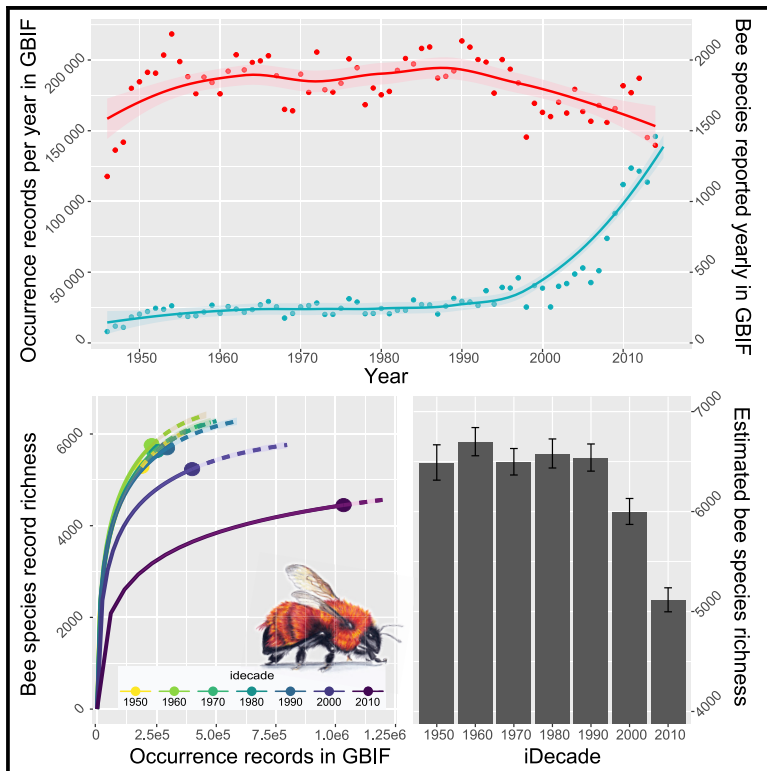


# Worldwide occurrence records suggest a global decline in bee species richness

## Graphical abstract



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## In brief

Wild bees are key to pollination of wild and crop plants, and local and regional reports of their decline are cause for concern. Since there are no global long-term datasets of bee diversity, we analyzed historical occurrence data from collections and observations gathered by the Global Biodiversity Information Facility and found that the number of bee species worldwide has been steadily decreasing since the 1990s as a result of either concerted changes in data-gathering strategies or, most likely, an actual global decline in bee diversity.

## Highlights

- The number of bee species found each year in GBIF data has declined since the 1990s
- Approximately 25% fewer species were found between 2006 and 2015 than before 1990
- As records increase as a result of enhanced data mobilization, analysis uncertainty decreases
- Both obstacles to data mobility and drivers of actual bee decline need addressing



## Article

# Worldwide occurrence records suggest a global decline in bee species richness

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**SCIENCE FOR SOCIETY** Wild bee pollination is fundamental to the reproduction of hundreds of thousands of wild plant species and is key to securing adequate yields in about 85% of food crops. Declines in the abundance and diversity of bee species have been reported at local, regional, and country levels on different continents, but up to now there has not been a long-term assessment on global trends. We turned to publicly available data on specimen collections and observations gathered at the Global Biodiversity Information Facility, mostly coming from museum and academic collections and complemented by citizen-science efforts. We found that the number of bee species being collected or observed over time has been steadily declining since the 1990s. Although these results might in part reflect increased impediments to specimen collection and data mobilization, as well as reduced sampling coverage, they could also reflect a worldwide decline in bee diversity given that many species are becoming rarer and less likely to be found.

## SUMMARY

Wild and managed bees are key pollinators, ensuring or enhancing the reproduction of a large fraction of the world's wild flowering plants and the yield of ~85% of all cultivated crops. Recent reports of wild bee decline and its potential consequences are thus worrisome. However, evidence is mostly based on local or regional studies; the global status of bee decline has not been assessed yet. To fill this gap, we analyzed publicly available worldwide occurrence records from the Global Biodiversity Information Facility spanning over a century. We found that after the 1990s, the number of collected bee species declines steeply such that approximately 25% fewer species were reported between 2006 and 2015 than before the 1990s. Although these trends must be interpreted cautiously given the heterogeneous nature of the dataset and potential biases in data collection and reporting, results suggest the need for swift actions to avoid further pollinator decline.

## INTRODUCTION

Insects are the most speciose group of animals and are estimated to encompass a large fraction of Earth's living biomass.<sup>1</sup> Given their historical abundance and ubiquity, along with the many familiar examples of extreme resilience to natural or intentional extermination, some insects have been viewed traditionally as the ultimate survivors of most apocalyptic scenarios. However, in the last two decades, a series of high-profile reports based mostly on local or regional evidence have repeatedly warned of a significant decline in insect diversity and biomass and raised the alarm about the potential consequence of this decline for the delivery of many ecosystem services.<sup>2–5</sup> Among the affected ecosystem services is plant pollination: insects are

the main vectors for pollen transfer of most wild and crop flowering plant species.<sup>6–10</sup> Bees (Hymenoptera: Apoidea: Anthophila), a lineage that includes about 20,000 described species, are the most important group of insect pollinators.<sup>11,12</sup> Wild bee species are key not only to the sexual reproduction of hundreds of thousands of wild plant species<sup>7</sup> but also to the yield of about 85% of all cultivated crops.<sup>6,13,10</sup> There is mounting evidence that a decline in wild bee populations might follow or even be more pronounced than overall trends in insect decline.<sup>12,14–17</sup> Such differential vulnerability might result from a high dependence of bees on flowers for food and a diversity of substrates for nesting, resources that are greatly affected by land conversion to large-scale agriculture, massive urbanization, and other intensive land uses.<sup>18–20</sup> However, most studies on “bee decline” to

date are either focused on particular bee taxa (e.g., *Bombus*<sup>21</sup>) or based on local-, regional-, or country-level datasets and have a strong bias toward the Northern Hemisphere, particularly North America and Europe, where most long-term research projects capable of generating multidecadal datasets have been conducted.<sup>4,12,22,23</sup>

To find an alternative approach to assess whether bee decline is a global phenomenon affecting all major bee lineages, we used the data publicly available at the Global Biodiversity Information Facility (GBIF).<sup>24</sup> The GBIF collects and provides “data about all types of life on Earth” from “sources including everything from museum specimens collected in the 18<sup>th</sup> and 19<sup>th</sup> centuries to geotagged smartphone photos shared by amateur naturalists in recent days and weeks.”<sup>24</sup> GBIF ingests data from a widely diverse range of data sources, localities, recording strategies, geographic areas, sampling intensities, etc., and each data source is potentially plagued by both systematic and idiosyncratic biases.<sup>25–28</sup> Although usage of GBIF data has been heavily criticized because of its inherent biases,<sup>22,25,29–31</sup> most criticisms are usually aimed at using its occurrence data to reconstruct and model species’ distribution ranges. Reconstructing geographic ranges and abundances from such “messy” datasets is indeed challenging.<sup>32</sup> However, a binning approach in which a simpler question (“has a species been recorded anywhere in the world during a given period?”) yields a yes/no answer can potentially be much more robust to sampling-effort heterogeneity and geographic uncertainty.<sup>33</sup> We reasoned that if bees have been experiencing a global decline in the last few decades, then a generalized decrease in population size and range would result in increased rarity, diminished chance of observation and collection, and consequently, a diminished number of total species being observed and recorded worldwide each year. This approach assumes that none of the artifactual trends caused by potential observation biases in the data are stronger than the real trends in bee diversity. Thus, we also assess the potential influence of some sources of bias and suggest how improving data collection and sharing could alleviate bias and reduce uncertainty.

