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BatFly: A database of Neotropical bat-fly interactions

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Substantive Area:	Community Ecology < Substantive Area, Species Interactions < Community Ecology < Substantive Area, Parasitism < Species Interactions < Community Ecology < Substantive Area, Data paper < Data < Substantive Area
Organism:	Bats < Mammals < Vertebrates < Animals, Flies, Mosquitoes < Insects < Arthropods < Invertebrates < Animals
Habitat:	
Geographic Area:	South America < Geographic Area, Central America < Geographic Area, Mexico < North America < Geographic Area, Puerto Rico < United States < North America < Geographic Area, Southeast US (DC, DE, FL, GA, MD, NC, SC, WV, VA) < United States < North America < Geographic Area, Southcentral US (AL, AR, KS, KY, LA, MO, MS, OK, TN, TX) < United States < North America < Geographic Area, Southwest US (AZ, CA, CO, NM, NV, UT) < United States < North America < Geographic Area
Key words/phrases:	Antagonism, bats, bat flies, Chiroptera, diseases, ectoparasites, hematophagy, Nycteribiidae, Streblidae, specialization, species interactions, zoonosis
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	but so far, our knowledge is restricted to fragmented records at a local scale. To help boost research, we have assembled a data set of bat-fly interactions from 174 studies published between 1904 and 2022, plus three original data sets. Altogether, these studies were carried out at 650 sites in the Neotropics, mainly distributed in Mexico, Brazil, Argentina, southern USA and Colombia, among other countries. In total, our data set contains 3,984 interaction records between 237 bat species and 255 fly species. The bat species with the largest number of recorded interactions were Carollia perspicillata (357), Artibeus jamaicensis (263), and Artibeus lituratus (228). The fly species with the largest number of recorded interactions were Trichobius joblingi (256), Megistopoda aranea (235), and Megistopoda proxima (215). The interaction data were extracted, filtered, taxonomically harmonized, and made available in a tidy format together with linked data on bat population, fly population, study reference, sampling methods and geographic information from the study sites. This interconnected structure enables the expansion of information for each interaction record, encompassing where and how each interaction occurred, as well as the number of bats and flies involved. We expect BatFly to open new avenues for research focused on different levels of ecological organization and spatial scales. It will help consolidate knowledge about ecological specialization, resource distribution, pathogen transmission, and the drivers of parasite prevalence over a broad spatial range. It may also help answer key questions, such as: are there differences in fly prevalence or mean infestation across Neotropical ecoregions? What ecological drivers explain those differences? Or how do specialization patterns vary among fly species in the Neotropics? Furthermore, we expect BatFly to inspire research aimed at understanding how climate and land-use changes may impact host-parasite interactions and disease outbreaks. This kind of research may help us reach Sustainable Development Goal 3, Good Health and Wellbeing, outlined by the United Nations.

Note: The following files were submitted by the author for peer review, but cannot be converted to PDF. You must view these files (e.g. movies) online.

Data_S1.zip

SCHOLARONE™ Manuscripts

BatFly: A database of Neotropical bat-fly interactions

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Abstract: Global changes have increased the risk of emerging infectious diseases, which can be prevented or mitigated by studying host-parasite interactions, among other measures. Bats and their ectoparasitic flies of the families Streblidae and Nycteribiidae are an excellent study model, but so far, our knowledge is restricted to fragmented records at a local scale. To help boost research, we have assembled a data set of bat-fly interactions from 174 studies published between 1904 and 2022, plus three original data sets. Altogether, these studies were carried out at 650 sites in the Neotropics, mainly distributed in Mexico, Brazil, Argentina, southern USA and Colombia, among other countries. In total, our data set contains 3,984 interaction records between 237 bat species and 255 fly species. The bat species with the largest number of recorded interactions were *Carollia perspicillata* (357), *Artibeus jamaicensis* (263), and *Artibeus lituratus* (228). The fly species with the largest number of recorded interactions were *Trichobius joblingi* (256), *Megistopoda aranea* (235), and *Megistopoda proxima* (215). The interaction data were extracted, filtered, taxonomically harmonized, and made available in a tidy format together with linked data on bat population, fly population, study reference, sampling methods and geographic information from the study sites. This interconnected structure enables the expansion of information for each interaction record, encompassing where and how each interaction occurred, as well as the number of bats and flies involved. We expect BatFly to open new avenues for research focused on different levels of ecological organization and spatial scales. It will help consolidate knowledge about ecological specialization, resource distribution, pathogen transmission, and the drivers of parasite prevalence over a broad spatial range. It may also help answer key

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Key words/phrases: Antagonism, bats, bat flies, Chiroptera, diseases, ectoparasites, hematophagy, Nycteribiidae, Streblidae, specialization, species interactions, zoonosis.

Open Research: The complete data set is available as Supporting Information at: [*to be completed at proof stage*]. Associated data is also available at: BatFly: A database of Neotropical bat-fly interactions *https://doi.org/10.5281/zenodo.10019756*

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METADATA

CLASS I. DATA SET DESCRIPTOR

A. Data set identity

Title: BatFly: A database of Neotropical bat-fly interactions

B. Data set identification

Data set identity codes:

BatFly_References.csv

BatFly_Sites.csv

BatFly_Sampling.csv

BatFly_Bat_Pop.csv

BatFly_Fly_Pop.csv

Batfly_Species.csv

C. Data set description

Principal Investigator(s):

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Abstract:

Global changes have increased the risk of emerging infectious diseases, which can be prevented or mitigated by studying host-parasite interactions, among other measures. Bats and their ectoparasitic flies of the families Streblidae and Nycteribiidae are an excellent study model, but so far, our knowledge is restricted to fragmented records at

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D. Keywords

Antagonism, bats, bat flies, Chiroptera, diseases, ectoparasites, hematophagy, Nycteribiidae, Streblidae, specialization, species interactions, zoonosis.

E. Description

Our world faces urgent problems related to global changes caused by human activities, which we strive to solve by following the United Nation's 17 Sustainable Development Goals (UN 2015). Goal 3, "Good Health and Wellbeing", is the focus of research by scientists from many areas under a transdisciplinary approach known as One Health (OHITF 2008). Under this approach, it is of paramount importance to understand the interactions between hosts and their parasites to prevent disease transmission and spillover (Giraudoux et al. 2022).

Bats play a crucial role in the dynamics of emerging infectious diseases because of their huge ecological diversity (Wilson and Reeder 2005), which includes a myriad of interactions with endo and ectoparasites (Klimpel and Mehlhorn 2016) that carry pathogens associated with zoonosis (Szentiványi et al. 2018). The most important bat ectoparasites are dipterans of the families Streblidae and Nycteribiidae, also known as bat flies (Dick and Patterson 2006). Bat flies (hereafter just flies) share a tight evolutionary history with bats, as they are found exclusively on them (Dick and Dittmar 2014). Consequently, both fly families exhibit intricate morphological and ecological adaptations for living on bats (Dittmar et al. 2015). In addition, they are considered host-specific, with most fly species parasitizing from one to three bat species only (Pilosof et al. 2012).

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Host specificity has received large attention in the ecological literature, being used as a model to study ecological specialization (Hiller et al. 2021), resource distribution (Hiller et al. 2018), pathogen transmission (Szentiványi et al. 2018), and the drivers of parasite prevalence (Frank et al. 2016). Despite this remarkable effort to study the ecology of flies (Patterson, Dick, and Dittmar 2007), so far knowledge is restricted to fragmented interaction records at a local scale. Therefore, we need synthesis aimed at compiling information and publishing it in data papers that filter, organize, and curate large data sets, opening avenues for addressing a broader range of questions.

In the present data paper, we compiled information on bat-fly interactions derived from 174 studies with multiple scopes, including taxonomic reviews, checklists, and assessments of species interactions, and we have also included three original data sets. These reference studies were published between 1904 and 2022, with most being published after the year 2000 (Fig. 1A). Overall, our database contains information recorded at 650 sites spanning from the northern limit of the Neotropics to southern South America (Fig. 1B). Those sites are primarily located in Mexico (143 sites from published studies and 3 sites from original datasets), Brazil (89), Argentina (62), southern USA (62), Peru (55), Cuba (32), the Dominican Republic (32), Honduras (26), and Colombia (19 sites from published studies and 15 sites from original datasets), among other countries (Fig. 1B). For 95% of the sites, there is information on entire assemblages of bats and flies. The remaining 5% report parasites collected from a single bat species (Fig. 1B).

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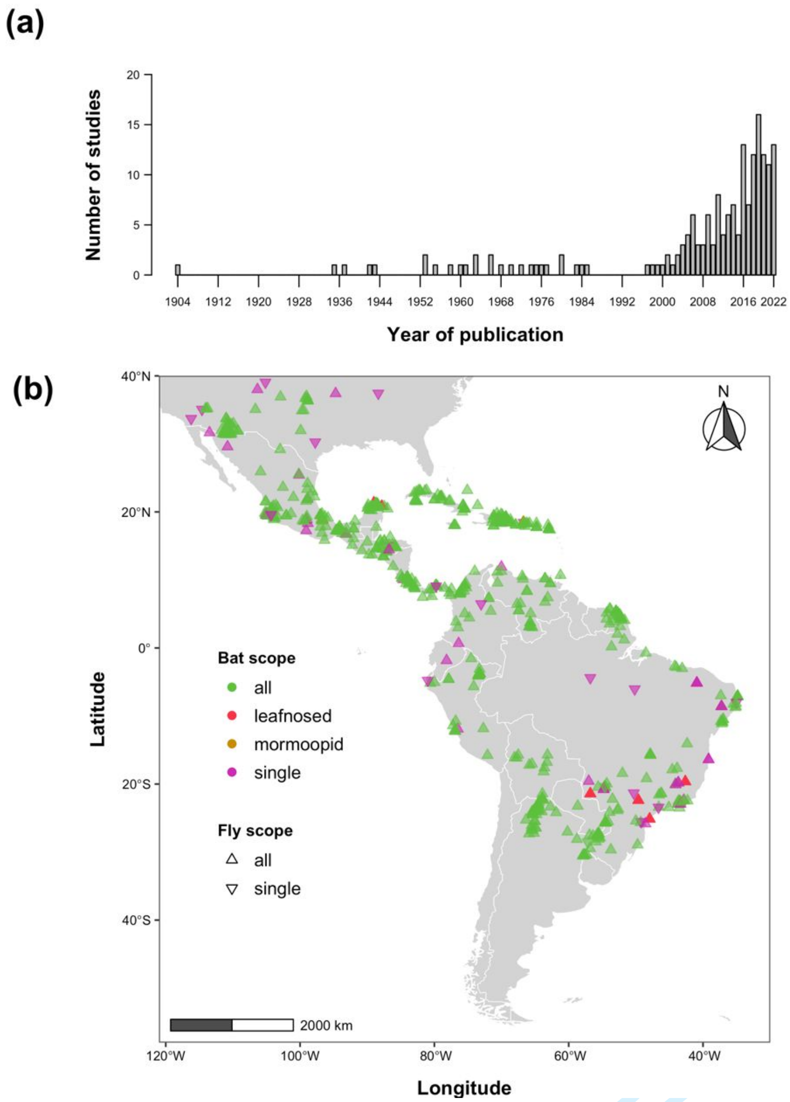

Figure 1. Temporal and spatial distribution of the references included in BatFly. (A) Number of studies published per year in the time range (1904 – 2022) included in BatFly. (B) Distribution of the sampling sites included in BatFly. Triangles represent sampling sites. Colors represent the taxonomic scope of sampling for bats, and triangle orientation (up/down) represents the taxonomic scope of sampling for flies. “Single” represents studies focused on a single fly species. “All” represents studies that assessed all fly species found at the site.

Our database comprises interactions made by bats of nine families, 76 genera, and 237 species. For flies, it comprises two families, 29 genera, and 255 species. The 15 most frequently recorded bat species made 57% of all interactions, with *Carollia perspicillata* as the species with most records (357), followed by *Artibeus jamaicensis* (263) and *Artibeus lituratus* (228) (Fig. 2A), all of which are members of the Phyllostomidae (Fleming et al. 2020). Over 57 bat species were shown to have only one interaction (singletons). Half of the interactions were made by 15 fly species, with *Trichobius joblingi* having the highest number of records (256), followed by *Megistopoda aranea* (235) and *Megistopoda proxima* (215) (Fig. 2B).

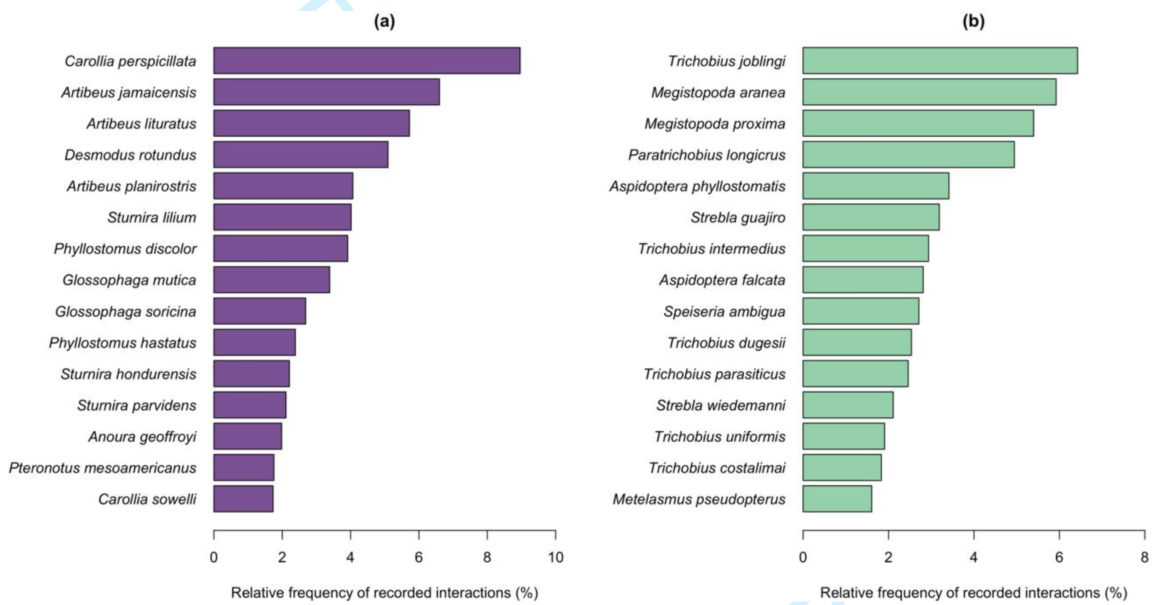

Figure 2. Relative frequency of interactions made by the top 15 (A) bat species and (B) fly species with most records.

In summary, BatFly has a total of 3,984 interaction records between bat and fly species. Among bats, the family Phyllostomidae shows the richest set of interactions (140 fly species), followed by Vespertilionidae (48 fly species), and Mormoopidae (36 fly species). Most bat families within our records interact more frequently with fly species of the family Streblidae, except for Vespertilionidae and Thyropteridae, which interact more frequently with the Nycteribiidae. Furthermore, in the bat families Furipteridae, Noctilionidae, and

Natalidae no interaction with Nycteribiidae species was recorded (Fig. 3A). Those interactions between bat and fly species form a densely connected network, in which a large group of interconnected bat and fly species (giant component of the network) can be observed. This kind of structure was unexpected due to the high specificity that these interactions are assumed to have (Fig. 3B). However, this network was made with all interactions included in BatFly, even uncommon interactions, which may mask the true host specificity in the bat-fly interactions, so it should be interpreted with caution.

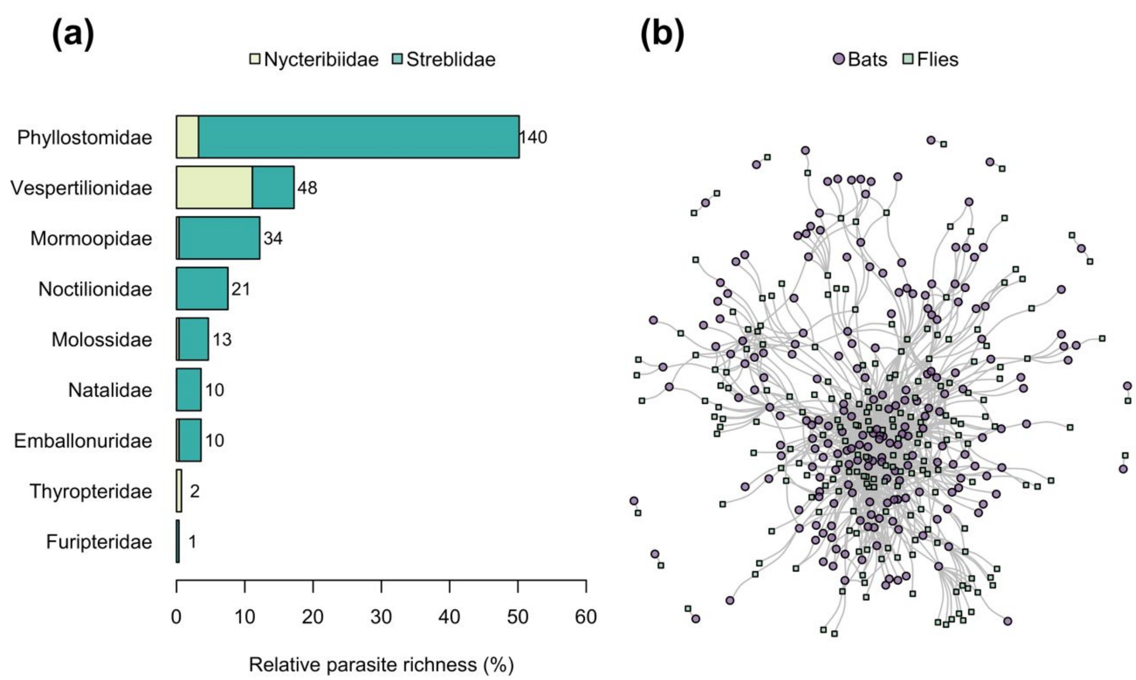

Figure 3. Overview of bat-fly interactions included in BatFly. (A) Relative richness of fly families (Nycteribiidae and Streblidae) per bat family. The number in front of the bars depicts the total number of fly species found parasitizing each bat family. (B) Bat-fly network built for the entire Neotropical region with all records included in our data set, even uncommon associations. Lines depict interactions between bat species (purple circles) and fly species (green squares). Most nodes belong to the giant component (largest subgroup of interconnected species) and there are also ten minor components (dyads).

BatFly represents the largest dataset of antagonistic interactions made by bats in both geographical and taxonomic terms. All records were taxonomically harmonized, i.e., bat and fly scientific names were checked and updated. In addition to interaction records, our database includes information about references, study sites, sampling methods, and bat and fly populations organized in six linked data sheets (Fig. 4): “references”, “sites”, “sampling”, “bat population”, “fly population”, and “species interactions”. The “references” data sheet (Fig. 4A) contains information on the original sources from which the data were obtained. Each reference study was assigned a unique reference code (e.g., BFR001), enabling identification of each reference study in all other data sheets. The data sheets “sites” (Fig. 4B) and “sampling” (Fig. 4C) contain information about where, when and how the data were collected at each site, including study sites characteristics (e.g., mean annual temperature, annual rainfall, and vegetation type) which are known to influence bat-fly interactions (Pilosof et al. 2012). Each study site was assigned a unique site code (e.g., BFA001), with which each study site can be identified in within “sites”, “sampling”, “bat population”, “fly population” and “species interactions” data sheets.

