10. Mountain biodiversity: the case of invertebrates (and some birds)

R. Viterbi[1, 2], C. Cerrato[1], A. Provenzale[2]

[1]Gran Paradiso National Park, Torino, Italy
[2]CNR-IGG, National Research Council, Institute of Geosciences and Earth Resources, Pisa, Italy

Introduction

In the last decades, species extinction and biodiversity decline have reached an alarming rate (Thomas et al., 2004; Butchart et al., 2010), indicating an urgent need to monitor and understand factors that influence biodiversity variations and identify priority areas and sensitive taxonomic groups for conservation purposes (Yoccoz et al., 2001; Magurran et al., 2010).

In this framework, mountain ecosystems are of particular interest. Mountain landscapes, owing to their physical, topographic and climatic heterogeneity, create a mosaic of habitats along the altitudinal gradient (Körner, 2000; Beniston, 2003). Such heterogeneity determines high levels of biodiversity, usually higher than those recorded in adjacent lowland areas (Körner, 2000; Theurillat et al., 2003). Compared to latitudinal variations, altitudinal gradients allow for investigating the relationships between biodiversity and abiotic/biotic parameters on a reduced spatial scale, where fauna and flora are often characterized by a similar biogeographical history (Rahbek, 1995; Körner, 2000).

Mountains host some of the world's most rare and fragile ecosystems (Diaz et al., 2003; Pauchard et al., 2009). Populations at high elevations are typically small, isolated and prone to local extinction, are often poor dispersers and are characterised by high levels of endemism (EEA, 2010). Mountains are very sensitive to environmental changes and global warming (Huber et al., 2005; Beniston, 2006) hosting a high number of species adapted to low temperature conditions (Pauli et al., 2004). Long-term records provide evidence for ongoing climate warming in mountain environments and in the Alps (Beniston, 2006; Auer et al., 2007; Rebetez and Reinhard, 2008), that has already impacted the life cycle, pattern of activity, distribution and range size of various plant and animal species (Thuiller et al., 2005; Pauli et al., 2007; Bässler et al., 2010).

Mountains are also outstanding heritage sites and their biodiversity is linked with the cultural patrimony of the people living therein. The European Alps have a long history of human presence and exploitation: during the last millennium, agro-pastoral activities determined a lowering of the treeline ecotone and shaped community composition of plants and animals (Theurillat and Guisan, 2001; Chemini and Rizzoli, 2003). Currently, high levels of recreational activities, as well the abandonment of traditional farming systems can negatively affect mountain biodiversity (Patthey et al., 2008; Brambilla et al., 2010). In addition, the loss of more sedentary and specialized elements in favour of more vagile and tolerant species could determine an impoverishment of the biotic structure (e.g., Dirnböck et al., 2011).

For these reasons, the identification of factors that determine biodiversity patterns has important implications on conservation and management decisions. Altitudinal gradients are particularly useful to test traits for their long-term adaptive nature, and allow for covering different belts along the vertical zonation of the vegetation pattern. Clearly, elevation must be seen as a proxy for the environmental conditions associated with it (Körner, 2000). The knowledge of the relation with altitude becomes especially important in a time of global climate change, and it allows to assess which species will be more threatened by the temperature rise (e.g., Fleishman et al., 1998).

To gain a comprehensive understanding of biodiversity patterns, comparison of elevation trends between taxa and between different mountain ranges is necessary (Lomolino, 2001). Information gained with a multi-taxa approach can be used as a primary tool to recognise areas of high natural value, to address management actions and to develop a more effective response to biodiversity loss than the standard 'simply maintaining the site's status quo' (Hannah et al., 2002).

In this chapter we report about a long-term study, partially funded by NextData, based on a standardized protocol for monitoring the biodiversity of multiple taxa in the Italian Alps, focusing on biodiversity changes along altitudinal transects encompassing three vegetation belts (montane, subalpine and alpine), in three protected areas (Viterbi et al., 2013). The study started in 2006 and it is still ongoing, and it is being extended to other national parks in the Italian Alps.

10.1 Mountain biodiversity monitoring during the NextData project

In the framework of the NextData project, field activities have been carried out in fixed plots, already considered for monitoring during a previous period (2007-2008). They represent the implementation and continuation of a previous existing *in situ* project, promoted by Gran Paradiso National Park (GPNP) in 2006 and continued with the cooperation between CNR ISAC and other two protected areas in NW Italian Alps, Orsiera Rocciavré Natural Park (ORNP) and Veglia Devero Natural Park (VDNP).

The aim of the research activity is the development of an accessible historical dataset, on the base of already existing data and with the new data collected during the project, and the improvement of some of the methodologies used in monitoring animal biodiversity.

Monitoring activities during 2012-2013 have been carried out in the three above-mentioned Parks (Gran Paradiso National Park, Orsiera-Rocciavré Natural Park, Veglia Devero Natural Park). Thirteen altitudinal transects, characterised by an altitudinal development ranging from 600 m to 1000 m, were set covering an altitudinal gradient chosen between 500 m a.s.l. and 2700 m a.s.l., interesting three vegetation belts (montane, subalpine, alpine).

Sampling units are circular plots (100 m radius), for a total of 75 units, where monitoring activities have been carried out to provide presence/absence and relative abundance data of species belonging to the taxa selected as bio-indicators. The selected taxa are: *Lepidoptera Rhopalocera* (butterflies), *Orthoptera* (grasshoppers/crickets), birds, surface-active macro-arthropods (*Coleoptera Carabidae, Coleoptera Staphylinidae, Araneae, Hymenoptera Formicidae*).

For each taxonomic group, we used semi-quantitative sampling techniques that are, as much as possible, easy to apply, standardized, cheap and repeatable. Birds were monitored by means of point counts and each plot was visited twice during the reproductive season. We sampled butterflies and grasshoppers/crickets using linear transects along the diameter of the plot (200 m in length), walked at uniform speed. We collected surface-active arthropods using pitfall traps (plastic cups, diameter of 7 cm, filled with 10 cc of white vinegar and a drop of soap). All collected specimens were stored, preserved in alcohol 70%, and identified at the species-level, by expert taxonomists.

Monitoring activities included also the collection of:

- micro-climatic data, through the positioning of temperature data-logger (iButton DS1922), one per each sampling station, located in field for all the sampling season;
- macro-environmental (topographic variables) and micro-environmental parameters (percentage of land coverage and estimate of floristic diversity).

During 2014-2017, field activities were carried out in selected plots and focused on birds (30 plots), butterflies (13 plots) and micro-climate (30 plots), while in 2018-2019 the three protected areas repeated in all the plots the whole monitoring protocol.

The results of the monitoring activities are databases, constituted by lists of species, with data on relative abundance for each taxon and each sampling plot. Moreover, each plot is accompanied by the characterisation of environment and micro-climate. These data are now stored in appropriate databases.

Since 2013, three other protected areas agreed to share the objectives of the monitoring activities promoted by PNGP in 2006 and to follow the sampling protocols already adopted by PNGP, PNOR and PNVD. These protected areas are Stelvio National Park (CPNS), Val Grande National Park (PNVG), Dolomiti Bellunesi National Park (PNDB). During spring 2013 (March-April), PNGP researchers trained the personnel of these parks, in order to obtain comparable data and create the appropriate databases for common data storage. CNPS, PNVG and PNDB also repeated in 2018-2019 the whole monitoring campaign.

The results of the first two monitoring campaigns (2006-2008; 2012-2013), from the first three involved protected areas, have already been analysed (Viterbi et al., 2013, Rocchia, 2016, Cerrato et al., 2019, to which we refer for details), following two approaches: *i)* the description of α- and ß-diversity along the altitudinal gradient; *ii)* the analysis of temporal changes.

10.2 Organisation and storage of the raw data

The biodiversity data, collected since 2006by the three protected areas partners of the project (PNGP, PNOR and PNVD), have been stored in a relational database, hosted by the PNGP server and integrated in the systems of archives of the NextData project. In the following, we provide a short description of the database (Table 1), composed of 9 "sampling" databases (one per each of the 8 taxa sampled during the project, plus one related to the faunal observations), 3 "measure" databases (referred to faunal contour data), 2 "geographic" databases (describing the geographic position of the sampling sites), 3 "environmental" databases (with floral, land cover and micro-climatic data).

Sampling databases

• ***Coleoptera Carabidae***. Relative abundance and ecological information of the ground beetles (carabids) sampled through pitfall traps during the two sampling periods of the project (PNGP, 2006-2007-2012-2013; PNOR, 2007-2008-2012-2013; PNVD, 2007-2008-2012-2013). We followed the nomenclature proposed by Brandmayr et al. (2005).

• ***Coleoptera Staphylinidae***. Relative abundance and ecological information of the rove beetles (staphylinids) sampled through pitfall traps during the two sampling periods of the project (PNGP, 2006-2007-2012-2013; PNOR, 2007-2008-2012-2013; PNVD, 2007-2008-2012-2013). The specimens belonging to the sub-family *Aleocharinae* have been determined at the species level only in 2006 in PNGP. We followed the nomenclature proposed by Horion (1963, 1965, and 1967).

