1	Continental-scale determinants of population trends in European
2	amphibians and reptiles
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4	Running title: Continental determinants of population trends
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17 Abstract

18

The continuous decline of biodiversity is determined by the complex and joint effects of 19 multiple environmental drivers. Still, a large part of past global change studies reporting and 20 explaining biodiversity trends have focused on a single driver. Therefore, we are often unable 21 to attribute biodiversity changes to different drivers, since a multi-variable design is required 22 to disentangle joint effects and interactions. In this work, we used a meta-regression within a 23 Bayesian framework to analyze 843 time-series of population abundance from seventeen 24 European amphibian and reptile species over the last 45 years. We investigated the relative 25 26 effects of climate change, alien species, habitat availability, and habitat change in driving trends of population abundance over time, and evaluated how the importance of these factors 27 differs across species. A large number of populations (54%) declined, but differences between 28 species were strong, with some species showing positive trends. Populations declined more 29 often in areas with a high number of alien species, and in areas where climate change has 30 caused loss of suitability. Habitat features showed small variation over the last 25 years, with 31 an average loss of suitable habitat of 0.1% / year per population. Still, a strong interaction 32 between habitat availability and the richness of alien species indicated that the negative 33 34 impact of alien species was particularly strong for populations living in landscapes with less suitable habitat. Furthermore, when excluding the two commonest species, habitat loss was 35 the main correlate of negative population trends for the remaining species. By analyzing 36 37 trends for multiple species across a broad spatial scale, we identify alien species, climate change, and habitat changes as the major drivers of European amphibian and reptile decline. 38

39

40 KEYWORDS

- 41 Alien species, climate change, demography, land-cover change, meta-analysis, population
- 42 trends, species distribution models

43 INTRODUCTION

44 Biodiversity is declining at an unprecedented rate (Butchart et al., 2005; IPBES, 2018). Understanding the main causes of these changes is a major endeavor for the scientific 45 46 community, should we want to anticipate and mitigate future impacts. Climate change, landuse change, spread of alien species, atmospheric CO₂ increase, anthropogenic nitrogen 47 deposition, and spread of disease are all drivers known to strongly influence the structure and 48 distribution of biodiversity (Bateman et al., 2016; Gallardo, Clavero, Sánchez, & Vilà, 2016; 49 Tracewski et al., 2016). These drivers do not affect biodiversity independently, rather they act 50 in synergistic or antagonistic ways. For instance, in a global study comprising multiple taxa, 51 52 Mantyka-Pringle, Martin, & Rhodes (2012) found that the negative effects of habitat loss and fragmentation on species abundance and diversity were magnified in areas where average 53 rainfall has decreased in the past. Multi-variable studies, taking into account more than one 54 driver of global change, are thus essential to disentangle the relative importance of different 55 threats (Didham, Tylianakis, Gemmell, Rand, & Ewers, 2007). Nevertheless, a large part of 56 57 past global change studies focused on one single driver, perhaps because it is difficult to retrieve standardized data across broad spatial extents, or because integrating multiple factors 58 can result in overly complex models. In the last years, attention is growing toward the 59 60 importance of disentangling the effects of multiple drivers (e.g. Campbell Grant et al., 2016; Northrup, Rivers, Yang, & Betts, 2019), because knowing the relative impact of different 61 drivers on the different biodiversity facets is essential to identify conservation priorities and 62 management strategies (Brook, Sodhi, & Bradshaw, 2008). 63

Global change drivers impact populations in multiple ways and can, for instance,
impact morphology, breeding success, survival, and abundance (Ficetola et al., 2016; Ficetola
& Maiorano, 2016; Menzel et al., 2006; Saino et al., 2011). Trends of population abundance
are connected to extinction risk and are commonly used to evaluate the conservation status of

species, thus population trends are one of the key demographic parameters to assess the 68 effects of global change drivers on biodiversity (Flesch, Rosen, & Holm, 2017; IUCN, 2012). 69 However, studies on population abundance are generally local, thus limiting the possibility of 70 drawing broad-scale, generalizable inference. Quantitative analyses of the results of multiple 71 studies (meta-regressions) can alleviate this issue, as they allow to summarize information 72 from a broad range of sources. Meta-regressions showed excellent performance in the analysis 73 of multiple demographic time series and helped to obtain general inference on patterns of 74 global change (Bonardi et al., 2011; Gurevitch, Koricheva, Nakagawa, & Stewart, 2018; 75 Hadfield & Nakagawa, 2010). 76

