

## 1- Introduction

Understanding how ecological communities are organized across space scales is a long-standing question in community ecology with a well-established conceptual framework ((Decaëns, 2010); (Azaele et al., 2015)). In these works, authors highlight the importance of considering the spatial  
5 scale in analysis. Thus, spatial scale is the targeted area where samplings are done. In this area, multiple spatial processes are played out, creating unique biodiversity patterns. Moreover, these processes are possible thanks to filtering, that is to say, environmental influences that limit biodiversity (Hutchinson, 1957). Similarly, biologic interactions within species tends to limit biodiversity as major part of them constrains individual. However, understanding the relative part of  
10 spatial process, environmental filtering and biotic interactions in multi-trophic community assemblage still deserve much works. The importance of holding area constant in analysis has been accentuated, as is the notion that different environmental factors exhibit measurable heterogeneity at different scales (Wells et al., 1999) proposed and (Whittaker et al., 2001). In other words, the ecological filters do not affect the diversity with the same intensity (Whittaker et al., 2001), (Chase  
15 et al., 2019). It's important to identify how species richness change across spatial scale and what are the main drivers of these changes (Chase et al., 2019) to guide preservation and protection of biodiversity (Whittaker et al., 2001).

A large amount of metrics are available to estimate biodiversity (Pulleman et al., 2012) ; (Konopiński, 2020) ; (Tuomisto, 2010). Most metrics also have advantages, drawbacks, and habitat  
20 or scales preferences (Pulleman et al., 2012; Dopheide et al., 2020; Willis, 2019).  $\alpha$ -diversity informs about a single and target location.  $\beta$ -diversity refers to compositional changes between samples.

$\alpha$ -,  $\beta$ - and  $\gamma$ -diversity are under the influence of many factors, such as geographic distance, environmental variables or biotic interactions (Rodriguez-Artigas et al., 2016). The  $\beta$ -biodiversity  
25 is not equally influenced across spatial scale (Steiner & Leibold, 2004). This is why, (Ferrier et al., 2007) explained how to study  $\beta$ - diversity with a global dissimilarity model. In order to understand how spatial scale described  $\alpha$ -diversity, (Joseph, 2002) showed the additive partitioning model, in adequation with null model which create a pattern where diversity is only explained by randomness.

While many studies focused on aboveground communities and their dynamics through time and  
30 space, the belowground part of the ecosystems still remain poorly studied (Vaněk, 1975); (Nielsen et al., 2010). The soil hosts a huge amount of diversity, as well as it contains many terrestrial fauna families (Gongalsky, 2021), We only know at best a tiny fraction of the existing species diversity, and our knowledge of both the distribution and abundance of many known species remains very

poor (Wilson & Barker, 2019); (Decaëns, 2010); (Turner, 2021). In addition, soil organisms are  
35 involved in ecosystems functioning and biogeochemical cycles, putting compounds into movement,  
accelerating decomposition and mineralization (Bradford et al., 2002); (Lal et al., 2015)

In this context, mountains ecosystem represents a unique matrix, where soils are diverse in  
composition, structure and thus, biodiversity hosted. In this logic, it might be interesting to invest  
mountain biodiversity patterns in order to better know these ecosystems.

40 Several researches have used elevation gradient to highlight the factor structuring soil fauna  
(Fischer et al., 2011).; (Peters et al., 2016); (Yin et al., 2017). These researches are focusing on  
elevation gradient as a synthesis a lot of direct and indirect factors, such as pH, temperature, water  
deficit, incident light. The number of variables involved in an altitudinal gradient makes this system  
very unique (Körner, 2007). Elevation gradients exhibit complex variation in abiotic conditions  
45 over short distances (McCain & Colwell, 2011). It is known that biodiversity tends to decrease as  
elevation increases, because of shelter function at low elevation (Keppel et al., 2017) and harshness  
of the environment at high elevation (Fischer et al., 2011). In order to understand how species are  
distributed in space, it is also relevant to depict the relative role of ecological gradients (Perrigo et  
al., 2020).

50 Soil (macro)fauna (between 1mm and 5 cm) is very diverse and includes many animal families  
(Gongalsky, 2021), leading to complex and different interactions between organisms themselves  
and with abiotic parameters (Fischer et al., 2011) (Perrigo et al., 2020). Recently, (Calderón Sanou,  
2022) found that along elevation gradients, the driving factors differ across trophic guilds revealing  
the relative weight of four main mechanisms (Habitat heterogeneity, Energy, Abiotic Tolerance and  
55 Resource Heterogeneity). Habitat heterogeneity represents soil structure, Energy represents the  
amount of energy that the ecosystem receives, Abiotic Tolerance represents the physiological stress  
that organisms experience (PS), and Resource Heterogeneity the diversity in resources available  
for organisms.