The “bat population” (Fig. 4E) and “fly population” (Fig. 4F) data sheets contain taxonomic identification and information about the populations of interacting species. Also, we included bat species traits, such as the roost types used by bats, which are important drivers of parasite dynamics (Patterson, Dick, and Dittmar 2007). Each population was assigned a unique population code for bats (e.g., BFBPOP000) and flies (e.g., BFFPOP000), allowing its identification of each population in the “species interactions” data sheets. Finally, the “species interactions” data sheet (Fig. 4F) contains the species-species interaction records, and information about number of infested bats, prevalence, mean fly intensity, and

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mean fly abundance. Each interaction record was assigned an interaction code (e.g, BFSSI000) associated to bat population and fly population codes, and also associated to site, and references codes shared between data sheets (foreign keys). This interconnected structure enables the expansion of information for each interaction record encompassing where and how the interaction was collected, as well as the number of bats and flies involved in a specific record.

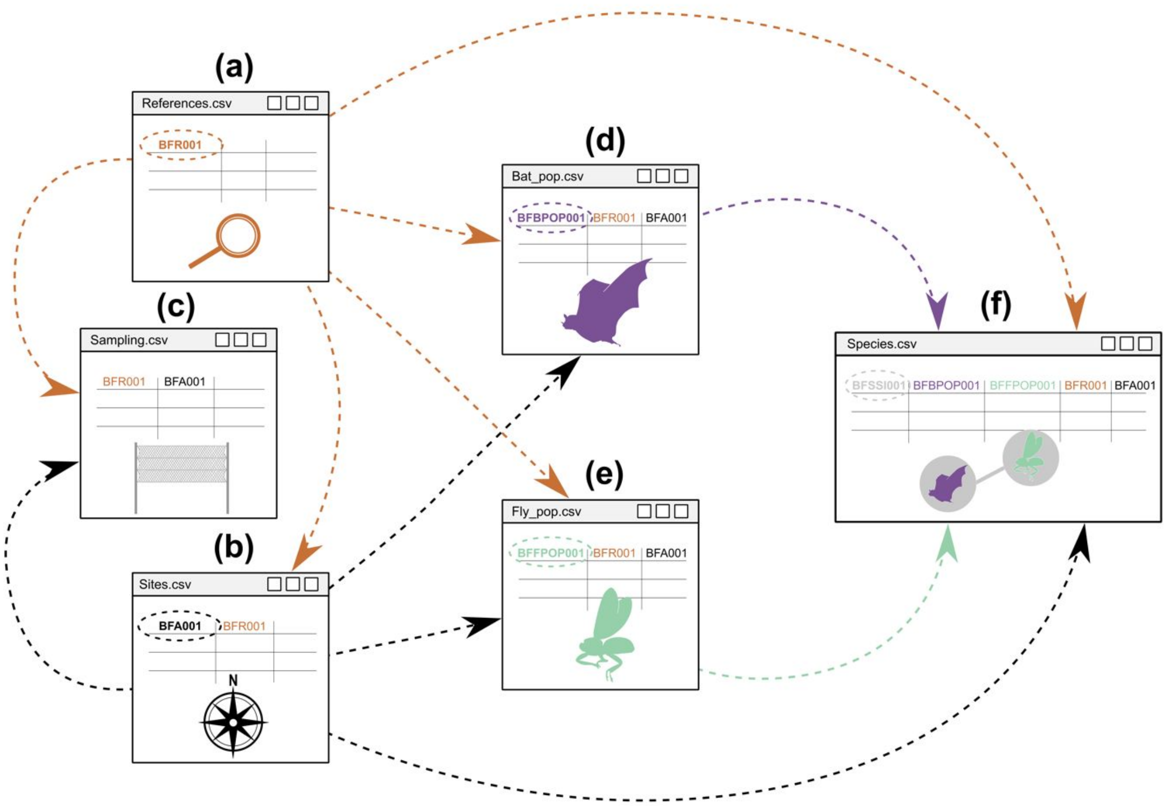

Figure 4. Structure of the BatFly database. BatFly is integrated by six interconnected datasheets. (a) References data sheet. (b) Site data sheet. (c) Sampling data sheet. (d) Bat population data sheet. (e) Fly population data sheet. (f) Species interaction data sheet. Each interaction record has a unique interaction code (primary key) associated to reference, site, bat and fly population codes shared between datasheets (foreign keys). In the graphical representation, dashed ovals indicate the first appearance of a code within the database.

Dashed lines illustrate the relationships between BatFly's datasheets. Each code is designated with a distinct color. For example, the reference code (colored orange), which first appears on the reference datasheet (a), can be found on all other datasheets, denoted by five orange lines.

BatFly was designed to boost the use of bat-fly interactions as a model for addressing questions at different levels of ecological organization and spatial scales. We expect BatFly to inspire researchers to continue consolidating knowledge about ecological specialization, resource distribution, pathogen transmission, and the drivers of parasite prevalence over a broader spatial range. It may also help answer key questions, such as: are there differences in fly prevalence or mean infestation across Neotropical ecoregions? What ecological drivers explain those differences? Or how do specialization patterns vary among fly species in the Neotropics? We also expect to inspire research aimed at understanding how bat-fly interactions can be affected by climate and landscape changes. Ultimately, we expect BatFly to help understand host-parasite interactions, facilitate predicting zoonotic outbreaks, and provide information to address the UN's SDG 3 Good Health and Wellbeing.

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CLASS II. RESEARCH ORIGIN DESCRIPTORS

A. Overall project description

Identity: A compilation of bat-fly interactions.

Period of study: Data of publication reported in the references range from 1904 to 2022.

Objective: We aimed to summarize and make available all bat-fly interaction records found in the literature plus three new data sets in a tidy format, to be used in studies on community ecology, interaction networks, and macroecology, and disease spillover, among other topics.

Abstract: Global changes have increased the risk of emerging infectious diseases, which can be prevented or mitigated by studying host-parasite interactions, among other measures. Bats and their ectoparasitic flies of the families Streblidae and Nycteribiidae are an excellent study model, but so far, our knowledge is restricted to fragmented records at a local scale. To help boost research, we have assembled a data set of bat-fly interactions from 174 studies published between 1904 and 2022, plus three original data sets. Altogether, these studies were carried out at 650 sites in the Neotropics, mainly distributed in Mexico, Brazil, Argentina, southern USA and Colombia, among other countries. In total, our data set contains 3,984 interaction records between 237 bat species and 255 fly species. The bat species with the largest number of recorded interactions were *Carollia perspicillata* (357), *Artibeus jamaicensis* (263), and *Artibeus lituratus* (228). The fly species with the largest number of recorded interactions were *Trichobius joblingi* (256), *Megistopoda aranea* (235), and *Megistopoda proxima* (215). The interaction data were extracted, filtered, taxonomically harmonized, and made available in a tidy format together with linked data on bat population, fly population, study reference, sampling methods and geographic information from the study sites. This interconnected structure enables the expansion of information for each interaction record, encompassing where and how each interaction occurred, as well as the number of bats and flies involved. We expect BatFly to open new avenues for research focused on different levels of ecological organization and spatial scales. It will help consolidate knowledge about ecological specialization, resource distribution, pathogen transmission, and the drivers of parasite

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Sources of funding: NZM, SMB, and JH were funded by Ministerio de Ciencia, Tecnología e Innovación de Colombia (MinCiencias, Convocatoria Doctorados en el Exterior 860 and 906). NZM and SMB were funded by the Brazilian Coordination for the Improvement of Higher Education Personnel (CAPES, 88887.467879/2019-00 and 88887.388097/2019-00). GG was funded by National Council for Scientific and Technological Development (CNPq# 308119/2022-3). MARM was funded by the Alexander von Humboldt Foundation (AvH, 1134644), National Council for Scientific and Technological Development (CNPq, 304498/2019-0), São Paulo Research Foundation (FAPESP, 2018/20695-7 and 2023/02881-6), and Dean of Research of the University of São Paulo (PRP-USP, 18.1.660.41.7).

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B. Specific subproject descriptions

Data compilation: We performed a comprehensive systematic review of the literature, following the Preferred Reporting Items for Systematic review and Meta-Analyses (PRISMA) protocol designed as a guide to improve clarity and transparency in the reporting of systematic reviews (Page et al. 2021). We also added information from papers that did not appear in our systematic search, but which we were aware of, and invited authorities to contribute with their unpublished data (Fig. 5).

The systematic search was conducted utilizing the Web of Knowledge and Scopus databases. There were no date restrictions, and the search was performed in 2021. The search utilized keywords in three languages: English, Portuguese, and Spanish. The following keywords were employed: “bat*” OR “murciélago*” OR “morcego*” OR “chiroptera” OR “chiroptero” OR “quiroptera” OR “quiroptero” AND “bat fly” OR “bat flies” OR “streblid*” OR “streblidae” OR “nycteribiid*” OR “nycteribiidae” OR “parasite*” OR “parásito*” OR “ectoparasite*” OR “ectoparásito*” OR “ectoparasita*” OR “diptera*” OR “díptero” OR “mosca”. With the results from this naive-term search we extracted potential keywords using the Rapid Automatic Keyword Extraction (RAKE) algorithm (Grames et al. 2019). Those automatic extracted keywords underwent manual verification, filtering, and sorting. Subsequently, a search was performed using the following refined keywords: "tropical bat" OR "tropical bats" OR "bat" OR "bats" OR "neotropical bats" OR "neotropical bat" OR "chiroptera" OR "chiropteran hosts" OR "chiropteran species" AND "blood-sucking flies" OR "blood-sucking fly" OR "diptera" OR "dipterans" OR "nycteribiidae" OR "streblidae" OR "streblid*" OR "bat flies" OR "bat fly" OR "ectoparasite*" OR "nycteribiid*" OR "bat parasite*" OR "bloodsucking diptera" OR "bloodsucking dipterans" OR "batfly" OR "batflies" AND "parasitizing" OR "interaction*" OR "interacted" OR "interact" OR "parasitological" OR "association*" OR "host-parasite" OR "system*" OR "vertebrate-parasite" OR "network*" "parasite assemblage*" OR "intensity" OR "infection" OR "infestation" OR "load*" "host potential" OR "parasitism" OR "prevalence" OR "parasited" OR "hematophagous" OR

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"relationship*" OR "specificity" OR "specialization" OR "specialisation" OR "inhabiting" OR "fly-host" OR "host-specific" OR "parasitology" OR "bat-parasite" OR "specialized" OR "specialised" OR "specialize" OR "specialise" OR "host" OR "hosted" OR "hosting" OR "hosts". We compiled information on bat fly interactions from a total of 102 references, 99 studies found in this systematic search and 3 unpublished data sets collected by the authors. As we did our first systematic search in 2021, we did an update with additional search restricted to studies published in 2022, with keywords: "streblid*" OR "streblidae" OR "nycteribiid*" OR "nycteribiidae", adding ten references for 2022 year. Finally, we included 65 references provided by one of the authors, Gustavo Graciolli (Fig. 5). These 65 references did not come up in the search due to most of them are not indexed in the databases used.

For a study to be included in our database, it had to meet the following inclusion criteria: (1) be a primary study, so we discarded literature reviews or compilations of interactions from other studies; (2) contain naturally occurring interactions, so we ignored host preference studies carried out under controlled conditions; and (3) contain spatial information of where the interactions were recorded, as coordinates, country and locality. Finally, with the studies found in the first systematic search done in 2021 (99), the studies found in the second systematic search (update, 10) and 65 studies provided by one of the authors, BatFly contains 174 published studies and 3 original datasets (177 references in total; Fig. 5).

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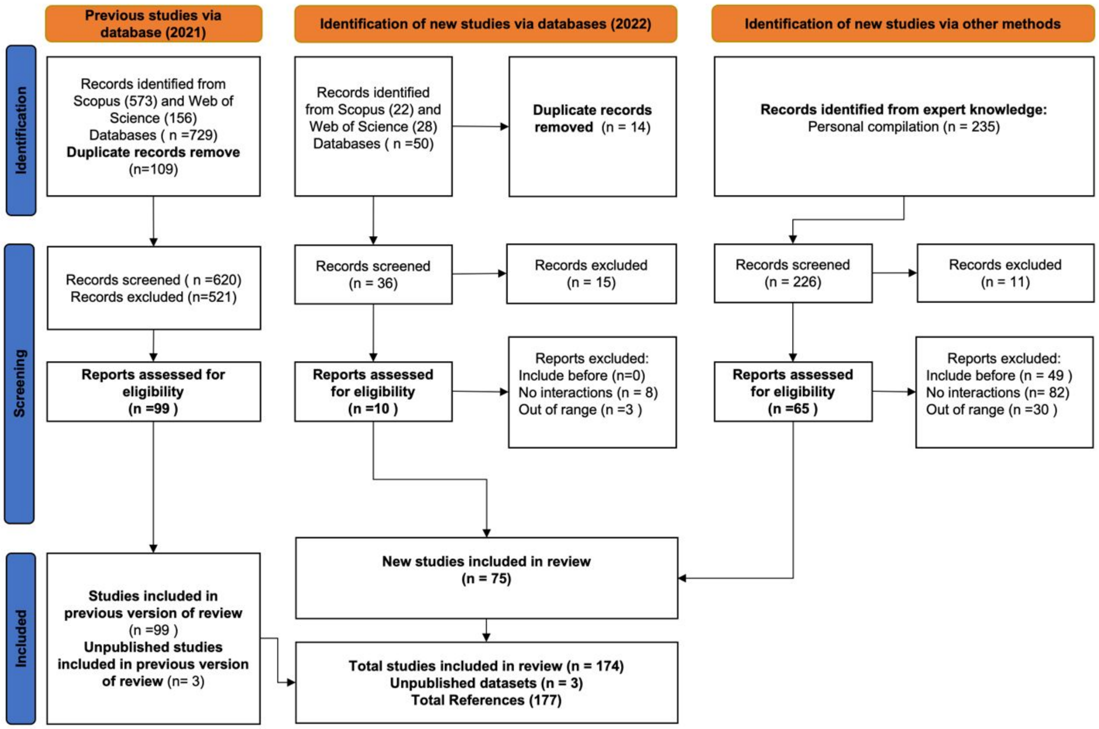

Figure 5. Workflow of the updated systematic review carried out to acquire data, which included database searches, additional records, and other sources, following PRISMA 2020 (Page et al. 2021).

Research methods: We included only studies that reported bat-fly interactions recorded from wild assemblages. Their scopes range from new fly records and community ecology and endosymbiont diversity in bat flies (bacteria and fungi), along with information on bat hosts. Information on sampling methods and host population was also extracted. We also included geographical information from study sites (latitude, longitude, locality, municipality, state, and country), and site characteristics (ecoregion, type of vegetation, height, average annual temperature). Missing information was coded as “NA”.

We compiled information on bat-fly interactions published between 1904 and 2022 from 174 references: Brues 1904; Curran 1935; Guimarães 1937; 1966; 1972;

1977; E. Dias et al. 1942; Augustson 1943; Fox and Stabler 1953; Hoffmann 1953; Parmalee 1955; Zeve 1958; Peterson 1960; 1963; Bradshaw and Ross 1961; Tonn and Arnold 1963; Uberlaker 1966; Maa 1968; Peterson and Maa 1970; Peterson and Hůrka 1974; Whitaker and Easterla 1975; Reisen, Kennedy, and Reisen 1976; Hoffmann, Palacios-Vargas, and Morales-Malacara 1980; Overal 1980; Fritz 1983; Coimbra jr, Guimarães, and Mello 1984; Peterson and Lacey 1985; Capllonch et al. 1997; Komeno and Linhares 1999; Claps, Autino, and Barquez 2000; 2005; Chavez 2001; Ritzi et al. 2001; Azevedo and Linardi 2002; Guzmán-Cornejo et al. 2003; Moura, Bordignon, and Graciolli 2003; Autino and Claps 2004; González D., Santos M, and Miranda 2004; ter Hofstede, Fenton, and Whitaker, Jr. 2004; Bertola et al. 2005; Villegas-Guzman, López-González, and Vargas 2005; Dick and Gettinger 2005; Anderson and Ortencio Filho 2006; Dick and Wenzel 2006; Oscherov, Chatellenaz, and Milano 2006; Oscherov, Idoeta, and Milano 2012; Graciolli et al. 2006; Graciolli, Zortéa, and Carvalho 2010; Graciolli, Guerrero, and Catzeflis 2019; Voigt and Kelm 2006; Shockley and Murray 2006; Graciolli and Bianconi 2007; Dick, Gettinger, and Gardner 2007; Kurta et al. 2007; Rojas et al. 2008; Sebastián Tello, Stevens, and Dick 2008; P. A. Dias et al. 2009; Autino et al. 2009; 2011; Autino, Claps, and Barquez 2014; Autino et al. 2016; 2018; 2020; Dittmar et al. 2009; 2011; Valdez, Ritzi, and Whitaker 2009; Santos et al. 2009; 2013; Graciolli and Dick 2009; 2012; Almeida et al. 2011; Camilotti et al. 2010; Aguiar and Antonini 2011; Eriksson, Graciolli, and Fischer 2011; Muñoz-Romo, Burgos, and Kunz 2011; J. R. R. da Silva and Ortêncio Filho 2011; Lourenço and Esbérard 2011; Esbérard et al. 2012; 2014; Morse et al. 2012; Dick 2013; Moras et al. 2013; Saldaña-Vázquez et al. 2013; Soares et al. 2013; 2016; 2017; França et al. 2013; Urbieta and Torres 2014; Moreno Valdéz 1998; Camacho et al. 2014; Lourenço

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et al. 2014; 2020; Velazco, Autino, and Claps 2014; Tarquino-Carbonell et al. 2015; Tlapaya-Romero et al. 2015; Tlapaya-Romero, Ibáñez-Bernal, and Santos-Moreno 2019; Tlapaya-Romero, García-Méndez, and Ramírez-Martínez 2022; Cuxim-Koyoc et al. 2015; 2016; 2018; Judson, Frank, and Hadly 2015; Patricio and Lourenço 2016; de Vasconcelos et al. 2016; Hernández-Arciga, Herrera M., and Morales-Malacara 2016; Frank et al. 2016; Reeves et al. 2016; Barbier and Graciolli 2016; Bezerra, de Vasconcelos, and Bocchiglieri 2016; Zarazúa-Carbajal et al. 2016; Barbier, Prado-Neto, and Bernard 2016; Barbier et al. 2017; 2018; 2019; Barbier, Graciolli, and Bernard 2019; Barbier et al. 2020; Barbier, Falcão, and Bernard 2021; Fagundes, Antonini, and Aguiar 2017; Dornelles and Graciolli 2017; Rivera-García et al. 2017; Cordero-Schmidt et al. 2017; Walker et al. 2018; Abundes-Gallegos et al. 2018; Bolívar-Cimé et al. 2018; Colín-Martínez, Morales-Malacara, and García-Estrada 2018; Salinas-Ramos et al. 2018; Calonge-Camargo and Pérez-Torres 2018; Estrada-Villegas et al. 2018; do Amaral et al. 2018; Bezerra and Bocchiglieri 2018; 2022; Hrycyna, Martins, and Graciolli 2019; S. S. P. da Silva, Guedes, et al. 2019; S. S. P. da Silva et al. 2021; Torres et al. 2019; Hernández-Martínez et al. 2019; Trujillo-Pahua and Ibáñez-Bernal 2019; 2020; Smit and Miller 2019; Durán et al. 2019; S. S. P. da Silva, Neves, et al. 2019; Vieira et al. 2019; Liévano-Romero, Rodríguez-Posada, and Cortés-Vecino 2019; Orta-Pineda et al. 2019; Ribas, Batista, and Aranha 2020; Ascuntar-Osnas, Montoya-Bustamante, and González-Chávez 2020; Bonifaz, Mena, and Oporto 2020; Raigosa Álvarez et al. 2020; Zamora-Mejías et al. 2020; Ikeda et al. 2020; Palheta et al. 2020; de Groot et al. 2020; Oliveira et al. 2020; Menezes Júnior et al. 2021; Minaya, Mendoza, and Iannacone 2021; Vidal, Bernardi, and Talamoni 2021; Urbieta, Graciolli, and Vizentin-Bugoni 2021; Hiller et al. 2021; Lira-Olguin, Guzmán-

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Cornejo, and León-Paniagua 2021; Mello et al. 2021; Ramalho, Diniz, and Aguiar 2021; Gómez-Corea et al. 2022; Alcantara et al. 2022; Speer et al. 2022; da Silva Biz et al. 2021; Castillo-Urbina et al. 2022; Carvalho et al. 2022; Herrera and Jara 2008; González-Ávalos et al. 2014; Bellizzi et al. 2022; Almeida et al. 2010; Dornelles et al. 2017; Ramírez-Martínez et al. 2016; Mello et al. 2022; da Silva Reis et al. 2022.