77 Amphibians and reptiles are two vertebrate groups particularly threatened by global 78 changes (Böhm et al., 2013; Hoffmann et al., 2010). Amphibian populations are declining at a greater pace than the other vertebrates, and their decline is determined by the combined 79 effects of multiple threats, notably land-use change, climate change, and alien species (Hof, 80 Araújo, Jetz, & Rahbek, 2011; Stuart et al., 2008). While the global reptile assessment has not 81 been completed yet, land-use change, climate change, and alien species are listed as major 82 threats also for reptiles (Todd, Willson, & Gibbons, 2010). Furthermore, climate change is 83 expected to have a particularly strong impact on ectothermic vertebrates, because it can affect 84 85 essential life-history processes that depend on the characteristics of the environment (Buckley, Hurlbert, & Jetz, 2012; Flesch et al., 2017). Finally, the response of local 86 populations to global drivers vary across taxa and geographic areas. It is thus important to 87 88 assess whether different species show heterogeneous responses, in order to understand the generality of patterns of change (Muths et al., 2017). 89

In this study, we used meta-regression to quantify the relative importance of different
global change drivers on population trends of European amphibians and reptiles (Figure 1). In
particular, we tested four hypotheses:

i) Population trends are determined by changes in climatic suitability. Climatic 93 suitability is a measure of how much the climate of an area is suitable for a 94 particular species (Araújo, Alagador, Cabeza, Nogués-Bravo, & Thuiller, 2011). 95 Suitability can provide a better measure of the impact of climate change compared 96 to climatic velocity since it accounts for the geographic position of a population. 97 For instance, in a situation of poleward shift of the geographic range of a species, 98 populations nearest to the pole can gain suitability, while the farthest ones often 99 lose suitable space (Parmesan et al., 1999). We thus predict that a decrease in 100 climatic suitability negatively affects population trends and vice versa; 101

- ii) Population trends are negatively influenced by alien species. Alien species exert
 multiple impacts on native biodiversity (Gallardo et al., 2016). Negative impacts
 increase with the abundance and richness of alien species (Vilà et al., 2010), thus
 we predict a negative relationship between the richness of alien species and
 population trends;
- iii) Population trends are determined by habitat availability. The amount of available 107 habitat in the landscape is a key parameter influencing species distribution and 108 109 population dynamics (Flesch, 2017; Seibold et al., 2017). For example, a low 110 amount of suitable habitat leads to reduced carrying capacity and vital rates, and to a decrease in the amount of source populations that could provide migrants from 111 the surrounding landscape (Hodgson, Thomas, Wintle, & Moilanen, 2009). 112 113 Because these processes can affect the long-term dynamics of populations and their probability of persistence, we predict a positive relationship between the 114 amount of suitable habitat and population trends; 115
- iv) Population trends are determined by changes in habitat availability. Land-use has
 undergone heavy changes in the last decades, with the conversion of natural

vegetation to urban or agricultural land-use in some areas and forest gain in others
(Hansen et al., 2013). Habitat loss is considered the main cause of decline for the
vast majority of vertebrates, hence we predict a negative relationship between the
decrease in habitat availability and population trends (Hoffmann et al., 2010).

We used data on long-term population abundance of reptiles and amphibians to evaluate the support of these hypotheses and also investigated possible interactions among drivers. Furthermore, we appraised whether the response of populations to these drivers was heterogeneous across taxa.



FIGURE 1 General framework of the study. We assessed the relative importance of multipleglobal change drivers on population trends of European amphibians and reptiles.

131 MATERIALS AND METHODS

132

133 Abundance data

The study area included Europe plus Anatolia, with eastern limit in the Ural Mountains and 134 the Caucasus. We performed a literature search in February 2017. Published data on 135 abundance for reptile and amphibian species were collected by searching in the ISI Web of 136 Science for keywords "demography", "population", and "decline", associated with "reptile", 137 and "amphibian" keywords. We reviewed the text and selected data of populations with at 138 least 4 years of sampling. Shorter time series were discarded to ensure more relevant 139 140 estimates of temporal trends. We also analyzed the data associated to the Houlahan, Findlay, Schmidt, Meyer, & Kuzmin (2000) paper on amphibian population trends, and retrieved all 141 the time series from the study area, for which enough information was available to reconstruct 142 the population locality. We also added two unpublished population times series for which we 143 directly collected data for the period 2010-2016 (Manenti R., unpublished data). We obtained 144 a total of 16 studies, comprising time-series for 843 populations of 17 different species (see 145 Supporting Information Table S1 for a complete list of references). 146

From these time series, we derived population trends by calculating, for each population, the Pearson's correlation (r) between years of sampling and log-transformed population abundance. We then used Fisher's Z to calculate the effect size of temporal trends and the associated variance for each population (Ficetola & Maiorano, 2016). To identify the drivers of population trends, we then assessed the relationships between population trends (effect sizes) and four drivers: (i) climatic suitability changes, (ii) alien species richness, (iii) habitat availability, (iv) changes in habitat availability.

