

A global synthesis of animal phenological responses to climate change

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Shifts in phenology are already resulting in disruptions to the timing of migration and breeding, and asynchronies between interacting species^{1–5}. Recent syntheses have concluded that trophic level¹, latitude⁶ and how phenological responses are measured⁷ are key to determining the strength of phenological responses to climate change. However, researchers still lack a comprehensive framework that can predict responses to climate change globally and across diverse taxa. Here, we synthesize hundreds of published time series of animal phenology from across the planet to show that temperature primarily drives phenological responses at mid-latitudes, with precipitation becoming important at lower latitudes, probably reflecting factors that drive seasonality in each region. Phylogeny and body size are associated with the strength of phenological shifts, suggesting emerging asynchronies between interacting species that differ in body size, such as hosts and parasites and predators and prey. Finally, although there are many compelling biological explanations for spring phenological delays, some examples of delays are associated with short annual records that are prone to sampling error. Our findings arm biologists with predictions concerning which climatic variables and organismal traits drive phenological shifts.

Global climate change has important ecological consequences^{4,8} and perhaps the best studied are advancements in the timing of seasonal activities, or phenology, of organisms^{1–3,5,7,9–13}. Understanding the factors that influence phenological shifts is critical because these shifts can impact the fitness of organisms by altering the availability of resources^{2–4}. In addition, phenological shifts can cause species declines by generating asynchronies or 'mismatches' between plants and pollinators¹², plants and herbivores¹⁴, migrant birds and their prey¹¹ or floral resources¹⁵, and hosts and parasites¹⁶. Several recent syntheses have made inroads to understanding how the phenology of species is shifting with climate change^{1,5–7,13}. For example, primary consumers were demonstrated to be shifting their phenology faster than other species in the UK¹, species are shifting their phenology faster in spring than in autumn in China⁵, and the strength of phenological responses to climate change is dependent on the way responses are measured (for example, by the types of behaviour observed or the number of observations⁷).

Despite these insights, several critical knowledge gaps preclude accurate predictions of the sensitivity of organisms to climate change on a global level. First, although many phenological syntheses assume climate change as an important driver, few explicitly test for the effects of climate (but there are exceptions^{1,5,6}), and among those that do, climate data have rarely been standardized across studies to confirm the link between changes in phenology and climate. Therefore, it remains unclear which climatic variables, such as temperature or precipitation, are driving shifts in phenology, and

whether the broad geographical heterogeneity in these climate variables impacts their power to explain and predict ecological trends. Second, recent syntheses have relied on country-level data, and no synthesis in over a decade has addressed phenological responses to climate change across the globe. Global analyses are important because they cover a greater extent of climatic conditions than local or regional analyses. For example, global syntheses are critical to test broad-scale latitudinal hypotheses about phenological shifts, such as the hypothesis that the climatic factors driving seasonality across latitudes also drive phenological changes. Third, it is unclear why some species show delayed spring phenologies despite an overall trend towards advancement^{10,17}. Finally, it is also unclear whether certain ecologically important characteristics of organisms are predictive of strong phenological responses. For example, phylogeny or body size may be an important factor in determining the magnitude of phenological response to climate change because smaller organisms acclimate more quickly to changing conditions than larger organisms (J.R.R., manuscript in preparation). In addition, ectotherms may exhibit stronger phenological responses than endotherms because they cannot thermoregulate independently of their environments and are therefore more sensitive to changes in environmental conditions. Because of these knowledge gaps, a general global framework is still missing for predicting the direction and magnitude of phenological shifts based on ecological context and organismal traits.

To address these gaps, we conducted a global synthesis of animal phenological time series from 127 studies (Supplementary Tables 1 and 2), spanning 5 continents and 15 classes of animals including insects, mammals, reptiles and birds. We focused on spring phenological events in animals because phenological responses to climate change in plants have recently been synthesized¹⁸, some of our primary questions could only be answered using animal data, and the evidence for advancement in animal phenology is more conflicting and controversial than it is for plants⁹ (see Supplementary Information). Here, we synthesized the multivariate effects of climate change on phenology, as well as testing predictors of this complex phenomenon (such as latitude, endo- or ectothermy), with a unique meta-analysis approach that jointly modelled phenological shifts, the effects of climate on phenology and climate change (the 50 yr correlation between climate and year) using a trivariate mixed-effects model^{19,20} (see Supplementary Fig. 1; see Methods). Unlike previous univariate meta-analyses that strictly synthesize phenological shifts^{2,3}, our trivariate approach assessed whether phenology is dependent on climate and climate change and whether the magnitude and direction of these relationships is dependent on 10 climate variables (for example, mean, minimum and maximum temperature, precipitation, snowfall²¹, see Methods). All climate variables were standardized across all time series by accessing a single source of historical point-based climate data (the National Oceanic and

Atmospheric Administration (NOAA) NCDC-3 data²²) with data that were specific to the region and time of each study, reliably allowing us to identify which aspects of climate were driving phenological shifts. Importantly, this approach facilitated evaluation of whether climate change, rather than just long-term climate means, was associated with changes in phenology. Further, our trivariate mixed-effects meta-analysis also accounted for dependencies of effects among related taxa due to their shared phylogenetic history²³ (see Supplementary Code). We were able to compare relationships between phenology and year for 1,011 time series and relationships among phenology, year and climate for a subset of these including 321 time series.

The meta-analysis revealed that, on average, animals have advanced their phenology significantly since 1950 ($\beta = -0.318$ (mean slope), d.f. = 937, $P = 0.01$; Fig. 1a; Supplementary Table 3), advancing by 2.88 days per decade. Across all species and sites, mean temperature increased significantly over time (Fig. 1a; Supplementary Table 4). The meta-analysis also revealed that temperature is closely related to phenological date independent of year, and that phenology is more closely linked with mean temperature in areas that have experienced more climate change (Fig. 1b), suggesting that climate change is indeed the driver of these shifts (Fig. 1a; Supplementary Table 4). Phenological shifts were not heavily biased by the

phylogenetic history of taxa, which accounted for only about 4.5% of the variance (phylogenetic τ^2) between phenology and year, and 0–6% between phenology and climate (Supplementary Tables 3–8). Between-study variance accounted for 8–9% of the total variance accounted for in all models (Supplementary Tables 3–8).

The direction of phenological shifts may differ among taxa, with some species showing delays rather than advances of spring phenology^{5,10,13,17,18}—such as delays in seabird egg-laying as a consequence of reduced sea ice¹⁰ or delays in phenology (flowering, for example) after short winters that fail to induce vernalization¹⁷. To test whether a phenomenon similar to vernalization might be responsible for phenological delays among animals (positive relationships between phenological date and year), we examined whether the magnitude of the delay could be predicted by the increase in winter temperatures (defined here as the relationship between year and average temperature during the year's three coolest consecutive months), controlling for latitude. We found no support for the hypothesis that winter temperatures predicted phenological delays, instead finding that they predicted advancements ($\beta = -0.296$ (slope), d.f. = 321, $P < 0.001$ in models with all time series) or were not significantly predictive ($\beta = -0.125$, d.f. = 68, $P = 0.32$ among time series with delays only). In fact, winter temperatures were positively correlated with spring temperatures that are well

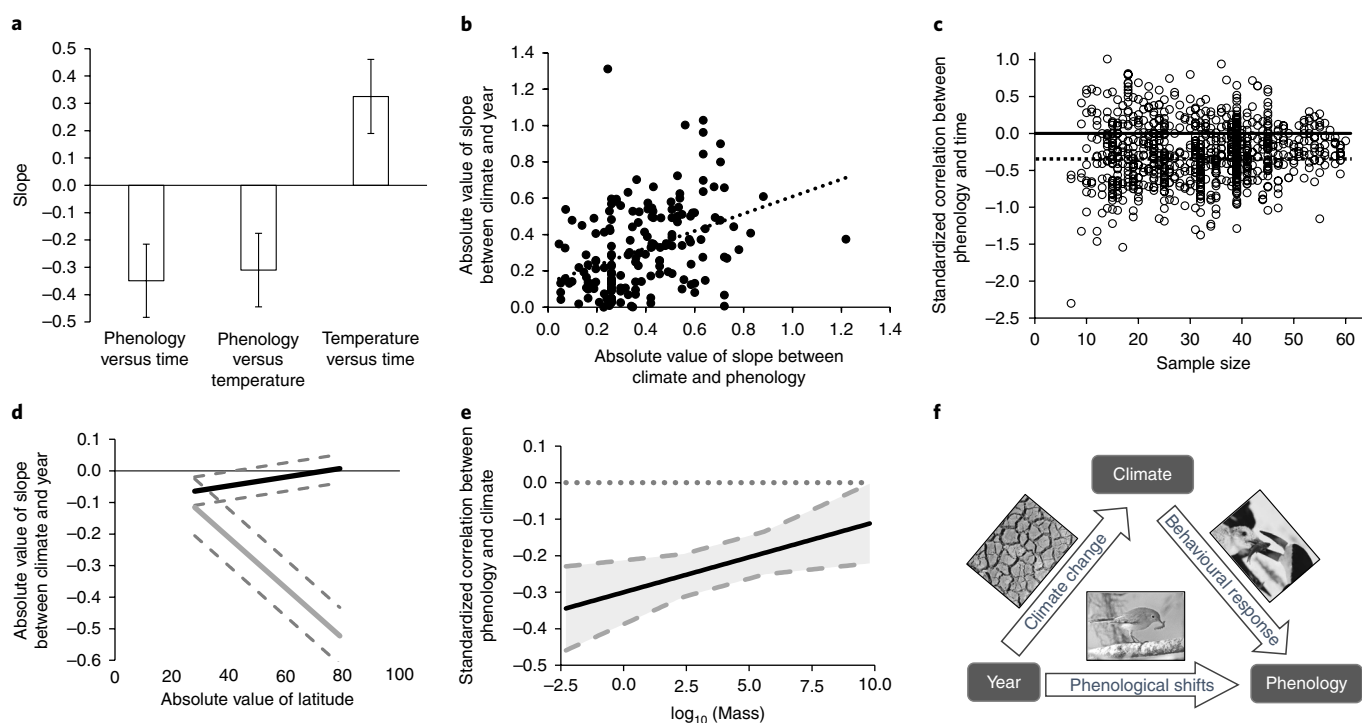


Fig. 1 | Improving how we understand advancements in phenology due to climate change. **a**, Across 1,011 time series, phenology occurred earlier through time as temperature increased and the increases in temperature were negatively correlated with phenology (see Supplementary Fig. 3 for precipitation). Error bars represent s.e.m. **b**, Phenology was more closely linked with mean temperature (x axis) in areas with more climate change (y axis; $R^2 = 0.152$, d.f. = 175, $P < 0.0001$). **c**, A funnel plot comparing sample sizes (total years in time series) with standardized effect sizes (correlation between phenology and time quantified via Fisher's z effect sizes (standard score)) reveals that studies with small sample sizes have large variation with both the positive and negative shifts, suggesting that species that appear to delay their phenology in spring might sometimes be spurious products of sampling error. The solid line is the zero line and the dotted line represents the grand mean effect size (-0.349). **d**, Precipitation becomes more important in driving phenological responses (that is, more negative values) as one moves towards the Equator from temperate regions (orange line with 95% confidence band), whereas temperature becomes important as one moves away from the Equator towards temperate regions (blue line with 95% confidence band; test for different slopes: $P < 0.0001$). Data on time series of phenological shifts close to the equator are unfortunately unavailable. **e**, The slope between log-transformed body mass and the correlation between phenological date and mean temperature is positive in a non-phylogenetically controlled trivariate meta-analysis model, suggesting that smaller organisms might track their phenology with temperature more closely than larger organisms. Data points are not shown to reduce clutter and 95% confidence intervals are provided in grey. **f**, Conceptual figure explaining the meaning of the slope and correlation terms on the other panels, which represent relationships between year, climate and phenology.

documented as drivers of phenological advancements ($\beta = 0.298$, d.f. = 321, $P < 0.0001$ for all time series, $\beta = 0.202$, d.f. = 68, $P = 0.03$ among delays). Alternatively, many apparent spring delays might be sampling artifacts of short annual records. Indeed, a funnel plot revealed that many studies based on short time series (small sample sizes) had both delays and strong advances in phenology, but when sample sizes were large, phenology advanced more uniformly (Flinger–Killeen test for homoscedasticity: $\chi^2 = 112.72$, $P < 0.0001$; Fig. 1c; see Extended Data Fig. 2 for comparisons of effect sizes with variance). In addition, there was no evidence of funnel plot asymmetry (Egger's test: $z = -0.724$, $P = 0.47$), suggesting that the representation of phenological delays in our dataset does not differ from what would be expected by chance. While this result does not exclude true and biologically relevant spring delays in phenology (see examples above), it suggests that reports of delays are probably sensitive to sampling error; in fact, the duration of time series has previously been found to influence observed phenological trends in marine species⁷.

We also hypothesized that phenological shifts would be associated with the climatic variables that drive seasonality locally—such as temperature at mid-latitudes (that is, temperate zones) and precipitation at low latitudes (that is, tropical and subtropical zones). Moreover, because climate change is resulting in greater changes in temperature than precipitation²⁴, we hypothesized greater phenological shifts in temperate than tropical zones. In support of these hypotheses, as the absolute value of latitude increased, changes to temperature became more predictive of the magnitude of phenological shifts, and as latitude decreased, precipitation became a more important predictor of phenology (test for different slopes²⁵: $t = 7.89$, d.f. = 1650, $P < 0.0001$; Fig. 1d; Supplementary Table 5). Further, there was a greater increase in temperature than

precipitation through time (Extended Data Fig. 3), and the correlation between phenology and temperature in the temperate zones was stronger than the correlation between phenology and precipitation near the tropics (Fig. 1d). These results indicate that different climatic variables are triggering phenology in temperate and tropical regions. While past syntheses have hypothesized that species should shift their phenology faster at higher latitudes in response to greater warming in these regions^{2,3,6}, low-latitude species may also be shifting their phenology in response to changes in rainfall. Given that the majority of phenological studies are from northern temperate climates⁷ (especially North America and Europe; Fig. 2), and emphasize temperature over precipitation, additional phenological time series from low latitudes are needed to quantify the full effects of precipitation shifts on tropical phenology. However, the effects of precipitation on phenology may be less closely associated with latitude than the effects of temperature simply because latitude is more strongly correlated with temperature than precipitation.

