundance of mites and various variables of interest, no research is reported where possible non-linear relationships are identified. Due to the above, this research proposes the use of GAM models (Wood, 2017), whose characteristics are discussed below.

MATERIALS AND METHODS

GENERALIZED ADDITIVE MODEL

The Generalized Additive Model (GAM) proposed by Hastie and Tibshirani (1986) is an extension of the Generalized Linear Model (GLM) of Nelder and Wedderburn (1972). It is a non-parametric regression that relaxes the assumption of linearity between the response variable and the covariates, which allows the discovery of non-linear relationships between them. The linear predictor of the GAM models is expressed as:

$$g(\mu_p) = X_i^* \theta + f_1(x_{1p}) + f_2(x_{2p}) + f_3(x_{3p}, x_{4p}) + \dots$$

Where $X_i^* \theta$ is a fixed effects function such that X_i^* is the i -th row of the design matrix of the fixed effects model θ is a parameter vector. smoothing functions $f_i(x_p)$, they allow, in a very flexible way, to specify the dependency between the response and the covariates (Wood, 2017). In particular, $E[y_i] = \mu_p$, where has a distribution belonging to the exponential family and it is a known function, called the link function that connects to with the linear predictor. Like the GLMs, the GAMs allow the modeling of response variables with distributions belonging to the exponential family, which includes both continuous (normal, gamma, and inverse Gaussian) and discrete (binomial and Poisson) distributions. A distribution belonging to the exponential family can be written as:

$$f_\theta(y) = \exp \left[\frac{y(\theta) - b(\theta)}{a(\phi)} + c(y, \phi) \right]$$

where a , b and c are arbitrary functions, θ is a natural parameter of the distribution and ϕ a scale parameter. It must be noted that a difference between the GLM and GAM models is that the former are restricted to modeling independent observations in contrast to the latter, which can model dependent and independent observations, through time or space (Toriz-Robles et al., 2019). Additionally, the GAM models have been adapted to incorporate the negative binomial distribution, $X \sim BN(\theta^*, \mu)$, where $\text{prob} = \theta^* / (\theta^* + \mu)$, θ^* is the dispersion parameter, μ represents the number of failures before achieving desired number of successes, in particular, $\text{var}(X) = \mu + \frac{\mu^2}{\theta^*}$; $\theta^* > 0$). The link function for this distribution is $g = \log$.

REPRESENTATION OF A SMOOTHING FUNCTION

A smoothing function depends on the observations of a given point known as a node (knot, for its acronym in English) and the neighboring observations. The most commonly used smoothing functions are polynomials (splines). The nodes divide the range of each covariate (x) in regions. Splines depend on three elements, the degree of the polynomial, the number of nodes, and the location of the nodes. The most used function is the cubic spline, which is a curve built through the sum of polynomials around each node, which are assembled to form a continuous curve. Their flexibility lies in the fact that they have continuous second derivatives and inflection points (Mamouridis, 2011 and Wood, 2017). GAM models are preferred over lowees models (locally weighted least squares regression (Cleveland, 2007), because the latter can produce predictions less than zero or greater than 1 when dealing with binomial data (Agresti, 2015).

A smoothing function: (f) can be represented as:

$$f(x) = \sum_{i=1}^q b_i(x)\beta_i$$

where $b_i(x)$ is a known basis function, q is the degree of the polynomial, and β_i is the regression parameter associated with: $b_i(x)$. A spline of degree, is a curve, formed by sections of polynomials. For example for the cubic spline ($q=3$), the bases are: $b_1(x) = 1$, $b_2(x) = x$, $b_3(x) = x^2$, $b_4(x) = x^3$. Regression versus smoothing functions (f) it is also known as spline regression (Wood, 2017). It must be noted that the R software has at least two types of smoothing functions, for the cases: isotropic, that is, for when the covariates are on the same scale; and the tensor product, for when the covariates have a different unit of measurement or have a different variance (Wood, 2003).

ESTIMATION OF THE SPLINE PARAMETERS

For the case of an explanatory variable, the penalized maximum likelihood estimation of the vector: $\beta = (\beta_1, \beta_2, \dots, \beta_q)$ is achieved by minimizing by maximum likelihood the expression:

$$\|y - x\beta\|^2 + \lambda\beta^T S\beta \quad (1)$$

where S is a matrix of known coefficients associated with the basis functions: $(b(x))$ and λ is the smoothing parameter, which sets a tradeoff between goodness-of-fit and smoothness, allowing less overfitting. The second component of (1) penalizes for the excess “waviness” of the “spline”. The estimator of: β is $\beta = (X^T X + \lambda S)^{-1} X^T y$. In the case of covariates, the likelihood function to be maximized can be written.