- ***Araneae***. Relative abundance and ecological information of the spiders sampled through pitfall traps during the first sampling period of the project (PNGP, 2006-2007; PNOR, 2007-2008; PNVD, 2007-2008). The specimens collected during the second sampling period are still under the control of taxonomist, due to a few determination uncertainties, but soon they will be ready for storage in the archive. We followed the nomenclature proposed by Platnick (2014).
- ***Hymenoptera Formicidae***. Relative abundance and ecological information of the ants sampled through pitfall traps during the second sampling period of the project (PNGP, 2012-2013; PNOR, 2012-2013; PNVD, 2012-2013). We followed the nomenclature proposed by Ruffo and Stoch (2005).
- ***Lepidoptera Rhopalocera***. Relative abundance and ecological information of the butterflies sampled through linear transects during the two sampling periods of the project (PNGP, 2006-2007-2012-2013; PNOR, 2007-2008-2012-2013; PNVD, 2007-2008-2012-2013). Butterflies have also been collected every year in 13 selected plots in PNGP (2006-2015). We followed the nomenclature proposed by Balletto et al. (2014).
- ***Orthoptera***. Relative abundance and ecological information of the grasshoppers and crickets sampled through counts on delimited surface along linear transects during the two sampling periods of the project (PNGP, 2006-2007-2012-2013; PNOR, 2007-2008-2012-2013; PNVD, 2007-2008-2012-2013). We followed the nomenclature proposed by Massa et al. (2012).
- ***Aves***. Relative abundance and ecological information of the birds sampled through point counts during the two sampling periods of the project (PNOR, 2007-2008-2012-2013; PNVD, 2007-2008, 2012-2013) and continuously, in every year, in PNGP (2006-2015). We followed the nomenclature proposed by BirdLife International (2015).
- ***Odonata***. Relative abundance and ecological information of the damselflies and dragonflies sampled through linear transects around bogs, ponds and wet areas present inside the sampling plots (PNVD, 2007-2008-2013). Suitable plots have been found only inside PNVD. We followed the nomenclature proposed by Riservato et al. (2014).
- ***Observations***. Faunistic (and also floristic) observations collected in a non-standardised way inside the sampling plots of the project but also along the paths walked by the researchers moving from one plot to another. Such data have been collected during the sampling years of the project (PNGP, from 2006 to 2015; PNOR, 2007-2008-2009-2012-2013; PNVD, 2007-2012-2013). The data collected are not only related to the taxa monitored inside the project but depend on the expertise and observation ability of the individual researchers. These data are consequently not directly comparable across time and space and cannot be directly used as semi-quantitative data.

Measurement databases

- ***Biomass***. Measurements of the volume and mass occupied by all arthropods (isolated from the other invertebrates and the few vertebrates), sampled inside the pitfall traps during the second monitoring period (2012-2013, PNGP, PNOR, PNVD).
- ***Activity Density***. This represents the number of traps active and emptied during each biweekly sessions of the pitfall traps sampling, in all years of the project (PNGP, 2006-2007-2012-2013; PNOR, 2007-2008-2012-2013; PNVD, 2007-2008-2012-2013). We distinguished the traps found empty in

field from the traps that have been destroyed due to various causes (e.g., animals, bad weather conditions) and that consequently did not provide any sampling unit. Such information is important to obtain a more realistic quantification of the sampling effort for the pitfall trapping and to make fully comparable data obtained for different plots and years.

- ***Morphometry***. Morphometric measurements were done on 5 species of Coleoptera Carabidae (*Carabus depressus*, *Calathus melanocephalus*, *Pterostichus externpunctatus*, *Pterostichus flavofemoratus*, *Pterostichus multipunctatus*), sampled inside the pitfalls located in field in the three protected areas, during the field season 2012. Eleven morphometric traits have been sampled for each specimen, and each measurement have been done independently by three operators. The protocol describes the morphometric traits and the tools used to obtain them.

Geographic databases

- ***Traps***. Geographic coordinates of the position of each pitfall trap and of each temperature data-logger positioned in the field during the two sampling periods (first period 2006-2007-2008; second period 2012-2013). There could be some small differences in the location of the traps during the first and the second sampling period, due to field error in finding them or to imprecision in the GPS positioning.
- ***Plots***. Coordinates of the plot centre and shapefiles of the plots (buffers with a radius of 100 meters around the centre). The plot is the sampling units of the project.

Environmental databases

- ***Environment***. Information referred to the micro-habitat and the general environmental characteristics of each plot. These data have been collected in 2012-2013.
- ***Temperature***. Data include hourly measurements provided by the plot data-logger, validated through a quality control procedure; daily measurements of the ARPA weather stations located inside or near to the boundary of each park; procedure of temperature construction and extrapolation to obtain a temperature map at parks level. We also stored all the steps that were followed to obtain the temperature maps (spatial resolution of 250x250 m).
- ***Vegetation***. There are several data types (floral lists, semi-quantitative data deriving from linear transects, quantitative description of tree biomass, shapefile deriving from photo-interpretation). Vegetation/land cover data are not currently homogeneous across the three protected areas.

Data	**Group**	**Time period**	**Spatial Coverage**
Sampling databases	Coleoptera Carabidae	2006, 2007, 2012, 2013	PNGP (30 plots)
	Coleoptera Carabidae	2007, 2008, 2012, 2013	PNOR (20 plots), PNVD (24 plots)
	Coleoptera Staphylinidae	2006, 2007, 2012, 2013	PNGP (30 plots)
	Coleoptera Staphylinidae	2007, 2008, 2012, 2013	PNOR (20 plots), PNVD (24 plots)
	Araneae	2006, 2007, 2012, 2013	PNGP (30 plots)

Data	Group	Time period	Spatial Coverage
	Araneae	2007, 2008, 2012,	PNOR (20 plots), PNVD (24 plots)
	Hymenoptera Formicidae	2012, 2013	PNGP (30 plots), PNOR (20 plots), PNVD (24 plots)
	Lepidoptera Rhopalocera	2006, 2007, 2012, 2013	PNGP (30 plots)
	Lepidoptera Rhopalocera	2007, 2008, 2012, 2013	PNOR (20 plots), PNVD (24 plots)
	Lepidoptera Rhopalocera	2006-2015 (continuously)	PNGP (selected areas)
	Orthoptera	2006, 2007, 2012, 2013	PNGP (30 plots)
	Orthoptera	2007, 2008, 2012, 2013	PNOR (20 plots), PNVD (24 plots)
	Aves	2007, 2008, 2012, 2013	PNOR (20 plots), PNVD (24 plots)
	Aves	2006-2015 (continuously)	PNGP (30 plots)
	Odonata	2007, 2008, 2013	PNVD (5 plots)
	Observations	2006-2015	PNGP, PNOR, PNVD
Measure databases	Activity Density	2006, 2007, 2012, 2013	PNGP (30 plots)
	Activity Density	2007, 2008, 2012, 2013	PNOR (20 plots), PNVD (24 plots)
	Biomass	2012, 2013	PNGP (30 plots), PNOR (20 plots), PNVD (24 plots)
	Morphometry	2012	PNGP (30 plots), PNOR (20 plots), PNVD (24 plots)
Geography databases	Traps	2007, 2012	PNGP (30 plots), PNOR (20 plots), PNVD (24 plots)
	Plots	2007	PNGP (30 plots), PNOR (20 plots), PNVD (24 plots)
Environmental databases	Environment	2012, 2013	PNGP (30 plots), PNOR (20 plots), PNVD (24 plots)
	Temperature	2006, 2007, 2012, 2013	PNGP (30 plots), PNOR (20 plots), PNVD (24 plots)
	Temperature	2006-2014 (continuously)	PNGP (selected areas)
	Vegetation	2007, 2014	PNGP (30 plots)
	Vegetation	2007	PNOR (20 plots), PNVD (24 plots)

Table 1. *List of the available biodiversity data. The time span and the spatial coverage of each of data set are indicated.*

The metadata describing this database have been compiled following the EnvEurope (LTER-Europe)/ExpeER Metadata Specification for Dataset Level based on the EML (Ecological Metadata Language) specification. Our metadata provide information on both the biological databases and the sites of data collection (synthetic information about the three protected areas, PNGP, PNOR, PNVD). In particular, metadata of the biological databases include: *i)* a title and an abstract describing the main purpose of each database; *ii)* the extent of the data collection in time and space; *iii)* a detailed description of the field methodologies adopted to obtain the data and of the identification procedures (e.g., the identity of the expert taxonomist who identified the specimens, the followed nomenclature); *iv)* the contact point for the databases (author and owner of the data, both for the database and the collected specimens) and its use regulations.

The ecological databases are not only related to the presence and abundance of different species in the selected plots and across time. It also contains other important information: *i)* a value corresponding to the quality of the data (some specimens can be determined only at the genus or family level, lowering the quality of the determination); *ii)* the ecological characteristics of each species (derived both from literature and expert opinion, and the related references we used); *iii)* information, if available, on the single specimens (age classes, sex, behavioural observation).

To obtain a complete collection of data and metadata and to make the future repetition of the sampling procedure (and also any kind of data analysis) as reproducible as possible, we also stored:

- a detailed description of the sampling design and protocol;
- the field sheet used to collect the data;
- a template of the Excel file used to digitally archive all the data.

10.3 Results of the Data Analysis

10.3.1 Patterns of biodiversity from the first sampling season

The analysis of the data obtained during the 2007 sampling year, reported in Viterbi et al. (2013), to which we refer for details, indicate that, for the altitudinal gradient explored in this project, the curve of the overall species richness was hump-shaped, with a peak in richness at intermediate elevations and a stronger decline at increasing elevations (Figure 1a). In the sampling sites analyzed here, the lower-elevation portion of the curve, was strongly influenced by xeric conditions (3 plots in the Orsiera Rocciavrè Parks) and by higher levels of human impact, compared to the belts at higher altitude.

Altitudinal gradients can be taken as a proxy for a large number of inter-linked variables that can affect biological diversity (Brehm et al., 2003). As observed elsewhere (e.g., Oommen and Shanker, 2005), we found that temperature was the most important variable associated with altitude. This held for almost all taxonomic groups and for the overall species richness. Only butterflies and carabids showed a slightly different pattern, as they were more influenced by environmental variables. In the case of butterflies, higher structural diversity and higher amount of herbaceous layer positively influenced species richness, while in the case of carabids the major driver was the amount of herbaceous layer. This is presumably due to the fact that carabids are extremely sensitive to grassland management (Grandchamp et al., 2005), and also because carabid species richness is not clearly related to habitat characteristics (Gobbi et al., 2007). In the case of butterflies, higher structural diversity means higher availability of different habitats at a local scale, allowing for the coexistence of a higher number of species (e.g., Krauss et al., 2003).