For already included references, if applicable, we accommodated studies that partially or totally used the same data sets as "Associated References", assuring not to duplicate interaction records (see Table 1).

Taxonomic information: All records were taxonomically harmonized. Scientific names were checked and updated. For bats, taxonomic harmonization was performed by Marcelo Nogueira. The main reference for bat taxonomic arrangement and nomenclature adopted here was Simmons and Cirranello (2023). However, when considering the taxonomy of *Glossophaga* we followed Diaz et al. (2021). Also, in the case of *Dermanura*, we followed Cirranello et al. (2016) in treating this taxon as a subgenus of *Artibeus*. Diaz et al. (2021) and Gardner (2008) were the general references for the geographic distribution of each species, but we also consulted country-wide compilations (e.g., York et al. 2019; Martínez-Fonseca et al. 2020; Turcios-Casco et al. 2020; Mora, López, and Espinal 2021; Velazco et al. 2021; Garbino et al. 2022) and primary references (e.g., species descriptions and systematic revisionary works), and species accounts, including Solari and Baker (2006); Genoways and Baker (1996); McDonough et al. (2008); Velazco, Gardner, and Patterson (2010); Velazco and Simmons (2011); Moratelli et al. (2011); Mantilla-Meluk (2014); Mantilla-Meluk and Muñoz-Garay (2014); Pavan and Marroig (2016); Pavan, Bobrowiec, and Percequillo (2018); Velazco and Patterson (2019); Basantes et

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al. (2020); Loureiro, Engstrom, and Lim (2020); Rodríguez-Posada et al. (2021); Velazco et al. (2021); Calahorra-Oliart, Lira-Noriega, and León-Paniagua (2022); Calderón-Acevedo, Bagley, and Muchhala (2022); Esquivel et al. (2022). When there was a situation in which more than one species could be associated to a previous species record within the same bat assembly, as *Platyrrhinus helleri* and *Pteronotus parnellii*—please refer to Velazco, Gardner, and Patterson (2010) and Pavan, Bobrowiec, and Percequillo (2018) for newly described taxa related to these species—the updated identification was retained at genus level.

For flies, taxonomic harmonization was performed by Gustavo Graciolli. Taxonomic changes in the current name of species were made following Alcantara, Graciolli, and Nihei (2019); Hrycyna et al. (2022); Tlapaya-Romero, García-Méndez, and Ramírez-Martínez (2023); Graciolli and Dick (2012); Graciolli, Santos, and Rebêlo (2022). In the records that were not identified to the species level, whenever possible, the taxonomic complex or group to which they belong was reported.

Bat roost information: We report the roost type used by each bat species included in the database. Bat roost play an important role in fly species lifecycle due to fly species pupal development is carried out in these places (Dittmar et al. 2009). All possible roost types were classified into eight categories: cave (hot caves, caverns, and crevices), tree cavity (hollow trees, fallen trees, and loose bark), human-made structure (buildings, bridges, tunnels, and culverts), foliage (branches and leaves), tent, termite nest, rocky cliff, and river cliff. We compiled this information from the literature (Kunz and Lumsden 2003; Rodríguez-Durán 2020).

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C. Data limitations and potential enhancements

BatFly has limitations related to the scope of the studies used as data sources and how information was reported in them. There are many gaps in information in the references used, as unfortunately commonly observed in studies on species interactions (see another paper with recommendations to solve this problem: Kita et al. 2022)

First, there are sampling information limitations. As several references are checklists of fly species also reporting their hosts, most studies do not provide information about the methods used for capturing bats, e.g., the number of sampling hours or the number of mist nets used, hindering the estimation of sampling effort. Only 117 study sites (18%) informed their sampling effort following the widely used method of Straube and Bianconi (2002).

Second, there are geographical information limitations. Sixteen site studies (2.5%) report interactions accumulated from several locations, hindering the use of their data at smaller spatial scales. In those cases, we recorded all data available from the locations of the study in the observation column (see Table 2). A single SiteCode was assigned with the coordinates of the centroid of the polygon formed by the coordinates reported in the study (see Table 2).

Third, there are interaction information limitations. Not all studies have information that allows quantifying the interaction, 490 (12%) interactions were recorded only as occurrence (binary information), hindering the use of their data in studies that aim to analyze the interaction by incidence of fly species on bat species. Furthermore, information provided by most studies is limited to the number of individuals of a given fly species found on a given bat species, excluding other key information useful to quantify the interaction such as prevalence, mean intensity, and

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mean abundance. Only 978 (25%) of the interaction records provide us with information on prevalence.

Four, there are representativeness limitations. Our database is biased by the method through which bats are sampled, since most studies were based on mist-netting, and different bat species have different capturability (Francis 1989). Mist nets are much more efficient for capturing phyllostomids than bats from other families (Tschapka 1998). So, potential users of BatFly should have this in mind, for example when carrying out studies aimed at analyzing fly incidence in different bat families or species from different bat families.

CLASS III. DATA SET STATUS AND ACCESSIBILITY

A. Status

Latest update: October 2023.

Latest archive date: October 2023.

Metadata status: Last updated in October 2023, version submitted.

Data verification: Data were compiled as presented in the sources. We corrected transcription errors, checked the geographic coordinates of the study sites, and made taxonomic harmonization of species names.

B. Accessibility

Storage location and medium: The complete data set (in .CSV format) and scripts to replicate the figures of this metadata are available on https://doi.org/10.5281/zenodo.10019756

Contact persons: Natalya Zapata-Mesa (zapatamesan@gmail.com) & Marco A. R. Mello (marmello@usp.br).

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Copyright restrictions: Creative Commons Attribution 4.0 International License.

Proprietary restrictions: Please cite this data paper, if the data are used in any kind of publication related to research, outreach, and teaching activities, such as papers, books, book chapters, monographs, bibliographies, reports, patents, posters, talks, keynotes, and lectures.

Costs: None.

CLASS IV. DATA STRUCTURAL DESCRIPTORS

A. Data set file

Identity and size:

BatFly_References.csv 66KB

BatFly_Sites.csv 142KB

BatFly_Sampling.csv 46KB

BatFly_Bat_Pop.csv 334KB

BatFly_Fly_Pop.csv 303KB

Batfly_Species_Interactions.csv 585KB

Format and storage mode: Data frames with comma-separated values (.csv).

Header information: See variable description in Variable information section.

Alphanumeric attributes: Mixed.

Special characters/fields: Each table contains a column named “Observations”. This column may have additional information or comments. For example, in Table 2, Observations column may have additional information about the study site reported by the reference, as a pool of coordinates from a study site. “NA” indicates no information available for a given cell.

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477 **B. Variable information**

478 **Table 1.** BatFly_References: Information of the references used as data sources in our
479 database.

Variable	Description	Levels	Example
RefCode	Identification code of each reference	BFR001 – BFR179	BFR002
Author	Short name of the author(s); if there are three or more authors, we use *et al.*		Graciolli *et al.*
Year	Year of publication of each reference		2010
Type	Type of reference	Article, Book, Unpublished data	Article
Reference	Full bibliographic reference		Graciolli G., Zortéa M., Carvalho L. F. A. C. (2010) Bat flies (Diptera, Streblidae and Nycteribiidae) in a Cerrado area of Goiás state, Brazil. Revista Brasileira de Entomologia 54: 511-514. https://doi.org/10.1590/S0085-56262010000300025
BatVouchers	Name of the biological collection where voucher bat specimens were deposited		Chiroptera Collection of “Universidade Federal de Goiás, Campus Jataí” (CCUFG)

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FlyVouchers	Name of the biological collection where voucher fly specimens were deposited		Zoological Collection of "Universidade Federal do Mato Grosso do Sul"
Associated References	Full bibliographic reference of studies that fully or partially uses the same data of the Reference		Pedro, W.A., Passos F.C. & B.K Lim. 2001. Morcegos (Chiroptera; Mammalia) da Estação Ecológica dos Caetetus, Estado de São Paulo. Chiroptera Neotropical, Brasília, 7: 136-140

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Table 2. BatFly_Sites: Information of the study sites from the references included in our database.

Variable	Description	Levels	Example
SiteCode	Identification code of each study site. A single publication may contain multiple study sites. Different studies could share the same study site and consequently the same SiteCode	BFA001 – BFA653	BFA002
RefCode	Identification code of each reference	BFR001 – BFR179	BFR002
Country	English name of the country where the study was carried out		Brazil
State	State, Province or Department of the study site as described in the source or identified from its geographic coordinates		Goiás
Municipality	Municipality of the study site as described in the reference or identified from its geographic coordinates		Serranópolis
Locality	Local name of the study site as described in the reference or identified from its geographic coordinates		Reserva Particular do Patrimônio Natural Pousada das Araras
Latitude	Corrected and transformed coordinates of the latitude in decimal degrees (Datum WGS84)		-20.772227
Longitude	Corrected and transformed coordinates of the longitude in decimal degrees (Datum WGS84)		-54.785154
PrecisionClass	Coordinate precision classes of the study site. Precise: coordinates of the grid, transect or vegetation patch are reported in the reference. Not precise: coordinates of	precise, not precise	precise

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	the municipality are reported, or the coordinates do not match the information provided in the reference		
Vegetation	Vegetation type as described in the reference		Tropical rainforest
VegType	Vegetation type according to Oliveira-Filho (2017)		Rainforest
Ecoregion	Ecological region according to Oliveira-Filho (2017)		Cauca Valley montane forests
Domain	Tectonic domain according to Oliveira-Filho (2017)		Northern Andean
Elevation	Elevation above sea level in meters (m) reported in the reference		700
DatasetElevation	Elevation above sea level in meters (m), extracted from the GTOPO30 dataset (United States Geological Survey – USGS, 2001. Global 30 arc-seconds Elevation)		700
MeanAnnTemp	Mean annual temperature in Celsius degrees (ºC) from WorldClim 2.1 with 30 arc seconds resolution.		23.3
MeanAnnRain	Mean annual rainfall in millimeters (mm) from WorldClim 2.1 with 30 arc seconds resolution.		1429
Observations	Additional information or comments		

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485 **Table 3.** BatFly_Sampling: Information on the sampling methods used to record interactions
486 included in our database.

Variable	Description	Levels	Example
SiteCode	Identification code of each study site from each reference. A single publication may contain multiple study sites.	BFA001 – BFA653	BFA002
RefCode	Identification code of each reference	BFR001 – BFR179	BFR002
YearStart	Year of the beginning of sampling		2000
YearFinish	Year of the end of sampling		2001
Duration	Unstandardized duration of sampling (in months)		11
SamplingEffort	Sampling effort, accounting for the area of the mist nets used and the duration of the survey, in hours*square meters (following Straube and Bianconi 2002). Since many studies do not report mist net size or model, this standardized measure is common for comparing bat inventories		13608
BatEcologicalScale	Reported bat assemblage. all: the whole bat species captured was reported. leafnosed: only leaf-nosed bats (Phyllostomidae) were reported. mormoopid: only mormoopid bats (Mormoopidae) were reported. single: a single bat species was reported	all, leafnosed, mormoopid, single	all
FlyEcologicalScale	Reported fly assemblage. all: the whole fly species capture was reported. Single: a single fly species was reported.	all, single	all
BatSamplingMethod	Method used to capture bats. Direct refers to collection by hand or devices such as hand nets or harp traps.	direct, harp traps, mist nets, hand net	mist nets

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SamplingNights	Total number of capture nights	0 to 36	10
SamplingHours	Duration of capture per night, i.e., the number of hours the mist nets were kept open each night	1 to 12	1
SamplingMistnets	Number of mist nets used, regardless of manufacturer, type, size, mesh, or material	1 to 14	1
SamplingStrata	Vertical strata of the habitat where bats were captured: understory, from canopy to understory, below canopy, canopy	U, UC, BC, C	U
SamplingSeason	Sampling season reported in the reference	dry, wet, both	wet
Observations	Additional information or comments		

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Table 4. BatFly_Bat_Pop: Information on the bat populations sampled, which were involved in the recorded interactions included in our database.

Variable	**Description**	**Levels**	**Example**
BatPopulationCode	Identification code of each bat population	BFBPOP001 – BFBPOP2187	BFBPOP001
RefCode	Identification code of each reference	BFR001 – BFR179	BFR001
SiteCode	Identification code of each study site in each reference	BFA001 – BFA653	BFA001
BatFamily	Current scientific name of the bat family		Noctilionidae
BatGenus	Current scientific name of the bat genus		*Noctilio*
BatSpecies	Scientific name of the bat species as reported in the reference		*Noctilio leporinus*
CurrentBatSpecies	Current scientific name of the bat species according to Simmons and Cirranello (2023)		*Noctilio leporinus*
BatSubspecies	Scientific subspecies name of the Bat as reported in the reference (checked and updated)		
BatRoost	Roosting site of the bat species reported in Kunz and Lumsden (2003) and Rodríguez-Durán (2020)	cave, tree cavity, foliage, tent, termite nest, human-made structure	caves
BatCaptureNumber	Total number of captured bats of the population	1 to 3173	25
BatMarks	Whether or not captured bats were marked. For studies where no marks were used, BatCaptureNumber might include recaptured	yes, no	no

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	individuals		
BatFemales	Number of captured bats that are females of the population	0 to 235	11
BatMales	Number of captured bats that are males of the population	0 to 182	21
BatJuvenile	Number of captured bats that are juveniles of the population	0 to 290	41
BatAdult	Number of captured bats that are adults of the population	0 to 127	5
BatLactatingFemales	Number of captured bats that are lactating females of the population. Bats can be lactating and pregnant at the same time	0 to 21	20
BatNonreproductiveFemales	Number of captured bats that are nonreproductive females of the population	0 to 34	3
BatPregnantFemales	Number of captured bats that are pregnant females of the population	0 to 18	4
BatNonreproductiveMales	Number of captured bats that are nonreproductive males of the population	0 to 37	6
BatScrotalTestesMales	Number of captured bats that are males with scrotal testes of the population	0 to 32	30
Observations	Additional information or comments		

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491 **Table 5.** BatFly_Fly_Pop: Information on the fly populations sampled, which were involved
492 in the recorded interactions included in our database.

Variable	**Description**	**Levels**	**Example**
FlyPopulationCode	Identification code of each bat fly population	BFFPOP001 – BFFPOP2969	BFFPOP001
RefCode	Identification code of each reference	BFR001 – BFR179	BFR001
SiteCode	Identification code of each study site in each reference	BFA001 – BFA653	BFS001
FlyFamily	Current scientific name of the fly family	Streblidae, Nycteribiidae	Streblidae
FlyGenus	Current scientific name of the fly genus		*Megistopoda*
FlySpecies	Scientific name of the fly as reported in the reference		*Megistopoda aranea*
CurrentFlySpecies	Current scientific name of the fly		*Megistopoda aranea*
Flysubspecies	Scientific subspecies name of the fly as reported in the reference (checked and updated)		
FlyCaptureNumber	Total number of captured flies of the population	1 to 2197	2
FlyFemales	Total number of flies that are females of the population	0 to 1105	20
FlyMales	Total number of flies that are males of the population	0 to 2042	4
FlyUndetermined	Total number of flies that were not sex identified		

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494 **Table 6.** Batfly_Species_Interactions: Information on the bat-fly species-species interactions
495 recorded in our database.

Variable	Description	Levels	Example
InteractionSpeciesCode	Identification code of each species-species interaction record	BFSSI0001 – BFSSI4014	BFSSI0001
BatPopulationCode	Identification code of each bat population	BFBPOP001 – BFBPOP2187	BFBPOP0010
FlyPopulationCode	Identification code of each fly population	BFFPOP001 – BFFPOP2969	BFFPOP0015
RefCode	Identification code of each reference	BFR001 – BFR179	BFR004
SiteCode	Identification code of each study site in each reference	BFA001 – BFA653	BFA051
CurrentBatSpecies	Current scientific name of the bat species according to Simmons and Cirranello (2023)		*Noctilio leporinus*
BatSubspecies	Scientific subspecies name of the bat as reported in the reference (checked and updated)		
CurrentFlySpecies	Current scientific name of the fly		*Megistopoda aranea*
Flysubspecies	Scientific subspecies name of the fly as reported in the reference (checked and updated)		
TransientInteractionorError	Uncommon association. It may be an association that will not last over time (transient) or the researcher's error in the collection or identification	yes, no	no
NumberInteractions	Number of flies captured on	0 to 2197	2197

	the bat species		
NumberInteractionsByFlyFemales	Number of female flies captured on the bat species	0 to 1105	291
NumberInteractionsByFlyMales	Number of male flies captured on the bat species	0 to 1091	351
NumberInteractionsByFlyUndetermined	Number of undetermined flies captured on the bat species	0 to 2042	781
BatInfested	Number of bats infested with one or more individuals of the fly species	0 to 278	201
BatInfestedFemales	Number of female bats infested with one or more individuals of the fly species	0 to 40	21
BatInfestedMales	Number of male bats infested with one or more individuals of the fly species	0 to 33	33
Prevalence	Prevalence (Number of bats infested divided by the total number of bat captures) as reported in the reference	0 to 100	80
PrevalenceOnBatFemales	Prevalence (Number of female bats infested divided by the total number of bat captures) as reported in the reference	0 to 100	50
PrevalenceOnBatMales	Prevalence (Number of male bats infested divided by the total number of bat captures) as reported in the reference	0 to 100	20
MeanFlyIntensity	The total number of flies of the species parasitizing the bat species divided by the number of individual bats infested with the fly	1 to 4.66	1
MeanFlyIntensityOnBatFemales	The total number of flies of the species parasitizing females of the bat species divided by the number of individual female bats infested with the fly	1 to 8	4
MeanFlyIntensityOnBatMales	The total number of flies of the species parasitizing males of the bat species divided by the number of individual male bats infested	1 to 2.53	2.1

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	with the fly		
MeanFlyAbundance	The total number of flies of the species parasitizing the bat species divided by the number of individual bats (including non-infested individuals)	0 to 24.1	24.1
MeanFlyAbundanceOnBatFemales	The total number of flies of the species parasitizing females of the bat species divided by the number of individual female bats (including non-infested individuals)	0 to 2.6	1.5
MeanFlyAbundanceOnBatMales	The total number of flies of the species parasitizing males of the bat species divided by the number of individual male bats (including non-infested individuals)	0 to 1.6	1
Observations	Information about reference or comments		

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C. Data anomalies: If there is no information available for a specific cell in a given datasheet, it is indicated as “NA”.

CLASS V. SUPPLEMENTAL DESCRIPTORS

A. Data acquisition

Data entry/verification procedures: Screening and data extraction were always performed by the same person. The information included in BatFly’s sheets, such as codes and scientific names, was validated with logical and set tests implemented in R to reduce typing errors.

