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 Synchrony in adult survival is remarkably strong among common temperate songbirds across France

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- **Open Research:** Data necessary to reproduce the analyses are provided on the Dryad repository 38
- https://doi.org/10.5061/dryad.vx0k6djv3 (Ghislain et al. 2022a) and novel code is provided on 39
- the Zenodo repository https://doi.org/10.5281/zenodo.8172390 (Ghislain et al. 2022b). 40

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- **Keywords**: adult survival; common songbirds; demography; mark-recapture; migration; Moran
- *effect; precipitation; temporal synchrony; temperature.*

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44 Abstract

45	Synchronous variation in demographic parameters across species increases the risk of
46	simultaneous local extinction, which lowers the probability of subsequent recolonization.
47	Synchrony therefore tends to destabilize meta-populations and meta-communities. Quantifying
48	interspecific synchrony in demographic parameters, like abundance, survival or reproduction, is
49	thus a way to indirectly assess the stability of meta-populations and meta-communities.
50	Moreover, it is particularly informative to identify environmental drivers of interspecific
51	synchrony since those drivers are important across species. Using a Bayesian hierarchical multi-
52	site multi-species mark-recapture model, we investigated temporal interspecific synchrony in
53	annual adult apparent survival for 16 common songbird species across France for the period
54	2001–2016. Annual adult survival was largely synchronous among species (73%, 95% credible
55	interval [47-94%] of the variation among years was common to all species), despite species
56	differing in ecological niche and life-history. This result was robust to different model
57	formulations, uneven species sample sizes, and removing the long-term trend in survival.
58	Synchrony was also shared across migratory strategies, which suggests that environmental
59	forcing during the 4-month temperate breeding season has a large-scale, interspecific impact on
60	songbird survival. However, the strong interspecific synchrony was not easily explained by a set
61	of candidate weather variables we defined a priori. Spring weather variables explained only
62	1.4% [0.01–5.5%] of synchrony, while the contribution of large-scale winter weather indices
63	may have been stronger but uncertain, accounting for 12% [0.3–37%] of synchrony. Future
64	research could jointly model interspecific variation and covariation in breeding success, age-

- dependent survival and age-dependent dispersal to understand when interspecific synchrony in
- abundance emerges and destabilizes meta-communities.

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Introduction

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Synchrony corresponds to the coincident change in individual, population or species characteristics over extended areas, up to thousands of km (Liebhold et al. 2004). Understanding the causes of synchronous variations in population size is important in ecology and conservation because the greater the synchrony, the higher the risk of population, metapopulation, and metacommunity extinction (Liebhold et al. 2004, Koenig and Liebhold 2016). When populations go down in numbers simultaneously the risk of synchronous local extinctions increases and the opportunity for subsequent demographic rescue through immigration diminishes (Tavecchia et al. 2016). If extinctions occur simultaneously for multiple co-occurring species, communities and ecosystem functioning can be disrupted (Loreau and de Mazancourt 2008, Kahilainen et al. 2018). However, differences in life-history and niche across species should increase community stability by decreasing interspecific synchrony (Pandit et al. 2013). A major theoretical and empirical challenge is to disentangle the respective roles of the three processes that can cause synchrony. The first process, termed the Moran effect, corresponds to extrinsic forcing: populations that are affected by the same environmental variables are synchronized due to the spatial correlation in constraints (Liebhold et al. 2004, Olmos et al. 2019). In particular, climate forcing may directly drive variation in survival and reproduction (Post and Forchhammer 2004, Cattadori et al. 2005, Hansen et al. 2013, Sheppard et al. 2015, Koenig and Liebhold 2016, Black et al. 2018, Kahilainen et al. 2018, but see Vik et al. 2004). Climate forcing in wintering areas is expected to synchronize survival among species that share the same wintering range (e.g., Telensky et al. 2020). The second process is synchronization through interactions with another trophic level. This includes synchrony due to variation in the

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abundance of shared prey, notably mast-seeding for seed-eating species (Liebhold et al. 2004, 92 Klapwijk et al. 2018), predators (Huitu et al. 2004), or parasites (Cattadori et al. 2005). Variation 93 in abundance in the trophic level responsible for synchrony may itself be driven by climate 94 forcing (e.g., Dubos et al. 2018). The third process is dispersal, which may synchronize 95 fluctuations in population size for connected populations (Paradis et al. 1999, Liebhold et al. 96 97 2004, Martin et al. 2017; but see Sanz-Aguilar et al. 2016, Tayecchia et al. 2016). More generally, any type of simultaneous movement of individuals, including seasonal migratory 98 movements, can synchronize population sizes across distant sites. 99 100 Synchrony has mainly been investigated across populations within species, i.e., as the spatial covariance in temporal changes in population sizes or vital rates (Liebhold et al. 2004). 101 However, evidence accumulates that different species can show a strong degree of synchrony 102 over wide areas even when they are ecologically, functionally and phylogenetically divergent 103 (Post and Forchhammer 2004, Hansen et al. 2013, Black et al. 2018). In vertebrate animals this 104 interspecific synchrony (Liebhold et al. 2004) has mainly been studied using two study systems 105 that are subject to trivial environmental forcing: species thriving in cold-driven environments 106 following cyclic dynamics (Post and Forchhammer 2004, Jones et al. 2003, Hansen et al. 2013, 107 108 Koenig and Liebhold 2016, Huitu et al. 2004, Liebhold et al. 2004) and seabirds that gather at a few colonies close to shared, large foraging areas (Lahoz-Monfort et al. 2011, 2013, 2017, 109 Robinson et al. 2013). Existing evidence of interspecific synchrony in population sizes across a 110 111 wide range of species comes mainly from large-scale censuses of common wintering birds: six species from the UK (Swallow et al. 2016) and 49 species from North America (Koenig and 112 113 Liebhold 2016).

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To our knowledge, until recently interspecific synchrony in vital rates, rather than population 114 sizes, had been studied only for a small number of species at a single site or region: one study on 115 two duck species (Péron and Koons 2012), two studies on two salmon species (Malick and Cox 116 2016, Malick et al. 2017), and all others on two to six seabird species (Lahoz-Monfort et al. 117 2011, 2013, 2017, Robinson et al. 2013). Recently, Telensky et al. (2020) estimated the 118 119 synchronizing effect of weather variables on breeding sites and wintering sites for the survival of 16 songbird species across Czech Republic during 2004–2014, albeit without estimating 120 synchrony explicitly. In addition, Morrison et al. (2022) estimated species-specific synchrony -121 122 but not overall interspecific synchrony - in reproduction and survival using 26 songbird species across 336 European sites. The lack of research on interspecific synchrony of vital rates likely 123 results from (i) the lack of theory and methods to root (meta)community dynamics in processes 124 operating at the individual level (but see Lahoz-Monfort et al. 2017), and (ii) the complexity of 125 methods required to analyze multi-species, multi-site, long-term vital rate data (Grosbois et al. 126 2009, Lahoz-Monfort et al. 2011, 2013, 2017, Swallow et al. 2016). 127 In the present study, we take advantage of a Constant Effort Sites (CES) mist-netting scheme 128 to investigate interspecific synchrony in yearly fluctuations of annual adult apparent survival for 129 130 a set of 16 common songbirds species at 242 sites across France (Fig. 1) over a 16 year period. We analyzed interspecific synchrony using the variance partitioning method of Lahoz-Monfort 131 et al. (2011), splitting between-year variance into a synchronous component common to all 132 133 species, and an asynchronous component corresponding to a year by species interaction. Since our analyses involved species with distinct ecological niches (Appendix S1: Table S1) and since 134

synchrony is expected to be lower with higher species diversity (Pandit et al. 2013), we expected

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low interspecific synchrony. Further, our species differ in terms of migratory strategies and wintering range: nine species are resident or short-distance migrants, with year-round exposure to temperate climate, whereas seven species are trans-Saharan migrants that winter under the west-African climate (Appendix S1). Therefore, we expected that synchrony would be stronger within a given migratory strategy and that migratory strategy would explain a significant proportion of year-to-year variation among species. If that was the case it would point to a synchronizing role of conditions on wintering grounds. Winter harshness is commonly proposed to explain a large proportion of year-round mortality in small organisms like songbirds (Grosbois et al. 2006, Robinson et al. 2007, Salewski et al. 2013, Johnston et al. 2016, Saether et al. 2016), including in migratory species (Robinson et al. 2007, Woodworth et al. 2017b). Factors explaining winter mortality could include water availability in arid wintering areas (Telenský et al. 2020) and the cost of thermoregulation in extreme cold or hot conditions (Boyles et al. 2011). On the other hand, if survival was to covary more synchronously and across migration strategies, it would point towards a synchronizing role of conditions on the breeding grounds, possibly due to climate forcing. In addition to factors that explain mortality during winter, climate forcing during the breeding season could synchronize species through its effect on the cost of reproduction through primary and secondary productivity (see details in discussion). To assess the role of climate forcing during the breeding season (i.e. common to all species) vs. non-breeding season (i.e. common to species wintering in the same climatic region), we estimated the proportion of synchronous variation in annual survival that could be ascribed to local temperatures and precipitations at the breeding sites during the breeding season, and to

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global climate indices related to conditions on the wintering grounds during the non-breeding season (the winter North Atlantic Oscillation and the summer Sahel rainfalls, see Methods). We predicted that synchronous variation in survival should be in part explained by spring weather conditions.

METHODS

Study sites and species

Mark-recapture data were collected by volunteer bird banders under the French Constant-ringing-Effort-Site (CES) banding survey (Julliard and Jiguet 2002). The full CES dataset is available on request through https://crbpo.mnhn.fr/. We selected data over the period 2001–2016, with the goal of estimating annual apparent survival and recapture probabilities. We consider "apparent survival", rather than "true survival", as our data cannot distinguish between mortality and permanent emigration. At each CES site the local bird community is sampled 3.17 \pm 1.06 SD times per breeding season (first session on May 21 \pm 15 days, last session on July 4 \pm 12 days), with 14 \pm 7 mist nets (12 m long, 3-to-4 m high, 16 mm mesh size) spread over an area of ~ 3 hectares (4 to 5 mist nets per hectare). A capture session typically starts at dawn and lasts until midday. For every site the number, dates, hours of capture sessions, and mist net locations are held constant across sessions and years. Sites are monitored for an average of six \pm four years. Sites are typically located in low canopy habitats such as shrublands, open woodlands and reed beds, where birds are easily captured with 3.5 m high mist nets. Each bird captured is marked with a metal band bearing a unique identifier, identified at the species level, aged

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(juvenile or adult), sexed (Svensson 1992), and released at the point of capture. All recaptures of marked individuals are recorded.

To ensure robustness of site-level parameter estimates we retained only data for species with an average of at least five adult individuals captured per year. Juvenile mortality is highly confounded with dispersal (Johnston et al. 2016) and so we did not consider juvenile data. After excluding the first year of capture for each individual to handle transients (see below), our mark-recapture dataset consists of 20,912 adults from 16 species, including 5,198 individuals recaptured at least once across years (see Appendix S1), across 242 sites (Fig. 1 and Appendix S2: Figure S1) over a period of 16 years (Dehorter and CRBPO 2017).

Bayesian survival data analysis

We modeled annual apparent survival and recapture probabilities using mark-recapture histories of individual birds with species- and time-dependent Cormack-Jolly-Seber (CJS) models (Lahoz-Monfort et al. 2011). Inter-annual adult apparent survival probability (ϕ) is the probability that a bird alive in year t is still alive and present at the same CES site in year t+1. The recapture probability (p) is the probability that a bird alive and present in the same CES site where it was formerly captured (on year t-1 or before) is recaptured in year t. Individuals that were captured only once were considered as transient individuals that do not pertain to the local population (Johnston et al. 2016) and were discarded by starting mark-capture histories only at the second year of capture. We also attempted to explicitly model transient rates, but the models were prohibitively long to run. Therefore our estimates are conditional on each bird being alive and present at a same site for at least two years. Goodness-of-fit tests for the general group-by-

time-dependent CJS model (where group was site-by-sex) were then run separately for each
 species using the R2ucare package (Gimenez et al. 2018; Appendix S3).

We built a Bayesian formulation of the CJS model applying a Markov Chain Monte Carlo (MCMC) sampling procedure (Lahoz-Monfort et al. 2011) implemented in JAGS (Plummer 204 2003) called from R version 3.5.1 (R Development Core Team 2015) using the R-package R2jags version 4.2.0 (Su and Yajima 2015). For our base model (model 1 thereafter), the survival probability ($\phi_{i,t}$) of an individual i at time t was modeled as

 $logit(\phi_{i,t}) = \mu_{sp(i)} + \beta_{sex}sex_i + u_{site(i)} + u_{year(t)} + u_{year:species(i,t)}$, where $\mu_{sp(i)}$ is a species-specific intercept, β_{sex} is the effect of the bird being female, and $u_{site(i)}$ is a random deviation for the site i on which the bird breeds; we assume that those deviations follow a normal distribution of mean zero and variance σ_s^2 , which we write as $u_{site} \sim N(0, \sigma_s^2)$. Further, the random deviation for years follows $u_{year} \sim N(0, \sigma_\delta^2)$, and the random deviations for species within years follow $u_{year:species} \sim N(0, \sigma_\varepsilon^2)$. Following Grosbois et al. (2009), the year random variance (σ_δ^2) quantifies the amount of between-year variation that is common to all species, across all sites (synchronous, country-level, inter-annual variation), and the Year-by-Species random variance (σ_ε^2) quantifies the between-year variation that differs between species (asynchronous, country-level, inter-annual variation). Note that σ_δ^2 and σ_ε^2 are parameters common to all species.