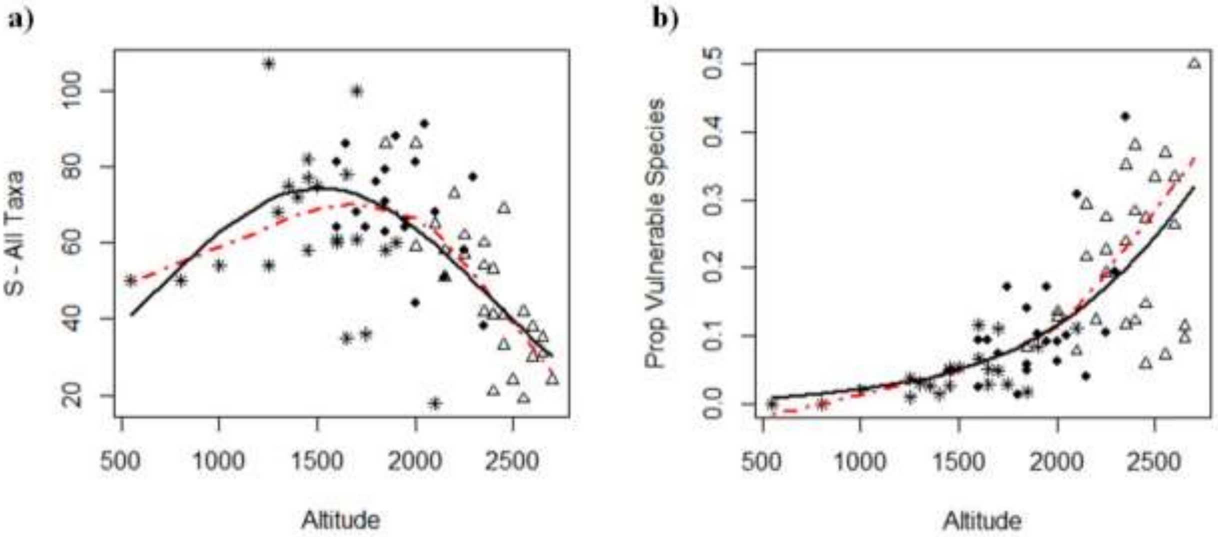

Figure 1. *Scatterplots of the total species richness per site for all taxa pooled together (a) and of the proportion of vulnerable species (b) along the altitudinal gradient. The LOWESS regression curve is represented as a dashed line, while the significant regression curve is represented as a solid line. Montane belt (stars), Subalpine belt (diamonds), Alpine belt (triangles). [From Viterbi et al. 2013]*

The data analysis showed that the highest levels of species richness was in the Subalpine belt, as expected from the fact that this is a transition area where different habitats coexist (Lomolino, 2001; Oommen and Shanker, 2005). The Subalpine belt in the areas of study was characterized by the presence of some species that are exclusive to this area, as well as of species shared with the surrounding belts. Some authors claim that responses in mountain ecosystems can stronger at ecotones, owing to the possibility of different trends in adjacent habitats (Beniston, 2003). Consequently, the Subalpine belt is potentially one of the most endangered, because its peculiar community composition could be disrupted. Both the general trend of reforestation in the mountains of Europe (e.g. EEA 2010) and a warmer climate could determine an increase of species from lower altitude and a decrease of species shared with the Alpine belt.

In Viterbi et al. (2013), it was also observed a significantly larger proportion of vulnerable and endemic species in the Alpine belt, which thus emerged as a priority area (Figure 1b). Moreover, it was observed that vulnerable species were the ones with the greatest explained variance (more than 50%): their richness was clearly influenced by the shared effect of temperature and altitude. Endemic and vulnerable species often present very narrow ranges and their abundance peaks are not necessarily coherent with species richness, being often shifted to higher altitudes (Kessler, 2001; Schmitt, 2009). In addition, the Alpine belt is characterized by environmental constraints (severe climatic conditions, short summer periods, slope, and natural hazards) and by the importance of direct and indirect effects of climatological factors, in particular low temperatures (Beniston, 2003; Pauli et al., 2004; Körner et al., 2011). High altitude biota are thus poorer and more fragile: localized and strongly adapted elements are prone to higher levels of threat and are vulnerable to climatic and environmental changes (Parmesan, 2006; Dirnböck et al., 2011).

On the technical side, the results reported in Viterbi et al. (2013) indicate that α-diversity indices, which weight all species in the same way or consider only their relative abundances, are not enough to describe habitat vulnerability and to identify conservation priority areas, particularly in mountain ecosystems. The number of species and the ecological characteristics of single elements must be taken into account, to identify which areas are important for the different conservation purposes (e.g., Orme et al. 2005).

10.4 Modelling approach at species level

The aim of this part of the work was to develop and test an exportable modelling approach to obtain the probability of occurrence of invertebrate target species, using the data obtained in the Biodiversity Monitoring Project (sampling years 2006-2008; protected areas involved PNGP, PNOR, PNVD). Modelling has been carried out at the scale of the three protected areas and at high spatial resolution (250x250 m cells).

To this end, we applied *species distribution models* (SDM) following a multi-scale technique, combining two spatial scales and two different kinds of models (regional and local models). The main steps of the approach were:

- acquisition and evaluation of predictor variables (temperature and land cover), through the creation of climatic maps of the study areas and the comparison between different sources of land cover data;
- acquisition of species data and reconstruction of their climatic niche using presence-only data and climatic variables at regional scale (Northern Italy). The local model was built using environmental variables (land cover data) and presence/absence data within park boundaries;
- a combination of the two models, to obtain potential distributions and uncertainty maps of the chosen species.

During the previous steps of the project, we create temperature maps using in situ data and we selected the "Forestry and other land-use categories map of the Piedmont Region (FPM)" as the best available land-cover map. The last step was the construction of the species distribution modelling approach, combining two different kinds of models with different explanatory variables. The scheme in Figure 2 briefly summarizes such combined approach.

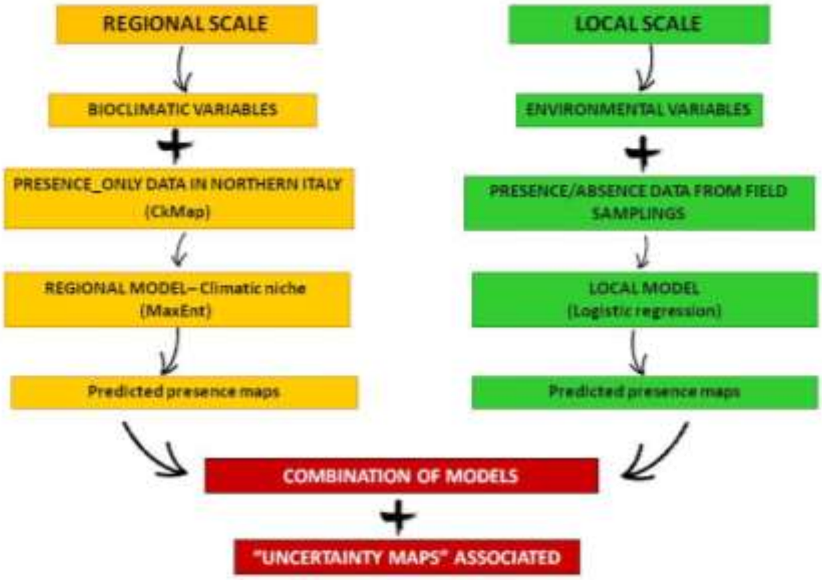

Figure 2. *Conceptual scheme of the modelling approach.*

The approach adopted here is characterised by the combination of two models, developed at different spatial scales, following the suggestion of Vicente et al. (2011). This combined approach differs from traditional methods (in which all variables are analysed inside the same modelling procedure) because it is based on two distinct models, which are in turn based on different predictor variables. Each of the two probabilities of presence are then combined to obtain the final model.

The steps of this modelling approach are:

- division of response variables in two groups (over-regional and local scales);
- modelling of the selected species, independently for each set of variables;
- projection of each model onto high-resolution spatial grids (250x250 m), covering each protected area;
- combination of both projections in the final model, through the product of the individual probabilities.

At over-regional scale, bioclimatic variables were used. Climate can influence species distribution at continental scale (Vicente et al., 2011) and, to obtain a precise description of the links between probability of presence and climate, it is necessary to analyse a large portion of the species range. We estimated that our sampling approach (three protected areas, altitudinal range 800-2600 m) was not enough to fully capture the range of climatic tolerance for the selected species.

The variables considered at local scale are related to topography and land cover. Our sampling stations are distributed over the protected areas and cover most of the present environmental variability. Multi-scale approaches can give information related to variables, which are otherwise difficult to obtain, when working on one single spatial scale (Vicente et al., 2011). Multi-scale approaches can thus provide useful information from the conservation point of view, also giving a robust starting point for simulations (Elith and Leathwick, 2007).

We tested our approach on three taxa (*Coleoptera Carabidae*, *Orthoptera*, *Lepidoptera Rhopalocera*), that were selected because of the presence of bibliographical references on their climatic tolerance. We chose two species per taxon, selecting species with different altitudinal specialisation.

Over-regional scale

At the over-regional scale, we estimated the climatic niche of the selected species, using presence data furnished by CKMap (Ruffo and Stoch, 2005). CkMap is an atlas of the Italian fauna, with spatial information collected over low resolution spatial grids (10x10 km), deriving from non-standardised data (only presence information). In our case, we focused on the grids over northern Italy (1397 grid cells). Each cell is characterised by the value of “1” in case of presence and “NA” in case of unknown information. Temperature data have been obtained from the maps of Metz et al. (2014). We obtained the climatic niche using MaxEnt (Philips et al., 2006).

The analysis have been done with the software R, using the package *biomod2* (Thuiller et al., 2014). We used 80% of the initial dataset as a *training set*, to calibrate each model, and the remaining 20% as a *test set*, to validate the models (100 iterations). For each iteration, we evaluate model goodness of fit through AUC (Receiver Operating Characteristica/Area Under the Curve) and TSS (True Skill Statistic) (Thuiller et al., 2014). We used the iteration with a TSS value > 0.7 to execute an *ensemble forecasting*, a global model representing the climatic niche of each species.

Local scale

The local scale analysis, taken as a starting point, used field data collected inside the Biodiversity Monitoring Project since 2006, to determine, through logistic regression, the relationships between presence/absence data and topographic and land cover data.

Explanatory variables are:

- altitude (100 m bands);
- percentage of tree cover (broadleaves and coniferous – 20% increase);
- percentage of herbaceous layer (20% increase);
- rock presence (yes/no);
- slope (low/high);
- aspect (cosin component);
- index of structural diversity (Shannon index of different structural layer).