B. Publications and results

Partial data of unpublished reference BFR102 (see Table 1) was used in Pastrana-Montiel, M. R., Ballesteros-Correa, J., & Chacón-Pacheco, J. (2019). First record of the parasite bat fly *Basilia mimoni* Theodor & Peterson, 1964 (Diptera: Nycteribiidae) in Colombia. Oecologia Australis, 23(3).): 685-689. https://doi.org/10.4257/oeco.2019.2303.27

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BatFly: A database of Neotropical bat-fly interactions

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Abstract: Global changes have increased the risk of emerging infectious diseases, which can be prevented or mitigated by studying host-parasite interactions, among other measures.

Bats and their ectoparasitic flies of the families Streblidae and Nycteribiidae are an excellent study model, but so far, our knowledge is restricted to fragmented records at a local scale. To help boost research, we have assembled a data set of bat-fly interactions from 174 studies published between 1904 and 2022, plus three original data sets. Altogether, these~~Those~~ studies were carried out at 650 sites in the Neotropic~~al regions~~s, mainly distributed in Mexico ~~(146)~~, Brazil ~~(89)~~, Argentina ~~(62)~~, southern USA ~~(62)~~, and Colombia~~Peru (55)~~, among other countries. In total, our data set contains 3,984 interaction records between 237 bat species and 255 fly species. The bat species with the largest number of recorded interactions were *Carollia perspicillata* (357), *Artibeus jamaicensis* (263), and *Artibeus lituratus* (228). The fly species with the largest number of recorded interactions were *Trichobius joblingi* (256), *Megistopoda aranea* (235), and *Megistopoda proxima* (215). The interaction data were extracted, filtered, taxonomically harmonized, and made available in a tidy format together with linked data on bat population, fly population, study reference, sampling methods and geographic information from the study sites. This interconnected structure enables the expansion of information for each interaction record, encompassing where and how each interaction occurred, as well as the number of bats and flies involved. We expect BatFly to open new avenues for research focused on different levels of ecological organization and spatial scales. It will help consolidate knowledge about ecological specialization, resource distribution, pathogen transmission, and the drivers of parasite prevalence over a broad spatial range. It may also help answer key questions, such as: are there differences in fly prevalence or mean infestation across Neotropical ecoregions? What ecological drivers explain those differences? Or how do specialization patterns vary among fly species in the Neotropics? Furthermore, we expect BatFly to inspire research aimed at understanding how climate and land-use changes may impact host-parasite interactions and disease outbreaks.

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This kind of research may help us reach Sustainable Development Goal 3, Good Health and Wellbeing, outlined by the United Nations.~~The data were organized, taxonomically harmonized, and made available in a tidy format together with rich metadata on bats, flies, and sites. We expect BatFly to open new avenues for research focused on different levels of ecological organization and spatial scales.~~

Key words/phrases: Antagonism, bats, bat flies, Chiroptera, diseases, ectoparasites, hematophagy, Nycteribiidae,~~ parasitism,~~ Streblidae, specialization, species interactions, zoonosis.

Open Research: The complete data set is available as Supporting Information at: [to be completed at proof stage]. Associated data is also available at: BatFly: A database of Neotropical bat-fly interactions https://doi.org/10.5281/zenodo.10019756

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~~INTRODUCTION~~

~~Our world faces urgent problems related to global changes caused by human activities, which we strive to solve by following the United Nation's 17 Sustainable Development Goals (UN 2015). The third goal, Good Health and Wellbeing, is the focus of research by scientists from many areas under a transdisciplinary approach known as One Health (OHITF 2008). Under this approach, it is of paramount importance to understand the interactions between hosts and their parasites to prevent emerging diseases (Giraudoux et al. 2022).~~

~~Bats play a crucial role in emerging diseases because of their huge ecological diversity (Wilson and Reeder 2005), which includes a myriad of interactions with endo and ectoparasites (Klimpel and Mehlhorn 2016) that carry pathogens associated with zoonoses (Szentiványi et al. 2018). The most important bat ectoparasites are dipterans of the families Streblidae and Nycteribiidae, also known as bat flies (Dick and Patterson 2006). Bat flies share a tight evolutionary history with bats, as they are found exclusively on them (Dick and Dittmar 2014). Consequently, both streblids and nycteribiids exhibit intricate morphological and ecological adaptations for living on bats (Dittmar et al. 2015). In addition, they are considered host-specific, with most fly species parasitizing from one to three bat species only (Pilosof et al. 2012).~~

~~Host specificity has received large attention in the ecological literature, being used as a model to study ecological specialization (Hiller et al. 2021), resource distribution (Hiller et al. 2018), pathogen transmission (Szentiványi et al. 2018), and the drivers of parasite prevalence (Frank et al. 2016). Despite this remarkable effort to study the ecology of bat flies (Patterson, Dick, and Dittmar 2007), so far knowledge is restricted to fragmented interaction records at a local scale. Therefore, we need syntheses aimed at compiling~~

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~~information and publishing it in data papers that filter, organize, and curate large data sets, opening avenues for addressing a broader range of questions.~~

~~In the present data paper, we compiled information on bat-fly interactions derived from 177 studies with multiple scopes, including taxonomic reviews, checklists, and assessments of species interactions. Altogether, our database comprises information recorded at 650 sites distributed from the northern frontier of the Neotropics (including Mexico, southern USA, and the Caribbean), until southern South America (Fig. 1). Summarizing a total of 3,984 interaction records between 237 bat species and 255 fly species, BatFly represents the largest dataset of antagonistic interactions made by bats in both geographical and taxonomic terms.~~

~~Most interaction records compiled in BatFly came from published data, and we have also included three original data sets. All records were taxonomically harmonized, i.e., bat and fly scientific names were checked and updated. In addition, our database includes additional information about study sites characteristics (e.g., mean annual temperature, annual rainfall, and vegetation type). Also, we included bat species traits, such as the roost types used, which is considered an important driver of parasite dynamics (Patterson, Dick, and Dittmar 2007). BatFly was designed to boost the use of bat-fly interactions as a model for addressing questions at different levels of ecological organization and spatial scales.~~

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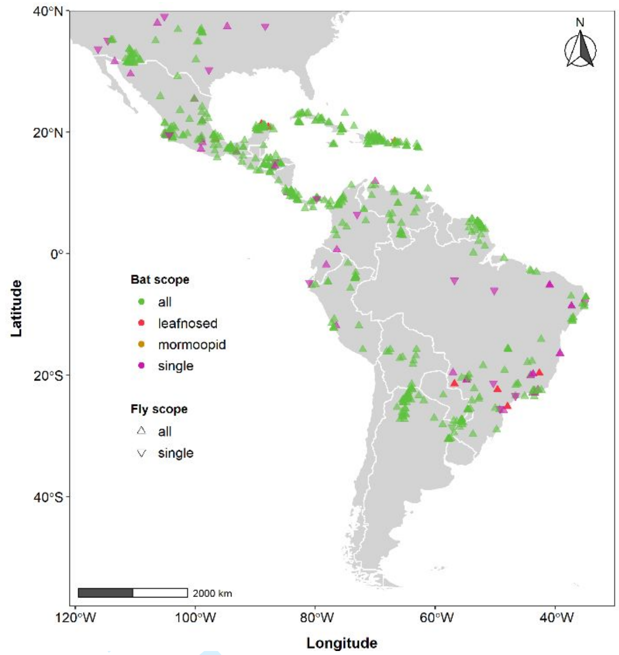

~~**Figure 1.** Distribution of the sampling sites included in BatFly. Triangles represent sampling sites. Colors represent the taxonomic scope of sampling for bats, and triangle orientation (up/down) represents the taxonomic scope of sampling for flies. "Single" represents studies focused on one bat species. "All" represents studies that assessed all bat species found at the sampling site.~~

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METADATA

CLASS I. DATA SET DESCRIPTOR

A. Data set identity

Title: BatFly: A database of Neotropical bat-fly interactions

B. Data set identification

Data set identity codes:

BatFly_References.csv

BatFly_Sites.csv

BatFly_Sampling.csv

BatFly_Bat_Pop.csv

BatFly_Fly_Pop.csv

Batfly_Species.csv

C. Data set description

Principal Investigator(s):

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2. Marco A. R. Mello. Departamento de Ecologia, Instituto de Biociências, Universidade de São Paulo, São Paulo, SP, Brazil.

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Abstract:

Global changes have increased the risk of emerging infectious diseases, which can be prevented or mitigated by studying host-parasite interactions, among other measures. Bats and their ectoparasitic flies of the families Streblidae and Nycteribiidae are an excellent study model, but so far, our knowledge is restricted to fragmented records at a local scale. To help boost research, we have assembled a data set of bat-fly interactions from 174 studies published between 1904 and 2022, plus three original data sets. Altogether, these studies were carried out at 650 sites in the Neotropics, mainly distributed in Mexico, Brazil, Argentina, southern USA and Colombia, among other countries. In total, our data set contains 3,984 interaction records between 237 bat species and 255 fly species. The bat species with the largest number of recorded interactions were *Carollia perspicillata* (357), *Artibeus jamaicensis* (263), and *Artibeus lituratus* (228). The fly species with the largest number of recorded interactions were *Trichobius joblingi* (256), *Megistopoda aranea* (235), and

Megistopoda proxima (215). The interaction data were extracted, filtered, taxonomically harmonized, and made available in a tidy format together with linked data on bat population, fly population, study reference, sampling methods and geographic information from the study sites. This interconnected structure enables the expansion of information for each interaction record, encompassing where and how each interaction occurred, as well as the number of bats and flies involved. We expect BatFly to open new avenues for research focused on different levels of ecological organization and spatial scales. It will help consolidate knowledge about ecological specialization, resource distribution, pathogen transmission, and the drivers of parasite prevalence over a broad spatial range. It may also help answer key questions, such as: are there differences in fly prevalence or mean infestation across Neotropical ecoregions? What ecological drivers explain those differences? Or how do specialization patterns vary among fly species in the Neotropics? Furthermore, we expect BatFly to inspire research aimed at understanding how climate and land-use changes may impact host-parasite interactions and disease outbreaks. This kind of research may help us reach Sustainable Development Goal 3, Good Health and Wellbeing, outlined by the United Nations.~~Global changes have increased the risk of emerging infectious diseases, which can be prevented or mitigated by studying host-parasite interactions, among other measures. Bats and their ectoparasitic flies of the families Streblidae and Nycteribiidae are an excellent study model, but so far, our knowledge is restricted to fragmented records at a local scale. To help boost research, we have assembled a data set of bat-fly interactions from 174 studies published between 1904 and 2022, plus three original data sets. Those studies were carried out at 650 sites in the Neotropical region, distributed in Mexico (146), Brazil (89), Argentina~~

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~~(62), southern USA (62), and Peru (55), among other countries. In total, our data set contains 3,984 interaction records between 237 bat species and 255 fly species. The bat species with the largest number of recorded interactions were *Carollia perspicillata* (357), *Artibeus jamaicensis* (263), and *Artibeus lituratus* (228). The fly species with the largest number of recorded interactions were *Trichobius joblingi* (256), *Megistopoda aranea* (235), and *Megistopoda proxima* (215). The data were organized, taxonomically harmonized, and made available in a tidy format together with rich metadata on bats, flies, and sites. We expect BatFly to open new avenues for research focused on different levels of ecological organization and spatial scales.~~

D. Keywords

Antagonism, bats, bat flies, Chiroptera, diseases, ectoparasites, hematophagy, ~~ectoparasites,~~ Nycteribiidae~~, parasitism~~, Streblidae, specialization, species interactions, zoonosis.

E. Description

Our world faces urgent problems related to global changes caused by human activities, which we strive to solve by following the United Nation’s 17 Sustainable Development Goals (UN 2015). Goal 3, “Good Health and Wellbeing”, is the focus of research by scientists from many areas under a transdisciplinary approach known as One Health (OHITF 2008). Under this approach, it is of paramount importance to understand the interactions between hosts and their parasites to prevent disease transmission and spillover (Giraudoux et al. 2022).

Bats play a crucial role in the dynamics of emerging infectious diseases because of their huge ecological diversity (Wilson and Reeder 2005)□□, which includes a myriad of interactions with endo and ectoparasites □□(Klimpel and Mehlhorn 2016) that carry

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pathogens associated with zoonosis (Szentiványi et al. 2018).□ The most important bat ectoparasites are dipterans of the families Streblidae and Nycteribiidae, also known as bat flies (Dick and Patterson 2006). Bat flies (hereafter just flies) share a tight evolutionary history with bats, as they are found exclusively on them □(Dick and Dittmar 2014). Consequently, both fly families exhibit intricate morphological and ecological adaptations for living on bats (Dittmar et al. 2015). In addition, they are considered host-specific, with most fly species parasitizing from one to three bat species□ only (Pilosof et al. 2012).

Host specificity has received large attention in the ecological literature, being used as a model to study ecological specialization □□(Hiller et al. 2021), resource distribution (Hiller et al. 2018)□, pathogen transmission (Szentiványi et al. 2018), and the drivers of parasite prevalence (Frank et al. 2016). Despite this remarkable effort to study the ecology of flies (Patterson, Dick, and Dittmar 2007), so far knowledge is restricted to fragmented interaction records at a local scale. Therefore, we need synthesis aimed at compiling information and publishing it in data papers that filter, organize, and curate large data sets, opening avenues for addressing a broader range of questions.

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In the present data paper, we compiled information on bat-fly interactions derived from 174 studies with multiple scopes, including taxonomic reviews, checklists, and assessments of species interactions, and we have also included three original data sets. ~~The database includes references published between 1904 and 2022 (Fig. 2).~~These reference studies were published between 1904 and 2022, with most being published after the year 2000 (Fig. 1A). Overall, our database contains information recorded at 650 sites spanning from the northern limit of the Neotropics to southern South America (Fig. 1B). Those sites are primarily located in Mexico (143 sites from published studies and 3 sites from original datasets), Brazil (89), Argentina (62), southern USA (62), Peru (55), Cuba (32), the Dominican Republic (32), Honduras (26), and Colombia (19 sites from published studies and 15 sites from original datasets), among other countries (Fig. 1B). For 95% of the ~~study~~ sites, ~~we have~~there is information on entire ~~communities~~ assemblages of bats and flies. The remaining 5% report parasites collected from a single bat species (Fig. 1B). ~~Information gathered here came from 650 study sites, located mainly in Mexico (146), Brazil (89), Argentina (62), southern USA (62), Peru (55), Cuba (32), Dominican Republic (32), and Honduras (26) (Fig. 1). On average, each reference contributed to the database with information from one study site. However, there are 19 references that contain information from over 10 study sites, which represent studies focused on recording all fly species and their hosts from a country or state (e.g., bat flies of Paraguay).~~

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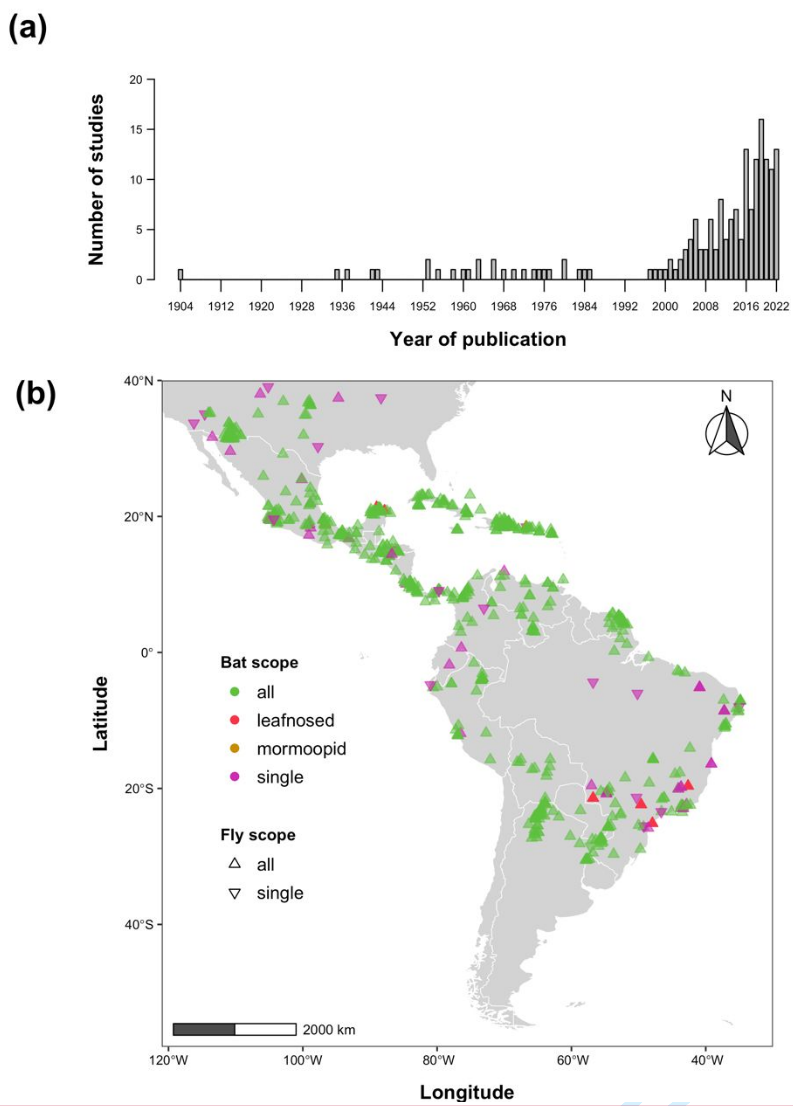
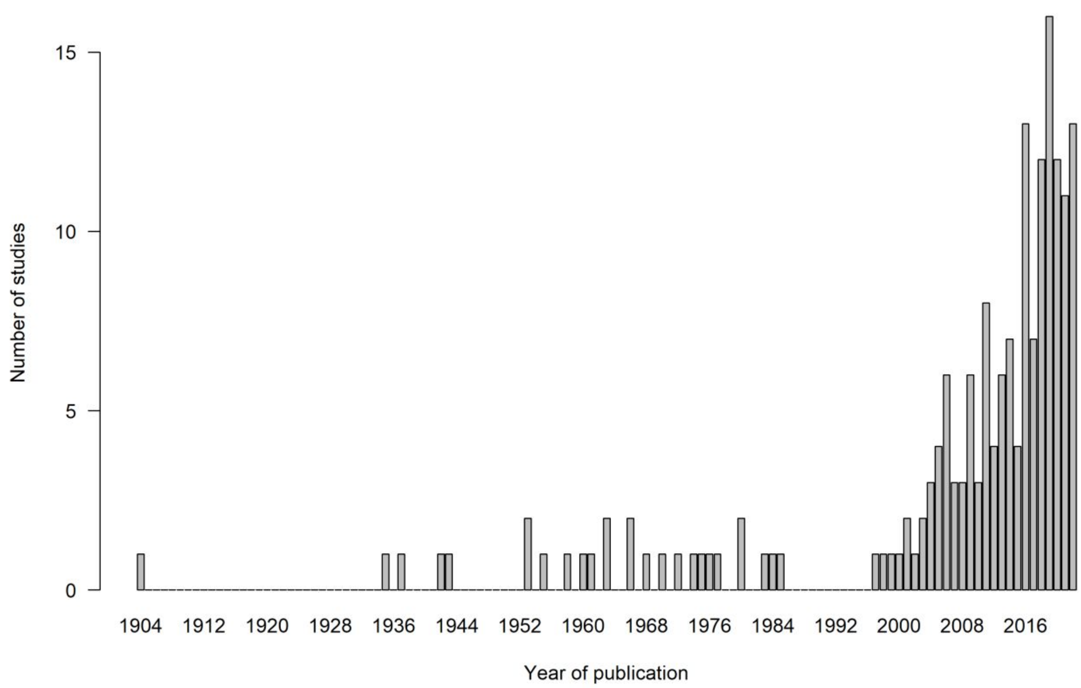


Figure 1. Temporal and spatial distribution of the references included in BatFly. (A) Number of studies published per year in the time range (1904 – 2022) included in BatFly. (B) Distribution of the sampling sites included in BatFly. Triangles represent sampling sites. Colors represent the taxonomic scope of sampling for bats, and triangle orientation (up/down) represents the taxonomic scope of sampling for flies. "Single" represents studies focused on a single fly species. "All" represents studies that assessed all fly species found at the site.

