

# **FragSAD: A database of diversity and species abundance distributions from habitat fragments**

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## INTRODUCTION

Although habitat loss and fragmentation have long been known to be a threat to biodiversity (e.g., Wallace 1880), it was MacArthur and Wilson's (1967) exposé on island biogeography and its later applications to habitat fragmentation that provided solid theoretical grounds for understanding this threat (e.g., Haila 2002). When formerly large and continuous habitat is transformed by humans into small habitat 'islands' within a matrix of nominally less hospitable landscape, biodiversity can be greatly affected (e.g., Saunders et al. 1991, Ewers and Didham 2006). Indeed, habitat loss and fragmentation are consistently considered to be two of the predominant threats to biodiversity on the planet (Millennium Ecosystem Assessment 2005, Tittensor et al. 2014). As a result of the ubiquitous and conspicuous nature of habitat fragmentation, there have been hundreds of studies on the ecological consequences of habitat fragmentation, including changes to biodiversity and ecosystem functions within the remnant habitats (reviewed in e.g., Saunders et al. 1991, Harrison and Bruna 1999, Collinge 2009, Lindenmayer and Fischer 2013). Nevertheless, debate remains as to the predominant outcomes of these studies (e.g., Fahrig 2003, 2013, 2017, Didham et al. 2012, Hanski 2015, Fletcher et al. 2018, Fahrig et al. 2019).

Some syntheses have claimed that habitat fragmentation has profound effects on biodiversity in the habitats remaining, because of reduced dispersal rates, increased demographic stochasticity and edge effects, and/or increased disturbance rates (e.g., Haddad et al. 2015, 2017, Barlow et al. 2016). Others have claimed that habitat fragmentation might result in biodiversity loss because of habitat loss, but not as a result of differential effects on species in the remaining habitats (e.g., Fahrig 2013). One of the primary reasons for this inconsistency in results is that the variable most typically measured in these studies, species richness, is a highly scale-dependent measure that depends critically on sampling methodology. As a result, quantitative measures of change in diversity (i.e., effect size) depend critically on this sampling methodology and scale, which can create largely incomparable results among studies (e.g., Chase and Knight 2013, Chase et al. 2018).

To be able to more consistently compare and contrast habitat fragmentation studies and their influence on species assemblages, we compiled a set of studies where abundances and

identities of species were available and sampling methodology known. Specifically, our goal was to gather data sets from studies that collected data on an entire species assemblage from large, intact habitats and small fragments within the same region, so that the relative abundances of species could be compared in a consistent way (e.g., using rarefaction curves, estimates of evenness/diversity, etc). Sampling effort was also recorded, so that comparisons can be made more directly and statistical adjustments made if appropriate. Some data sets consisted of a dichotomous comparison of two treatments (e.g., large/intact versus small/fragmented), while others consisted of gradients of habitat area from very large to very small.

We compiled 117 data sets that constitute the largest assembly of data available to compare directly species assemblages in habitat islands of different areas. The compilation includes studies on plants (woody and non-woody) and animals (vertebrate and invertebrate) where the numbers of individuals from standardized sampling protocols were available. Most data sets came from tropical forests, including data on several taxa from the iconic Biological Dynamics of Forest Fragmentation Project in the Brazilian Amazon (see e.g., Laurance et al. 2011), but our compilation includes data from temperate and boreal forests, grasslands, shrublands, and even a wetland system. Note that our data set only includes single temporal snapshot data from studies that have collected data over time.

We explored other similar data compilation efforts. Although ostensibly on a similar topic, our data set has extremely low overlap with another data compilation project on fragmentation effects on biodiversity, BIOFRAG (Pfeifer et al. 2014). The BIOFRAG database has exact location points for each sampling location of fragments within a landscape and as a result restricted the number of data sets from habitat fragments that could be included. Our FragSAD database has less stringent criteria for exact location data, which limits the kinds of questions that can be asked, but allows a broader range of data sets to be included. Furthermore, most of the data sets in BIOFRAG did not meet our criteria for inclusion, which required estimates of habitat fragment area surrounded by a habitat matrix, so that comparisons could be made among a gradient of within patch habitat area. Nevertheless, a few of the studies from BIOFRAG, which is currently not open access, overlap with the criteria for our study. Some of those BIOFRAG studies had data available from the published work, and we included those here by re-extracting the data. Data from one other study where data were not available in the

publication, but present in BIOFRAG, are reproduced here with permission of the data owner (Slade et al. 2013).

We also searched the PREDICTS database (Hudson et al. 2017), which examined species responses to a wide variety of anthropogenic disturbances. Some of those studies also directly fit into our criteria. We do not reproduce those data here, but point the reader specifically to the PREDICTS open access database. Specifically, the relevant studies are Ewers et al. (2007) (only data from within fragments, not the matrix), Caceres et al. (2010), Stouffer et al. (2011), Fernández and Simonetti (2013) (two data sets, one from fragments surrounded by an urban matrix, one from fragments surrounded by an agricultural matrix), and Garmendia et al. (2013) (data from fragments only, not the matrix).

