

rees. Each phylogenetic tree bears species with varying degrees of vulnerability to climate change. Plain circles at the tips of each tree Figure S1: Hypothetical example depicting the possible consequences of climate change on the evolutionary history of phylogenetic depict species, with a color gradient from blue to red standing for low to high vulnerability. The red bars across branches depict the branches that will be lost when species go extinct. The three scenarios are: species vulnerability is A) increased for species with the east redundant evolutionary history; B) structured such as the youngest species (i.e. with the shortest terminal branches and more redundant evolutionary history) are the most vulnerable; C) randomly distributed and replicated drawings provide a basis for null model testing.

97.5%

Resulting PD = 5.24

Resulting PD = 3.6

5.03





**Figure S2**: Workflow diagram depicting the different steps of the analysis performed in this study. Different steps are the forecasting of future species distributions under climate change, the reconstruction of large-scale phylogenetic trees, and the analysis of projected loss of phylogenetic diversity relative to extinction scenarios.



Figure S3: Representation of the strengh of the phylogenetic signal of species sensitivity to climate change as a function of study time slices and climate change scenarios (A: plants, B: birds and C: mammals). Each boxplot represents the variation in the two estimated values (Blomberg's K and Pagel's Lambda) over the 100 available phylogenetic trees for each group of species.



**Figure S4:** Variation of p-values obtained for the tests of phylogenetic signal on predicted changes in habitat suitability (CSC), based on three tests, namely Abouheif test (left column), Blomberg's K (central column), and Pagel's lambda (right column), and ran over the 100 phylogenetic trees available for each study group (A: plants, B: birds and C: mammals). Results are also detailed for different time sclices and climate change scenarios.

Figure S5 A Plants



Figure S5 B – Birds



Figure S5 C – Mammals



**Figure S5:** Representation of the predicted loss in habitat suitability (LSC) under the A1FI scenario by 2080, onto the phylogenetic tree of each species' group. Colors are black when LSC is lower than 15%, yellow when LSC ranges from 15 to 30%, orange when loss ranges from 30 to 50% and red when LSC is higher than 50%. The tree was taken at random from the 100 trees available for the three species groups.



**Figure S6**: Projected change of phylogenetic diversity compared with scenarios of random extinctions for the European plants, birds and mammals, in the case of two climatic scenarios (A1F1 and B1) using LSC rather CSC for inferring probability of extinctions. Black and blue lines represent the median (plain), minimum and maximum values of PD (dashed) predicted under current and future conditions respectively, while integrating over the 100 phylogenetic trees used for each study group. Graphs also depict the quantiles (0.025-0.975) (grey shading) of the random extinction scenarios and the remaining PD estimated when probability of extinction was positively related with the most or least original species (red lines).



**Figure S7**: Sensitivity analysis to investigate the effects of variations across species distribution models (SDMs) and global circulation models (GCMs) on the projected change of phylogenetic diversity on birds compared with scenarios of random extinctions. As for Figure S6, Black and blue lines represent the median (plain), minimum and maximum values of PD (dashed) predicted under current and future conditions respectively, while integrating over the 15 combinations of Models and GCMs. Graphs also depict the quantiles (0.025-0.975) (grey shading) of the random extinction scenarios.



**Figure S8**: Predicted change in phylogenetic diversity under scenario A1 HadCM3 for 2080 after accounting for species richness. To make sure the change in the spatial phylogenetic diversity was not only due to the change in species richness, we mapped the residuals of a generalised additive model with phylogenetic diversity as the response variable and species richness as the explanatory variable under both current and future conditions. A) Map of residuals from the generalised additive regression model from current phylogenetic diversity and species richness. When positive, phylogenetic diversity is higher than expected given the mean species richness, and reciprocally. B) Map of residuals from the generalised additive species richness; C) Difference between current residuals (B) and future residuals (A). When positive, change in phylogenetic diversity is higher than expected given change in species richness, and reciprocally. For plants and birds, the spatial variation in alpha PD is the average PD across the 100 trees.

