

Supplementary information

APPENDIX 1

Selecting ecological characteristics for plant species classification.

For each of selected dominant plant species ($n = 136$), we chose species features or traits to represent six key-life history characteristics: dispersal ability, response to competition for light (whether they germinate and grow under specific light conditions), resistance to disturbance (grazing and mowing), competitive effects (estimated through the height of the species), tolerance to abiotic conditions (ecological niche) and demography (life form, longevity, age of maturity). Dispersal ability was taken and adapted from (Vittoz & Engler, 2007). This typology is based on the most efficient dispersal mode, plant height, habitat, seed mass and dispersal attributes (e.g., wings, pappi). It identifies seven classes that discriminate a log-increase of dispersal distances. To estimate the response to competition for light, we used an ecological indicator value for species light requirements adapted to the study region (Landolt *et al.*, 2010). Following the same idea of competition for light, species' competitive effect was measured by plant height. In the Bauges regional park, since domestic stock is the main disturbance regime we used a palatability index based on forage values for cattle to represent species response to grazing. This forage value for cattle represents an ordinal variable made of 9 categories (from from poisonous to best forage value) made by experts following (Briemle, 1992; Jouglet, 1999). We measured species tolerance to abiotic conditions using species distribution models (SDMs) calibrated on each of 136 plant species and in function of a set of uncorrelated climatic, soil and topographic variables at 100m resolution (Thuiller *et al.*, 2009; Thuiller *et al.*, 2014). From the calibrated SDMs, we calculated the ecological niche overlap between species following Broennimann *et al.* (2012). Given the limited amount of available data and uncertainty related to species demography (e.g., longevity), we used a pre-classification based on Raunkiaer's life forms (Raunkiaer, 1934) that represent the main differences in demographic traits such as individual longevity, age at maturity, and fecundity (phanerophyte, chamaephyte, and herbaceous). Most traits values were extracted from ANDROSACE database (Thuiller, *et al.* unpublished, Table S1) and additional available (Kühn *et al.*, 2004) and local database. Concerning the diet of the chamois, we built a regular five-class variable to summarize the relative abundance of each plant species (measured by eDNA) within the chamois faeces (from zero to high relative abundance).

Database	Reference
Field measurements	Choler, P (2005). Consistent shifts in Alpine plant traits along a mesotopographical gradient. <i>Artic, Antartic and Alpine Research</i> , 37, 444-453.
Field measurements	Albert, C.H., Thuiller, W, Yoccoz, N.G., Soudant, A., Boucher, F., Saccone, P., Lavorel, S. (2010). Intraspecific functional variability : extent, structure and sources of variation. <i>Journal of Ecology</i> , 98, 604-613.
Field measurements	Lavorel, S., Grigulis, K, Lamargue, P. et al. (2011). Using plant functional traits to understand the landscape distribution of multiple ecosystem services. <i>Journal of Ecology</i> , 99, 135-147.
Field measurements	Chalmandrier, L., Münkemüller, T., Lavergne, S., Thuiller, W. (2014). Effect of species's similarity and dominance on the functional and phylogenetic structure of a plant meta-community. <i>Ecology</i> , 96, 143-153.
Flora Indicativa	Landolt, E., Bäumler, B., Erhardt, A. et al. (2010). Flora Indicativa. Ecological indicator values and biological attributes of the flora of Switzerland and the Alps. Berne, Haupt Verlag.
BiolFlor	Kuhn,I., Durka, W., Klotz, S. (2004). BiolFlor - a new plant-trait database as a tool for plant invasion ecology. <i>Diversity & Distributions</i> , Vol. 10, No. 5-6, 363.

Databases used for species traits or characteristics. They all form the database ANDROSACE that compiles trait values from field measurements in the study area and other trait databases containing species from the study area or nearby.

Classification procedure. For each life form group (phanerophyte, chamaephyte, and herbaceous), we built a distance matrix using Gower's formula to integrate both categorical and quantitative traits. Niche overlap between each species pair was converted into Euclidean distance. We used the Unweighted Pair Group Method with Arithmetic Mean clustering algorithm (UPGMA, (Kaufman & Rousseeuw, 1990) to build the different PFGs from the combination of these two distance matrices.

The Dunn index, the R-squared (Halkidi *et al.*, 2001), the index of Calinski & Harabasz (1974), and the average silhouette (Kaufman & Rousseeuw, 1990) were calculated to choose the optimal number of groups for each life form.

PFGs description. The classification identified two chamaephyte groups (C1-C2), eight herbaceous groups (H1-H8) and six phanerophyte groups (P1-P6). The species list is given for each group.