## RESULTS AND DISCUSSION

### Fewer bee species have been recorded since the 1950s

To test our hypothesis of global bee decline, we queried GBIF for all occurrence records of Hymenoptera prior to 2020 with either “preserved specimen” or “human observation” bases of record<sup>34</sup> (see [experimental procedures](#)). Records of preserved specimens originate in vouchered collections such as those from museums and universities or associated with biodiversity surveys and molecular barcoding initiatives, among others. Human observations, on the other hand, are records in which a given species was observed but no voucher was collected; this category of records has been growing exponentially since citizen-science initiatives became increasingly popular.<sup>35</sup> Because the preserved specimen records are likely to represent the most taxonomically traceable source of information within the GBIF dataset,<sup>35,36</sup> we made parallel analyses for both the full dataset and the specimen-only subset. We filtered the datasets to six families of the superfamily Apoidea that comprise the Anthophila or “true bees”: Melittidae, Andrenidae, Halictidae,

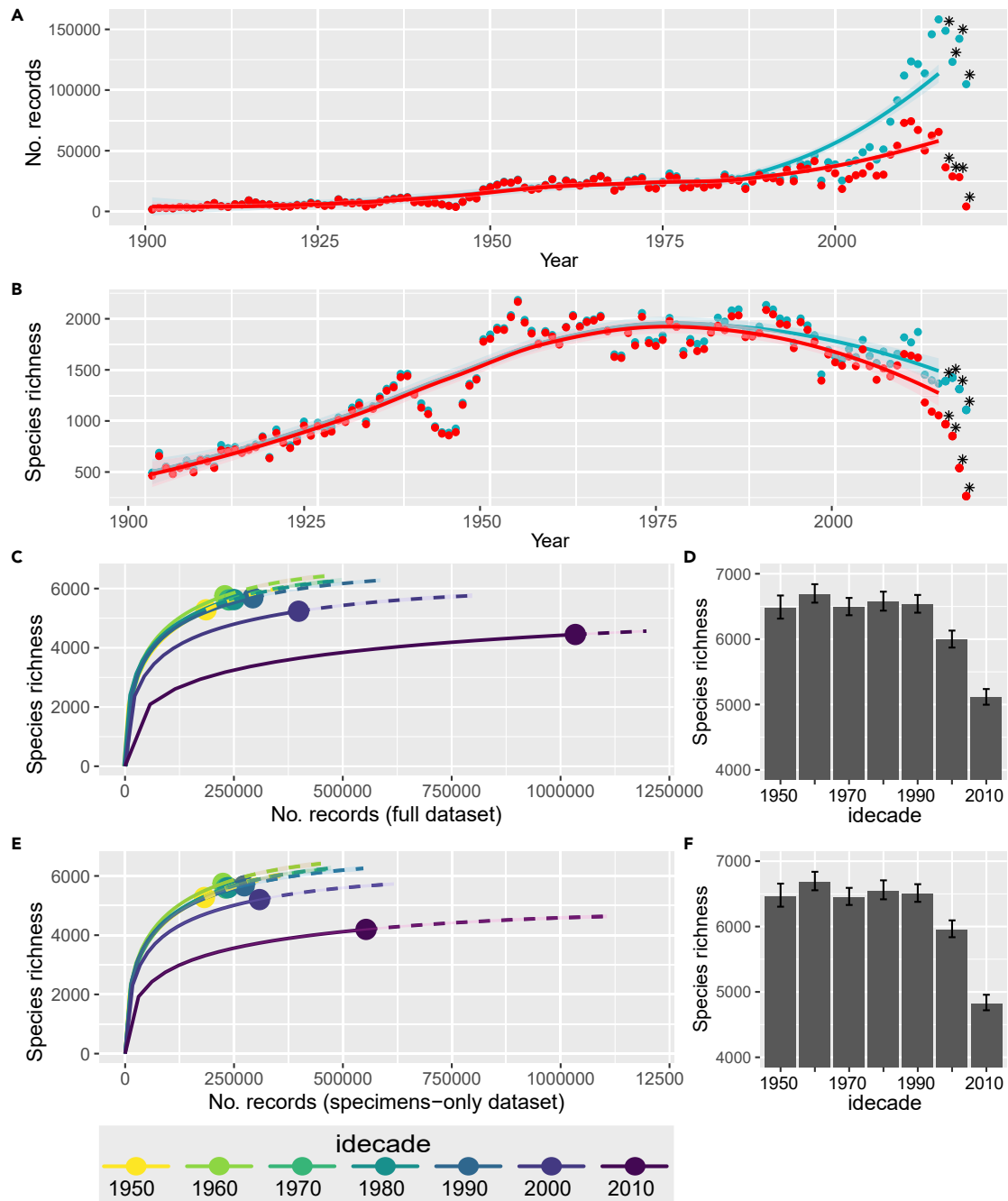
Colletidae, Megachilidae, and Apidae (we excluded the small family Stenotritidae from our analysis, since it has only 21 species restricted to Australia).<sup>11</sup>

Plotting the total number of records per year in both datasets shows that the number of worldwide bee occurrence records follows a mostly monotonic increasing trend that becomes steeper after 1990 ([Figure 1A](#)). Since the four most recent years (2016–2019, marked with an asterisk in [Figure 1A](#)) show a noticeable drop in records, most likely because of time lags in data entry,<sup>37</sup> we excluded those years from further analyses to avoid a downward bias in the most recent years. In contrast, while the number of recorded species per year during the same period also increases initially, it reaches a steady maximum after 1950 but then shows a noticeable decline starting near the end of the 20<sup>th</sup> century ([Figure 1B](#)). This negative temporal trend persisted even when number of records and of contributing collections, institutions, and datasets were considered (generalized least squares estimate + SE for the period 1986–2016:  $-31.9 \pm 11.0$ ,  $t$  value  $-2.9$ ,  $p = 0.008$ ). Thus, fewer species have been reported globally within GBIF records since approximately the 1990s.

To remove potential biases introduced by year-to-year heterogeneity of data sources, we binned records every 10 years starting from 1946 (after the end of World War II, which caused a noticeable dip in collection intensity; see [Figure 1A](#)) until 2015 (inclusive); we call these bins “idecades” and name them by the multiple-of-10 year in the middle (e.g., “1960” for the period between 1956 and 1965). We then used rarefaction-based interpolation/extrapolation (iNEXT) curves and asymptotic richness estimators<sup>38,39</sup> to compare idecadal changes in richness of species records. This assumes that (1) relative sampling of rare versus common species and (2) representation of biodiversity hotspots are both consistent across decades and that inconsistencies between years are averaged out by idecadal binning. In this analysis, accumulation curves are very similar from the 1950s to the 1990s but flatten considerably to reach lower asymptotes for the 2000s and 2010s ([Figures 1C](#) and [1E](#)). By comparing the values of the asymptotic richness estimators, we found a reduction of about 8% during the 2000s in both datasets and a reduction of 22% and 26% during the 2010s for the full and specimen-only datasets, respectively ([Figures 1D](#) and [1F](#)). These results suggest that the number of species among bee specimens collected worldwide is showing a sharp decline.

### Patterns of record richness show phylogenetic structure

Bee families in our dataset are heterogeneous in terms of richness and abundance, and the observed trends might be driven by just a few bee clades. To make a more phylogenetically explicit analysis exploring whether bees show a differential temporal trend compared with that of their closest relatives and whether particular bee families are more endangered than others, we re-analyzed the specimen dataset and this time also retained records for two families of carnivorous apoid wasps, Crabronidae and Sphecidae, that are sister to Anthophila and for another highly diverse, non-apoid hymenopteran family, the Formicidae (ants).<sup>40</sup> The results show different patterns of species richness in records of each family with noticeable phylogenetic structure ([Figure 2](#)). Long-tongued bees (Megachilidae



**Figure 1. Despite increasing number of specimen records, the number of worldwide recorded bee species is sharply decreasing**

(A) Number of worldwide GBIF records of Anthophila (bees) occurrences per year in the full (cyan) and specimen-only (red) datasets. The curves represent loess fits with a smoothing parameter of  $\alpha = 0.75$  up to 2015. The four most recent years (2016–2019, labeled with an asterisk) were excluded from further analysis.

