Nine simple ways to make it easier to (re)use your data

Ethan P. White, Elita Baldridge, Zachary T. Brym, Kenneth J. Locey, Daniel J. McGlinn, and Sarah R. Supp

Ethan P. White (ethan.white@usu.edu), Dept. of Biology and the Ecology Center, Utah State University, Logan, UT, USA, 84341

Elita Baldridge (elita.baldridge@usu.edu), Dept. of Biology and the Ecology Center, Utah State University, Logan, UT, USA, 84341

Zachary T. Brym (zachary.brym@usu.edu), Dept. of Biology and the Ecology Center, Utah State University, Logan, UT, USA, 84341

Kenneth J. Locey (kenneth.locey@usu.edu), Dept. of Biology, Utah State University, Logan, UT, USA, 84341

Daniel J. McGlinn (daniel.mcglinn@usu.edu), Dept. of Biology and the Ecology Center, Utah State University, Logan, UT, USA, 84341

Sarah R. Supp (sarah.supp@usu.edu), Dept. of Biology and the Ecology Center, Utah State University, Logan, UT, USA, 84341

Abstract

Sharing data is increasingly considered to be an important part of the scientific process. Making your data publicly available allows original results to be reproduced and new analyses to be conducted. While sharing your data is the first step in allowing reuse, it is also important that the data be easy to understand and use. We describe nine simple ways to make it easy to reuse the data that you share and also make it easier to work with it yourself. Our recommendations focus on making your data understandable, easy to analyze, and readily available to the wider community of scientists.

Introduction

Sharing data is increasingly recognized as an important component of the scientific process (Whitlock et al. 2010). The sharing of scientific data is beneficial because it allows replication of research results and reuse in meta-analyses and projects not originally intended by the data collectors (Parr and Cummings 2005, Poisot et al. 2013). In ecology and evolutionary biology, sharing occurs through a combination of formal data repositories like GenBank (http://www.ncbi.nlm.nih.gov/genbank/) and Dryad (http://datadryad.org/), and through individual and institutional websites.

While data sharing is increasingly common and straightforward, much of the shared data in ecology and evolutionary biology are not easily reused because they do not follow best practices in terms of data structure, metadata, and licensing (Jones et al. 2006). This makes it more difficult to work with existing data and therefore makes the data less useful than it could be (Jones et al. 2006, Reichman et al. 2011). Here we provide a list of 9 simple ways to make it easier to reuse the data that you share.

Our recommendations focus on making your data understandable, easy to work with, and available to the wider community of scientists. They are designed to be simple and straightforward to implement, and as such represent an introduction to good data practices rather than a comprehensive treatment. We contextualize our recommendations with examples from ecology and evolutionary biology, though many of the recommendations apply broadly across scientific disciplines. Following these recommendations makes it easier for anyone to reuse your data including other members of your lab and even yourself.

1. Share your data

The first and most important step in sharing your data is to share your data. The recommendations below will help make your data more useful, but sharing it in any form is a big step forward. So, why should you share your data?

Data sharing provides substantial benefits to the scientific community (Fienberg and Martin 1985) and the researchers sharing the data. For the scientific community it allows 1) the results of existing analyses to be reproduced and improved upon (Fienberg and Martin 1985, Poisot et al. 2013), 2) data to be combined in meta-analyses to reach general conclusions (Fienberg and Martin 1985), 3) new approaches to be applied to the data and new questions asked using it (Fienberg and Martin 1985), and 4) approaches to scientific inquiry that could not be considered without broad scale data sharing (Hampton et al. 2013). As a result, data sharing is increasingly required by funding agencies (Poisot et al. 2013, e.g., NSF, NIH, NSERC, FWF), journals (Whitlock et al. 2010), and potentially by law (e.g. FASTR, OSTP Policy). For data collectors, data sharing provides credit for publication of data products (Poisot et al. 2013) and can increase citation metrics (Piwowar et al. 2007, Piwowar and Vision 2013). In addition, data that are well-documented and standardized make future reuse easier for the original investigator.

Despite these potential benefits to the community, individual incentives have historically been insufficient to encourage widespread data sharing. Reluctance to share data is largely due to concerns about 1) competition for publications based on the shared data, 2) a lack of recognition for sharing data, and 3) a perception that sharing data is technically difficult and time consuming (Palmer et al. 2004, Parr and Cummings 2005, Hampton et al. 2013). However, changes in how data is treated and shared have increasingly ameliorated these issues. First, many data sharing initiatives allow for data embargoes or limitations on direct competition that allow authors to develop their publications and thus avoid competition for deriving publications from the data. Second, as mentioned above, datasets are now considered citable entities and data providers receive recognition in the form of increased citation metrics and credit on CVs and grant applications (Piwowar et al. 2007, Piwowar and Vision 2013, Poisot et al. 2013). Finally, data archives have become increasingly common and easy to use (Parr and Cummings 2005, Hampton et al. 2013), and in some cases sharing data requires no more effort than uploading a file to a website. As a result, it is increasingly beneficial to the individual researcher to share data.