Therefore, our models accounted for the variation of apparent survival and recapture probabilities between sexes (assuming effects common to all species), species and sites (see Appendix S4 and code shared on Zenodo). We addressed only synchrony across all sites, ignoring the spatio-temporal variance (i.e., Site:Year random variance) and the within species

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spatio-temporal variance (i.e., Species:Site:Year random variance) in apparent adult survival probability. Such a full, hierarchical partitioning of variance was not achievable with the amount of mark-recapture data available within the year by site by species combinations.

We modeled recapture probability for individual *i* at time *t* as

 $logit(p_{i,t}) = v_{sp(i)} + \gamma_{sex}sex_i + \gamma_{het}het_i + v_{site(i)} + v_{year(t)}$, where $v_{sp(i)}$ is a species-specific intercept, γ_{sex} is the effect of the bird being female, and γ_{het} is the effect of between-individual heterogeneity in capture probability (detailed in Appendix S4). Finally, v_{site} and v_{year} are both normally distributed with means of zero and variances to be estimated.

We chose weakly informative priors for all parameters. Details on specification of prior distributions for the parameters and satisfactory convergence criteria are provided in Appendix S4. We report posterior modes as point estimates and 95% highest posterior density credible intervals to show estimation uncertainty. We report posterior probabilities, pMCMC, computed as twice the proportion of MCMC values above 0, for a negative point estimate, or below 0, for a positive point estimate (analog to a two-sided frequentist p-value). All calculations were done for the full posterior distribution in order to propagate uncertainty.

Interspecific synchrony in survival

From model 1, we calculated a between-species intra-class correlation (*ICC*) of temporal variation to quantify country-level, between-year synchrony in adult survival across species, on the logit scale, defined as $ICC = \sigma_{\delta}^2/(\sigma_{\delta}^2 + \sigma_{\varepsilon}^2)$.

The approach used for model 1 differs from Lahoz-Monfort et al. (2011) in that we defined σ_{ε}^2 and ICC common to all species, while Lahoz-Monfort et al. (2011) estimated species-specific parameters, $\sigma_{\varepsilon species}^2$ and $ICC_{species} = \frac{\sigma_{\delta}^2}{(\sigma_{\delta}^2 + \sigma_{\varepsilon species}^2)}$. We also fitted the model corresponding to Lahoz-Monfort et al. (2011) and name it model 2. In this model, survival follows the same equation as for model 1, except that $u_{year:species} \sim N(0, \sigma_{\epsilon species}^2)$, i.e. the random deviations for species within years follow different distributions for each species, with one $\sigma_{especies}^2$ estimated for each of the 16 species. From model 2, we calculated the average of the 16 ICC_{species} point estimates and compared it to the global ICC calculated from model 1. Model 2 allows us to test for effects explaining variation in ICC_{species} among species. Thus, we fitted a general linear model of ICC_{species} as a function of either of two species characteristics: migratory class, a factor with two levels, long-distance vs. short-distance or resident species, or species sample size; we integrated the model over each sample of the full posterior distributions of ICC_{species} to propagate estimation uncertainty. We explain other pros and cons of model 1 and model 2 in Appendix S4. Note that we report ICCs on the logit scale, not on the natural scale of survival probability. Arguably, ICC on the logit scale is more biologically relevant because it expresses differences as log odds-ratios and

does not depend on average survival probability. For the range of parameter values considered

(mean survival, variance on the logit-scale, and ICC), the difference between ICCs on the two

258 scales is minimal (see Appendix S4).

Migratory strategy (model 3)

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Because of shared conditions among species wintering in the same regions, migratory strategy could explain part of the overall synchrony in annual survival. To quantify the importance of this effect, we fitted Model 3, a variation of Model 1 with a random effect for the interaction year-by-migratory strategy (long-distance vs. short-distance migrant or resident). The equation for survival thus became:

- $logit(\phi_{i,t}) = \mu_{sp(i)} + \beta_{sex}sex_i + u_{site(i)} + u_{year(t)} + u_{year:species(i,t)} + u_{year:migration(i,t)}, \text{ with }$
- 266 $u_{year:species} \sim N(0,\sigma_{\varepsilon w}^2)$ and $u_{year:migration} \sim N(0,\sigma_m^2)$.
- We thus modeled a year-by-migratory strategy variance σ_m^2 , while σ_δ^2 remained the Yearvariance common to migratory strategies and species, and $\sigma_{\varepsilon w}^2$ was the within-migratory strategy within-species year variance. The proportion of total annual variance attributed to migratory
- strategy (i.e., synchrony within migratory strategy) was estimated as $ICC_m =$
- 271 $(\sigma_m^2)/(\sigma_\delta^2 + \sigma_m^2 + \sigma_{\varepsilon w}^2)$. The proportion of total annual variance common to all species was
- estimated as $ICC = \frac{\sigma_{\delta}^2}{(\sigma_{\delta}^2 + \sigma_m^2 + \sigma_{\varepsilon w}^2)}$. If migratory strategy explains no synchronous variation,
- the *ICC* from model 3 will approach the *ICC* calculated from model 1.
- Yearly weather covariates (models 4 and 5)
- Weather conditions during the breeding period (April to July) were characterized for each site and year using daily mean temperature and daily sum precipitation (as in Grosbois et al. 2006, Eglington et al. 2015, Gaüzère et al. 2015, Dubos et al. 2018) from the "E-OBS" meteorological
- dataset (available at https://www.ecad.eu/), with a 0.25° pixel (approximately 20 km by 28 km)
- 279 resolution using the R-package climateExtract (available at https://github.com/RetoSchmucki).
- Since organisms are expected to be adapted to average local conditions (e.g. Dubos et al. 2019),
- we tested for an effect of departure from local average weather conditions, i.e., local spring

weather anomalies. Anomalies were computed for each variable, site and year as the difference 282 between the local value for a given spring and the mean over the 2001–2016 period (as in Dubos 283 et al. 2018). For the effect sizes for temperature and precipitation to be comparable, anomalies 284 were standardized by dividing them by the standard deviation across all sites and years. 285 However, we then used the yearly averages of anomalies across all sites to capture the 286 287 synchronizing effect of weather variables (Appendix S5: Figure S1). To explain between-species synchrony in annual survival variations that could be attributed to 288 large-scale fluctuations in spring weather conditions, we fitted Model 4, which added terms to 289 Model 1 including fixed effects for the linear and quadratic effects of spring temperature (θ) and 290 precipitation (π) anomalies, effects known to explain bird survival (Boyles et al. 2011, Pomara 291 & Zuckerberg 2017), plus the four pairwise interactions between temperature and precipitation: 292 $\beta_{\theta}\theta_{i,t} + \beta_{\pi}\pi_{i} + \beta_{\theta2}\theta_{i,t}^{2} + \beta_{\pi2}\pi_{i,t}^{2} + \beta_{\theta:\pi}(\theta_{i,t}\pi_{i,t}) + \beta_{\theta:\pi2}(\theta_{i,t}\pi_{i,t}^{2}) + \beta_{\theta2:\pi}(\theta_{i,t}^{2}\pi_{i,t}) + \beta_{\theta2:\pi2}(\theta_{i,t}^{2}\pi_{i,t}^{2}),$ 293 where, for instance $\beta_{\theta 2:\pi}$ is the coefficient for the interaction between squared standardized 294 temperature deviations and standardized precipitation deviations and $(\theta_{i,t}^2\pi_{i,t})$ is the product of 295 squared standardized temperature deviations and standardized precipitation deviations. 296 We included quadratic and interactive effects a priori, without performing model selection. 297 This approach should be seen as an attempt to estimate an upper bound to the variance, and thus 298 synchrony, that can be ascribed to the weather variables available, rather than an attempt to test 299 the potential causal effects of weather presented in introduction or to produce a predictive 300 301 model. Following Nakagawa and Schielzeth (2013), we estimated the synchronous variance 302 explained by spring weather (σ_{sw}^2) as the variance in partial model predictions (that is, the linear 303

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combination of the products of each parameter estimate by the corresponding weather variable): 304 $\sigma_{sw}^2 = var(\sum_{h=1}^8 \beta_h \dot{x}_{ht})$ where h indexes the eight model parameters related to spring weather, β_h 305 is the parameter estimate for the effect of h, and \dot{x}_{ht} is the mean value of the weather variable h306 in year t (across all sites). By definition σ_{sw}^2 captures only synchronous variation. Therefore we 307 calculated the proportion of synchronous variation related by spring weather as $\sigma_{sw}^2/(\sigma_{\delta}^2 + \sigma_{sw}^2)$, 308 and the new $ICC = (\sigma_{sw}^2 + \sigma_{\delta}^2)/(\sigma_{sw}^2 + \sigma_{\delta}^2 + \sigma_{\varepsilon}^2)$. 309 In Model 5, we added covariates related to winter weather to Model 1. For resident and short-310 distance migrants, which spend the winter in western Europe or North-Africa, we used the North 311 Atlantic Oscillation during winter (wNAO, averaged from December to March, available at 312 http://www.cru.uea.ac.uk/~timo/datapages/naoi.htm). The wNAO captures broad scale weather 313 variation in Western Europe and North Africa (Forchhammer & Post 2004), which explains 314 variations in over-winter survival in several European bird species (Robinson et al. 2007, 315 Salewski et al. 2013). For long-distance migrants that winter in Western Africa, we used the 316 Sahel Rainfall during summer (sSR, averaged from July to September, available at 317 http://research.jisao.washington.edu/data_sets/sahel/). The sSR is often used as a proxy of winter 318 Sahel suitability for wintering songbirds, considering that habitat quality in December–February 319 is driven by rainfall during the previous summer (Robinson et al. 2007, Salewski et al. 2013). 320 As was done for spring weather covariates, we fitted linear and quadratic effects for wNAO 321 and sSR. We estimated the synchronous variance explained by winter weather (σ_{ww}^2) as the 322 variance in partial model predictions from the linear and quadratic effects of wNAO and sSR. 323 The synchronous variance due to winter climate (σ_{ww}^2) is the variance among years in survival, 324 averaged over species, predicted from differences in wNAO and sSR only, which we write as 325

- 326 $\sigma_{ww}^2 = var_t(E_{species}(\phi | \text{winter climate}))$. We can decompose the average between the two
- 327 migratory strategies as
- 328 $\sigma_{ww}^2 = var_t(mE_{migratory}(\phi|sSR) + (1-m)E_{resident}(\phi|wNAO))$ where *m* is the proportion of
- 329 long-distance migratory species. The two conditional averages are the sum of an average
- 330 survival independent of winter climate and anomalies due to the effects of winter climate:
- 331 $\sigma_{ww}^2 = var_t$
- 332 $(m\alpha_1 + m(\beta_{SSR}SSR + \beta_{SSR2}SSR^2) + (1-m)\alpha_2 + (1-m)(\beta_{wNAO}wNAO + \beta_{wNAO2}wNAO^2))$, where α_1
- and α_2 are baseline survival probabilities independent of winter climate and are scalars, hence
- 334 $\sigma_{ww}^2 = var_t(m(\beta_{sSR}sSR + \beta_{sSR2}sSR^2) + (1-m)(\beta_{wNAO}wNAO + \beta_{wNAO2}wNAO^2))$ (see Appendix S6
- 335 for formula validation).
- This variance is a function of the effect of sSR among migratory species, of the effect of wNAO
- among resident species, and of the small negative covariance between sSR and wNAO (the two
- 338 indices are expected to be independent, but the empirical Pearson correlation coefficient was -
- 339 0.12, 95% confidence interval [-0.58;0.40]). The proportion of synchronous variance related to
- winter weather was calculated as $(\sigma_{ww}^2)/(\sigma_{\delta}^2 + \sigma_{ww}^2)$, and the $ICC = (\sigma_{ww}^2 + \sigma_{\delta}^2)/(\sigma_{ww}^2 + \sigma_{\delta}^2 + \sigma_{\epsilon}^2)$.
- 341 All parameter estimates for all models are provided in Appendix S7.