Given that temperature and precipitation drive phenology unequally across the globe and particular taxa exhibit differential sensitivities to extreme temperatures and moisture levels, we hypothesized that the phenology of specific taxonomic groups might be more strongly associated with temperature or precipitation. For example, we expected amphibians to respond to precipitation more strongly than any other taxonomic group because of their considerable reliance on moist conditions for survival and reproduction. However, across all taxa synthesized, phenology was associated more strongly with temperature than with precipitation (temperature, $\bar{\beta} = -0.310$, d.f. = 1579, $P = 0.02$; precipitation, $\bar{\beta} = -0.054$, d.f. = 1579, $P = 0.54$; Extended Data Fig. 4; Supplementary Table 4), and different components of temperature (mean, minimum and maximum) did not significantly differ from one another at predicting phenology. As

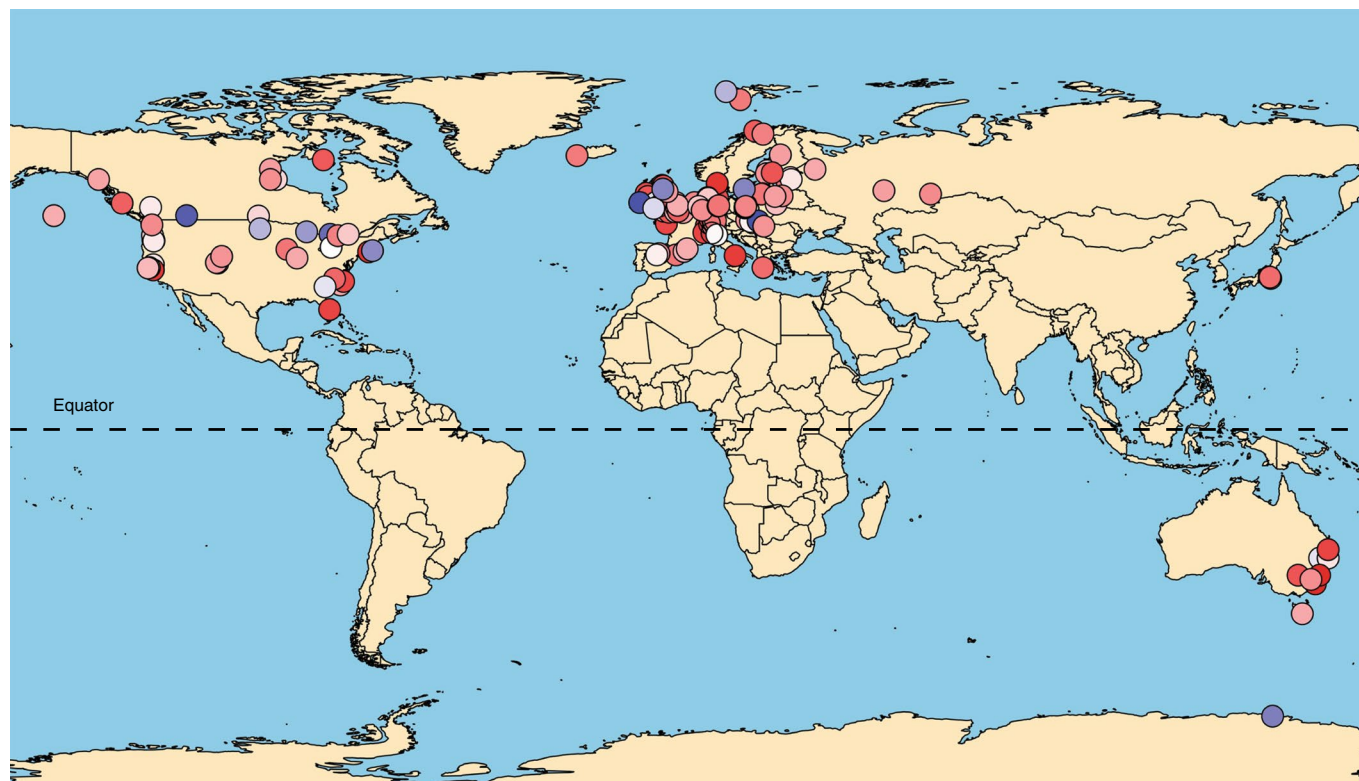


Fig. 2 | The uneven global distribution of published studies exploring the phenology of animals. There are hundreds of published phenological time series from North America and Europe, but much less is known about phenology on the other five continents with particularly large gaps in the tropics and marine systems. Red points indicate advancements in phenology over time and blue points indicate delays. The strength of the color indicates the magnitude of the relationship between phenology and time (as quantified with a Fisher's z effect size).

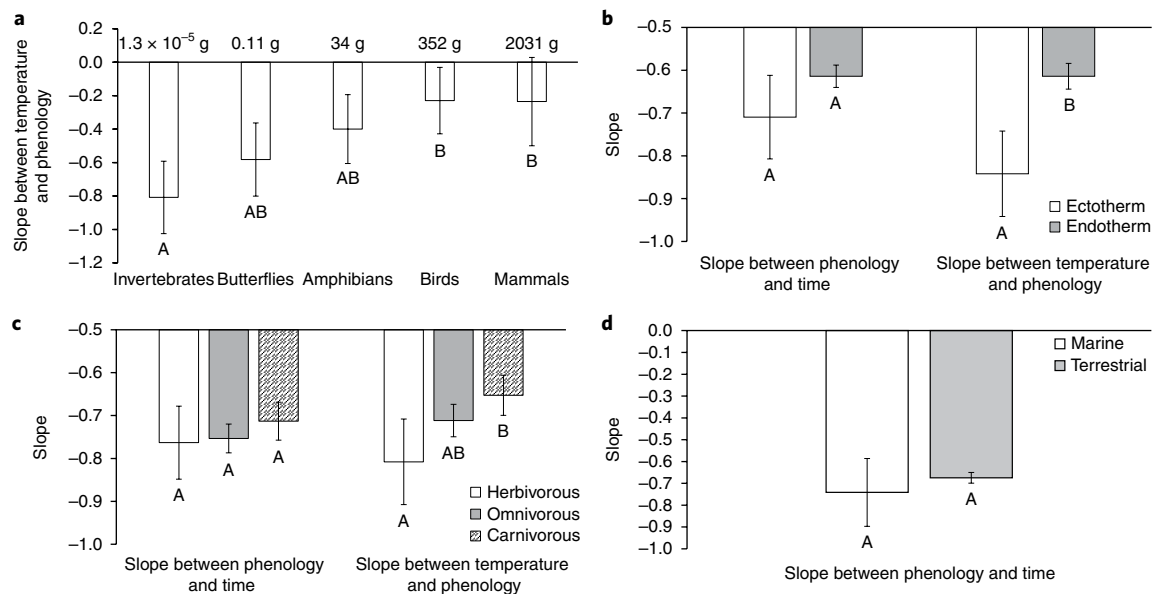


Fig. 3 | The ability of phenology to track temperature varies among taxonomic classes of animals, ecto- or endothermy, and trophic level. a–b, In models including body size and ecto- or endothermy as covariates, smaller taxa (**a**) and ectotherms (**b**) tracked temperature closer than larger animals and endotherms. Generally, taxa with smaller body sizes shifted at faster rates than larger taxa (mean body sizes are reported above bars). **c,** Herbivores had a greater association between temperature and phenology than carnivores, possibly because herbivores were reacting to shifts in plant phenology associated with temperature. **d,** However, we did not observe a difference in phenological response between terrestrial and marine organisms. We report relationships between phenology and both temperature and time (except in **d**, because we lack climate data for marine organisms) to highlight that even if groups are apparently advancing their phenology at similar rates, they could be responding to changing climates at dissimilar rates if they come from regions that are experiencing different rates of climate change. Error bars represent the s.e.m. for the slope parameters from trivariate mixed-model meta-regressions. Different letters denote statistically significant differences in effect sizes.

predicted, amphibians exhibited the strongest association between precipitation and phenology among all taxa ($\bar{\beta} = -0.172$, d.f. = 1564, $P = 0.16$; Extended Data Fig. 4b; Supplementary Table 6). Although Thackeray et al. found that amphibian phenology was not sensitive to precipitation in the UK¹, this might only be the case at high latitudes where the effects of precipitation are less pronounced.

Next, we sought to identify general ecologically important characteristics of taxa that might predict the strength of phenological responses to climate change. Here, we hypothesized that ectotherms and smaller organisms should be more sensitive to shifts in climate than endotherms and larger organisms (because thermal inertia is positively associated with body size²⁶; J.R.R., manuscript in preparation). When we tested for the effects of body size in a phylogenetically controlled model, there was no significant effect of body size, at least partly because body size is correlated with phylogeny (for example, almost all birds have greater mass than all insects). However, smaller invertebrate groups advanced their phenology faster than larger vertebrates (Fig. 3a; Supplementary Table 7); non-insect invertebrates (mean body mass: 5.3×10^{-6} g) advanced their phenology 4.93 days per decade, insects (0.15 g) advanced 4.15 days per decade, amphibians (34 g) advanced 3.23 days per decade and birds (352 g) advanced 2.24 days per decade. In addition, body size was a significant predictor of phenological shifts in a model without phylogenetic controls ($\beta = 0.0544$, d.f. = 921, $P < 0.01$), suggesting that it may be a factor influencing the strength of phenological shifts. As predicted, the phenology of ectotherms was more strongly correlated with temperature than the phenology of endotherms (Fig. 3b; Supplementary Table 7), even when controlling for phylogeny. Finally, herbivore phenology tracked temperature

more closely than carnivore phenology (Fig. 3c; Supplementary Table 7), possibly because herbivores are also responding to shifts in the timing of plant phenology²⁷, and supporting similar conclusions by Thackeray et al. in the UK¹. Additionally, we did not observe a difference between the phenological responses of terrestrial and aquatic species (Fig. 3d; Supplementary Table 7), although there are admittedly few aquatic species in the dataset (18 total) and all are marine.

Finally, we posited that the type of phenological responses, such as peak seasonal abundance, arrival (migration) and breeding/rearing (calling, nesting, laying, hatching or weaning), may differ in their sensitivities to climate change, as recently concluded by a synthesis on marine systems⁷. We predicted that arrival would be least correlated with climatic factors because migrants are probably reacting to climatic conditions where they left from rather than conditions where they are arriving²⁸. Phenological responses related to arrival tracked climate the most poorly (Extended Data Fig. 5; Supplementary Table 8), and those based on peak abundance tracked temperature changes the most closely—possibly because peak abundance is more often documented with smaller invertebrates that phenologically respond strongly to climate. Unfortunately, because there are very few phenological time series from equatorial regions, and arriving species often come from multiple departure locations, we could not test whether the timing of departures for spring migrations tracked temperature better than arrivals (but see ref. ²⁹).

Our findings add to the growing evidence of direct ecological consequences of climate change on ecological systems and provide strong evidence linking climate change to phenological shifts.

Our synthesis unveiled previously unidentified generality in the phenological responses of organisms to climate, indicating that the phenology of species at high latitudes most strongly responds to temperature, while species at lower latitudes are responding to temperature and precipitation equally; thus, different components of climate drive phenology in different regions of the globe. We also found that different taxa respond to the same climatic signals but do so at different rates, and that the strength of these phenological shifts may be predictable based on two easily measured traits: thermoregulation and body size. As climate change intensifies in the next century, our results suggest that advances in phenology are likely to become more exaggerated, potentially further desynchronizing interactions between species that vary considerably in their body sizes, such as mutualistic, predator–prey, and host–parasite interactions. However, the synthesis presented here now equip climate biologists with knowledge regarding the specific components of climate and the traits of interacting species that can drive phenological shifts, providing new opportunities to forecast mismatches and mitigate their adverse effects.

Methods

Methods, including statements of data availability and any associated accession codes and references, are available at <https://doi.org/10.1038/s41558-018-0067-3>.

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Author contributions

J.M.C., M.J.L., and J.R.R. contributed ideas and devised the analyses. J.M.C. assembled the database of phenological time-series and collected climate data. M.J.L. designed and conducted the analyses. J.M.C., M.J.L. and J.R.R. wrote the paper.

Competing interests

The authors declare no competing interests

Additional information

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Methods

Literature survey and data requirements. We conducted a literature search in September 2012 on Web of Science for the term ‘phenology AND climate’ within the following fields: environmental sciences and ecology, zoology, developmental biology, reproductive biology, life sciences (other), entomology, behavioural sciences, physiology, biodiversity and conservation, fisheries, evolutionary biology, parasitology, marine and freshwater biology, infectious diseases and oceanography. This search generated 6,989 studies that were examined for phenological time series. References in these papers and the USA National Phenology Network (<https://usanpn.org>) database were also examined for time series. Time series were not used if they: (1) contained data spanning <10 yr; (2) contained data for fewer than seven individual years; (3) described autumn migrations; or (4) described data that were redundant with data we had already compiled from another paper. We also eliminated raw data from before 1950, because this is considered to be before significant global climate change³⁰. Our exclusion criteria are similar to those from previous meta-analyses^{1,2}.

Data extractions. We extracted raw time series data from figures plotting day of year of phenological event (including date of first or median arrival, first calling, nesting, laying, peak abundance, oestrus, or weaning) against year using Datathief III Version 1.6 (Bas Tummars). Correlation coefficients between phenological date and year, standard errors or surrogates, and slopes were also calculated for each time series when they were not reported in the original text (all analyses were conducted in R 3.1.0; stats package, glm function). Correlation coefficients (r) and standard deviations were available for 1,011 of these time series (representing 127 studies) that were used in the meta-analysis examining the relationship between phenology and year. Approximately 400 time series from about 100 papers provided raw data and were used in the meta-analyses examining the relationships between phenology, year and climate (the actual numbers varied between different climate variables because some variables were not available at certain geographic locations). Sampling variances (used as weights) were derived from all correlation coefficients, and coefficients and variances were standardized using Fisher's z -transformation before all meta-analysis modelling.

External climate data. Climate data were obtained from the NOAA National Climatic Data Center (NCDC; www.ncdc.noaa.gov) worldwide database of monthly observational data corresponding to the nearest location (within 100 km) and all years in every time series that provided raw data and geographic coordinates. Ten climate variables were obtained for each site and year (see Extended Data Fig. 4) and they generally were related to temperature or precipitation. Climate variables were used individually in models instead of as covariates (see below). Yearly averages of climate variables were compiled for all variables in all locations and for the years in all time series only when data were available for all 12 months. Within each time series, correlation coefficients and standard errors were compiled for all correlations between all annual climate variables year, all climate variables and phenology, and phenology and year (stats package, glm function). We did not have any climate data for marine species and did not include these time series in any analyses testing the effects of climate.

Independent fixed-effects variables. Independent variables collected for each time series included taxonomic classification of the focal species, absolute value of latitude, elevation, form of thermoregulation (ectothermy or endothermy), trophic level, habitat (terrestrial or marine), country (to control for geography), log-transformed body mass (see below) and type of phenological event (endpoint measured). Taxonomic classification was assessed to the class level. Elevation specific to the locations where time series were observed was extracted from Worldclim elevation rasters (www.worldclim.org) (raster package, extract function). Trophic levels were assigned categorically as ‘herbivore’, ‘omnivore’, or ‘carnivore’. If a species typically eats plants and animals it was designated an omnivore, but if it mostly relies on either prey or plants and only occasionally ate the other, it was assigned to ‘carnivore’ or ‘herbivore’ respectively. Phenological events were categorized as either ‘arrival’ (migrations), ‘breeding/rearing’ (calling, nesting, laying, hatching, or weaning) or ‘peak abundance’ (peak population abundance).