154

155 Climatic suitability changes

We used species distribution models (SDM) to assess changes in climatic suitability through 156 157 time for each population. To build SDM, species presence was derived from the European Herpetological Atlas (Sillero et al., 2014), at a resolution of 0.5°. All the frogs of the 158 hybridogenic complex *Pelophylax* spp. were modeled as a single taxon; the distribution range 159 of the grass snake Natrix natrix extends outside the boundaries of the European 160 Herpetological Atlas, thus presences for this species were integrated with points obtained 161 162 from the global biodiversity information facility (https://www.gbif.org/); The distribution records of newts (Triturus cristatus and Lissotriton vulgaris) were taken from Wielstra et al., 163 (2018) and Wielstra, Sillero, Vörös, & Arntzen (2014). 164

165 SDM were calibrated on the climatic conditions in the last 51 years (averaged from 1966 to 166 2016), obtained from an updated version of the Climatic Research Unit dataset (Harris, Jones, Osborn, & Lister, 2014) (CRU TS v. 4.01), which reports monthly values of precipitation and 167 temperature for the time-period 1901-2016. We used four climatic variables: mean annual 168 temperature, total annual precipitation, annual temperature standard deviation, annual 169 precipitation coefficient of variation. Minimum annual temperature and maximum annual 170 temperature, and minimum / maximum temperature during breeding seasons, are additional 171 172 variables important for tolerance and activity of ectotherms but are strongly correlated to 173 mean temperature and standard deviation (Appendix S1). We thus also re-ran the SDMs using min/max values instead of mean and standard deviation of temperature and for subsequent 174 analyses we used models with higher performance values (see results). Models were built 175 176 within the biomod2 R package (Thuiller, Georges, Engler, & Breiner, 2016), running an ensemble of the following models: boosted regression trees, generalized additive models, 177 classification tree analysis, multivariate adaptive regression splines, and random forests. For 178 each species, we selected 3,000 pseudo-absence points within a radius of 1,000 km from the 179 species distribution range. To get a meaningful evaluation of the models and to avoid over-180

fitting, models were repeated five times to perform cross-validation, and for each run we used a random sample of 67% of the initial occurrence data to calibrate the models and the remaining 33% for evaluation. Models performance was assessed using the True Skill Statistic (TSS) and the Area Under the receiver operating characteristic Curve (AUC) (Liu, White, & Newell, 2011). Finally, we obtained an ensemble model through a weighted sum of the probability of occurrence, proportional to the cross-validated TSS.

Subsequently, to assess changes in climatic suitability through time, the overall 187 bioclimatic SDM for each species (calibrated for 1966-2016) was projected on the climatic 188 conditions for the years for which information on population abundance was available. This 189 190 allowed obtaining time series of climatic suitability for each population. Specifically, we 191 calculated the trend of SDM suitability for each population by calculating the correlation between years of sampling and climatic suitability. Correlation coefficients were then 192 transformed to Fisher's Z to obtain comparable measures of effect size. The trend of climatic 193 suitability was considered as independent variable to measure the effect of changes of climatic 194 suitability. 195

196

197 Alien species

198 The richness of alien species was obtained from the Global Alien Species First Record Database (Seebens et al., 2017), which reports the first year of detection of alien species at the 199 regional level resolution. At this scale, alien species richness can be a good proxy to measure 200 negative effects on native biodiversity, because the number of impacts is higher in areas with 201 more alien species (Latombe et al., 2017; Vilà et al., 2010). For each population, we extracted 202 203 the total number of alien species starting from 1901 to the last year of sampling by summing the total number of vertebrates and crustaceans, as these taxa are known to have a major 204 impact on amphibians and reptiles (Ficetola et al., 2011; Kats & Ferrer, 2003). The database 205

reports the occurrences of alien species at the regional level, but the considered regions had a 206 207 coarser resolution than the localities used for our analyses. Therefore, the number of alien species obtained using this approach probably overestimates the actual number of alien 208 species at a given locality. Nevertheless, the Global Alien Species First Record Database has 209 210 the advantage that the alien species records are temporally explicit, thus allowing analyses of temporal processes. Furthermore, the number of alien species is strongly related to economic 211 and political factors of territories, thus we expect a strong correlation between regional-level 212 and local abundance of alien species (Pysek et al., 2010). For each time series, the total 213 number of alien species from the year 1901 to the last year of the time series was considered 214 as independent variable to measure the effect of alien species. 215