~~The BatFly database contains 3,984 interaction records complied and curated from 177 references, including three original data sets. For 95% of the study sites, we have~~

~~information on entire communities of bats and flies. The remaining 5% report parasites collected from a single bat species (Fig. 1). Information gathered here came from 650 study sites, located mainly in Mexico (146), Brazil (89), Argentina (62), southern USA (62), Peru (55), Cuba (32), Dominican Republic (32), and Honduras (26) (Fig. 1). On average, each reference contributed to the database with information from one study site. However, there are 19 references that contain information from over 10 study sites, which represent studies focused on recording all fly species and their hosts from a country or state (e.g., bat flies of Paraguay). The database includes references published between 1904 and 2022 (Fig. 2).~~



~~**Figure 2.** Growth in the number of studies on bat-fly interactions over the years (1904 – 2022).~~

Our database comprises interactions made by bats ~~belonging to~~of nine families, 76 genera, and 237 species. For flies, it comprises two families, 29 genera, and 255 species. ~~Those interactions form a highly connected network, in which a giant component can be observed. This kind of structure was unexpected due to the high specificity that these interactions are assumed to have (Fig. 3).~~

The 15 most frequently recorded bat species made 57% of all interactions, with *Carollia perspicillata* ~~(357)~~ as the species with most records (357), followed by *Artibeus jamaicensis* (263) and *Artibeus lituratus* (228) (Fig. 2~~4~~A), all of which are ~~all three~~ members of ~~the~~ the Phyllostomidae (Fleming et al. 2020)□. Over 57 bat species were shown to have only one interaction (singletons). Half of the interactions were made by 15 fly species, with *Trichobius joblingi* having the highest number of records (256), followed by *Megistopoda aranea* (235)~~,~~ and *Megistopoda proxima* (215) (Fig. 2~~4~~B).

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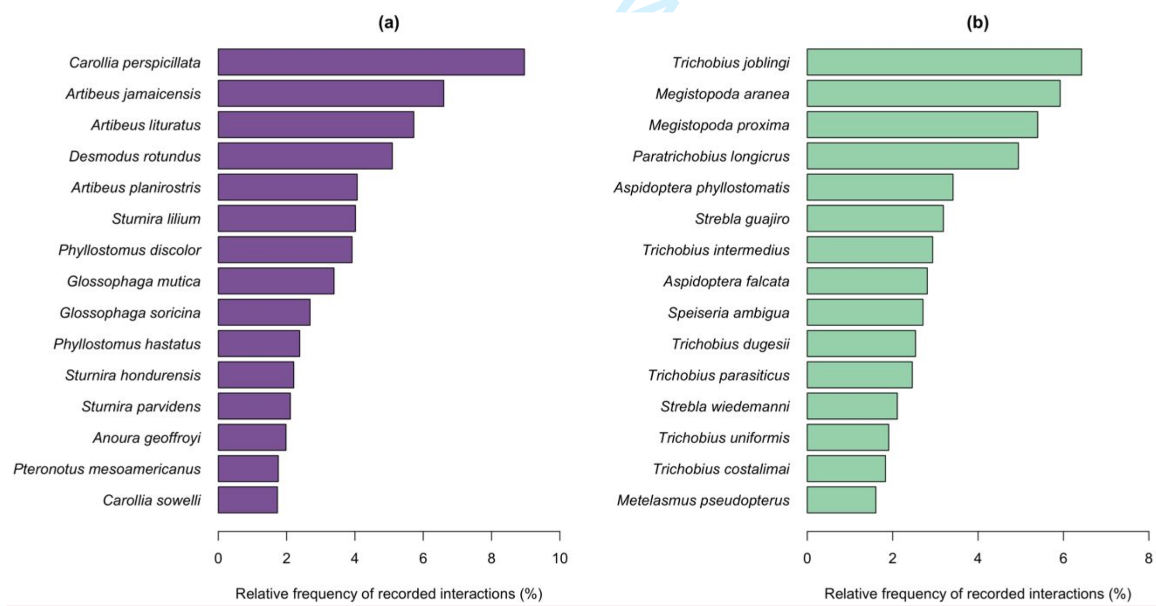
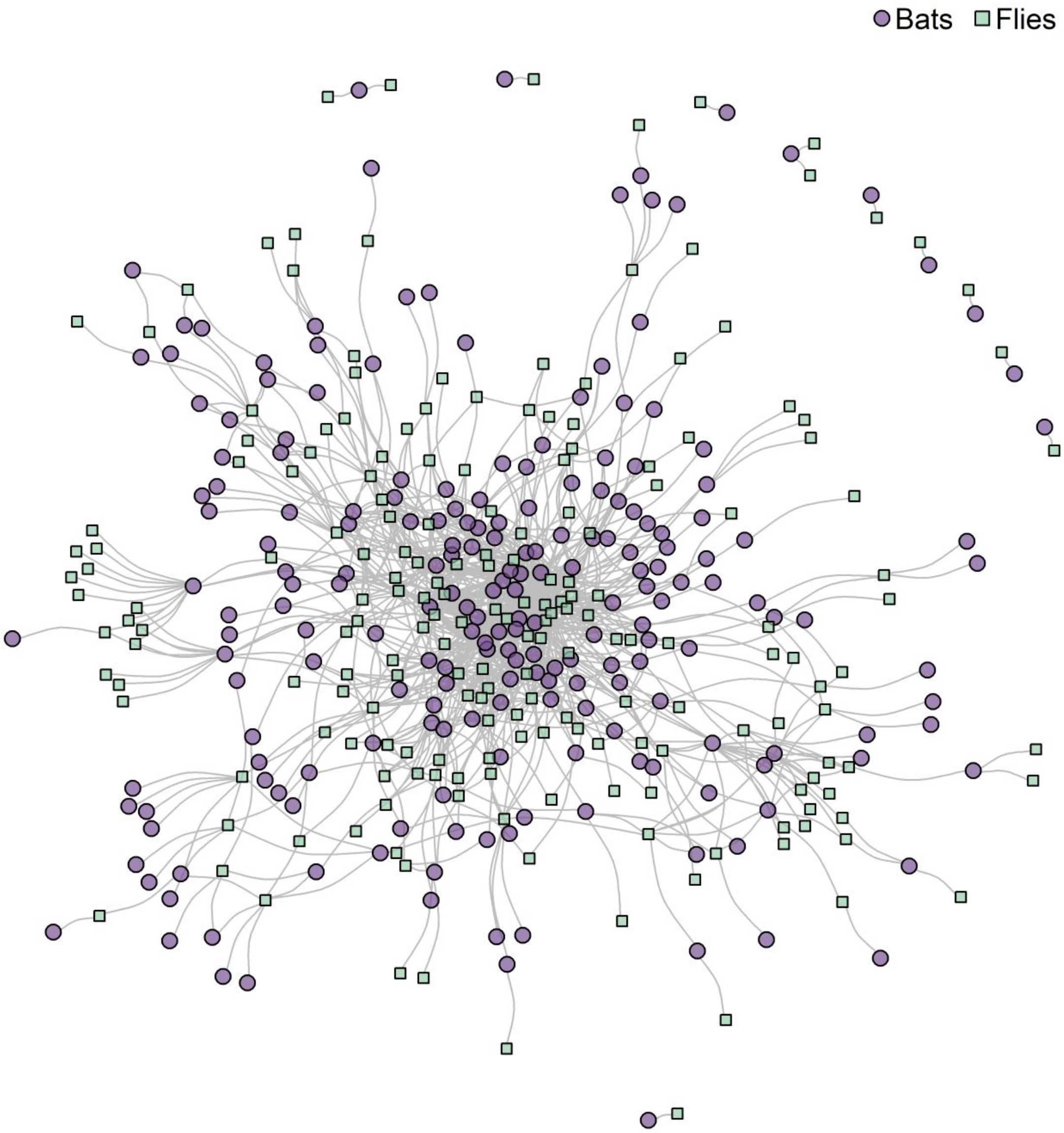
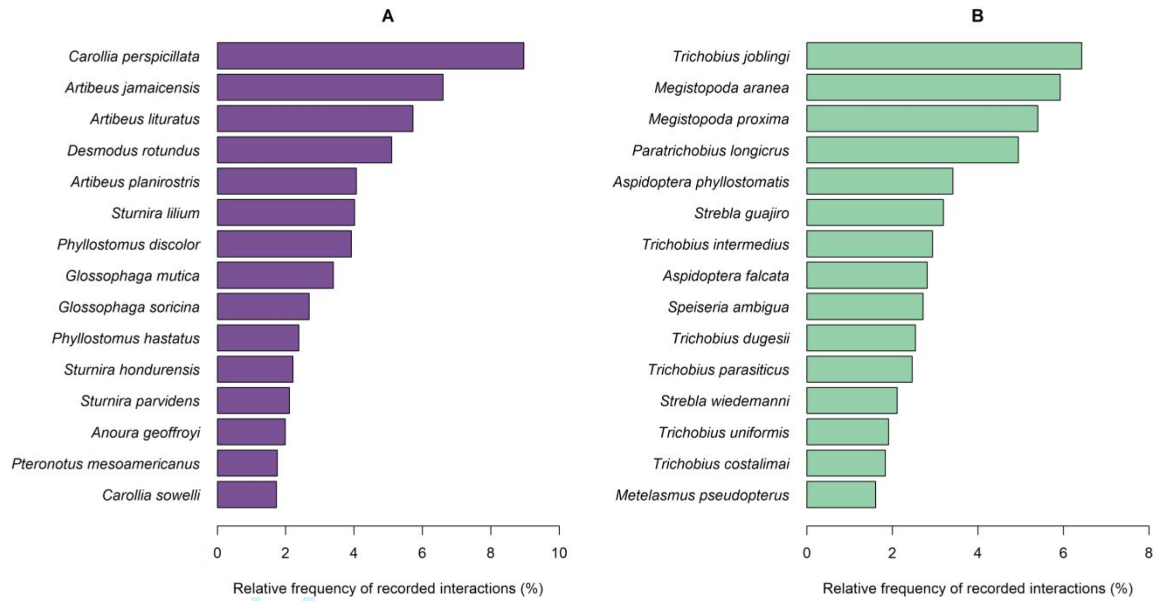


Figure 2. Relative frequency of interactions made by the top 15 (A) bat species and (B) fly species with most records.

In summary, BatFly has a total of 3,984 interaction records between bat and fly species.



~~Figure 3. The bat-fly network built for the entire Neotropical region with all records included in our data set. Lines depict interactions between bat species (purple circles) and bat fly species (green squares). Most nodes belong to a giant component and there are also ten minor components.~~



~~Figure 4. Relative frequency of interactions made by the top 15 (A) bat species and (B) fly species with most records.~~

~~Those interactions form a highly connected network, in which a giant component can be observed. This kind of structure was unexpected due to the high specificity that these interactions are assumed to have (Fig. 3). Most bat species recorded in our data set, according to the IUCN Red List of Threatened Species (https://www.iucnredlist.org), are categorized as least concern (152 species). However, two of them are considered vulnerable, while the species *Leptonycteris nivalis* and *Lonchophylla dekeyseri* are considered endangered (Fig. 5)~~

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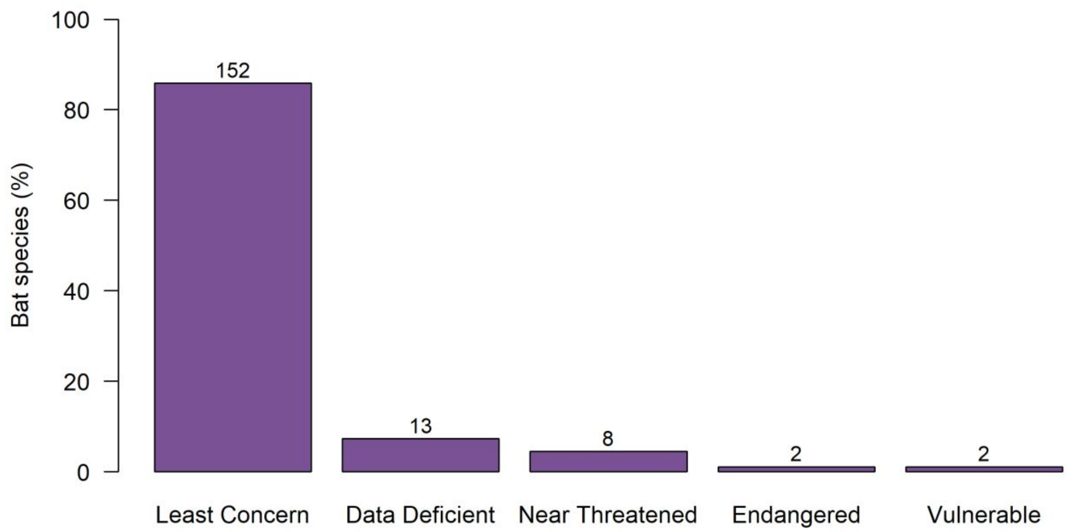
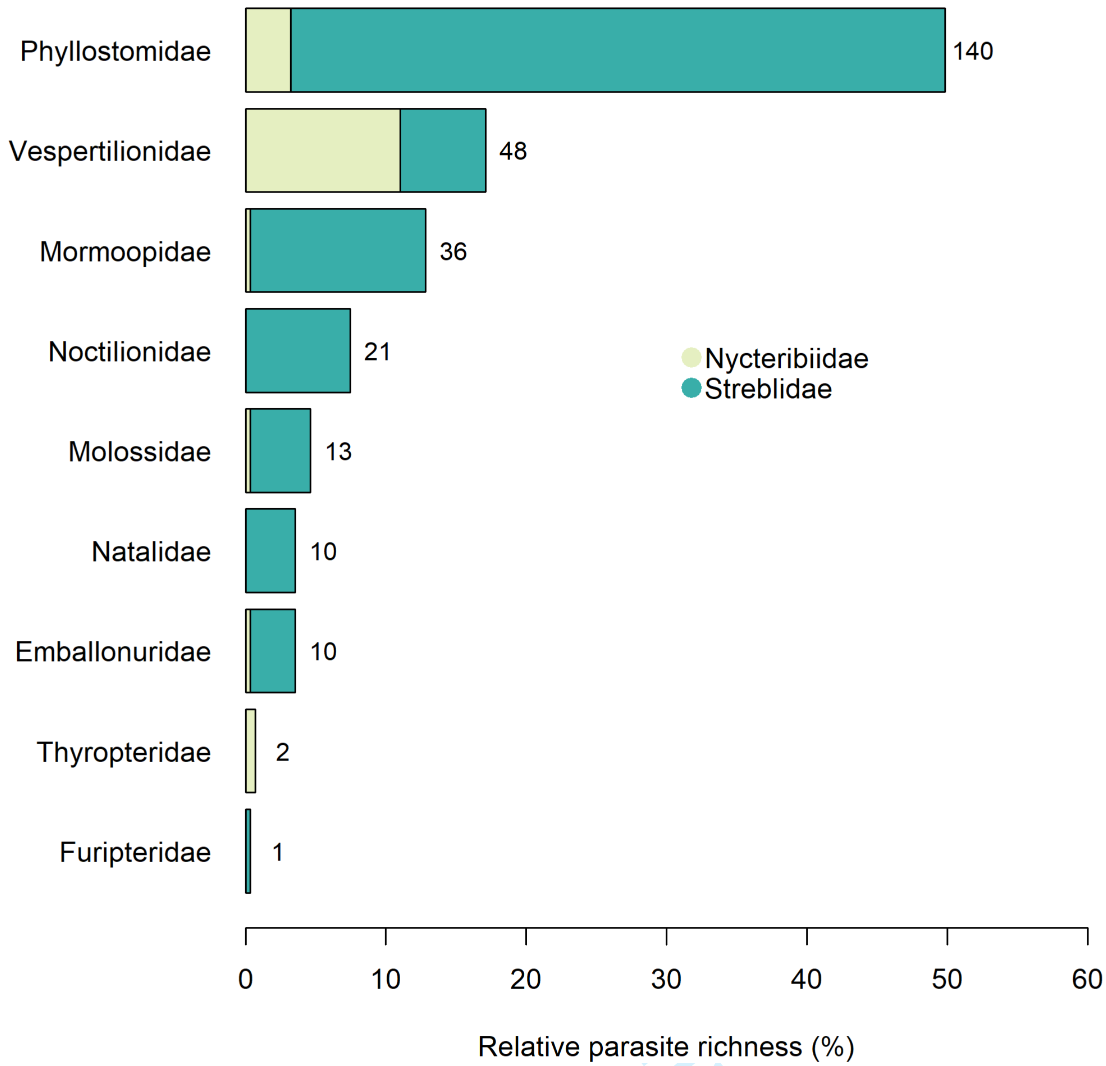


~~Figure 5. IUCN conservation status of the bat species.~~

Among bats,~~Species within~~ the family Phyllostomidae shows the richest set of interactions (140 fly species), followed by Vespertilionidae (48 fly species), and Mormoopidae (36 fly species). Most bat families within our records interact more frequently with fly species ~~belong to~~of the family Streblidae, except for Vespertilionidae and Thyropteridae, which ~~that~~ interact more frequently with the ~~the~~ Nycteribiidae. Furthermore, in the bat families Furipteridae, Noctilionidae, and Natalidae no interaction with ~~species of~~ Nycteribiidae species was recorded (Fig. 3A~~6~~). Those interactions between bat and fly species form a densely connected network, in which a large group of interconnected bat and fly species (giant component of the network) can be observed. This kind of structure was unexpected due to the high specificity that these interactions are assumed to have (Fig. 3B). However, this network was made with all interactions included in BatFly, even uncommon interactions, which may mask the true host specificity in the bat-fly interactions, so it should be interpreted with caution.