Following (Calderón Sanou, 2022), we focused on macrofauna (not studied in their work) (1) to  
60 depict soil macrofauna biodiversity patterns at various nested scales from soil sample to mountain  
range and (2) to elucidate the relative role of geographic distance, ecological filtering and biotic  
interactions.

The first hypothesis is, that larger spatial scale should explain more diversity than smaller scales, as  
supported by (Pyron & Wiens, 2013), (Qian & Ricklefs, 2007).

65 The second assumption states that, geographic distance is the main factor driving communities at  
larger spatial scales. In other terms, colonization abilities and biogeography should be the principal  
obstacles in organism spreading, as (Drake, 1990) already supported. In addition at intermediate  
scale, we suspect a role of habitat variable, like the vegetation opening or climate influence  
(Beaugrand, 2023). At a lower spatial scale, biologic interactions such as vegetation composition,  
70 predations, competitions should drive communities  $\beta$ -diversity (Calderón Sanou, 2022).  
Finally, we make the assumptions that factors influencing every trophic guild are not totally the  
same, because each trophic guild respond to their own pressure factors (Calderón Sanou, 2022).

## 2- Material and Methods

### 75 2.1. Sampling sites

All the sampling sites are being monitored by Orchamp Observatory (<https://orchamp.osug.fr>). The  
11 studied altitudinal gradients were located in the Alps and the Pyrenees mountains, both in their  
French part : **Argentièrre** (Chamonix Mont-Blanc - 45.985496, 6.947277), **Armenaz** (Ecole –  
45.625926, 6.228909), **Cauterets** (Cauterets – 42.831, 0.174), **Chaillol** (Chaillol – 44.721,  
80 6.187555), **Forêt du Bout** (Pinsot – 45.324, 6.107), **Lac Vert/Vallée du Lys** (Saint Mamet -  
42.72073, 0.5675), **Mounier** (Beuil – 44.142, 6.983), **Pécloz** (Ecole – 45.638226, 6.217314),  
**Ristolas** (Ristolas – 44.724622, 7.031392), **Saint-Barthélémy** (Montségur – 42.838705, 1.797797),  
**Tania** (Courchevel – 45.414, 6.601), **Valloire** (Valloire – 45.126224, 6.397591), and **Ventoux Nord**  
(Beaumont du Ventoux – 44.177, 5.251). Samplings have been realized in 2021 and 2022 during  
85 early Autumn (September to October).

### 2.2. Plots

The permanent plots measure 900 m<sup>2</sup>, and are spaced from each other by a minimum altitude of 200  
m, for every gradient. The lowest starts at 1130 m (Ventoux Nord), and the highest one is placed at  
2940 m (Chaillol). In average, four plots are placed in every gradient. Every plot has the same  
90 orientation, has a homogeneous topography, don't include water stream, are far from paths but can  
include pasture.

### 2.3. Sampling methods

As every organism isn't present at the same depth of the soil, don't have the same physical niche,  
and the same moving pattern, we need to use multiple methods to capture them.

95           **Pitfall traps**

In every plot, six pitfall traps have been placed 15 m apart in two lines at the edges of the permanent plot. A pitfall trap was made of a 125 ml plastic pot, buried up to its superior border and filled with about 40 ml of vinegar over saturated in salt. This solution killed organisms, avoided consumption and conserved individuals. To limit additional organic matter and water filling by rain, a cap was placed 5 cm over the pot. The traps were collected 1 month after their setting. Back at the laboratory, organisms were desalted into tap water during two days and then stored in 98° alcohol.

**Soil hand sorting**

In every plot, four soil monoliths were excavated outside the corners of the permanent plot. Before digging, vegetation was removed and animals in plant litter were hand sorted. Soil blocks were 25 x 25 cm in surface and up to 20 cm in depth. Then, macrofauna was hand sorted from soil blocks and stored in 98° alcohol.

**2.4. Identification**

Lumbricinae, Carabidae, Isopoda and Diplopoda, part of Araneae, part of Myriapoda have been identified precisely to species (or at least to genus) by specialists in laboratory (See Acknowledgements part). For this, the identification keys used were Lumbricinae (Bouché, 1972): Araneae :(Nentwig et al., 2014) Isopoda :(Vandel, 1960) Carabidae :(Coulon & Pupier, 2011), (Jeannel, 1942), Myriapoda :(Demange, 1981) (Brolemann, 1930)

Among all the individual sampled during sampling campaign, 60% have been identified in laboratory.. The other individuals (the remaining 40% of individuals) have been proposed for identification by citizen science through to the web-application Inaturalist. All observations can be found here: [https://www.inaturalist.org/projects/orchamp\\_global](https://www.inaturalist.org/projects/orchamp_global)

Individuals were grouped by morphotypes in each sample. On average two pictures, namely dorsal and ventral view, have been taken for each morphotype. Photographs of small organisms are obtained under binocular magnifier equipped with a 20MP USB3.0 CMOS Camera. The software Capture V2.4 stacks a live video at different focal distances to get a stacked photo. Larger organisms are placed under a Panasonic Lumix 25-600 at ~30 cm from the device.