(B) Number of bee species found each year in the full (cyan) and specimen-only (red) datasets.

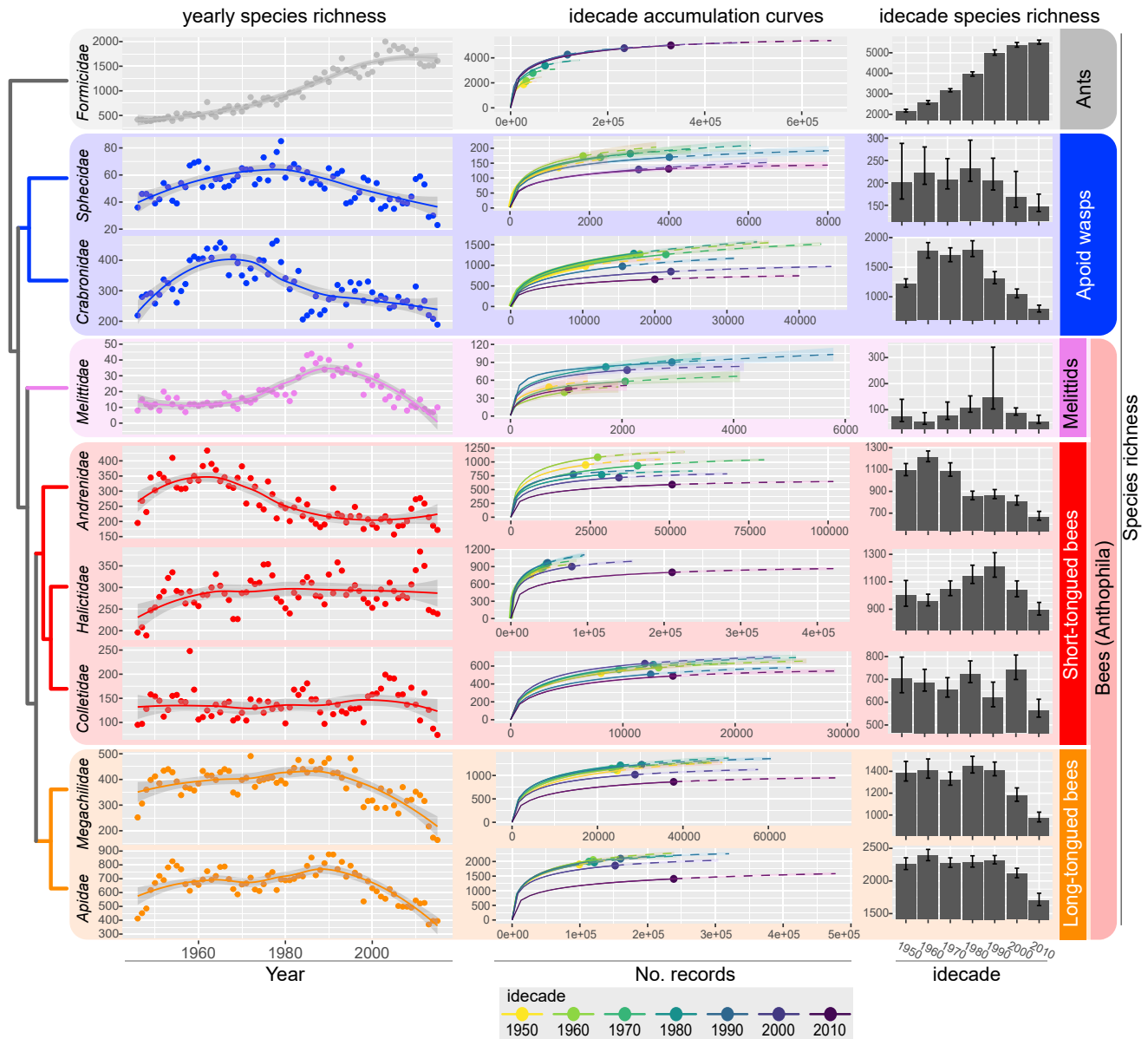
(C) Chao's interpolation/extrapolation (iNEXT) curves based on the full dataset. Data were binned into 10-year periods (*idecades*) from 1946 to 2015. The circles show actual number of specimen records and separate interpolated (left, full line) from extrapolated (right, dashed line) regions of each curve.

(D) Values of the asymptotic richness estimator by decade (see main text) for the full dataset (error bars mark upper and lower 95% confidence intervals).

(E) Chao's iNEXT curves based on the specimen-only dataset.

(F) Values of the asymptotic richness estimator by decade for the specimen-only dataset.

See also [Figures S2–S6](#).

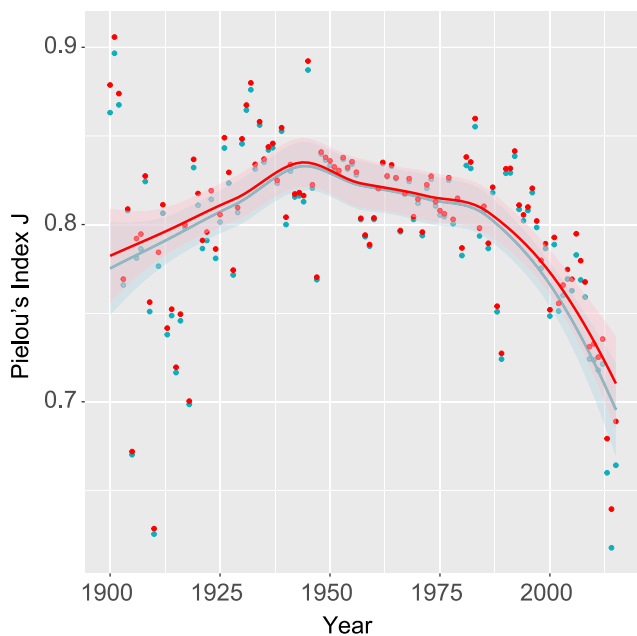


**Figure 2. Patterns of decline in worldwide records of bees are generalized but phylogenetically structured**

Phylogenetic relationships among each of the six families of bees (Anthophila, lower six rows), two related families of non-flower-associated apoid wasps (second and third rows), and the less-related, highly speciose ant family (top row). The left column shows the number of species per year in GBIF records from 1946 to 2015 according to the preserved specimen dataset; the curves represent loess fits with a smoothing parameter of  $\alpha = 0.75$ . The middle column shows Chao's iNEXT curves based on GBIF records, grouped by idecade for the period 1946–2015. The right column shows the asymptotic estimates of richness by idecade for the same period (error bars mark upper and lower 95% confidence intervals). See also [Figure S1](#).

and Apidae) show a steepening decline starting in the 2000s, whereas short-tongued bees show declines starting earlier (Andrenidae and Halictidae) or later (Colletidae). These declines in richness of recorded species relative to the average number found between 1950 and 1990 ranged from 17% for Halictidae to over 41% for Melittidae. Comparisons between Anthophila families and two families of apoid wasps sister to bees and a more distantly related family, the true ants (Formicidae), revealed contrasting trends (Figure 2). While both wasp families also show declining trends, they present different patterns than bees do.