Phyllostomidae
140
Vespertilionidae
48
Mormoopidae
36
Noctilionidae
21
Molossidae
13
Natalidae
10
Emballonuridae
10
Thyropteridae
2
Furipteridae
1
Nycteribiidae
Streblidae
0
10
20
30
40
50
60
Relative parasite richness (%)

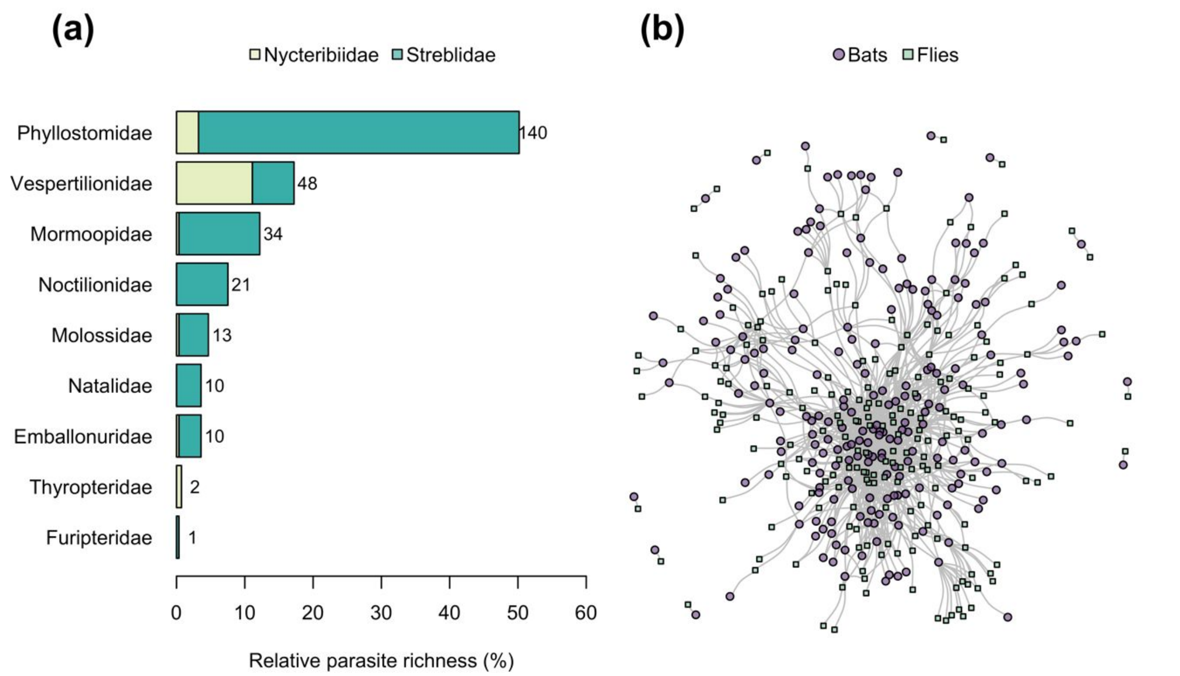
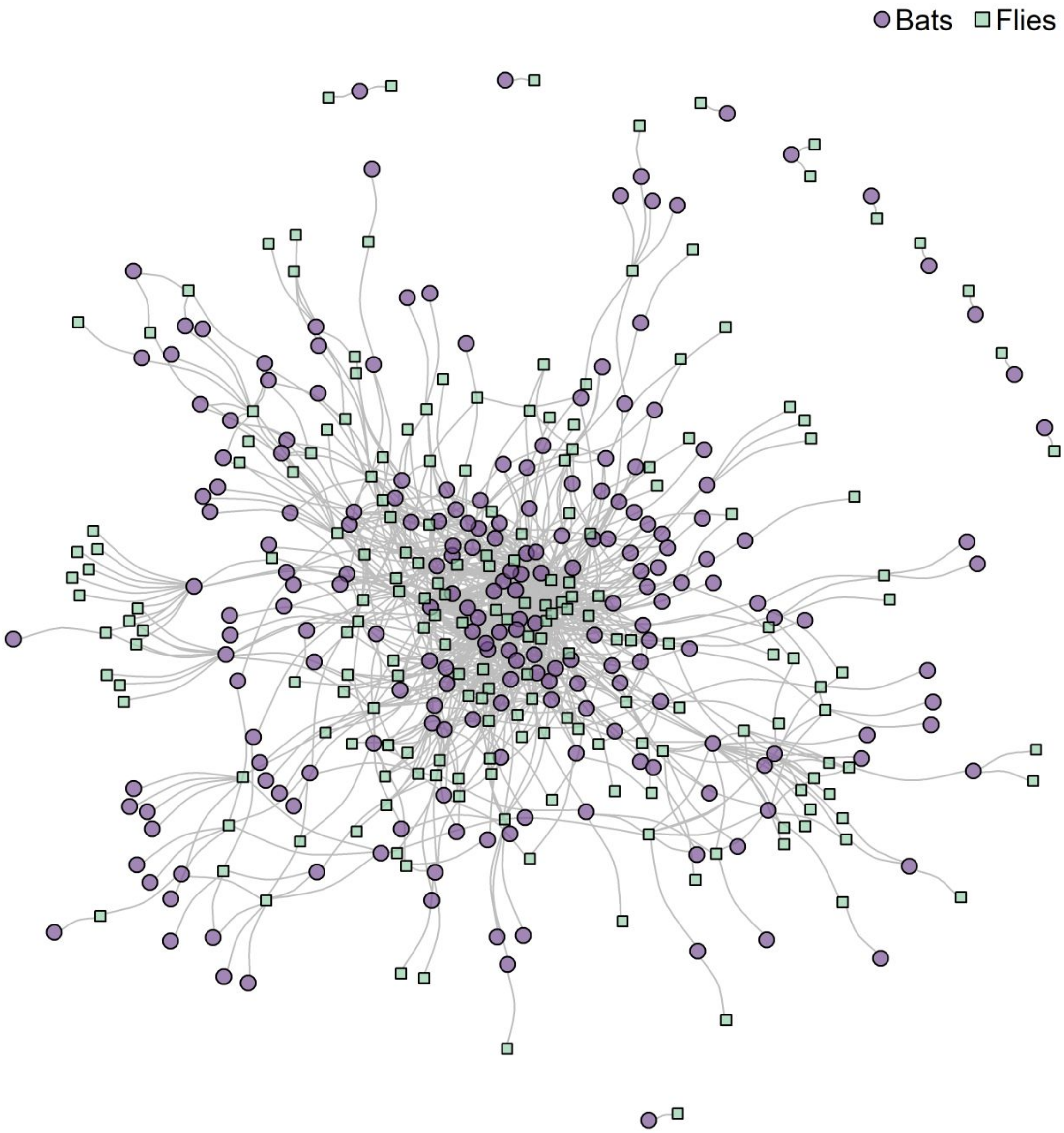


Figure 3~~6~~. Overview of bat-fly interactions included in BatFly. (A) Relative richness of ~~bat~~ ~~flies~~fly families (Nycteribiidae and Streblidae) per bat family. The number in front of the bars depicts the total number of ~~bat~~ fly species found parasitizing each bat family. (B) Bat-fly network built for the entire Neotropical region with all records included in our data set, even uncommon associations. Lines depict interactions between bat species (purple circles) and fly species (green squares). Most nodes belong to the giant component (largest subgroup of interconnected species) and there are also ten minor components (dyads).



~~**Figure 3.** The bat-fly network built for the entire Neotropical region with all records included in our data set. Lines depict interactions between bat species (purple circles) and bat fly species (green squares). Most nodes belong to a giant component and there are also ten minor components.~~

BatFly represents the largest dataset of antagonistic interactions made by bats in both geographical and taxonomic terms. All records were taxonomically harmonized, i.e., bat and fly scientific names were checked and updated. In addition to interaction records, our database includes information about references, study sites, sampling methods, and bat and fly populations organized in six linked data sheets (Fig. 4): “references”, “sites”, “sampling”, “bat population”, “fly population”, and “species interactions”. The “references” data sheet (Fig. 4A) contains information on the original sources from which the data were obtained. Each reference study was assigned a unique reference code (e.g., BFR001), enabling identification of each reference study in all other data sheets. The data sheets “sites” (Fig. 4B) and “sampling” (Fig. 4C) contain information about where, when and how the data were collected at each site, including study sites characteristics (e.g., mean annual temperature, annual rainfall, and vegetation type) which are known to influence bat-fly interactions (Pilosof et al. 2012). Each study site was assigned a unique site code (e.g., BFA001), with which each study site can be identified in within “sites”, “sampling”, “bat population”, “fly population” and “species interactions” data sheets.

The “bat population” (Fig. 4E) and “fly population” (Fig. 4F) data sheets contain taxonomic identification and information about the populations of interacting species. Also, we included bat species traits, such as the roost types used by bats, which are important drivers of parasite dynamics □(Patterson, Dick, and Dittmar 2007). Each population was assigned a unique population code for bats (e.g., BFBPOP000) and flies (e.g., BFFPOP000), allowing its identification of each population in the “species interactions” data sheets. Finally, the “species interactions” data sheet (Fig. 4F) contains the species-species interaction records, and information about number of infested bats, prevalence, mean fly intensity, and mean fly abundance. Each interaction record was assigned an interaction code (e.g, BFSSI000) associated to bat population and fly population codes, and also associated to site, and references codes shared between data sheets (foreign keys). This interconnected structure

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enables the expansion of information for each interaction record encompassing where and how the interaction was collected, as well as the number of bats and flies involved in a specific record.

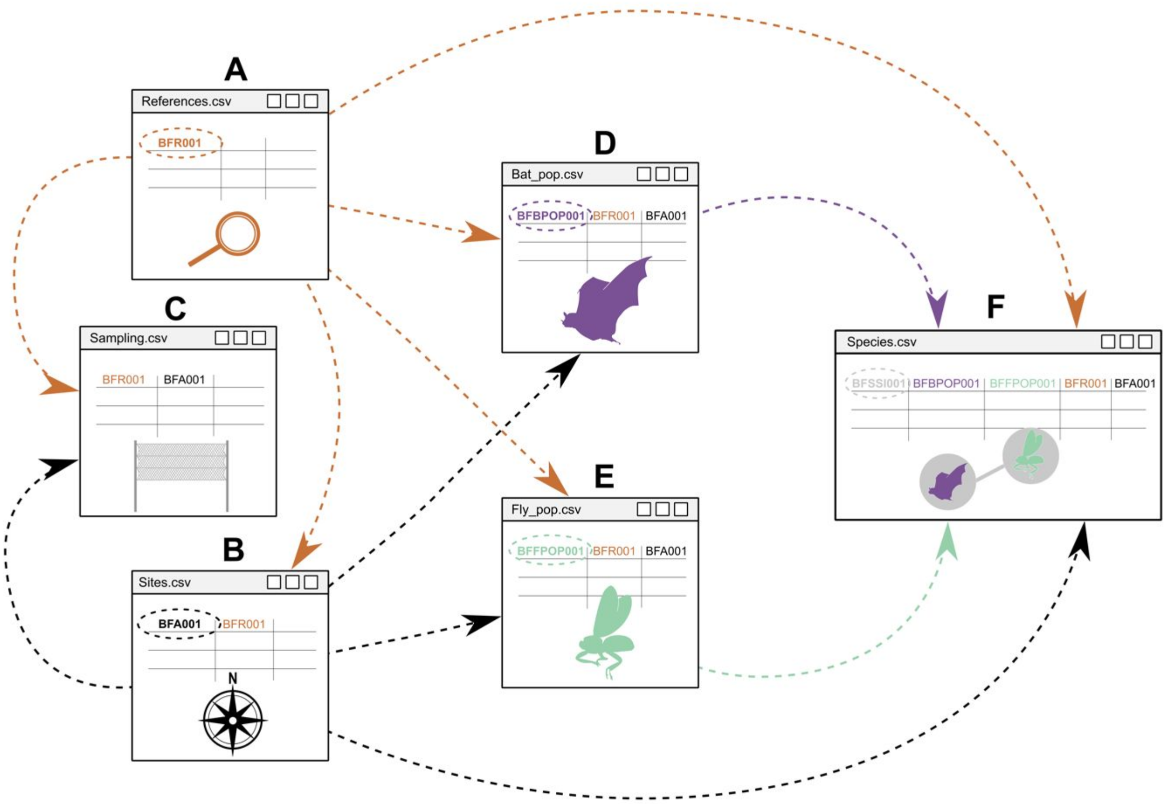

Figure 4. Structure of the BatFly database. BatFly is integrated by six ~~interconected~~interconnected datasheets. (a) References data sheet. (b) Site data sheet. (c) Sampling data sheet. (d) Bat population data sheet. (e) Fly population data sheet. (f) Species interaction data sheet. Each interaction record has a unique interaction code (primary key) associated to reference, site, bat and fly population codes shared between datasheets (foreign keys). In the graphical representation, dashed ovals indicate the first appearance of a code within the database. Dashed lines illustrate the relationships between BatFly's datasheets. Each code is designated with a distinct color. For example, the reference code (colored

orange), which first appears on the reference datasheet (a~~A~~), can be found on all other datasheets, denoted by five orange lines.

~~In the graphical representation, dashed ovals indicate the first appearance of a code within a specific datasheet. Dashed lines depict the relationships between BatFly's datasheets, showing where each code first appears (indicated by the start of the dashed line) and in which datasheets it is shared (indicated by the dashed line arrow). Each code is assigned a different color. For instance, the reference code (colored orange), which initially appears on the reference datasheet (A), can be located on all other datasheets, represented by five orange lines.~~

BatFly was designed to boost the use of bat-fly interactions as a model for addressing questions at different levels of ecological organization and spatial scales. We expect BatFly to inspire researchers to continue consolidating knowledge about ecological specialization, resource distribution, pathogen transmission, and the drivers of parasite prevalence over a broader spatial range. It may also help answer key questions, such as: are there differences in fly prevalence or mean infestation across Neotropical ecoregions? What ecological drivers explain those differences? Or how do specialization patterns vary among fly species in the Neotropics? We also expect to inspire research aimed at understanding how bat-fly interactions can be affected by climate and landscape changes. Ultimately, we expect BatFly to help understand host-parasite interactions, facilitate predicting zoonotic outbreaks, and provide information to address the UN's SDG 3 Good Health and Wellbeing.

~~Bat species included here use different types of roosts, mainly caves, tree cavities, human-made structures, and foliage. Most bat species use caves and tree cavities (32 and~~

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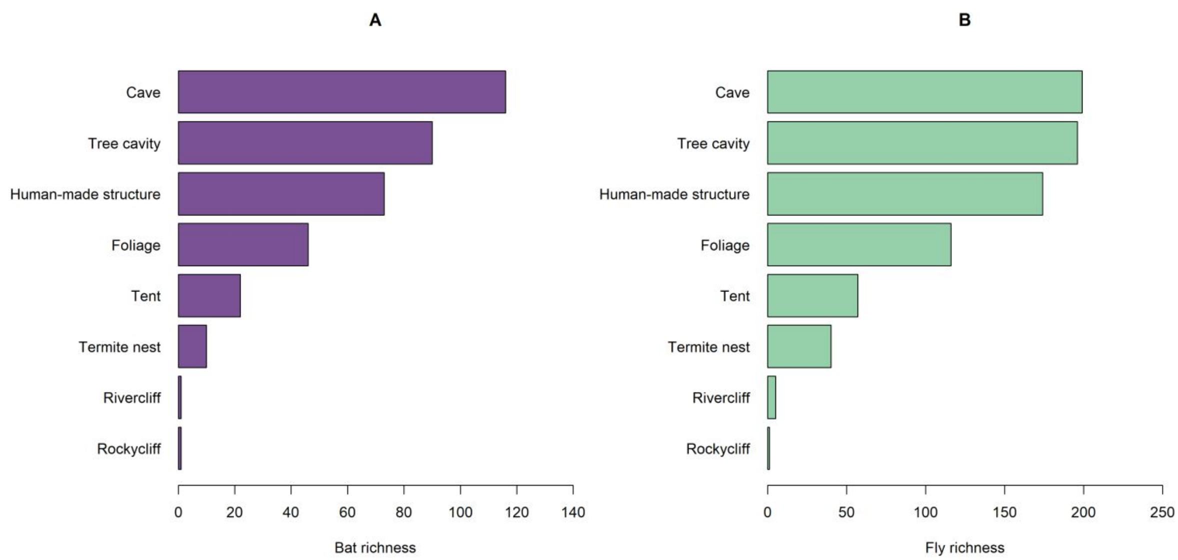
~~25%, respectively) (Fig. 7A). Others use termite nests as roosts, mainly bats that belong to the genera *Lophostoma*, *Phyllostomus*, and *Tonatia*. In addition, *Sturnira tildae* and *Nyctinomops laticauda* were the only species reported using river cliff roosts and rocky cliff roosts, respectively. The highest species richness of flies was found to be linked to bat species inhabiting caves (25%) and tree cavities (25%) (Fig. 7B).~~



~~**Figure 7.** (A) Bat richness according to the type of roost used. (B) Fly richness according to the type of roost used by their bat hosts. Considering that the same bat species might use more than one type of roost, the sum of bar values does not match the total number of bat and fly species included in our data set.~~

CLASS II. RESEARCH ORIGIN DESCRIPTORS

A. Overall project description

Identity: A compilation of bat-fly interactions.

Period of study: Data of ~~collection~~ publication reported in~~on~~ the references range from 19044 to 2022.

Objective: We aimed to summarize and make available all bat-fly interaction records found in the literature plus three new data sets in a tidy format, to be used in studies on community ecology, interaction networks, and macroecology, and disease spillover, among other topics.

Abstract: Global changes have increased the risk of emerging infectious diseases, which can be prevented or mitigated by studying host-parasite interactions, among other measures. Bats and their ectoparasitic flies of the families Streblidae and Nycteribiidae are an excellent study model, but so far, our knowledge is restricted to fragmented records at a local scale. To help boost research, we have assembled a data set of bat-fly interactions from 174 studies published between 1904 and 2022, plus three original data sets. Altogether, these studies were carried out at 650 sites in the Neotropics, mainly distributed in Mexico, Brazil, Argentina, southern USA and Colombia, among other countries. In total, our data set contains 3,984 interaction records between 237 bat species and 255 fly species. The bat species with the largest number of recorded interactions were *Carollia perspicillata* (357), *Artibeus jamaicensis* (263), and *Artibeus lituratus* (228). The fly species with the largest number of recorded interactions were *Trichobius joblingi* (256), *Megistopoda aranea* (235), and *Megistopoda proxima* (215). The interaction data were extracted, filtered, taxonomically harmonized, and made available in a tidy format together with linked data on bat population, fly population, study reference, sampling methods and geographic information from the study sites. This interconnected structure enables the expansion of information for each interaction record, encompassing where and how each interaction occurred, as well as the number of bats and flies involved. We expect BatFly to open new avenues for research focused on different levels of ecological

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organization and spatial scales. It will help consolidate knowledge about ecological specialization, resource distribution, pathogen transmission, and the drivers of parasite prevalence over a broad spatial range. It may also help answer key questions, such as: are there differences in fly prevalence or mean infestation across Neotropical ecoregions? What ecological drivers explain those differences? Or how do specialization patterns vary among fly species in the Neotropics? Furthermore, we expect BatFly to inspire research aimed at understanding how climate and land-use changes may impact host-parasite interactions and disease outbreaks. This kind of research may help us reach Sustainable Development Goal 3, Good Health and Wellbeing, outlined by the United Nations.

~~Same as above.~~

Sources of funding: NZM, SMB, and JH were funded by Ministerio de Ciencia, Tecnología e Innovación de Colombia (MinCiencias, Convocatoria Doctorados en el Exterior 860 and 906). NZM and SMB were funded by the Brazilian Coordination for the Improvement of Higher Education Personnel (CAPES, 88887.467879/2019-00 and 88887.388097/2019-00). GG was funded by National Council for Scientific and Technological Development (CNPq# 308119/2022-3). MARM was funded by the Alexander von Humboldt Foundation (AvH, ~~, 3.2-BRA/~~1134644~~ and 3.4- 1134644-BRA-GA~~), National Council for Scientific and Technological Development (CNPq, 304498/2019-0), São Paulo Research Foundation (FAPESP, 2018/20695-7 and 2023/02881-6), and Dean of Research of the University of São Paulo (PRP-USP, 18.1.660.41.7).

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B. Specific subproject descriptions

Data compilation: We performed a comprehensive systematic review of the literature, following the Preferred Reporting Items for Systematic review and Meta-Analyses (PRISMA) protocol designed as a guide to improve clarity and transparency in the reporting of systematic reviews ~~protocol~~ (Page et al. 2021). We also added information from ~~articles~~ papers that did not appear in our systematic search, but which we were aware of, and invited authorities to contribute with their unpublished data (Fig. 5~~8~~).