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# Supplementary table

**Table S1** Results of the tests for phylogenetic signal on predicted changes in habitat suitability (CSC), namely Abouheif test, randomization tests for Blomberg's K, and likelihood ratio test for Pagel's lambda. Reported values are the number of times the tests were significant over the 100 retained phylogenetic trees for each study group (from 0 to 100).

		Plants		Birds		Mammals				
		Abouheif	Κ	Lambda=0	Abouheif	Κ	Lambda=0	Abouheif	Κ	Lambda=0
A1	2020	64	32	0	0	0	100	0	40	0
	2050	64	37	0	99	2	100	60	53	0
	2080	61	51	0	99	5	100	71	63	0
A2	2020	63	32	0	0	0	100	0	36	0
	2050	60	33	0	99	1	100	66	54	0
	2080	62	46	0	98	24	100	66	57	0
B1	2020	65	36	0	0	0	100	0	38	0
	2050	61	32	0	99	2	100	62	63	0
	2080	62	47	0	98	3	100	63	71	0
B2	2020	64	33	0	0	0	100	0	39	0
	2050	58	30	0	99	2	100	67	73	0
	2080	62	44	0	99	8	100	66	68	0

# SUPPLEMENTARY METHODS

#### **Data and Methods**

#### Species data

We modelled 1760 European species (1,280 plants<sup>1</sup>, 140 mammals<sup>2</sup> and 340 birds<sup>3</sup>). Species with fewer than 20 records and bird species with strictly aquatic and marine habitats were not modelled. The original grid is based on the Atlas Florae Europaeae (AFE)<sup>1</sup>, with cell boundaries typically following the 50-km lines of the Universal Transverse Mercator (UTM) grid. The European mapped area (2,434 grid cells) excludes most of the eastern European countries (except for the Baltic States) where recording effort was both less uniform and less intensive<sup>4</sup>.

### Climate data

A set of aggregated climate parameters were derived from the Climate Research Unit at 10' resolution. Average monthly temperature and precipitation in grid cells covering the mapped area of Europe were used to calculate mean values of four different climate parameters for the period 1961–1991 (referred to as 'baseline data'). Variables included mean temperature of the coldest month (°C), mean annual summed precipitation (mm), mean annual growing degree days (> 5° C), and a moisture index calculated as the ratio of mean annual actual evapotranspiration over mean annual potential evapotranspiration. Choice of variables was made to reflect two primary properties of the climate (energy and water) that have known roles in imposing constraints upon species distributions as a result of widely shared physiological limitations. All data were developed at a spatial resolution of 10' and then projected onto the AFE 50 km grid system using bilinear interpolation for the modeling part.

The CRU CL 2.0<sup>5</sup> and CRU CL 2.1<sup>6</sup> dataset at resolution of 10' was chosen to represent current climate (average from 1961 to 1990). The CRU TYN SC 1.0 dataset<sup>6</sup> at resolution of 10' was chosen to represent future climate projections for the periods of 1991-2020 (referred as 2020), 2021-2050 (2050), and 2051-2080 (2080) from three global climate models (GCM: CGCM2, CSIRO2, and HadCM3) made available through the Climate Research Unit data center (http://www.cru.uea.ac.uk/cru/data/hrg/). Originally, all GCMs were built by the Climate Research Unit as a comprehensive set of high-resolution grids of monthly climate at spatial resolutions of 10 minutes for Europe. Information about the constructions of the data associated uncertainties and be found here: http://www.ipcccan data.org/docs/tyndall working papers wp55.pdf. Five climate variables were included: temperature, diurnal temperature range, precipitation, vapour pressure, and cloud cover. The set comprised the observed climate record (1901–2000), a control scenario (1901–2100) and 16 scenarios of projected future climate (2001-2100). The 16 climate change scenarios represented all combinations of four emissions scenarios and four global climate models (GCMs: PCM2, CSIRO2, HadCM3, CGCM2), covering 93% of the range of uncertainty in global warming in the 21st century published by the Intergovernmental Panel on Climate Change (2007). Thus these scenarios permitted to assess climate change impacts while taking into account all major sources of uncertainty in future climate. The scenarios were constructed by combining time-series of global warming and patterns of change from GCMs with the baseline climate and sub-centennial variability from the observed record. Thus these grids provided homogenous 200-year transient scenarios (1901-2100) for users projecting the future impacts of climate change using environmental models.