Record richness of sphecid and crabronid wasps both show a smoother decrease initiating earlier than the 2000s. In contrast, ants show very little evidence of global record richness decline but rather a trend toward an increase in the number of recorded species. Although the limited number of bee families precludes a formal analysis of phylogenetic patterning, closely related families (e.g., Apidae and Megachilidae, or Colletidae and Halictidae) seem to share more similar trends in terms of timing and magnitude of species richness decline than less-related families. This hint of phylogenetic patterning becomes even more apparent



**Figure 3. Overall representation of bee species within global records is becoming increasingly uneven over time**

Estimate of Pielou's index of sample evenness per year in the full (blue) and specimen-only (red) datasets from 1900 to 2016. The lines show respective loess-fit curves with a smoothing parameter of  $\alpha = 0.75$ . See also Figure S5.

when considering the two apoïd wasp families, Crabronidae and Sphecidae (Figure 2). Interestingly, a very similar pattern—in which bees show a strong, recent decline; wasps show a gentler decline starting earlier; and ants remain steady—was recently reported by a quite different analytical approach on a substantially different and more geographically limited dataset.<sup>41</sup> All together, family-specific trends and asymptotic richness estimates show that the apparent overall decline in global bee record richness is not driven by any particular family. Instead, a generalized decline seems to be a pervasive feature within the bee lineage.

To rule out the possibility that the method we used to estimate richness does not correlate with actual bee diversity, we compared the asymptotic estimator of total richness for each family according to GBIF records with the total known number of species and found a linear correlation between both estimates across families (Figure S1). Another potential artifact causing a decline in recorded bee diversity in the last two decades could be an increasing loss in taxonomic expertise during that period.<sup>42–44</sup> Under such scenario, we would expect the fraction of records unidentified to the species level—a reasonable proxy for lack of expertise<sup>35</sup>—should have stayed approximately constant until the last two decades and then increased noticeably. Whereas the fraction of records missing species' identification shows an overall increase in the last 120 years, this trend has actually reversed since the 2000s (Figure S2). This result is consistent with previous analyses of the GBIF dataset<sup>35</sup> and shows that potential loss of taxonomic expertise cannot explain the decline in bee record diversity seen in the last two decades.

### Most continents contribute to recorded species decline

Next, we explored the geographic distribution of the dataset by subsetting the data by continent and repeating the analyses. Overall, GBIF has a strong bias toward North American and European records,<sup>37</sup> and this bias results in a very uneven contribution of each continent to the decadal number of records (Figure S3). North America (including Central America and the Caribbean) has the largest and most even representation of records across decades (between 46% and 75% of global records) and shows its steepest apparent decline in species richness between the 1990s and the 2010s (Figure S4). In contrast, Europe shows two separate periods of decline, one between the 1960s and the 1970s and a more recent drop between the 1980s and 1990s, but stabilizes afterward (Figure S4). Africa appears to show a sustained fall in species richness since the 1980s, whereas in Asia the decline seems to have started two or three decades earlier (Figure S4). The trend in South America is less clear, although estimated richness also decreases in the last 10 years of the dataset (Figure S4). Overall, analyses of the dataset at a continental scale show heterogeneity in both the proportional and the absolute contributions to the records and in the timing and magnitude of the decline in species richness. However, despite large differences in data availability, all continents except for Oceania seem to be contributing to the observed global decline in species richness of bee records.

### Relative species representation is increasingly uneven

A global decline in bee record diversity could relate to a proportional decrease in bee abundance so that rare species become rarer or even extinct and abundant species become less abundant. Alternatively, the less abundant species could be declining strongly, whereas abundant species might be declining at a lower rate or even thriving. These different scenarios are expected to leave a distinctive signature in the temporal pattern of relative record abundances. Under the first scenario, the sharp decrease in species richness estimates should not be accompanied by a decrease in evenness, a measure of how equally total record abundance is partitioned among species, whereas under the second scenario there should be a parallel decrease in record evenness. As expected from the hypothesis of an abundance-related differential species decline, plotting Pielou's index (a common measure of evenness<sup>45</sup>) per year of bee records shows a strong decreasing trend since the 1990s for both datasets (Figure 3). Therefore, this decline in species richness of records can relate to a global change in how an invariant bee diversity is sampled, leading to more infrequent reporting of many species and much more frequent reporting of a few other species. Alternatively, this trend of decreasing evenness can reflect a true global biological phenomenon by which thousands of species are becoming too rare to be sampled while fewer species are becoming dominant and perhaps even increasing in abundance. These two alternatives are not mutually exclusive, but the global trend of decreasing evenness is consistent with reported regional trends of increasing dominance by one or a few bee species associated with large-scale anthropogenic disturbance.<sup>46,47</sup>

### Global records agree with regional bee decline reports

Our results support a hypothesis of overall decline in bee diversity at a global scale. If trends in species richness of GBIF records are



reflecting an actual trend in bee diversity, then this decline appears to be occurring with distinctive characteristics in every bee family and on most continents. Interestingly, this trend appears to be a relatively recent phenomenon that accentuated in the 1990s, at the beginning of the globalization era, and continues to the present. The globalization era has been a period not only of major economic, political, and social change but also of accelerated land-use transformation.<sup>48</sup> Bees thrive in heterogeneous habitats, even those driven by humans,<sup>18,49</sup> where they find a diversity of floral and nesting resources. However, land devoted to agriculture, particularly to monoculture, has expanded in several regions of the world since the 1990s.<sup>48</sup> This has led not only to higher habitat homogeneity, which can relate by itself to more impoverished and spatially homogeneous bee assemblages,<sup>18,50</sup> but also to higher use of pesticides and other agriculture chemical inputs that have direct and indirect lethal and sublethal effects on bee health.<sup>51</sup> Effects of climate change on shrinking bee geographical ranges have been also documented in Europe and North America.<sup>4</sup> Lastly, a booming international bee trade has involved the co-introduction of bee pathogens, which may cause bee decline, like in the emblematic case of the giant Patagonian bumble bee, *Bombus dahlbomii*.<sup>52</sup> These drivers can act synergistically, which could have accelerated a process of bee decline. Phylogenetic patterning in the trend of recorded species diversity among the different bee families (Figure 2) suggests that different lineages can be differentially affected by different drivers, most likely via both their common geographical distribution and their shared clade-specific biological and ecological traits.<sup>22,53,54</sup>

Associated with the declining trend of richness of species records is a trend of increasing dominance of records by a few species. Increasing dominance by one or a few species can be observed at the regional scale, like the case of *Bombus terrestris* in Scandinavia within its native geographical range<sup>46</sup> and in southern South America within its invaded range<sup>55</sup> or the western honeybee *Apis mellifera* in the Mediterranean.<sup>47</sup> In particular, the western honeybee has been introduced into every continent except Antarctica from its original geographical range in Europe and Africa. Although both domesticated and wild populations of the western honeybee seem to be declining in several countries, this species is still thriving globally.<sup>56</sup> Correspondingly, an increasing fraction of the total global bee records is composed of *Apis mellifera* occurrences (Figure S5). A consequence of increasingly less diverse and uneven bee assemblages could be an increase in pollination deficits, causing a reduction in the quantity and quality of the fruits and seeds produced by both wild and cultivated plants. Less diverse bee assemblages at both local and regional scales have been associated with lower and less stable yields of most pollinator-dependent crops.<sup>13</sup>