Also for this modelling effort, we used the R package *biomod2* (Thuiller et al., 2014). In this case, we used as a training set the 60% of the original data (40% as a test set; 100 iterations). Model evaluation and ensemble forecasting have been performed as for the over-regional scale. To obtain the final representation of probability of presence for each cell, we multiplied the individual probabilities (over-regional and local scale), assuming the values obtained from the two models were independent on each other.

We show in Figure 3, as an example, the maps obtained for *Aeropus sibiricus* (Orthoptera, Acrididae) in the Gran Paradiso National Park.

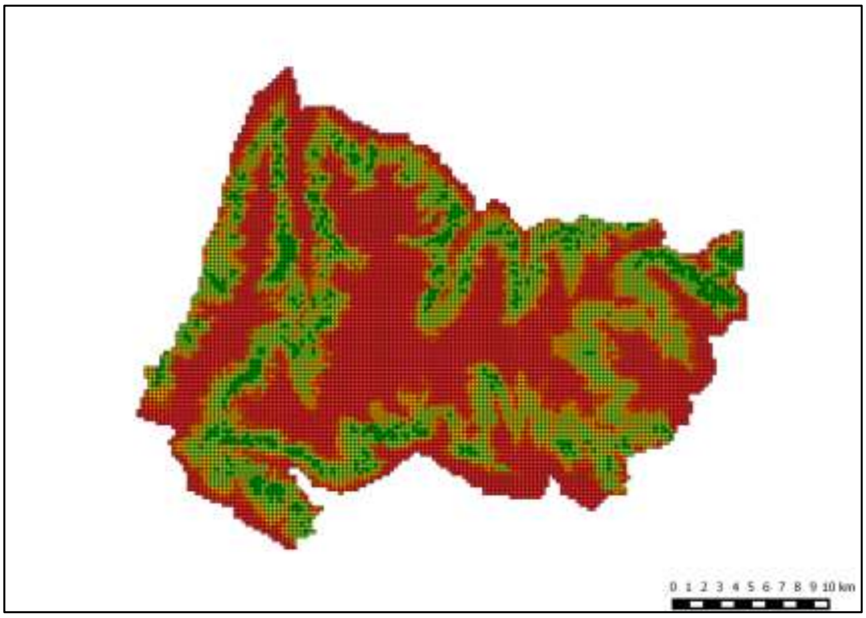

Figure 3. *Map representing the probability of presence for Aeropus sibiricus in the Gran Paradiso National Park, following the model at the over-regional scale (climatic niche) and the model at the local scale. The map shows the final probability, obtained by multiplying the probabilities provided by each model. Probability of presence increases from red to green.*

As a general conclusion of this part, we note that:

- the modelling approach reported here represents a good compromise to obtain the probability of presence at high resolution spatial scale, also integrating data from the whole climatic niche of the species. Such a modelling approach can be used for conservation purposes and as a starting point for the application of climate and environmental change scenarios;

- some drawbacks and weak points have been identified. In particular, the data at the over-regional scale are at very coarse spatial resolution (10x10 km), while a low precision of land cover maps at the local scale can strongly influence the quality of the results.

Future work should consider better way to combine the two models (over-regional and local scale), both in term of probability of occurrence and in term of uncertainty maps, taking advantage of the large data sets produced during the project.

10.5 Butterfly communities along altitudinal gradients: exploring changes over five years

This part summarizes the work "Butterfly distribution along altitudinal gradients: temporal changes over a short time period", (Cerrato et al., 2019).

The main threats to biodiversity are climate warming and land use changes. Other drivers may also interact with climate and land use changes to amplify the impact on biodiversity. Substantial changes in terrestrial species populations and distributions have already been detected worldwide, mainly in response to these impacts (Mantyka-Pringle et al., 2012). Exploring the temporal patterns of biodiversity is thus of central relevance, because the future warming and the related environmental changes are expected to cause substantial modifications in the species spatial distribution and temporal turnover.

Long-term monitoring programs are essential tools to assess the temporal changes of biodiversity on a long-time scale. However, most data series are still rather short. Therefore, it is important to extract as much information as possible from short time series, to explore the ongoing biodiversity response and try to understand whether we are witnessing the beginning of a biodiversity temporal change pattern or just a temporary fluctuation.

In this framework, we analysed butterfly data obtained from the two sampling periods (1st, 2006-2008; 2nd, 2012-2013) of the Biodiversity Monitoring Project and we compared them both at species and community level.

Species Distribution and Altitudinal Range

To understand whether and how the species distribution changes over time, we analysed changes in occupancy between the two selected time periods. We defined occupancy as the number of plots occupied by each species in each sampling session (1st *vs* 2nd) and compared these numbers by using a t-test for paired samples (significance level assessed after 999 randomizations, following Legendre and Legendre, 2012). To identify which group of species changes the most through time, we analysed if the occupancy equally increases/decreases between functional groups. We compared the changes in the number of plots per species (delta plot, 2nd sampling session *minus* 1st sampling session) between the ecological groups of conservation interest by using non-parametric tests (Kruskal-Wallis or Mann-Whitney tests, depending on the number of ecological categories). We followed the classification proposed by Balletto et al. (2015), concerning: feeding specialization (from polyphagous to monophagous); altitudinal range (generalist, medium altitude, specialised); alpine species; light ("shade loving", "sun loving"), temperature and water preferences; dispersal capacity; habitat preferences (woodland, ecotone, open areas, screes); length of flight period; reproduction frequency (monovoltine, multivoltine); hibernation strategy (egg, larva, pupa, adult). We also described the altitudinal range of each species with the following parameters:

- altitudinal optimum (mean and median value);
- higher limit (absolute maximum, 90th percentile);
- lower limit (absolute minimum, 10th percentile).

To quantify the amount of change, we compared these parameters between sampling periods using the t-test for paired samples (significance level assessed after 999 randomizations, following Legendre and Legendre 2012). As in the case of occupancy rates, we also compared the changes in altitudinal range between the ecological groups.

As a general result, we observed an increase in mean occupancy levels. However, the occupancy did not change equally among ecological groups. Concerning feeding specialisation, specialised (monophagous) species differed from the other feeding groups, even showing a slight decrease in the number of plots per species. We also recorded significant differences regarding the relationship with altitude. Altitudinal specialists increased less than the generalists, and also high-altitude species showed a significantly less marked increase. "Shade loving" species showed on the opposite the highest increase in mean occupancy levels.

We also observed significant differences in the changes in the altitudinal range between ecological groups. In particular, "high altitude" species, compared to the others, showed a significant increase in the mean, median and 10th percentile values. "Shade loving" species, compared to the "sun loving" ones, lowered their minimum and 10th percentile values. Strongly vagile species increased their minimum boundary, while the others lowered it.

Monophagous, altitudinal specialists and high-altitude species appeared to be more limited than the others. Such categories include species with high level of specialisation, consequently less prone to colonise new environments, even if climatic or environmental constraints will be relaxed. In particular, monophagous species are strictly limited by the presence and the quality of their single larval host plant and are already observed, and also predicted to be highly vulnerable to climatic/environmental changes (Romo et al. 2014). The present results concerning butterfly specialisation are quite interesting and mirror what has been observed in central Europe concerning habitat specialisation, where a decrease of specialised and low vagile species has been observed along with an increase of generalists and good dispersers (Habel et al., 2016).

High-altitude species are already limited in their distribution. Their presence is, in many cases, limited by minimum temperatures (Pellisier et al., 2013) and, consequently, they cannot lower their altitudinal range, neither in many cases, raise it, due to drastic changes in vegetation cover (a high occurrence in rock cover and a strong reduction of the availability of herbs and grasses). Moreover, permafrost reduction, which is a relatively new and rapid phenomenon, can increase instability of high altitude rocks and screes, possibly preventing colonisation by plant species (Cannone et al., 2007). High altitude species also showed a significantly larger increase in their mean, median and 10th percentile altitudinal parameters, corresponding to a reduction in their lower altitudinal boundary and in the available surface. However, we should also consider a limit of our sampling design, as we do not consider plots above 2700 m a.s.l., consequently reducing the possibility to observe expansion toward higher altitudes and colonisation of new plots by high altitude species. A significantly larger increase in plot occupancy by "shade-loving" species, compared to the others, can be associated to a tendency towards a higher cover of shrubs in open areas at low and medium altitude. In the European Alps, the effect of climate change is regionally confused by human activities. Cattle grazing in alpine pastures has been decreasing throughout the last century, allowing a fast recolonization by trees and shrubs (e.g., Vittoz et al., 2008; EEA, 2010).

Species richness

To analyse how species richness per plot changed through time, we compared different sampling periods with t-test for paired samples (significance level assessed after 999 randomizations, following Legendre and Legendre 2012). To understand if changes in species richness were mainly related to specific plots' characteristics, we considered altitude, temperature, geographic location, dominant vegetation cover (habitat type), and dominant land use. We considered as dependent variable the rate-of-change (hereinafter ROC), defined as the differences in species richness between sampling sessions, divided per the species richness of the first sampling session. We analysed ROC through linear regression and we compared variables in a multi-model context.

Species richness significantly increased from the first to the second sampling season (t-test, n = 62, t = -9.76, p = 0.001, change = 8.82 ± 0.90). The analysis of the ROC showed a significant effect of both land cover and land use: wooded habitats and managed plots increased the most.

Consequently, we can conclude that butterflies showed significant changes in species richness per plot in the analysed period. Butterfly communities are known to quickly change their arrangement because of environmental changes (Thomas, 2005), and previous studies indicated that butterflies might be responding even faster than other taxa (Devictor et al., 2012).

The highest rate of change was observed in wooded areas, while ecotonal places (transitional areas, dominated by shrubs and mainly located inside the subalpine belts) showed the lowest rate. Other studies obtained similar results, although mainly focusing on individual species abundances. For instance, a higher increase in species abundances, simultaneously to an increase of temperature, was observed in forest areas (Sgardeli et al., 2016). In days with high temperature and solar radiation, wooded areas can exert a tampon effects, protecting the individuals from extreme temperatures and reducing temperature leaps, contrary to what happens in open areas where temperature extremes are exacerbated (Oliver and Morecrof, 2014).