What: $l_p = l(\beta) - \frac{1}{2} \sum_j \lambda_j = \lambda_j \beta^T S_j \beta$, where is the likelihood function of a generalized linear model and λ_j ; $j = 1, 2, \dots, p$, are the smoothing

parameters that are estimated rather than set arbitrarily (Wood, 2017).

EVALUATION OF A GAM MODEL

The most important measures to evaluate a GAM model are the deviance and the GCV score. The first is defined as:

$$D = 2[l(\hat{\beta}_{max}) - l(\hat{\beta})]\phi$$

where $\hat{\beta}_{max}$ is the maximum likelihood function of the saturated model and $l(\hat{\beta})$ is the maximum likelihood function of the fitted model. The saturated model is a model with one parameter for each data. The scaled deviance is: $D^* = D/\phi$, where ϕ is a scale parameter. Scaled deviances play an important role in likelihood ratio tests, since the difference in scaled deviances of two models is a distribution:

χ^2 , with y degrees of freedom. The GCV score is the generalized cross-validation function of the fitted GAM model. The GCV score can be used as the Akaike and Shewhartz information criteria are used, to compare various models (Wood, 2017). when known: ϕ , one measure for comparing models is the

Unbiased Risk Estimator (UBRE), which is a scaled AIC.

The software R (2019) and RStudio (2022), in its version 4.2.0, was used to generate the results.

STUDY CASE

The study to determine the abundance of Mesostigmatamites was carried out in the boreal forest, located 90 km northwest of Peace River, Alberta, Canada (Longitude: -118.419712, -118.324707. Latitude: 56.745673, 56.818255). This forest was included in the Ecosystem Management Emulating Natural Disturbance (EMEND) project. EMEND is a large-scale (1000 ha) variable retention forest harvesting experiment established within an area of 7000 ha. The climate of this region is characterized

by long, cold winters and short, moderately hot summers. Average temperatures range between $-15.4\text{ }^{\circ}\text{C}$ in January and $16.4\text{ }^{\circ}\text{C}$ in July, the frost-free period is less than 90 days, and the average annual rainfall is 378 mm, occurring mainly in June and July (Environment Canada, 2011). The study area is located at an elevation between 689 and 838 masl with a gently undulating topography. The soils have formed predominantly on fine-textured glaciolacustrine parent materials, with the exception of the southwestern part of the experimental site where the soils developed on heterogeneous sediments of glacial “till” origin (Lindsay et al., 1958). Most of the area is Luvisols Orthic and Dark Gray soils, while soils of the Brunisols, Gleysolic and Solonetzic orders are found in a smaller proportion (Kishchuk, 2004); soils vary from fair to imperfectly drained depending on texture and slope position.

In this study, the abundances of Mesostigmata litter mites in naturally disturbed forests were evaluated, that is, the control stands constituted three types of successional vegetation cover that originated from forest fires ~80 and 140 years ago. In the control forests, there are no records of

disturbance by recent fires or insect outbreaks, nor any form of anthropogenic disturbance in the last 80 years. Based on the type of tree cover, they were classified as: i) Deciduous or coniferous forest with $> 70\%$ trembling aspen (*Populus tremuloides* Michx.), ii) Coniferous forest dominated by $> 70\%$ white spruce (*Picea glauca* (Moench) Voss), and iii) Mixed forest composed of approximately 35% *P. glauca* and 65% *P. P. tremuloides*.

FIELD SAMPLE

For this study, three replicate stands of each forest type with an extension of ~10 ha each, distributed randomly in the EMEND project area, were chosen. The stands of the deciduous forest were 852, 862 and 940, those of the mixed forest were 867, 902 and 928 and those of the coniferous forest were 889, 918 and 930 (Figure 1).