PFG	Species list
C1	<i>Clematis vitalba, Cornus sanguinea, Crataegus monogyna, Hedera helix, Ligustrum vulgare, Lonicera xylosteum, Rubus fruticosus.</i>
C2	<i>Arctostaphylos uva-ursi, Helianthemum nummularium, Polygala chamaebuxus, Rhododendron ferrugineum, Vaccinium myrtillus, Vaccinium uliginosum, Vaccinium vitis-idaea.</i>
H1	<i>Ajuga reptans, Briza media, Bromus erectus, Carex panicea, Filipendula ulmaria, Gagea villosa, Geranium robertianum, Gymnadenia conopsea, Leontodon hispidus, Polygonum viviparum, Potentilla erecta, Salvia pratensis, Sanguisorba minor, Teucrium chamaedrys.</i>
H2	<i>Anthoxanthum odoratum, Astrantia major, Carex sempervirens, Festuca rubra, Geranium sylvaticum, Heracleum sphondylium, Knautia arvensis, Nardus stricta, Onobrychis montana, Phyteuma orbiculare, Pimpinella major, Rhinanthus alectorolophus, Rumex arifolius, Silene dioica, Trollius europaeus.</i>
H3	<i>Carex ferruginea, Gentiana lutea, Leucanthemum adustum, Plantago atrata, Rumex pseudalpinus, Sesleria caerulea, Trifolium badium.</i>
H4	<i>Brachypodium rupestre, Cirsium palustre, Lysimachia vulgaris, Mentha aquatica, Origanum vulgare, Phragmites australis, Solidago gigantea.</i>
H5	<i>Arnica montana, Campanula rhomboidalis, Carduus defloratus, Centaurea uniflora, Chaerophyllum hirsutum, Deschampsia flexuosa, Epilobium angustifolium, Gentiana purpurea, Globularia nudicaulis, Homogyne alpina, Hypericum richeri, Juncus filiformis, Knautia dipsacifolia, Laserpitium latifolium, Linum alpinum, Luzula sieberi, Pulsatilla alpina, Ranunculus tuberosus, Sempervivum tectorum, Serratula tinctoria, Traunsteinera globosa, Valeriana montana.</i>
H6	<i>Aruncus dioicus, Athyrium filix-femina, Cardamine pentaphyllos, Dryopteris filix-mas, Galium odoratum, Hieracium murorum, Hordelymus europaeus, Lamium galeobdolon, Melica uniflora, Mercurialis perennis, Phyteuma spicatum, Prenanthes purpurea, Saxifraga rotundifolia.</i>
H7	<i>Anthyllis vulneraria, Campanula rotundifolia, Carex elata, Dactylis glomerata, Deschampsia cespitosa, Euphorbia cyparissias, Fragaria vesca, Hippocrepis comosa, Holcus lanatus, Lathyrus pratensis, Linum catharticum, Lotus corniculatus, Plantago lanceolata, Trifolium pratense, Urtica dioica.</i>

H8	<i>Carex flacca, Carex sylvatica, Listera ovata, Thymus serpyllum.</i>
P1	<i>Acer campestre, Sorbus aria, Sorbus aucuparia.</i>
P2	<i>Corylus avellana, Juniperus communis, Sambucus nigra, Sorbus chamaemespilus, Viburnum lantana.</i>
P3	<i>Abies alba, Acer pseudoplatanus.</i>
P4	<i>Fagus sylvatica, Picea abies.</i>
P5	<i>Alnus alnobetula.</i>
P6	<i>Fraxinus excelsior.</i>

PFG classification traits values. Traits values were attributed to each group using the mean across species for continuous traits and the majority class for ordinal values, after removing outlier species. The three life forms classes are P=Phanerophytes, C=Chamaephytes, and H=Herbaceous. There are seven dispersal classes with increasing median distance (Short: 0.1-2m; Medium: 40-100m; Long: 400-500m). Light classes increase with decreasing shade tolerance. Plant height is given in cm. Palatability (forage value for cattle) ranges from 0 (not grazed) to 9 (grazed, with high nutritional value). Diet preference for chamois from 1 (not important in chamois diet) to 5 (really important in chamois diet). Habitat represents climatic niche in 3 categories (C=collinean; M=mountainous; S=subalpine) that can be represented at the same time depending on the preferences of the species within the PFGs.

PFG	Growth form	Dispersal distance	Light preference	Height (cm)	Palatability	Diet preference	Habitat
C1	C	Medium (5)	Any (3)	217	1	4	C-M
C2	C	Medium (4)	Any (3)	21	1	5	M-S
H1	H	Medium (4)	Full light (4)	20	2	4	C-M-S
H2	H	Long (7)	Full light (4)	37	3	3	M-S
H3	H	Long (6)	Full light (4)	35	4	4	S
H4	H	Medium (4)	Full light (4)	98	1	2	C
H5	H	Short (3)	Any (3)	34	2	2	S
H6	H	Short (3)	Shade (2)	49	5	2	M
H7	H	Long (7)	Full light (4)	23	6	4	C-M
H8	H	Long (6)	Any (3)	42	3	1	M
P1	P	Long (6)	Any (3)	1167	1	4	M
P2	P	Long (6)	Any (3)	248	1	4	C-M-S
P3	P	Medium (4)	Shade (2)	2000	1	2	M

P4	P	Long (6)	Shade (2)	2500	1	1	M
P5	P	Short (3)	Full light (5)	300	3	4	S
P6	P	Medium (5)	Any (3)	2000	1	1	C-M

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Appendix 2

Distribution data of the chamois

We used different source of data to map the spatial locations of chamois. At both the BNRP and NGWR scales, hunters recorded spatial locations of chamois harvested since 2004 (n = 3830). Such data were completed within the NGWR by data recorded during yearly censuses, long-term resightings of marked animals and GPS locations of chamois fitted with GPS collars. Yearly censuses were based on repeated foot surveys along 3 to 6 pre-defined paths (since 1995) and from 12 fixed points (since 2013) covering the NGWR and repeatedly done (3-6 times) each year by a restricted number of professionals. During these surveys, all group seen (from 1 to 94 animals, average = 5.95) were spatially located (based on a 100x100m grid size or directly pointed on a map; n = 2686). Chamois were also trapped and re-sighted each year since 1985 within the 3-4 main alpine pastures composing the NGWR. Captures were done using traps and drop nets baited with salt licks and trapped chamois were marked with collared/numbered collars. More recently (2003-2015), part of trapped chamois were also fitted with GPS collars Lotek 3300S (Engineering Inc.). Re-sightings of groups including marked chamois provided 10,805 spatial locations and 38,491 spatial locations from GPS collars for 67 different animals. GPS data were screened for erroneous locations following Bjørneraas *et al.* (2010). All non-harvested data collected within the NGWR (censuses, re-sightings and GPS) were pooled and subsequently sub-sampled to get a balanced design in term of sample size with harvesting data collected at the BNRP scale. This step was performed to avoid an over-sampling of a very local zone over the study area which may artificially biased the point process model. Data sampling was in accordance with guidelines approved by the American Society of Mammalogists (Gannon *et al.*, 2007).