In grazed areas, we observed an increase in species richness that was about twice that in unmanaged areas. This could be explained by the low intensity, sustainable grazing present in those managed areas. Previous works suggest that grazing can increase the presence of plant species belonging to *Poaceae* and *Fabaceae* (Fischer and Wipf, 2002), which represent the most used plant families as larval host plant by many butterfly species. Moreover, grazing maintains woodland clearings and open herbaceous areas below the tree line that would be rapidly colonised by shrubs and trees without management activities (Nagy and Grabherr, 2009).

Community composition

We analysed community compositions by testing both for changes in location (significant changes in community composition per site over time) and dispersion over the years (significant changes in observed differences in community composition between sites over time). Changes in location were tested by applying non-parametric MANOVA to Bray-Curtis distance matrixes, to test if the multivariate centroids of species composition were, or were not, similar in the two groups (Anderson, 2001). Non-parametric MANOVA is an analysis of variance using distance matrixes and was performed by the function *adonis* of the *vegan* package (Oksanen et al., 2016). The significance of the test was assessed by using F-tests based on sequential sums of squares obtained from permutations of the raw data (999 permutations). Since we had to keep the temporal structure and spatial dependencies of our sampling design (62 sites at 2 points in time), we applied a restricted randomisation, which did not allow for permutations across samples. Changes in dispersion were tested by the *betadisper* function of the package *vegan*, a multivariate analogous of the Levene's test for comparing group variances (Anderson, 2001). Non-Euclidean distances between objects and group centroids were handled by reducing the original distances to principal coordinates. To test for significance, we applied a similar randomisation approach as described previously.

In the analysis, we did not observe substantial differences in community composition. These results were expected, as a consequence of the short time frame of analysis. Works that demonstrate variations in butterfly community composition consider longer time frames (e.g., Habel et al., 2016) and, to our knowledge, no significant changes in community composition were observed on shorter time frames.

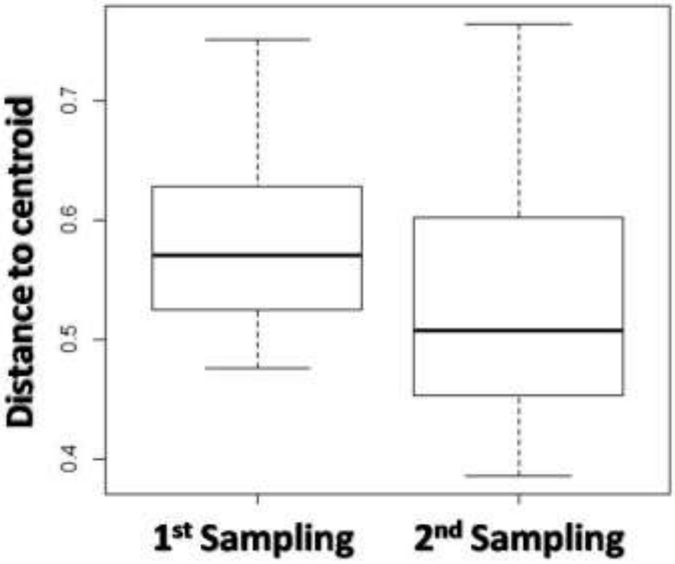

Figure 4. *Box-plot of the distances to the centroid of community composition, during each of the sampling periods. A reduction in species heterogeneity at community level from the first to the second period can be seen.*

We instead observed significant changes in dispersion between seasons, with a lower dispersion around the median during the second sampling session (Figure 4), indicating some tendency toward biotic homogenization in butterfly community composition. With the term biotic homogenization, we refer to the increase in biological similarity among communities, a replacement process leading to a decrease in distinctiveness in community composition over time, as a result of the replacement of some specialist species with other generalists, which become more uniformly distributed across previously different assemblages (Olden and Rooney, 2006). Indeed, species respond individually to the changing environmental conditions, depending mainly on their physiological characteristics and habitat requirements. This determines new species assemblages, which can be appreciated only by the examination of the entire communities throughout time (e.g., Wilson et al., 2007). For example, a similar change in community composition over time, accompanied by an increase in community similarity, has been observed in the analysis of data from the UK Butterfly Monitoring Scheme through a period of 20 years (Gonzalez-Megias et al., 2008). The tendency toward biotic homogenisation has been observed during the last decades in different taxa, following land cover and climatic changes (e.g., Buhler and Roth, 2011). Such phenomena often determine an increase in the generalist and highly vagile species, to the detriment of the others (e.g., Bonelli et al., 2011).

Community Temperature Index

The "Species Temperature Index" (STI) provides a quantitative description of the realised climatic niche of a species (Tayleur et al., 2016). To obtain such quantification over the Italian territory, we used presence data given by the database CkMap (Ruffo and Stoch, 2005). In our case, because we wanted STI referred to the Alpine populations, we only focused on northern Italy, considering 1396 cells. Every cell had a value of "1" (if occupied by the species) or "0" (if the species presence was not certain). Temperature data were obtained by the maps of Metz et al. (2014), already described above. In this way, we calculated mean temperature values for each species (realised niche optimum). We used STI to calculate the "Community Temperature Index" (CTI), quantified as the mean STI of all the species present in a given community. We calculated CTI for each community (plot) and sampling period and we analysed the changes in CTI through time.

We compared CTI between sampling period by using a t-test for paired samples. As in the case of ROC, we analysed the temporal change in CTI (Delta CTI) through linear regression in a multi-model context regression, as a function of the same environmental variables and models. We observed that CTI significantly increased from the first to the second sampling period. Change in CTI through time was mainly dependent on the geographic position of the sampling plots, with a significantly higher increase in the plots located in the colder areas, representing a clear threat for the altitudinal specialists and microthermic species of the alpine belt. Our results are consistent with an increase in CTI already observed in other geographic areas (e.g., in Greece by Zografou et al., 2014 over 13 years; in the Swiss Alps by Roth et al., 2014 over 8 years). In any case, this trend has been observed over a shorter time frame, and if confirmed during the next monitoring sessions it could represent a serious warning signal for the alpine butterfly fauna.

Prelimianry analyses on temporal changes have been conducted also using other two taxonomic groups, birds (*Aves*) and carabids (*Coleoptera Carabidae*) (Rocchia, 2016). Both taxa, in particular carabids, showed a higher degree of stability through time if compared with butterflies, with no significant changes in species richness and no decrease in heterogeneity in community composition between sampling seasons. Only the continuation of the monitoring campaigns will allow to understand whether carabids and birds display a time lag in their response to environmental changes.

10.6 Functional diversity along altitudinal gradients

An important aspect of the data collected in this monitoring project is the possibility to analyse functional diversity along elevational and climatic gradients. Functional diversity is extremely relevant, since it is strictly linked to ecosystem processes and to the resilience and resistance of ecosystems to changes.

In this framework, during 2017 and 2018, this issue has been explored for the seven taxa that were monitored (*Lepidoptera Rhopalocera*, *Orthoptera*, *Coleoptera Carabidae*, *Coleoptera Staphylinidae*, *Araneae*, *Hymenoptera Formicidae*, *Aves*) and for the species list obtained in the monitoring campaigns carried out from 2005 to 2016.

For two taxa (*Hymenoptera Formicidae*, *Orthoptera*), the collected information is currently preliminary, but for the other five taxa (*Lepidoptera Rhopalocera*, *Coleoptera Carabidae*, *Coleoptera Staphylinidae*, *Araneae*, *Aves*) a functional database has been created and analysed. This work represents a substantial part of the master thesis of Cristina Tha, graduated at the University of Turin (Tha et al. 2017).

For each of the five taxa, the functional databases have different precision levels, based on the bibliographic information available in the literature. Table 2 shows the completeness of each functional database and the number of bibliographic sources consulted.

Taxon	Number of species	Number of traits	Completeness	Number of bibliographic sources
Birds	90	16	99.31	9 articles; 3 web sites
Butterflies	160	13	100.00	7 articles; 2 web sites; expert opinion
Carabids	127	8	98.92	66 articles; 6 web sites; expert opinion
Staphylinids	240	6	89.69	15 articles; expert opinion
Spiders	291	5	90.49	8 articles; 1 web sites

Table 2. *For each taxon, the columns report the number of species present in the database, the number of functional traits for each species, the completeness of the database (expressed as a percentage of traits * species for which the information is available), and the number and nature of bibliographic sources consulted.*

The completeness of the databases was always high, but for some groups the number of quantified traits had to be reduced, owing to the limited bibliographic information available. In Table 3, for each taxon we report the quantified functional features.

Taxon	Trait	Category	Description
Birds	Wing span	Morphological	Mean value between minimum and maximum size
	Body mass	Morphological	Mean value between minimum and maximum weight
	Diet	Feeding	All feeding type that contribute to the adult diet
	Foraging stratum	Behavioural	Vertical level of the vegetation where the adults feed
	Territoriality	Behavioural	Attitude to defend nest site and/or foraging place during the breeding season
	Migration	Behavioural	Whether the species overcomes the winter in the same place where it breeds or if it moves to a warmer place
	Breeding period	Behavioural	Number of months that occur from the beginning to the end of the breeding season
	Phenology	Behavioural	Whether the breeding occurs early in the year or not
	Nest site	Behavioural	Environmental layer where adults are used to build the nest
	Clutch size	Life history	Mean number of eggs weighted by the number of broods per year
	Habitat openness	Behavioural	Main habitat where adults breed and feed
	Habitat specialization	Behavioural	Species presence in Corine Land Cover patches