343

RESULTS

- 344 Interspecific synchrony of annual adult apparent survival
- Inter-annual variation in adult apparent survival probabilities was largely synchronous across
- the 16 study species (Fig. 2). Model 1 *ICC* of 73%, 95% highest posterior density credible

interval = [47–94%] indicates that most of the temporal variance in apparent survival 347 probabilities was common to all species (Table 1: Model 1). Conversely, this implies that 348 within-species variation corresponded to only 27% [6–53%] of temporal fluctuations of survival 349 probabilities. 350 Species showed considerable variation in Model 2 *ICC*_{species} (Fig. 3), although estimates came 351 with broad credible intervals. There was no significant association between the value of IC 352 C_{species} and migratory strategy (Fig. 3; pMCMC=0.48) nor with species sample size 353 (pMCMC=0.31). The mean of the 16 species posterior mode estimates for ICC_{species} was 76% 354 355 (Table 1: Model 2). This strong synchrony was robust to (i) the uneven contributions of species to the mark-356 recapture dataset (ICC = 65% [28-90%], Appendix S8), (ii) the removal of the part of synchrony 357 due to a potential linear trend in survival probabilities (ICC = 56% [23–86%], Appendix S9; 358 note that this calculation necessarily excludes some true synchrony), (iii) the choice of prior 359 distributions (Appendix S10), and (iv) the effects of weather and migratory strategy presented 360 below. 361 Graphically, some years seemed to deviate more from the mean survival probability (Fig. 2) 362 and may have contributed more to synchrony: estimates of survival probabilities between the 363 years 2001–2002, 2002–2003 were larger than average while estimates for the years 2005–2006 364 and 2008–2009 were particularly low (Appendix S11: Figure S2). However, our ad hoc 365 approach using model estimates failed at identifying statistical support for variability in yearly 366 contributions to interspecific synchrony (Appendix S11). 367

Contributions of migratory strategy to synchrony in survival probabilities

In Model 3 the interaction between year and migratory strategy captured only a small amount of asynchronous-variation in survival among species, with $ICC_m = 9\%$ [0–32%] (Table 1). After removing the synchrony within migratory strategy the variance common to all species was ICC = 65% [30–91%]. This low dependence of synchrony on migratory strategy is apparent in Fig. 2 and Fig. 3.

Contributions of weather to synchrony in survival probabilities

According to Model 4, spring weather variables taken together explained only 1.4% [0.01–5.5%] of synchrony, whereas according to Model 5, the winter weather variables explained 12% [0.3–37%] of the synchrony. Assuming spring and winter weather variables are uncorrelated, together they explain 13% [0.8–39%] of synchrony and 10% [0.6–23%] of the total temporal variance (Table 1). There was no clear evidence for an effect of any of the weather-related parameters on survival probability, with all credible intervals overlapping zero (across all species, i.e. additive effects; Appendix S5: Table S1). Higher spring precipitation and more extreme spring temperatures tended to increase survival probability (Appendix S5: Figure S1). Regarding winter weather covariates, survival probability appeared a bit higher for high Sahara rainfall values during summer (sSR), while there was no discernible effect of the North Atlantic Oscillation during winter (wNAO) across all species (i.e. additive effects; Appendix S5: Figure S2).

DISCUSSION

Unexpectedly, annual fluctuations in adult apparent survival were largely synchronous across the 16 songbird species that dominate bird communities in France: 73% [47–94%] of between-

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differences in migratory strategy among species, uneven species sample sizes, and time detrending. This strong synchrony is remarkable given that these species differ in various properties linked to apparent survival: they cover the range of songbird migratory strategies. body mass (8 to 88 g) and number of broods per year, and they partly differ in habitat and ecological specialization (Appendix S1). Moreover, our estimates represent minimal synchrony since they are not controlled for potentially desynchronizing factors like intra- and interspecific negative density dependence. Estimated synchrony should be higher if we could control for those factors (Péron and Koons 2012, Swallow et al. 2016). Our estimates of interspecific synchrony are as high as estimates of spatial synchrony in apparent survival probabilities across some populations of a same species, with for instance values of 67% and 71% in two long-lived birds (Jenouvrier et al. 2009, Grosbois et al. 2009), and higher than the interspecific synchrony in survival (49%) estimated for two closely related duck species (Péron and Koons 2012). Shortlived vertebrate animals, such as our study species, are under stronger environment-dependence than long-lived species (Saether et al. 2016), which may contribute to the high interspecific synchrony observed. The species-specific synchronies ($ICC_{species}$) varied from very high to low (Figure 4). This

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year variance in survival probabilities was common to all species. This result was robust to

The species-specific synchronies ($ICC_{species}$) varied from very high to low (Figure 4). This means that within some species, such as the Cetti's Warbler, $Cettia\ cetti$ (with ICC = 0.12, 95%CI [0.03; 0.60]), there was considerable temporal variability in adult survival, probably due to the species' high sensitivity to winter harshness (Moussus 2010). Conversely, in other species such as the widespread Eurasian Blackcap, $Sylvia\ atricapilla$ (with ICC = 0.99, 95% CI [0.61;1]), the temporal variability in adult survival corresponded almost entirely to the average

variability across the 16 species. Morrison et al. (2022) also reported a wide range of species-
specific synchronies, although our estimates were generally a bit higher: Our point estimates
were never below 0.10 (vs. a minimum of 0.03) and were above 0.80 for 9 out of 16 species (vs.
2 out of 26 species). The broader geographic range covered by Morrison et al. (2022), spanning
eight European countries, may contribute to the lower $ICC_{species}$. Differences in $ICC_{species}$ may be
influenced by heterogeneity in the spatio-temporal distribution of captures among species (see
Fig. 1), but we did not find a clear pattern explaining differences in synchrony among species
(i.e., range, migration class, sample size, habitat), and species-specific synchronies were
estimated with broad confidence intervals. Therefore, the determinants of interspecific
synchrony remain to be identified with a larger dataset, if possible involving more species, more
diverse life history traits, and more years. Drivers that differ between species and determine
local survival dynamics must occur and operate at the level of sites or regions (Giraud et al.
2013, Gaüzère et al. 2015, Cayuela et al. 2019, Morrison et al. 2013, 2021). In any case, our
moderate and high estimates of $ICC_{species}$ indicate that the drivers of annual variations in adult
apparent survival at the country level are largely common to many species.
Climate forcing could be responsible for synchronous events of high mortality among species,
either through direct or indirect effects. A few studies have shown that climate forcing was
responsible for at least a part of the observed interspecific synchrony in abundances or vital rates
in common songbirds (Jones et al. 2003, Grosbois et al. 2006, Koenig and Liebhold 2016,
Swallow et al. 2016, Telenský et al. 2020). However, within species, neither broad scale climatic
variables nor local weather variables explained synchronous survival variation in blue tit
populations (Bastianelli et al. 2021), and synchronous survival in little auk populations was

better explained by trophic interactions than climate (Reiertsen et al. 2021). In the present study we failed to identify a statistically significant role for any climatic variables, and altogether those variables explained only 13% [0.8–39%] of the interspecfic synchrony. Nevertheless, we likely underestimated the importance of climate. First, the variables we used did not explicitly consider weather properties such as extreme temperature or precipitation events (e.g., Gardner et al. 2022), or species-specific periods of sensitivity to weather (van de Pol et al. 2016). Second, we used variables averaged either over spring or winter, which is unlikely to represent the cumulative effect of climatic variations experienced throughout the year. Finally, our modeling investigated the direct effects of weather whereas indirect or delayed effects may be more influential, particularly weather-driven primary and secondary productivity and their effects on the cost of reproduction (see below).

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Apart from direct climate forcing other mechanisms could synchronize adult annual local survival across species (Reiertsen et al. 2021). First, synchronous variation in prey abundance could generate interspecific synchrony. Since all songbirds feed their chicks exclusively with invertebrates, a high invertebrate abundance could lower the foraging effort of breeding adults during chick rearing, decrease exposure to predators, and ultimately increase adult survival (Eglington et al. 2015). Therefore, the survival of songbird species could be synchronized by a spatial synchrony in invertebrate abundance, itself possibly caused by high precipitation and hot temperatures (Jones et al. 2003, Sheppard et al. 2015, Eglington et al. 2015, Kahilainen et al. 2018, Dubos et al. 2018, 2019). A remarkable food-supplementation experiment even demonstrated that food availability during breeding has a direct effect on annual adult survival in a long-distance migratory species: simply increasing food availability during reproduction (i.e.,

over 4–5 months) increased annual survival by 5% (Seward et al. 2013). Moreover, in highly productive years, a higher proportion of adults engage in rearing a second brood (Visser et al. 2003), potentially at a supplementary cost in terms of survival (Woodworth et al. 2017a). If facultative multi-brooding species (62% of studied species; Appendix S1) are synchronous in their choice to lay a second brood, their adult survival could be synchronized by the cost of reproduction. Schaub et al. (2015) demonstrated that the probability of double brooding was actually the most synchronous vital rate across the 9 populations of an aerial insectivorous songbird, the Barn Swallow, *Hirundo rustica*.

Second, intra- and interspecific competition for shared resources likely operate at the level of the local songbird community, potentially resulting in large-scale, weather-driven density-dependent regulations of adult survival. Nevertheless, intraspecific density-dependence can also be a source of asynchrony across species (Péron and Koons 2012, Martin et al. 2017). The net role of community-level density-dependence in synchronizing adult survival probabilities across species remains to be properly investigated (Swallow et al. 2016).

Third, breeding dispersal could contribute to interspecific synchrony in adult apparent survival. Apparent survival results from survival and residency (i.e. absence of dispersal, Saracco et al. 2010) at the scale of study sites. Interspecific synchrony in apparent survival could occur if individuals of different species tend to disperse more synchronously in some years than in others. Following a bad reproductive experience at one location (e.g., weather-driven early reproductive failure) a higher proportion of adults settles away in the following year (e.g., Arlt and Part 2008). However, only a small proportion of adults typically emigrates between breeding events, even in long-distance migrants (Greenwood and Harvey 1982), and males, the most

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resident sex in birds (Amrhein et al. 2012), represent a majority (64%) of individuals in our dataset. Therefore, synchronous breeding dispersal alone seems unlikely to have caused the estimated high interspecific synchrony in adult apparent survival.

Could conditions during the non-breeding season explain the high synchrony in adult survival across songbirds in France? Across long-distance migrants, short-distance migrants and residents, we found that winter conditions explained 12% [0.3–37%] of the interspecific synchrony. This proportion is low, but potentially significant biologically, and, as already explained, we likely underestimate the synchronizing importance of weather. Winter harshness is commonly proposed to explain variation in year-round mortality in small organisms like songbirds (Grosbois et al. 2006, Robinson et al. 2007, Salewski et al. 2013, Johnston et al. 2016, Saether et al. 2016), including in migratory songbirds (Robinson et al. 2007, Woodworth et al. 2017b). Recent studies on multi-species population synchrony have also emphasized a major role of winter climate forcing, but these few studies were biased towards cold-driven ecosystems, like high latitude populations that are subject to extreme winter events such as rainon-snow icing events (Post & Forchhammer 2004, Jones et al. 2003, Hansen et al. 2013, Pomara & Zuckerberg 2017). Restricting the analysis to long-distance migrant species only, Telenský et al (2020) found that water availability on the wintering grounds explained 15% of the temporal variation in survival, but the result was not statistically significant. Overall, it seems likely that conditions on the non-breeding grounds, especially climate, contribute somewhat to the interspecific synchrony in adult survival, even though the 16 studied species spread from France to Central Africa during the winter.

Differences in migratory strategy explained little temporal variation in survival probability. Synchrony across all species, calculated after removing the synchrony within migration classes, was similar to synchrony calculated without accounting for migratory strategy (Table 1: Model 3). This high synchrony in adult survival across resident and long-distance migrant species, wintering on two different continents (at a distance of 2000–3000 km and 35–45° in latitude) has profound implications for our understanding of the regulation of migratory bird populations. Breeding habitat degradation appears as the major cause of ongoing massive, synchronous population declines (Eglington and Pearce-Higgins 2012), including in migratory species (Morrison et al. 2013). Our results and these studies suggest that habitat quality or productivity over breeding areas is critical for year-round songbirds population dynamics, even for migratory species that spend only 3-4 months per year on their breeding grounds (Morrison et al. 2013).

At least graphically (Fig. 2), some years appear to increase synchrony, with large interspecific deviations in survival probabilities. Synchrony is expected to be heterogeneous across years, or even transitory (Klapwijk et al. 2018), and to be largely attributable to the occurrence of environmental disturbances in some years (Cattadori et al. 2005, Keitt 2008). For instance, Jenouvrier et al. (2009) showed that the high spatial synchrony (71%) in Scopoli's shearwater adult apparent survival was attributed to only two 'low' years out of eight. In 'normal' years, species specificities (e.g., ecological niche differentiation) would dominate and drive variation in survival probabilities (Liebhold et al. 2004, Robinson et al. 2013). As climate warms and increasingly fluctuates through time with stronger and more frequent extreme weather events, spatial synchrony and interspecific synchrony are likely to increase in strength

(Post and Forchhammer 2004, Hansen et al. 2013, Koenig and Liebhold 2016, Hansen et al. 2020) over wider spatial scales (Black et al. 2018). A longer timer series would be necessary to properly assess the yearly contributions to synchrony and to quantify differences in synchrony over different time periods. Analytical methods are also not yet readily implementable to such multi-year, multi-site, multi-species mark-recapture dataset (Cattadori et al. 2005, Lahoz-Monfort et al. 2017).

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The accumulation of data over several decades should also allow fitting of more complex models. In the present work we ignored interactions between site and species or time. However, modeling fine-scale time by space by species variation in survival across sites would provide a more nuanced view of the dynamics of survival. By exploiting the heterogeneity among sites in environmental conditions and species community compositions, such modeling could be used to investigate the causes for differences in interspecific synchrony among sites. It would also allow disentangling the effects of global cross-sites weather effects that generate broad-scale synchrony in average survival, from local site-level weather events that necessarily desynchronize survival among sites (Fig. 4 in Wan et al. 2022, Morrison et al. 2021).