Leaf litter samples from each replicate were collected for Mesostigmata predatory mites in September 2006. Three subsamples were collected from each replicate stand in three of the six permanent plots (which are 2m x 40m in width and length). m); which were randomly selected in each replica of each experimental

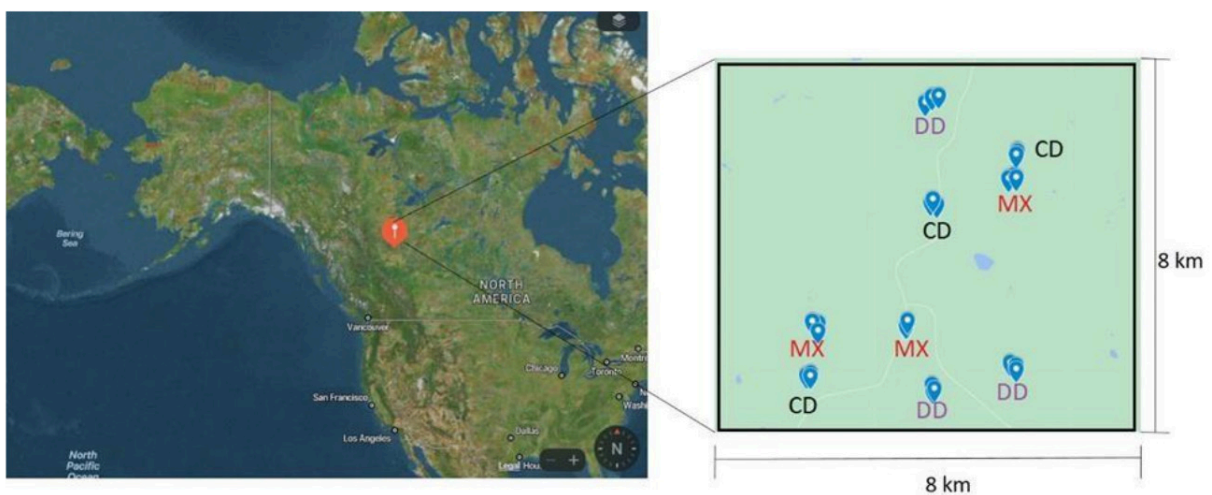


Figure 1. Study zone. Country Canada. Province: Alberta. Region: Northern Alberta. Length: $-118.419712,-118.324707$. Latitude: $56.745673, 56.818255$.

stand (for more details, see Volney et al., 1999), obtaining a total of 9 subsamples per forest type and analyzing a total of $n=27$ subsamples. To avoid interference with other projects and minimize the influence of human disturbance, sampling points were set 10m apart from the left side along the 40m vertical side of each permanent plot.

Predatory mites were the least abundant, constituting <5 to 20% of the total Acari found in litter and soil (Petersen and Luxton, 1982). In this study, a 25 cm diameter metal cylinder was used to take samples of the forest litter and guarantee the collection of a greater number of individuals in each sample. At each sampling site, three measurements of explanatory variables were taken, such as forest litter thickness and temperature, around the cavity in the L-F-H organic horizons, using a digital thermometer. In addition, additional samples of the litter were taken at each sampling point to determine the moisture content and estimate the pH, with a 0.01 M CaCl₂ solution, in a ratio of 1:10 using 10 g of ground litter (Davey and Conyers, 1988).

The litter samples were placed in hermetically sealed plastic bags and stored in a portable cooler for transport, maintaining an average temperature of 10°C using cryopacks for transport and once in the laboratory, the samples were stored at 5 °C until the extraction of the mites (for more details on the collection of litter variables, see Díaz-Aguilar et al., 2013).

MITE EXTRACTION AND IDENTIFICATION

Mesostigmata mites were extracted from litter samples using Tullgren-type funnels (24.8 cm in diameter) according to the recommendation of Crossley Jr. and Blair (1991) and Edwards (1991), who recommend them for organic soils; in most cases the

extraction efficiency exceeded 80% (van Straalen and Rijninks, 1982). The samples were kept in the funnels for ~5 days and the litter microarthropods were collected in plastic vials with 70% ethanol. Mesostigmatan mites were separated, sorted and counted under a stereoscopic microscope at 15 to 40x magnification, rinsed in 85% lactic acid for one to several hours depending on the degree of transparency required for each specimen, mounted on slides in medium. PVA (polyvinyl alcohol from BioQuip Products Inc.) and then dried at 45°C for 4-5 days using a hot iron.

A total of 4,045 specimens were counted, including adults and immature stages such as deutonymphs and protonymphs, they were classified into morphospecies and, later, mites of the order Mesostigmata were identified under optical and phase contrast microscopy, identifying those of the Gamasina and Uropodina cohorts, as well as the mites of the Sejida suborder, for this the use of electronic keys at different taxonomic levels such as those of Walter and Proctor (2001) and Walter (2006) was required.