Cited references Appendix 2

- Bjørneraas, K., Van Moorter, B., Rolandsen, C.M. & Herfindal, I. (2010) Screening Global Positioning System Location Data for Errors Using Animal Movement Characteristics. *Journal of Wildlife Management*, 74, 1361-1366.
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APPENDIX 3

R Code to run the point process model of the chamois. The following lines of code were used to fit a ppm model on the chamois data using the R package *spatstat*.

```
rm(list=ls())

#Set library
library(raster)
library(rgdal)
library(biomod2)
library(spatstat)
library(ecospat)

#Set directories
path_input <- "SDM_chamois/"
path_data_save <- "SDM_chamois/"
path_output <- "PPM_chamois/"

#Mask of BRP
mask <- raster(paste0(path_input,"MASK_100m.img"))
quad <- xyFromCell(mask,which(mask[]==0))

#Load occurrences
pts<-get(load("/PPM_chamois/pts.RData"))

#Load PFG data
pfg.names <- c("C2", "H1", "H4", "H6", "H7", "P2")
nbPFGs <- length(pfg.names)
y <- 850
PFG.files <- paste0("FATE_Bauges/RESULTS/ABUND_perPFG_allStrata/Abund_YEAR_",y,"_",
  "_STRATA_all.tif")
PFG.stk <- stack(PFG.files)
names(PFG.stk) <- sub("Abund_YEAR_850_", "",names(PFG.stk))
names(PFG.stk) <- sub("_STRATA_all", "",names(PFG.stk))
```

```

# Load environmental data
path_ras <- c(paste0("SDM_chamois/Bauges_ClimVar_SELECTED/",c("bio_1_img", "slope.img")))

#Projecting on the mask and converting data to a table
stk_ras <- stack(path_ras)
stk_ras <- stack(stk_ras,PFG.stk)
stk_ras <- projectRaster(stk_ras,mask)
nam_stk = names(stk_ras)
mask1 = mask
mask1[which(mask1[]==0)] = 1
stk_ras <- stk_ras*mask1
names(stk_ras) = nam_stk
env.data = as.data.frame(stk_ras)
env.data = na.exclude(env.data)

#Setting up the study window
ux = sort(unique(quad[,1])) #x coordinates
uy = sort(unique(quad[,2])) #y coordinates"
nx = length(ux)
ny = length(uy)
col.ref = match(quad[,1], ux) # index of x coordinates of quad within ux
row.ref = match(quad[,2], uy)
all.vec = rep(NA, max(row.ref)*max(col.ref))
vec.ref = (col.ref - 1)*max(row.ref) + row.ref
all.vec[vec.ref] = 1
Bauges.mask = matrix(all.vec, max(row.ref), max(col.ref),dimnames = list(uy, ux))
Bauges.win = as.owin(im(Bauges.mask, xcol = ux, yrow = uy))

#Creating point pattern
ppp.dat = ppp(pts$x, pts$y, window = Bauges.win, check = FALSE)

#Quadrature points are the same pixels of the original mask, as their grid resolution is 100m
quads = ppp(quad$x, quad$y, window = Bauges.win)

```

```

Q = quadscheme(data = ppp.dat, dummy = quads, method = "grid",ntile = c(nx, ny), npix = c(nx, ny))

#Variables selection by a forward AIC algorithm

#Polynomial with all the possible variables
X.des = poly(env.data$bio_1_0, env.data$slope,
             sqrt(env.data$H1), sqrt(env.data$C2), sqrt(env.data$H4),sqrt(env.data$H6),
             sqrt(env.data$H7),sqrt(env.data$P2), degree = 2, raw = TRUE)

#Converting to a list
int.list = list()
for (i in 1:dim(X.des)[2]){
  all.vec = rep(NA, max(row.ref)*max(col.ref))
  vec.ref = (col.ref - 1)*max(row.ref) + row.ref
  all.vec[vec.ref] = X.des[,i]
  int.list[[i]] = im(matrix(all.vec, max(row.ref), max(col.ref),dimnames = list(uy, ux)), xcol = ux, yrow = uy)
}
names(int.list) = paste0("V", 1:dim(X.des)[2])
pred.list = int.list
list.names<-names(int.list)

nbVar <- length(int.list)
not_chosen <- 1:nbVar
prev_list <- list()
ordre <- aic_final <- vector()

#Every loop we add to the model the variable that optimise the AIC
for (i in 1:nbVar){
  aic<-vector()
  #Loop to select the variable that optimise the AIC
  for(j in not_chosen){
    newVarlist<-prev_list
    newVarlist[[length(newVarlist)+1]]<-int.list[[j]]
    names(newVarlist)<-c(ordre, list.names[j])
    #Fit the model we the new added variable and evaluate the likelihood
    int.form = as.formula(paste("~", paste(names(newVarlist), collapse = "+")))