Models could also be improved by explicitly accounting for spatial auto-correlation in survival across sites. In the present study we ignored spatial auto-correlation, primarily because of the necessity to limit model complexity. One might therefore expect our models to underestimate uncertainty in parameter estimates. However, in the present dataset, results should be robust to this simplification: a post-hoc analysis exploring the potential spatial auto-correlation of survival estimates across sites, using the random site-level effect estimates (BLUPs), revealed a weak and negative spatial auto-correlation (Moran's I = -0.05, null

expected I = -0.004, null expected I standard deviation = 0.028, p-value=0.10): survival tends to be more dissimilar among closer sites than among distant sites. Nonetheless, future models investigating simultaneous intra-specific and interspecific synchrony could benefit from accounting for spatial auto-correlation to ensure estimation robustness and to gain more biological insight.

The present study focused on synchrony in adult apparent survival, but population size fluctuations can be asynchronous despite synchrony in some vital rates. Indeed, vital rates taken separately are expected to be more commonly synchronized than population sizes, due to "compensatory mechanisms" such as life-history trade-offs, demographic buffering (Schaub et al. 2015, Saether et al. 2016), and intra- and interspecific density-dependence regulations (Péron and Koons 2012, Tavecchia et al. 2016, Lahoz-Monfort et al. 2017). Ultimately, it is synchrony in population sizes that can cause extinction. Nevertheless, studying synchrony only in population sizes does not allow inference about the mechanisms driving synchrony, and impedes predicting their respective role in future extinction risk. Future research should aim to jointly model synchronous variation and covariation in breeding success, age-dependent survival, and age-dependent dispersal for several co-occurring species. Such modeling would not only allow the study of synchrony of population growth rate and population size, but would also help identify (a)synchronizing mechanisms at complementary organizational levels (individuals, populations, communities).

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TABLE 1. Variance component estimates for survival probability under different models. Model 1 is the base model and captures all of the synchrony in the Year variance parameter. Other models include various effects that may or may not explain some of the synchrony, thus leaving a corrected synchrony as the Year variance parameter. Estimates are posterior modes and 95% highest probability density credible intervals.

Variance	Model 1	Model 2	Model 3	Model 4	Model 5
component	Base model	Species-specific	Migration:Year	Spring weather	Winter weather
		synchrony		a	a
Year	0.098	0.090	0.091	0.091	0.092
(synchrony)	[0.031–0.234]	[0.016-0.203]	[0.009–0.205]	[0.023-0.216]	[0.019–0.214]
Model-specific	-	_ b	0.011	0.001	0.008
synchrony term			[0-0.036]	[<0.001-0.0029]	[<0.001-0.020]
Year:Species	0.034	0.026 °	0.032	0.034	0.036
(asynchrony)	[0.012–0.068]		[0.007-0.065]	[0.007-0.062]	[0.010-0.066]
Site	0.155	0.157	0.152	0.156	0.152
	[0.076–0.232]	[0.088-0.237]	[0.085-0.226]	[0.081-0.232]	[0.087–0.226]
Variance sum ^d	0.287	-	0.286	0.287	0.286
ICC e	73% [47–94]	Mean 76%	65% [30–91]	72% [47-93]	68% [36-95]

Notes: a. Weather variables were introduced as fixed effects and the variance they explain was computed post-hoc, while all other variance components were directly estimated as random effects.b. In model 2 synchrony is estimated separately for each of the 16 species, see Fig. 3. c.

Mean of the 16 species-specific point estimates. d. The sum of the variances is expected to be constant, but may vary slightly due to rounding, and because survival is not directly observed but predicted as a latent variable (i.e., survival does not have a defined variance observable independently of a model). e. Intra-class correlations (see Methods) are estimates of synchrony across species, i.e., the proportion of Year variance over 'total' temporal variance, which varies across models.

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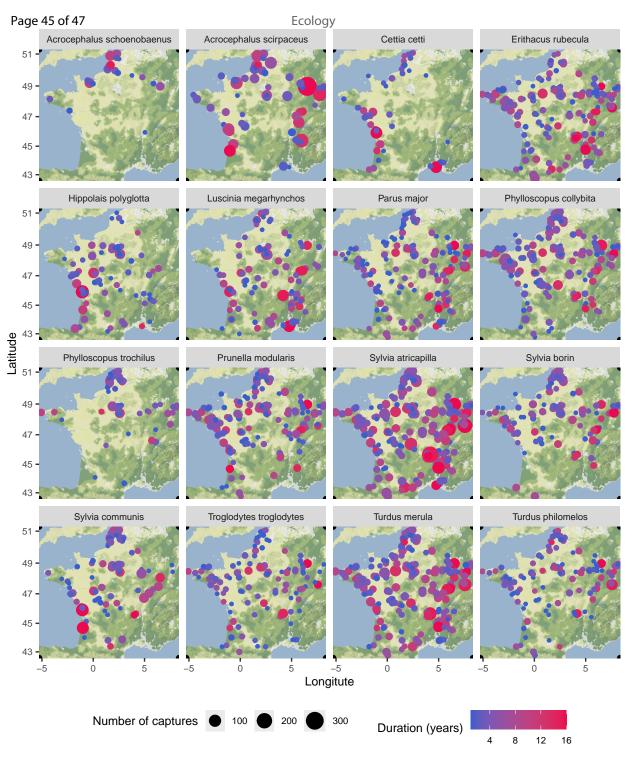
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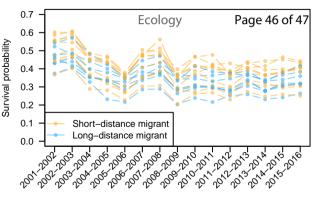
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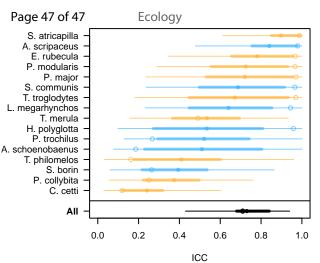
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FIGURE 1. For each species, spatio-temporal distribution of the 242 sites across continental France used in this study. Color corresponds to the number of years for which we estimated survival in our models. The true duration of the monitoring at the site is always at least one more year. Point size indicates the total number of captures used in analyses, excluding transient individuals, for a given site. FIGURE 2. Inter-annual fluctuation of local survival probabilities by species for adult individuals. Estimates were obtained independently for each species (with resident males as intercept) from a model with fully Year-dependent survival and explicitly modeling an interaction between Year and Migratory behavior (resident/short-distance migrants versus long-distance migrants, i.e. model 5). FIGURE. 3. Interspecific synchrony for each species and overall. Estimates of Intra-Class Correlations measuring interspecific synchrony in adult survival, for each species separately, and across all species taken together. A lower species-specific synchrony means that mean survival probability is more variable in that species. Species-specific estimates were obtained from model 2, while the overall estimate was obtained from model 1. Yellow lines represent short-distance migrants, blue lines represent long-distance migrants. Filled circles represent posterior means, empty circles posterior modes, thick lines 50% quantile CI and thin lines 95% HPD CI.

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Supporting Information for:

Authors:

Manon Ghislain, Timothée Bonnet, Ugoline Godeau, Olivier Dehorter, Olivier Gimenez, and Pierre-Yves Henry

Title:

Synchrony in adult survival is remarkably strong among common temperate songbirds across France

Journal: **Ecology**

APPENDIX S1. DESCRIPTION OF STUDIED SPECIES

TABLE S1. List of species considered, with summary information on sample sizes, mean value of the individual covariate for capture heterogeneity (see Appendix S4), average apparent survival probability (with 95% credible interval), migratory strategy, habitat traits, number of broods per year and body mass.

Species	Number of adult individuals	Number of individuals with at least one recapture in another year	Individual covariate for heterogeneity in recapture probability (relative mean) ¹	Apparent survival probability ²
Acrocephalus schoenobaenus	335	60	1	0.365 [0.314–0.42]
Acrocephalus scirpaceus	2149	740	0.86	0.470 [0.438–0.502]
Cettia cetti	455	166	0.99	0.416 [0.377–0.456]
Erithacus rubecula	1433	269	0.84	0.360 [0.328–0.394]
Hippolais polyglotta	740	151	0.74	0.410 [0.369–0.451]
Luscinia megarhynchos	1189	441	0.74	0.503 [0.471–0.535]
Parus major	939	143	0.56	0.369 [0.332–0.407]
Phylloscopus collybita	1769	279	0.78	0.296 [0.267–0.326]
Phylloscopus trochilus	539	118	0.82	0.365 [0.326–0.407]
Prunella modularis	1408	453	0.69	0.464 [0.434–0.494]
Sylvia atricapilla	3890	744	0.67	0.431 [0.403–0.459]
Sylvia borin	1038	246	0.73	0.457 [0.421–0.494]
Sylvia communis	1111	244	0.83	0.370 [0.335–0.405]
Troglodytes troglodytes	568	99	0.74	0.307 [0.27–0.348]
Turdus merula	2800	936	0.57	0.499 [0.47–0.528]
Turdus philomelos	549	109	0.55	0.465 [0.423–0.509]

Species	Habitat specialization index ³	Habitat ³	Migratory behavior ³
Acrocephalus schoenobaenus	34.1	Humid shrub land (reed)	Long-distance migrant
Acrocephalus scirpaceus	23.8	Humid shrub land (reed)	Long-distance migrant
Cettia cetti	21	Humid shrub land (reed)	Sedentary or short-distance migrant
Erithacus rubecula	29.7	Terrestrial shrub land / Forest	Sedentary or short-distance migrant
Hippolais polyglotta	43.2	Terrestrial shrub land / Forest	Long-distance migrant
Luscinia megarhynchos	28.4	Terrestrial shrub land / Forest	Long-distance migrant
Parus major	40.3	Terrestrial shrub land / Forest	Sedentary or short-distance migrant
Phylloscopus collybita	31.3	Terrestrial shrub land / Forest	Sedentary or short-distance migrant
Phylloscopus trochilus	28.3	Terrestrial shrub land / Forest	Long-distance migrant
Prunella modularis	38.7	Terrestrial shrub land / Forest	Sedentary or short-distance migrant
Sylvia atricapilla	39.6	Terrestrial shrub land / Forest	Sedentary or short-distance migrant
Sylvia borin	33.4	Terrestrial shrub land / Forest	Long-distance migrant
Sylvia communis	25.2	Terrestrial shrub land / Forest	Long-distance migrant
Troglodytes troglodytes	31.5	Terrestrial shrub land / Forest	Sedentary or short-distance migrant
Turdus merula	39.1	Terrestrial shrub land / Forest	Sedentary or short-distance migrant
Turdus philomelos	33.1	Terrestrial shrub land / Forest	Sedentary or short-distance migrant

Notes. ¹ The recapture probability heterogeneity index is defined in Appendix S4. Values were averaged across individuals of the same species; and species means were standardized across species (with *A. schoenobaenus* as reference). ²Annual, adult, apparent survival probabilities have been estimated for resident males (*i.e.* males recaptured at least once at the same site) with Model 1, and averaged across years. ³ Habitat species specialization index values come from Godet et al. (2015); the lowest the value, the more the species is specialized. Other traits were obtained from Storchová and Hořák (2018).

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APPENDIX S2. SPECIES NUMBER PER SITE

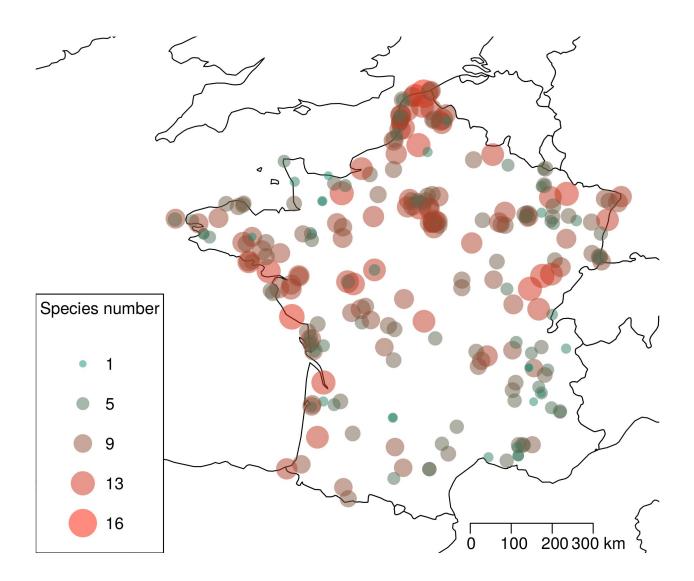


Fig S1. Number of species per site included in the dataset. There are 242 sites spread over continental France, and 16 species.

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APPENDIX S3. GOODNESS-OF-FIT TESTS

TABLE S1. Details of goodness-of-fit tests for the Cormack-Jolly-Seber (CJS) model for each species.