In addition to data on species assemblages from the different forest fragments and the specific nature of sampling, our metadata also include categorical estimates of how long it was from the time the habitats were fragmented (if available), the categories of the quality and condition of the matrix between habitat islands. Given that species identities (or operational taxonomic units when taxa were not specifically identified to species) and their relative abundances are given for each habitat island within a study, these data can be used to estimate within-habitat patterns of biodiversity (number of species per area, relative abundances, etc) and to compare compositional differences among habitat islands that differ in their size. Unfortunately, most studies did not provide explicit information on other landscape variables, such as habitat isolation/connectance to other habitat types. However, this could be estimated for many of the data sets using information from the publication and/or independently from geospatial data if one wanted to extend the database to be more informative for landscape-level questions.

## **METADATA**

### CLASS I. DATA SET DESCRIPTORS

#### A. Data set identity

Title: FragSAD: A database of diversity and species abundance distributions from habitat fragmentation studies

#### B. Data set identification code

Data available on the Dryad Digital Repository: <https://doi.org/10.5061/dryad.595718c>.

Suggested data set identification codes:

*metadata\_utf8.csv*

*abundances\_utf8.csv*

#### C. Data set description

##### 1. Originators

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##### 2. Abstract

The data set consists of 117 studies that examined how species assemblages varied across habitat patches that were fragmented, but differed in their area. Studies included sampled species assemblages from at least 2 patch sizes (typically replicated), and ranged to as many as 53 habitat patches in a given study (median number of patches per study was 10). Details of each individual study, including full reference, biogeographic data (coordinates, biome, climate,

continent, etc) and sampling details are provided in the metadata table. A second table provides the patch and plots names, and the name and abundance of species present. Both tables have a common identifying column called *refshort* allowing one-to-many matches comparably to a relational database structure. Here we overview the structure of the entire data set. There are no copyright restrictions. Please cite this data paper and the associated Dryad data set (doi:10.5061/dryad.595718c) if the data are used in publications.

Figure 1 illustrates the geographic distribution of the studies. The majority (76/117) of studies come from tropical forests in Central and South America, with 37 studies coming from Brazil alone. Other continents were more-or-less equally represented, with 13 studies in Africa, 20 in Asia, 14 in Europe and 5 in North America. Studies in temperate regions of North America (e.g., Canada) and Asia (e.g., Russia, China) were conspicuously sparse. Note, in several instances, more than one study was taken from the same location (habitat fragments); in these cases, different taxa were measured from the same sites.

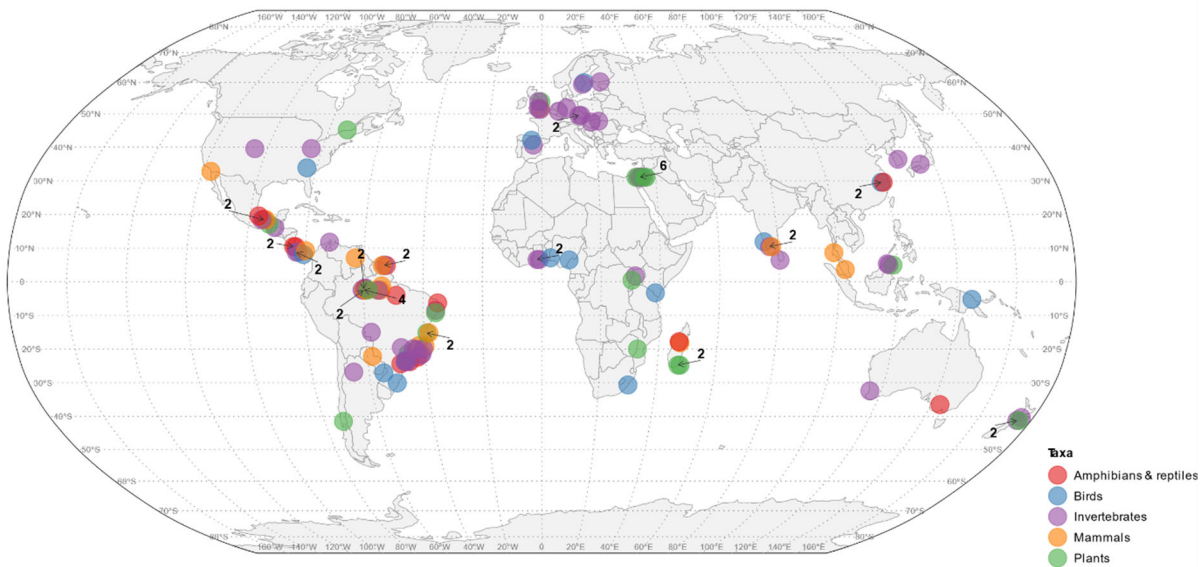


Figure 1. Geographic location of each data set. Colors indicate different categories of taxa that were the focus of the study. Some sites had multiple data sets from a single set of fragments, and these are indicated by a number pointing to a given point.



The majority of studies were from forested biomes (101/117 data sets). There were also studies from shrubland/steppe (12), grasslands (3), and one study from a fragmented wetland system (Guadagnin et al. 2005). Figure 2 consists of photos from some of the field sites.