2. Provide metadata

The first key to using data is understanding it. Metadata is information about the data including how it was collected, what the units of measurement are, and descriptions of how to best use the data (Michener and Jones 2012). Clear metadata makes it easier to figure out if a dataset is appropriate for a project. It also makes data easier to use by both the original investigators and by other scientists by making it easy to figure out how to work with the data. Without clear metadata, datasets can be overlooked or go unused due to the difficulty of understanding the data (Fraser and Gluck 1999, Zimmerman 2003). Undocumented data also becomes less useful over time as information about the data is gradually lost (Michener et al. 1997).

Metadata can take several forms, including descriptive file and column names, a written description of the data, images (i.e., maps, photographs), and specially structured information that can be read by computers (i.e., machine readable metadata). Good metadata should provide the following information (Michener et al. 1997, Zimmerman 2003, Strasser et al. 2012):

- The what, when, where, and how of data collection.
- How to find and access the data.
- Suggestions on the suitability of the data for answering specific questions.
- Warnings about known problems or inconsistencies in the data, e.g., general descriptions of data limitations or a column in a table to indicate the quality of individual data points.
- Information to check that the data are properly imported, e.g., the number of rows and columns in the dataset and the total sum of numerical columns.

Just like any other scientific publication, metadata should be logically organized, complete, and clear enough to enable interpretation and use of the data (Zimmerman 2007). Specific metadata standards exist (e.g., Ecological Metadata Language EML, Directory Interchange Format DIF, Darwin Core DWC (Wieczorek et al. 2012), Dublin Core Metadata Initiative DCMI, Federal Geographic Data Committee FGDC (Reichman et al. 2011, Whitlock 2011, Michener and Jones 2012). These standards are designed to provide consistency in metadata across different datasets and also to allow computers to interpret the metadata automatically. This allows broader and more efficient use of shared data because computers can be relied on to identify (and potentially combine) data from many different datasets for synthetic analyses (Brunt et al. 2002, Jones et al. 2006). While following these standards is valuable, the most important thing is having metadata regardless of the specific form.

Writing good metadata does not necessarily require a lot of extra time. The easiest way to develop metadata is to start describing your data during the planning and data collection stages. This will help you stay organized, make it easier to work with your data after it has been collected, and make eventual publication of the data easier. If you decide to take the extra step and follow metadata standards, there are tools designed to make this easier including: KNB Morpho, USGS xtme, and FGDC workbook.

3. Provide an unprocessed form of the data

Often, the data used in scientific analyses are modified in some way from the original form in which they were collected. Values are averaged, units are converted, or indices are calculated from direct measurements or observations to address the focal research questions and to fix issues associated with the raw data. However, the best way to process data depends on the question being asked and corrections for common data limitations often change as better approaches are developed. It can also be very difficult to combine data from multiple sources that have each been processed in different ways. Therefore, to make your data as useful as possible it is best to share the data in as raw a form as possible. That means providing your data in a form that is as close as possible to the field measurements and observations from which your analysis started.

This is not to say that your data are best suited for analysis in the raw form, but providing it in the raw form gives data users the most flexibility. Of course, your work to develop and process the data is also very important and can be quite valuable for other scientists using your data. This is particularly true when correcting data for common limitations. Providing both the raw and processed forms of the data, and clearly explaining the differences between them in the metadata, is an easy way to include the benefits of both data forms. An alternate approach is to share the unprocessed data along with the code that process the data to the form you used for analysis. This allows other scientists to assess and potentially modify the process by which you arrived at the values used in your analysis.

4. Use standard data formats

Everyone has their own favorite tools for storing and analyzing data. To make it easy to use your data it is best to store it in a standard format that can be used by many different kinds of software. Good standard formats include the type of file, the overall structure of the data, and the specific contents of the file.

Use standard file formats

You should use file formats that are readable by most software and, when possible, are non-proprietary (Borer et al. 2009, Strasser et al. 2011, 2012). Certain kinds of data in ecology and evolution have well established standard formats such as FASTA files for nucleotide or peptide sequences (http://zhanglab.ccmb.med.umich.edu/FASTA/) and the Newick files for phylogenetic trees (http://evolution.genetics.washington.edu/phylip/newicktree.html). Use these well-defined formats when they exist, because that is what other scientists and most existing software will be able to work with most easily.