A unique ID was attributed to each individual that has been photographed. Then photographs were posted on Inaturalist, with metadata (spatial coordinates, date of sampling) and a proposed identification that was then challenged and improved by INaturalist participants. The present dataset

125 corresponds to an extraction from INaturalist the 02/06/2023 that has been merged to identification  
matrix obtained from the Eco&Sols lab thanks to the unique ID attributed to each photographs.

## 2.5. Trophic Guilds creation

In order to create trophic guilds, we looked after the species database composition. We decided to

Variable	Meaning	Unite	Trophic group	Variable Category
TmeanY.mean	Annual Mean Temperature	Kelvin (°K)	The four guilds	Physical stressing variable
TG1.degrees.mean	Annual Mean Temperature (1cm above ground)	Kelvin (°K)		
TG4.degrees.mean	Annual Mean Temperature (4 cm above ground)	Kelvin (°K)		
DSN_T_ISBA.mean	Snow thickness	meter (m)		
PtotY.mean	Annual Precipitations	millimeters (m)		
pH mean	pH	none		
ndvi.mean	The mean of NDVI	none		Energy related variables
ndvi.min	The minimum of NDVI	none		
ndvi.max	The maximum of NDVI	none		
PRCTMOmean	Organic matter content	%		
matrix_l	Vegetal dissimilarity matrix	none (from 0 to 1)		
Rveg	Vegetal specific richness	none (number of species)		
Milieu	The opening of the environnement	0 : open habitat, 1 : forest		Habitat complex factors
Alt	Altitude	meters(m)		
X_L93 and Y_L93	Geographic coordinates	meters(m)		Geographic
Nmean	Nitrogen content	g/kg	Detritivores	Nutrient content
Almean	Aluminium content	g/kg		
Camean	Calcium content	g/kg		
Fermean	Iron content	g/kg		
mgmean	Magnesium content	g/kg		
Mnmean	Manganese content	g/kg		
Phosmean	Phosphore content	g/kg		
Kmean	Potassium content	g/kg		
Namean	Sodium content	g/kg		
Argilemean	Clay content	g/kg		
Calcmean	Calclerous content	g/kg		

155 *Tableau 1: Variables elected for Global Dissimilarity Modeling, with heir meaning, unite, supposed guild influences and categorie belonging*

group Chrysomelidae family and Orthoptera order together as representatives of Herbivores group or green chain. We associated with this group the “Pitfall Trap” method, because it’s mostly species that walk on the ground. Predators group is composed by Carabidae family. The “Pitfall Trap” is also chosen. Detritivores were represented by Clitellata and Diplopoda class, Isopoda order. As they belong to underground organisms, we selected the soil hand sorting method. Finally, parasitoid trophic guild are composed by all the Hymenoptera we gathered, except the Formicidae family. They can be captured thanks to the “pitfall trap” method (Brown & Matthews, 2016).

## 2.6. Environmental data

The selection of variables groups has been done regarding (Calderón Sanou, 2022). Physical Stressing variables come from Physical Tolerance Hypothesis, Variables related to energy are inspired from Energy Hypothesis, and Resource Heterogeneity Hypothesis. Complex Driving factor (Altitude and Opening of Habitat) and Geographic factor have been added, from my own choice, in order to observe the potential hidden effect of these kind of variables (Fischer et al., 2011), and to test dispersal hypothesis. Then, we created the

dissimilarity matrix for plant species (matrix\_1, biotic variable) to compare with main community matrix, also with vegdist. The distance used was Bray-Curtis distance.

For Detritivores, we added a pool of variables, in line with (Tiunov & Scheu, 2004), (Curry & Schmidt, 2007). We decided not to include Habitat heterogeneity group elsewhere than in Detritivores groups, because it's composed of soil characteristics, less important for other trophic guilds (Calderón Sanou, 2022). The variables used for analysis, for all the groups can be found in tableau1.

For every computed GDM, I have tested the significance of predictors by cross validation (function *gdm.crossvalidation*). Unfortunately, the significance is not presented here, by a lack of space.

## 2.7. Scales of analysis

Spatial scales of study targeted for the Additive Diversity Partitioning was between sample ( $\beta_1$  : dissimilarity between samples), between plot ( $\beta_2$  : Dissimilarity between permanent plots), between gradients ( $\beta_3$  : Dissimilarity between elevation gradients).