We then only selected three of the four GCMs because some anomalies from PCM2 global circulation models presented extreme anomalies. We then used 4 emissions scenarios (A1FI, A2, B2, B1). These four represent 68% of the range of uncertainty in emissions published by

SRES, as measured by the cumulative carbon dioxide emissions (1990–2100), compared to the full set of 40 SRES scenarios (IPCC, 2000, Table SPM-3a). These emission scenarios were used in combination with different GCMs, as described in the table M1 below.

	SCENARIO				
		A1FI	A2	B1	B2
	Csiro2		Х		
GCM	HadCM3	Х	Х	Х	Х
	Cgcm2		Х		

Table M1: Scenarios and global emission scenarios used in the analyses

We show below the temporal trends over Europe of four common bioclimatic variables, as projected by the four different emission scenarios (Figure M1). Side bars represent projections uncertainty from GCMs for each scenario. The four scenarios have similar trends until 2020-2050 and then diverge afterwards. The varability in climatic forecasts from different GCMs is represented and demonstrates a higher variability across GCMs for the most extreme scenario (A1FI) whereas the variability is rather low for the least extreme scenarios (B1 and B2).





**Figure M1**: Overall trends in the four variables used in the analyses for the 4 emission scenarios. The variability across GCMs in 2080 is represented on with the vertical bars wth colors associated to the scenarios.

# Habitat Suitability Modeling

An ensemble of forecasts of species distributions models (SDM)<sup>7-9</sup> was obtained for each one of the 1760 species considered. The ensemble included projections with Generalised Linear Models (GLM), Generalised Additive Models (GAM), Boosting Regression Trees (BRT), Classification Tree Analysis (CTA), Artificial Neural Networks (ANN), Mixture Discriminant Analysis (MDA). Models were calibrated for the baseline period using 80% random sample of the initial data and evaluated against the remaining 20% data, using the area under the curve (ROC)<sup>10</sup>, and the True Skill Statistic (TSS)<sup>11</sup>. This analysis was repeated 10 times, thus providing a 10-fold internal cross validation of the models. For the final assessment, models were calibrated using 100% of the species distributions data as it has been shown that random removal of presence records adds a non-trivial amount of uncertainty in future projections<sup>12</sup>. All models were run using the BIOMOD package<sup>13,14</sup> in R. Models were calibrated on the 50km resolution and then projected onto the 10' resolution grids as in <sup>12,15</sup>.

#### Assessing species' vulnerability to climate change

Each ensemble of species projections for current and future conditions were converted into the two metrics of species' vulnerability. The first measures the relative change in climate suitability (CSC, or species range change) and is presented in the main text as the measure of species' vulnerability. It corresponds to the total suitable area projected into the future under the assumption of unlimited dispersal minus the total suitable area projected onto the current conditions divided by the total suitable area projected onto the current conditions.

 $CSC = \frac{(\text{Future suitable climatic area}) - (\text{Current suitable climatic area})}{\text{Current suitable climatic area}} *100$ 

The second measures the relative loss of current suitable climate (LSC). It measures the remaining current suitable climatic area into the future under the assumption of no dispersal.

$$LSC = \frac{\text{Overlap(Future suitable climatic area - Current suitable climatic area)}}{\text{Current suitable climatic area}} *100$$

Each metric was derived from each Species x Model x Scenario x GCM combinations.

Given the extremely large datasets generated (see Figure S2, 1140 projections per species) and that computionnaly intensive analyses (see Phylogenetic signal in species' vulnerability part and Effects of climate change on the tree of life part) had to be carried out on these data, we firstly investigated the variations in LSC and CSC across the different SDMs and GCMs combinations, while keeping species and scenarios constant.

The figure M2 represents the multiple correlations between estimates of CSC for all combinations of SDM and CGM, for each time slice and each scenario for the bird dataset. Each bar corresponds to 225 correlations tests (5 SDM x 3 GCMs => 15x15 combinations).