216

217 Habitat availability and habitat changes

For each species, we identified a list of suitable land-cover classes in order to calculate the 218 extent of suitable habitat (ESH) by integrating the habitat preferences obtained from the 219 IUCN Red List with land-use information (see Table S2 for details; Rondinini et al., 2011). 220 Land-use information was obtained from the time series of the European Space Agency 221 Climate Change Initiative Land Cover project (https://www.esa-landcover-cci.org/). This map 222 223 is available from 1992 and does not cover the whole 1972-2016 period. Hence, analyses which considered land use variables were limited to populations sampled in the period 1992-224 2016 (N = 705 populations). Previous analyses showed that ESH maps, built on the basis of 225 226 the occurrence of suitable land-use classes, allow a good representation of the actual habitat that can be exploited by species, and provide useful information to estimate species trends 227 (Ficetola, Rondinini, Bonardi, Baisero, & Padoa-schioppa, 2015; Rondinini et al., 2011; 228 Tracewski et al., 2016). We used ESH to calculate the habitat availability at the beginning of 229 the study period, and the trend of suitable habitat during the study period. Habitat variables 230

were calculated within the 9×9 km cell surrounding each population; we selected this resolution because about 90% of amphibian species have a maximum dispersal ability of ~4.5 km (Smith & Green, 2005), and because it matched well the accuracy of population localities in our dataset.

Habitat availability at the beginning of the period. We extracted the percentage cover of ESH in the first year of monitoring within the 9×9 km cell surrounding each population. We considered cover at the beginning of time series since we aimed at testing whether initial habitat amount can affect subsequent abundance changes within that landscape. We also repeated analyses using ESH at the end of the period and obtained very consistent results.

Habitat changes. To assess the impact of the change of ESH on population trends, we calculated the ESH within the 9×9 km cell surrounding each population in each year of monitoring, obtaining a time series of ESH. Hence, we calculated the Fisher's Z of the correlation between years of sampling and ESH, and considered this value as the trend of ESH (hereafter habitat change).

245

246 Statistical analyses

247 We used meta-regression to identify the most influential drivers of population trends 248 (Gurevitch et al., 2018). Global change drivers were related to population trends through Bayesian generalized linear mixed models, using the effect size of population trends (Fisher's 249 Z) as the dependent variable. First of all, the overall trend averaged across all the populations 250 251 was assessed by performing a model of the mean (i.e. a meta-regression model including the intercept and without independent variables) (Kéry, 2010). We also ran a separate model of 252 253 the mean for each species, in order to assess the average species trend. Then, four separate meta-regressions were run to assess the single-variable relationships between population 254 trends at each locality and: (i) trend of climatic suitability, (ii) richness of alien species, (iii) 255

habitat availability at the beginning of the period, (iv) trend of habitat availability (Figure 1). 256 257 Independent variables used, and time period considered for each single-variable model are described in Table S3. Finally, we performed a multi-variable model including all four 258 independent variables, for the period 1992-2016. We also tested pairwise interactions between 259 the four variables and, in the final model, we considered only interactions with 95% credible 260 intervals (CIs) not overlapping zero. The biological rationale of tested interactions is listed in 261 Table S4. Our multi-variable meta-regression included data from all the species, in order to 262 evaluate the overall pattern. Subsequently, to assess if the effects were consistent across 263 species, we re-run the meta-regression separately for the two commonest species (the 264 265 common toad Bufo bufo and the common frog Rana temporaria) and then considering all the 266 species except common toad and common frog.

Before the analysis, we tested the collinearity among the global change drivers and 267 found no strong correlations (|r| < 0.4, Table S5). In meta-regressions we included as random 268 effects: the study source of the data; species, family, order, and class, fitted as nested random 269 intercepts, to consider the phylogeny; the id of the 0.5° cell, to take into account the non-270 independence of nearby populations (i.e. populations within the same cell). Furthermore, for 271 272 models including alien species, we included region identity as an additional random effect 273 because alien species data are derived from a regional-level database (Seebens et al., 2017). To take into account different variances of Fisher's Z among studies, we weighted the records 274 by using the "mev" argument in the MCMCglmm function, considering 1 / variance of Z as 275 276 weight (following Hadfield & Nakagawa, 2010). All models were run for 2,000,000 iterations, with 1,000,000 burn-in and a thinning of 250. The number of alien species was log-277 278 transformed and all variables were scaled (mean = 0, SD = 1) before analyses to allow comparison of their estimated effects. Finally, we used respectively Moran's I and Pagel's 279 lambda, to assess whether the residuals of meta-regressions showed spatial or phylogenetic 280

correlation. To test the phylogenetic signal, we used a phylogeny tree including all the 17
species, derived from the phylogenetic tree of the European tetrapods (Roquet, Lavergne, &
Thuiller, 2014).