Data that does not have a well-defined standard format is often stored in tables. To increase reuseability, tabular data should be stored in a format that can be opened by any type of software, i.e. text files. These text files use delimiters to indicate different columns. Commas are the most commonly used delimiter (i.e., comma-delimited text files with the .csv extension). Tabs can also be used as a delimiter, although problems can occur in displaying the data correctly when importing data from one program to another. In contrast to plain text files, proprietary formats such as those

used by Microsoft Excel (e.g, .xls, .xlsx) can be difficult to load into other programs. In addition, these types of files can become obsolete, eventually making it difficult to open the data files at all if the newer versions of the software no longer support the original format (Borer et al. 2009, Strasser et al. 2011, 2012).

When naming files you should use descriptive names so that it is easy to keep track of what data they contain (Borer et al. 2009, Strasser et al. 2011, 2012). If there are multiple files in a dataset, name them in a consistent manner to make it easier to automate working with them. You should also avoid spaces in file names, which can cause problems for some software (Borer et al. 2009). Spaces in file names can be avoided by using camel case (e.g, RainAvg) or by separating the words with underscores (e.g., rain_avg).

Use standard table formats

Data tables are ubiquitous in ecology and evolution. Tabular data provides a great deal of flexibility in how data can be structured. However, this flexibility also makes it easy to structure your data in a way that is difficult to (re)use. We provide three simple recommendations to help ensure that tabular data are properly structured to allow the data to be easily imported and analyzed by most data management systems and common analysis software, such as R and Python.

- Each row should represent a single observation (i.e., record) and each column should represent a single variable or type of measurement (i.e., field) (Borer et al. 2009, Strasser et al. 2011, 2012). This is the standard formatting for tables in the most commonly used database management systems and analysis packages, and makes the data easy to work with in the most general way.
- Every cell should contain only a single value (Strasser et al. 2012). For example, do not include units in the cell with the values (Figure 1) or include multiple measurements in a single cell, and break taxonomic information up into single components with one column each for family, genus, species, subspecies, etc. Violating this rule makes it difficult to process or analyze your data using standard tools, because there is no easy way for the software to treat the items within a cell as separate pieces of information.
- There should only be one column for each type of information (Borer et al. 2009, Strasser et al. 2011, 2012). The most common violation of this rule is cross-tab structured data (http://en.wikipedia.org/wiki/Cross_tabulation), where different columns contain measurements of the same variable (e.g., in different sites, treatments, etc.; Figure 1).

While cross-tab data can be easier to read and may be appropriate for data collection, this format makes it difficult to link the records with additional data (e.g., the location and environmental conditions at a site) and it cannot be properly used by most common database management and analysis tools (e.g., relational databases, dataframes in R and Python, etc.). If tabular data are currently in a cross-tab structure, there are tools to help restructure the data including functions in Excel, R (e.g., melt() function in the R package reshape; Wickham 2007), and Python (e.g., melt() function in the Pandas Python module http://pandas.pydata.org/).