Taxon	Trait	Category	Description
	Mean altitude	Physiological	Mean value between minimum and maximum optimal altitude
	Altitudinal range	Physiological	Altitudinal range where the species occurs, calculated as the difference between the maximum and the minimum optimal altitude value
	Bio1	Physiological	Annual mean temperature of species distribution area
	Bio7	Physiological	Temperature annual range of species distribution area
Butterflies	Wing span	Morphological	Mean of female and male wing span values
	Voltinism	Life history	Number of generations an individual completes per year
	Flight period	Behavioural	Number of months the adult is active during the year
	Overwintering stage	Behavioural	Main developmental stage used to overcome winter
	Habitat openness	Behavioural	Habitat type mainly used by adults
	Stenophagy	Feeding	Diet preference of larvae measured as number of host plants
	Myrmecophily	Behavioural	Degree of positive association with ants in a scale from 0 to 6
	Stratum use	Feeding/Behavioural	Stratum use of larvae defined by host plant form according to Ellenberg's definition
	Host plant Nitrogenous request	Feeding	Average Ellenberg Nitrogen values of host plants present in the study area
	Altitude	Physiological	Altitudinal range where species occurs
	Bio1	Physiological	Annual mean temperature of species distribution area
	Bio7	Physiological	Temperature annual range of species distribution area
	Moisture	Physiological	Adults adaptation to live with specific level of moisture
Carabids	Body size	Morphological	Mean value between minimum and maximum body size
	Wing morphology	Morphological	Most common wing development of the adults
	Colour	Morphological	Colour of the upper surface of the body (head, pronotum and elytra)
	Habitat openess	Behavioural	Main habitat type where adults occur
	Altitude	Physiological	Altitudinal range
	Moisture	Physiological	Adults adaptation to live with particular level of moisture
	Diet	Feeding	Feeding strategy of the adults
	Breeding period	Behavioural	Species breeding period within the year
Staphylinids	Diet	Feeding	Main feeding guild
	Environmental specialization	Behavioural	Whether the species is specialized on particular environment or not
	Habitat openess	Behavioural	Main habitat type where the species occurs
	Microhabitat	Behavioural	Main microhabitat type where the species occurs
	Altitude	Physiological	Altitudinal range
	Moisture	Physiological	Species adaptation to live with specific level of moisture
Spiders	Body size	Morphological	Mean value between female and male body size
	Hunting method	Feeding	Hunting strategy used by the species
	Microhabitat	Behavioural	Main microhabitat type where the species occurs
	Stratum use	Behavioural	Vertical level of the vegetation where the species lives, breeds and feeds

Taxon	**Trait**	**Category**	**Description**
	Phenology	Behavioural	Sum of months during which males and females are active within the year

Table 3. *For each taxon, the columns report the functional traits that have been quantified, the category to which they can be ascribed (Morphology, Behaviour, Feeding, Life history, Physiology) and a brief description of the traits themselves.*

The presence/absence data obtained from the monitoring campaigns carried out in PNGP, PNOR and PNVD during the first two sessions of the biodiversity project (2006-2008, 2012-2013) have been used to estimate selected functional diversity indices:

- Functional Richness, FRic;
- Functional Evenness, FEve;
- Functional Divergence, FDiv;
- Functional Dispersion, FDis.

The indices were calculated separately for each taxon and session, to identify individual trends.

The relationship between species richness and functional diversity was analysed to directly investigate whether the two parameters can be used interchangeably, that is, to understand whether communities that are richer in species correspond also to greater functional diversity. For each taxon and monitoring session, the relationship between these two quantities was compared with the theoretical curves proposed in the literature (Michaelis-Menten saturation, exponential, linear, quadratic, null model). The analyses were based on non-linear regressions, carried out using the software R and the *nlstools* package (Baty et al. 2015); the best-fit curve was selected using AICc (Akaike's information criterion with sample size correction).

As shown in Table 4, different patterns were observed, depending on the taxon and the sampling session.

	First sampling session (2006-2008)				Second sampling session (2012-2013)			
Taxon	**FDis**	**FDiv**	**FEve**	**FRic**	**FDis**	**FDiv**	**FEve**	**FRic**
Birds	M-M	Quadratic	ns	Quadratic	M-M	ns	ns	Linear
Butterflies	M-M	ns	Linear	Linear	M-M	M-M	Quadratic	Linear
Carabids	M-M	M-M	Linear	M-M	M-M	M-M	ns	M-M
Spiders	ns	Linear	M-M	Quadratic	-	-	-	-
Staphylinids	ns	ns	ns	M-M	M-M	M-M	ns	Quadratic

Table 4. *For each taxon, monitoring session and functional diversity index, the curve that best explains the relationship with species richness is reported. M-M: Michaelis-Menten model; ns: the best model turned out to be the null model; sampling data are not currently available.*

The most represented models were:

- the Michaelis-Menten curve (Figure 5), which corresponds to a saturation model, for which, beyond a certain level of species richness, functional diversity saturates leading to situations of functional redundancy in the most species-rich communities;
- the linear curve (Figure 6), for which a direct proportionality between species richness and functional diversity is present.

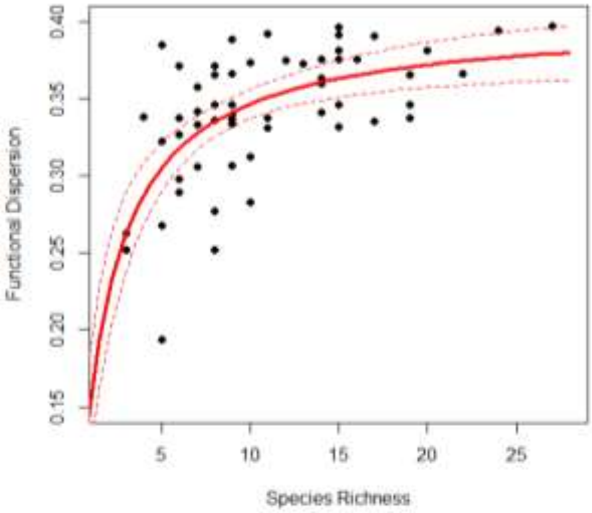

Figure 5. *Scatterplot of the relationship between functional dispersion and species richness, obtained using data from carabids (Coleoptera Carabidae) sampled during the first monitoring session. Each black dot represents a sampling station. The red solid line represents the non-linear regression curve corresponding to the best model (in this case the Michaelis-Menten curve); the limits of the 95% confidence interval are indicated by the red dotted curves.*

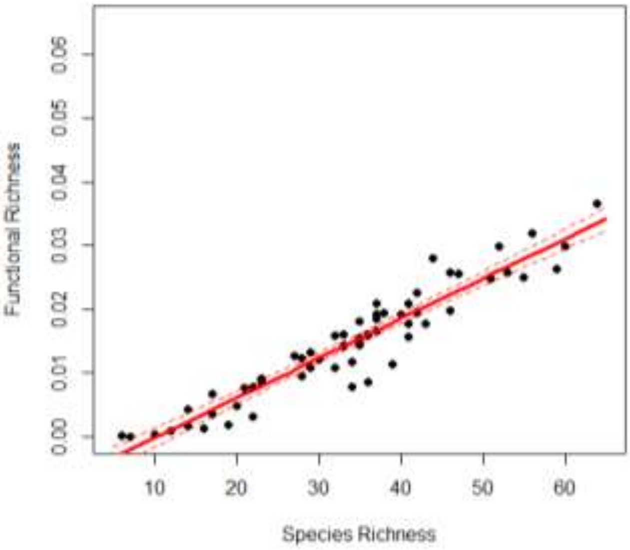

Figure 6. *Scatterplot of the relationship between functional dispersion and species richness, obtained using data from butterflies (Lepidoptera Rhopalocera) sampled during the second monitoring session. Each black dot represents a sampling station. The red solid line represents the non-linear regression curve corresponding to the best model (linear model in this case); the limits of the 95% confidence interval are indicated by the red dotted curves.*

As a second step, the role of altitude and temperature in determining the functional diversity pattern was investigated. Differences between taxa and over time have emerged, but generally, the results indicated an important role of altitude and temperature in determining the functional diversity of invertebrate communities. As shown in Figure 8 as an example, the most commonly observed pattern is a hump-shaped curve, which corresponds to higher values of functional diversity at intermediate altitude, corresponding to the subalpine belt.

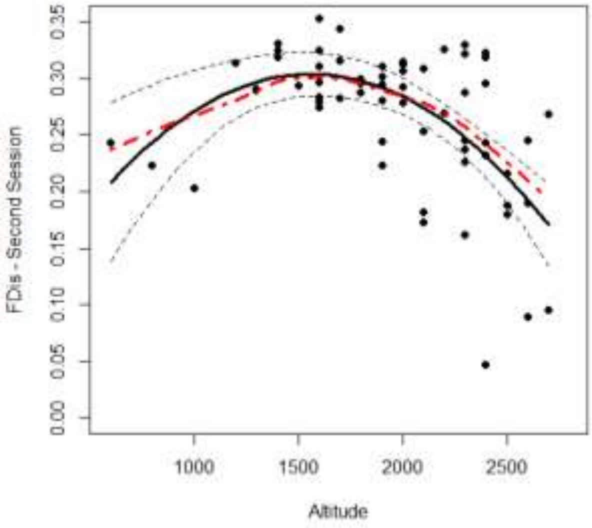

Figure 7. *The observed relationship between functional dispersion and altitude, obtained using staphylinids (Coleoptera Staphylinidae) sampled during the second monitoring session. Each black dot represents a sampling station. The solid black line represents the regression curve corresponding to the best model (in this case a quadratic relationship), whereas the limits of the 95% confidence interval is indicated by the black dotted curves. The non-parametric LOWESS curve is shown by the red dot-dashed curve.*

Finally, we started to explore changes in functional diversity between the first and second sampling sessions (2006-2008 vs. 2012-2013). The aim here is to assess whether the changes have been uniformed within the investigated elevational gradient or whether certain areas or altitudes have been affected, despite the short time span, more than others. In many cases, it was also observed that changes in species richness have already led to changes in functional diversity, as shown as an example in Figure 8.

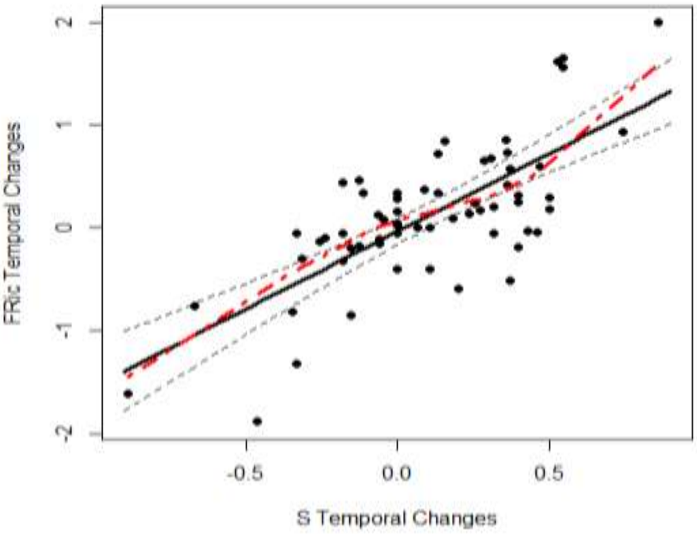

Figure 8. *Existing relationship between temporal changes in species richness and functional richness, using bird data. Each black dot represents a sampling station. The continuous black line represents the regression curve corresponding to the best model (in this case a linear type relationship), while the black dotted lines indicate the limits of the 95% confidence interval. The non-parametric LOWESS curve is shown by the red dotted curve.*

In conclusion, the work performed in these years has achieved a good level of completeness, leading to the definition of new databases. For some taxa, such as spiders and staphylinids, more data are needed. Moreover, the ecological and life-history information for species that are endemic to the Alps or specialised to the alpine environment are not always available.