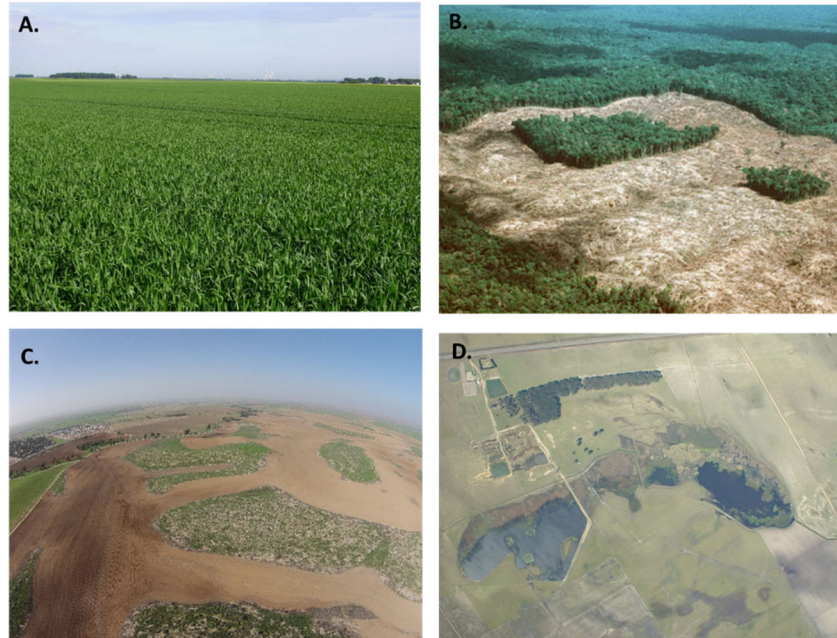


Figure 2. Photos of some representative sites included in FragSAD A. Forest fragments in the distance amidst an agricultural matrix in western Germany (from Kappes et al. 2009; Photo credit: Heike Kappes). B. Two of the experimental fragments within the Biological Dynamics of Forest Fragments Project near Manaus, Brazil where several data sets were collected (Photo credit: Richard Bierregaard). C. Israel scrub habitat surrounded by an agricultural matrix where several data sets were collected (Photo Credit: Yaron Ziv). D. Aerial view of fragmented wetlands of southern Brazil (from Guadagnin et al. 2005; photo credit: Demetrio Luis Guadagnin)

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Almost one-half of the studies (54/117) in our database were for invertebrate assemblages, and most (42) of those studies were on insects (15 on beetles, 9 on moths and butterflies, 9 on bees and the rest on different groups). Spiders and harvestmen (8 studies) and mollusks (2 studies) made up the remainder of invertebrate studies. There were 19 studies on mammals, 11 of which were on small and medium sized mammals (mostly rodents), 7 of which were on bats and one on large mammals. There were 16 studies on birds. There were 13 studies

on amphibians and reptiles, which were often studied and captured together (though some also targeted species groups, such as frogs, lizards or snakes). And there were 15 studies on plants, 14 of which were on seed plants, 1 on ferns and 2 on bryophytes.

#### D. Key words

Disturbance; habitat fragmentation; habitat loss; species abundance distribution; species-area relationship; species richness

### CLASS II. RESEARCH ORIGIN DESCRIPTORS

#### A. Overall project description

1. Identity: Same as above.
2. Originators: Same as above.
3. Period of study

Collection of published data ranges from the 1980s to 2018

#### 4. Objectives

We compiled this data set to gather widely spread information on the effect of habitat fragmentation on abundances of species within assemblages, and make it readily available in a single database. Our immediate objectives were to develop this database for use to examine key hypotheses about the influence of habitat fragment size on biodiversity variables, while controlling for sampling and scale. However, we expect that the data set will be useful for a number of questions and analyses addressing fragmentation effects on species and communities.

#### 5. Abstract

Habitat destruction is the single greatest anthropogenic threat to biodiversity. Decades of research on this issue have led to the accumulation of hundreds of data sets comparing species

assemblages in larger, intact, habitats to smaller, more fragmented, habitats. Despite this, little synthesis or consensus has been achieved, primarily because of non-standardized sampling methodology and analyses of notoriously scale-dependent response variables (i.e., species richness). To be able to compare and contrast the results of habitat fragmentation on species' assemblages, it is necessary to have the underlying data on species abundances and sampling intensity, so that standardization can be achieved. To accomplish this, we systematically searched the literature for studies where abundances of species in assemblages (of any taxa) were sampled from many habitat patches that varied in size. From these, we extracted data from several studies, and contacted authors of studies where appropriate data were collected but not published, giving us 117 studies that compared species assemblages among habitat fragments that varied in area. More than half (76) came from tropical forests, but there were many studies from temperate forests and grasslands from all continents except Antarctica. Fifty-four of the studies were on invertebrates (mostly insects), but there were several studies on plants (15), birds (16), mammals (19), and reptiles and amphibians (13). We also collected qualitative information on the length of time since fragmentation. With data on total and relative abundances (and identities) of species, sampling effort, and affiliated meta-data about the study sites, these data can be used to more definitively test hypotheses about the role of habitat fragmentation in altering patterns of biodiversity.

## 6. Sources of funding

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## B. FragSAD database project description

### 1. Site description

Data sets comprise studies from all continents except Antarctica, as well as some near continent islands (Figure 1). Studied ecosystems are fragments of different areas isolated from each other by a more or less impassable matrix, e.g. forest fragments separated by intensive agricultural fields.