The systematic search was conducted ~~in three languages: English, Portuguese, and Spanish,~~ utilizing the Web of Knowledge and Scopus databases. There were no date restrictions, and the search was performed in 2021~~The systematic search was conducted across three languages English, Portuguese, and Spanish, on the Web of Knowledge and Scopus databases~~. The search utilized keywords in three languages: English, Portuguese, and Spanish. The following keywords were employed: ~~The systematic search was made on the databases *Web of Knowledge* and *Scopus*, using the following search terms:~~ “bat*” OR “murciélago*” OR “morcego*” OR “chiroptera” OR “chiroptero” OR “quiroptera” OR “quiroptero” AND “bat fly” OR “bat flies” OR “streblid*” OR “streblidae” OR “nycteribiid*” OR “nycteribiidae” OR “parasite*” OR “parásito*” OR “ectoparasite*” OR “ectoparásito*” OR “ectoparasita*” OR “diptera*” OR “díptero” OR “mosca”. With the results from this~~ese~~ naive-term search we extracted potential keywords using the Rapid Automatic Keyword Extraction (RAKE) algorithm (Grames et al. 2019). ~~We performed an additional search based on t~~Those automatic extracted keywords underwent manual verification, filtering, and sorting. Subsequently, a search was performed using the following~~se~~ refined keywords: "tropical bat" OR "tropical bats" OR "bat" OR "bats" OR "neotropical bats" OR

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"neotropical bat" OR "chiroptera" OR "chiropteran hosts" OR "chiropteran species" AND "blood-sucking flies" OR "blood-sucking fly" OR "diptera" OR "dipterans" OR "nycteribiidae" OR "streblidae" OR "streblid*" OR "bat flies" OR "bat fly" OR "ectoparasite*" OR "nycteribiid*" OR "bat parasite*" OR "bloodsucking diptera" OR "bloodsucking dipterans" OR "batfly" OR "batflies" AND "parasitizing" OR "interaction*" OR "interacted" OR "interact" OR "parasitological" OR "association*" OR "host-parasite" OR "system*" OR "vertebrate-parasite" OR "network*" "parasite assemblage*" OR "intensity" OR "infection" OR "infestation" OR "load*" "host potential" OR "parasitism" OR "prevalence" OR "parasited" OR "hematophagous" OR "relationship*" OR "specificity" OR "specialization" OR "specialisation" OR "inhabiting" OR "fly-host" OR "host-specific" OR "parasitology" OR "bat-parasite" OR "specialized" OR "specialised" OR "specialize" OR "specialise" OR "host" OR "hosted" OR "hosting" OR "hosts"~~hose automatically extracted keywords~~. We compiled information on bat fly interactions from a total of 102~~77~~ references, ~~(~~99~~174~~ ~~papers~~ studies found ~~and 3 unpublished data sets)~~ in this systematic search and 3 unpublished data sets collected by the authors ~~in a first source of information~~. As we did our first systematic search in 2021, we did an update with additional search restricted to ~~works~~ studies published in 2022, with keywords: “streblid*” OR “streblidae” OR “nycteribiid*” OR “nycteribiidae”, adding ten references for 2022 year. Finally, we included 65 references provided by one of the authors, Gustavo Graciolli (Fig. 5~~8~~). These 65 references did not come up in the search due to most of them are not indexed in the databases used.

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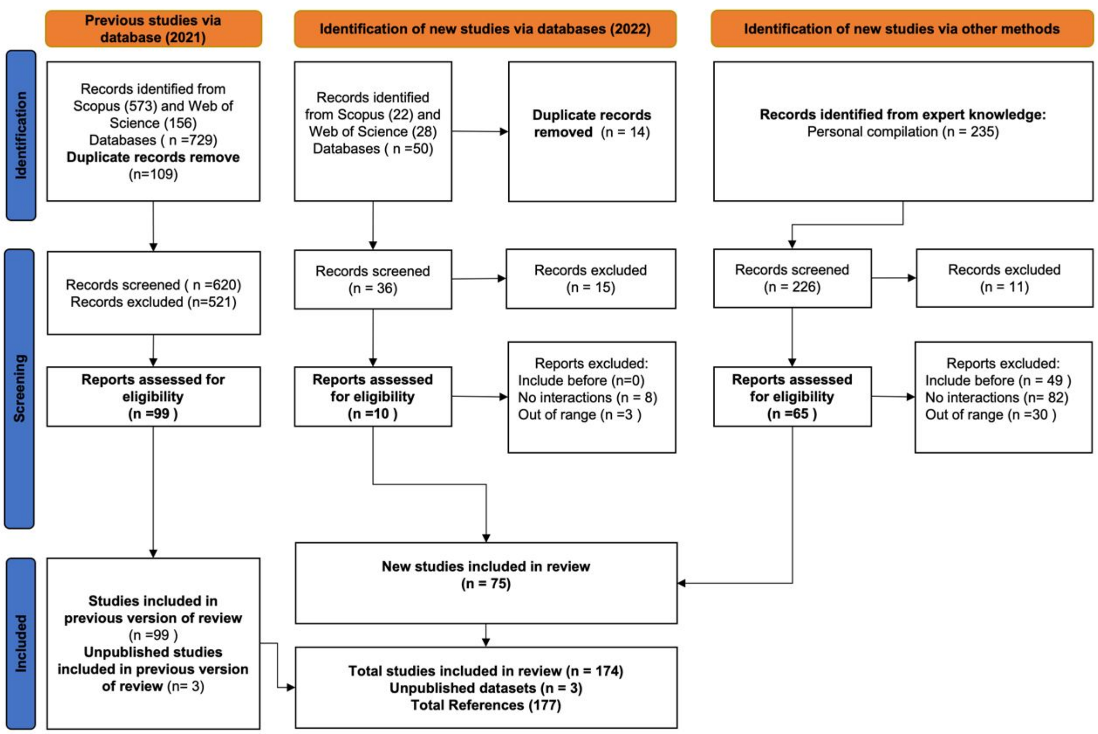
For a study to be included in our database, it had to meet the following inclusion criteria: (1) be a primary study, so we discarded literature reviews or compilations of interactions from other studies; (2) contain naturally occurring interactions, so we ignored host preference studies carried out under controlled conditions; and (3) contain spatial ~~geographic~~ information of where the interactions were recorded, as coordinates, country and locality. Finally, with the studies found in the first systematic search done in 2021 (99), the studies found in the second systematic search (update, 10) and 65 studies provided by one of the authors, BatFly contains 174 published studies and 3 original datasets (177 references in total; Fig. 5).~~Finally, with three sources (previous~~



~~review, update, and personal compilation) BatFly contains 174 studies and 3 original datasets (Fig. 8).~~

Figure 5~~8~~. Workflow of the updated systematic review carried out to acquire data, which included database searches, additional records, and other sources, following PRISMA 2020 (Page et al. 2021).

Research methods: We included only studies that reported bat-fly interactions recorded from wild assemblages. Their scopes range from new fly records and community ecology and endosymbiont diversity in bat flies (bacteria and fungi), along with information on bat hosts. Information on sampling methods and host population was also extracted. We also included geographical information from study sites (latitude, longitude, locality, municipality, state, and country), and site characteristics (ecoregion, type of vegetation, height, average annual temperature). Missing information was coded as "NA".

We compiled information on bat-fly interactions published between 1904 and 2022 from 174 references: ~~(~~Brues 1904; Curran 1935; Guimarães 1937; 1966; 1972; 1977; E. Dias et al. 1942; Augustson 1943; Fox and Stabler 1953; Hoffmann 1953; Parmalee 1955; Zeve 1958; Peterson 1960; 1963; Bradshaw and Ross 1961; Tonn and Arnold 1963; Uberlaker 1966; Maa 1968; Peterson and Maa 1970; Peterson and Hůrka 1974; Whitaker and Easterla 1975; Reisen, Kennedy, and Reisen 1976; Hoffmann, Palacios-Vargas, and Morales-Malacara 1980; Overal 1980; Fritz 1983; Coimbra jr, Guimarães, and Mello 1984; Peterson and Lacey 1985; Capllonch et al. 1997; Komeno and Linhares 1999; Claps, Autino, and Barquez 2000; 2005; Chavez 2001; Ritzi et al. 2001; Azevedo and Linardi 2002; Guzmán-Cornejo et al. 2003; Moura, Bordignon, and Graciolli 2003; Autino and Claps 2004; González D., Santos M, and Miranda 2004; ter Hofstede, Fenton, and Whitaker, Jr. 2004; Bertola et al. 2005; Villegas-Guzman, López-González, and Vargas 2005; Dick and Gettinger 2005; Anderson and Ortencio

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Filho 2006; Dick and Wenzel 2006; Oscherov, Chatellenaz, and Milano 2006; Oscherov, Idoeta, and Milano 2012; Graciolli et al. 2006; Graciolli, Zortéa, and Carvalho 2010; Graciolli, Guerrero, and Catzeflis 2019; Voigt and Kelm 2006; Shockley and Murray 2006; Graciolli and Bianconi 2007; Dick, Gettinger, and Gardner 2007; Kurta et al. 2007~~, n.d.~~; Rojas et al. 2008; Sebastián Tello, Stevens, and Dick 2008; P. A. Dias et al. 2009; Autino et al. 2009; 2011; Autino, Claps, and Barquez 2014; Autino et al. 2016; 2018; 2020; Dittmar et al. 2009; 2011; Valdez, Ritzi, and Whitaker 2009; Santos et al. 2009; 2013; Graciolli and Dick 2009; 2012; Almeida et al. 2011; Camilotti et al. 2010; Aguiar and Antonini 2011; Eriksson, Graciolli, and Fischer 2011; Muñoz-Romo, Burgos, and Kunz 2011; J. R. R. da Silva and Ortêncio Filho 2011; Lourenço and Esbérard 2011; Esbérard et al. 2012; 2014; Morse et al. 2012; Dick 2013; Moras et al. 2013; Saldaña-Vázquez et al. 2013; Soares et al. 2013; 2016; 2017; França et al. 2013; Urbieta and Torres 2014; Moreno Valdéz 1998; Camacho et al. 2014; Lourenço et al. 2014; 2020; Velazco, Autino, and Claps 2014; Tarquino-Carbonell et al. 2015; Tlapaya-Romero et al. 2015; Tlapaya-Romero, Ibáñez-Bernal, and Santos-Moreno 2019; Tlapaya-Romero, García-Méndez, and Ramírez-Martínez 2022; Cuxim-Koyoc et al. 2015; 2016; 2018; Judson, Frank, and Hadly 2015; Patricio and Lourenço 2016; de Vasconcelos et al. 2016; Hernández-Arciga, Herrera M., and Morales-Malacara 2016; Frank et al. 2016; Reeves et al. 2016; Barbier and Graciolli 2016; Bezerra, de Vasconcelos, and Bocchiglieri 2016; Zarazúa-Carbajal et al. 2016; Barbier, Prado-Neto, and Bernard 2016; Barbier et al. 2017; 2018; 2019; Barbier, Graciolli, and Bernard 2019; Barbier et al. 2020; Barbier, Falcão, and Bernard 2021; Fagundes, Antonini, and Aguiar 2017; Dornelles and Graciolli 2017; Rivera-García et al. 2017; Cordero-Schmidt et al. 2017; Walker et al. 2018; Abundes-Gallegos et al.

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2018; Bolívar-Cimé et al. 2018; Colín-Martínez, Morales-Malacara, and García-Estrada 2018; Salinas-Ramos et al. 2018; Calonge-Camargo and Pérez-Torres 2018; Estrada-Villegas et al. 2018; do Amaral et al. 2018; Bezerra and Bocchiglieri 2018; 2022; Hrycyna, Martins, and Graciolli 2019; S. S. P. da Silva, Guedes, et al. 2019; S. S. P. da Silva et al. 2021; Torres et al. 2019; Hernández-Martínez et al. 2019; Trujillo-Pahua and Ibáñez-Bernal 2019; 2020; Smit and Miller 2019; Durán et al. 2019; S. S. P. da Silva, Neves, et al. 2019; Vieira et al. 2019; Liévano-Romero, Rodríguez-Posada, and Cortés-Vecino 2019; Orta-Pineda et al. 2019; Ribas, Batista, and Aranha 2020; Ascuntar-Osnas, Montoya-Bustamante, and González-Chávez 2020; Bonifaz, Mena, and Oporto 2020; Raigosa Álvarez et al. 2020; Zamora-Mejías et al. 2020; Ikeda et al. 2020; Palheta et al. 2020; de Groot et al. 2020; Oliveira et al. 2020; Menezes Júnior et al. 2021; Minaya, Mendoza, and Iannacone 2021; Vidal, Bernardi, and Talamoni 2021; Urbieta, Graciolli, and Vizentin-Bugoni 2021; Hiller et al. 2021; Lira-Olguin, Guzmán-Cornejo, and León-Paniagua 2021; Mello et al. 2021; Ramalho, Diniz, and Aguiar 2021; Gómez-Corea et al. 2022; Alcantara et al. 2022; Speer et al. 2022; da Silva Biz et al. 2021; Castillo-Urbina et al. 2022; Carvalho et al. 2022; Herrera and Jara 2008; González-Ávalos et al. 2014; Bellizzi et al. 2022; Almeida et al. 2010; Dornelles et al. 2017; Ramírez-Martínez et al. 2016; Mello et al. 2022; da Silva Reis et al. 2022~~)~~.

For already included references, if applicable, we accommodated studies that partially or totally used the same data sets as “Associated References”, assuring not to duplicate interaction records (see Table 1).

Taxonomic information: All records were taxonomically harmonized. Scientific names were checked and updated. For bats, taxonomic harmonization was performed by Marcelo Nogueira. The main reference for bat taxonomic arrangement and

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nomenclature adopted here was Simmons and Cirranello (2023). H~~We, h~~owever, when considering the taxonomy of *Glossophaga* we followed Diaz et al. (2021). Also, in the case of *Dermanura*, we followed Cirranello et al. (2016) in treating this taxon as a subgenus of *Artibeus*. ~~followed Diaz et al. (2021) when considering the taxonomy of *Glossophaga*. In the case of *Dermanura*, we followed Cirranello et al. (2016) in treating this taxon as a subgenus of *Artibeus*.~~ Diaz et al. (2021) and Gardner (2008) were the general references for the geographic distribution of each species, but we also consulted country-wide compilations (e.g., York et al. 2019; Martínez-Fonseca et al. 2020; Turcios-Casco et al. 2020; Mora, López, and Espinal 2021; Velazco et al. 2021; Garbino et al. 2022) and primary references (e.g., species descriptions and systematic revisionary works), and species accounts, including Solari and Baker (2006); Genoways and Baker (1996); McDonough et al. (2008); Velazco, Gardner, and Patterson (2010); Velazco and Simmons (2011); Moratelli et al. (2011); Mantilla-Meluk (2014); Mantilla-Meluk and Muñoz-Garay (2014); Pavan and Marroig (2016); Pavan, Bobrowiec, and Percequillo (2018); Velazco and Patterson (2019); Basantes et al. (2020); Loureiro, Engstrom, and Lim (2020); Rodríguez-Posada et al. (2021); Velazco et al. (2021); Calahorra-Oliart, Lira-Noriega, and León-Paniagua (2022); Calderón-Acevedo, Bagley, and Muchhala (2022); Esquivel et al. (2022). When there was a situation in which more than one species could be associated to a previous species record within the same bat ~~community~~assembly, as *Platyrrhinus helleri* and *Pteronotus parnellii*—please refer to Velazco, Gardner, and Patterson (2010) and Pavan, Bobrowiec, and Percequillo (2018) for newly described taxa related to these species— ~~When more than one species could be associated to a previous record, as was the case for *Platyrrhinus helleri* and *Pteronotus parnellii*—see Velazco, Gardner, and Patterson~~

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~~(2010) and Pavan, Bobrowiec, and Percequillo (2018) for new taxa related to these species —~~the updated identification was retained at genus level.

For flies, taxonomic harmonization was performed by Gustavo Graciolli. Taxonomic changes in the current name of species were made following Alcantara, Graciolli, and Nihei (2019); Hrycyna et al. (2022); Tlapaya-Romero, García-Méndez, and Ramírez-Martínez (2023); Graciolli and Dick (2012); Graciolli, Santos, and Rebêlo (2022). In the records that were not identified to the species level, whenever ~~was~~ possible, the taxonomic complex or group to which they belong was reported.

Bat roost information: We report the roost type used by each bat species included in the database. Bat roost play an important role in fly species lifecycle due to fly species pupal development is carried out in these places (Dittmar et al. 2009). All possible roost types were classified into eight categories: cave (hot caves, caverns, and crevices), tree cavity (hollow trees, fallen trees, and loose bark), human-made structure (buildings, bridges, tunnels, and culverts), foliage (branches and leaves), tent, termite nest, rocky cliff, and river cliff. We compiled this information from the literature (Kunz and Lumsden 2003; Rodríguez-Durán 2020).

C. Data limitations and potential enhancements

BatFly has limitations related to the scope of the studies used as data sources and how information was reported in them. There are many gaps in information in the references used, as unfortunately commonly observed in studies on species interactions (see another paper with recommendations to solve this problem: ~~(~~Kita et al. 2022~~)~~)

~~BatFly has limitations related to the scope of the studies used as data sources.~~ First, there are sampling information limitations. ~~a~~As several references are checklists of fly species also reporting their hosts, ~~many lack information on bat sampling~~

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~~methods.~~ most studies do not provide information about the methods used for capturing bats, e.g., the number of sampling hours or the number of mist nets used, hindering the estimation of sampling effort. Only 117 study sites (18%) informed their sampling effort following the widely used method of Straube and Bianconi (2002).

Second, there are geographical information limitations. Sixteen site studies (2.5%) report interactions accumulated from several locations, hindering the use of their data ~~in studies~~ at smaller spatial scales. In those cases, we recorded all ~~the~~ data available ~~data~~ from the locations of the study in the observation column (see Table 2). A single SiteCode was assigned with the coordinates of the centroid of the polygon formed by the coordinates reported in the study (see Table 2).

Third, there are ~~sampling~~ interaction information limitations. ~~Most studies do not provide information about the methods used for capturing bats, e.g., the number of sampling hours or the number of mist nets used, hindering the estimation of sampling effort. Only one hundred and seventeen (18%) studies informed their sampling effort following (Straube and Bianconi 2002). Fourth, N~~Not all studies have information that allows quantifying the~~about~~ interaction~~ weight~~, ~~and~~ 490 (12%) interactions were recorded only as ~~incidence~~ occurrence (binary information), hindering the use of their data in studies that aim to analyze the interaction by incidence of fly species on bat species.~~.~~ Furthermore, information provided by most studies is limited to the number of individuals of a given fly species found on a given bat species, excluding other key information useful to quantify the interaction such as prevalence, mean intensity, and mean abundance. Only 978 (25%) of the interaction records provide us with information on prevalence.