A particularly interesting feature of the fauna was the great diversity of species of zerconids of the genus *Mixozercon* (Halašková, 1963), including *M. albertainensis*, *M. jasoniana* and *M. borealis*, species found exclusively in western boreal forests.

RESULTS AND DISCUSSION

The descriptive statistics of 27 observations of the abundance of mites (Table 1), showed the presence of overdispersion by showing a variance much greater than the mean. The significance levels to test the null hypothesis regarding the Poisson and negative binomial distributions were zero and 0.08, respectively. Therefore, all analyzes were performed with the negative binomial distribution.

The software used was R (2022) and RStudio (2022). The main packages used were:

Variable	Average	Variation	D.E. [†]	Min	Max
Abundance (frequency)	145.81	7553.39	86.91	6.00	341.00
Elevation (msn)	750.72	2853.405	53.42	689.70	838.30
Humidity (%)	74.99	177.84	13.34	55.21	100.00
Temperature (°C)	10.44	1.97	1.40	8.50	14.10
pH	4.90	0.31	0.55	3.60	5.80
Depth (cm)	8.46	15.67	3.96	4.00	20.50

[†] D.E. Standard deviation. Minimum: Minimum. Max: Maximum.

Table 1. descriptive statistics of the chemical and physical variables of litter and abundance of Mesostigmata mites from boreal forest in Alberta, Canada.

dplyr: pipeline programming, RcmdrMisc: descriptive statistics, ggplot2: plotting, fitdistrplus: negative binomial distribution fit, vcd: goodness-of-fit for discrete distributions, car: qq plots, MASS: BN regression, grDevices: font backgrounds, mgcv: fit of GAM models and mgcViz: analysis of residuals of GAM models

The GAM model adjusted with $k=3$ knots was:

$$g(y_i) = B_j + te(ele, k) + te(temp, k) + te(pro, k) + te(ph, k) + te(hum, k) + te(X, Y, k) + e_i$$

$$y_i \sim BN(\theta^* = 1.91, \mu = 145.81) \quad y \sim g = \log(2)$$

Where:

y_i : number of mites; B_j : type of forest, where $j=1$: coniferous forest, $j=2$: deciduous forest, $j=3$: mixed forest; *ele*: Elevation in msnm; *temp*: temperature in degrees centigrade; *pro*: depth in cm; *ph*: pH; *hum*: moisture in %; *X*: Longitude in geographic coordinates, *Y* Latitude in geographic coordinates and e_i experimental error with normal distribution and constant variance. the softener *te* is the product tensor and $k=3$ is the number of knots.

The explained deviance of the model was 71.8%, with a value of UBRE= 14.79 and a scale statistic =1. This model indicated that the number of mites in the coniferous forest

(CD) was equal to (DD), but different from the mixed (MX) with a value of $p < 0.05$ (Figure 2).

The Shapiro Wilks test indicated that the distribution of the residuals was normal (p -value= 0.679). The residuals presented a random behavior (Figure 3) and the regression between the adjusted values explained by the predicted ones showed an intercept with a value of 8.0317 that was not significant (p -value = 0.679) and a slope with a value of 0.9437 that was significant (p -value = 1.84). $e-08$).

The relationship between each predictor with the response variable was significant and non-linear, the smoothing functions were of second degree (Figure 4).

The highest abundances of mites predicted by model 2 were obtained at elevations below 730 masl. The temperature between 11 and 14 °C favors the abundance of Mesostigmata mites. Depths greater than 13 cm, acid pH (below 4.5) and humidity below 70% and above 90% also favor the presence of Mesostigmata mites (Figure 4).

Elevation, in combination with temperature between 11 and 120 °C, increases the presence of mites (Figure 5). The same happens in combination with the depth between 13 and 18 cm (Figure 6) and with a pH below 4.5.