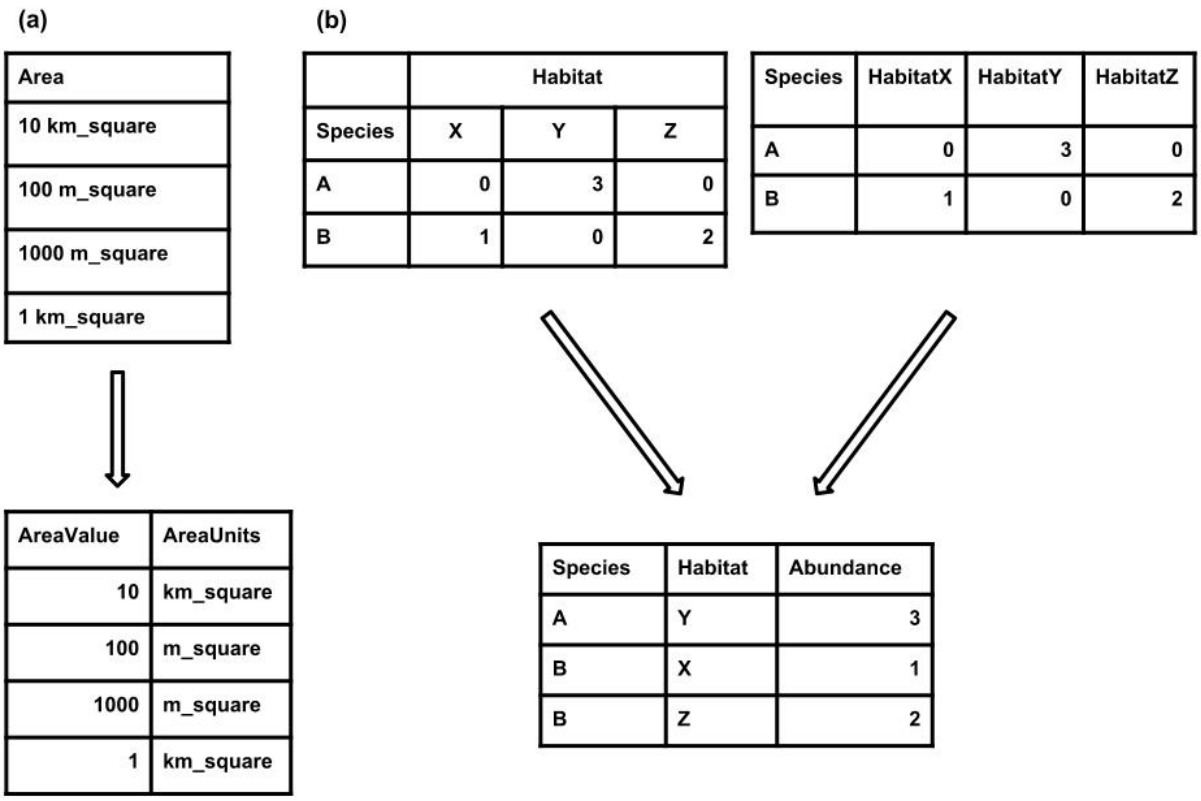

Figure 1: Examples of how to restructure two common issues with tabular data. (a) Each cell should only contain a single value. If more than one value is present then the data should be split into multiple columns. (b) There should be only one column for each type of information. If there are multiple columns then the column header should be stored in one column and the values from each column should be stored in a single column.

In addition to following these basic rules you should also make sure to use descriptive column names (Borer et al. 2009). Descriptive column names make the data easier to understand and therefore make data interpretation errors less likely. As with file names, spaces can cause problems for some software and should be avoided.

Use standard formats within cells

In addition to using standard table structures it is also important to ensure that the contents of each cell do not cause problems for data management and analysis software. Specifically, we recommend that you:

- Be consistent. For example, be consistent in your capitalization of words, choice of delimiters, and naming conventions for variables.
- Avoid special characters. Most software for storing and analyzing data works best on plain text, and accents and other special characters can make it difficult to import your data (Borer et al. 2009, Strasser et al. 2012).
- Avoid using your delimiter in the data itself (e.g., commas in the notes filed of a comma-delimited file). This can make it difficult to import your data properly. This means that if you are using commas as the decimal separator (as is often done in continental Europe) then you should use a non-comma delimiter (e.g., a tab).
- When working with dates use the YYYY-MM-DD format (i.e., follow the ISO 8601 data standard).

While these standard approaches make it easier to use your data, the most important thing is to document the approach that you have taken in your metadata (e.g., specify the date format) so that data users can understand how to work with the data.

5. Use good null values

Most ecological and evolutionary datasets contain missing or empty data values. Working with this kind of "null" data can be difficult, especially when the null values are indicated in problematic ways. There are many ways to indicate a missing/empty value and little agreement on which approach to use. We recommend choosing a null value that is both compatible with most software and unlikely to cause errors in analyses (Table 1).

The null value that is most compatible with the software commonly used by biologists is the blank (i.e., nothing; Table 1). Blanks are automatically treated as null values by R, Python, SQL, and Excel. They are also easily spotted in a visual examination of the data. Note that a blank involves entering nothing, it is not a space, so if you use this option make sure there are no hidden spaces. There are two potential issues with blanks that should be considered:

1. It can be difficult to know if a value is missing or was overlooked during data entry.
2. Blanks can be confusing when spaces or tabs are used as delimiters in text files.

"NA" and "NULL" are reasonable null values, but they are only handled automatically by a subset of commonly used software (Table 1). "NA" can also be problematic if it is also used as an abbreviation (e.g., North America, Namibia, *Neotoma albigula*, sodium, etc.). We recommend against using numerical values to indicate nulls (e.g., 999, -999, etc.) because they typically require an extra step to remove from analyses and can be accidentally included in calculations. We also recommend against using non-standard text indications (e.g., No data, ND, missing, —) because they can cause issues with software that requires consistent data types within columns). Whichever null value that you use, only use one, use it consistently throughout the data set, and indicate it clearly in the metadata.