### 2. Experimental or sampling design

This data set provides exclusively data obtained from published papers.

### 3. Research methods

#### *Data acquisition*

Given that we required a very specific and detailed kind of data for this meta-study (i.e., species abundance data from different sized habitat islands from within a given study), we cast as broad a net as possible to find potentially appropriate studies. Our first approach was to systematically search the literature using Google Scholar with combinations of key words including “fragment\*”, “habitat loss”, “area”, “island”, “matrix”, “diversity”, “richness”, “abundance”. Titles, and if promising, abstracts were scanned to determine whether the appropriate data were potentially available. We scanned methods, tables, figures and appendices to determine whether data were provided in the paper itself (or in an associated data repository such as Dryad). If so, data were extracted and harmonized using a variety of tools. For a study to be included, it needed to clearly report the abundance of individual species within assemblages of sampled species, sampling methods, survey design and fragment sizes. When an appropriate study was found, we also followed the papers that cited that paper, as well as papers cited by that study, in order to broaden our pool of possible data sets available. Searches were conducted over a period from 2014-2019. During this time, networks of colleagues also pointed us to other potential studies, which we scanned as above.

Data from more than 40 studies were available in published papers, appendices or associated repositories. When it was clear from the methods that the necessary data were likely

collected (i.e., information on species abundances), but the data were not present in the paper itself (or in various data repositories), we contacted authors directly asking whether they could provide the necessary data. In total, we contacted authors of more than 200 studies that appeared to fit our criteria. Of those, about one-third provided the data needed and most are listed as co-authors here (others did not respond or were not able/willing to provide the data). As described above, data from five studies that meet the same criteria are available in the open access PREDICTS database (Hudson et al. 2017).

### *Data harmonization*

Each data set consisted of data on abundances of species within an assemblage where multiple habitat fragments could be delineated and measured. Fragment areas were typically given in text (or sometimes by the authors) and units of hectares. Sometimes, the largest areas were defined with a rough value in text, in which case this value was kept as the site size. Other times, no values were given, in which case, fragment size was coded as ‘continuous’. For most analyses, exceptionally large areas with a defined area (e.g., >10,000 ha) are effectively the same as studies where the reference was coded as ‘continuous’.

Each data set consisted of comparable sampling events where an assemblage (i.e., group of species) readily sampled using the same methodology were targeted. Sampling events included, among others, quadrats for enumerating plants, traps (e.g., pitfall traps, live traps, mist nets) for catching animals, and transects for counting birds or mammals, and numerous other methods. Sampling methods are provided in the metadata table in 14 dedicated columns describing sampling effort, methods, devices, intensity, hierarchy, density and duration. Because of the complex and highly divergent ways in which data were collected for each study, we do not try to quantify sampling effort in any sort of standardized way (e.g., per unit area) for comparisons *across* studies. For example, even when studies collect the same kinds of organisms (e.g., frogs) using the same kinds of sampling devices (e.g., pitfall traps) one study might sample along a transect every 10 meters, and another every 5 meters. Even the size of the sample varies considerably among studies (e.g., different sized pitfall traps left out for different amounts of time). Therefore, we made no attempts to standardize to a realistic number for comparisons among studies, and strongly caution against attempts to do so.

Although we did not attempt to harmonize data among studies, we spent considerable attention to try to account for sampling effort within studies so that appropriate standardizations could be made. Here, in addition to requiring data on the abundance of each individual of each species sampled in a given assemblage, we required there to be information on the sampling effort the investigator put into sampling the assemblage in each habitat fragment, and used similar methodology. Although such standardization is highly heterogeneous in the literature (which is why synthesis heretofore was not possible), it is essential for comparing abundances and diversities among fragment sizes within studies. Sampling effort critically influences comparisons of diversity estimates among habitat fragments that differ in area (Chase et al. 2019). For the studies that we collated, there were generally three qualitatively distinct situations regarding sampling effort among sites:

- In most cases (74), sampling was standardized among fragments. That is, the same sampling effort was used in small and large fragments. In these cases, the *sampling\_effort* column is labelled as '1' for all fragments within a study to denote equal sampling. In these cases, *sampling\_effort\_unit* is labeled as 'balanced'.
- In three cases, the entirety of fragments was sampled (or large areas within continuous areas). Here, sample effort is simply proportional to fragment size (i.e., a fragment 2x the size of another fragment also had 2x the sampling effort), and *sampling\_effort* typically gave the area of the fragment.
- In all other cases (40), sampling was variable among different sized fragments. Typically, but not always, sampling increased semi-proportional to habitat size. In these cases, *sampling\_effort* was measured by the authors, usually as the duration of the sampling. *sampling\_effort\_unit* gives the proper unit and it is the same for all sites of a given study.

The variable *sampling\_design* indicates the sampling structure and data organization as best as could be gleaned from the study. In some cases, multiple plots/samples were taken per fragment and this information was available, in which case *sampling\_design* was coded as *standardized\_fragment* or *standardized\_subsamples*. In other cases, plots/samples in a given fragment were pooled and *sampling\_design* is coded as *pooled*. When pooled, the *sample\_effort*

column can be used to standardize effort. When separated, the numbers of samples should be considered for standardization to an average per sample. Regarding sampling design and methods, as much information as possible was extracted from papers or obtained from authors directly, and organized in dedicated variables (variable definitions in Table 1).