Meta-analysis models. A trivariate mixed-effects meta-analysis was used to analyse three effect sizes per study that jointly quantify the pairwise relationships among phenology, time and a single climate variable (Fig. 1f). Preserving the trivariate structure of effect sizes has the advantage of accounting for the correlations within the three non-independent effect sizes (because of sampling variability and covariances), while also explicitly accounting for any existing correlations among these three effect size groups (via a multivariate random-effects model). Our overall model had a hierarchical structure in which we modelled the sampling variances and covariances among the three effect sizes (within-study weighting to account for study sampling error), between-study random-effects for each effect size triplicate that were allowed to be correlated but differ among groups (that is, a multivariate version of the between-study variance component typically included in traditional random-effects meta-analysis) and finally an

unstructured random-effect modeling the phylogenetic correlations among taxa (see Supplementary Code). For all models, the *rma.mv* function from the R package *metafor*³¹ was used, with the variance–covariance matrix as the variance–covariance matrix of the sampling errors, and all random effects (trivariate between-study variances, and phylogenetic) were based on restricted maximum likelihood estimator using a nlminb numerical optimizer. However, we did not include phylogenetic random-effects in our initial analysis of the relationship between phenology and body size because phylogeny and body size are highly correlated and thus controlling for phylogeny also indirectly eliminates much of the body size variation. See Supplementary Code for the R script used in these analyses.

Species-level body mass data. We collected species-level body masses from several existing datasets and sources^{32–40}. We calculated mass based on body length for some insects as described by previous studies^{41,42} when we could not find published estimates of body mass. For species for which we could not obtain or calculate reliable body mass data (including several amphibian and invertebrate species), we estimated mass by taking the mean of the mass of species in the lowest taxonomic level occupied by that species. Although this method is relatively coarse, we were not concerned about obtaining highly specific values of mass because across the organisms in our dataset mass varied by >10 orders of magnitude and mass was log-transformed in our analyses. To plot the relationship between body mass and phenology, we used the ggplot2 package⁴³, ggplot function.

Trivariate mixed-effects meta-regression model. In matrix notation, our trivariate and phylogenetic mixed-effects meta-analysis can be described with this regression model:

$$\mathbf{z} = \mathbf{M}\mathbf{W}\boldsymbol{\beta} + \boldsymbol{\varepsilon} + \mathbf{M}\mathbf{u} + \sigma_p^2\mathbf{P}\mathbf{J}, \quad (1)$$

where \mathbf{z} denotes a $(k \times 1)$ column vector containing all of the k number of effect sizes. For each i th of m number of studies there can be three effect sizes (specifically Fisher's Z transformed correlation coefficients): the standardized correlation ($Z_{t,p}$) between time (t) and phenology (p), the correlation ($Z_{t,c}$) between time and the climate variable (c) and the correlation between phenology and the climate variable ($Z_{p,c}$). Therefore \mathbf{z} can have length $k = m \times 3$. However, for some climate variables, data were incomplete such that $Z_{t,c}$ and $Z_{p,c}$ could not be calculated. The indicator matrix \mathbf{M} models this availability of effect sizes among studies. It has a block diagonal design with its main diagonal defined by \mathbf{I} , a vector whose i th elements are either a 3×3 identity matrix when the three effect sizes are available or a 1×1 identity matrix when otherwise (for example, designating studies with only $\delta_{t,p}$ available). The second matrix in equation (1) (\mathbf{W}) is the regression design matrix of $m \times (p + 1)$ size, with p number of covariates, and where the first column of \mathbf{W} contains only ones (for example, the model intercept). The regression coefficient of this model is defined by $\boldsymbol{\beta}$ which is a column vector of size $(p + 1) \times 3$. Because covariates (predictors) are included in our model and are treated as fixed effects, our meta-analysis model can also be described as a trivariate mixed-effects meta-regression.

The within-study sampling error and sampling covariances (further defined below in the Within study sampling error of trivariate effect sizes section) among the effect sizes is modelled as a block diagonal matrix $\boldsymbol{\varepsilon}$, which on its main diagonal contains the elements of an $m \times 1$ column vector of sampling variance–covariance matrices. The $\boldsymbol{\varepsilon}$ matrix models the weighting of effect sizes based on their sampling error, and models the non-independence of the trivariate effects that share common dependent variables. Also, as assumed by all random-effects meta-analysis, a between-study variance τ^2 component is estimated; however, here our among-study variance component (as well as covariance) is estimated for each of the three main underlying effects. For simplicity, it is assumed that the main effects have the following multivariate normal (MVN) between-study random-effects distribution:

$$\begin{bmatrix} u_{t,p} \\ u_{t,c} \\ u_{p,c} \end{bmatrix} \sim \text{MVN} \left(0 = \begin{bmatrix} 0 \\ 0 \\ 0 \end{bmatrix}, u = \begin{bmatrix} \tau_{t,p}^2 & \tau(t,p), (t,c) & \tau(t,p), (t,c) \\ \text{sym} & \tau_{t,c}^2 & \tau(t,c), (p,c) \\ & & \tau_{p,c}^2 \end{bmatrix} \right) \quad (2)$$

Where u is a 3×3 variance–covariance matrix defining the trivariate between-study variance. Multivariate among-study variance components are estimated via maximum likelihood using the *ram.mv* function in the *metafor* R package. In addition to the multivariate among-study random affects, the phylogenetic effects are modelled as random factor with an unstructured multivariate distribution $\sigma_p^2\mathbf{P}\mathbf{J}$. Here σ_p^2 is the estimated phylogenetic variance, and following ref. ⁴⁴, \mathbf{J} is a secondary indicator matrix that links the phylogenetic correlations (\mathbf{P}) to individual effect sizes and when multiple effect sizes are derived from single species it specifies their shared covariance to one. Finally, \mathbf{P} is the phylogenetic correlation matrix; details about \mathbf{P} are described below under the Non-independence due to shared evolutionary history among taxa section.

Marginally, this trivariate and phylogenetic mixed-effects meta-regression model can be described as:

$$z_i \sim \text{MVN}(\text{MW}\beta, \epsilon + \text{Mu} + \sigma_p^2 P)$$

Within-study sampling error of trivariate effect sizes. We accounted for the non-independence that occurs when combining and comparing multiple effect sizes that share common variables (phenology, climate and year) by including their estimated sampling covariances in the off-diagonals of the variance-covariance ϵ matrix used as weights for meta-analysis (as done in a previous study¹⁹). This ϵ matrix has a block-diagonal design, where each block can represent a 1×1 matrix containing the sampling variance of an effect size (cases where only $Z_{t,p}$ was available for a study), or a 3×3 matrix where its main diagonal contains the sampling variances (var) of each of three Fisher's Z transformed correlation (effect size):

$$\text{var}\left(Z_{t,p} = \text{var}(Z_{t,c}) = \text{var}(Z_{p,c}) = \frac{1}{n-3}\right), \quad (3)$$

where each variance is the predicted sampling variance of the pairwise Fisher's Z transformed correlation for three variables (t , p and c). All correlations share a common sample size (n). The covariance between two Z correlations, for example $Z_{t,p}$ and $Z_{t,c}$, is $\text{cov}(Z_{t,p}, Z_{t,c})$, where $Z_{t,p}$ is the effect size for a correlation between variables time and phenology, and $Z_{t,c}$ is the effect size for the correlation between time and climate. Further, the raw correlations (Pearson product moment correlation coefficient) are needed to estimate these covariances, where for example between t and p the correlation will be $\rho_{t,p}$. Following two previous studies^{45,46}, the covariance between two Fisher's Z effect sizes with a t common dependent variable, $\text{cov}(Z_{t,p}, Z_{t,c})$, is estimated as:

$$\begin{aligned} \text{cov}(Z_{t,p}, Z_{t,c}) \\ = \frac{\rho_{p,c}(1-\rho_{t,p}^2-\rho_{t,c}^2) + 0.5 \times \rho_{t,p} \times \rho_{t,c} \times \rho_{p,c} - 0.5(\rho_{t,p} \times \rho_{t,c})(1-\rho_{t,p}^2+\rho_{t,c}^2)}{(n-3)(1-\rho_{t,p}^2)(1-\rho_{t,c}^2)} \end{aligned} \quad (4)$$

The covariance was estimated for all pairwise correlations among the phenology, time and climate variables. For example, the variance-covariance matrix for i th of the effect size triplicates can be described with this symmetric matrix:

$$\begin{bmatrix} \text{var}(Z_{t,p}) & \text{cov}(Z_{t,p}, Z_{t,c}) & \text{cov}(Z_{t,p}, Z_{p,c}) \\ \text{cov}(Z_{t,p}, Z_{t,c}) & \text{var}(Z_{t,c}) & \text{cov}(Z_{t,c}, Z_{p,c}) \\ \text{cov}(Z_{t,p}, Z_{p,c}) & \text{cov}(Z_{t,c}, Z_{p,c}) & \text{var}(Z_{p,c}) \end{bmatrix} \quad (5)$$

The matrices for each i th study were then stacked diagonally into a single matrix for meta-analysis (ϵ). When needed, individual matrices described in equation (5) that were not positive definite were fixed following an earlier work⁴⁷.

Testing for impacts of shorter winters on spring phenological delays. We examined whether the magnitude of a phenological delay could be positively predicted by an increase in winter temperatures (defined as the relationship between year and average temperature during the year's three coolest consecutive months), controlling for latitude (glm function, stats package). We tested this using the full dataset and a subset containing only time series with delayed phenology (positive relationships between phenology and year). We also tested whether winter warming correlated with spring warming (change in average temperature in three months following 'winter' over time), also controlling for latitude.

Funnel plot statistics. To evaluate our funnel plot (Fig. 1b) for asymmetry in effect sizes (slopes of phenology versus year), we conducted an Egger's regression test for funnel plot asymmetry (*regtest* function, *metafor* package). To test whether the variance in effect sizes decreased with increasing sample size, we conducted a Fligner-Killeen test of homogeneity of variances (*fligner.test* function, *stats* package).

Non-independence due to shared evolutionary history among taxa. To account for the correlational structures among taxa due to their shared evolutionary history²³, we treated the phylogenetic correlations (P) derived from a composite phylogenetic tree of all taxa in our study (see equation (1)) as an unstructured random-effect in our trivariate meta-regressions. These phylogenetic correlations in P were extracted from an ultrametric tree using the *vcv* function of the *ape* package in R⁴⁸, and explicitly assume trait evolution via Brownian motion⁴⁹. Our composite phylogeny of all 475 species used the topology and internode divergence times from published sources when available. The deep divergence times among phyla

were based on ref.⁵⁰. Among vertebrates, the topology and estimated divergence times among fish were compiled from ref.⁵¹, mammals from ref.⁵², and amphibians from refs.^{53,54}. The topology and divergence times among birds were derived from a random sample of the Bayesian tree pool provided by the online avian phylogeny generating tool⁵⁵. Among invertebrates, the topology and divergence times among hexapods, calanoids and branchiopods were based two previous studies^{56,57}. The topology and divergence times among insect orders were compiled using an earlier work⁵⁸. However, within insect orders topologies were only available for moths and butterflies^{57,59,60}, and dragonflies and damselflies⁶¹. Because the divergence times within Lepidoptera and Odonata were unavailable, we arbitrarily scaled branch-lengths distances using a published method⁴⁹ while assuming ρ to the power of 1.0 to create divergence times fitting a Brownian motion model of evolution.

Code availability. The code used to generate trivariate model results is available as Supplementary Code.

Data availability. The data that support the findings of this study are available from the corresponding author upon request.

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A global synthesis of animal phenological responses to climate change

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9 **Supplementary Information Guide:**

10 Supplementary Discussion

11 Supplementary Figures S1-S6

12 Supplementary Tables S1-S8

13 Supplementary Code

14 Supplementary References

15 PRISMA Checklist

16 **Supplementary Discussion**

17 *Use of annual climate data in models.* For each phenological time series, we originally extracted both mean annual climate data and
18 mean climate data for the month prior to the average phenological date in the time series (seasonal data). We chose to use annual,
19 rather than seasonal, climate data because we did not want to bias the models with climate from the specific month that the phenology
20 of a given species was measured. For example, insect phenology might be routinely measured later in the year than avian phenology
21 because of different methodological approaches by different researchers or different measured phenological activities. In this scenario,
22 climate data from cooler seasons may be disproportionately represented in conjunction with avian time series and imply that they are
23 responding to different conditions than insects. Further, we were comfortable using annual climate data in our models because it
24 correlates strongly with spring data ($R^2=0.93$, $p<0.00001$ across our time series; Extended Data Fig. 6). Finally, our effect sizes are
25 based on inter-annual trends in phenology—finer scale monthly phenological data are not consistently available across species and
26 thus would drastically reduce our sample sizes.

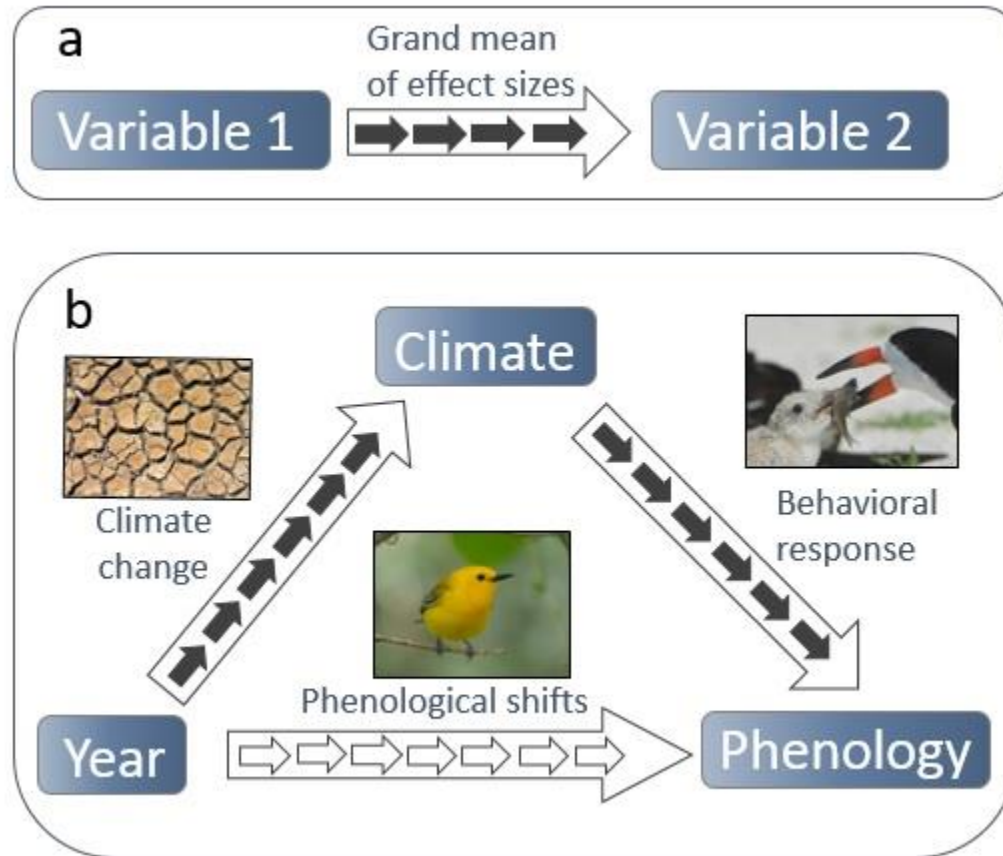
27 Future analyses should also explore effects of intra-annual trends. However, when approaching analyses at this finer scale, it
28 requires a detailed understanding of how short-term variability influences long-term variability—however, identifying the mechanisms
29 for these fine-scale sources of variability across many phenological datasets can be challenging. Presently, by examining inter-annual
30 trends, we were able to focus on broad-scale sources of variability, such as climate change and geographic variability in effects of
31 climate change.