GBIF is certainly not a source of systematically collected data, and this should be borne in mind when interpreting the results of our analyses.<sup>22,28,37,57,58</sup> Spatial and temporal biases in collection intensity (e.g., targeted programs might enrich the abundance of specific species or groups at specific spans and regions) can generate spurious trends. In our analysis, we counted every species only once per year regardless of how many records it had for a given year; this filters out biases due to sporadic intensive sampling campaigns. Biases introduced as a result of targeted collection efforts or local or regional events (e.g., changes in research and conservation policies, economic downturns, and social un-

rest) are possible, yet most such biases tend to be spatially and temporally restricted and are less likely to systematically affect trends at the global, multidecadal scale of this analysis. Plausible biases could enhance the appearance of a declining trend; others might act to hide it. For example, an increasing tendency for collectors targeting rare species would be expected to enrich the number of species (unless many species are becoming so scarce that they just cannot be found). By contrast, shifts in collection trends (driven by changing museum priorities, restrictions on the movement of biological material from biodiversity hotspots, defunding of natural history research and taxonomy, or the implementation of systematic monitoring programs) could lead to a shift away from rare to common species, thus creating a false signal of decline in apparent species richness. Supplementation of dwindling specimen collection data with exponentially growing citizen-science observations is not devoid of issues either,<sup>28,35,59</sup> including less reliable species identification and a strong bias toward sampling well-populated, more accessible areas rather than more remote and potentially more biodiverse areas (which could result in observing a general declining trend that is actually driven by species being lost mostly in urban and suburban areas). Although focusing on the presence or absence of species across large areas may make our analytical approach more robust to many of these sources of bias, they are not to be dismissed, and thus results should be approached with caution.

Despite the above concerns, and consistent with the hypothesis of a global decline in recorded bee richness, our continent-level analysis showed that regions with the best temporal and spatial coverage (i.e., Europe and North America; Figure S3) are the ones exhibiting the clearest signal of decline (Figure S4); our results agree with several existing reports at local, national, and subcontinental levels.<sup>14,16,17,41,60–65</sup> Furthermore, none of those biases can explain the noticeable phylogenetic contagion seen in the trends (Figure 2) better than the fact that the hymenopteran groups we analyzed have a considerable phylogenetic signal in their ecology and life history traits and would be expected to show phylogenetic clustering in their response to drivers of decline.<sup>54</sup>

Unsurprisingly, when data are disaggregated by country, agreement between country-level results and existing reports improves as the number of records increases. For example, our data reflect a clear and continuous decline in bee diversity in the United States<sup>60,61,64</sup> (with over one million records) and a decline in Brazil<sup>65</sup> during the last two decades (~190,000 records) but show no clear loss of richness in Great Britain (~25,000 records) and much uncertainty in an apparent trend in bee species loss in Panama (~9,000 records) despite reports of bee decline in all those countries<sup>14,16,17,66</sup> (Figure S6). Interestingly, reports on the decline of British bees are based on occurrence data that are not publicly available, i.e., ~300,000 records from the Bees, Wasps & Ants Recording Society (<http://www.bwars.com/>). This suggests that, in addition to data source heterogeneity, obstacles to data mobilization are a major source of bias and inaccuracy of results derived from GBIF data, highlighting the need to increase efforts to remove barriers to data sharing and encourage funding agencies to implement policies that minimize data sequestration while implementing a system of incentives to promote data sharing by privately funded natural history societies and private collectors. Seeing that a larger number of records

also reduces uncertainty is also encouraging since it implies that a much better picture would be obtained as vast troves of information currently held within institutional and private collections become digitized and added to the public domain. For example, a recent specimen record digitization effort from the collections of a single Chilean institution has increased 4-fold the number of bee records for this South American country,<sup>67</sup> proving that even a relatively modest investment can yield a sizable improvement in occurrence record numbers of data-deficient regions. Thus, while the inherent heterogeneity and biases of aggregated datasets such as those offered by GBIF may make them unreliable as a direct (i.e., unfiltered or uncorrected) data source of predictive models, they can still be used within a hypothesis-driven framework to test whether bees (or any other taxon) as a group are declining worldwide. In this context, our results largely agree with the hypothesis that current regional reports of declining bee diversity reflect a global phenomenon.

## Conclusions

One of the most important pieces of missing information from the IPBES Assessment Report on Pollinators, Pollination and Food Production<sup>68</sup> was the lack of data on global bee decline, despite the many local and few regional reports pointing out that this decline could reflect a global phenomenon. With all of its shortcomings, GBIF still is probably the best global data source available on long-term species occurrence and has the potential to contribute to filling this critical knowledge gap. Our analysis supports the hypothesis that we are undergoing a global decline in bee diversity that needs the immediate attention of governments and international institutions. Under the most optimistic interpretation—that bees are not declining and that the trends we find are an artifact of heterogeneous data collection—our results would indicate that global efforts to record and monitor bee biodiversity are either decreasing over time or becoming increasingly focused on widespread species and/or outside biodiversity hotspots. However, given the current outlook of global biodiversity,<sup>4,5,10,12</sup> it is more likely that these trends reflect existing scenarios of declining bee diversity. In the best scenario, this can indicate that thousands of bee species have become too rare; under the worst scenario, they may have already gone locally or globally extinct. In any case, a decline in bee diversity driven by either increasing rarity or irreversible extinction will affect the pollination of wild plants and crops and have broader ecological and economic consequences.<sup>8,12</sup> In this context, plans to establish national monitoring programs for native bees (as recently proposed for the United States) could help fill the information gaps and perhaps serve as a model for a more global effort.<sup>69</sup> Slowing down and even reversing habitat destruction and land conversion to intensive uses, implementing environmentally friendly schemes in agricultural and urban settings, and creating programs to re-flower our world are urgently required. Bees cannot wait.

## EXPERIMENTAL PROCEDURES

### Resource availability

#### Lead contact

Further information and requests for resources and code should be directed to and will be fulfilled by the lead contact, Eduardo E. Zattara (ezattara@comahue-conicet.gob.ar).

### Materials availability

This study did not generate new unique materials.

### Data and code availability

Occurrence record data used in this paper can be downloaded from <https://doi.org/10.15468/dl.yjzm4x>; original sources are traceable via <https://GBIF.org>. The R language scripts used for analyzing the data and reproducing reported results and plots are available at <http://doi.org/10.5281/zenodo.4312055>; this code is open and can be used and/or modified for analyzing updated datasets and additional taxa.

### Dataset

An initial query to the database of occurrence records at GBIF (<http://www.gbif.org>) using the filters [Scientific Name = “Hymenoptera”, Basis of Record = “PRESERVED\_SPECIMEN” | “HUMAN\_OBSERVATION”, Year <2020] on May 7, 2020, resulted in 9,176,688 total records involving 2,374 datasets.<sup>34</sup> Data were downloaded as a text file and filtered for records identified to species levels and belonging to Anthophila (defined as the families Melittidae, Andrenidae, Halictidae, Colletidae, Megachilidae, and Apidae; 3,459,086 records). We also retrieved records for two closely related families of apoid wasps (Crabronidae and Sphecidae; 283,331 records) or true ants (Formicidae; 1,121,857 records). Phylogenetic relations among all nine of these families follow recent phylogenomic results.<sup>40</sup>

### Analyses

Data were analyzed with a customized script written and executed within the R computing environment.<sup>70</sup> The complete annotated script can be used to fully reproduce all results or be adapted to re-run the analyses on other datasets.<sup>71</sup> Data were processed with the `tidyr`,<sup>72</sup> `dplyr`,<sup>73</sup> and `data.table`<sup>74</sup> packages.