For several cases, we were only able to glean data from the published paper itself (attempted contacts with authors of the paper did not result in raw data). Here, it was often the case that averages, or compilations, of data were provided. For example, averages or totals from small fragments were given in one column and large or continuous habitats in another column. In these cases, we simply reported the data as reported in the published work, as well as the respective sampling effort, though some information is missing (e.g., within fragment variation).

Sampling effort value and unit are provided in *metadata\_utf8.csv* as well as several variables describing the sampling design and methods. All site per species data sets obtained from papers cited below were aggregated in a long format table (*abundances\_utf8.csv*) in which each row corresponds to one record of a species in a given site and plot (Table 2). Each record hence provides identifiers for the paper, the site and the plot besides scientific name and abundance value. The definitions for variables in *metadata\_utf8.csv* and *abundances\_utf8.csv* are given in Table 1 and Table 2 respectively.

In addition to recording the location and taxa sampled for each data set, we qualitatively categorized studies according to two criteria that could influence biodiversity responses: (1) We categorized studies in three categories based on the time elapsed following habitat fragmentation (when the sampling occurred), including ‘recent’ (fragmentation occurred less than 20 years previous to the study), ‘intermediate’ (fragmentation occurred 20-100 years previous to the study), and ‘long’ (fragmentation occurred more than 100 years previous to when the study took place). (2) We categorized studies into three groups based on the quality of the matrix in between habitat fragments, as described by the authors in their papers. This included three qualitative categories: ‘light’, where remnant habitat fragments were surrounded by a matrix of relatively hospitable habitats (e.g., second growth forest, shade grown coffee); ‘intermediate’, where remnant habitats occurred within a matrix of different, but relatively lightly used habitats (e.g., forests surrounded by successional gradients or livestock grazing); and ‘harsh’ where remnant

habitats occurred within a matrix of relatively inhospitable matrix (e.g., intense agriculture, water when reservoirs were built, leaving behind islands).

### *Sources*

We gathered 117 data sets from 108 individual studies. Data sets stem from the following sources: Aguiar and Gaglione 2012, Aizen and Feinsinger 1994, Almeida-Gomes and Rocha 1994, Amaral Nogueira and Pinto-da-Rocha 2016, Andresen 2003, Báldi and Kisbenedek 1999, Barradas Paciencia and Prado 2005, Baz and Garcia-Boyero 1995, Bell and Donnelly 2006, Benedick et al. 2006, Benítez-Malvido et al. 2016, Berg 1997, Bernard and Fenton 2007, Bolger et al. 1997, Bossart and Antwi 2016, Bossart et al. 2006, Bragagnolo et al. 2007, Brosi et al. 2008, Brosi et al. 2009, Cabrera-Guzmán and Reynoso 2012, Cadotte et al. 2002, Carneiro et al. 2016, Cayuela et al. 2006, Chiarello 1999, Cosson et al. 1999, da Fonseca and Robinson 1990, Dami et al. 2013, Dauber et al. 2006, Davies et al. 2003, de La Sancha 2014, de Souza and Brown 1994, Dickman 1987, Didham et al. 1998, Ding et al. 2013, Dixo and Metzger 2009, Dominguez-Haydar and Armbrecht 2011, Echeverría et al. 2007, Edwards et al. 2010, Estrada and Coates-Estrada 2002a, Estrada and Coates-Estrada 2002b, Filgueiras et al. 2011, Fujita et al. 2008, Gavish et al. 2012, Gibson et al. 2013, Giladi et al. 2011, Giraudo et al. 2008, Gonçalves-Souza et al. 2007, Goodman and Rakotondravony 2000, Guadagnin et al. 2005, Halme et al. 1993, Henry et al. 2007, Horváth et al. 2009, Jauker et al. 2019, Jung et al. 2014, Jyothi and Nameer 2015, Kapoor 2008, Kappes et al. 2009, Klein 1989, Knapp and Řezáč 2015, Lambert et al. 2003, Lasky and Keitt 2010, Lima et al. 1999, Lima et al. 2015, Lion et al. 2014, Lion et al. 2016, Lövei 2000, Mac Nally and Brown 2001, Manu et al. 2007, Martensen et al. 2012, McCollin 1993, McIntyre 1995, Meyer and Kalko 2008, Montgomery 2014, Nemésio and Silveira 2007, Nemésio and Silveira 2010, Neuschulz et al. 2011, Nufio et al. 2009, Nyeko 2009, Nyelele et al. 2014, Owen 2008, Pardini 2004, Pineda and Halfpeter 2004, Raheem et al. 2009, Rocha et al. 2017, Sam et al. 2014, Savilaakso et al. 2009, Schnitzler 2008, Silva and Porto 2009, Silva et al. 2016, Silveira et al. 2015, Slade et al. 2013, Sridhar et al. 2008, Stireman et al. 2014, Storck-Tonon and Peres 2017, Struebig et al. 2008, Tellería and Santos 1995, Tonhasca et al. 2003, Uehara-Prado et al. 2007, Ulrich et al. 2016, Usher and Keiller 1998, Vallan 2000, Vasconcelos et al. 2006, Vieira et al. 2009, Vulinec et al. 2008, Wang et al. 2012, Williams 2011, Zartman 2003, Ziter et al. 2013.