```

```

ft.int = ppm(Q, trend = as.formula(int.form), covariates = newVarlist)
aic <- c(aic,AIC(ft.int))
}
keep <- not_chosen[which(aic==min(aic))] # Which variable induces the lowest AIC
ordre <- c(ordre,list.names[keep]) # Update the order of chosen variable
not_chosen <- not_chosen[-which(not_chosen==keep)] # Remove selected variable
aic_final <- c(aic_final,min(aic)) # Add AIC of the last updated model
prev_list[[length(prev_list)+1]] <- int.list[[keep]] # Update the list of chosen variables
names(prev_list) <- ordre

cat(paste0("\n selected variable: ", list.names[keep]))
cat(paste0("\n AIC value: ", min(aic)))
}

#Take variables corresponding to the AIC minimum
int.list<-prev_list[1:which(aic_final==min(aic_final))]

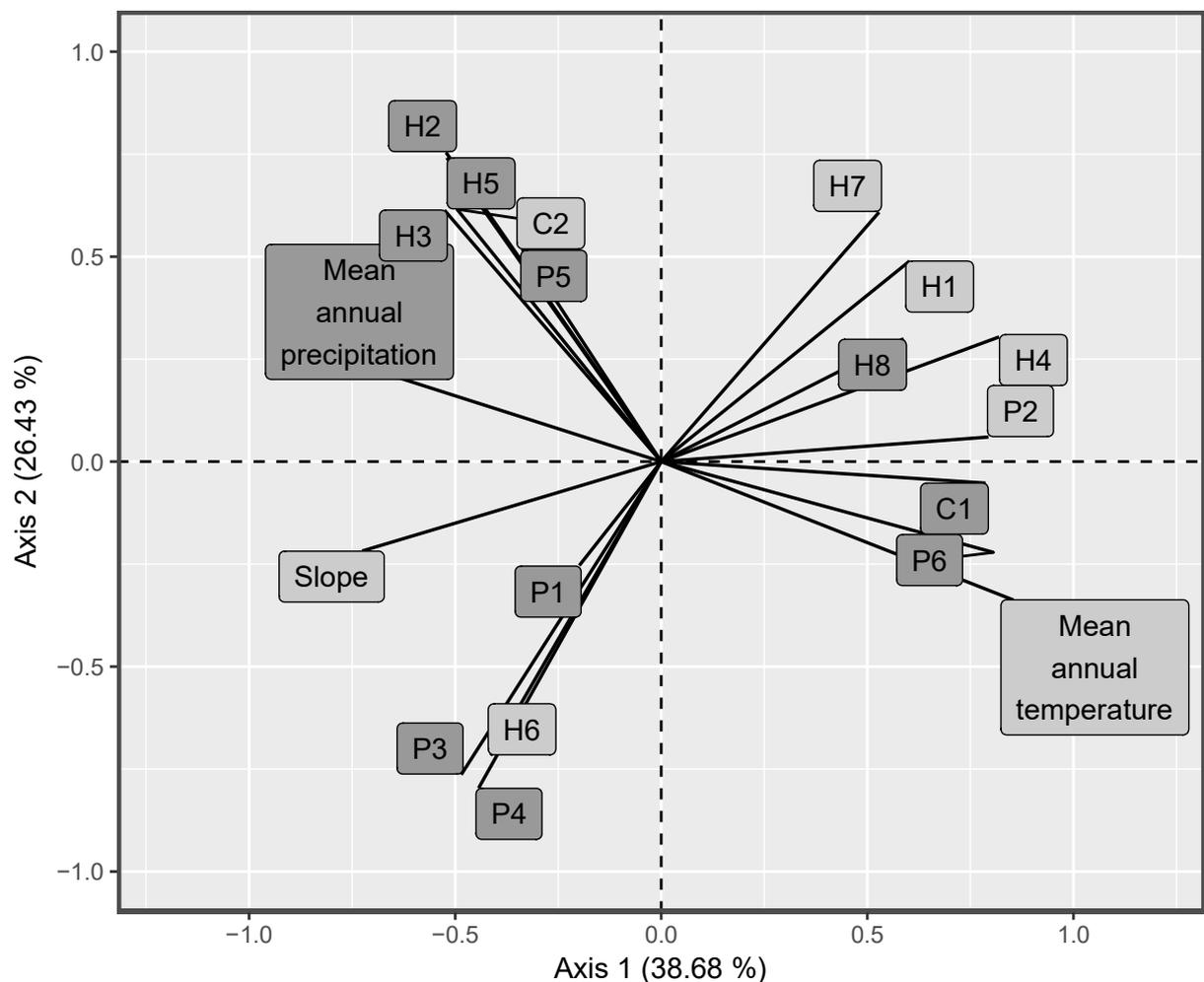
#Final formula
int.form = as.formula(paste("~", paste(ordre[1:which(aic_final==min(aic_final))], collapse = "+")))
#Fitting the model
ft.int = ppm(Q, trend = as.formula(int.form), covariates = int.list)

```

Appendix 4

PCA shows the correlation between PFG abundances. Correlated PFGs are representative of the same habitat. It is the case of P1, P3 and P4, trees characteristics of low altitude forests, or C2, P5, H2, H3, H5 that, on the contrary, represent subalpine habitats.

To build the final set of PFGs to be used into the chamois' model, we chose among every correlated group of PFGs the one that was the most important in chamois diet (highlighted in light grey). To prevent temperature from over-driving the model, we excluded P6 and C1 because they were highly correlated with it. As precipitations and temperature were highly inversely correlated, we only kept temperature.