The exploratory analyses described here indicate the existence of interesting patterns. In particular, it emerged that:

- in most cases, species richness cannot be considered as a substitute for functional diversity, thus requiring considering also this aspect in the analysis of biodiversity patterns through space and time;
- in many cases, functional diversity shows a clear pattern along the altitudinal gradient, thus allowing to identify the most vulnerable areas from the functional point of view. It is very important for management purposes to quantify and investigate aspects related to functional redundancy, as an estimate of the vulnerability of the communities and ecosystems;
- despite the short time frame between the two monitoring sessions, differences in terms of functional diversity have already emerged, partly owing to changes in species richness of single taxa.

10.7. Discussion

The database on invertebrate biodiversity obtained during the NextData project, is an important source of information on ecosystem and community changes taking place in Alpine areas. This database is made available upon request and can be considered as a base information set for many studies.

In particular considering butterflies, the results of the analysis of these data suggest that, even if the timeframe under analysis is relatively short, we already observed a significant amount of changes. This is especially interesting, and somewhat alarming, considering that we have been working in protected areas where habitat alteration by direct human effects was strongly reduced.

To summarise, over a period of five years, we observed:

- general increase in mean occupancy level and species richness;
- no significant changes in mean altitudinal optimum, but significant changes in altitudinal limits.

Moreover, the observed changes differed across species, determining:

- an increase in shared species (tendency to biotic homogenisation) among communities, even if the overall community composition did not change;
- a significant increase in the Community Temperature Index (CTI).

Functional traits are an important addition to estimate the vulnerability of the communities and ecosystems.

Considering these results, it is now even more important to continue the monitoring effort to understand if the patterns observed here represent only transient changes or are the first signals of a long-term trend.

References

Anderson M.J., 2001. A new method for non-parametric multivariate analysis of variance. Austral Ecol., 26:32-46.

Auer I., Böhm R., Jurkovic A., Lipa W., Orlik A., Potzmann R., Schöner W., Ungersböck M., Matulla C., Briffa K., Jones P., Efthymiadis D., Brunetti M., Nanni T., Maugeri M., Mercalli L., Mestre O., Moisselin J. M., Begert M., Müller-Westermeier G., Kveton V., Bochnicek O., Stastny P., Lapin M., Szalai S., Szentimrey T., Cegnar T., Dolinar M., Gajic-Capka M., Zaninovic, K., Majstorovic Z., Nieplova E., 2007. HISTALP – Historical instrumental climatological surface time series of the greater alpine region 1760-2003. Int. J. Climatol., 27:17-46.

Balletto E., Bonelli S., Barbero F., Casacci L.P., Sbordoni V., Dapporto L., Scalercio S., Zilli A., Battistoni A., Teofili C., Rondinini C. (compilatori), 2015. Lista Rossa IUCN delle Farfalle Italiane - Ropaloceri. Comitato Italiano IUCN e Ministero dell'Ambiente e della Tutela del Territorio e del Mare, Roma.

Balletto E., Cassulo L. A., Bonelli S., 2014. An annotated checklist of the Italian Butterflies and Skippers, (Papilionoidea, Hesperiioidea). Zootaxa, 2853.

Bässler C., Müller J., Hothorn T., Kneib T., Badeck F. & Dziock F., 2010. Estimation of the extinction risk for high-montane species as a consequence of global warming and assessment of their suitability as cross-taxon indicators. Ecol. Indic., 10:341–352.

Baty F., Ritz C., Charles S., Brutsche M., Flandrois J. P., Delignette-Muller M. L., 2015. A Toolbox for Nonlinear Regression in R: The Package nlstools. J. Stat. Soft., 66:1-21.

Beniston M., 2003. Climatic change in mountain regions: a review of possible impacts. Climatic Change, 59:5-31.

Beniston M., 2006. Mountain weather and climate. A general overview and a focus on climatic change in the Alps. Hydrobiologia, 562:3-16.

BirdLife International, 2015. The IUCN Red List of Threatened Species 2015. Version 2018-2.

Bonelli S., Cerrato C., Loglisci N., Balletto E., 2011. Population extinctions in the Italian diurnal Lepidoptera: an analysis of possible causes. J. Insect Conserv., 15:879-890.

Brambilla M., Casale F., Bergero F., Bogliani G., Crovetto M., Falco R., Roati M., Negri I., 2010. Glorious past, uncertain present, bad future? Assessing effects of land-use changes on habitat suitability for a threatened farmland bird species. Biol. Conserv., 143:2770-2778.

Brandmayr P., Zetto T., Pizzolotto R., 2005. I coleotteri carabidi per la valutazione ambientale e la conservazione della biodiversità: manuale operativo. APAT, Manuali e Linee Guida, Roma.

Brehm J., Homeier J., Fiedler K., 2003. Beta diversity of geometrid moths (Lepidoptera: Geometridae) in an Andean montane rainforest. Divers. Distrib., 9:351-366.

Bühler C. and Roth T. 2011. Spread of common species results in local-scale floristic homogenization in grassland of Switzerland. Divers. Distrib., 17:1089-1098.

Butchart S.H., Walpole M., Collen B., van Strien A., Scharlemann J. P., Almond R. E., Baillie J. E., Bomhard B., Brown C., Bruno J., Carpenter K. E., Carr G. M., Chanson J., Chenery A. M., Csirke J., Davidson N. C., Dentener F., Foster M., Galli A., Galloway J. N., Genovesi P., Gregory R. D., Hockings M., Kapos V., Lamarque J. F., Leverington F., Loh J., McGeoch M. A., McRae L., Minasyan A., Hernández Morcillo M., Oldfield T. E., Pauly D., Quader S., Revenga C., Sauer J. R., Skolnik B., Spear D., Stanwell-Smith D., Stuart S. N., Symes A., Tierney M., Tyrrell T. D., Vié J. C., Watson R., 2010. Global Biodiversity: Indicators of Recent Declines. Science, 328:1164-1168.

Cannone N., Sgorbati S., Guglielmin M., 2007. Unexpected impacts of climate change on alpine vegetation. Front. Ecol. Environ., 5:360–364.

Cerrato C., Rocchia E., Brunetti M., Bionda R., Bassano B., Provenzale A., Bonelli S., Viterbi R. 2019. Butterfly distribution along altitudinal gradients: temporal changes over a short time period. Nat. Conserv., 34:91-118.

Chemini C., Rizzoli A., 2003. Land use change and biodiversity conservation in the Alps. J. Mt. Ecol., 7:1-7.

Devictor V., van Swaay C., Brereton T., Brotons L., Chamberlain D., Heliölä J., Herrando S., Julliard R., Kuussaari M., Lindström Å., Reif J., Roy D. B., Schweiger O., Settele J., Stefanescu C., Van Strien A., Van Turnhout C., Vermouzek Z., WallisDeVries M., Wynhoff I., Jiguet F., 2012. Differences in the climatic debts of birds and butterflies at a continental scale. Nat. Clim. Change, 2:21-124.

Diaz H. F., Grosejeanan M., Graumlich L., 2003. Climate variability and change in high elevation regions: past, present and future. Climatic Change, 59:1-4.

Dirnböck T., Essl F., Rabitsch W., 2011. Disproportional risk for habitat loss of high-altitude endemic species under climate change. Glob. Change Biol., 17:990-996.

EEA - European Environment Agency 2010. Europe's ecological backbone: recognising the true value of our mountains. Office for Official Publ. of the European Communities.

Elith J., Leathwick J. R., 2007. Predicting species distributions from museum and herbarium records using multiresponse models fitted with multivariate adaptive regression splines. Divers. Distrib., 13:265-275.

Fischer M. and Wipf S., 2002. Effect of low-intensity grazing on the species-rich vegetation of traditionally mown subalpine meadows. Biol. Conserv., 104:1-11.

Fleishman E., Austin G. T., Weiss A. D., 1998. An empirical test of Rapoport’s rule: elevational gradients in montane butterfly communities. Ecology, 79:2482-2493.

Gobbi M., Rossaro B., Vater A., De Bernardi F., Pelfini M., Brandmayr P., 2007. Environmental features influencing Carabid beetle (Coleoptera) assemblages along a recently deglaciated area in the Alpine region. Ecol. Entomol., 32:282-289.

Gonzalez-Megias A., Menendez R., Roy D., Brereton T., Thomas C. D., 2008. Changes in the composition of British butterfly assemblages over two decades. Glob. Chang. Biol., 14:1464-1474.

Grandchamp A. C., Bergamini A., Stofer S., Niemela J., Duelli P., Scheidegger C., 2005. The influence of grassland management on ground beetles (Carabidae, Coleoptera) in Swiss montane meadows. Agr. Ecosyst. Environ., 110:307-317.

Habel J.C. M., Segerer A., Ulrich W., Torchyk O., Weisser W., Schmitt T., 2016. Butterfly community shifts over 2 centuries. Conserv. Biol., 30:754-762.

Hannah L., Midgley G. F., Millar D., 2002. Climate change-integrated conservation strategies. Glob Ecol. Biogeogr., 11:485-495.

Horion A., 1963. Faunistik der Mitteleuropäischen Käfer, Bd 9.Staphylinidae 1. Teil (Micropeplinae bis Euaesthetinae). Ph. C. W. Schmidt Verlag, Überlingen-Bodensee.

Horion A., 1965. Faunistik der Mitteleuropäischen Käfer, Bd 10. Staphylinidae 2. Teil (Paederinae bis Staphylininae). Ph. C. W. Schmidt Verlag, Überlingen-Bodensee.