After records without “year” data were removed, yearly counts of records and species were plotted with `ggplot2`.<sup>75</sup> We tested the significance of a negative trend by fitting yearly counts of records, species, collections, institutions, and datasets with a generalized least-squares model with the formula  $sp \sim year + records + collections + institutions + datasets$  and an autoregressive-moving average autocorrelation structure of order (1,0). Then, each year was assigned to a 10-year period termed “idecade” (for interdecade) corresponding to a regular decade shifted 4 years into the past (e.g., the 1990s idecade spans 1986–1995). Records by species and idecade were counted and stored in a matrix of  $m$  species  $\times$  7 idecades (1950s–2010s). We used this matrix as abundance data input for the `iNEXT` function of the `iNEXT` package<sup>39</sup> to estimate rarefaction-based `iNEXT` curves and Chao1 asymptotic estimators of species richness.<sup>38</sup> We also compared the asymptotic estimator of species richness for each family with the total number of species listed for each family in the taxonomic framework of the Integrated Taxonomic Information System (<http://www.itis.gov>).

To estimate potential biases caused by changes in taxonomic expertise over time, we re-filtered the initial GBIF query without excluding records without a species ID and then counted the number of records with or without a species ID per year.<sup>35</sup> To analyze trends at the continental level, we added a “continent” field to the base dataset via table joining to a list of countries, country codes, and continents from <https://datahub.io/JohnSnowLabs/country-and-continent-codes-list>. We then repeated the analyses by splitting the dataset by continent. Continent- and country-specific shapes were taken from <https://github.com/djaiss/mapsicon>. To show trends in equitability of species abundance across records over time, we calculated Pielou’s evenness index,<sup>45</sup>  $J = \sum p_i \ln(p_i) / \log(S)$ , for  $i = 1$  to  $S$ , the total number of species, for each year between 1900 and 2018 by using the diversity functions from the package `vegan`.<sup>76</sup> The contribution of a given species (e.g., *Apis mellifera*) was calculated as yearly number of the species records divided by the total number of records for that year and plotted as a function of year.

## SUPPLEMENTAL INFORMATION

Supplemental information can be found online at <https://doi.org/10.1016/j.oneear.2020.12.005>.



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**AUTHOR CONTRIBUTIONS**

Conceptualization, E.E.Z. and M.A.A.; data curation, E.E.Z.; formal analysis, E.E.Z. and M.A.A.; visualization, E.E.Z.; writing – original draft, E.E.Z. and M.A.A., writing – review & editing, E.E.Z. and M.A.A.

**DECLARATION OF INTERESTS**

The authors declare no competing interests.

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**ONEEAR, Volume 4**

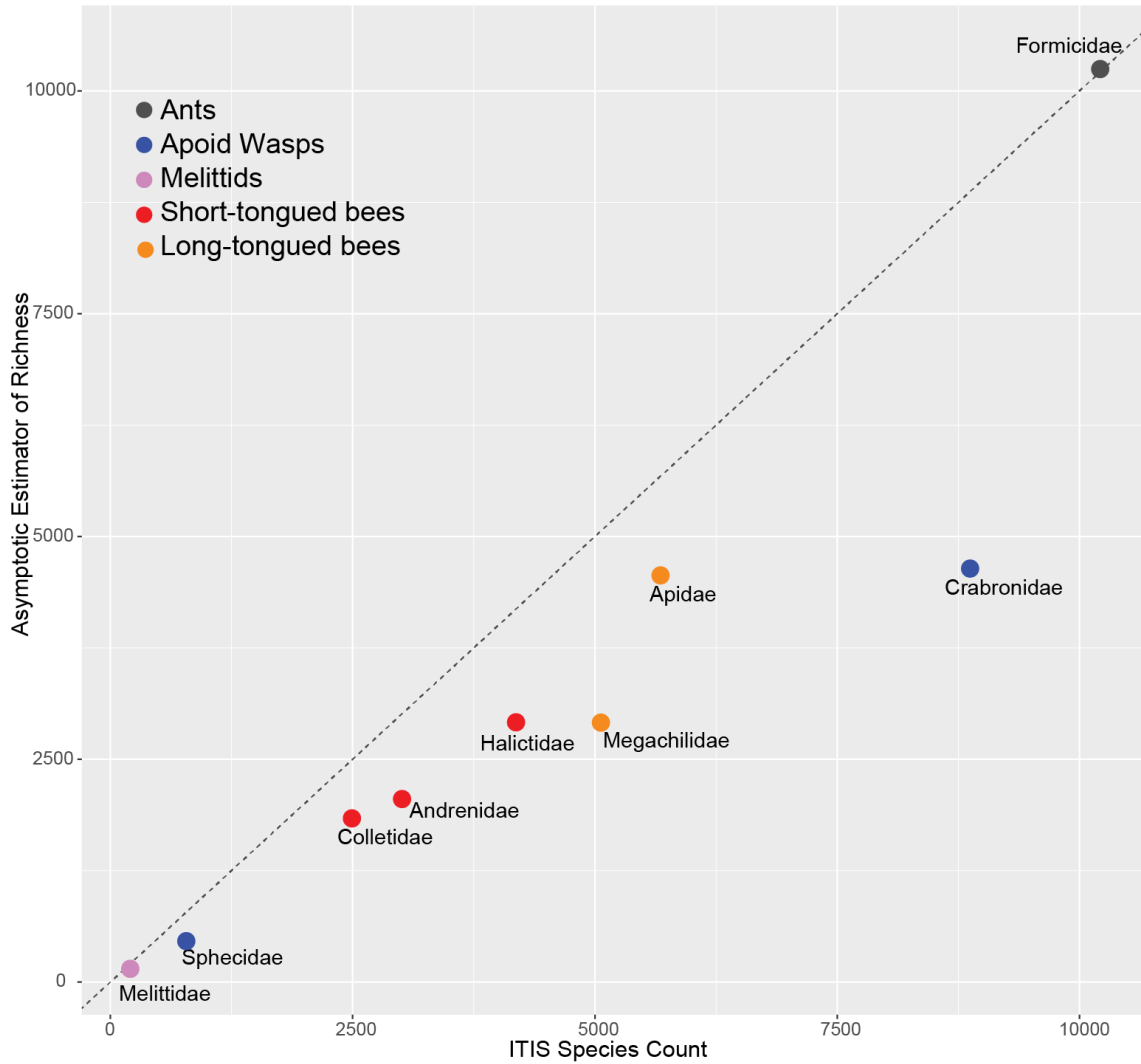
## **Supplemental Information**

**Worldwide occurrence records suggest  
a global decline in bee species richness**

**Eduardo E. Zattara and Marcelo A. Aizen**

## Supplemental Figures

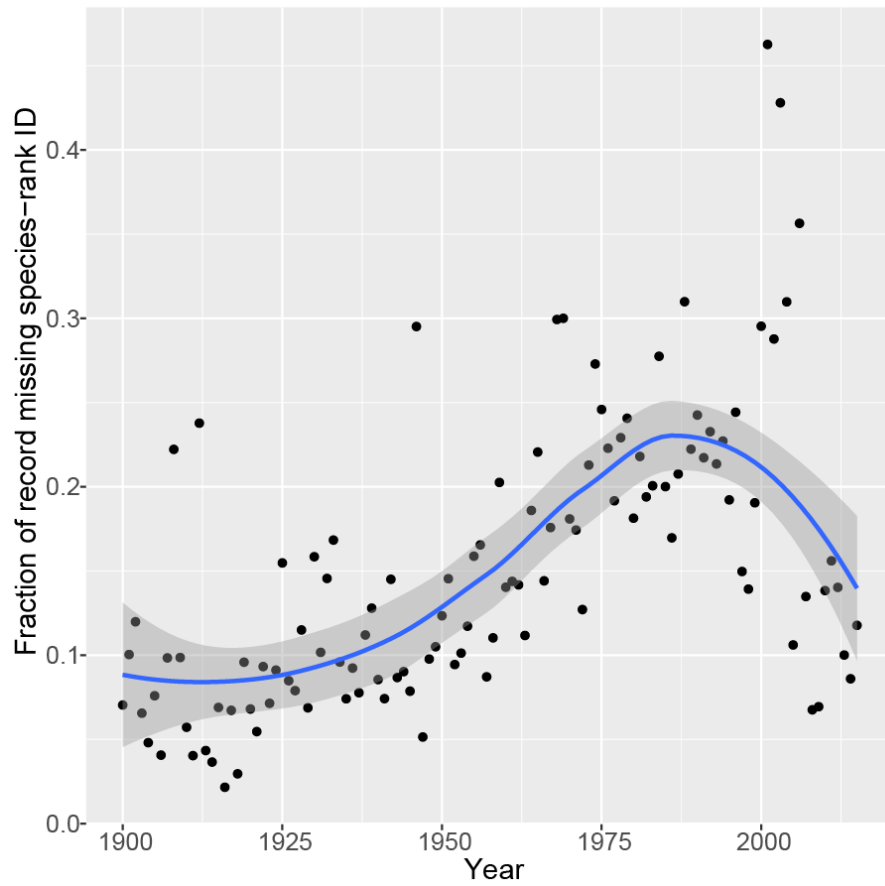
**Figure S1. Correlation of family species richness values between asymptotic estimators and total known species. Related to Figure 2.**