32

33 *Use of animal phenological data.* The primary question that initially motivated the meta-analysis concerned the nature of the
34 relationship between phenological shifts and body size, given that there is evidence that small organisms acclimate to new conditions
35 faster than larger organisms^{1,2}. However, body size questions are challenging to address using plants because below-ground mass is
36 often difficult or impossible to quantify and some plants grow clonally, making the definition of an individual unclear. Other
37 questions, such as the influence of thermoregulation on phenology, also could not be addressed using plants because none are
38 endothermic. Thus, we initially created our dataset with animal records of phenological shifts only.

39

40 **Supplementary Figures**

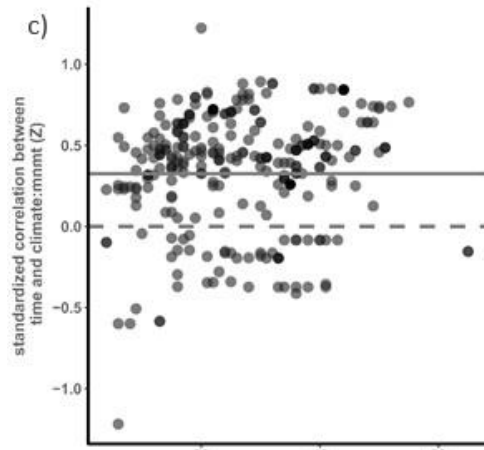
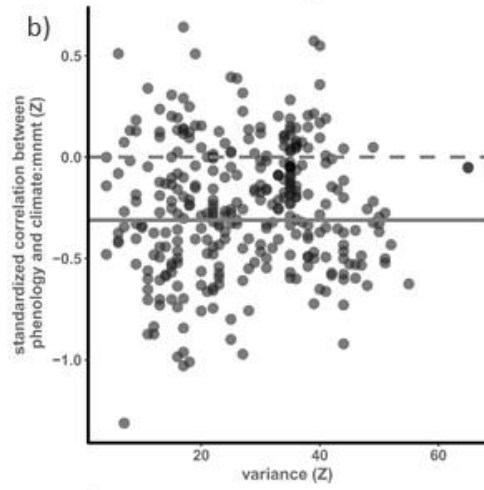
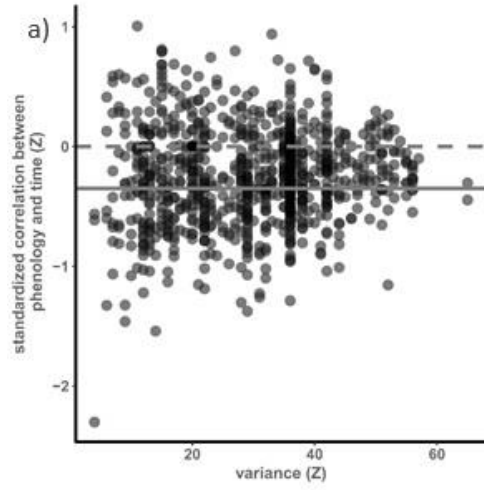


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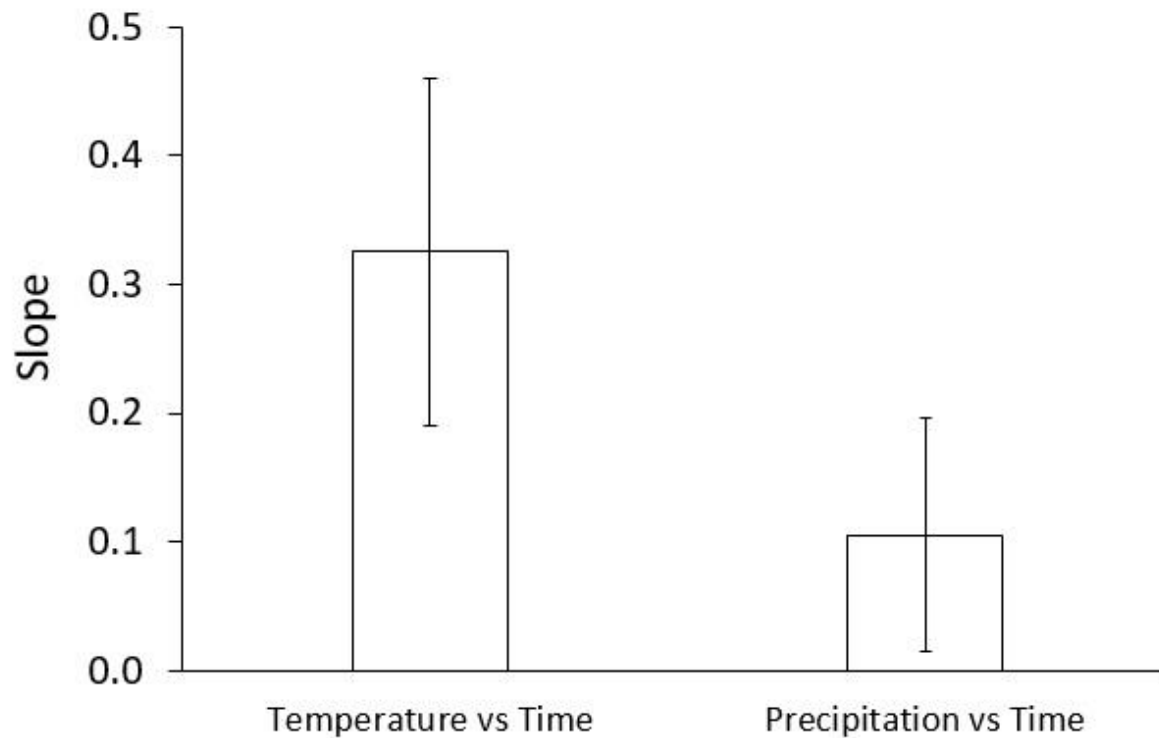
42 **Supplementary Figure 1. Structure of trivariate meta-analysis examining the relationship between phenology, climate, and**
 43 **year.** Conceptual schema contrasting the structure of (a) a typical (univariate) meta-analysis summarizing the relationship
 44 (correlation) between two variables using the grand mean of one effect size (large arrows) composed of many effect sizes reported in
 45 the literature (small arrows) and (b) the trivariate meta-analysis used in this study which summarizes the relationship among three
 46 variables using three effect sizes (standardized correlations). Filled arrows represent direct effects (i.e., the effect of climate on
 47 phenology) and open arrows represent indirect effects (i.e., the effect of year on phenology). This trivariate meta-analysis allowed us

48 to jointly analyze the three effect sizes quantifying the pairwise relationships between phenology, time, and climate. Further, it
49 enabled us to account for the correlations within the three non-independent effect sizes (because of common sampling variability),
50 while also explicitly accounting for any existing correlations among them (via a multivariate random-effects model). See Methods for
51 further details.

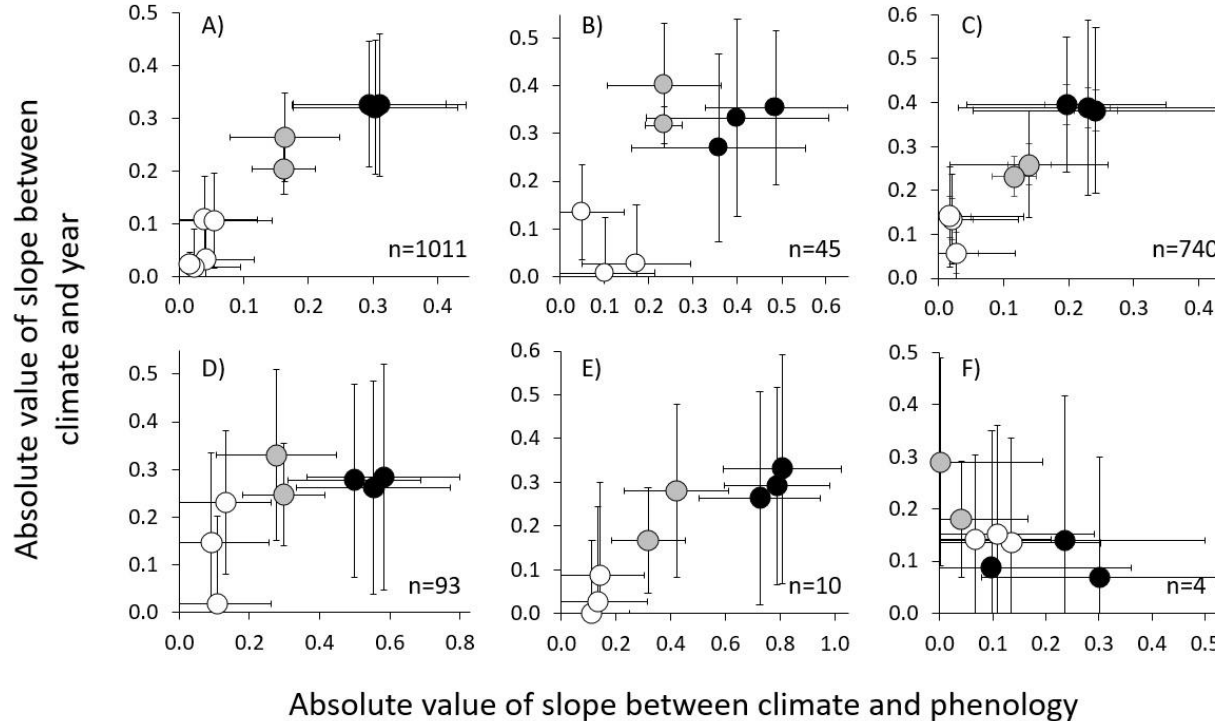
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54 **Supplementary Figure 2. Funnel plots of the three effect size datasets used in the trivariate meta-analysis.** Depicted are variance
55 and z-scores of the correlation coefficients describing the relationships between (a) phenology and year, (b) phenology and annual
56 mean temperature, and (c) year and annual mean temperature. Dashed lines are the null effect (0.0) and solid lines are the grand mean
57 effect sizes from a trivariate meta-analysis corrected for phylogenetic history.



Supplementary Figure 3. Shifts in climate variables over time. In the locations of the time series in this study, mean temperature and total precipitation both increased over time, but temperature increased more than precipitation. Because recent major shifts in temperature have occurred alongside phenological advancements, the two phenomena have been closely associated with each other. Error bars represent standard errors.

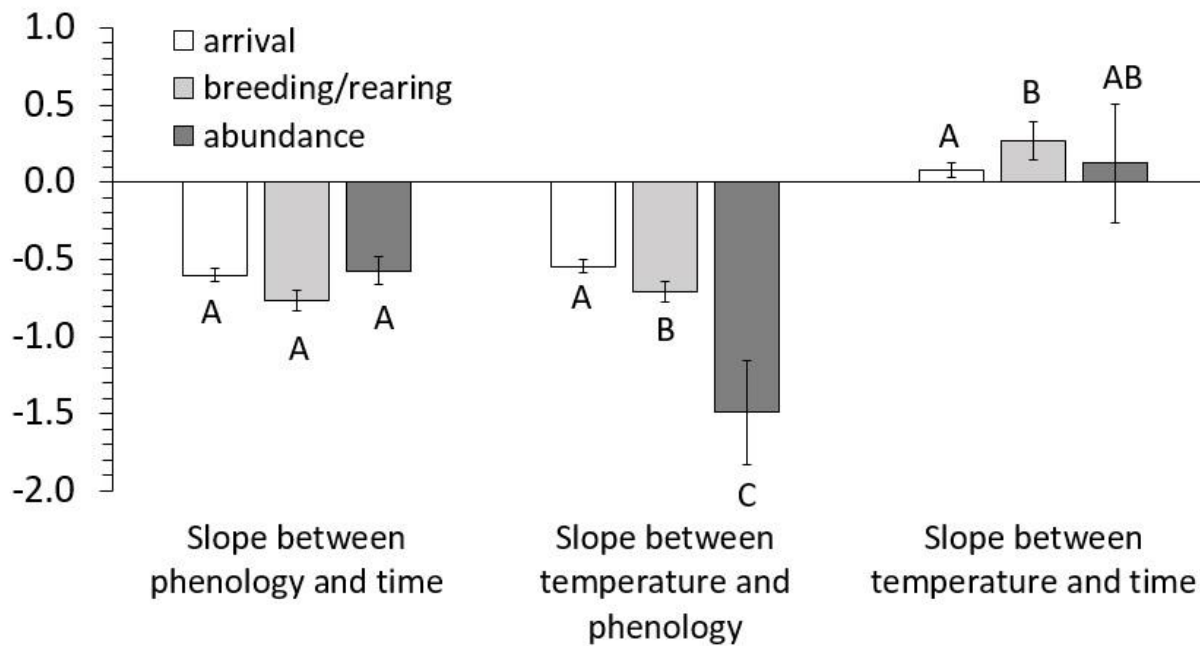


Supplementary Figure 4. Generality of climatic conditions influencing changes in phenology. Absolute values of grand means of slopes between phenology and climate (x-axis) and between climate and time (y-axis) for the ten climatic variables used in the analysis (points). Variables that changed over time and were predictive of animal phenology appear in the upper right-hand corner, while variables that did not change much over time and did not match animal phenology well appear in the lower-left corner. Error bars represent standard errors for the regression slope parameters. We plotted absolute values to highlight the magnitude (rather than the direction) of the effect, because different climate variables affect phenology in different directions. We found a strong relationship between temperature variables (black circles) and phenology for (a) all taxa, (b) amphibians, (c) birds, and (d) butterflies. Relationships between temperature and phenology for (e) non-insect invertebrates and (f) mammals are presented as well. Meanwhile, relationships between phenology and precipitation variables (white circles) and precipitation and time were generally weaker than relationships between phenology and temperature variables and temperature and time, respectively. Of all the taxonomic groups, only amphibians had a significant relationship between precipitation (white circles) and phenology, but precipitation was still a weaker

76 predictor of amphibian phenology than temperature. Gray circles represent variables derived from temperature (see methods for a list
77 of variables in each category).

