**MATERIALS AND METHODS**

***Study design and sampling protocol***

***Statistical analyses***

[OVERVIEW OF HMSC]. We analyzed the data with Hierarchical Modelling of Species Communities (HMSC; Ovaskainen et al. 2017 ELE; Ovaskainen and Abrego 2020 book). HMSC is a joint species distribution model (Warton et al. 2015 TREE) which includes a hierarchical layer asking how species responses to environmental covariates depend on species traits and phylogenetic relationship (Abrego et al. 2017 JE). Here we will utilize spatially structured latent variables proposed by Ovaskainen et al. (2016 MEE) and later expanded to big spatial data by Tikhonov et al. (2020 Ecology).

[STUDY DESIGN AND DATA SELECTION]. The data comprises the abundances of 763 plant species surveyed in 2208 Central European forest plots, with each plot surveyed at two time-points: the first one during year 1953-1998 and the second one in year 2002-2018. We excluded those species that had less than 10 occurrences in these data, and thus our analyses concerns of . To examine if the 349 rare species excluded from the HMSC analyses showed systematically different responses from the common, we additionally fitted two univariate models, where we modelled the species richness of the rare species or the common species as a function of the same explanatory variables included in the HMSC model.

[SAMPLING UNITS AND RESPONSE VARIABLE]. As sampling unit, we used the individual visits to the study plots, thus there being sampling units. As the response variable (the matrix **Y** of HMSC; see Ovaskainen et al. 2017 ELE), we used the counts of each of the 414 species. Due to the zero-inflated nature of the data, we applied a hurdle model, i.e., one model for presence-absence and another one for abundance conditional on presence (henceforth abundance COP model). We applied probit regression in the presence-absence model, and linear regression for transformed count data in the abundance COP model. The count data were transformed by declaring zeros as missing data, log-transforming, and then scaling the data to zero mean and unit variance within each species.

[PREDICTORS]. We included as fixed effects (the matrix **X** of HMSC; see Ovaskainen et al. 2017 ELE; where is the number of species-specific regression parameters to be estimated) the survey time (categorical variable with two classes; old and new), the mean altitude of the plot and the area of the surveyed plot. While our primary interest was in the effect of the survey time, we controlled for altitude for its known influence on plant communities, and for plot area to control for variation in sampling effort.

[TRAITS AND PHYLOGENY] HMSC involves a hierarchical structure examining how species responses to environmental covariates depend on species traits and phylogenetic relationships. [As species traits, we included log-transformed body mass, and the categorical variable of migratory status.] In this study we did not have any trait data, but we examined if variation in species niches was phylogenetically structured, i.e., if closely related species had more similar environmental responses than distantly related species. As phylogenetic data, we included a quantitative phylogenetic tree derived from xxx. To account for the spatial nature of the study design, we included a spatially explicit random effect, implemented through the predictive Gaussian process for big spatial data (Tikhonov et al. 2020 Ecology). We note that the plot-level random effect controls for unexplained variation at the plot level on top of the explicitly modelled effects of the altitude and plot area.

[MODEL FITTING]. We fitted the HMSC model with the R-package Hmsc (Tikhonov et al. 2020 MEE) assuming the default prior distributions (see Chapter 8 of Ovaskainen and Abrego 2020 book). We sampled the posterior distribution with four Markov Chain Monte Carlo (MCMC) chains, each of which was run for 3750,000 iterations, of which the first 125,000 were removed as burn-in. The chains were thinned by 1000 to yield 250 posterior samples per chain and so 1000 posterior samples in total. We examined MCMC convergence by examining the potential scale reduction factors (Gelman and Rubin 1992) of the model parameters.

[POSTPROCESSING OF RESULTS]. We examined the explanatory and predictive powers of the probit models through species-specific AUC (Pearce & Ferrier 2000) and Tjur’s R2 (Tjur 2009) values. The explanatory and predictive powers of the abundance COP models were measured by R2. To compute explanatory power, we made model predictions based on models fitted to all data. To compute predictive power, we performed 5-fold cross-validation, in which the sampling units were assigned randomly to five folds, and predictions for each fold were based on model fitted to data on the remaining four folds.

To quantify the drivers of community structure, we partitioned the explained variation among the fixed and random effects included in the model. To address our main study question, i.e., if and how species communities have changed over the study period, we examined species responses to the categorical explanatory variable of study period, counting what proportion of species showed a positive or negative response with at least 95% posterior probability.