## 2.8. Statistical analysis

### 2.8.1. Additive Species Diversity Partitioning

We performed an additive partitioning of species diversity to quantify differences in species composition at various nested spatial scales: the sample scale ( $\sim 10^0 \text{ m}^2$ ), plot scale ( $\sim 10^3 \text{ m}^2$ ), elevation gradient scale ( $\sim 10^6 \text{ m}^2$ ). Mean values of species diversity at lower spatial scale ( $\alpha$  diversity, sample) of a sampling hierarchy ( $\beta$  diversity between plots and gradients) are compared to the total diversity in the entire data set ( $\gamma$  diversity, Northern Alps+Southern Alps+Pyrénées).  $\beta_1$  is the compositional diversity between samples, that is to say, between pit traps, or between monoliths of soils.  $\beta_2$  is the compositional diversity between permanent plots and  $\beta_3$  is the compositional diversity between elevation gradients. At the highest sampling level, the diversity components are calculated as  $\beta_m = \gamma - \alpha_m$ . For each lower sampling level as  $\beta_i = \alpha_{(i+1)} - \alpha_i$ . Then, the additive partition of diversity is  $\gamma = \alpha_1 + \sum(\beta_i)$ . In tableau 1, you can find shannon gamma diversity for every four trophic guild.

Guild	Gamma
1 Herbivore	2.56589950958946
2 Predator	2.90040922543079
3 Detritivore	2.36154006169698
4 Parasitoid	1.94591014905531

Tableau 1: Gamma diversity for the four trophic guilds

We used the function `adipart()` from the `vegan` package. We used Shannon diversity to evaluate  
185 diversity. We specified the argument ‘prop’ for weighting diversity index by abundance, and  
performed 150 permutations.

$$H' = - \sum_{i=1}^S p_i \cdot \log_2(p_i)$$

Here is the Shannon Diversity Index Formula :

Where  $p_i$  the proportional abundance of a species,  $s_i$  : the number of individuals for a species,  $N$  :  
total number of individuals, and  $S$  : the number of species.

### 190        **2.8.2. Global Dissimilarity Model (GDM)**

The Global Dissimilarity Model analyses beta biodiversity patterns. Here, it allows us to identify  
the main predictors influencing  $\beta$  diversity, by relating compositional dissimilarity between sites to  
how much sites differ in their environmental conditions (environmental distance) and how isolated  
they are from one another (geographical distance). For the each trophic guilds, we created  
195 dissimilarity matrices between samples ( $\beta_1$ ), between plots ( $\beta_2$ ) and between gradients ( $\beta_3$ ) using  
the function `vegdist()` from the package `vegan`, Bray-Curtis distance. We compared the magnitude  
of effects of the predictors between trophic guilds at each spatial scale. Predictors associated-  
coefficient don’t have any unite

### 200        **2.8.3. Fitted relationships between Predicted Ecological Distance and Observed Dissimilarity (Fitted splines)**

This relationship allows us to observe trophic guild response to ecological gradient. It have been  
done thanks to the GDM package. The correlation plot is automatically calculated when we perform  
the `gdm()` function on the pairwise matrix previously created. “The predicted ecological distance  $\eta$   
(is) derived as the sum across all predictor variables of the absolute differences in the model  
205 transformed predictor values (...) between sites”(Mokany et al., 2022). The Observed Dissimilarity  
is calculated when we previously created the pairwise matrix.

All the analyses were performed on RStudio version 4.2.3.1. Scripts, data and figures are available  
at <https://github.com/Aurelien-Navarro/Macrofauna>

## **3- Results**

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### 3.1. Species diversity partitioning

Species diversity was mostly explained by compositional difference (20-30%%) at larger scale :  $\beta_3$   
215 between elevation gradients) for predators and detritivores. Herbivore diversity is mostly explained  
between plots (20%).

Parasitoids diversity is shared equally between plot and between gradients.

Shannon diversity only accounts for 10% to 15% of explanation between samples. In general,  
across all scales, Herbivores respond differently. Detritivore diversity explained by alpha is quite  
220 poor (10%) in comparison with herbivore diversity (20%).

### 3.2. Predictors of $\beta$ -diversity

Between samples ( $\beta_1$ ), the variables related to energetic constraints are the most important drivers,  
followed by variables reflecting physical stress (figure 2). Geographical distance affected changes  
225 in herbivores, predators and parasitoids species composition, but not that of detritivores.

Between plots ( $\beta_2$ ), physical stressing variables explain most of the dissimilarity (relative  
coefficient = 3). Energy related variables (E) are also good predictors, except for detritivore, where  
Nutrient Content (NC) is important. Complex variables (CF) such as the opening of habitat and  
Altitude have light relative coefficient, as the geographic factor. Theses two categories don't affect  
230 detritivores dissimilarity.