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Four~~ifth~~, there are representativeness limitations. Our database is biased by the method through which bats are sampled, since most studies were based on mist-netting, and different bat species have different capturability (Francis 1989). Mist nets are much more efficient for capturing phyllostomids than bats ~~of~~ from other families (Tschapka 1998). So, potential users of BatFly should have this in mind, for example when carrying out studies aimed at analyzing fly incidence in different bat families or species from different bat families.~~Thus, our database with 1,023 unique interactions represents only a small subset of all bat-fly interactions that probably occur in nature. The rarefaction curve is far from reaching an asymptote despite being based on 3,984 interactions records and 1,023 unique interactions, made at 650 study sites (Fig. 9).~~

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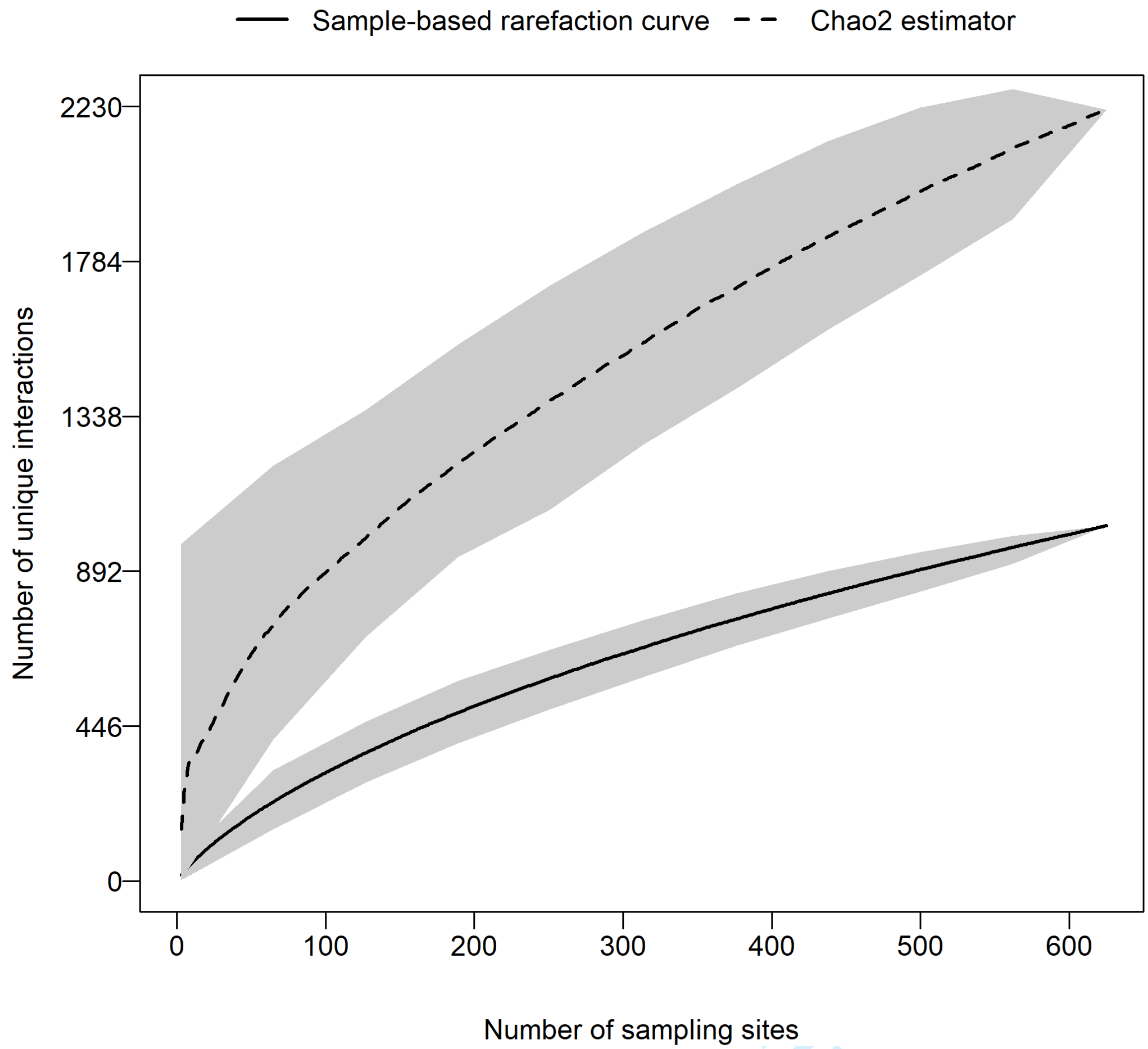

~~**Figure 9.** Number of unique interactions estimated by the Chao2 non-parametric estimator. Plotted values for Chao2 are means of 1,000 permutations per sampling site, with the gray area along the line representing 95% confidence intervals. 95% confidence intervals are also showed for the sample-based rarefaction curve. When all sampling sites are pooled (1,023 unique interactions detected), the estimator suggests that 1,198 unique interactions remain undetected.~~

CLASS III. DATA SET STATUS AND ACCESSIBILITY

A. Status

Latest update: ~~November~~ October 2023~~2~~.

Latest archive date: ~~November~~ October 2023~~2~~.

Metadata status: Last updated in Octo~~Novem~~ber 2023~~2~~, version submitted.

Data verification: Data were compiled as presented in the sources. We corrected transcription errors, checked the geographic coordinates of the study sites, and made taxonomic harmonization of species names.

B. Accessibility

Storage location and medium: The complete data set (in .CSV format) and scripts to replicate the figures of this metadata are available on https://doi.org/10.5281/zenodo.10019756 ~~https://doi.org/10.5281/zenodo.7814543.~~

Contact persons: Natalya Zapata-Mesa (zapatamesan@gmail.com) & Marco A. R. Mello (marmello@usp.br).

Copyright restrictions: Creative Commons Attribution 4.0 International License.

Proprietary restrictions: Please cite this data paper, if the data are used in any kind of publication related to research, outreach, and teaching activities, such as papers, books, book chapters, monographs, bibliographies, reports, patents, posters, talks, keynotes, and lectures.

Costs: None.

CLASS IV. DATA STRUCTURAL DESCRIPTORS

A. Data set file

Identity and s~~ and s~~ize:

BatFly_References.csv 66KB

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BatFly_Sites.csv 142~~2~~KB

BatFly_Sampling.csv 46KB

BatFly_Bat_Pop.csv 334KB

BatFly_Fly_Pop.csv 303KB

Batfly_Species_Interactions.csv 585~~5~~KB

Format and storage mode: Data frames with comma-separated values (.csv).

Header information: See variable description in Variable information section.

Alphanumeric attributes: Mixed.

Special characters/fields: Each table contains a column ~~of~~ named “O~~o~~bservations”. This column may have additional information or comments. For example, in Table 2, Observations column may have additional information about the study site reported by the reference, as a pool of coordinates from a study site.~~This column may have additional information or comments. For example, a pool of coordinates from a study site.~~ “NA” indicates no information available for a given cell.

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B. Variable information

Table 1. BatFly_References: Information ~~about~~ of the references used as data sources in our database.

Variable	Description	Levels	Example
RefCode	Identification code of each reference	BFR001 – BFR179	BFR002
Author	Short name of the author(s); if there are three or more authors, we use *et al.*		Graciolli *et al.*
Year	Year of publication of each reference		2010
Type	Type of reference	Article, Book, Unpublished data	Article

Reference	Full bibliographic reference		Graciolli G., Zortéa M., Carvalho L. F. A. C. (2010) Bat flies (Diptera, Streblidae and Nycteribiidae) in a Cerrado area of Goiás state, Brazil. Revista Brasileira de Entomologia 54: 511-514. https://doi.org/10.1590/S0085-56262010000300025
BatVouchers	Name of the biological collection where voucher bat specimens were deposited		Chiroptera Collection of "Universidade Federal de Goiás, Campus Jataí" (CCUFG)
FlyVouchers	Name of the biological collection where voucher fly specimens were deposited		Zoological Collection of "Universidade Federal do Mato Grosso do Sul"
Associated References	Full bibliographic reference of studies that fully or partially uses the same data of the Reference		Pedro, W.A., Passos F.C. & B.K Lim. 2001. Morcegos (Chiroptera; Mammalia) da Estação Ecológica dos Caetetus, Estado de São Paulo.

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			Chiroptera Neotropical, Brasília, 7: 136-140

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Table 2. BatFly_Sites: Information ~~about~~ of the study sites from the references included in our database.

Variable	Description	Levels	Example
SiteCode	Identification code of each study site. A single publication may contain multiple study sites. Different studies could share the same study site and consequently the same SiteCode	BFA001 – BFA653	BFA002
RefCode	Identification code of each reference	BFR001 – BFR179	BFR002
Country	English name of the country where the study was carried out		Brazil
State	State, Province or Department of the study site as described in the source or identified from its geographic coordinates		Goiás
Municipality	Municipality of the study site as described in the reference or identified from its geographic coordinates		Serranópolis
Locality	Local name of the study site as described in the reference or identified from its geographic coordinates		Reserva Particular do Patrimônio Natural Pousada das Araras
Latitude	Corrected and transformed coordinates of the latitude in decimal degrees (Datum WGS84)		-20.772227
Longitude	Corrected and transformed coordinates of the longitude in decimal degrees (Datum WGS84)		-54.785154
PrecisionClass	Coordinate precision classes of the study site. Precise: coordinates of the grid, transect or vegetation patch are reported in the reference. Not precise: coordinates of	precise, not precise	precise

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	the municipality are reported, or the coordinates do not match the information provided in the reference		
Vegetation	Vegetation type as described in the reference		Tropical rainforest
VegType	Vegetation type according to Oliveira-Filho (2017)		Rainforest
Ecoregion	Ecological region according to Oliveira-Filho (2017)		Cauca Valley montane forests
Domain	Tectonic domain according to Oliveira-Filho (2017)		Northern Andean
Elevation	Elevation above sea level in meters (m) reported in the reference		700
Dataset~~Elevationfrom~~Elevation	~~Meters~~ Elevation above sea level in meters (m), extracted from the GTOPO30 dataset (United States Geological Survey – USGS, 2001. Global 30 arc-seconds Elevation)		700
MeanAnnTemp	Mean annual temperature in Celsius degrees (ºC) from WorldClim 2.1 with 30 arc seconds resolution.		23.3
MeanAnnRain	Mean annual rainfall in millimeters (mm) from WorldClim 2.1 with 30 arc seconds resolution.		1429
Observations	Additional information or comments		

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Table 3. BatFly_Sampling: Information on the sampling methods used to record interactions included in our database~~Information about the sampling and methods in our database~~.

Variable	Description	Levels	Example
SiteCode	Identification code of each study site from each reference. A single publication may contain multiple study sites.	BFA001 – BFA653	BFA002
RefCode	Identification code of each reference	BFR001 – BFR179	BFR002
YearStart	Year of the beginning of sampling		2000
YearFinish	Year of the end of sampling		2001
Duration	Unstandardized duration of sampling (in months)		11
SamplingEffort	Sampling effort, accounting for the area of the mist nets used and the duration of the survey, in hours*square meters (following Straube and Bianconi 2002). Since many studies do not report mist net size or model, this standardized measure is common for comparing bat inventories		13608
BatEcologicalScale	Reported bat assemblage. all: the whole bat species captured was reported. leafnosed: only leaf-nosed bats (Phyllostomidae) were reported. mormoopid: only mormoopid bats (Mormoopidae) were reported. single: a single bat species was reported	all, leafnosed, mormoopid, single	all
FlyEcologicalScale	Reported fly assemblage. a~~A~~ll: the whole fly species capture was reported. Single: a single fly species was reported.	all, single	all
BatSamplingMethod	Method used to capture bats. Direct refers to collection by	direct, harp traps, mist	mist nets

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	hand or devices such as hand nets or harp traps.	nets, hand net	
SamplingNights	Total number of capture nights	0 to 36	10
SamplingHours	Duration of capture per night, i.e., the number of hours the mist nets were kept open each night	1 to 12	1
SamplingMistnets	Number of mist nets used, regardless of manufacturer, type, size, mesh, or material	1 to 14	1
SamplingStrata	Vertical strata of the habitat where bats were captured: understory, from canopy to understory, below canopy, canopy	U, UC, BC, C	U
SamplingSeason	Sampling season reported in the reference	dry, wet, both	wet
Observations	Additional information or comments		

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Table 4. BatFly_Bat_Pop: Information on the bat populations sampled, which were involved in the recorded interactions included in our database~~Information about the bat populations sampled in the references included in our database~~.

Variable	Description	Levels	Example
BatPopulationCode	Identification code of each bat population	BFBPOP001 – BFBPOP2187	BFBPOP001
RefCode	Identification code of each reference	BFR001 – BFR179	BFR001
SiteCode	Identification code of each study site in each reference	BFA001 – BFA653	BFA001
BatFamily	Current scientific name of the bat family		Noctilionidae
BatGenus	Current scientific name of the bat genus		*Noctilio*
BatSpecies	Scientific name of the bat species as reported in the reference		*Noctilio leporinus*
CurrentBatSpecies	Current scientific name of the bat species according to Simmons and Cirranello (2023)		*Noctilio leporinus*
BatSubspecies	Scientific subspecies name of the Bat as reported in the reference (checked and updated)		
BatRoost	Roosting site of the bat species reported in Kunz and Lumsden (2003) and Rodríguez-Durán (2020)	cave, tree cavity, foliage, tent, termite nest, human-made structure	caves
BatCaptureNumber	Total number of captured bats of the population	1 to 3173	25
BatMarks	Whether or not captured bats were marked. For studies where no marks were used,	yes, no	no

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	BatCaptureNumber might include recaptured individuals		
BatFemales	Number of captured bats that are females of the population	0 to 235	11
BatMales	Number of captured bats that are males of the population	0 to 182	21
BatJuvenile	Number of captured bats that are juveniles of the population	0 to 290	41
BatAdult	Number of captured bats that are adults of the population	0 to 127	5
BatLactatingFemales	Number of captured bats that are lactating females of the population. Bats can be lactating and pregnant at the same time	0 to 21	20
BatNonreproductiveFemales	Number of captured bats that are nonreproductive females of the population	0 to 34	3
BatPregnantFemales	Number of captured bats that are pregnant females of the population	0 to 18	4
BatNonreproductiveMales	Number of captured bats that are nonreproductive males of the population	0 to 37	6
BatScrotalTestesMales	Number of captured bats that are males with scrotal testes of the population	0 to 32	30
Observations	Additional information or comments		

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Table 5. BatFly_Fly_Pop: Information on the fly populations sampled, which were involved in the recorded interactions included in our database.~~Information about the fly populations sampled in the references included in our database.~~

Variable	Description	Levels	Example
FlyPopulationCode	Identification code of each bat fly population	BFFPOP001 – BFFPOP2969	BFFPOP001
RefCode	Identification code of each reference	BFR001 – BFR179	BFR001
SiteCode	Identification code of each study site in each reference	BFA001 – BFA653	BFS001
FlyFamily	Current scientific ~~name~~ name of the fly family	Streblidae, Nycteribiidae	Streblidae
FlyGenus	Current scientific ~~name~~ name of the fly genus		*Megistopoda*
FlySpecies	Scientific name of the fly as reported in the reference		*Megistopoda aranea*
CurrentFlySpecies	Current s~~S~~cientific name of the ~~bat~~ fly		*Megistopoda aranea*
Flysubspecies	Scientific subspecies name of the fly as reported in the reference (checked and updated)		
FlyCaptureNumber	Total number of captured flies of the population	1 to 2197	2
FlyFemales	Total number of flies that are females of the population	0 to 1105	20
FlyMales	Total number of flies that are males of the population	0 to 2042	4
FlyUndetermined	Total number of flies that were not sex identified		

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Table 6. Batfly_Species_Interactions: Information ~~about~~ on the bat-fly species-species interactions recorded in our database.

Variable	Description	Levels	Example
InteractionSpeciesCode	Identification code of each species-species interaction record	BFSSI0001 – BFSSI4014	BFSSI0001
BatPopulationCode	Identification code of each bat population	BFBPOP001 – BFBPOP2187	BFBPOP0010
FlyPopulationCode	Identification code of each ~~bat~~ fly population	BFFPOP001 – BFFPOP2969	BFFPOP0015
RefCode	Identification code of each reference	BFR001 – BFR179	BFR004
SiteCode	Identification code of each study site in each reference	BFA001 – BFA653	BFA051
CurrentBatSpecies	Current scientific name of the bat species according to Simmons and Cirranello (2023)		*Noctilio leporinus*
BatSubspecies	Scientific subspecies name of the bat as reported in the reference (checked and updated)		
CurrentFlySpecies	Current scientific name of the ~~bat~~ fly		*Megistopoda aranea*
Flysubspecies	Scientific subspecies name of the fly as reported in the reference (checked and updated)		
TransientInteractionorError	Uncommon association. It may be an association that will not last over time (transient) or the researcher's error in the collection or identification	yes, no	no
NumberInteractions	Number of ~~bat~~ flies captured on the bat species	0 to 2197	2197

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NumberInteractionsByFlyFemales	Number of female ~~bat~~ flies captured on the bat species	0 to 1105	291
NumberInteractionsByFlyMales	Number of male ~~bat~~ flies captured on the bat species	0 to 1091	351
NumberInteractionsByFlyUndetermined	Number of undetermined ~~bat~~ flies captured on the bat species	0 to 2042	781
BatInfested	Number of bats infested with one or more individuals of the fly species	0 to 278	201
BatInfestedFemales	Number of female bats infested with one or more individuals of the fly species	0 to 40	21
BatInfestedMales	Number of male bats infested with one or more individuals of the fly species	0 to 33	33
Prevalence	Prevalence (Number of bats infested divided by the total number of bat captures) as reported in the reference	0 to 100	80
PrevalenceOnBatFemales	Prevalence (Number of female bats infested divided by the total number of bat captures) as reported in the reference	0 to 100	50
PrevalenceOnBatMales	Prevalence (Number of male bats infested divided by the total number of bat captures) as reported in the reference	0 to 100	20
MeanFlyIntensity	The total number of flies of the species parasitizing the bat species divided by the number of individual bats infested with the fly	1 to 4.66	1
MeanFlyIntensityOnBatFemales	The total number of flies of the species parasitizing females of the bat species divided by the number of individual female bats infested with the fly	1 to 8	4
MeanFlyIntensityOnBatMales	The total number of flies of the species parasitizing males of the bat species divided by the number of individual male bats infested with the fly	1 to 2.53	2.1

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MeanFlyAbundance	The total number of flies of the species parasitizing the bat species divided by the number of individual bats (including non-infested individuals)	0 to 24.1	24.1
MeanFlyAbundanceOnBatFemales	The total number of flies of the species parasitizing females of the bat species divided by the number of individual female bats (including non-infested individuals)	0 to 2.6	1.5
MeanFlyAbundanceOnBatMales	The total number of flies of the species parasitizing males of the bat species divided by the number of individual male bats (including non-infested individuals)	0 to 1.6	1
Observations	Information about reference or comments		

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C. Data anomalies: If there is no information available for a specific cell in a given datasheet, it is indicated as ~~if there is no information available for a given cell, this is indicated as~~ "NA".

CLASS V. SUPPLEMENTAL DESCRIPTORS

A. Data acquisition

~~**Data forms or acquisition methods:** The full data set is composed of six data sheets: references, sites, sampling, bat population, fly population, and interactions species-species. The references data sheet has the information of the original sources from the data was obtained. The data sheets sites and sampling contain information about where, when and how the data were collected on each site. The data sheets bat population and~~

~~fly population contain taxonomic identification and information about the populations of interacting species. Finally, the interaction data sheet contains interaction records linked to bat population and fly population, and information about number of bats infested, prevalence, mean fly intensity, and mean fly abundance.~~

Data entry/verification procedures: Screening and data extraction were always performed by the same person. The information included in BatFly's ~~the tables~~sheets, such as codes and scientific names, was validated with logical and set tests implemented in R to reduce typing errors.

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B. Publications and results

Partial data of unpublished reference BFR102 (see Table 1) was used in Pastrana-Montiel, M. R., Ballesteros-Correa, J., & Chacón-Pacheco, J. (2019). First record of the parasite bat fly *Basilia mimoni* Theodor & Peterson, 1964 (Diptera: Nycteribiidae) in Colombia. Oecologia Australis, 23(3).): 685-689. https://doi.org/10.4257/oeco.2019.2303.27

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