All analyses were performed in the R environment (R Core Team, 2017), using the packages compute.es (del Re, 2013) to compute population trends effect sizes and variance, raster (Hijmans, 2016) and rgeos (Bivand & Rundel, 2017) to process maps, biomod2 (Thuiller et al., 2016) to create SDMs, MCMCglmm (Hadfield, 2010) to perform Bayesian generalized linear mixed models, EcoGenetics (Roser, Ferreyra, Saidman, & Vilardi, 2017) to test spatial autocorrelation, and caper (Orme et al., 2018) to test phylogenetic autocorrelation.

290

291 **RESULTS**

Overall, we obtained 843 time-series for 17 species, covering 11 European countries across the period 1972-2016 (Figure S1; Appendix S2). 705 time-series were included in the period for which land cover information was available (after 1992, Appendix S3).

295

296 General trend

297 Out of the 843 populations, 458 (54%) showed negative population trends, 383 (45%) 298 positive trends and two remained stable (|r| < 0.01). The averaged population trend (effect size), obtained from the models of the mean of the different species, was negative for ten 299 species and positive for seven species (Figure 2). 95% CIs of the estimates of population 300 301 trends did not overlap zero in seven out of 17 species (41%), however, there were strong differences of trends across populations (Figure 2). The population trend averaged across the 302 populations of all species, was negative but credible intervals overlapped zero (mean = -303 0.084; 95% CI = -0.284 / 0.152). 304

306 Single-variable relationships

307 *Climatic suitability changes.* All bioclimatic models showed very good or excellent 308 performance (Figure S2). The models built with mean annual temperature and annual 309 temperature standard deviation showed higher TSS and AUC values than models including 310 minimum and maximum annual temperature (Table S6) and were hence used to calculate 311 climatic suitability.

Climatic suitability increased through time for 309 populations, decreased for 520 312 populations, and remained stable for 14 populations. For the period 1972-2016, the average 313 change of climatic suitability/year was -0.15% (SD = 2.4%). The relationship between 314 315 climatic suitability and population trends was positive, indicating more positive trends in populations experiencing improvement of suitability. Nevertheless, 95% CIs slightly 316 overlapped zero (effect size = 0.046; 95% CI = -0.021 / 0.107). The pattern was similar when 317 we limited analyses to the period 1992-2016, even though the effect size of the relationship 318 between climatic suitability and population trends was slightly weaker (effect size = 0.038). 319

320

Alien species. The average number of alien species per region was 45 (SD = 24), and population trends declined in regions with more alien species. For the period 1972-2016, the 95% CIs of this relationship slightly overlapped zero, while 90% CIs did not (effect size = -0.061; 95% CI = -0.125 / 0.004; 90% CI = -0.112 / -0.008). When we limited analyses to 1992-2016, the effect size was significantly lower than zero (effect size = -0.093, 95% CI = -0.166 / -0.022).

327

Habitat availability. Average cover of suitable habitat was 29% (SD = 20%), and population trends were more positive in landscapes with high habitat availability (effect size = 0.069; 95% CI = 0.002 / 0.130; Table S7a). *Habitat change.* Cover of suitable habitat increased for 33 populations, decreased for 396 populations, and remained stable for 276 populations ($|\mathbf{r}| < 0.01$); the average absolute value of habitat change across all the populations was 0.17% / year (SD = 0.39%). The singlevariable relationship between habitat change and population trends was weak, with CIs broadly overlapping zero (Table S7a).

337

338 Multi-variable analysis

Out of the six possible paired interactions among the four candidate drivers, only the interaction between the richness of alien species and the initial habitat availability showed 95% CIs not overlapping zero and was included in the meta-regression analysis including all the predictors and all the populations (full model; N = 705 populations). The effect sizes of predictors were nearly identical between the models and without the interaction (Table S7b, S7c).

The full model confirmed that population trends were negatively related to the 345 richness of alien species (Figures 3 and 4b). There was a positive relationship between the 346 347 trend of climatic suitability and population trends (Figure 4a) and, even though the 95% CIs 348 slightly overlapped zero, the 90% CIs did not (Figure 3; Table S7c). Population trends were positively related to habitat availability and to the habitat trend (Figure 4c and 4d), but 349 credible intervals overlapped zero for both variables (Figure 3). Furthermore, there was a 350 351 strong interaction between habitat availability and richness of alien species, showing that the negative impact of alien species was particularly strong in landscapes with a low amount of 352 suitable habitat (Figure 5). Values of random intercepts for the multiple regression model are 353 listed in Table S8. The residuals of the model showed no significant spatial or phylogenetic 354

autocorrelation (Moran's *I* = 0.001; 95% CIs = -0.009 - 0.010; Pagel's Lambda = 0; 95% CIs
= 0 - 0.503).