Although some divergences between combinations occur, the correlations are very high demonstrating a relatively low variation across the SDMs and GCMs.



**Figure M2:** Correlations between estimated change in suitable climate from the different combinations of SDM and GCM for each scenario and time slice.

In summary, although future distributions have been showed to be sensitive to SDMs and to a lesser extent to GCMs  $^{16,17}$ , the integrative metrics provided in our study, i.e., LSC and CSC, were not very sensitive. Given this result, for each species x scenario combinations, we took the median as recently recommended by Araújo et al.<sup>12</sup> and Marmion et al.<sup>8</sup>.

We also conducted a sensitivity analysis to investigate the influence of variations in LSC and CSC due to GCMs and SDMs on the effects of climate change on the tree of life (see below, and Figure S7).

#### Phylogenetic tree constructions

For mammals, we used 100 phylogenetic trees based on Fritz et al<sup>18</sup> with the polytomies resolved using Polytomy Resolver v1. by Kuhn et al. (submitted, Methods in Ecology and Evolution). Polytomy Resolver v1. applied a birth-death model using a new two-steps approach to simulate branch lengths and randomly resolved the polytomies in the original supertree<sup>19</sup>. More explanation can be found here:

http://www.sfu.ca/~amooers/papers/Kuhn\_etal\_MEEman\_10.pdf.

Phylogenetic trees for the birds and plants datasets were constructed with sequence data available in GenBank, which were downloaded with the SeqinR package in R. The supermatrices of birds and plants and their respective best ML phylogenetic trees have been incorporated to Treebase: http://purl.org/phylo/treebase/phylows/study/TB2:S10770

For the bird phylogeny, we downloaded 10 mitochondrial gene regions (12S, ATP6, ATP8, COII, COIII, ND1, ND3, ND4, ND5, ND6 ) plus 6 nuclear regions (28S, c-mos, c-myc, RAG1, RAG2, ZENK) for each genus, to create a consensus sequence using BioEdit15 in order to maximize the representation of study taxa in our supermatrix. We also downloaded three widely represented regions in GenBank, namely cyt B, ND2 and COI, for each species (Table M2). These three regions, which were represented at 86,7%, 76,1% and 58% among study species, respectively, allowed us to further resolve our tree at the species level. All sequences were aligned with 4 methods (ClustalW16, Kalign17, MAFFT18, MUSCLE19). The best alignment for each region was selected and depurated with TrimAl20. The DNA matrices were concatenated to obtain a supermatrix.

Gene regions included on the birds dataset	% of taxa representation
128	63.9
28S	9.6
ATP6	37.4
ATP8	27
c-mos	31.8
c-myc	34.1
COI	79.6
COII	16.1
COIII	21.3
Cyt b	96.7
ND1	30.3
ND2	82.9
ND3	37.9
ND4	20.9
ND5	31.3
ND6	31.3
RAG1	62.6
RAG2	17.1
ZENK	25.1

**Table M2:** Percentage of taxa (genera) represented in Genbank for each region included in

 the study

For the plants dataset, we downloaded 2 conserved chloroplastic gene regions (rbcL, matK) plus 14 regions for a single family or order (ndhF for Brassicales; rps16 for Ranunculales; PHYA for Brassicaceae; trnL-F for Aizoaceae, Amaranthaceae, Brassicaceae, Caryophyllaceae, Polygonaceae, Rosaceae; ITS for Amaranthaceae, Brassicaceae, Caryophyllaceae, Papaveraceae, Ranunculaceae) (Table M3).