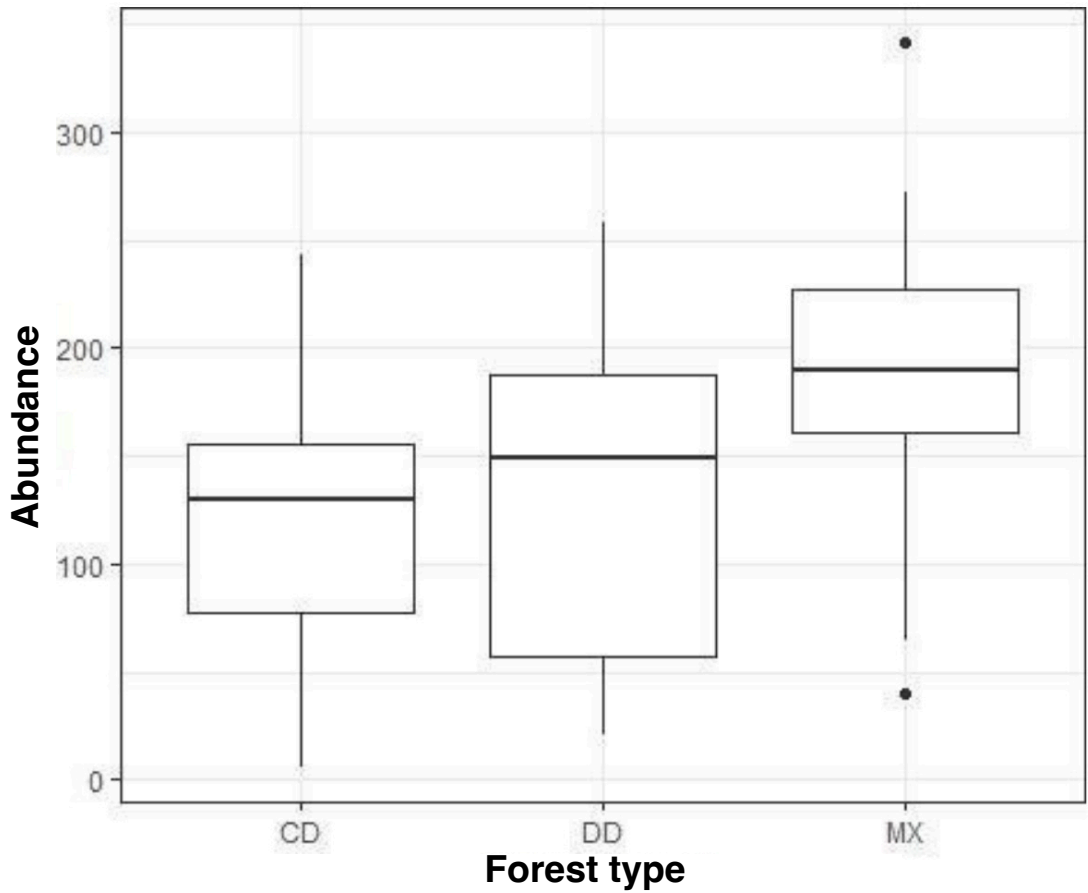


Figure 2. Box-and-whisker plot of the number of Mesostigmata mites in coniferous (CD), deciduous (DD) and mixed (MX) forests.

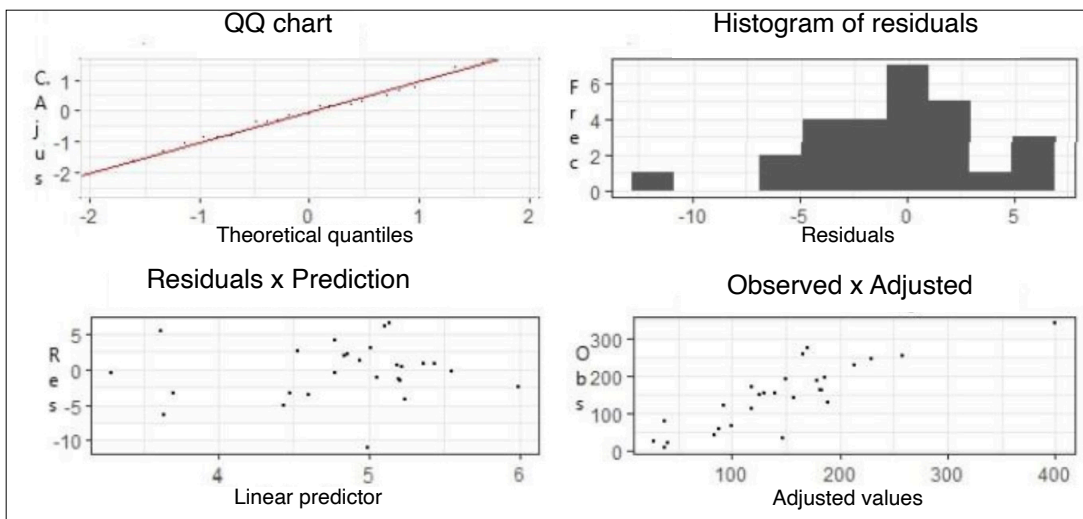


Figure 3. Plots for Residual Analysis.