357

358 **Robustness to interspecific variation**

When we repeated meta-regression including only common toad populations, results were 359 generally consistent with the full analysis. Common toad population trends were more 360 negative in sites with more alien species, were positively related to the trend of climatic 361 suitability and were more positive in landscapes with higher habitat availability, even though 362 95% intervals were broader than in the analysis including all the species. Conversely, trends 363 364 were unrelated to habitat change and to the interaction between habitat availability and richness of alien species (Figure 6a). Common frog populations showed a different pattern 365 compared to the full analysis, as population trends only showed a weak positive relationship 366 with habitat change (Figure 6b). 367

Results remained partially consistent when we repeated analyses excluding the two 368 most common species (the common toad and the common frog), even though credible 369 intervals were much broader than in the full analysis. Population trends were positively 370 related to climatic suitability trend and negatively related to alien species. While the effect 371 372 size of habitat availability was close to zero, this analysis confirmed the interaction between habitat availability and richness of alien species (Figure 6c). Moreover, in this analysis we 373 observed a strong positive effect of habitat changes, indicating that population trends were 374 375 more positive in landscapes were the extent of suitable habitat increased through time (Figure 6c). 376



FIGURE 2 Average population trend of species, with 95% credible intervals. Point size is
proportional to the number of populations considered in this study. Amphibians are shown in
green, reptiles in brown.



383

FIGURE 3 Density plots of the posterior distribution for the relationships between trends of 705 populations of amphibians and reptiles and the candidate drivers (from top to bottom: trend of climatic suitability, richness of alien species, initial habitat availability, habitat change through time, interaction between initial habitat availability and richness of alien species). Thick vertical lines represent the average effect size, outer lines represent the 95% credible interval, inner colors represent the 75% credible interval. The y-axis indicates the frequency of posterior distributions and it is consistent for the five plots.



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FIGURE 4 Relationship between the four independent variables and population trends, as predicted by the full model. In each plot the dark line shows the predicted value of population trends (Fisher's Z) and the shaded area indicates the 95% credible interval.



FIGURE 5 Interaction between habitat availability and alien species. Plots show the relationship between the richness of alien species and the population trends predicted by the full model at different levels of habitat availability: a) habitat availability = 5%, b) habitat availability = 30%, c) habitat availability = 70%. In each plot the dark line shows the predicted value of population trends and the shaded area indicates the 95% credible interval.



406 FIGURE 6 Density plots of the posterior distribution for the relationships between population trends and the candidate drivers (from top to bottom: trend of climatic suitability, richness of 407 alien species, initial habitat availability, habitat change through time, interaction between 408 initial habitat availability and richness of alien species), considering a) common toad 409 populations only, b) common frog populations only and c) all data except for common toad 410 and common frog populations. Thick vertical lines represent the average effect size, outer 411 lines represent the 95% credible interval, inner colors represent the 75% credible interval. 412 Arrows represent the mean effect size of the analysis including all the species. The y-axis 413 414 indicates the frequency of posterior distributions and it is consistent for all the plots.

415

416 **DISCUSSION**

417

Our study provides one of the first broad-scale and long-term assessments of the impact of 418 multiple global change drivers on population trends of amphibians and reptiles. Despite 419 amphibians and reptiles having a major functional role in ecosystems, these vertebrates 420 remain underrepresented in population trend analyses, and they only account for a tiny part of 421 studies even in global databases of species abundance (Dornelas et al., 2018; Santini, Isaac, & 422 Ficetola, 2018). Our work summarized the trends of multiple European amphibian and reptile 423 populations through 45 years and showed that climate change, alien species, habitat 424 425 availability, and habitat change have complex impacts on their dynamics, even though their 426 importance differed among taxa (Figures 3 and 6).

Population trends of amphibians and reptiles were jointly determined by multiple 427 drivers. In the multi-variable analysis, alien species showed the largest effect, followed by 428 climate change and habitat availability (Figure 3), indicating that they might be among the 429 most influential drivers of population trends for many amphibians and reptiles. Alien species 430 have a major impact on the European native fauna (Vilà et al., 2010); unfortunately, the 431 number of alien species is quickly growing in all the continents, stressing the urgency of 432 433 prevention and mitigation actions in order to limit the intensification of impacts in the future (Seebens et al., 2017; Vilà et al., 2010). Nevertheless, the effect of alien species differed 434 across taxa, as they showed a negative effect on the common toad and on other amphibians 435 436 and reptiles, while were unrelated to the trends of common frogs (Figure 6). Other studies on population trends detected heterogeneous responses to broad-scale environmental stressors 437 (Campbell Grant et al., 2016; Flesch et al., 2017; Muths et al., 2017). For instance, Muths et 438 al. (2017) analyzed the demographic response of amphibian populations to climate and 439 observed that the magnitude and direction of the response were highly heterogeneous across 440

taxa and even within species. This confirms the importance of studies including species with
various ecological tolerances, in order to disentangle the heterogeneous effects of global
changes on natural populations.