While often underestimating the known richness of each family, Chao's asymptotic estimators of species richness based on all-times GBIF global records of preserved specimens show a linear correlation with actual species diversity. The dotted line shows the identity diagonal. ITIS stands for Integrated Taxonomic Information System ([www.itis.gov](http://www.itis.gov)).

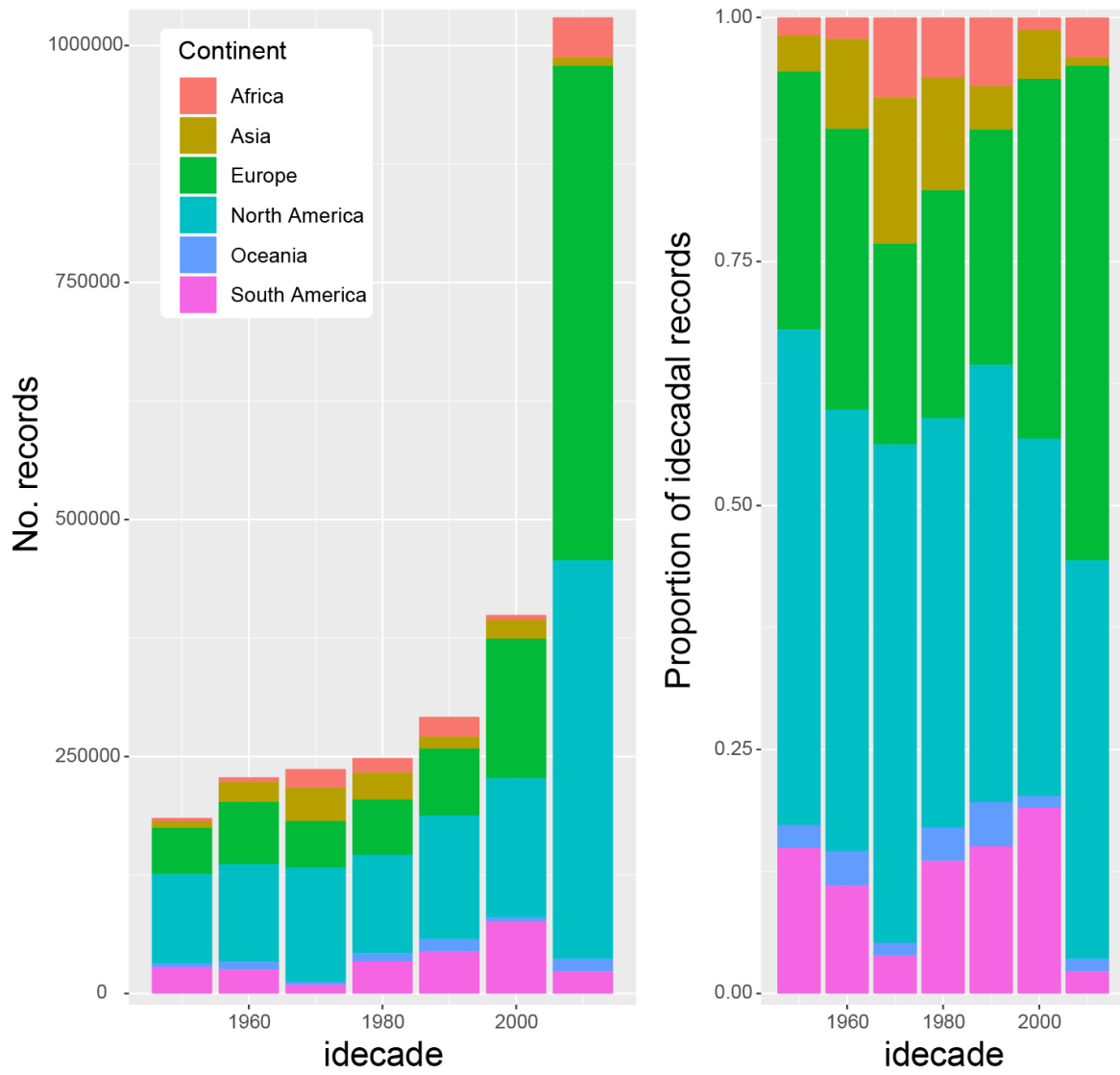


Figure S2. Fraction of the dataset records that lack a species ID. Related to Figure 1.



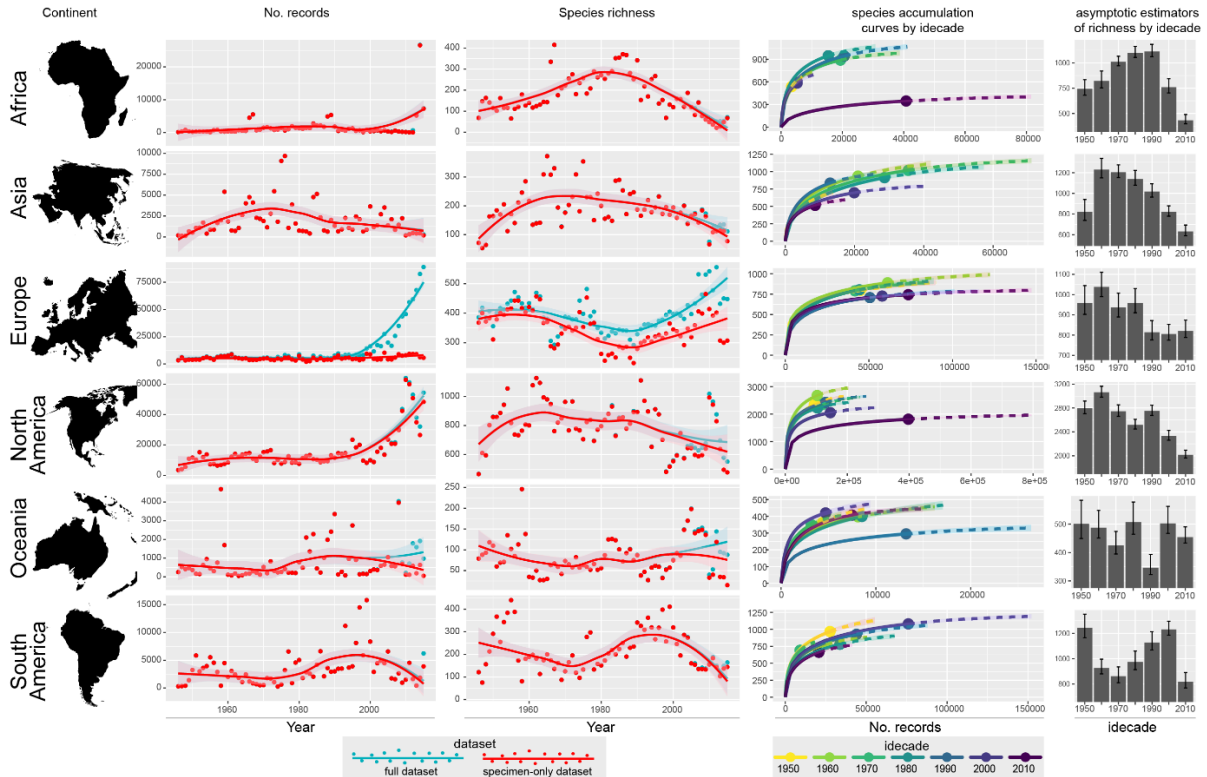
Points show the proportion of records unidentified at the species level in a given year, relative to the total number of records for that year. The curve shows a loess-smoothed trend line with a smoothing parameter  $\alpha = 0.75$ .