### C. Data limitations and potential enhancements

#### *Sampling effort*

Measures of diversity depend critically on sampling effort. Therefore, one must carefully consider the issue of sampling effort when using these data, particularly for meta-analyses and comparisons among studies. At least two issues associated with sampling must be carefully considered when using these data to make inferences and comparisons:

1) Sample grain and extent of a study can greatly influence the diversity measured in a given site, as does the difference in diversity among sites (e.g., small vs large fragments). This data set is intended primarily for comparisons within studies, where similar sampling strategies were used even if sampling effort was different. Thus, care must be taken to standardize sampling effort (e.g., via rarefactions) to make meaningful comparisons.

2) As described above, we discourage attempts to combine data from these studies with heterogeneous sampling designs. For example, if some sampling strategies are more prone to capture some types of species (i.e., more common or mobile species), whereas other sampling strategies are more prone to capture other types of species (i.e., rarer or more sedentary species), combining them into a single analysis can produce bias in comparisons. Even studies of the same taxa often used different sampling methodologies (e.g., visual surveys vs baited traps), different intensities, different seasons, and were otherwise variable in a number of sampling approaches.

#### *Space for time*

Also inherent to data we compiled are implicit assumptions associated with substituting space for time. That is, when comparing patterns of biodiversity from smaller to larger fragments, we often infer some sort of dynamical process of biodiversity change that happened as a result of fragmentation. This is because we do not typically have the temporal data on biodiversity change as larger habitats are fragmented into smaller habitats (e.g., Fukami and Wardle 2005, Ewers et al. 2013). Instead, we assume that small fragments are a reasonable comparison of what might have happened during the transition from large/intact habitats to smaller/fragmented habitats. Although this is a very frequent approach, it is important to

recognize that we are making several assumptions (e.g., homogeneity of habitat prior to fragmentation) when making these comparisons.

#### *Taxonomy and systematics*

Species names or broader taxonomic groupings are not standardized among studies. Instead, we have simply provided the data as given and analyzed in the original studies. Certainly, a taxonomic backbone among studies would enhance the utility of the data set for certain purposes. However, again we emphasize that the main purpose of this data set is for comparison within data sets and then comparisons across those (e.g., synthetic meta-analyses). Thus, we do not feel that taxonomic standardization among studies is necessary, and would be extremely difficult or impossible in many cases. Importantly, a number of data sets do not provide the full latin binomial of all species encountered, and in many cases, operational taxonomic units (OTUs) are provided. This was especially true for studies on invertebrates, wherein identifications can be extremely difficult, especially for immature individuals. We feel that their inclusion in this database is useful, however, as this is a standard practice in local community ecology studies, while we have to trust the investigator that individuals given a particular OTU code are consistent within a given study (but not across studies). In most such cases, identifications could be made to genus or in rarer cases, higher taxonomic categories (e.g., family). For clarity, common abbreviations (e.g. sp., msp. (morphospecies), var., aff., cf.) were homogenized and misprints in scientific names were corrected.

#### *Missing data and habitat/geographical bias*

Our data set represents the largest compilation of fragmentation studies available. Nevertheless, there are many relevant studies for which data are not listed in the compilation. First, although we cast as broad a net as possible during our literature searches, we did not find all of the studies available in the literature. Even though we did the majority of our searches during an intense period in 2016, we serendipitously continued to find studies with relevant data in subsequent years. Second, although we attempted to contact all authors from studies we did find, we received negative or no response from more than 70 studies with possibly appropriate data; we hope to continue adding these and other relevant studies to the database in the future. Third, as can be seen from Figure 1, there is a clear geographical bias in the location of the

studies that we did find, although a similar geographical bias is present in almost all such data complications. Fourth, the majority of studies in our compilation are from tropical forests. Ideally, we would target more studies from temperate and boreal forests, and from grasslands and shrublands, to be able to compare fragmentation responses among biome types as well.

Nevertheless, despite these limitations (most of which are inherent to any meta-study or compilation), our compilation brings together a massive amount of data and effort into one easily accessible database. We hope this represents a useful resource for a number of projects that can analyze these data directly, and/or build on this data compilation towards novel future objectives.