Supplementary Figures

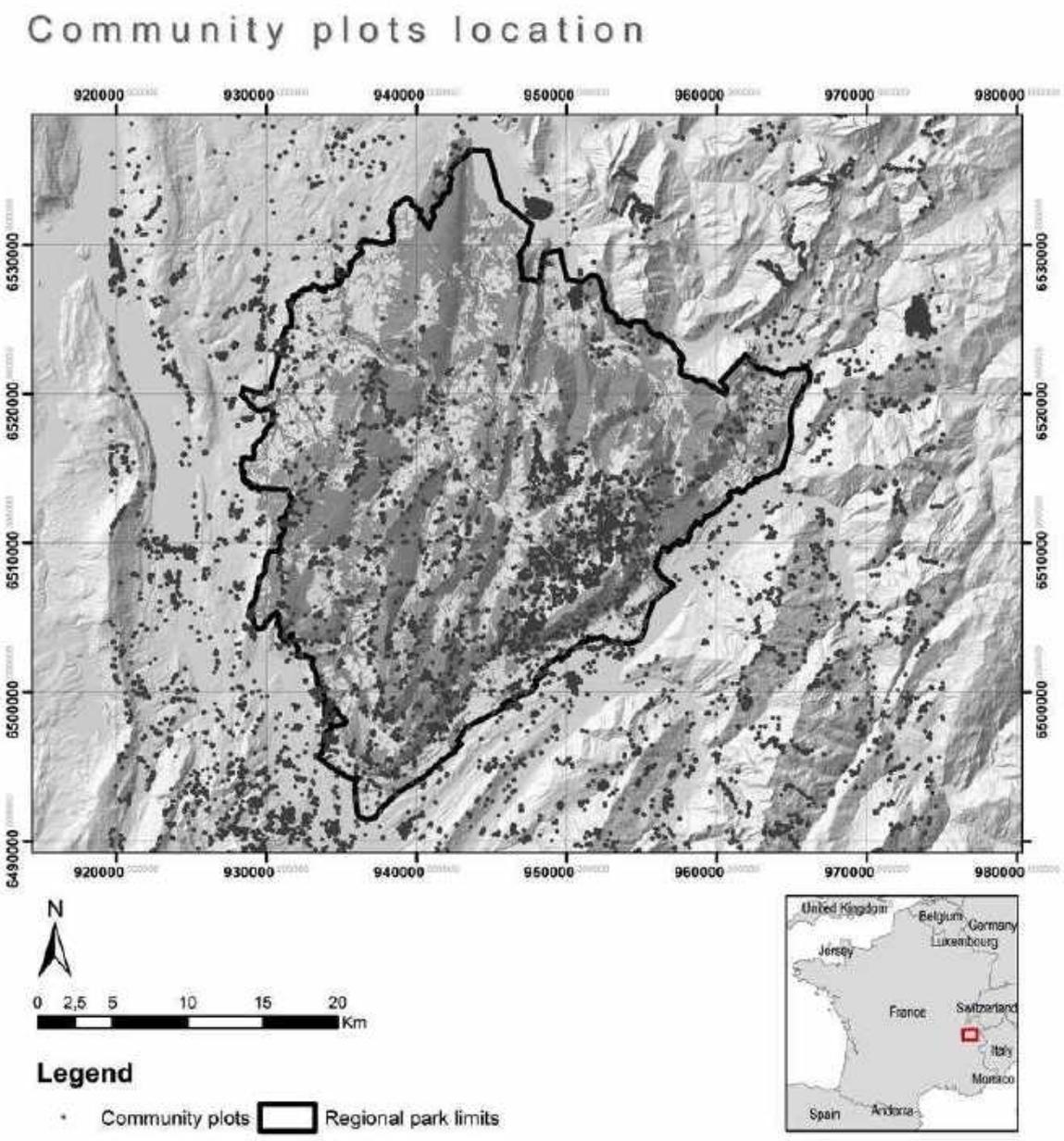


Figure S1. Spatial distribution of the vegetation plots used to select the dominant species list and to model the habitat suitability of the plant functional groups.