Horion A., 1967. Faunistik der Mitteleuropäischen Käfer Bd 11. Staphylinidae 3. Teil (Habrocerinae bis Aleocharinae, ohne subtribus Athetae). Ph. C. W. Schmidt Verlag, Überlingen-Bodensee.

Huber U., Reasoner M., Bugmann H., 2005. Global Change and Mountain Regions: An Overview of Current Knowledge. Advances in Global Change Research. Springer-Verlag, Berlin.

Kessler M. S., Herzog K., Fjeldsai T., Bach K., 2001. Species richness and endemism of plant and bird communities along two gradients of elevation, humidity and land use in the Bolivian Andes. Biodivers. Distrib., 7:61-77.

Körner C., 2000. Why are there global gradients in species richness? Mountains may hold the answer. Trends Ecol. Evol., 15:513-514.

Körner C., Paulsen J., Spehn E.M., 2011. A definition of mountains and their bioclimatic belts for global comparisons of biodiversity data. Alpine Bot., 121:73-78.

Krauss J., Steffan-Dewenter I., Tscharntke T, 2003. How does landscape context contribute to effects of habitat fragmentation on diversity and population density of butterflies? J. Biogeogr., 30:889-900.

Legendre P. and Legendre L., 2012. Numerical Ecology. 3rd English Edition. Elsevier, Amsterdam.

Lomolino J. W., 2001. Elevation gradients of species-density: historical and prospective views. Global Ecol. Biogeogr., 10:3-13.

Magurran A. E. , Baillie S. R. , Buckland S. T., Dick J. M., Elston D. A., Scott E. M., Smith R. I., Somerfield P. J., Wat A. D., 2010. Long-term datasets in biodiversity research and monitoring: assessing change in ecological communities through time. Trends Ecol. Evol., 25:574-582.

Mantyka-pringle C. S., Martin T. G., Rhodes J. R., 2012. Interactions between climate and habitat loss effects on biodiversity: a systematic review and meta-analysis. Glob. Change Biol., 18:1239-1252.

Massa B., Fontana P., BuzzettiI F.M., Kleukers R. & Odè B., 2012. Orthoptera. Fauna d'Italia. Vol. XLVIII. Calderini, Bologna, 563 pp.

Metz M., Rocchini D., Neteler M., 2014. Surface temperatures at the continental scale: tracking changes with remote sensing at unprecedented detail. Remote Sens., 6:3822-3840.

Nagy L. and Grabherr G., 2009. The biology of alpine habitats. Oxford University.

Oksanen J., Guillaume Blanchet F., Kindt R., Legendre P., Minchin P. R., O'hara R. B., Simpson G. L., Solymos P., Stevens M. H., Wagner H., Oksanen M. J., 2016. Package “vegan”, community ecology package.

Olden J. D. and Rooney T. P., 2006. On defining and quantifying biotic homogenization. Glob. Ecol. Biogeogr., 15:113-120.

Oliver T. H., and Morecroft M. D., 2014. Interactions between climate change and land use change on biodiversity: attribution problems, risks, and opportunities. WIREs Clim. Change, 5:317-335.

Oommen M. A., Shanker K., 2005. Elevational species richness patterns emerge from multiple local mechanisms in Himalayan woody plants. Ecology, 86:3039-3047.

Orme C. D. L., Davies R. G., Burgess M., Eigenbrod F., 2005. Global hotspots of species richness are not congruent with endemism or threat. Nature, 436:1016-1019.

Parmesan C., 2006. Ecological and Evolutionary Responses to Recent Climate Change. Annu. Rev. Ecol. Sys., 37:637-669.

Patthey P., Wirthner S., Signorell N., Arlettaz R., 2008. Impact of outdoor winter sports on the abundance of a key indicator species of alpine ecosystems. J. Appl. Ecol., 45:1704-1711.

Pauchard A., Kueffer C., Dietz H., Daehler C. C., Alexander J., Edwards P. J., Arévalo J. R., Cavieres L. A., Giusan A., Haider S., Jakobs G., McDougall K., Millar C. I., Naylor B. J., Parks C. G., Rew L. J., Seipel T., 2009. Ain't no mountain high enough: plant invasions reaching new elevations. Front. Ecol. Environ., 7:479-486.

Pauli H., Gottfried M., Hohenwallner D., Reiter K., Casale R., Grabherr G., 2004. The GLORIA field manual. Multi-summit approach. DG Research, EUR 21213, Official Publications of the European Communities, Luxembourg.

Pauli H., Gottfried M., Reiter K., Klettner C., Grabherr G., 2007. Signals of range expansions and contractions of vascular plants in the high Alps: observations (1994–2004) at the GLORIA*master site Schrankogel, Tyrol, Austria. Glob. Change Biol., 13:147-156.

Pellissier L., Alvarez N., Espindola A., Pottier J., Dubuis A., Pradervand J-N., Guisan A., 2013. Phylogenetic alpha and beta diversities of butterfly communities correlate with climate in the western Swiss Alps. Ecography, 36:541-550.

Phillips S. J., Anderson R. P., Schapire R. E., 2006. Maximum entropy modeling of species geographic distributions. Ecol. Mod., 190:231-259.

Platnick N. I., 2014. The world spider catalog, version 14.5. American Museum of Natural History.

Rahbek C 1995 The elevational gradient of species richness: a uniform pattern? Ecography, 18:200-205.

Rebetez M., Reinhard M., 2008. Monthly air temperature trends in Switzerland 1901-2000 and 1975-2004. Theor. Appl. Climatol., 91:27-34.

Riservato E., Festi A., Fabbri R., Grieco C., Hardensen S., La Porta G., Landi F., Siesa M. E., Utzeri C., 2014. Odonata – Atlante delle libellule italiane. Società Italiana per lo Studio e la Conservazione delle Libellule. Edizioni Belvedere, Latina “Le scienze”.

Rocchia E., 2016. Temporal variation of species distribution and species morphological traits along altitude in the Alps. PhD Thesis, Università degli Studi di Milano-Bicocca.

Romo H., Baros G., Marquez A. L., Moreno J. C., Real R., 2014. Effects of climate change on the distribution of ecologically interacting species: butterflies and their main food plants in Spain. Ecography, 37:1063-1072.

Roth T., Plattner M. & Amrhein V., 2014. Plants, birds and butterflies: short-term responses of species communities to climate warming vary by taxon and with altitude. PLoS One, 9:e82490.

Ruffo S., Stoch F. (eds.), 2005. Checklist e distribuzione della fauna italiana. Memorie del Museo Civico di Storia Naturale di Verona, 2.serie, Sezione Scienze della Vita 16.

Schmitt T., 2009. Biogeographical and evolutionary importance of the European high mountain systems. Front. Zool., 6:1-9.

Sgardeli, V., Zografou K., Halley J. M., 2016. Climate change versus ecological drift: Assessing 13 years of turnover in a butterfly community. Basic Appl. Ecol., 17:283-290.

Tayleur C. M., Devictor V., Gauzere P., Jonzen N., Smith H. G., Lindstrom A., 2016. Regional variation in climate change winners and losers highlights the rapid loss of cold-dwelling species. Divers. Distrib., 22:468-480.

Tha C., Cerrato C., Viterbi R., Provenzale A., 2017. Functional diversity along altitudinal gradients: a multi-taxa approach in the Western Alps. In: Book of abstracts – 1st International Conference on Comunity Ecology, Budapest, 28-29 September 2017, p.95.

Theurillat J. P., Guisan A., 2001. Potential impact of climate change on vegetation in the European Alps: a review. Climatic Change, 50:77-109.

Theurillat J. P., Schlüssel A., Geissler P., Guisan A., Velluti C., Wiget L., 2003.Vascular plant and bryophyte diversity along elevational gradients in the Alps. In: Nagy L, Grabherr G, Körner C, Thompson DBA, editors. Alpine Biodiversity in Europe. Springer, Berlin, Germany, pp.185-193.

Thomas C. D., Cameron A., Green R. E., Bakkenes M., Beaumont L. J., Collingham Y. C., Erasmus B. F. N., Ferreira de Siqueira M., Grainger A., Hannah L., Hughes L., Huntley B., van Jaarsveld A. S., Midgley G. F., Miles L., Ortega-Huerta M. A., Peterson A. T., Phillips O. L., Williams S. E., 2004. Extinction risk for climate change. Nature, 427:145-148.

Thomas J.A., 2005. Monitoring change in the abundance and distribution of insects using butterflies and other indicator groups. Philos. Trans. R. Soc. Lond. B. Biol. Sci., 360:339-357.

Thuiller W., Georges D., Engler R., 2014. BIOMOD2: Ensemble platform for species distribution modeling. R package version 2.1.7/r560.

Thuiller W., Lavorel S., Arau´jo M. B., Sykes M. T., Prentic I. C., 2005. Climate change threats to plant diversity in Europe. Proc. Natl. Acad. Sci. U.S.A., 102:8245-8250.

Vicente J., Randin C. F., Gonçalves J., Metzger M. J., Lomba Â., Honrado J., Guisan A., 2011. Where will conflicts between alien and rare species occur after climate and land-use change? A test with a novel combined modelling approach. Biol. Inv., 13:1209-1227.

Viterbi R., Cerrato C., Bassano B., Bionda R., von Hardenberg A., Provenzale A., Bogliani G., 2013. Patterns of biodiversity in the northwestern Italian Alps: a multi-taxa approach. Community Ecol. 14:18-30.

Vittoz P., 2008. Effects of climate and land-use change on the establishment and growth of cembran pine (Pinuscembra L.) over the timberline-treeline ecotone in the Central Swiss Alps. Arctic. Ant. Alp. Res., 40:225-232.

Wilson R., Gutiérrez D., Gutiérrez J., Monserrat V. J., 2007. An elevational shift in butterfly species richness and composition accompanying recent climate change. Glob. Change Biol., 13:1873-1887.

Yoccoz N. G., Nichols J. D., Boulinier T., 2001. Monitoring of biological diversity in space and time. Trends Ecol. Evol., 16:446-453.

Zografou K., Kati V., Grill A., Wilson R.J., Tzirkally E. L., Pamperis L. N., Halley J. M., 2014. Signals of climate change in butterfly communities in a Mediterranean protected area. PLoS One, 9:e87245.