### CLASS III. DATA SET STATUS AND ACCESSIBILITY

#### A. Status

1. Latest update: April 2019
2. Latest archive date: July 2019
3. Metadata status: Last updated July 2019, version submitted
4. Data verification: Data verification process was followed until July 2019

#### B. Accessibility

1. Storage location and medium: The data set is provided open access on the Dryad Data Repository.
2. Contact person: Jonathan Chase ([jonathan.chase@idiv.de](mailto:jonathan.chase@idiv.de))
3. Copyright restrictions: None
4. Proprietary restrictions: Please cite this data paper and the associated Dryad data set ([doi:10.5061/dryad.595718c](https://doi.org/10.5061/dryad.595718c)) if the data are used in publications.
5. Costs: None

## CLASS IV. Data structural descriptors

### A. Data set files

#### 1. Identity

*metadata\_utf8.csv*

*abundances\_utf8.csv*

#### 2. Size

*metadata\_utf8.csv*; 2074 rows (excluding the header row), 33 columns; one row=one plot; 1437.88 kbytes

*abundances\_utf8.csv*; 43571 rows (excluding the header row), 7 columns; one row=one species record; 2809.16 kbytes

#### 3. Format and storage mode

Both tables are available as comma-separated values text tables (\*.csv), column-separator is ',', field quoting character is '"'. To ensure that all author names and site names are correctly written, UTF-8 encoding was used. As a consequence, both files contain many special characters that will not be correctly displayed if encoding is not set to UTF-8. For the same reason, the relationship between both tables based on *refshort*, *site\_id* and *plot\_id* will not work if encoding is not properly set for both tables.

If files appear to be corrupted, file integrity can be checked using md5 checksums, either online (e.g. using <http://onlinemd5.com/>) or in R using the command `tools::md5sum()`.

- *metadata\_utf8.csv*; file integrity md5 checksum:  
"de248d74a7d2140e6507d56b92aaa557"
- *abundances\_utf8.csv*; file integrity md5 checksum:  
"361e67626e01373891653cdd2572b6ce"

#### 4. Header information

See section Class IV, B. Variable information for a complete description.

#### 5. Alphanumeric attributes

Mixed

### B. Variable information

#### 1. Metadata and sampling descriptions: *metadata\_utf8.csv*

This file contains metadata concerning the identity, origin, environmental characteristics and sampling information of the data sets. Variable definitions are provided below in Table 1.

Table 1: Variables of the *metadata\_utf8.csv* table.

<b>Variable</b>	<b>Variable definition</b>	<b>Datatype</b>
id	Row number	numeric
refshort	Unique identifier built following the pattern “Author_year”. When several study cases were extracted from a single article, a letter was added to the identifier.	categorical
reference	Full reference of the original study.	string
country	Country where the study was conducted.	categorical
climate	Climate type in the studied area. Can be either <i>Tropical</i> (absolute latitude < 23.5°) or <i>Temperate</i> .	binary
continent	Continent where the study was conducted: Africa, Asia, Europe, North America, Oceania, or South America.	categorical

latitudeN	Latitude North of the approximate study location (decimal degrees, WGS 84).	numeric
longitudeE	Longitude East of the approximate study location (decimal degrees, WGS 84).	numeric
environment_type_fragment	Description of the fragment environment. Can be either <i>terrestrial</i> or <i>aquatic</i> .	binary
environment_type_matrix	Description of the matrix surrounding the fragments. Can be either <i>terrestrial</i> or <i>aquatic</i> .	binary
biome	Biome of the study region.	categorical
taxa	Name of the taxa investigated. Can be either <i>Arthropoda</i> (one study sampled all available Arthropods), <i>Insecta</i> , <i>Arachnida</i> , <i>Mollusca</i> , <i>Amphibia &amp; Squamata</i> , <i>Aves</i> , <i>Mammalia</i> , or <i>Plantae</i> .	categorical
time_since_fragmentation	Time between fragmentation and investigation of the original study.	categorical
matrix_category	Describes the matrix between fragments depending on its susceptibility to impair species dispersion. Can be <i>light filter</i> (e.g. light secondary forest, crops, etc), <i>intermediate</i> or <i>harsh filter</i> (intense agriculture, urban, flooded area, etc).	categorical
site_id	Original site name.	string
plot_id	Within site plot number.	integer
site_size	Site area in hectares. Can be either a numerical value or <i>continuous</i> .	numeric / categorical

sampling_design	Describes how community abundances are given depending on whether plots were the same size or not, or whether subsamples were pooled or not (see section Data harmonization for details). Can be either <i>pooled</i> , <i>standardized_fragment</i> or <i>standardized_subsamples</i> .	categorical
sampling_method	Broad description of the sampling method used. Can be <i>trap</i> , <i>net</i> , <i>bird survey</i> , <i>visual search</i> , <i>manual sampling</i> or <i>combined methods</i> .	categorical
method_category	Sub-categories describing sampling methods. Traps can be <i>pitfall traps</i> , <i>scented traps</i> , <i>pan traps</i> and <i>nets</i> can be <i>sweep nets</i> , <i>entomological nets</i> or <i>mist nets</i> , etc.	categorical
sampling_device_size	Size of sampling devices: diameter of pitfall traps, mesh size of nets, diameter of sweep net etc.	numeric
device_size_unit	Unit of the measure of the sampling device and additional information on the sampling devices.	string
intensity	If sampling is hierarchical within blocks (plots, transects, etc), intensity gives the number of traps, nets, listening points per block. If sampling design is not hierarchical, <i>intensity</i> gives the size of sampled areas (transect length, plot area, etc).	numeric / string
intensity_unit	Unit of the measure of sampling intensity (if hierarchical, <i>pitfalls per transect</i> , <i>traps per plot</i> , etc.; if non-hierarchical, <i>m<sup>2</sup> quadrat</i> , <i>minutes walking</i> , etc) and additional information.	string