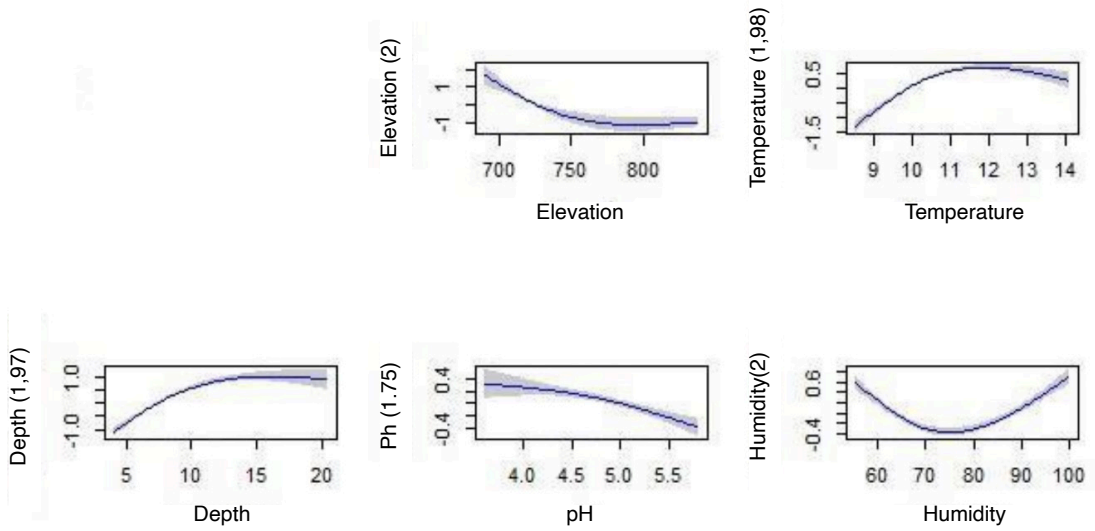


Figure 4. Relationship between predictor variables (horizontal axis) and Mesostigmata mite abundance (vertical axis)).

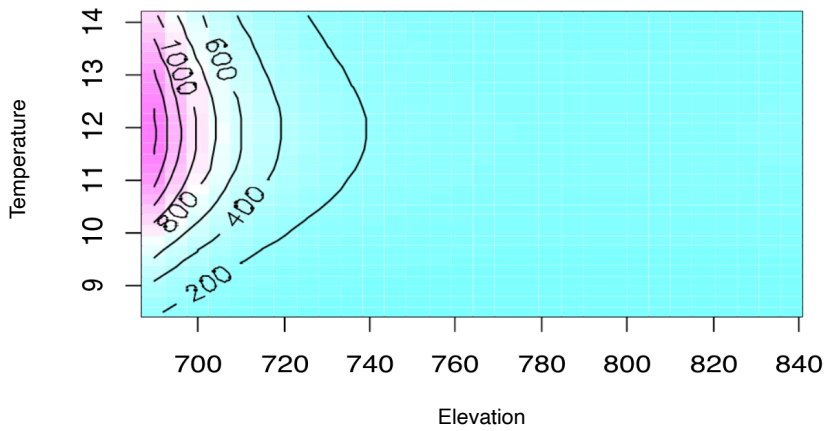


Figure 5. Prediction of Mesostigmata mites as a function of elevation and temperature.

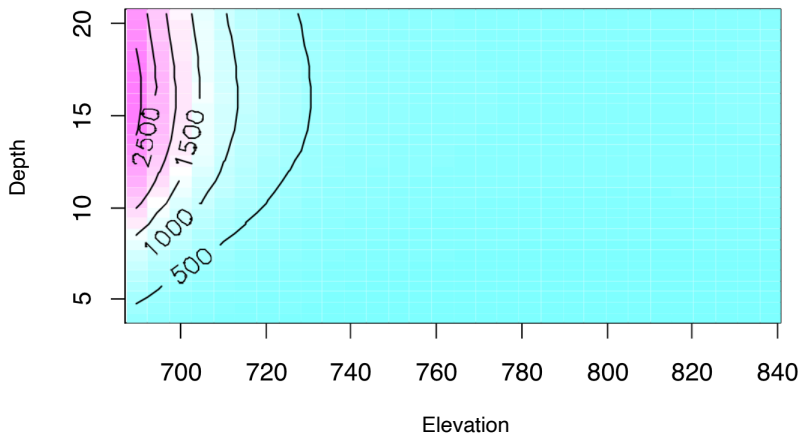


Figure 6. Prediction of Mesostigmata mites as a function of elevation and depth.