Between gradients ( $\beta_3$ ), almost all predictors influencing beta diversity belong to physical stressing  
category. Energy associated variable (NDVI) only influencing predators guild. The opening of  
habitat have a light coefficient (0,5 in average) for herbivores and parasitoids. Detritivores  
dissimilarity is also caused by a Habitat Heterogeneity (HH) : Coarse silt content, with a relative  
235 coefficient of 0,5.

Predictors coefficients are the lighters between gradients.



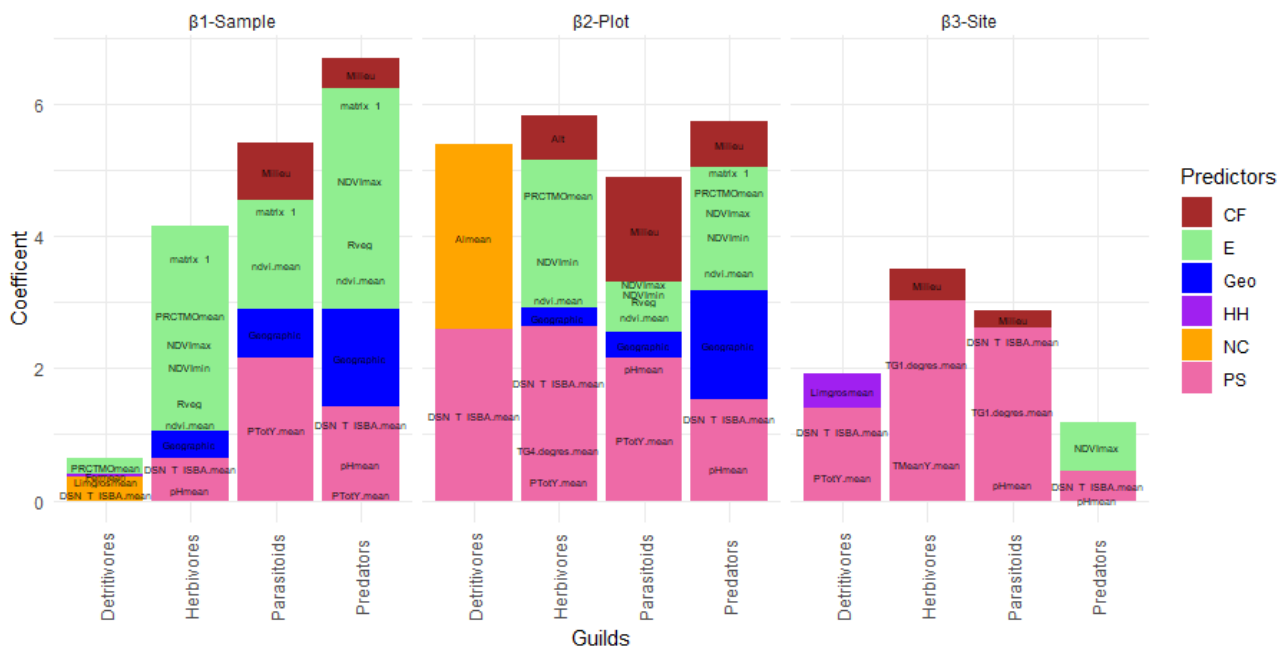


Figure 2: Barplot of the relative contribution of predictors to beta diversity in three scales and for four trophic guilds