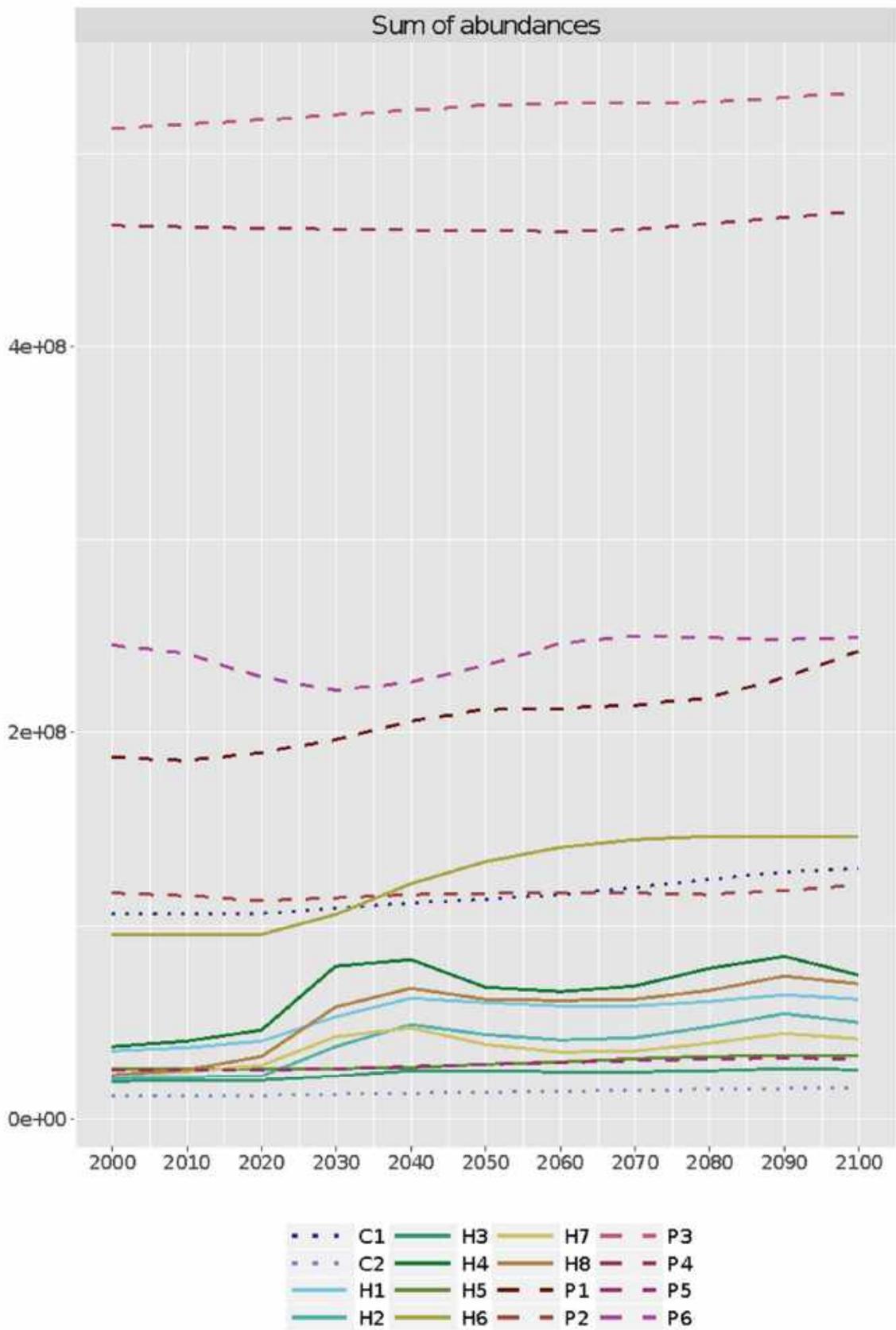


Figure S2. Change in mean abundance of the modeled PFGs through time under the scenario RCP 8.5.

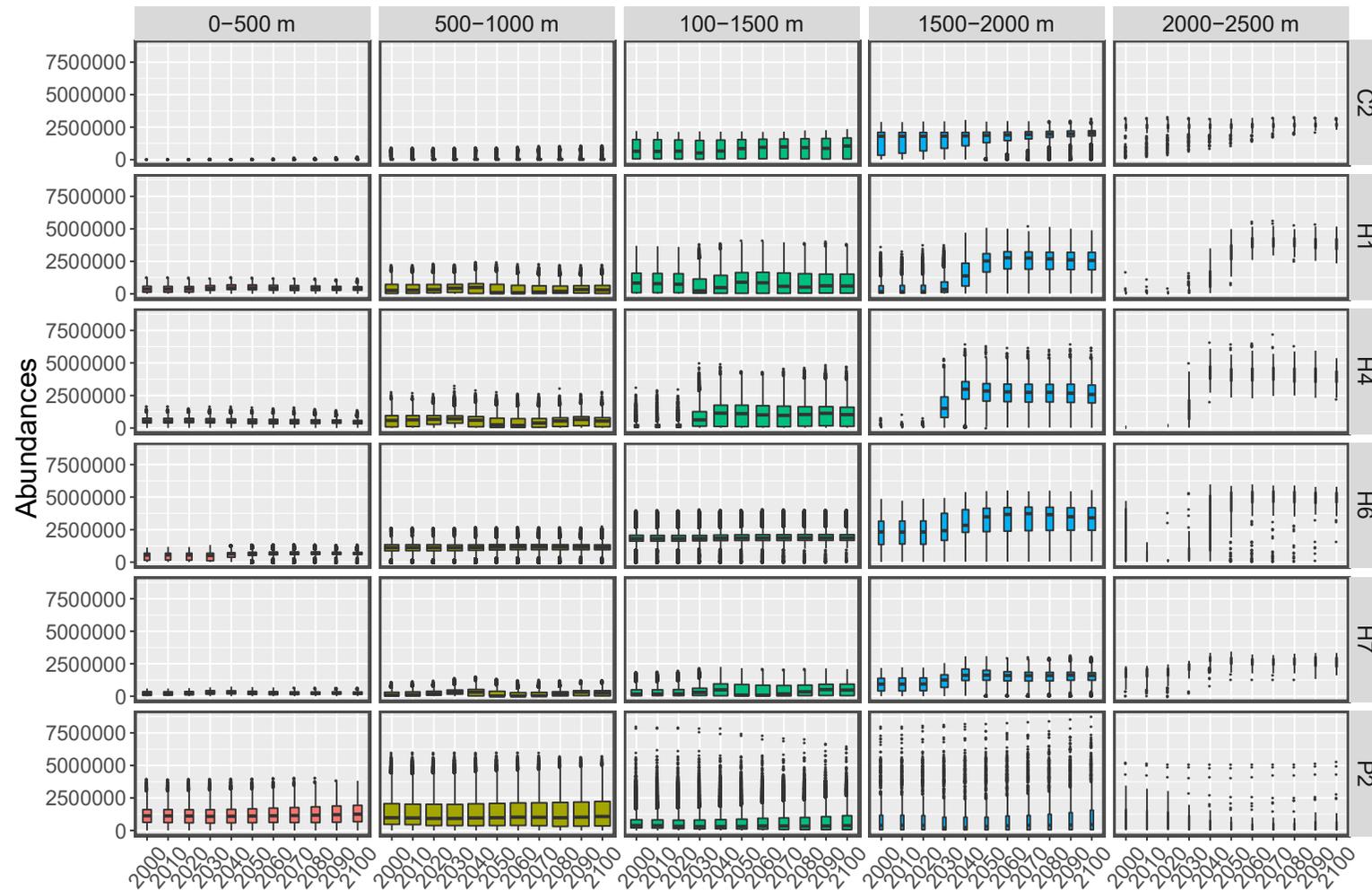


Figure S3. Change in mean PFGs' abundance through the Bauges Regional Park in function of altitude (columns with different colors). Only the retained PFGs in the point-process models of the chamois are shown. The width of the boxplot is proportional to the relative available area. C2, H1, H4 and H6 are predicted to increase their abundances mostly at high altitude (>1500m).