Gene regions included on the plants	% of taxa	% of taxa representation within family or		
dataset	representation	order		
matK	55.6	NA		
rbcL	61.9	NA		
ndhF (Brassicales)	13.8	46		
rps16 (Ranunculales)	2.1	16.7		
ITS (Amaranthaceae)	9.5	94.7		
ITS (Brassicaceae)	25.4	88.9		
ITS (Caryophyllaceae)	8.2	30.1		
ITS (Fumariaceae)	1.1	44.4		
ITS (Papaveraceae)	1.9	87.5		
ITS (Ranunculaceae)	5	41.3		
PHYA (Brassicaceae)	9.5	33.3		
trnL-F (Aizoaceae)	1.6	66.7		
trnL-F (Amaranthaceae)	4.8	47.4		

trnL-F (Brassicaceae)	16.4	57.4
trnL-F (Caryophyllaceae)	3.2	11.7
trnL-F (Polygonaceae)	1.9	77.8
trnL-F (Rosaceae)	5.3	100

**Table M3**: Percentage of taxa (genera) represented in Genbank for each region included in

 the study

Phylogenetic analyses were conducted using Maximum Likelihood within RaxML<sup>20,21</sup>. To avoid problems derived from nucleotide saturation and patchiness in the datasets, we applied a tree prior constraint at the ordinal level for the birds dataset (based on <sup>22</sup>) and at the family level for the plants dataset (based on <sup>23</sup>). This supertree constraint improved the speed of tree inference and final quality of estimated trees, as it represent widely demonstrated basal phylogenetic relationships, and thus indirectly allow to include more phylogenetic information into the analysis than the one included only in our genetic partitions.

A high proportion of nodes were supported by RaxML bootrap analyses in both plants and birds trees: 71.1 % for birds and 65.6 % of the nodes had a bootstrap equal or higher than 70%; only 20.8% of the nodes for birds and 17.9 % for plants were not supported (bootstrap < 50 %). Both trees were ultrametricised by penalized likelihood using r8s.

To account for uncertainty in the reconstruction of phylogenies we adopted the following approach: For birds, we used the 100 best ML trees. For plants, we randomly resolved terminal polytomies by applying a birth-death (Yule) bifurcation process within each genus and repeated this 100 times. Concretely, from the dated tree at the genus level, for each genus holding more than one species, we replaced the pendant edge by a random subtree following a birth only bifurcation process. The subtree was scaled so that the distance from the leaves to the root was equal to the corresponding pendant edge length (see explanatory Figure M3).

All analyses were thus conducted over the 100 estimated trees for each group. The phylogenetic trees for the birds and plants datasets were converted to chronograms by Penalized Likelihood<sup>24</sup>. The phylogenetic trees for mammals were already calibrated by Fritz et al.<sup>18</sup>



**Figure M3**: Schematic example of a random resolution of polytomies at a genus level to represent variability at the species level.

#### Phylogenetic signal in species' vulnerability

To estimate whether there was a phylogenetic signal in species' vulnerability we used three different tests that slightly differ in their assumptions and methods of estimations.

We first used a robust measure proposed by Abouheif to test for serial independence to detect a phylogenetic signal in phenotypic traits<sup>25</sup>. We used the Abouheif test implemented in the adephylo package in R<sup>26</sup> after having transformed each phylogenetic tree into dissimilarity matrices using the inverse of cophenetic distance. The exact test was performed with 999 randomizations. This test does not measure the strength of the phylogenetic signal but only test its significance. We also used the measure K proposed by Blomberg et al.<sup>27</sup> that estimates the strength of a phylogenetic signal and the associated test of significance using data randomizations. The randomization procedure tests the significant tendency for pairs of related species to have more similar sensitivity to climate change than species pairs taken at random. The test is based on the method of phylogenetic independent contrasts (PICS)<sup>28</sup>, and the fact that PIC variance is an unbiased estimator of the brownian variance parameter. Then the estimated PIC variance can be compared to the one computed through data randomizations. We used the implementation of K and the randomization procedure developed in the package *picante<sup>29</sup>* in R.

We also used a maximum-likelihood based measuremenet of phylogenetic signal, namely lambda model, as developped by Pagel<sup>30</sup>. This metric corresponds to a tree transformation parameter which gradually eliminates phylogenetic structure when varying from 1 to 0. Lambda transformation is performed by multiplying the off-diagonal elements of the variance/covariance matrix describing the tree topology and branch lengths. Lambda values of 1 correspond to a Brownian evolution, whereas at the other extreme a lambda value of 0 corresponds with the complete absence of phylognetic structure (star-like phylogeny).The estimated lambda can be compared to zero by computing a likelihood ratio and comparing it to a chi-square distribution with one degree of freedom. Hence testing for a significant phylogenetic signal, relative to phylogenetically unstructured data.