78

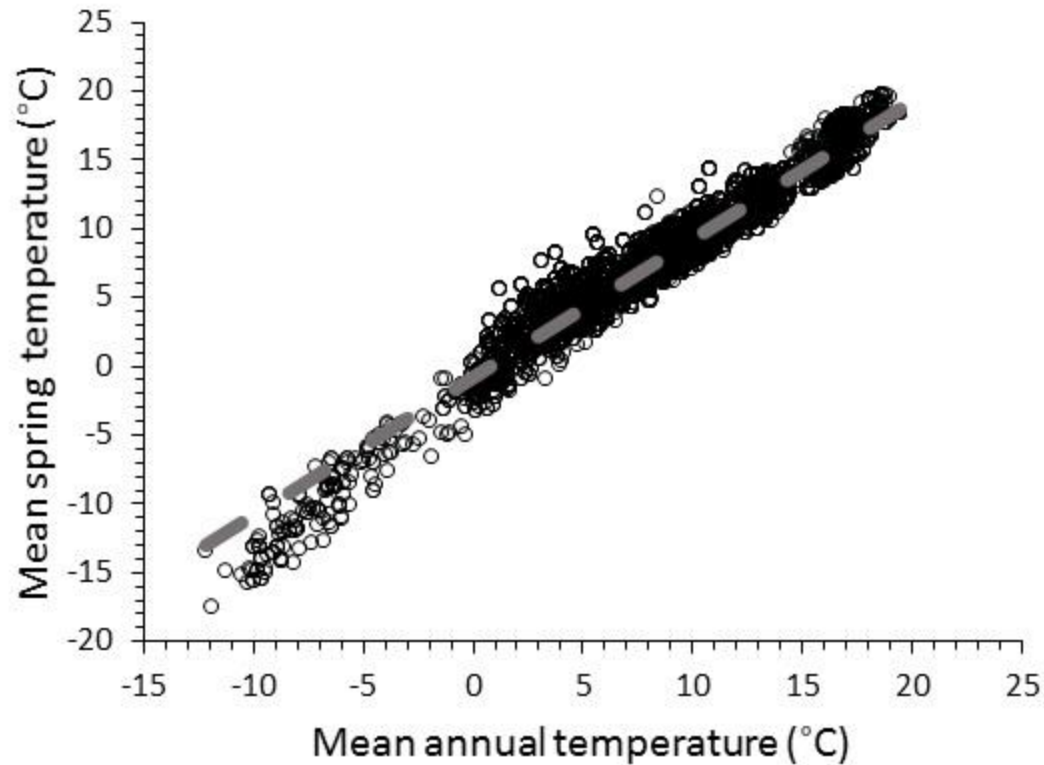
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80

81 **Supplementary Figure 5. Different types of phenological events respond differently to climate change.** We categorized
 82 phenological events as associated with either “arrival” (migration), “breeding/rearing” (calling, nesting, laying, hatching, weaning), or
 83 “abundance” (time of peak abundance). Controlling for body size, abundance phenology tracked temperature change more closely
 84 than arrival or breeding/rearing endpoints. Breeding/rearing phenology was more closely tied to temperature than arrival phenology,
 85 possibly because arrival phenology is dependent on the climatic conditions in the region from where the species was overwintering,
 86 which were not included in the analyses. Error bars represent standard errors for the slope parameters.

87



88

89 **Supplementary Figure 6. Relationship between spring and annual climate data.** Mean annual temperature (used in our analyses)
90 correlates strongly with mean spring temperature (mean of three months following three consecutive coldest months) across all of the
91 time points in our dataset ($R^2=0.93$, $p<0.00001$). We used annual data in our analyses for several reasons outlined in the
92 Supplementary Discussion.

93

94 **Supplementary Tables**

95 **Table S1. List of studies and time-series collected for meta-analysis.** Papers were included in the meta-analysis if they satisfied the
96 basic requirements detailed in Methods and provided raw time-series data on phenological date. Papers were included in the trivariate
97 meta-analysis (including climate in models) if they were at specific sites with locally corresponding terrestrial NOAA climate data
98 (papers not included are denoted with *). N indicates the number of time-series in the paper. The shift column indicates the median
99 days-per-decade shift among papers in the study.

Paper	Event	N	Class	Country	Time Span	Shift
Abraham and Sydeman 2004 ³	breeding	1	Aves	USA	1973- 2001	5.17
Adamik and Pietruszkova 2008* ⁴	arrival	1	Aves	Czech Republic	1964- 2004	-2.02
Adamik and Pietruszkova 2008* ⁴	arrival	1	Aves	Czech Republic	1964- 2004	-2.64
Ahas et al 1999 ⁵	arrival	1	Aves	Estonia	1952- 1996	-2.89
Ahola et al 2004 ⁶	arrival	1	Aves	Finland	1970- 2002	-2.66
Ahola et al 2004 ⁶	arrival	1	Aves	Finland	1970- 2002	-1.16
Ahola et al 2004 ⁶	breeding	1	Aves	Finland	1970- 2002	0.35
Anthes 2004 ⁷	arrival	1	Aves	Germany	1969- 2002	-2.95
Askeyev et al 2007 ⁸	arrival	4	Aves	Russia	1957- 2004	-0.46
Askeyev et al 2009a ⁹	arrival	1	Aves	Russia	1950- 2008	-1.49
Askeyev et al 2009b ¹⁰	arrival	4	Aves	Russia	1957- 2008	-0.94
Barbraud and Weimerskirch 2006 ¹¹	arrival	9	Aves	Antarctica	1951- 2005	2.48
Barbraud and Weimerskirch	breeding	5	Aves	Antarctica	1953-	0.24

2006 ¹¹					2001	
Barett 2002 ¹²	arrival	2	Aves	Norway	1978-2000	-0.35
Bauer et al 2010 ¹³	breeding	2	Aves	Czech Republic	1961-2007	-1.89
Bauer et al 2010 ¹³	arrival	1	Insecta	Czech Republic	1961-2007	-1.61
Beaumont et al 2006 ¹⁴	arrival	16	Aves	Australia	1960-2004	-7.25
Beebee 1995a ¹⁵	arrival	6	Amphibia	England	1978-1994	-1.78
Beebee 1995b ¹⁶	arrival	1	Amphibia	England	1978-1994	-2.02
Bertram et al 2001 ¹⁷	breeding	4	Aves	Canada	1975-1999	-
Blaustein et al 2001 ¹⁸	arrival	7	Amphibia	North America	1967-1999	11.44
Both and Visser 2001 ¹⁹	arrival	1	Aves	Netherlands	1980-2000	-0.58
Both and Visser 2001 ¹⁹	breeding	1	Aves	Netherlands	1980-2000	2.8
Both et al 2005a ²⁰	breeding	1	Aves	Netherlands	1950-2003	-4.03
Both et al 2009 ²¹	breeding	5	Aves	Netherlands	1985-2005	-1.83
Both et al 2009 ²¹	abundance	1	Insecta	Netherlands	1985-2005	-3.15
Bradley et al 1999 ²²	arrival	4	Aves	USA	1977-1998	-7.60
Carroll et al 2009* ²³	arrival	1	Amphibia	UK	1998-2007	-0.98
Chadwick et al 2006 ²⁴	arrival	2	Amphibia	England	1981-2005	4.79
Chadwick et al 2006 ²⁴	arrival	2	Amphibia	England	1981-2005	-6.43
Corn and Muths 2002 ²⁵	arrival	1	Amphibia	USA	1986-	-8.47
						-3.35

					2001	
Costello et al 2006* ²⁶	arrival	1	Maxillopoda	USA	1951-2003	2.85
Costello et al 2006* ²⁶	arrival	1	Tentaculata	USA	1950-2003	-14.4
Cotton 2003 ²⁷	arrival	1	Aves	England	1972-2000	-6.71
Cresswell and McCleery 2003 ²⁸	breeding	1	Aves	England	1960-1999	-2.4
Cresswell and McCleery 2003 ²⁸	breeding	1	Aves	England	1960-1999	-1.91
Crick and Sparks 1999* ²⁹	breeding	1	Aves	UK	1950-1995	0.61
Crick et al 1997* ³⁰	arrival	3	Aves	UK	1971-1995	-6.67
Croxton et al 2006 ³¹	arrival	10	Aves	England	1959-2005	-2.79
D'Alba et al 2010 ³²	breeding	1	Aves	Iceland	1977-2006	-2.86
Dell et al 2005 ³³	arrival	1	Insecta	Switzerland	1982-2002	-8.27
Dufour et al 2010* ³⁴	arrival	2	Actinopterygii	France/Spain	1967-2005	-5.82
Dufour et al 2010* ³⁴	arrival	2	Actinopterygii	France/Spain	1967-2005	-3.32
Dunn and Winkler 1999* ³⁵	arrival	1	Aves	USA	1959-1991	-2.86
Dyrce and Halupka 2009 ³⁶	breeding	1	Aves	Poland	1970-2007	-3.08
Elliot 1996 ³⁷	arrival	1	Insecta	England	1966-1995	-1.90
Elliot 1996 ³⁷	arrival	1	Insecta	England	1966-1995	-1.50
Forister and Shapiro 2003 ³⁸	arrival	1	Insecta	USA	1972-2002	-1.18
Gaston et al 2009 ³⁹	breeding	1	Aves	Canada	1990-	-2.71

					2007	
Gillet and Quentin 2006* ⁴⁰	arrival	1	Actinopterygii	France	1983-2001	-10.4
Gordo and Sanz 2005 ⁴¹	arrival	5	Aves	Spain	1950-2004	-3.16
Gordo and Sanz 2006* ⁴²	arrival	5	Aves	Spain	1950-2004	-0.8
Gordo and Sanz 2006* ⁴²	arrival	2	Insecta	Spain	1952-2004	0.57
Gordo et al 2005 ⁴³	arrival	6	Aves	Spain	1952-2003	1.49
Halupka et al 2008 ⁴⁴	breeding	1	Aves	Poland	1970-2006	-4.23
Harrington et al 2007* ⁴⁵	arrival	1	Insecta	Europe	1965-2000	-7.19
Huppopp and Huppopp 2003 ⁴⁶	arrival	6	Aves	Germany	1960-2000	-2.19
Hussell 2003 ⁴⁷	breeding	3	Aves	Canada	1969-2001	-1.66
Inouye et al 2000 ⁴⁸	arrival	1	Aves	USA	1974-1999	-4.26
Inouye et al 2000 ⁴⁸	arrival	1	Mammalia	USA	1976-1999	-10.2
Jarvinen 1989 ⁴⁹	breeding	1	Aves	Finland	1966-1987	-3.10
Jenkins and Watson 2000 ⁵⁰	arrival	2	Aves	Scotland	1974-1999	-
Kanuscak et al 2004 ⁵¹	arrival	1	Aves	Slovakia	1963-2003	10.12
Kennedy and Crozier 2010* ⁵²	abundance	1	Actinopterygii	Ireland	1978-2008	-0.19
Kobori et al 2012 ⁵³	arrival	6	Aves	Japan	1986-2007	-4.72
Koppman-Rumpf et al 2003 ⁵⁴	arrival	1	Mammalia	Germany	1972-1999	2.54
Kusano and Inoue 2008 ⁵⁵	arrival	4	Amphibia	Japan	1976-1999	-14.3
						-2.44

					2007	
Laaksonen et al 2006 ⁵⁶	breeding	1	Aves	Finland	1950-2003	0.35
Lane et al 2012 ⁵⁷	arrival	1	Mammalia	Canada	1992-2011	4.78
Lappalainen et al 2008 ⁵⁸	arrival	2	Aves	Finland	1952-2005	-3.65
Lappalainen et al 2008 ⁵⁸	arrival	1	Amphibia	Finland	1952-2005	-1.44
Lehikonen et al 2004 ⁵⁹	arrival	6	Aves	Finland	1965-2003	-3.32
Ludwichowski 1997 ⁶⁰	breeding	1	Aves	Germany	1979-1995	-8.3
MacInnes et al 1990 ⁶¹	breeding	3	Aves	Canada	1959-1986	-3.35
MacInnes et al 1990 ⁶¹	breeding	3	Aves	Canada	1959-1986	-4.07
Mackas et al 1998* ⁶²	abundance	1	Maxillopoda	Canada	1975-1996	-4.37
Mazaris et al 2008* ⁶³	breeding	1	Reptilia	Greece	1984-2002	-7.12
McCleery and Perrins 1998 ⁶⁴	breeding	1	Aves	England	1950-1997	-1.18
Miller-Rushing et al 2008 ⁶⁵	arrival	2	Aves	USA	1970-2002	0.9
Miller-Rushing et al 2008 ⁶⁵	arrival	2	Aves	USA	1970-2002	-0.96
Mills 2005 ⁶⁶	arrival	4	Aves	Canada	1975-2000	-3.84
Mills 2005 ⁶⁶	arrival	2	Aves	Canada	1975-2000	-3.35
Mitrus et al 2005 ⁶⁷	arrival	1	Aves	Poland	1973-2002	-2.76
Moe et al 2009 ⁶⁸	breeding	2	Aves	Sweden	1963-2008	0.06
Murphy-Klassen et al 2005 ⁶⁹	arrival	4	Aves	Canada	1950-	-1.02

					2001	
					1970-	
Nielsen and Moller 2006 ⁷⁰	breeding	6	Aves	Denmark	2004	-3.31
					1976-	
Ozgul et al 2010 ⁷¹	breeding	1	Mammalia	USA	2008	-1.88
Peintinger and Schuster 2006 ⁷²	arrival	8	Aves	Germany	1970-	
					2003	-4.93
					1952-	
Penuelas et al 2002 ⁷³	arrival	1	Aves	Spain	2000	3.03
					1953-	
Penuelas et al 2002 ⁷³	arrival	1	Insecta	Spain	2000	-2.42
					1973-	
Phillipart et al 2003* ⁷⁴	arrival	1	Bivalvia	Netherlands	2001	-4.39
					1983-	
Ptaszyk et al 2003 ⁷⁵	arrival	1	Aves	Poland	2002	-5.49
					1983-	
Ptaszyk et al 2003 ⁷⁵	arrival	1	Aves	Poland	2002	-0.89
					1980-	
Reading 1998 ⁷⁶	arrival	1	Amphibia	England	1998	-8.12
					1972-	
Reed et al 2009 ⁷⁷	breeding	1	Aves	USA	2005	-1.87
					1982-	
Rubolini et al 2007b ⁷⁸	arrival	4	Aves	Italy	2006	-1.23
					1982-	
Rubolini et al 2007b ⁷⁸	breeding	4	Aves	Italy	2006	-1.94
					1984-	
Sanz et al 2003 ⁷⁹	breeding	2	Aves	Spain	2001	-3.15
					1980-	
Schiegg et al 2002 ⁸⁰	breeding	2	Aves	USA	1998	-3.16
					1975-	
Schluter et al 2010* ⁸¹	arrival	2	Tentaculata	Germany	2004	-18.3
					1975-	
Schluter et al 2010* ⁸¹	arrival	1	Nuda	Germany	2004	-6.60
					1975-	
Schluter et al 2010* ⁸¹	arrival	1	Maxillopoda	Germany	2004	-7.00
Scott et al 2008 ⁸²	arrival	9	Amphibia	England	1994-	-9.53