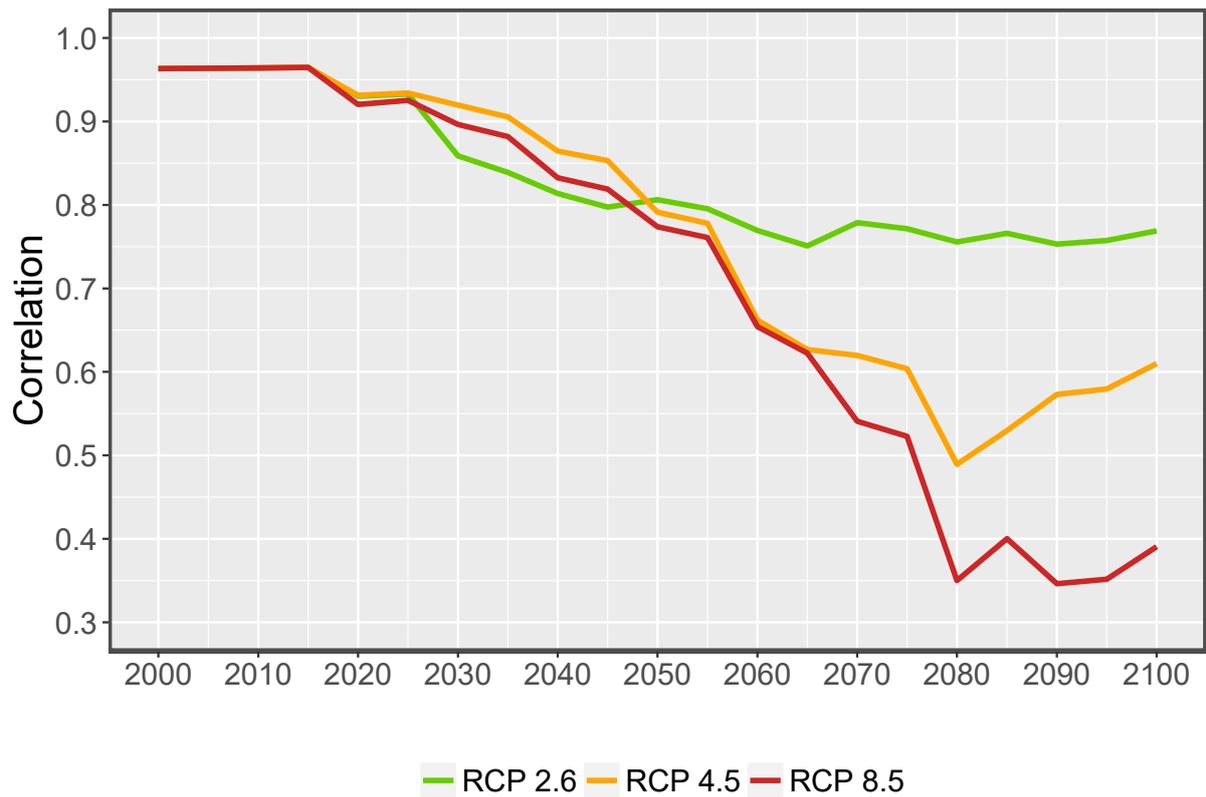


Figure S4. Change in Pearson' correlation between chamois' predictions from the climate-only model and the climate and vegetation model through time and for the three RCP scenarios.