**Figure S3: Contribution by idecade of each continent (Antarctica excluded) to the full bee record dataset. Related to Figure 1.**



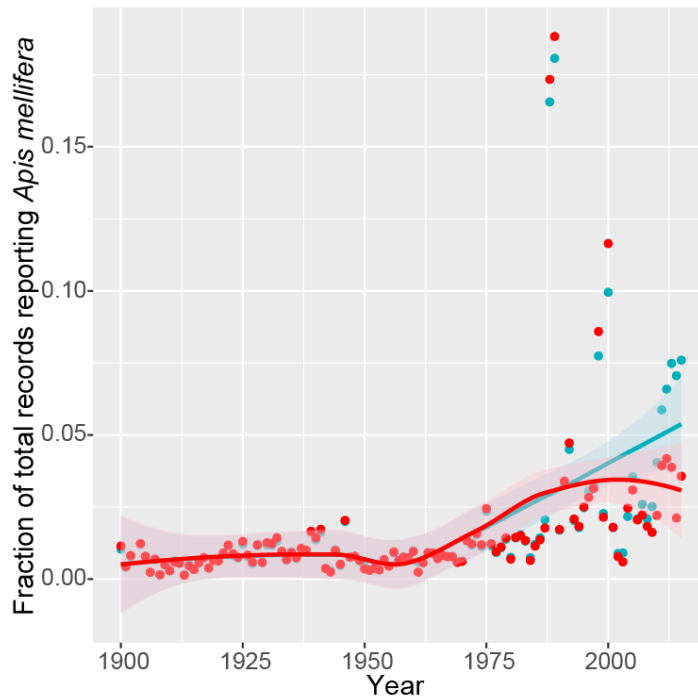
(A) Absolute number of GBIF records with a species ID for each continent, grouped by idecade since the 1950's. (B) Relative contribution of each continent to worldwide idecadal GBIF records with a species ID.

**Figure S4: Trends shown in GBIF records for each continent. Related to Figure 1**



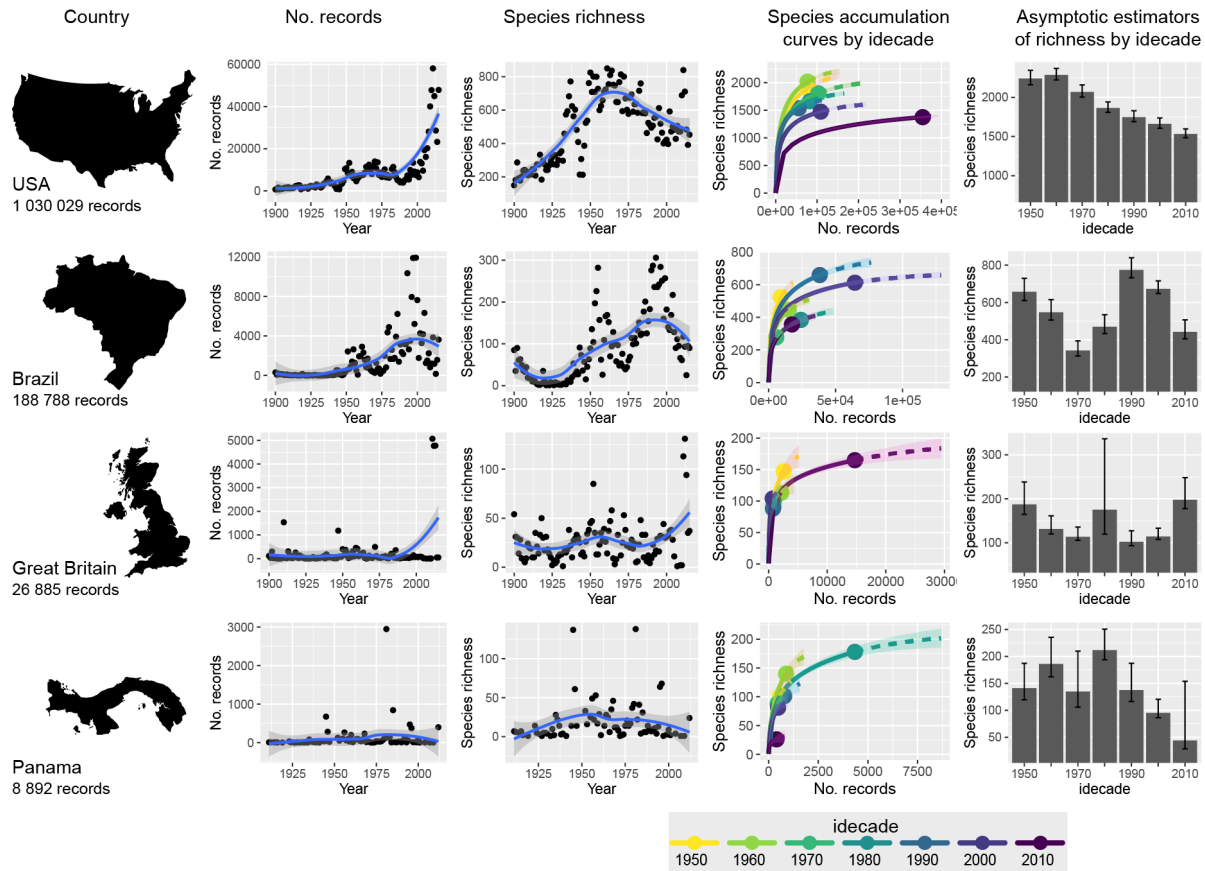
The left two rows of plots show number of yearly bee records and species in GBIF (blue: full dataset; red: specimen-only dataset); the right two rows show Chao's interpolation/extrapolation curves based on the specimen-only dataset grouped every ten years (idecades) for the period 1946-2015 and bar plots of the asymptotic estimates of richness by idecade for the same period (error bars mark upper and lower 95% confidence intervals).

**Figure S5: Representation of the honeybee *Apis mellifera* is increasing since the year 1900. Related to Figure 3.**



Fraction of global records of preserved specimens at GBIF represented by the honeybee *Apis mellifera* since the year 1900. Points represent yearly proportion of total records belonging to *A. mellifera* (cyan: full dataset; red: specimens-only dataset). Lines show respective loess fit curves with a smoothing parameter  $\alpha = 0.75$ .

**Figure S6: Reliability of trends shown in records of GBIF preserved specimens for specific countries increases with the number of records. Related to Figure 1.**



The left two rows of plots show number of yearly bee records and species in GBIF for each country – fitted trends are loess curves with a smoothing parameter  $\alpha = 0.75$ ; the right two rows show Chao's interpolation/extrapolation curves based on records grouped every ten years (idecades) for the period 1946-2015 and bar plots of the asymptotic estimates of richness by idecade for the same period (error bars mark upper and lower 95% confidence intervals).