Species	χ²	Degrees of freedom	P-value for global test	P-value for transient test (3.SR)	P-value for trap-dependence test (2.CT)
Acrocephalus schoenobaenus	14.974	19	0.724	0.309	1.000
Acrocephalus scirpaceus	65.079	53	0.123	0.010	0.598
Cettia cetti	22.114	30	0.850	0.766	0.397
Erithacus rubecula	Insufficient data	40	Insufficient data	0.012	Insufficient data
Hippolais polyglotta	42.113	38	0.297	0.104	0.261
Luscinia megarhynchos	44.548	49	0.654	0.497	0.331
Parus major	14.322	36	1.000	0.857	0.952
Phylloscopus collybita	16.877	34	0.994	0.452	1.000
Phylloscopus trochilus	Insufficient data	30	Insufficient data	0.951	Insufficient data
Prunella modularis	46.721	43	0.322	0.034	0.552
Sylvia atricapilla	55.768	50	0.267	0.004	0.821
Sylvia borin	36.322	42	0.718	0.626	0.292
Sylvia communis	47.939	43	0.279	0.006	0.612
Troglodytes	12.149	21	0.936	0.747	0.857

troglodytes

Turdus merula	64.940	54	0.146	0.100	0.111
Turdus philomelos	12.355	43	1.000	0.934	1.000

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Authors:

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APPENDIX S4. MODEL DETAILS

1.1 PARAMETER DEFINITIONS, PRIORS AND CONVERGENCE CRITERIA

Model parameter definitions and details on specification of prior distributions are provided in Table S1. In all models, local survival and recapture probabilities were adjusted for (i) sexdependency (three-level fixed effect: female, male, unknown, Amrhein et al. 2012, sexing was straightforward for sexually dimorphic species, i. e. 5 species out of the 16; dor the 9 other species, sexing was based on physiological evidence of reproductive activity, brood patch for females, cloacal protuberance for males, Svensson 1992), (ii) among-species differences (16 species, 16-level fixed effect), and (iii) among-site differences (random effect). Following Julliard 2004, heterogeneity across individuals (both within and across sites) was accounted for by including an individual heterogeneity index as an individual, linear covariate of recapture probabilities. This heterogeneity index was defined as $\ln\left(1+\frac{c-y}{y}\right)$ where c is the total number of captures for a given individual and *y* is the number of years with captures for that individual. We used a heterogeneity index rather than an individual random effect because the average number of recapture per individual was very low, and the modeling was implemented at the year level (1 data per individual per year), whereas this individual heterogeneity index allows to account also for within-year recaptures (without setting the model in a Robust Design framework, which would require too many parameters, and would be computationally too demanding). When a CES site was not monitored on a given year, the corresponding recapture probability was fixed to 0, to avoid biasing survival probabilities. We assumed that sex differences were common to all species. While this assumption is certainly inexact, it appears to be a reasonable compromise between model fit and model simplicity given that among temperate songbirds in general males

have a higher breeding philopatry (translating into higher apparent survival) and higher capture probability (Amrhein et al. 2012).

Convergence was considered to be satisfactory when R-hat < 1.1 for all parameters. All parameters of primary interest (i.e., variance parameters and fixed effects) had R-hat<1.05, showed good mixing on graphical inspection and had an effective sample size of at least 100. We run three chains of 50,000 iterations, including a burn-in of 12,500 iterations and a thinning rate of 37 (thinning was used to reduce the computer memory used by each model). We report posterior modes and 95% highest posterior density credible intervals.

TABLE S1. Prior distributions for parameters of the base model (Model 1).

Prior distribution (on logit-scale)

Survival probability parameters				
Species	N(0,1/1.5)			
Sex (for female)	N(-0.5, 1/2)			
Random(Site)	$N(0, 1/\sigma(Site)^2)$			
σ(Site)	U(0,10)			
Random(Year)	$N(0, 1/\sigma(Year)^2)$			
σ(Year)	U(0,10)			
Random(Year:Species)	$N(0, \sigma(Year:Species)^2)$			
σ(Year:Species)	U(0,10)			
Recapture probability parameters				
Species	N(0,1/3)			
Sex (for female)	N(-0.5,1/2)			
Individual recapture heterogeneity index	N(0,1/100)T(-10,10)			
Random(Site)	$N(0, 1/\sigma(Site)^2)$			
σ(Site)	U(0,10)			
Random(Year)	$N(0, 1/\sigma(Year)^2)$			
σ(Year)	U(0,10)			

Notes: In JAGS, N(m,p) represents a normal distribution of mean m and precision p, where the precision is the inverse of the variance (e..g, $\sigma(Site)^2$). We defined priors for standard deviations,

which are the square-roots of their respective variances (e.g., $\sigma(Site)$). In models considering the difference in migratory behavior (variable "group"), we used the same prior for Year:Group as for Year:Species. In models considering the effect of weather variables, all parameters were given a prior N(0,1/100)T(-10,10). N(0,100) represents a normal distribution of mean 0 and variance 100. T(-10,10) indicates that the distribution was truncated to allow only values between -10 and 10. In Jags, this truncated distribution remains a proper distribution, in contrast to WinBUGS. U(x,y) represents a uniform distribution between x and y. We checked that the posterior distribution of parameters did not reach the truncation boundaries for any parameters.

1.2 Pros and cons of model 1 vs. model 2

Our main goal was to quantify synchrony across species as a single value. A single value for synchrony corresponds directly to the parameterization of model 1 where synchrony is captured by a single ICC. In contrast, in model 2, to obtain the overall measure of synchrony we need to average 16 species-specific $ICC_{species}$, which is conceptually similar to our question of synchrony across species, but less direct. Further, we rely on sparse, hard to collect, mark-recapture data, and sample size limits the precision of estimates. In model 1, the ICC is estimated from all the data, while in model 2 the $ICC_{species}$ are each estimated from a fraction of the data only and therefore less precisely. Finally, model 2 has more variance parameters than model 1, which makes estimation more difficult algorithmically, although these extra parameters are not of direct interest for the estimation of overall synchrony. We observed that extensions of model 2 exploring factors contributing to synchrony (see below models 3-5) had difficulty converging, while the same extensions of model 1 converged. On the other hand, model 1 assumes that within-species time deviations came from a single distribution, with a variance common to all

species. This assumption may lead to a poor fit to the data. Model 2 relaxes the assumption and provides a sanity check: if the estimation of synchrony in model 1 is robust to the assumption of common distribution, then most species-specific $ICC_{species}$ in model 2 should be in the same range of values, and the average of $ICC_{species}$ should be similar to the ICC estimated in model 1. In summary, model 2 is useful to illustrate the variability, or lack of variability in ICC across species, and to check the statistical robustness to the imbalance of species sample sizes. Nevertheless, we favor model 1 as it provides a more direct measure of synchrony and, given sparse data as available here, allows a more powerful estimation of synchrony and test of the factors contributing to synchrony.

1.3 Approximate equality between ICC on the logit and data scales.

Note that we report ratios of variances (i.e., ICCs) on the logit scale, not on the natural scale of survival probability. Arguably, *ICC* on the logit scale is more biologically relevant because it expresses differences as log odds-ratio and does not depend on average survival probability. For instance, a change in survival probability from 0.45 to 0.50 (probability change of 0.05, logit change of 0.2) may be considered inconsequential for population dynamics, but a change from 0.94 to 0.99 (also a probability change of 0.05, but a logit change of 1.84) would be biologically dramatic, as would be a change in survival probabilities from 0.45 to 0.83 (also a logit change of 1.84. For mean probabilities very close to 0 or 1 (and also for very large variances on the logit scale) *ICCs* can differ substantially between the logit scale and the probability scale. The importance of the deviation depends on the logit-scale intercept and on the total variance on the logit scale (in particular through their combined effect on the mean probability), as well as on the *ICC* on the logit scale (Figure S1). Nevertheless, for most parameter values ratios of variances are approximately invariant to logit or inverse-logit transformations, particularly for medium-lived species as songbirds (annual adult survival in the range 0.2-0.8), and for the range of parameter values (mean survival, variance on the logit-scale and *ICC*) considered the difference is minimal (Figure S1). Therefore, the *ICCs* reported in the article can be thought of as close approximations of ICCs on the natural scale for probabilities, although we favor an interpretation on the logit scale.

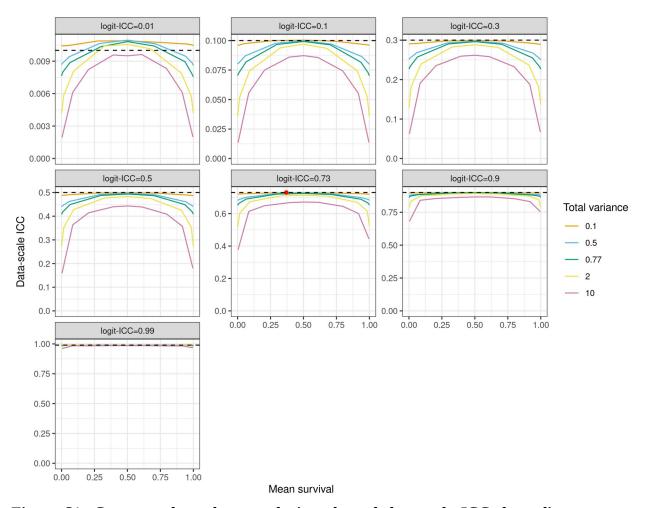


Figure S1: Correspondence between logit-scale and data-scale ICC depending on mean survival probability, logit-scale ICC and logit-scale total variance. The horizontal black dashed lines show the values of logit-ICC on the data-scale ICC axis. The red point in the panel logit-ICC=0.73 shows the coordinates of our point estimates for mean survival, total variance and logit-scale ICC. The curves were obtained by simulating logit-scaled data as the sum of an intercept, a grouping factor Gaussian process and a residual variance Gaussian process. Those data were back-transformed to data-scale probability using an inverse logit. The data-scale ICC was computed as the variance in the mean data-scale probability of each grouping factor, divided by the total variance in the data-scale probability. To obtain smooth curves we used 5 million points and 5000 grouping levels for each parameter combination.

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Supporting Information for:

Authors:

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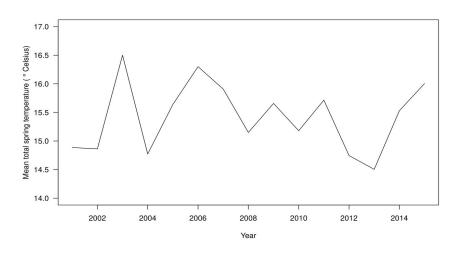
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APPENDIX S5. DEPENDENCE OF AVERAGE ANNUAL SURVIVAL PROBABILITY ON WEATHER VARIABLES





(b)

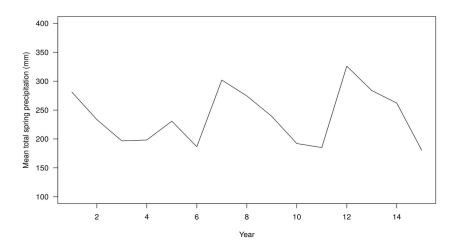


FIG. S1. Yearly variations in (a) mean temperature (in °C), and (b) mean total spring precipitation (in mm), averaged across all studied sites, for the whole study period. Note that temperature and precipitation vary across sites, but this variation is not represented here.

TABLE S1. Effects of weather covariates on average adult survival probability (additive effect across all species). In spring, covariates are common to all species; in winter, they depend on the species wintering range (i.e. migratory behavior class). Weather covariate symbols are shown for easier connection to the main text and other appendices.

Season	Species	Weather covariate	Mean [95% credible
			interval]
		Precipitation (π)	0.016 [-0.060–0.091]
		Precipitation ² (π^2)	0.036 [-0.006–0.077]
	All	Temperatures (θ)	0.007 [-0.092–0.107]
C		Temperatures ² (θ^2)	0.032 [-0.017–0.084]
Spring		Precipitation*Temperatures $(\pi \theta)$	0.036 [-0.41-0.110]
		Precipitation ² *Temperatures $(\pi^2 \theta)$	-0.005 [-0.014–0.005]
		Precipitation*Temperatures ² ($\theta \pi^2$)	0.000 [-0.043–0.047]
		Precipitation ² *Temperatures ² ($\theta^2 \pi^2$)	0.0175 [-0.013–0.051]
	Residents /	Winter North Atlantic Oscillation	0.009 [-0.135–0.139]
		Index (wNAO)	
Winter	short-distance migrants	Winter North Atlantic Oscillation	-0.016 [-0.141–0.093]
		$Index^2 (wNAO^2)$	
	Long-distance	Summer Sahel Rainfall index (sSR)	0.022 [-0.133–0.174]
	migrants	Summer Sahel Rainfall index ² (sSR^2)	0.074 [-0.067–0.219]

Notes: Posterior estimates were obtained from models 3 for spring and 4 for winter (Table 1), and are given on the logit-scale.

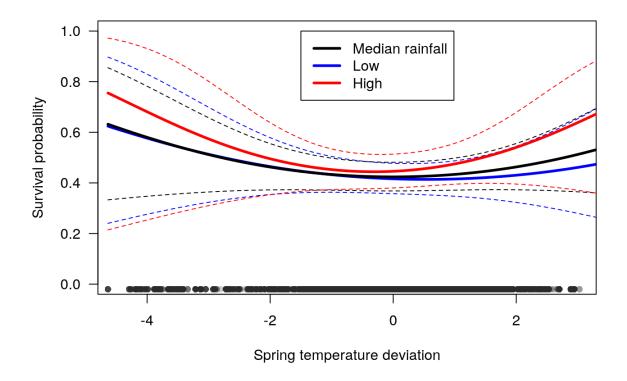


FIG. S2. Estimated survival probability according to spring weather. Local temperature anomalies (θ) are represented on the x-axis, while three different predictions are given for three values (median, 10% quantile and 90% quantile) of precipitations (π) . Bold lines represent the mean predictions and dashed lines represent the 95% credible interval. These predictions are based on the first-order and quadratic effects of precipitations and temperatures, and the four interactions presented in Table S1, and using the intercept for a median species. Black dots at the bottom represent data distribution over the range of observed temperature anomalies (with one value per site and year).