					2005	
					1994-	-
Sergio 2003 ⁸³	breeding	1	Aves	Italy	2002	11.33
					1954-	
Sims et al 2004* ⁸⁴	abundance	1	Actinopterygii	UK	1965	-30.4
					1957-	
Slater 1999 ⁸⁵	breeding	1	Aves	Wales	1997	-1.47
Sokolov and Gordienko 2008 ⁸⁶	arrival	6	Aves	Russia	1971-	0.01
Sokolov and Gordienko 2008 ⁸⁶	arrival	3	Aves	Russia	2005	0.62
					1971-	
Sokolov et al 1998 ⁸⁷	arrival	34	Aves	Russia	1959-	-1.01
					1996	
Sparks 1999 ⁸⁸	arrival	2	Aves	England	1954-	-2.8
					1996	
Sparks and Braslavska 2001 ⁸⁹	arrival	1	Aves	Slovakia	1961-	2.41
					2000	
Sparks and Mason 2001 ⁹⁰	arrival	2	Aves	England	1950-	-1.84
					1998	
Sparks and Yates 1997 ⁹¹	arrival	1	Insecta	Ireland	1976-	-1.52
					1993	
Sparks et al 2005 ⁹²	arrival	9	Aves	Europe	1959-	-2.73
					2002	
Sparks et al 2005 ⁹²	arrival	9	Aves	Europe	1959-	-3.51
					2002	
Sparks et al 2007b ⁹³	breeding	2	Aves	Europe	1978-	-6.89
					2004	
Sparks et al 2007b ⁹³	arrival	3	Amphibia	UK	1978-	-3.47
					2004	
Sparks et al 2010 ⁹⁴	arrival	1	Insecta	Poland	1985-	-13.4
					2009	
Strode 2003 ⁹⁵	arrival	16	Aves	USA	1950-	-
					2002	0.607
					USA	
Taylor 2008* ⁹⁶	arrival	1	Actinopterygii	(Alaska)	1972-	-2.43
Todd et al 2011 ⁹⁷	arrival	10	Amphibia	USA	2005	1.00
					1979-	

					2008	
Tryjanowski 2001 ⁹⁸	arrival	1	Aves	Poland	1983-2000	-3.4
Tryjanowski et al 2003 ⁹⁹	arrival	2	Amphibia	Poland	1978-2002	-3.34
Visser et al 1998 ¹⁰⁰	breeding	1	Aves	Netherlands	1973-1995	-1.52
Visser et al 1998 ¹⁰⁰	abundance	1	Insecta	Netherlands	1973-1995	-3.74
Waite and Strickland 2006 ¹⁰¹	breeding	1	Aves	Canada	1980-2005	-3.23
Wang et al 2002 ¹⁰²	breeding	1	Aves	USA	1975-1998	-3.63
Wanless et al 2009 ¹⁰³	breeding	13	Aves	UK	1971-2006	0.72
Wanless et al 2009 ¹⁰³	arrival	5	Aves	UK	1971-2006	-3.03
Wanless et al 2009 ¹⁰³	breeding	2	Aves	UK	1979-2006	-1.57
Weatherhead 2002 ¹⁰⁴	breeding	1	Aves	Canada	1974-2000	-0.78
Weishampel et al 2004* ¹⁰⁵	breeding	1	Reptilia	USA	1989-2003	-6.18
Wesolowski and Maziarz 2009 ¹⁰⁶	arrival	1	Aves	Poland	1976-2005	-1.46
Wesolowski and Maziarz 2009 ¹⁰⁶	breeding	1	Aves	Poland	1976-2005	-2.23
Wiebe and Gerstmar 2010 ¹⁰⁷	breeding	1	Aves	Canada	1998-2009	-0.56
Winder and Schindler et al 2004* ¹⁰⁸	abundance	1	Eurotifera	USA	1962-1995	-6.61
Winder and Schindler et al 2004* ¹⁰⁸	abundance	1	Branchiopoda	USA	1977-2002	7.23
Winkel and Hudde 1996 ¹⁰⁹	breeding	2	Aves	Germany	1970-1995	-2.45
Winkel and Hudde 1997 ¹¹⁰	breeding	2	Aves	Germany	1970-	-2.61

1995

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103 **Table S2. List of studies and time-series collected to calculate days-per-decade shift.** Papers were included in our calculation of
104 days-per-decade shift (in addition to the papers in Table S1) if they satisfied the basic requirements detailed in Methods. N indicates
105 the number of time-series in the paper. The shift column indicates the median days-per-decade shift among papers in the study.

Paper	Event	n	Class	Country	Time Span	Shift
Ahas et al 1999 ⁵	arrival	1	Aves	Estonia	1952-1996	1.14
Crick and Sparks 1999 ²⁹	breeding	7	Aves	England	1950-1995	NA
Jenkins and Watson 2000 ⁵⁰	arrival	32	Aves	Scotland	1974-1999	NA
Browne and Aebischer 2003 ¹¹¹	arrival	6	Aves	England	1963-2000	-0.05
Huppopp and Huppopp 2003 ⁴⁶	arrival	18	Aves	Germany	1960-2000	-1.41
Stervander et al 2005 ¹¹²	arrival	36	Aves	Sweden	1952-2002	-0.34
Mills 2005 ⁶⁶	arrival	9	Aves	Canada	1975-2000	-2.38
Mills 2005 ⁶⁶	arrival	9	Aves	Canada	1975-2000	-0.21
Murphy-Klassen et al 2005 ⁶⁹	arrival	92	Aves	Canada	1950-2001	-0.68
Both et al 2005b ¹¹³	breeding	1	Aves	Netherlands	1960-2003	NA
Lehikonen et al 2006 ¹¹⁴	arrival	1	Aves	Finland	1979-2004	NA
Lehikonen et al 2006 ¹¹⁴	arrival	1	Aves	Finland	1979-2004	NA
Zalakevicius et al 2006 ¹¹⁵	arrival	40	Aves	Lithuania	1971-2004	-2.81
Beaumont et al 2006 ¹⁴	arrival	29	Aves	Australia	1960-2004	-1.2
Jonzen et al 2006 ¹¹⁶	arrival	9	Aves	Italy	1980-2004	-2.39

Jonzen et al 2006 ¹¹⁶	arrival	9	Aves	Italy	1980-2004	-2.28
MacMynowski et al 2007 ¹¹⁷	arrival	45	Aves	USA	1969-2003	-2.22
Zalakevicius et al 2007 ¹¹⁸	arrival	20	Aves	Lithuania	1966-2000	-4.61
Sokolov and Gordienko 2008 ⁸⁶	arrival	7	Aves	Russia	1971-2005	-1.58
Vegvari et al 2010 ¹¹⁹	arrival	117	Aves	Hungary	1969-2007	-3.42
Neveu 2009 ¹²⁰	arrival	1	Amphibia	France	1984-2007	NA
Ahas et al 1999 ⁵	arrival	2	Actinopterygii	Estonia	1952-1996	-1.59
Hawkes et al 2007 ¹²¹	breeding	1	Reptilia	USA	1980-2005	NA
Telemeco et al 2009 ¹²²	breeding	1	Reptilia	Australia	1997-2006	NA
Pollard 1991 ¹²³	arrival	1	Insecta	UK	1976-1989	NA
Sparks and Yates 1997 ⁹¹	arrival	9	Insecta	Ireland	1976-1993	NA
Roy and Sparks 2000 ¹²⁴	abundance	35	Insecta	England	1976-1998	-1.66
Forister and Shapiro 2003 ³⁸	arrival	23	Insecta	USA	1972-2002	-1.68
Stefanescu et al 2003 ¹²⁵	arrival	18	Insecta	Spain	1988-2002	NA
Stefanescu et al 2003 ¹²⁵	arrival	18	Insecta	Spain	1988-2002	NA
Hassall et al 2007 ¹²⁶	arrival	25	Insecta	England	1960-2004	NA
Doi 2008 ¹²⁷	arrival	1	Insecta	Japan	1953-2005	4.69
Lappalainen et al 2008 ⁵⁸	arrival	5	Insecta	Finland	1953-2005	-0.83

Diamond et al 2011 ¹²⁸	arrival	44	Insecta	England	1976-2008	-3.92
Ellwood et al 2012 ¹²⁹	arrival	14	Insecta	Japan	1961-2004	0.74
Brown et al 1999 ¹³⁰	breeding	1	Aves	USA	1971-1998	-3.76
Penuelas et al 2002 ⁷³	arrival	4	Aves	spain	1952-2000	3.31
Tryjanowski et al 2002 ¹³¹	arrival	16	Aves	Poland	1970-1996	-4.18
Sanz 2002 ¹³²	breeding	12	Aves	Spain	1955-2000	-6.53
Howell and Gardali 2003 ¹³³	arrival	1	Aves	USA	1980-2000	0.07
Visser et al 2003 ¹³⁴	breeding	24	Aves	Europe	1979-2008	-3.31
Cotton 2003 ²⁷	arrival	19	Aves	England	1971-2000	-2.21
Both et al 2004 ¹³⁵	breeding	25	Aves	Europe	1980-2002	-1.64
Chambers 2005 ¹³⁶	arrival	5	Aves	Australia	1984-2003	-5.28
Torti and Dunn 2005 ¹³⁷	breeding	2	Aves	North America	1951-2000	0.02
Tottrup et al 2006 ¹³⁸	arrival	25	Aves	Denmark	1976-1997	-4.17
Tottrup et al 2006 ¹³⁸	arrival	25	Aves	Denmark	1976-1997	-1.57
Croxton et al 2006 ³¹	arrival	15	Aves	England	1959-2005	-0.92
Peintinger and Schuster 2006 ⁷²	arrival	95	Aves	Germany	1970-2003	-3.12
Jonzen et al 2006 ¹¹⁶	arrival	34	Aves	Scandinavia	1980-2004	-1.37
Jonzen et al 2006 ¹¹⁶	arrival	34	Aves	Scandinavia	1980-2004	-0.71

Hoye et al 2007 ¹³⁹	breeding	3	Aves	Greenland	1996-2005	-6.57
Saino et al 2007 ¹⁴⁰	arrival	9	Aves	Italy	1981-2004	-1.81
Sparks et al 2007a ¹⁴¹	arrival	108	Aves	England	1973-2002	-2.58
Miller-Rushing et al 2008 ⁶⁵	arrival	30	Aves	USA	1970-2002	0.11
Miller-Rushing et al 2008 ⁶⁵	arrival	30	Aves	USA	1970-2002	-0.77
Lappalainen et al 2008 ⁵⁸	arrival	15	Aves	Finland	1952-2005	-0.19
Adamik and Pietruszkova 2008 ⁴	arrival	3	Aves	Czech Republic	1964-2005	-4.87
Adamik and Pietruszkova 2008 ⁴	arrival	3	Aves	Czech Republic	1964-2005	-2.47
Swanson and Palmer 2009 ¹⁴²	arrival	88	Aves	USA	1964-2005	-1.99
van Buskirk et al 2009 ¹⁴³	arrival	58	Aves	USA	1961-2006	-0.94
van Buskirk et al 2009 ¹⁴³	arrival	58	Aves	USA	1961-2006	-0.69
Foster et al 2010 ¹⁴⁴	arrival	6	Aves	USA	1978-2005	2.21
Schneider et al 2010 ¹⁴⁵	arrival	12	Actinopterygii	USA	1966-2007	-2.14
Schneider et al 2010 ¹⁴⁵	abundance	12	Actinopterygii	USA	1966-2007	-1.45
Moyes et al 2011 ¹⁴⁶	breeding	1	Mammalia	Scotland	1980-2007	-2.6
Hoye et al 2007 ¹³⁹	arrival	3	Arachnida	Greenland	1996-2005	-7.77
Hoye et al 2007 ¹³⁹	arrival	1	Entognatha	Greenland	1996-2005	3.62
Hoye et al 2007 ¹³⁹	arrival	8	Insecta	Greenland	1996-2005	-17.6

106 **Table S3. Results of meta-analysis testing the shift in phenology over time independent of climate.** We calculated the slope
107 coefficient between phenology and time (p_t) across all time series. SE indicates standard error. The model was controlled for
108 phylogeny and study.

	Coefficient	SE	z-value	p-value
p_t	-0.3175	0.1258	-2.5228	0.0116

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111 **Table S4. Results of models testing the influence of climate variables on phenology across all taxa.** We calculated the slope
 112 coefficient between different climate variables (mean temperature and total precipitation) and both phenology and time. Correlation
 113 coefficients for three effect sizes (p_t = phenology-time, p_c = phenology-climate, t_c = time-climate) are reported. SE indicates
 114 standard error. The models were controlled for phylogeny and study.

Temperature	Coefficient	SE	z-value	p-value
p_t	-0.3497	0.1339	-2.6109	0.0090
p_c	-0.3102	0.1347	-2.3037	0.0212
t_c	0.3251	0.1355	2.3994	0.0164

Precipitation	Coefficient	SE	z-value	p-value
p_t	-0.3016	0.0887	-3.4002	0.0007
p_c	-0.0544	0.0898	-0.6056	0.5448
t_c	0.1057	0.0905	1.1681	0.2428

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117 **Table S5. Results of models testing how the correlation between climate variables and phenology changes with latitude.** We
 118 examined whether the slopes between different climate variables (temperature and days with heavy (>1 inch) precipitation) and
 119 phenology differ as latitude increased using trivariate meta-analysis models. Interactions are between one of three effect sizes (p_t =
 120 phenology-time correlation, p_c = phenology-climate correlation, t_c = time-climate correlation) and latitude. SE indicates standard
 121 error. The models were controlled for phylogeny and study.

Temperature	Coefficient	SE	z-value	p-value
intercept	-0.1086	0.1234	-0.8803	0.3787
p_t:Latitude	-0.0053	0.0005	-11.1918	<0.0001
p_c:Latitude	-0.0050	0.0005	-10.5132	<0.0001
t_c:Latitude	0.0069	0.0006	12.3861	<0.0001
Heavy Precip Days	Coefficient	SE	z-value	p-value
intercept	-0.0833	0.0735	-1.1325	0.2574
p_t:Latitude	-0.0037	0.0003	-10.7796	<0.0001
p_c:Latitude	0.0004	0.0003	1.2241	0.2209
t_c:Latitude	0.0014	0.0003	4.4480	<0.0001

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124 **Table S6. Results of models testing how individual taxa match their phenology to temperature and precipitation.** We calculated
125 the slope coefficient between different climate variables (temperature and precipitation) and both phenology and time for individual
126 taxa. Interactions are between one of three effect sizes (p_t = phenology-time correlation, p_c = phenology-climate correlation, t_c =
127 time-climate correlation) and latitude. SE indicates standard error. The models were controlled for phylogeny and study.