Humidity produces greater abundance below 60% and above 90%. This pattern was consistent with depth between 18 and 20 cm (Figure 7) and pH below 4.5 (Figure 8).

Temperature in the range of 11 to 13°C and a depth of 11 to 20 cm produces greater abundance of mites (Figure 9) and with pH values below 4.5 (Figure 10).

The relationship between abundance and geographic coordinates was fifth order, indicating that the greatest variation in abundance of predatory mites was the result of spatial variability. The greatest abundance was observed to the east and south (Figure 11).

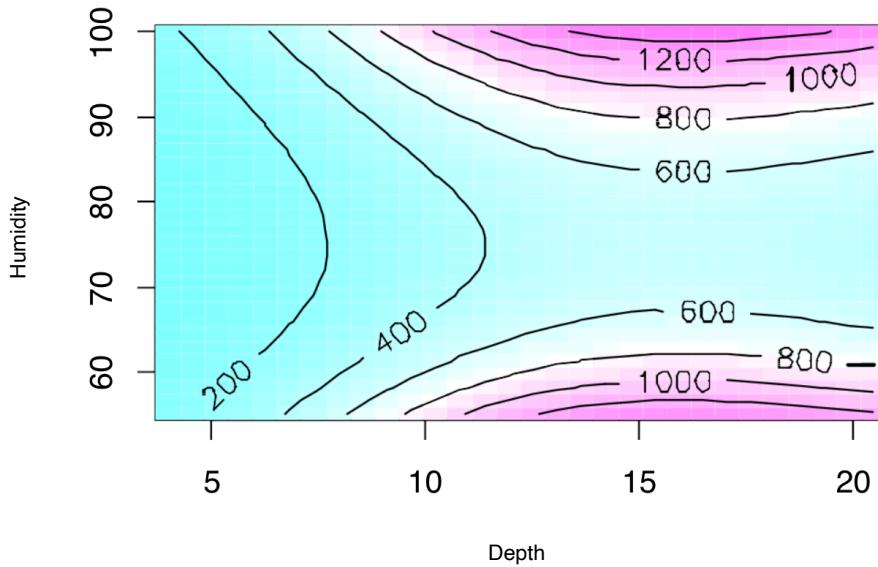


Figure 7. Prediction of Mesostigmata mites as a function of depth (cm) and humidity (%).

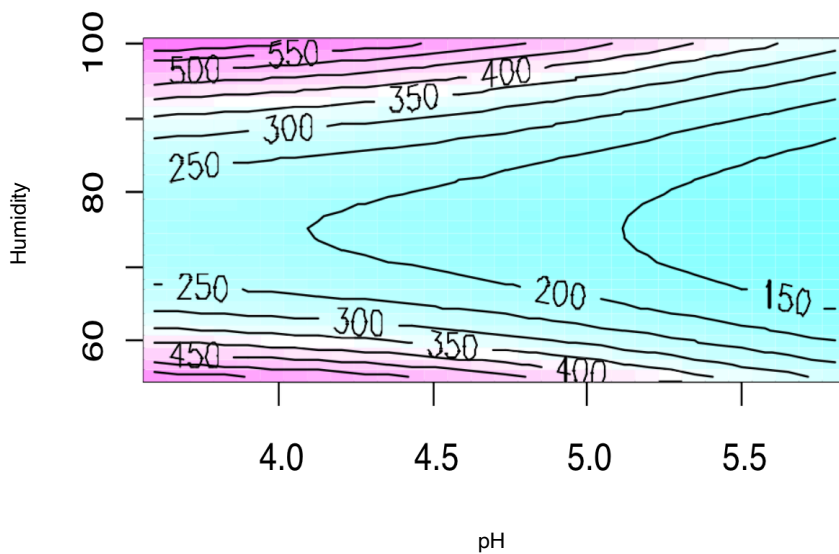


Figure 8. Prediction of Mesostigmata mites as a function of pH and humidity (%).