### 240 3.3. Diversity - distance decay relationships

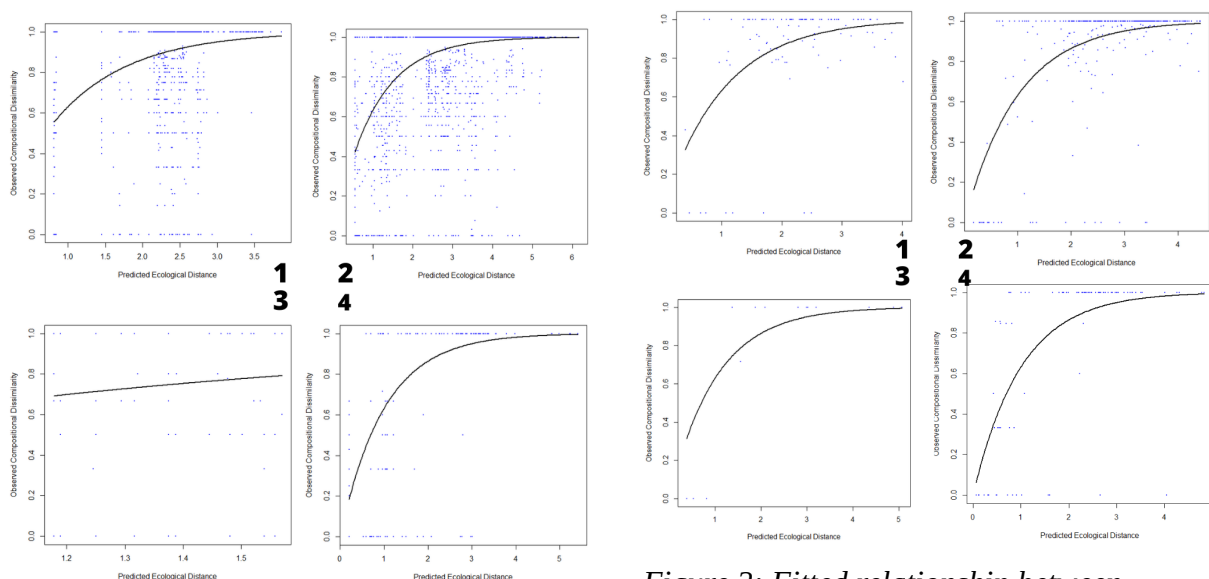
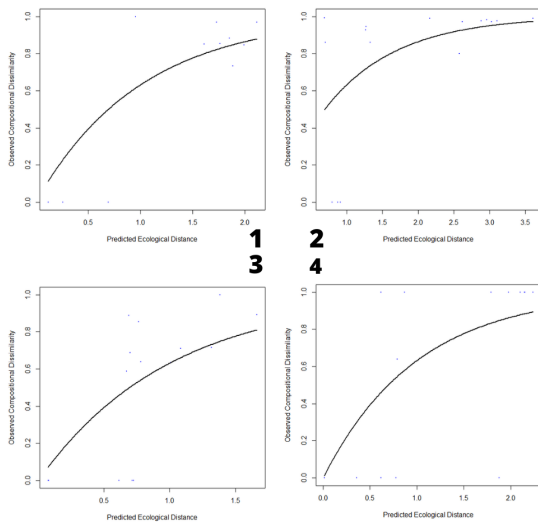


Figure 3: Fitted relationship between predicted ecological distance and observed compositional dissimilarity for 1) Herbivores, 2) Predators, 3) Detritivores, 4) Parasitoids, between samples (local- $\beta_1$ ).

Figure 2: Fitted relationship between predicted ecological distance and observed compositional dissimilarity for 1) Herbivores, 2) Predators, 3) Detritivores, 4) Parasitoids, between plots - $\beta_2$ .

Between samples, maximum dissimilarity in species composition of herbivores, parasitoids and predators was observed for an Ecological Distance of 3.5, 5.0 and 6.0, respectively (figure 3). Relations between herbivore and detritivores  $\beta_1$ -diversity and Ecological Distance were similar, with a minimum dissimilarity of 0.6, differing from those of predators and parasitoids that exhibited a minimum dissimilarity of 0.2



Between plot, herbivores and predators are reaching a maximum dissimilarity for an Ecological Distance of 4. The minimum dissimilarity is reached at 0.35 (herbivores) and 0,3 (predators and detritivores) for an ecological distance of 0. Detritivores curve is linear, with a maximum dissimilarity of 0,4, reached for an Ecological Distance of 0,3. (figure4) Parasitoids and detritivores reach their maximum dissimilarity of 1 for a distance of 5. Parasitoids dissimilarity at an ecological distance of 0 is almost 0 (0,05).

Figure 5: Fitted relationship between predicted ecological distance and observed compositional dissimilarity for 1) Herbivores, 2) Predators, 3) Detritivores, 4) Parasitoids, between gradient (global- $\beta_3$ ). Between gradients, herbivores predators and parasitoids dissimilarity correlations are similar, with a maximum dissimilarity reached for an Ecological Distance of 2, for herbivores and parasitoids, and 3.5 for predators.

For detritivores, the dissimilarity of 1 isn't totally reached. Nevertheless, the start of the curve is totally different. For an ecological distance of 0, herbivores dissimilarity between elevational gradients is 0,1, predators dissimilarity is 0,5 and parasitoids is almost 0. Detritivores curve stays more linear-like, where the maximum dissimilarity (0,6) is reached for an ecological distance of 1,5 in average. When ecological distance is minimum, dissimilarity between elevational gradients is 0,2.

## 4. Discussion

### 4.1. Variance partitioning

The first scale of study that encompassed biodiversity was gradient. It means that the difference between elevational gradients influences more the diversity than differences between plots ( $\beta_2$ ), or between sample ( $\beta_1$ ).

Indeed, the regional or landscapes scale more likely modifies diversity, than local, according with (Beaugrand, 2023), (Steiner & Leibold, 2004). Moreover, (Decaëns, 2010) precised that at a global scale, we observe more alpha diversity but also nested effect, that is to say, dissimilarity (high  $\beta$

diversity). It might be caused by dispersal capacities, colonization and history (Drake, 1990) or, as (Steiner & Leibold, 2004) proposed, a stochastic event can increase species dissimilarity among local communities, thus increasing  $\beta$  diversity.