Temperature	Coefficient	SE	z-value	p-value
p_t:amphibians	-0.3144	0.2089	-1.5052	0.1323
p_c:amphibians	-0.3999	0.2058	-1.9429	0.0520
t_c:amphibians	0.3329	0.2076	1.6037	0.1088
p_t:birds	-0.2920	0.1986	-1.4708	0.1414
p_c:birds	-0.2296	0.1989	-1.1544	0.2483
t_c:birds	0.3884	0.1994	1.9482	0.0514
p_t:butterflies	-0.3067	0.1827	-1.6788	0.0932
p_c:butterflies	-0.5823	0.2188	-2.6608	0.0078
t_c:butterflies	0.2838	0.2369	1.1981	0.2309
p_t:dragonflies	-0.1663	0.1914	-0.8688	0.3849
p_t:fish	-0.3991	0.2449	-1.6298	0.1031
p_t:invertebrates	-0.3680	0.1655	-2.2236	0.0262
p_c:invertebrates	-0.8084	0.2167	-3.7303	0.0002
t_c:invertebrates	0.3298	0.2623	1.2572	0.2087

p_t:mammals	-0.3585	0.2910	-1.2320	0.2180
p_c:mammals	-0.2356	0.2639	-0.8926	0.3721
t_c:mammals	0.1391	0.2785	0.4994	0.6175
p_t:reptiles	-0.5401	0.3013	-1.7927	0.0730

Precipitation	Coefficient	SE	z-value	p-value
p_t:amphibians	-0.3863	0.1277	-3.0259	0.0025
p_c:amphibians	-0.1717	0.1216	-1.4117	0.1580
t_c:amphibians	0.0265	0.1250	0.2124	0.8318
p_t:birds	-0.2725	0.1129	-2.4136	0.0158
p_c:birds	-0.0168	0.1134	-0.1478	0.8825
t_c:birds	0.1395	0.1140	1.2228	0.2214
p_t:butterflies	-0.2098	0.1154	-1.8176	0.0691
p_c:butterflies	-0.0910	0.1656	-0.5493	0.5828
t_c:butterflies	0.1472	0.1887	0.7800	0.4354
p_t:dragonflies	-0.1154	0.1287	-0.8970	0.3697
p_t:fish	-0.3829	0.1797	-2.1307	0.0331
p_t:invertebrates	-0.3533	0.1263	-2.7983	0.0051

p_c:invertebrates	-0.1344	0.1798	-0.7479	0.4545
t_c:invertebrates	0.0275	0.2156	0.1275	0.8985
p_t:mammals	-0.3384	0.2315	-1.4615	0.1439
p_c:mammals	0.1082	0.1836	0.5893	0.5557
t_c:mammals	0.1524	0.2072	0.7354	0.4621
p_t:reptiles	-0.5254	0.2470	-2.1274	0.0334

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131 **Table S7. Results of models testing associations between organismal traits and phenological shifts.** We examined whether the
 132 slopes between temperature, phenology and time differ between organisms that differ in thermy, trophic level, habitat, or whether they
 133 were vertebrates or invertebrates. Interactions are between one of three effect sizes (p_t = phenology-time correlation, p_c =
 134 phenology-climate correlation, t_c = time-climate correlation) and traits. SE indicates standard error. The models were controlled for
 135 phylogeny and study.

Temperature	Coefficient	SE	z-value	p-value
intercept	0.4861	0.1537	3.1624	0.0016
log(Mass)	-0.0165	0.0073	-2.2800	0.0226
p_c:ThermalEctotherm	-0.8420	0.1000	-8.4192	<0.0001
p_t:ThermalEctotherm	-0.7096	0.0977	-7.2593	<0.0001
t_c:ThermalEctotherm	-0.1050	0.1053	-0.9978	0.3184
p_c:ThermalEndotherm	-0.6140	0.0300	-20.484	<0.0001
p_t:ThermalEndotherm	-0.6776	0.0262	-25.8241	<0.0001

Temperature	Coefficient	SE	z-value	p-value
intercept	0.5152	0.1568	3.2853	0.0010
log(Mass)	-0.0132	0.0075	-1.7668	0.0773
p_c:Trophiccarnivorous	-0.6527	0.0468	-13.9478	<0.0001
p_t:Trophiccarnivorous	-0.7131	0.0444	-16.0438	<0.0001

t_c:Trophiccarnivorous	-0.1234	0.0505	-2.4438	0.0145
p_c:Trophicherbivorous	-0.8079	0.0997	-8.1003	<0.0001
p_t:Trophicherbivorous	-0.7631	0.0852	-8.9528	<0.0001
t_c:Trophicherbivorous	-0.1923	0.1090	-1.7645	0.0777
p_c:Trophicomnivorous	-0.7115	0.0378	-18.8196	<0.0001
p_t:Trophicomnivorous	-0.7534	0.0334	-22.5389	<0.0001

137

138

Temperature	Coefficient	SE	z-value	p-value
intercept	0.4424	0.1508	2.9343	0.0033
log(Mass)	-0.0158	0.0074	-2.1347	0.0328
p_t:Habitatmarine	-0.7414	0.1553	-4.7756	<0.0001
p_t:Habitatterrestrial	-0.6744	0.0247	-27.2527	<0.0001

139

140 **Table S8. Results of models testing associations between seasonal behaviors and phenological shifts.** We examined whether the
141 slopes between temperature, phenology and time differ between different seasonal behaviors measured by researchers. Interactions are
142 between one of three effect sizes (p_t = phenology-time correlation, p_c = phenology-climate correlation, t_c = time-climate
143 correlation) and traits. SE indicates standard error. The model was controlled for phylogeny and study.

Temperature	Coefficient	SE	z-value	p-value
intercept	0.3709	0.1295	2.8648	0.0042
log(Mass)	-0.0096	0.0069	-1.3896	0.1646
p_c:arrival	-0.5436	0.0472	-11.5105	<0.0001
p_t:arrival	-0.6006	0.0460	-13.0444	<0.0001
t_c:arrival	0.0760	0.0495	1.5343	0.1249
p_c:peakabundance	-1.4912	0.3365	-4.4316	<0.0001
p_t:peakabundance	-0.5744	0.0894	-6.4261	<0.0001
t_c:peakabundance	0.1213	0.3863	0.3141	0.7535
p_c:rearing	-0.7118	0.0646	-11.0102	<0.0001
p_t:rearing	-0.7690	0.0672	-11.441	<0.0001

144

145

146 **Supplementary Code**

147 **Code for trivariate meta-analysis.** Example code for constructing variance-covariance matrices, phylogenetic and study-level
148 random effects and fitting mixed-effects trivariate meta-analysis models.

```
149
150 # clear workspace and set working directory
151 rm(list = ls())
152
153 # remove current version and install custom metafor package by MJL that ignores positive definite errors
154 remove.packages("metafor")
155 install.packages("metafor_1.9-2_MJL.tar.gz", repos = NULL, type="source")
156
157 # get entire concatenated dataset with all climate variables
158 allData <- read.csv(file="phenology.csv", header=TRUE)
159
160 # remove rows with no effect size data
161 allData <- allData[which(!is.na(allData$z)),]
162
163 # parse dataset by climate variable and keep original order
164 climateDataList <- split(allData,
165                          factor(allData$sclimate, levels=unique(allData$sclimate)))
166
167 # parallelized rma.mv function
168 rma.parallel <- function(aClimateData,
169                          theRegressionModel,
170                          modelFileName)
171 {
172   # collect only complete cases for specified regression model
173   determineCompleteCases <- aClimateData[,c(labels(terms(theRegressionModel)))]
174   aClimateData <- aClimateData[which(complete.cases(determineCompleteCases)),]
175
176   # load phylogeny and convert to phylogenetic correlation matrix
177   phyloMatrix <- vcv(phy=read.tree(file="cohen_final_phylogeny_72214.tre"), corr=TRUE)
178   phyloMatrix <- forceSymmetric(phyloMatrix)
179
180   # construct VCV matrix for multivariate effect sizes and correct for positive definiteness
181   getV <- function(someData) {
182     dataList <- split(someData[,c("p_t", "p_c", "t_c")], someData$effect_ID)
183     theVList <- lapply(dataList,
184                        function(x) ifelse(nrow(x) == 1, return(as.matrix(x$p_t)), return(as.matrix(x))))
185     theVList_PosDef_fixed <- lapply(theVList, force_Positive_Definiteness)
186     return(as.matrix(bdiag(theVList_PosDef_fixed)))
```

```

187     }
188
189
190     # multi(tri)variate, multi-factor, mixed-model, meta-regression
191     theResults <- rma.mv(yi = z,
192                         V = getV(aClimateData),
193                         mods = update(theRegressionModel, ~ . + cor_ID),
194                         random = c(~ cor_ID | study_ID, ~ 1 | Genus_Species_NEWICK),
195                         R = list(Genus_Species_NEWICK = phyloMatrix),
196                         struct = "UN",
197                         data = aClimateData,
198                         control = list(optimizer = "nlminb"))
199
200     # save results and notify analysis completion
201     fileName <- paste(gsub("/", "/", getwd(), fixed = TRUE),
202                      "// results//", modelFileName, aClimateData$sclimate[1], ".rda", sep = "")
203     save(theResults, file = fileName)
204     return(theResults)
205 }
206
207 # parallelize meta-regressions among the 12 climate variables
208 library("parallel")
209 cl <- makeCluster(detectCores(logical = TRUE))
210 clusterEvalQ(cl,
211              { lapply(c("Matrix", "MASS", "corpcor", "metafor", "ape"), library, character.only = T); source("metaGear_v1_beta.r"); })
212
213
214 # available factors: VertInvert + Trophic + Thermal + Latitude + Longitude + Altitude + Habitat + TypeNEW
215 theRegressionModel <- ~ VertInvert + Trophic + Thermal + Latitude + Longitude + Altitude + Habitat + TypeNEW
216 modelFileName <- "all_factors_"
217 parLapply(cl, climateDataList, rma.parallel, theRegressionModel, modelFileName)
218
219 theRegressionModel <- ~ VertInvert + Trophic + Thermal + Latitude + Longitude + Altitude + Habitat + TypeNEW - 1
220 modelFileName <- "all_factors_noIntercept_"
221 parLapply(cl, climateDataList, rma.parallel, theRegressionModel, modelFileName)
222
223 stopCluster(cl)
224

```

225 **NEWICK (text) version of phylogenetic tree used for phylogenetic analyses.** The relationships between species in this tree were
 226 used to control for phylogeny in all mixed-effects meta-analyses because related species are non-independent because of their shared
 227 evolutionary history. The taxonomic composition of our meta-analytic dataset was broad and included 475 species, 289 genera, 119
 228 families, 45 orders, 12 classes, and 5 phyla. For details concerning the methodology behind the compilation of the tree, see Methods.
 229 The following pages include the full NEWICK (text) version of this tree.

230
 231 ((Beroe_gracilis:65,(Pleurobrachia_pileus:32.5,Mnemiopsis_leidyi:32.5):32.5):1082,(((Abramis_brama:100,Rutilus_rutilus
 232 :100):150,(((Oncorhynchus_gorbuscha:50,Salmo_salar:50):50,Esox_lucius:100):107,((Thunnus_alalunga:60,Thunnus_thynnus:60
 233):60,Platichthys_flesus:120):87):43):204.6,(((Hynobius_tokyoensis:217.5,((Triturus_alpestris:84,Triturus_cristatus:84)
 234 :84,(Triturus_helveticus:84,Triturus_vulgaris:84):84):16.4,((Ambystoma_opacum:62.2,Ambystoma_tigrinum:62.2):62.2,Ambys
 235 toma_talpoideum:124.4):57.3,Eurycea_quadridigitata:181.7):2.7):33.1):81.1,(Scaphiopus_holbrookii:212.1,(((Bufo_bufo:27
 236 .3,Bufo_calamita:27.3):27.3,(Bufo_boreas:36.4,(Bufo_fowleri:18.2,Bufo_terrestris:18.2):18.2):18.2):12.7,(Pseudacris_mac
 237 ulata:53.2,(Pseudacris_ornata:26.6,Pseudacris_crucifer:26.6):26.6):14.1):85.7,(Gastrophryne_carolinensis:118.8,(Rana_e
 238 sculenta:71.7,Rana_ornativentris:71.7,(Rana_sphenoccephala:47.8,(Rana_cascadae:23.9,Rana_temporaria:23.9):23.9):23.9):14
 239 .3,Rhacophorus_arboreus:86):32.8):34.2):59.1):86.5):62.6,((Glis_glis:62.4,(Marmota_flaviventris:31.2,Urocitellus_columb
 240 ianus:31.2):31.2):262.1,((((Cygnus_columbianus:48.94542262,((Chen_caerulescens:13.31646762,(Anser_anser:12.7686859,(An
 241 ser_fabalis:5.489252862,Anser_albifrons:5.489252862):7.279433036):0.5477817196):23.18266691,Branta_canadensis:36.499131
 242 87):12.44628809):37.60041847,(Oxyura_jamaicensis:81.77851461,((Somateria_mollissima:35.18954554,((Lophodytes_cucullatu
 243 s:19.21505334,(Mergus_serrator:5.358214526,Mergus_merganser:5.358214526):13.85683881):7.691978011,(Bucephala clangula:1
 244 9.06491558,Bucephala_albeola:19.06491558):7.842113109):8.282516859):4.115701449,(Aythya_nyroca:9.458353874,(Aythya_ful
 245 igula:5.722039301,Aythya_affinis:5.722039301):1.964407474,((Aythya_americana:3.33805485,Aythya_collaris:3.338052184):3.
 246 539111981,(Aythya_valisineria:1.822261348,Aythya_ferina:1.822261348):5.054905483):0.809279943):1.771907099):29.84689312
 247):3.008593052,((((Anas_penelope:5.507128753,Anas_americana:5.507128753):5.20633609,Anas_strepera:10.71346484):11.934703
 248 32,(Anas_platyrhynchos:15.76037069,Anas_crecca:15.76036803):0.651073238,Anas_acuta:16.41144393):6.236724231):3.3059923
 249 35,(Anas_querquedula:11.91346337,(Anas_discors:4.347291008,Anas_clypeata:4.347291008):7.566172359):14.04069713):16.3596
 250 8221):39.4646719):4.767331809):147.7363854,(Coturnix_coturnix:100.4651069,Lagopus_leucura:100.4651069):133.8171196):40.
 251 57485913,((Zenaida_macroura:90.2990266,(Columba_palumbus:54.85559862,Streptopelia_turtur:54.85560395):35.44343065):154.
 252 1564161,((((Oceanites_oceanicus:162.4786113,(((Fulmarus_glacialoides:20.55695541,Fulmarus_glacialis:20.55695541):12.7
 253 1006545,Macronectes_giganteus:33.2670182):2.479318985,Daption_capense:35.74633718):9.343498738,(Pagodroma_nivea:38.6685
 254 7896,Thalassoica_antarctica:38.66857896):6.421256958):117.388778):25.15052641,(Pelecanus_erythrorhynchos:168.298904,(Py
 255 goscelis_adeliae:63.805132,Aptenodytes_forsteri:63.80513733):104.493772):19.33023368):3.592201193,((((Platalea_leucoro
 256 dia:142.7518452,Plegadis_falcinellus:142.7518452):18.2552038,(Ciconia_nigra:43.28837202,Ciconia_ciconia:43.28837202):11
 257 7.7186797):22.52382062,Gavia_arctica:183.5308643):2.710455382,((Egretta_garzetta:103.4862712,(Casmerodius_albus:42.806
 258 70391,(Ardea_purpurea:22.00920233,(Ardea_herodias:10.21332907,Ardea_cinerea:10.21332907):11.79587327):20.79750158):38.8
 259 6419815,(Nycticorax_nycticorax:70.03049521,Ardeola_ralloides:70.03049521):11.64040952):21.81537446):33.59645867,(Ixobry
 260 chus_minutus:113.5033386,(Botaurus_lentiginosus:43.06850602,Botaurus_stellaris:43.06850602):70.43483263):23.57940188):4
 261 9.15858983):2.749323317,(Phalacrocorax_aristotelis:28.90562853,Phalacrocorax_auritus:28.90562853):160.0850171):2.230690
 262 55):20.81341022,((((Pluvialis_apricaria:4.458310264,Pluvialis_fulva:4.458310264):109.2970875,((Charadrius_dubius:55.0
 263 0429959,(Charadrius_hiaticula:34.42183385,Charadrius_vociferus:34.42183385):20.58246574):30.79259336,(Charadrius_bicinc
 264 tus:83.94426977,Vanellus_vanellus:83.9442751):1.852623174):24.45316139,(Recurvirostra_avosetta:46.25507162,Himantopus
 265 himantopus:46.25507162):26.90041253,Haematopus_ostralegus:73.15548681):37.09456752):3.505348778):36.68512537,Burhinus_o
 266 edicnemus:150.4405311):18.75075198,((Numenius_phaeopus:41.70172271,Numenius_arquata:41.70172271):71.97079982,((Limosa
 267 limosa:32.14749317,Limosa_fedoa:32.14749584):73.75750664,((Philomachus_pugnax:53.6865457,((Calidris_ferruginea:27.4373