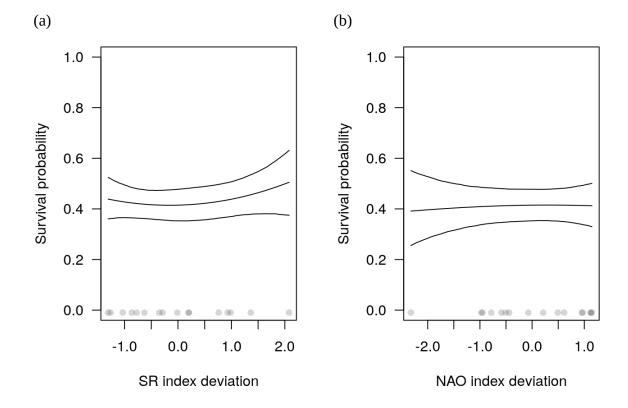


FIG. S3. Survival probability predicted by winter weather. The summer Sahel Rainfall index (sSR) is used for predictions of survival in long-distance migratory species and the winter North Atlantic Oscillation index (wNAO) is used for predictions of survival in resident or short-distance migratory species. First-order and quadratic effects are used. Grey dots show data distributions over the range of values for each weather index (with one value per year).

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APPENDIX S6. SIMULATIONS TO CHECK THE FORMULA FOR SYNCHRONOUS VARIANCE DUE TO WINTER WEATHER

We run simulations to check the equation computing the synchronous variance ascribed to winter climate. Code to run the simulations and produce the figure below is provided on the Zenodo repository.

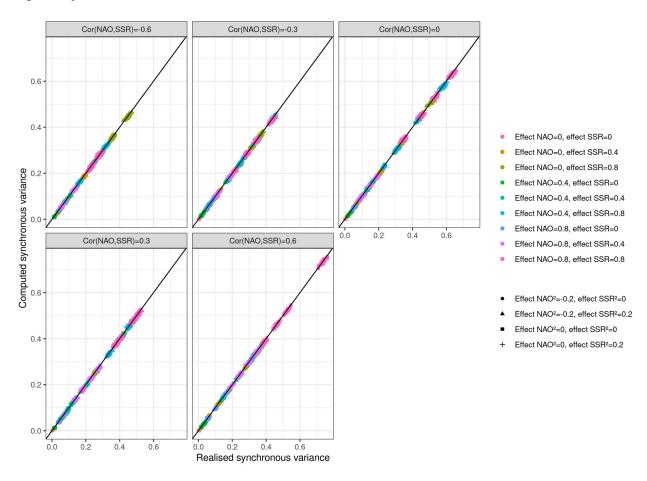


Figure S1: Synchronous variance computed with the formula presented in the manuscript vs. realized synchronous variance, for a range of parameters. The simulations assume that all synchronous variance comes from winter climate and assumes the two migratory classes represent 70% and 30% of species, respectively. For each combination of parameters (effects of NAO, NAO-squared, SSR, SSR-squared, and correlation between SSR and NAO) we ran 50 replicates. The black line represents the expectation of equality between the computed and realized synchronous variances.

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APPENDIX S7. ALL PARAMETER ESTIMATES

1.1 Model 1: Simple Interspecific synchrony

	mean	2.50%	97.50%
b1	-1.186	-1.335	-1.041
phi.sex[2]	-0.179	-0.279	-0.077
survival intercept S. atricapilla	-0.29	-0.521	-0.056
survival intercept A. schoenobaenus	-0.569	-1.006	-0.128
survival intercept A. scripaceus	-0.138	-0.364	0.098
survival intercept C. cetti	-0.361	-0.674	-0.035
survival intercept E. rubecula	-0.582	-0.865	-0.305
survival intercept H. polyglotta	-0.386	-0.715	-0.035
survival intercept L. megarhynchos	0.003	-0.244	0.247
survival intercept P. major	-0.561	-0.872	-0.251
survival intercept P. collybita	-0.876	-1.143	-0.601
survival intercept P. trochilus	-0.562	-0.887	-0.23
survival intercept P. modularis	-0.155	-0.4	0.091
survival intercept S. borin	-0.182	-0.457	0.092
survival intercept S. communis	-0.543	-0.828	-0.24
survival intercept T. troglodytes	-0.841	-1.208	-0.483
survival intercept T. merula	-0.02	-0.23	0.203
survival intercept T. philomelos	-0.146	-0.483	0.206
sigma.phi.site	0.39	0.295	0.496
sigma.phi.temps	0.303	0.177	0.484

	mean	2.50%	97.50%
sigma.phi.temps.species	0.185	0.109	0.26
p.sex[2]	-0.636	-0.793	-0.488
recapture intercept S. atricapilla	-0.17	-0.412	0.063
recapture intercept A. schoenobaenus	0.864	0.259	1.458
recapture intercept A. scripaceus	0.757	0.467	1.05
recapture intercept C. cetti	1.78	1.274	2.283
recapture intercept E. rubecula	0.527	0.177	0.899
recapture intercept H. polyglotta	0.11	-0.341	0.545
recapture intercept L. megarhynchos	0.542	0.241	0.841
recapture intercept P. major	-0.162	-0.564	0.253
recapture intercept P. collybita	0.756	0.39	1.138
recapture intercept P. trochilus	0.577	0.096	1.089
recapture intercept P. modularis	0.612	0.319	0.908
recapture intercept S. borin	0.206	-0.134	0.561
recapture intercept S. communis	0.629	0.227	1.055
recapture intercept T. troglodytes	0.627	0.096	1.19
recapture intercept T. merula	0.352	0.115	0.567
recapture intercept T. philomelos	-0.421	-0.831	0.003
sigma.p.site	0.669	0.543	0.812
sigma.p.temps	0.16	0.009	0.411

1.2 Model 2: Heterogeneous species variances

	Posterior mean	2.50%	97.50%
survival heterogenetiy	-1.19	-1.339	-1.041
survival sex female	-0.189	-0.291	-0.088
survival intercept S. atricapilla	-0.298	-0.502	-0.057
survival intercept A. schoenobaenus	-0.53	-1.018	0.006
survival intercept A. scripaceus	-0.134	-0.359	0.094
survival intercept C. cetti	-0.351	-0.807	0.111
survival intercept E. rubecula	-0.59	-0.868	-0.308
survival intercept H. polyglotta	-0.391	-0.786	-0.003
survival intercept L. megarhynchos	-0.002	-0.257	0.274
survival intercept P. major	-0.553	-0.867	-0.22
survival intercept P. collybita	-0.852	-1.168	-0.512
survival intercept P. trochilus	-0.545	-0.896	-0.143
survival intercept P. modularis	-0.158	-0.393	0.084
survival intercept S. borin	-0.137	-0.458	0.232
survival intercept S. communis	-0.544	-0.846	-0.233
survival intercept T. troglodytes	-0.824	-1.203	-0.443
survival intercept T. merula	-0.007	-0.231	0.247
survival intercept T. philomelos	-0.132	-0.547	0.308
survival site sigma	0.394	0.303	0.493
survival year sigma	0.288	0.164	0.493
survial year sigma S. atricapilla	0.078	0.002	0.235
survial year sigma A. schoenobaenus	0.351	0.011	0.991
survial year sigma A. scripaceus	0.11	0.004	0.312

	Posterior mean	2.50%	97.50%
survial year sigma C. cetti	0.587	0.204	1.092
survial year sigma E. rubecula	0.141	0.009	0.393
survial year sigma H. polyglotta	0.317	0.017	0.856
survial year sigma L. megarhynchos	0.22	0.027	0.522
survial year sigma P. major	0.18	0.005	0.537
survial year sigma P. collybita	0.4	0.154	0.728
survial year sigma P. trochilus	0.306	0.026	0.71
survial year sigma P. modularis	0.166	0.011	0.41
survial year sigma S. borin	0.396	0.105	0.777
survial year sigma S. communis	0.196	0.01	0.524
survial year sigma T. troglodytes	0.209	0.002	0.612
survial year sigma T. merula	0.272	0.079	0.504
survial year sigma T. philomelos	0.424	0.034	0.999
recapture sex female	-0.623	-0.773	-0.472
recapture intercept S. atricapilla	-0.149	-0.392	0.074
recapture intercept A. schoenobaenus	0.825	0.194	1.482
recapture intercept A. scripaceus	0.772	0.484	1.055
recapture intercept C. cetti	1.719	1.248	2.203
recapture intercept E. rubecula	0.556	0.203	0.914
recapture intercept H. polyglotta	0.112	-0.312	0.561
recapture intercept L. megarhynchos	0.555	0.249	0.84
recapture intercept P. major	-0.17	-0.58	0.234
recapture intercept P. collybita	0.728	0.347	1.124

	Posterior mean	2.50%	97.50%
recapture intercept P. trochilus	0.574	0.081	1.057
recapture intercept P. modularis	0.625	0.344	0.896
recapture intercept S. borin	0.185	-0.16	0.529
recapture intercept S. communis	0.64	0.23	1.043
recapture intercept T. troglodytes	0.608	0.07	1.157
recapture intercept T. merula	0.351	0.105	0.572
recapture intercept T. philomelos	-0.413	-0.84	-0.013
sigma.p.site	0.661	0.533	0.796
sigma.p.temps	0.161	0.02	0.4

1.3 Model 3: Migration

	mean	2.50%	97.50%
b1	-1.181	-1.33	-1.027
phi.sex[2]	-0.178	-0.278	-0.078
survival intercept S. atricapilla	-0.277	-0.51	-0.043
survival intercept A. schoenobaenus	-0.558	-1.003	-0.092
survival intercept A. scripaceus	-0.126	-0.364	0.118
survival intercept C. cetti	-0.347	-0.669	-0.02
survival intercept E. rubecula	-0.577	-0.849	-0.296
survival intercept H. polyglotta	-0.369	-0.7	-0.04
survival intercept L. megarhynchos	0.005	-0.242	0.261
survival intercept P. major	-0.534	-0.848	-0.212
survival intercept P. collybita	-0.869	-1.139	-0.582

	mean	2.50%	97.50%
survival intercept P. trochilus	-0.567	-0.889	-0.225
survival intercept P. modularis	-0.144	-0.377	0.106
survival intercept S. borin	-0.179	-0.455	0.113
survival intercept S. communis	-0.538	-0.824	-0.238
survival intercept T. troglodytes	-0.816	-1.179	-0.439
survival intercept T. merula	-0.007	-0.227	0.221
survival intercept T. philomelos	-0.134	-0.471	0.213
sigma.phi.site	0.387	0.299	0.482
sigma.phi.temps	0.289	0.147	0.499
sigma.phi.temps.groupe	0.087	0.008	0.219
sigma.phi.temps.species	0.173	0.083	0.255
p.sex[2]	-0.635	-0.785	-0.484
recapture intercept S. atricapilla	-0.169	-0.405	0.061
recapture intercept A. schoenobaenus	0.854	0.227	1.492
recapture intercept A. scripaceus	0.746	0.452	1.039
recapture intercept C. cetti	1.774	1.297	2.243
recapture intercept E. rubecula	0.543	0.176	0.904
recapture intercept H. polyglotta	0.107	-0.316	0.53
recapture intercept L. megarhynchos	0.548	0.253	0.846
recapture intercept P. major	-0.181	-0.572	0.243
recapture intercept P. collybita	0.756	0.372	1.141
recapture intercept P. trochilus	0.59	0.1	1.078

	mean	2.50%	97.50%
recapture intercept P. modularis	0.613	0.327	0.887
recapture intercept S. borin	0.213	-0.128	0.56
recapture intercept S. communis	0.628	0.206	1.047
recapture intercept T. troglodytes	0.594	0.069	1.139
recapture intercept T. merula	0.351	0.118	0.569
recapture intercept T. philomelos	-0.413	-0.831	-0.001
sigma.p.site	0.667	0.539	0.806
sigma.p.temps	0.164	0.014	0.386