Dissimilarity between plot also encompassed diversity, particularly for herbivores. It is possible that  
285 this trophic guild is under environmental influences present at the scale of plots

#### 4.2. Predictors of $\beta$ -diversity :

At local scale, for herbivores, predators and parasitoids, factors playing a role in  $\beta$  diversity are related to energy including biologic variables. Theses results are in line with c and my assumptions  
290 It's mainly possible that vegetal variables influence directly herbivores by organic matter available and indirectly predators and parasitoids, by trophic relationships.

Focusing on predators group, at local scale, the importance of energy variables is in accordance with paper, but the distance limit is more supported in (Drake, 1990) work. This results means that it's possible for predators species to be isolated by distance. In this case, we can observe a higher  
295 endemism than for other trophic guild. We can suppose that for Parasitoids, the influence of abiotic variables (PS) can be understood by the direct influence of precipitations on species survival (Kendall & Ward, 2016).

At an intermediate scale ( $\beta_2$ ), influences are both trophic (Energy) and abiotic (Physical Stressing : PS). As (Calderón Sanou, 2022) showed, with figure 3, Physiological tolerance hypothesis (here, represented by Snow cover), explains biodiversity with a great relative importance. It can be explain  
300 by three mechanisms highlighted by (Stein et al., 2014) : “First, an increase in environmental gradients and in the amount of habitat types, resources and structural complexity should increase the available niche space and thus allow more species to coexist [...]. Second, environmentally heterogeneous areas are more likely to provide shelter and refuges from adverse environmental  
305 conditions and periods of climate change, which in turn should promote species persistence [...]. Third, the probability of speciation events resulting from isolation or adaptation to diverse environmental conditions should increase with higher EH.” The influence of energy variables is in line with (Calderón Sanou, 2022) figure 2, where macrofauna phytophagous and are influenced by Ressource Heterogeneity.

310 Detritivores's case is particular. Between plots ( $\beta_2$ ), Physical Stressing Variables and Nutrient Contents influence biodiversity, as demonstrated by (Calderón Sanou, 2022) and ( $\beta_1$  and  $\beta_2$ ). Detritivores depends mostly on organic matter and nutrients to survive, as (Tiunov & Scheu 2004) showed, adding carbon into earthworms experiment fields. We still can add that the snow plays a major role as it influences, available water for theses organisms, and temperature (Sokratov &

315 Barry, 2002). The treeline effect could also explain detritivores pattern “both by the effect of environmental heterogeneity and of trophic resource quality which increases at the ecotone level” (Gabriac et al.2022). Further studies may be able to model and correlate the Treeline with detritivores  $\beta$ -diversity.

The first predictor of detritivores in for (Calderón Sanou, 2022) the energy available, while here, the  
320 nutrient content and climatic factor seem to play more. It’s quite surprising when we know how a detritivore depends on its environment for habitat and nutrition (Gabriac et al., 2022) Moreover, stated the fact for diverse communities, that the available energy is the first factor influencing biological patterns, in addition with precipitations and temperature.

Furthermore, (Moret, 2009), (Drake, 1990) showed in their study, that geographic distance can limit  
325 beta diversity, because of organism spreading. It’s an explication of the importance of geographic distance for herbivores, predators and parasitoids.

For parasitoids, the influence of Annual Temperature and Temperature above 1cm or soil is contrary to (Calderón Sanou, 2022), in which zooparasits are mostly influenced by energy availability ( $\beta_2$ ). Nevertheless, it can be approached by the influence of Annual Temperatures on  
330 plants growth and health, and by extend, their NDVI. Considering these consequences, results are in line with (Kendall & Ward, 2016), where their study showed that parasit wasps diversity is linked to vegetation type, and NDVI. This study also supports the fact that parasitoids are influenced by habitat, which is in accordance with  $\beta_1$  and  $\beta_2$  results, where the opening of habitat plays a role in parasitoids dissimilarity. In an another paper (Timms et al., 2016), it was found that a important  
335 factor for Ichneumonidae (parasitoid wasps) distribution at latitude scale was the availability of hosts, which we found at plot ( $\beta_2$ ) scale (smaller scale). This scale difference can be discussed thanks to (Hawkins et al. - 2023) where parasitoid biological patterns were largely influenced by host availability, at a  $\beta_2$  scale (population level).

The fact that physical stressing variables explain  $\beta_3$  diversity in general is in accordance with  
340 (Beaugrand, 2023), figure 2, showing that at a global ( $\beta_3$ ) scale, factors that influence diversity are climate factors, and sometimes biogeographical (like we can explain by the importance of the opening of the environment in our case). Temperature influence is also supported by (Peters et al., 2016), general conclusions. If herbivorous tend to be impacted by biological variables at a little scale, in regional context, it’s more environmental climatic variables which influence vegetation and  
345 indirectly, herbivores.