Global change scenarios suggest that climate change will have a growing impact on 444 biodiversity (Intergovernmental Panel on Climate Change, 2015). However, the impact of 445 climate change can be heterogeneous among species and even among populations within a 446 given species. For instance, in the northern hemisphere, climatic warming can determine the 447 extinction of populations in southern portions of species ranges, while can have positive 448 effects on northern populations (Parmesan et al., 1999). To assess the impact of climate 449 450 change it is thus important to develop appropriate measures of how climatic variation influences populations in different areas of the species' range. Climatic suitability can provide 451 information on the actual effect of climatic variation on populations because it considers the 452 differences that can occur across distant geographic areas. Therefore, in our analyses we 453 considered climatic suitability instead of raw temperature/precipitation change. Despite 95% 454 CIs slightly overlapping zero, the effects of suitability changes were consistent with our 455 predictions (Figures 3, 4 and 6) with negative changes in climatic suitability corresponding to 456 457 negative population trends. Studies relating the trends of amphibians and reptiles to climate 458 change obtained mixed results. For instance, Ficetola and Maiorano (2016) found that changes in precipitation can have a significant impact on amphibian trends, but did not detect 459 a clear effect of changes in temperature. Conversely, when using climatic suitability, we 460 found a consistent pattern across species (Figures 3 and 6). Changes in climatic suitability are 461 often used to explore potential impacts of future climate change on biodiversity (Araújo et al., 462 2011; Thuiller et al., 2011), while fewer studies have used this approach to understand the 463 impact of changes occurring in the past (e.g. Bateman et al., 2016; Fouquet, Ficetola, Haigh, 464 & Gemmell, 2010). Our analysis suggests that suitability can provide a measure of the impact 465

of climate change more comparable across species. The moderate effect of suitability change on population trends can also be related to the ability of populations to adapt in response to climate change (Seebacher, White, & Franklin, 2015). The integration of ongoing adaptive changes is a challenge for global change research and could allow to better understand the responses of populations and to make better predictions (Hoffman & Sgró, 2011).

While the effects of alien species and climate were generally consistent across taxa, 471 the effects of habitat availability and habitat change were more complex. Even though habitat 472 loss is described as the factor threatening the largest number of amphibians and reptiles 473 (Stuart et al., 2008), relationships between changes in habitat availability and population 474 475 trends were only detected in a subset of analyses. Population trends were more positive in landscapes with more habitat (Table S7a), but the effects of habitat availability were weak 476 when taking into account also other factors and potential interactions (Figure 3; Table S7b). 477 Several factors can explain the limited effects of habitat variables. First, a significant 478 interaction between habitat availability and the richness of alien species indicates that the 479 impact these two variables can be context dependent, complicating the detection of their 480 effects. Second, we assessed habitat change on the basis of broad-scale land cover maps, 481 which do not provide measures of the specific resources and conditions needed by different 482 483 species. Obtaining accurate measures of habitats is particularly complex for small vertebrates, which often exploit specific microhabitats (Ficetola, Lunghi, et al., 2018; Mendenhall, 484 Sekercioglu, Oviedo Brenes, Ehrlich, & Daily, 2011). For instance, agricultural 485 486 mechanization can determine loss of suitable micro-habitats (e.g. hedgerows, ditches) even in areas with a stable amount of agricultural lands, thus impacting species that can exploit semi-487 natural landscapes. Third, average rates of habitat change were extremely low during the 488 study period (average: ~0.1% / year). Such a limited variation is characteristic of broad areas 489 of Europe (Figure S3) but reduces the possibility to detect relationships and can explain the 490

weak effect of this driver. Furthermore, population declines often do not occur immediately 491 492 after environmental pressures (Dullinger et al., 2013), thus we might experience the legacy of present anthropogenic pressures in the next decades. Nevertheless, habitat change showed a 493 clear effect when we removed the commonest species (common toad and common frogs) 494 from our dataset, with more positive population trends in landscapes where the amount of 495 suitable habitat increased through time. Common toad and common frog are widespread, 496 generalist species that can exploit a very wide range of habitats (Table S2), therefore it may 497 be more difficult detecting their response to habitat change, compared to habitat specialists. 498 This further stresses the need of monitoring a wide range of species in order to obtain 499 500 generalizable information of the effects of global changes on biodiversity loss and highlights 501 the importance of comparing the responses of both widespread and specialized species.