268 9301,Calidris_acuminata:27.43739301):21.75064699,(Calidris_alpina:45.46777268,Calidris_minuta:45.46777268):3.720267322)
 269 :3.587107124,Calidris_canutus:52.77514979):0.9113985725):47.29269968,((Scolopax_rusticola:90.25208972,(Gallinago_gallin
 270 ago:5.985579417,Gallinago_hardwickii:5.985579417):84.26651297):9.539472462,(((Tringa_ochropus:57.54249226,((Catoptropho
 271 rus_semipalmatus:41.51727528,Tringa_flavipes:41.51727528):4.364401856,((Tringa_glareola:28.96528859,(Tringa_totanus:22.
 272 92428751,Tringa_stagnatilis:22.92428751):6.041003744):12.98381503,((Tringa_nebularia:25.60248845,Tringa_melanoleuca:25.
 273 60248845):7.02541731,Tringa_erythropus:32.62790576):9.321197857):3.932570857):11.66081246):26.72323968,(Actitis_macular
 274 ius:52.8879657,Actitis_hypoleucos:52.8879657):31.37776624):6.544746155,Steganopus_tricolor:90.81047009):8.981086762):1.
 275 187685857):4.925749101):7.767533375):48.05871602,((((Larus_ridibundus:12.53263136,(Larus_pipixcan:10.25630744,(Larus_d
 276 elawarensis:3.990684831,(Larus_cachinnans:1.797630683,Larus_argentatus:1.797630683):2.193051482):6.265622611):2.2763239
 277 21):5.710195789,Rissa_tridactyla:18.24282715):34.3780691,((Chlidonias_hybrida:11.15041124,(Chlidonias_niger:4.794060346
 278 ,Chlidonias_leucopterus:4.794060346):6.356350891):11.54498969,((Sterna_forsteri:16.11869622,Sterna_sandvicensis:16.1186
 279 9622):1.61589423,(Sterna_hirundo:12.2409739,Sterna_paradisaea:12.2409739):5.493616541):4.960813145):29.92549799):8.9404
 280 62159,((((Uria_aalge:11.56038652,Uria_lomvia:11.56038652):19.59710321,(Alle_alle:30.28180828,Alca_torda:30.28180828):0.
 281 8756787773):13.10901558,(Ptychoramphus_aleuticus:40.00476054,(Fratercula_arctica:12.55983705,Fratercula_cirrhata:12.55
 282 983972):10.83150277,Cerorhinca_monocerata:23.39134249):16.61342071):4.261739433):10.12681519,Catharacta_maccormicki:54.
 283 39331516):7.168040588):5.744508118,Glareola_pratincola:67.30586653):94.42537202):7.460036586):34.06282858,((Podilymbus
 284 podiceps:111.855046,(Aechmophorus_occidentalis:78.99269579,(Podiceps_nigricollis:71.13116871,(Podiceps_griseus:46.896
 285 32458,(Podiceps_cristatus:32.93024983,Podiceps_auritus:32.93024983):13.96607474):24.23484146):7.86152975):32.86234757):
 286 83.23444547,((Rallus_aquaticus:113.4618584,(Porzana_parva:109.057453,(Porzana_carolina:56.75827215,Porzana_porzana:56.
 287 75826949):20.02283252,(Gallinula_chloropus:50.86912819,(Fulica_atra:17.16585933,Fulica_americana:17.16585667):33.703271
 288 52):25.91197382):32.276351):4.404402696):36.25703962,(Grus_canadensis:21.1096606,Grus_grus:21.1096606):128.6092241):45.
 289 37059084):8.164617544):8.780642732):25.7993525,((Eudynamis_scolopaceus:121.5719552,(Scythrops_novaehollandiae:116.70164
 290 91,(Cuculus_canorus:80.18586224,(Cacomantis_variolosus:63.93739654,Cuculus_pallidus:63.93739654):16.2484737):36.5157815
 291 6):4.870306114):115.7826454,((((Falco_subbuteo:26.43311763,Falco_vespertinus:26.43311763):8.587292013,Falco_sparverius:
 292 35.02040965):191.1487851,(((Sayornis_phoebe:27.49448337,((Contopus_sordidulus:18.31686309,Contopus_cooperi:18.31686576
 293):7.958367714,(Empidonax_difficilis:24.32170987,Empidonax_minimus:24.32170987):1.953523599):1.219249894):25.99826111,(T
 294 yrannus_verticalis:20.7816116,Tyrannus_tyrannus:20.78161427):32.71112755):144.1100451,(Gerygone_olivacea:150.422482,(((
 295 (((Rhipidura_rufifrons:75.01578707,(Myiagra_rubecula:15.55132725,Myiagra_cyanoleuca:15.55132725):22.68194203,Monarcha
 296 _melanopsis:38.23326928):36.78252312):6.147760615,((Perisoreus_canadensis:54.22904409,(Pica_pica:44.14585503,Corvus_fru
 297 gilegus:44.14586036):10.08318906):22.89182515,(Lanius_minor:22.73044631,Lanius_collurio:22.73044364):54.39042559):4.042
 298 68379):4.834839557,Oriolus_oriolus:85.99840057):5.93117337,Vireo_gilvus:91.92956328):4.751556455,Pachycephala_rufivent
 299 is:96.6811304):5.229591276,(Coracina_tenuirostris:46.44461045,Lalage_sueurii:46.44461578):55.4661059):39.09621688,(((Pa
 300 rus_caeruleus:52.39244151,(Parus_major:45.94667117,Parus_ater:45.94667117):6.445767668):70.97720839,((((Sylvia_atricap
 301 illa:34.27027529,Sylvia_borin:34.27027529):7.503318848,(Sylvia_communis:31.32600186,(Sylvia_curruca:28.34279119,Sylvia_
 302 nisoria:28.34279119):2.983210672):10.44759228):22.20264902,((Hippolais_icterina:26.68546732,((Acrocephalus_paludicola:
 303 14.0467535,(Acrocephalus_schoenobaenus:9.301887842,Acrocephalus_melanopogon:9.301887842):4.744865657):5.952597251,Acroc
 304 ephalus_sciuraceus:19.99935075):1.486186057,(Acrocephalus_arundinaceus:5.109127599,Acrocephalus_stentoreus:5.109127599)
 305 :16.37640921):5.199930517):27.66164668,(Acrocephalus_palustris:37.3798434,(Locustella_fluviatilis:11.18477954,Locustell
 306 a_luscinoides:11.18478221):26.19506119):16.96727327):9.629129148):16.24485374,(((Petrochelidon_pyrrhonota:37.75066019
 307 ,Hirundo_rustica:37.75066019):0.2926837372,Delichon_urbicum:38.04334126,unknown_swallow:38.04334126):8.979740605,((Tach
 308 ycineta_bicolor:33.15673999,Riparia_riparia:33.15673999):2.62579147,(Stelgidopteryx_serripennis:31.31952431,Progne_subi
 309 s:31.31952698):4.463001819):11.24055307):27.17198693,(Phylloscopus_sibilatrix:36.8920736,(Phylloscopus_collybita:15.89
 310 511162,Phylloscopus_trochilus:15.89511162):20.99696465):2.360603979,Phylloscopus_trochiloides:39.25267758):34.94239388)
 311 :6.026028086):7.331527958,((Alauda_arvensis:22.87406121,Lullula_arborea:22.87406121):9.488771678,Eremophila_alpestris:3
 312 2.36283289):55.18979195):35.81702506):3.334824075,((Regulus_regulus:30.21005414,Regulus_calendula:30.21005414):91.3797

313 5566,(((Dumetella_carolinensis:47.98867324,Toxostoma_rufum:47.9886679):25.27432749,Sturnus_vulgaris:73.26300339):20.07
 314 293086,(((Catharus_ustulatus:27.54229458,Catharus_guttatus:27.54229458):34.70463066,(Turdus_viscivorus:45.95346326,(Tur
 315 dus_philomelos:43.43808595,(Turdus_iliacus:30.81185006,Turdus_merula:30.81185272):0.7443178975,(Turdus_migratorius:30.
 316 34757802,(((Turdus_naumanni:13.04530639,Turdus_torquatus:13.04530639):6.017511314,Turdus_pilaris:19.0628177):3.42761024
 317 1,Turdus_pallidus:22.49042795):7.857152742):1.208589935):11.88191799):2.515377318):16.29345931):27.02483204,(((Luscini
 318 a_megarhynchos:6.675078091,Luscinia_luscinia:6.675078091):43.36175488,Luscinia_svecica:50.0368383):7.324402659,(Erithac
 319 us_rubecula:57.07116423,(((Phoenicurus_phoenicurus:21.90067013,(Phoenicurus_ochruros:18.23231914,Phoenicurus_aureus:1
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Section/topic	#	Checklist item	Reported in...
TITLE			
Title	1	Identify the report as a systematic review, meta-analysis, or both.	Main text
ABSTRACT			
Structured summary	2	Provide a structured summary including, as applicable: background; objectives; data sources; study eligibility criteria, participants, and interventions; study appraisal and synthesis methods; results; limitations; conclusions and implications of key findings; systematic review registration number.	Main text
INTRODUCTION			
Rationale	3	Describe the rationale for the review in the context of what is already known.	Main text
Objectives	4	Provide an explicit statement of questions being addressed with reference to participants, interventions, comparisons, outcomes, and study design (PICOS).	Main text
METHODS			
Protocol and registration	5	Indicate if a review protocol exists, if and where it can be accessed (e.g., Web address), and, if available, provide registration information including registration number.	Supplement - Methods
Eligibility criteria	6	Specify study characteristics (e.g., PICOS, length of follow-up) and report characteristics (e.g., years considered, language, publication status) used as criteria for eligibility, giving rationale.	Supplement - Methods
Information sources	7	Describe all information sources (e.g., databases with dates of coverage, contact with study authors to identify additional studies) in the search and date last searched.	Supplement - Methods
Search	8	Present full electronic search strategy for at least one database, including any limits used, such that it could be repeated.	Supplement - Methods
Study selection	9	State the process for selecting studies (i.e., screening, eligibility, included in systematic review, and, if applicable, included in the meta-analysis).	Supplement - Methods
Data collection process	10	Describe method of data extraction from reports (e.g., piloted forms, independently, in duplicate) and any processes for obtaining and confirming data	Supplement - Methods

		from investigators.	
Data items	11	List and define all variables for which data were sought (e.g., PICOS, funding sources) and any assumptions and simplifications made.	Supplement - Methods
Risk of bias in individual studies	12	Describe methods used for assessing risk of bias of individual studies (including specification of whether this was done at the study or outcome level), and how this information is to be used in any data synthesis.	Supplement - Methods
Summary measures	13	State the principal summary measures (e.g., risk ratio, difference in means).	Supplement - Methods
Synthesis of results	14	Describe the methods of handling data and combining results of studies, if done, including measures of consistency (e.g., I^2) for each meta-analysis.	Supplement - Methods
Risk of bias across studies	15	Specify any assessment of risk of bias that may affect the cumulative evidence (e.g., publication bias, selective reporting within studies).	Supplement - Methods
Additional analyses	16	Describe methods of additional analyses (e.g., sensitivity or subgroup analyses, meta-regression), if done, indicating which were pre-specified.	Supplement - Methods
RESULTS			
Study selection	17	Give numbers of studies screened, assessed for eligibility, and included in the review, with reasons for exclusions at each stage, ideally with a flow diagram.	Main text
Study characteristics	18	For each study, present characteristics for which data were extracted (e.g., study size, PICOS, follow-up period) and provide the citations.	Supplement - Tables
Risk of bias within studies	19	Present data on risk of bias of each study and, if available, any outcome level assessment (see item 12).	Main text and Supplement - Tables
Results of individual studies	20	For all outcomes considered (benefits or harms), present, for each study: (a) simple summary data for each intervention group (b) effect estimates and confidence intervals, ideally with a forest plot.	Supplement - Tables
Synthesis of results	21	Present results of each meta-analysis done, including confidence intervals and measures of consistency.	Supplement - Tables
Risk of bias across studies	22	Present results of any assessment of risk of bias across studies (see Item 15).	Supplement - Tables

Additional analysis	23	Give results of additional analyses, if done (e.g., sensitivity or subgroup analyses, meta-regression [see Item 16]).	Supplement – Supplementary Results
DISCUSSION			
Summary of evidence	24	Summarize the main findings including the strength of evidence for each main outcome; consider their relevance to key groups (e.g., healthcare providers, users, and policy makers).	Main text
Limitations	25	Discuss limitations at study and outcome level (e.g., risk of bias), and at review-level (e.g., incomplete retrieval of identified research, reporting bias).	Main text and Supplementary Discussion
Conclusions	26	Provide a general interpretation of the results in the context of other evidence, and implications for future research.	Main text
FUNDING			
Funding	27	Describe sources of funding for the systematic review and other support (e.g., supply of data); role of funders for the systematic review.	Main text - Acknowledgments