As (Steiner & Leibold, 2004) showed, at higher scale ( $\beta_3$ ), fauna is still under the Scale Dependant Productivity Diversity Relationship, explaining why a variable (NDVI) belong to Ressource Heterogeneity category. The importance Physical Stressing Variable (here : Temperature) is

supported by (Beaugrand, 2023) and the METAL theory stipulates that climate is the main predictor  
350 for communities arranging. This theory is based on the concept of ecological niches (introduced by  
Hutchison) , When we are at the community level, , the interaction between the environment and  
the niche helps us to understand how communities are formed and modified (Beaugrand, 2023).

Trophic guilds seem not to be under same pool of variable, for lower spatial scales. The global  
355 scale tends to homogenous influence guilds. The Correlation between Community Dissimilarity and  
Ecological Distance should informs about how guilds are responding.

#### 4.3. Diversity - distance decay relationships

Measuring community dissimilarity by ecological distance gave us information about ecological  
360 niches of a trophic guild (Hutchinson, 1957) According to (Ferrier et al., 2007) (Mokany et al.,  
2022), when a high dissimilarity between elements is reached for a little ecological distance, (ie the  
slope of the curve) taxonomic composition is highly variable that is to say, the turnover is  
important. Moreover, (Mokany et al., 2022) specified that the model intercept, represented here by  
the dissimilarity for an ecological distance of 0 can explain “a real phenomenon derived through  
365 stochastic ecological processes, or may be an artefact of incomplete sampling and/or missing  
environmental predictor variables”.

Considering theses model interpretation keys, at  $\beta_1$  scale (**figure 3**), predators and parasitoids  
turnovers seem lower than herbivores and detritivores turnover, because maximum dissimilarity is  
reached with a higher ecological distance. This statement is supported by (Ingram et al., 2009), who  
370 demonstrated that the turnover of a trophic guild (ie how it's composition changes among elements  
of sampling) is intricately linked with the omnivory level. A trophic guild that have access to a  
larger range of resource is more taxonomically instable. Indeed, it is possible that detritivores and  
Herbivores have a more various diet than predators and parasitoids which, for some species can  
have a regime composed of only one specie, (or one host for parasitoids) (Wallin et al., 1992).  
375 Nevertheless, it might be possible that herbivores and predators group knew a stochastic or historic  
event, explaining the minimum dissimilarity of 0,6 for an ecological distance of 0 (named  
“intercept” for following explanations)

The omnivorous regime – turnover relationship is not observable at  $\beta_2$  scale (**figure 4**) where  
predators, parasitoids and herbivores curves are similar. Nevertheless, the hypothesis that  
380 herbivorous knew a stochastic even is consolidated here, where the intercept is almost 0,4.  
Finally, at  $\beta_3$  scale (**figure5**), herbivores, predators and parasitoids similar turnover pattern could be  
explained by the fact that both are mainly under climatic stressing variables (**figure,  $\beta_3$** ) leaving

supposition that this same variable category equally influences different trophic guilds, as (Calderón Sanou, 2022) main results showed in figure 2 and(Beaugrand, 2023)(general considerations). For predators, the relative lower turnover is still supported by (Ingram et al., 2009), because predators is a group of species which have specific diet in general. The high intercept is difficult to link with a possible stochastic event here, considering the low statistical individuals which helped to fit the model. Detritivore's case shows that this group is particularly sensible to ecological and/or environmental variations, in term of species compositions. In this case, species have smaller ecological niche (Ingram et al., 2009).

## 5. Conclusions and General Considerations

For the herbivores, predators and parasitoids trophic guilds, and at the three spatial scales,  $\beta$ -biodiversity pattern are pretty similar. It mainly concerns above ground creatures. A difference is visible for detritivores trophic guild, were part of species lives underground. Concerning global and regional scales, results are in line with assumptions about the impact of climate, biogeography. At smaller scale (between samples–  $\beta 1$ ), we observe a mix of energy related variables and nutrients/resource availability.

It this logic, it could be interesting to have a more precise look on trophic interactions, with a model in order to truly understand how this four trophic guilds are interacting with others.

The Global Dissimilarity Model offers a large range of applications. The one we wanted to explore was a focus on functional traits for every trophic guilds. It's a great way to model ecological impacts of trophic guild on ecosystem. However, parasitoids wasp traits are poorly documented, and poorly accessible. Additionally, it would be interesting to divide to group trophic guild in more precise groups, in order to model a more accurate trophic network.

Furthemore, the GDM allows to predict (here : trophic guild)  $\beta$ - diversity pattern in non-sampled regions, but also over time, thanks to environmental variable estimations (Mokany et al. 2022). It's a great way to predict how communities pattern can change through time or in association with the growing human impact

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