block_type	Type of block in a hierarchized design. Most common block types are <i>transect</i> , <i>plot</i> and <i>grid</i> . Transects are only considered a block when they are lined with traps or nets but not when they are a line along which an observer walks.	categorical
number_of_blocks_per_site	Number of blocks per site in hierarchized designs or left empty in non-hierarchized studies.	numeric
sampling_density	If sampling is hierarchical within blocks, <i>density</i> gives the density of sampling unit inside blocks. If sampling design is not hierarchical, <i>density</i> gives the density of sampling units inside the fragment.	numeric / string
density_unit	Gives the unit as “per fragment” or “per transect” and additional information.	string
sampling_duration	Duration of either each sampling events or survey (equivalent to a parent event), or number of surveys.	numeric
duration_unit	Unit of time ( <i>night</i> , <i>month</i> , <i>year</i> , etc) used for duration or additional information on the duration of each sampling event.	string
sampling_effort	Sampling effort per <i>site</i> (usually a plot, sometimes a whole site or mean values of several plots), measured as sampling hours per site, traps per site, or size of the site. Equal to 1 if the sampling effort is balanced among all plots in the data set.	numeric
sampling_effort_unit	Unit of the sampling effort corresponds to hours of walking, number of nets, area of the site, etc. If sampling effort is the same between all fragments, <i>balanced</i> is given.	string



sampling_note	Free text field summarizing details on sampling design and methods.	string
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2. Species per site records: *abundances\_utf8.csv*

The *abundances\_utf8.csv* table gives species records in sites. The three columns after *id* are hierarchized identifiers describing the study (*refshort*), the site or fragment name (*site\_id*), and the plot number (*plot\_id*).

Table 2: Variable definitions of *abundances\_utf8.csv*.

Variable	Variable definitions	Datatype
id	Row number	numeric
refshort	Unique id built following the pattern “Author_year”. Same entries as the <i>refshort</i> column of the metadata table.	categorical
site_id	Original name of the site: either a continuous forest site or a fragment.	categorical
plot_id	Plot-identifier of a sampling plot or a transect. If only one plot per site, 1 is given.	categorical / integer
scientific_name	Species names or species codes as given in the original publication or reviewed for misprints (details in section Taxonomy and systematics).	categorical
abundance	Abundance of a given species in a given plot.	numeric
tsn	Taxon code obtained from the ITIS database (Taxonomic Serial Number) when available.	categorical

## C. Data anomalies

If no information is available for a given record, the field contains “NA”.

## CLASS V. Supplemental descriptors

### A. Data acquisition

#### 1. Data forms or acquisition methods

Acquisition method is fully described in section Data acquisition in Class II, B, 3. Research Methods.

#### 2. Data entry verification procedures

Data entry was systematically checked to ensure that no typing or copy-pasting mistakes were transported to the final version of the data set. This thorough visual check allowed us to detect most mistakes such as software confusing a “l” letter for a “1” number or special characters at the end of species names (<sup>a</sup>, <sup>l</sup>, \*, †, etc.).

### B. Quality assurance/quality control procedures

Once all individual data sets were extracted and harmonized, they were aggregated into a single data set. With this, we again checked for missing, duplicate and erroneous entries. Misprints in scientific names were corrected and abbreviations were homogenized using regular expressions implemented in R (details in section Taxonomy and systematics). For example, spacing misinterpretation errors were identified and corrected.

### C. Related materials

No additional material.

## D. Computer programs and data-processing algorithms

We entered data within Microsoft Excel (2019 and previous versions). Data manipulation and verification was made using R version 3.6.0 (R Core Team 2019). No data transformations were made except when area or coordinate unit conversions were needed.

## E. Archiving

### 1. Archival procedures

The FragSAD data set was prepared with the objective of making it open-access and useful to the greater scientific community. The FAIR data principles were kept in minds to make it Findable, Accessible, Interoperable and Re-usable. Hence, the data set will be catalogued online following standard and searchable metadata, the data set will be made available open-access on Dryad repository, the data set is constituted of files in open formats only, and the data set structure and description ensure that it will be comprehensible and usable.

### 2. Redundant archive sites

The data set will be made available online on Dryad data repository. Following the Dryad rules, the data set will be associated to descriptive readme files describing the definition of variables. The DOI attributed to the data set is: doi:10.5061/dryad.595718c.

## F. Publications and results

No published results yet.

## G. History of data set usage

### 1. Data request history

The impetus for us to aggregate this data set came from our desire to address a number of questions that could not be addressed without more detailed data than was available in most publications, and to mobilize and make available a number of crucial data sets. The data set will be used in a number of forthcoming analyses by members of our team. FragSAD has not yet been shared or used outside of the team.

## 2. Data set update history

Since the beginning of this project, the data set has steadily grown and become more standardized and interoperable.

## 3. Review history

Comments from two reviewers (Rob Ewers and an anonymous reviewer) helped improve the structure and value of the data set. In addition, all of the co-authors on this data paper have helped to ensure their own data are adequately described and accurate.

## 4. Questions and comments from secondary users

The discrepancies between taxonomic names used in data sets extracted from different studies was raised as a limitation since it impairs between-study diversity analyses and species level analyses. This confirms our warnings from section Class II, C. Data limitations and potential enhancements.

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