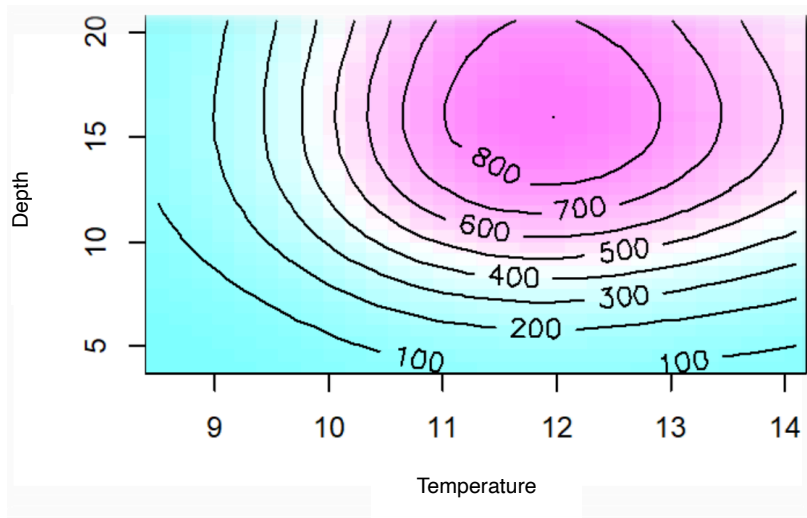


Figure 9. Prediction of Mesostigmata mites as a function of Temperature (0C) and depth (cm).

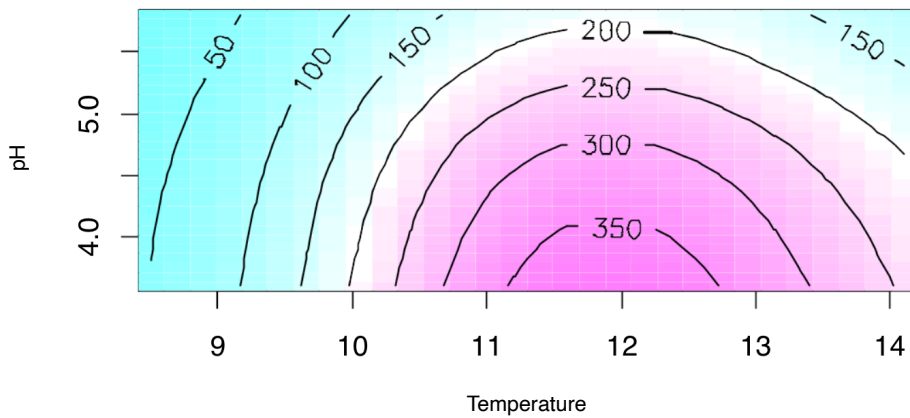


Figure 10. Prediction of Mesostigmata mites as a function of Temperature (0C) and pH.

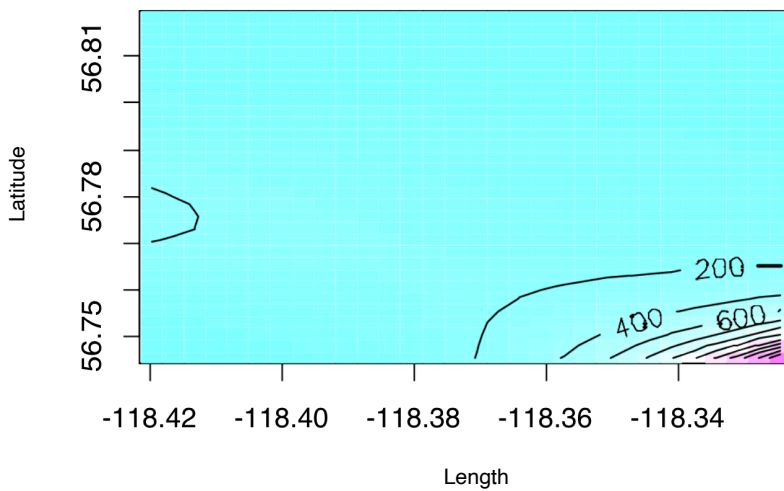


Figure 11. Prediction of Mesostigmata mites as a function of longitude and latitude in geographic coordinates.

CONCLUSIONS

The spatial variability of the physical and chemical variables of the litter, have a non-linear influence on the abundance of predatory mites. The mixed forest was characterized by having a higher number of Mesostigmata mites than the coniferous and deciduous forests. Geography, measured by geographic coordinates, significantly

influences the presence of mites, which have a greater presence to the east and south of the sampling area. It is concluded that the application of a statistical model is useful to quantify the abundance of mites in adjacent areas that were not sampled. The predicted total abundances were consistent with those found in the field, which validated the model.

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