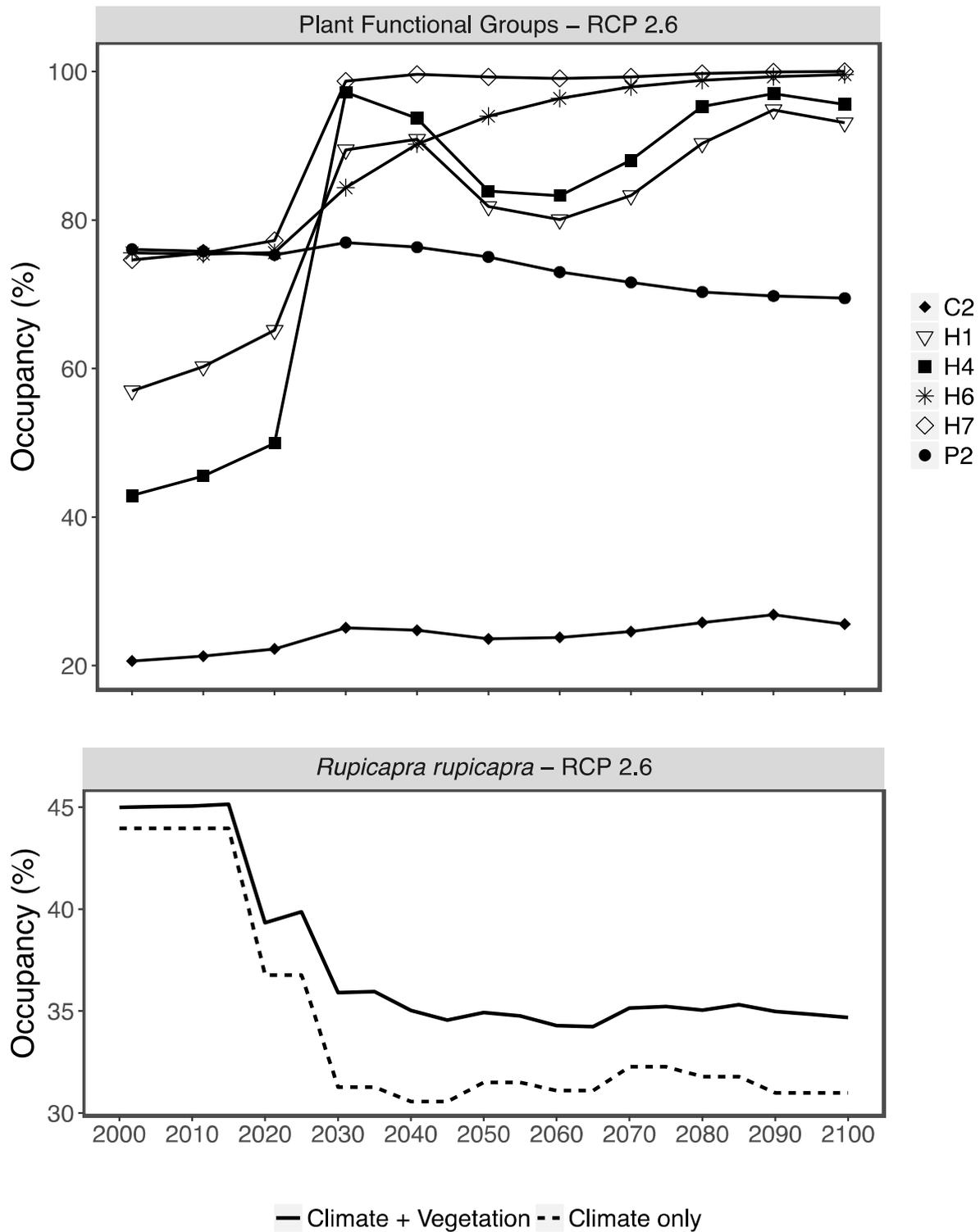


Figure S5 Change in the predicted species occupancy of the chamois (*Rupicapra rupicapra*) over time and for the two point-process models (i.e. climate-only and, climate and vegetation) in function of the RCP2.5 climate scenarios. The top figure represents the change in occupancy of the PFGs selected by the point-process model (climate and vegetation).

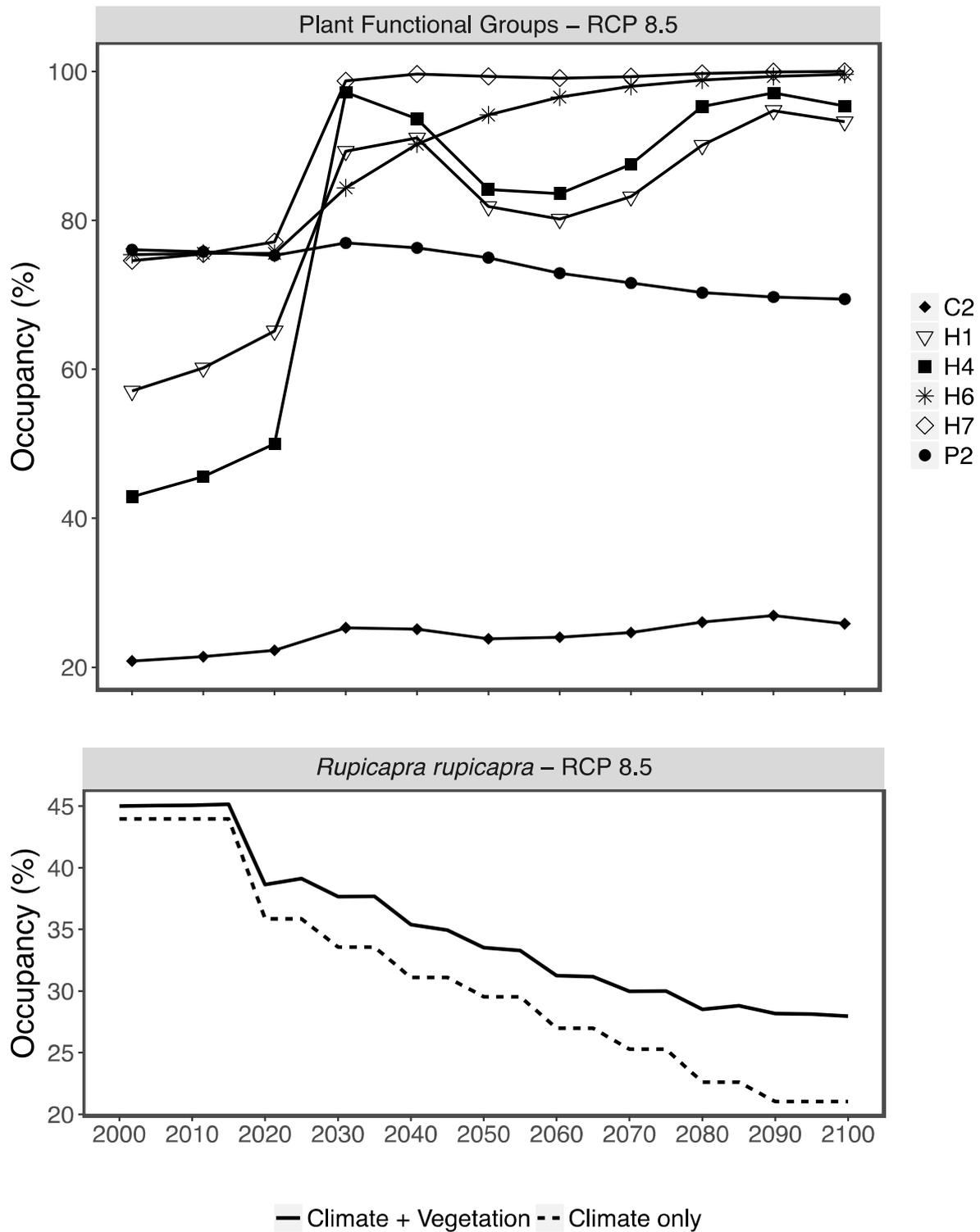


Figure S6 Change in the predicted species occupancy of the chamois (*Rupicapra rupicapra*) over time and for the two point-process models (i.e. climate-only and, climate and vegetation) in function of the RCP8.5 climate scenarios. The top figure represents the change in occupancy of the PFGs selected by the point-process model (climate and vegetation).