Habitat availability showed a strong interaction with the richness of alien species, as 502 the negative impact of alien species was particularly strong in landscapes with less habitat 503 availability (Figure 5). The importance of interactions among different drivers is increasingly 504 recognized by global change studies, as interactive effects can both magnify and mitigate the 505 impact of stressors (Blaustein & Kiesecker, 2002; Mantyka-Pringle et al., 2012). Alien 506 507 species show complex relationship with the availability of natural habitats, which can strongly 508 modify their impact. For instance, invasive species can be more abundant in human-modified landscapes, thus native populations living in landscape with a less natural habitat can suffer a 509 stronger impact by invasives (Blaustein & Kiesecker, 2002; Didham et al., 2007; Quinn, 510 511 Schooler, & Van Klinken, 2011). The complex interactions between alien species and habitat availability further stress the importance of conservation actions targeting multiple threats and 512 also considering synergies among drivers of decline in order to mitigate biodiversity loss 513 (Brook et al., 2008; Didham et al., 2007). 514

Despite the broad temporal and geographic extent, our analyses have some limitations. 515 516 Most of the data are from amphibian populations, and one species (the common toad, Bufo 517 bufo) accounted for more than half of populations (Table S9). This occurs because the common toad is one of the most abundant amphibians in Europe and is regularly monitored 518 519 by many citizen science programs. Common amphibians have a major role in ecosystem functioning and nutrient transfer (Beard, Eschtruth, Vogt, Vogt, & Scatena, 2003; Kyek, 520 521 Kaufmann, & Lindner, 2017). Several studies have shown negative trends in toad populations (e.g. Bonardi et al., 2011; Petrovan & Schmidt, 2016) and understanding the factors 522 underlying a common species decline is extremely important to maintain ecosystem 523 524 functioning (Gaston & Fuller, 2008). Alien species and climate change showed a similar 525 effect across most of the taxa: despite broader credible intervals, effect sizes pointed in the same direction even if we removed the most common species (Figure 6c), suggesting that 526 527 uneven sample size across species did not bias our conclusions. In our dataset we collected fewer data regarding reptiles than amphibians. This is a recurrent pattern in the herpetological 528 literature and hampered separate analyses of these taxa. Estimating the abundance of reptiles 529 is usually harder compared to amphibians, because reptiles often have low detection 530 531 probability, and estimating their abundance requires effort-demanding survey methods (e.g. 532 capture mark recapture instead of repeated counts) (Ficetola, Romano, Salvidio, & Sindaco, 2018). Increasing the monitoring efforts toward reptile populations is urgently required to 533 better assess the drivers of the decline of this group and guide future conservation efforts. 534 535 Finally, our analyses were limited both in space and in time by the availability of population and land-cover data. Continuous series of land-cover data are only available since 1992, thus 536 537 preventing us from assessing the effects of habitat availability during previous periods, when the velocity of habitat change in Europe was probably stronger than in recent years (Falcucci, 538 Maiorano, & Boitani, 2007). Furthermore, the majority of our data came from just two 539

European countries, potentially limiting the spatial representativeness of our dataset (Figure 540 S1). Despite not spanning the whole Europe, analyzed localities provide good coverage of the 541 features occurring through Europe for habitat availability and changes (Figure S4), richness of 542 alien species (Figure S5), and climatic features (with the exception of coldest climates; Figure 543 S6). Overall, the frequency of declining populations in our dataset was similar to previous 544 broad-scale estimates of trends of herps in Europe (e.g. Houlahan et al., (2000); 53% negative 545 and 43% positive trends). This suggests that our analyses can provide an accurate picture of 546 patterns occurring throughout most of Europe. 547

Population trends of European reptiles and amphibians are driven by the combined 548 549 effects of alien species, climate change, habitat features, and habitat changes, with complex 550 joint and interactive effects among factors. Even though we identified general patterns in the response to some environmental drivers, when retrieving broad-scale patterns it is important 551 552 to consider that the same factors can act differently among taxonomic groups (Campbell Grant et al., 2016; Muths et al., 2017). For instance, habitat change showed a contrasting 553 effect across species and its crucial role was only evident for a subset of them. Understanding 554 the impact of global change drivers is the first step for management. This requires drawing 555 556 general syntheses of the combined effects of multiple drivers but also considering how 557 responses can be different across species.

558

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