Results are in Figure S3, Figure S4, Table S1.

#### Phylogenetic diversity measures

Phylogenetic diversity was calculated as "the sum of the lengths of all the branches that are members of the corresponding minimum spanning path" <sup>31,32</sup>, in which 'branch' is a segment of a tree, and the minimum spanning path is the mimimum patristic distance between the two nodes. For all groups, the phylogenetic diversity was estimated using each of the 100 trees. The spatial variation in alpha phylogenetic diversity in Figure 3 and Figure S7 are thus the average PD over the 100 trees.

#### Effects of climate change on the tree of life.

To avoid converting estimates of range change (CSC & LSC) into extinction using subjective threshold, we instead used CSC and LSC as surrogates for probability of extinction (p(ext)) and weighted the edge length of the trees by the expected survival probabilities of each species (taken as 1 - p(ext)) under each time slice and scenario (e.g. Figure 2, Figure S6). The null model expectation was extracted by randomizing (p(ext)) across the tips and recalculating PD (Figure 2 and S5, grey shading).

We provide here an R script and associated figure (Figure M4) using artificial data to illustrate the approach first proposed by<sup>33</sup> (Prof. Arne Mooers, pers. comm.)

```
tree<- read.tree(text="(((Sp1:2, Sp2:2):1, Sp3:3):1, ((Sp4:0.5, Sp5:0.5):2,
(Sp6:1, Sp7:1):1.5):1.5):1;")
#The following data frame gives p(ext) for each species.
status<- data.frame(c(.50,.25,.25,.10,.75,.95,.75))
names(status)[1]<-"ExtinctionProbability"
row.names(status)<-tree$tip.label
#expected future PD
new.tree<-tree
for(i in 1:nrow(tree$edge)){
    node<- tree$edge[i,2]
    d<- node.leaves(tree, node)
    p.values<- status[which(row.names(status) %in% d),1]
    survival.prob<- 1-prod(p.values)
    new.tree$edge.length[i]<- new.tree$edge.length[i]*survival.prob
}
```

#The phylo object new.tree has the modified branch lengths. To get the total expected #future PD, just sum together the branch lengths: expectedPD<- sum(new.tree\$edge.length)</pre>

#compare old and "future" trees: yellow boxes are the extinction
probabilities, green boxes are the branch length.

```
par(mfrow=c(1,2))
plot(tree, no.margin=T, label.offset=0.2)
tiplabels(status$ExtinctionProbability)
edgelabels(tree$edge.length)
plot(new.tree, no.margin=T)
edgelabels(round(new.tree$edge.length,2))
```



**Figure M4**: Probabilistic approach to influence the tree of life by the probability of extinction of each species.

We did not display all projected PDs under random extinction (999 for each tree) but only the minimum and maximum of the quantiles 0.025 and 0.975 (area of significance at 0.05) across all trees (Figure 2 and Figure S3).

We also compared change in PD induced by climate change to two extreme scenarios where estimated probability of extinction (p(ext)) were positively or negatively assigned (red lines in Figure 2) to the most or to the least evolutionary distinct species<sup>34</sup>.

Results are in Figure 2 for CSC and Figure S6 for LSC.

# Sensitivity Analyses

To explore the sensitivity of our results to the decision of using the median across SDMs and GCMs, instead of using all combinations (which would be impractical), we conducted a formal sensitivity analysis applied to the bird data set by investigating the effects of climate change on their tree of life using one tree from the 100 available. We selected the bird dataset because of the intermediate number of species (340) and the fact that the phylogenetic trees are the most robust for this group (species-level phylogeny). For the selected tree, we conducted the analysis described above but across all combinations of GCMs and SDMs (5 Models and 3 GCMs) for the A1FI scenario. Results are in Figure S7

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