1.4 Model 4: Spring Climate

	mean	2.50%	97.50%
b1	-1.18	-1.324	-1.031
phi.sex[2]	-0.181	-0.281	-0.081
survival intercept S. atricapilla	-0.321	-0.557	-0.09
survival intercept A. schoenobaenus	-0.596	-1.029	-0.151
survival intercept A. scripaceus	-0.159	-0.399	0.096
survival intercept C. cetti	-0.389	-0.699	-0.056
survival intercept E. rubecula	-0.624	-0.898	-0.344
survival intercept H. polyglotta	-0.41	-0.747	-0.064
survival intercept L. megarhynchos	-0.024	-0.258	0.241
survival intercept P. major	-0.568	-0.876	-0.217

	mean	2.50%	97.50%
survival intercept P. collybita	-0.892	-1.146	-0.622
survival intercept P. trochilus	-0.576	-0.894	-0.24
survival intercept P. modularis	-0.174	-0.405	0.067
survival intercept S. borin	-0.206	-0.481	0.069
survival intercept S. communis	-0.566	-0.852	-0.273
survival intercept T. troglodytes	-0.866	-1.224	-0.498
survival intercept T. merula	-0.035	-0.246	0.195
survival intercept T. philomelos	-0.157	-0.516	0.204
sigma.phi.site	0.397	0.305	0.496
sigma.phi.temps	0.313	0.186	0.507
sigma.phi.temps.species	0.18	0.097	0.257
A_int_temp_prec_1	0.036	-0.041	0.11
A_int_temp_prec_2	-0.005	-0.014	0.005
A_int_temp_prec_3	0	-0.043	0.047
A_int_temp_prec_4	0.018	-0.013	0.051
A_prec_1	0.016	-0.06	0.091
A_prec_2	0.036	-0.006	0.077
A_temp_1	0.007	-0.092	0.107
A_temp_2	0.032	-0.017	0.084
p.sex[2]	-0.634	-0.783	-0.479
recapture intercept S. atricapilla	-0.178	-0.439	0.057
recapture intercept A. schoenobaenus	0.85	0.235	1.501
recapture intercept A. scripaceus	0.742	0.407	1.032

	mean	2.50%	97.50%
recapture intercept C. cetti	1.776	1.281	2.259
recapture intercept E. rubecula	0.542	0.182	0.921
recapture intercept H. polyglotta	0.109	-0.336	0.551
recapture intercept L. megarhynchos	0.537	0.235	0.823
recapture intercept P. major	-0.207	-0.647	0.226
recapture intercept P. collybita	0.725	0.322	1.118
recapture intercept P. trochilus	0.559	0.059	1.04
recapture intercept P. modularis	0.596	0.289	0.89
recapture intercept S. borin	0.193	-0.175	0.546
recapture intercept S. communis	0.611	0.172	1.03
recapture intercept T. troglodytes	0.609	0.066	1.144
recapture intercept T. merula	0.326	0.061	0.567
recapture intercept T. philomelos	-0.444	-0.879	0.007
sigma.p.site	0.661	0.523	0.808
sigma.p.temps	0.181	0.009	0.444

1.5 Model 5: Winter Climate

	mean	2.50%	97.50%
b1	-1.182	-1.331	-1.033
phi.sex[2]	-0.177	-0.28	-0.073
survival intercept S. atricapilla	-0.346	-0.607	-0.09
survival intercept A. schoenobaenus	-0.632	-1.098	-0.164
survival intercept A. scripaceus	-0.113	-0.381	0.141

	mean	2.50%	97.50%
survival intercept C. cetti	-0.339	-0.659	-0.018
survival intercept E. rubecula	-0.639	-0.942	-0.32
survival intercept H. polyglotta	-0.407	-0.779	-0.046
survival intercept L. megarhynchos	0.022	-0.236	0.293
survival intercept P. major	-0.538	-0.866	-0.211
survival intercept P. collybita	-0.937	-1.239	-0.646
survival intercept P. trochilus	-0.541	-0.876	-0.193
survival intercept P. modularis	-0.132	-0.382	0.128
survival intercept S. borin	-0.238	-0.538	0.068
survival intercept S. communis	-0.594	-0.911	-0.285
survival intercept T. troglodytes	-0.807	-1.174	-0.424
survival intercept T. merula	0.001	-0.236	0.24
survival intercept T. philomelos	-0.137	-0.487	0.212
sigma.phi.site	0.392	0.307	0.488
sigma.phi.temps	0.279	0.103	0.489
sigma.phi.temps.groupe	0.112	0.007	0.28
sigma.phi.temps.species	0.185	0.107	0.263
B_nao_1	0.009	-0.135	0.14
B_nao_2	-0.016	-0.141	0.093
B_sr_1	0.022	-0.133	0.174
B_sr_2	0.074	-0.067	0.219
p.sex[2]	-0.639	-0.792	-0.489

	mean	2.50%	97.50%
recapture intercept S. atricapilla	-0.176	-0.413	0.049
recapture intercept A. schoenobaenus	0.838	0.228	1.468
recapture intercept A. scripaceus	0.744	0.427	1.04
recapture intercept C. cetti	1.781	1.305	2.267
recapture intercept E. rubecula	0.515	0.142	0.881
recapture intercept H. polyglotta	0.062	-0.366	0.503
recapture intercept L. megarhynchos	0.536	0.239	0.823
recapture intercept P. major	-0.178	-0.598	0.222
recapture intercept P. collybita	0.739	0.346	1.129
recapture intercept P. trochilus	0.573	0.071	1.066
recapture intercept P. modularis	0.603	0.311	0.878
recapture intercept S. borin	0.203	-0.145	0.545
recapture intercept S. communis	0.6	0.196	1.019
recapture intercept T. troglodytes	0.586	0.038	1.151
recapture intercept T. merula	0.347	0.108	0.568
recapture intercept T. philomelos	-0.406	-0.834	0.026
sigma.p.site	0.663	0.535	0.806
sigma.p.temps	0.196	0.024	0.442

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APPENDIX S8. ROBUSTNESS OF INTERSPECIFIC SYNCHRONY

ESTIMATION TO UNBALANCED SAMPLE SIZES AMONG SPECIES

1.1 THE POTENTIAL PROBLEM

In our dataset, species were unevenly represented. Four species cumulated 51% of all individuals, and 52% of all inter-annual recaptures (Fig. S1). In principle our models account for the unbalanced sample sizes by allowing different species to have different residual variances (that is, variances in the random effects species-by-year). If the modelling of the random Species-by-Year term had failed to account for these unbalanced sample sizes, synchrony could indeed be the result of a methodological bias, and not of an actual biological process. It would indeed assess the synchrony of survival between individuals — and not between species — individuals being likely more synchronous within species than between species.

1.2 An empirical appraisal using data resampling

Methods

To assess this potential role of species uneven contribution in spuriously generating survival synchrony, we generated a more balanced dataset, where the number of individuals for the four dominating species (Fig. S1) was reduced to have an equivalent number of individuals to that of the three following most abundant species (about 1200 individuals; Fig. S1). Individuals to be deleted were chosen randomly.

Results

Estimates of ICC between the original and the reduced datasets were relatively close: 73% [63–85] and 61% [48–78], respectively. We can safely conclude that the observed temporal synchrony between species is an actual biological process, and is not generated by uneven species representation in the dataset.

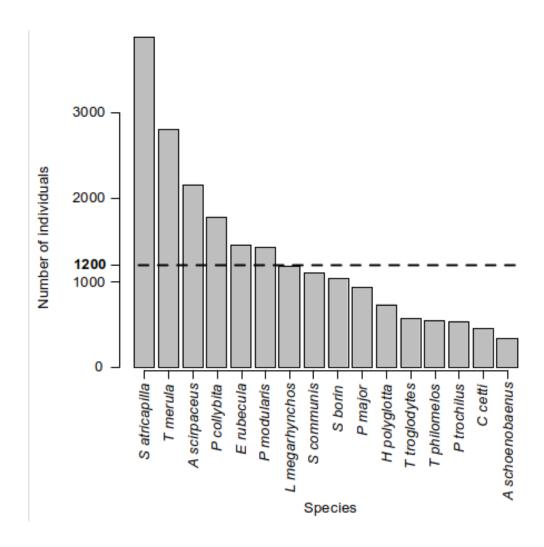


Fig. S1. Number of individuals per species in the total mark-recapture dataset. For assessing the robustness of survival synchrony estimates to uneven species contributions, a balanced dataset

was generated so that the most numerous species were limited to a maximal contribution to the dataset of 1200 individuals (dotted line).

1.3 An empirical verification using simulated data

The primary goal of this section is to test the idea that among-species heterogeneity in sample size might bias the estimation of synchrony among species. The verbal argument behind this concern is that the time-dynamic of the most common species might "spill over" the estimation of the time-dynamic common to all species. A suggested solution to this problem has been not to model synchrony explicitly, so that the model does not contain an across-species time-dynamic, but instead to estimate species-specific time dynamics independently, and reconstruct the synchrony a posteriori. Technically, this would be done by fitting a Species-by-Year random interaction without fitting the main random effect of time (but fitting the main random effect of species).

However, theory suggests that mixed models are generally able to handle unbalanced data, and that the estimation of synchrony should not be biased by unequal sample sizes (Pinheiro & Bates, 2000). Moreover, theory also suggests that the "solution" of not modeling synchrony explicitly but, instead, by reconstructing it *a posteriori* from model estimates is flawed and will generally lead to underestimation (Hadfield et al., 2010, Houslay & Wilson, 2017).

Here, we test that these two expectations hold for the special case of the mixed mark-recapture model structure used in the present study (Model 1), and that the results presented in the main text do not suffer from a bias due to unequal sample size among species. To this end, we first simulate multi-species mark-recapture data with synchrony among species (section 4.3.2) or with

no synchrony among species (section 4.3.3). We use the same sample size per year and per species as in the real data. We then analyze the simulated data either with a model that explicitly contains synchrony, or with a model that does not contain explicit synchrony but only allows for its reconstruction from species-specific estimates.

We first show that when interspecific synchrony is present in simulated data, a model explicitly modeling interspecific synchrony can recover it (section 4.3.2.1). We then show that on the same data, a model that does not explicitly model synchrony, but instead makes its estimation possible a posteriori underestimates synchrony (section 4.3.2.2). Finally, we show that the first model (explicitly modeling synchrony) does not detect synchrony if none is simulated in the data (section 4.3.3). The R code necessary to run these simulations is provided in the Zenodo repository (Ghislain et al. 2022).

1.3.2 Data with strong interspecific synchrony

1.3.2.1 Interaction model with explicit interspecific synchrony

Plotting these predictions, the synchrony is well recovered graphically as species-specific survival probabilities through years are parallel (Fig S2).

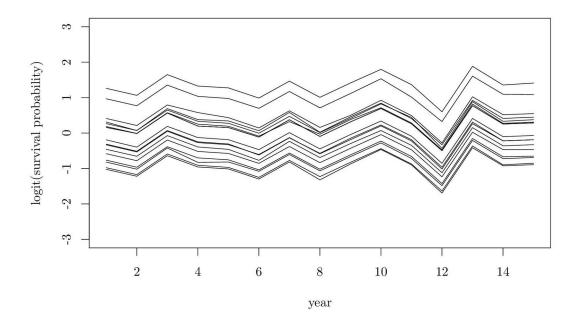


FIG. S2. Predicted latent values for survival for all species and years. The model used for predictions explicitly modeled interspecific synchrony, and the data were simulated with a strong interspecific synchrony. Interspecific synchrony is well recovered by the model, as evidenced by the parallel time-dynamics among species.

The intra-Class correlation is close to one (posterior mode = 0.972, see Fig. S3).

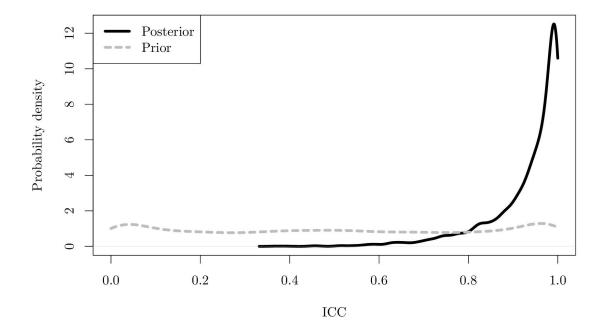


FIG. S3. Probability density distributions of the intra-class correlation (ICC) of Year, measuring the proportion of Year-variation in survival rate that is common to all bird species. Data were simulated with a strong interspecific synchrony (ICC close to one). Prior and posterior distributions are shown.

Note that the synchrony is apparent not only on the logit scale, but also on the scale of the data (Fig. S4).

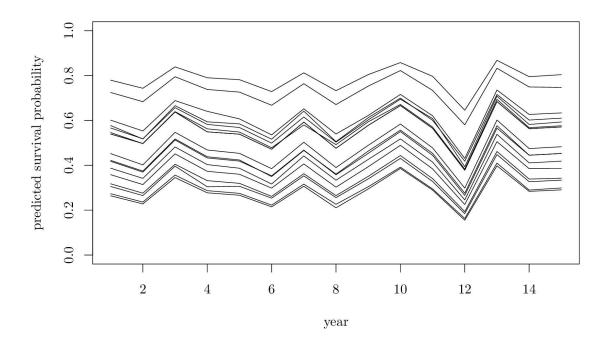


FIG. S4. Predicted survival probability by species and by year. Data were simulated with a strong synchrony (ICC close to one). The model used for prediction explicitly modeled synchrony.

1.3.2.2 Interactive model without explicit interspecific synchrony

We analyze the same data, but this time using a model that does not explicitly contain synchrony, that is, the model does not contain a year random effect, but only a species random effect and a year-by-species random effect. Graphically, much less synchrony is apparent (Fig. S5, S6).

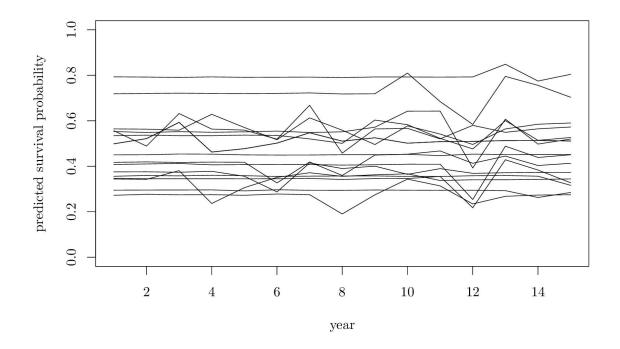


FIG. S5. Predicted latent values for survival for all species and years. The model used for predictions did not model explicit interspecific synchrony but allow for it with a Species-by-Year random interaction, and the data were simulated with a strong interspecific synchrony.

Interspecific synchrony is poorly recovered by the model, as evidenced by the lack of parallel time-dynamics among species.

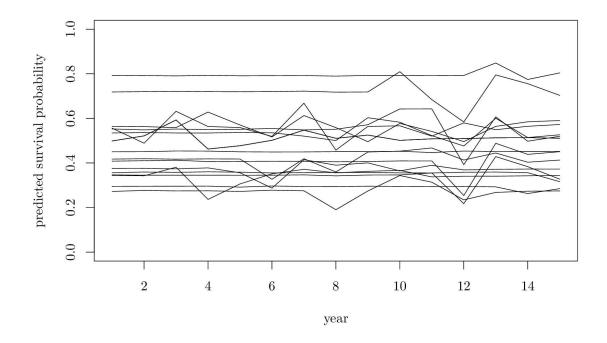


FIG. S6. Predicted survival probability by species and by year. Data were simulated with a strong interspecific synchrony (ICC close to one). The model used for prediction did not explicitly model interspecific synchrony.

The intra class correlation (ratio of temporal variance common to all species over the total temporal variance) is weak and close to zero (ICC point estimate = 0.127).

1.3.3 Model output when using data with no interspecific synchrony

We now simulate data without any synchrony to check whether a model would detect spurious synchrony because of the over-abundance of some species. That is, there is an effect of species and species-specific year effects on survival, but no year effects common to species. Each species has its own time variability in survival probability. We fit the model with explicit synchrony. Note that this model does not account for the heterogeneity in time variance among species that we simulated.

Graphically, no synchrony is apparent (Fig. S7, S8), what matches the data-generating process that did not have any synchrony.

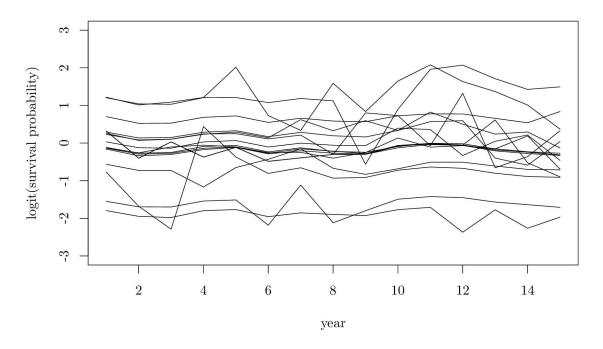


FIG. S7. Predicted latent values for survival for all species and years. The model used for predictions explicitly modeled interspecific synchrony, and the data were simulated without any interspecific synchrony. The model correctly identifies the lack of interspecific synchrony, as evidenced by the non-parallel year-dynamics among species.

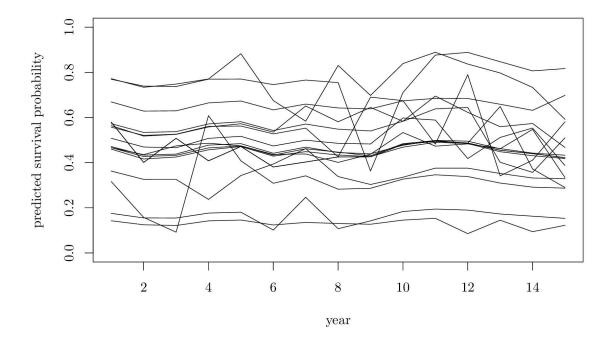


FIG. S8. Predicted survival probability by species and by year. Data were simulated without any interspecific synchrony (ICC close to zero). The model used for prediction explicitly modeled interspecific synchrony.

The intra-Class correlation is close to zero (ICC = 0.0714, Fig. S9) as expected.

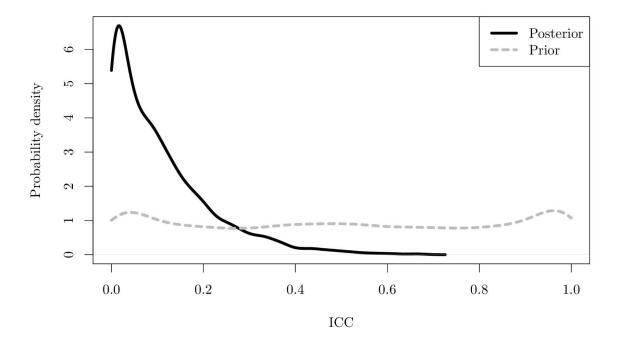


FIG. S9. Probability density distributions of the intra-class correlation (ICC) of Year, measuring the proportion of Year-variation in survival rate that is common to all bird species. Data were simulated without any interspecific synchrony (ICC close to zero). Prior and posterior distributions are shown.

In conclusion, the model does not detect spurious interspecific synchrony when none exists in the data generating process, despite heterogeneity in species sample sizes and in species variability.

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Ghislain, M., Bonnet, T., Godeau, U., Dehorter, O., Gimenez, O., & Henry, P.-Y. (2022). Novel code for: Synchrony in adult survival is remarkably strong among common temperate songbirds across France. Zenodo. https://doi.org/10.5281/zenodo.8172390

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APPENDIX S9. ROBUSTNESS OF THE INTERSPECIFIC SYNCHRONY ESTIMATE TO A TEMPORAL TREND IN SURVIVAL

To assess the potential contribution of a temporal trend in annual survival to synchrony, we included in Model 1 a linear Year effect on survival probability, common to all species (additive effect). This linear effect of Year proved to be statistically significant and negative (see the example of the Eurasian blackcap in Fig. S1). Estimate of ICC of the model with linear Year effect is smaller than in the original model: 56% [48–66] *versus* 73% [63–85] respectively, but still high. We can conclude that, even if part of the interspecific synchrony can be attributed to a temporal decline in adult survival (common to all species), the rest of yearly variations in survival were highly synchronous across species.

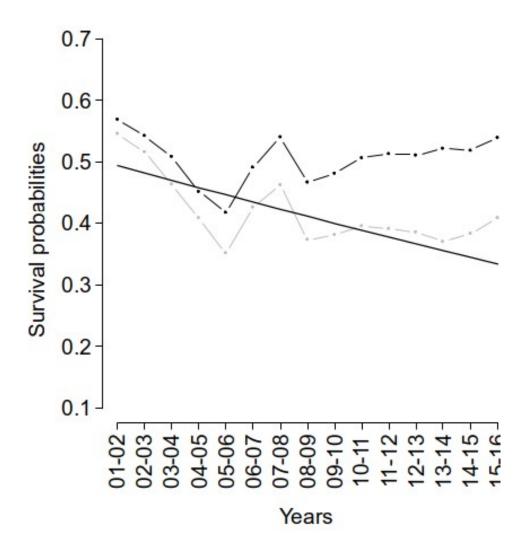


FIG. S1. Inter-annual fluctuations of local survival probabilities of adult male Eurasian blackcap with and without correction for temporal trend (respectively dotted lines black and grey). The black solid line represents the linear, temporal trend in adult survival probability for the Eurasian blackcap.

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APPENDIX S10. ROBUSTNESS OF THE INTERSPECIFIC SYNCHRONY ESTIMATE TO PRIOR DISTRIBUTION

Prior and posterior distributions for survival synchrony

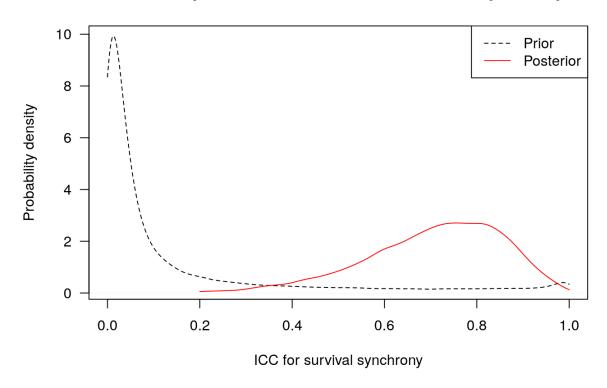


Fig. S1. Prior and estimated posterior probability density distributions of the intra-class correlation (ICC) for Year (see Methods). This figure shows estimation from real data. The posterior probability distribution shows no overlap with the parameter values with high prior probability, showing that the prior had no meaningful influence on estimation.

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APPENDIX S11. DIFFERENT CONTRIBUTIONS OF YEARS TO

INTERSPECIFIC SYNCHRONY

Methods

Some years may contribute more to interspecific synchrony than others, e.g. because of extreme conditions for all species. The random structures that we modelled assumed that all Year-Species random effects come from a single normal distribution, which prevents from formally computing year-specific variances in Year-Species effects from model estimates (Hadfield et al. 2010, Houslay and Wilson 2017, see Appendix S8: section 1.3). A formal estimation of yearly contributions to interspecific synchrony was computationally challenging and required more data than were available. As an alternative, we considered proxy indicators of the importance of some years using our model, by looking at the year-specific deviations common to all species (i.e., the components of σ_{δ}^2 ; defined in Methods), and at the variance in Year-Species deviations within each year (i.e, the components of σ_{ϵ}^2 in each year). The latter calculation is conservative because the model assumes all Year-Species deviations come from a single distribution common to all years, and should have limited power to detect differences in the spread of the deviations among years.

Results

The presented, *ad hoc* approach based on model estimates failed to identify yearly contributions: the 16 year-specific σ_{ε}^2 estimates ranged from 0.032 to 0.040, with their respective 95% credible intervals all covering at least [0.01–0.06] (Fig S1).

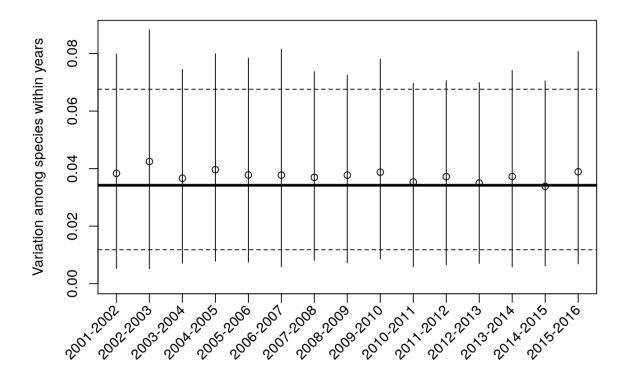


FIG. S1.Variances in year-species random deviations per year. The horizontal lines indicate the global estimate for the standard deviation in the random effect species-year, all with 95% credible intervals.

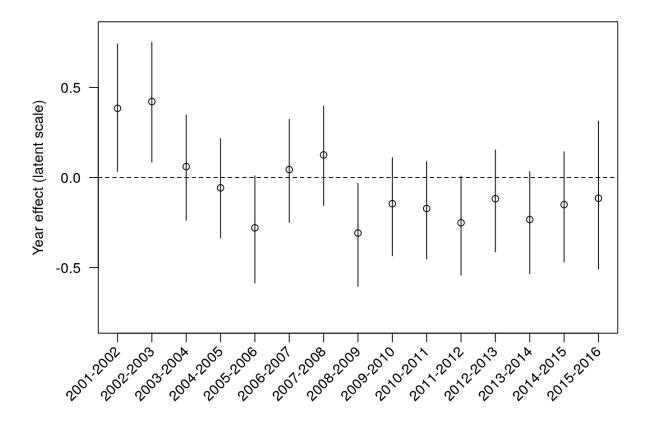


FIG. S2. Predictions of the deviation for the random effect Year on survival probability (with 95% credible intervals). The dashed line indicates the mean.

Literature Cited

Hadfield, J.D., A.J Wilson., D. Garant, B.C. Sheldon, and L.E.B. Kruuk. 2010. The misuse of BLUP in ecology and evolution. The American Naturalist 175:116–125.

Houslay, T.M. and A.J. Wilson. 2017. Avoiding the misuse of BLUP in behavioural ecology. Behavioural Ecology 28:948-952.

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Title:

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APPENDIX S12. LIST OF DATA CONTRIBUTORS

The following bird banders have provided data for the present study:

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PROVOST Romain, PROVOST Sébastien, RAITIERE Willy, REEBER Sébastien, REGNIER Marie-Claire, ROGER Thierry, RONDEL Stéphanie, ROUSSEAU Pierre, SALMON Franck, SAUVAGE Alain, SAVIN François, SCAAR Bertrand, SCHMITTER Lucien, SECHET Emmanuel, SELIQUER Pierre, SENECAL Didier, SENECHAL Cyril, SIBILLE Jean-Luc, SOURDRILLE Kévin, SPONGA Arnaud, STEIMER François, TARDIVO Gérard, TERNOIS Vincent, TEULIERE Jean-Michel, TEURQUETY Fabrice, THEILLOUT Amandine, THOUY Pèire, TILLO Stéphan, TOULOTTE Fabien, TRON François, URBINA-TOBIAS Patrice, URIOT Sylvain, VAN ACKER Bernard, VAN HECKE Benoît, VASLIN Matthieu, VEILLE Frantz, VENTROUX Julien, VIALLET Melchior, VIGOUR David, VRIGNAUD Nicolas, WILLIAMSON Thomas, WROBEL Sophie, ZEDDAM Pascal, ZUCCA Maxime.