Null values	Problems	Compatibility	Recommendation
0	Indistinguishable from a true zero		Never use
blank	Hard to distinguish values that are missing from those overlooked on entry. Hard to distinguish blanks from spaces, which behave differently.	R, Python, SQL	Best option
999, -999	Not recognized as null by many programs without user input. Can be inadvertently entered into calculations.		Avoid
NA, na	Can also be an abbreviation (e.g., North America), can cause problems with data type (turn a numerical column into a text column). NA is more commonly recognized than na.	R	Good option
N/A	An alternate form of NA, but often not compatible with software		Avoid
NULL	Can cause problems with data type	SQL	Good option
None	Can cause problems with data type	Python	Avoid
No data	Can cause problems with data type, contains a space		Avoid

Missing	Can cause problems with data type	Avoid
-,+,.	Can cause problems with data type	Avoid

Table 1: Commonly used null values, limitations, compatibility with common software and a recommendation regarding whether or not it is a good option. Null values are indicated as being a null value for specific software if they work consistently and correctly with that software. For example, the null value "NULL" works correctly for certain applications in R, but does not work in others, so it is not presented in the table as R compatible.

6. Make it easy to combine your data with other datasets

Ecological and evolutionary data are often combined with other kinds of data. You can make it easier to combine your data with other data sources by including contextual data that appears across similar data sources. Two of the most common kinds of contextual data in ecology and evolution are taxonomy and geographic location. While this type of data is known and recorded in most studies (e.g, in field notebooks, on maps) it is frequently not included with the data. In general, if you have collected additional data or notes about a study organism or field site, there is a good chance that it will be useful to someone else, so including it with your data when you share it is a good idea. This kind of information can be included either as part of the data itself (e.g., in a new column or an additional table) or can be included in the metadata (e.g., the geographic location of the study site). For geographic data it is also important to include the datum (e.g., WGS-84) and sufficient precision (e.g., 4 decimals places if using decimal degress) to allow the data to be combined with other geographic datasets.

When this data is included in a dataset it is often included as codes or abbreviations (e.g., DS instead of *Dipodomys spectabilis*, or site names instead of geographic coordinates). This can be useful for the data collector because it reduces data entry (e.g., typing a 1 into a plot column instead of entering both the latitude and longitude) and redundancy (e.g., a single column for a species ID rather than separate columns for family, genus, and species). However, without clear definitions these codes can be difficult to understand and make it more difficult to combine your data with external sources. One easy way to link your data to other datasets is to include additional tables that contain a column for the code and additional columns that describe the item in the standard way. For taxonomy, you might include a table with the species codes followed by their most current family, genus, and specific epithet. For site location, you could include a table with the site name or code followed by latitude and longitude, and other site information such as spatial extent, and temporal duration of sampling.

7. Perform basic quality control

Data, just like any other scientific product, should undergo some level of quality control (Reichman et al. 2011). This is true regardless of whether you plan to share the data because quality control will make it easier to analyze your own data and decrease the chance of making mistakes. However, it is particularly important for data that will be shared because scientists using the data will not be familiar with quirks in the data and how to work around them.

At its most basic, quality control can consist of a few quick sanity checks. More advanced quality control can include automated checks on data as it is entered and double-entry of data (Lampe and Weiler 1998, Michener and Jones 2012, Paulsen et al. 2012). This additional effort can be time consuming but is valuable because it increases data accuracy by catching typographical errors, reader/recorder error, out-of-range values, and questionable data in general (Lampe and Weiler 1998, Paulsen et al. 2012).

Before sharing your data we recommend performing a quick review. Start by performing a few basic sanity checks. For example:

- If a column should contain numeric values, check that there are no non-numeric values in the data.
- Check that empty cells actually represent missing data, and not mistakes in data entry, and indicate that they are empty using the appropriate null values (see recommendation 6).
- Check for consistency in unit of measurement, data type (e.g., numeric, character), naming scheme (e.g., taxonomy, location), etc.

These checks can be performed by carefully looking at the data or can be automated using common programming and analysis tools like R or Python.

Then, ask someone else to look over your metadata and data and provide you with feedback about anything they did not understand. In the same way that friendly reviews of papers can help catch mistakes and identify confusing sections of papers, a friendly review of data can help identify problems and things that are unclear in the data and metadata.

8. Use an established repository

For data sharing to be effective, data should be easy to find, accessible, and stored where it will be preserved for a long time (Kowalczyk and Shankar 2011). To make your data (and associated code) visible and easily accessible, and to ensure a permanent link to a well maintained website, we suggest depositing your data in one of the major well-established repositories. This guarantees that the data will be available in the same location for a long time, in contrast to personal and institutional websites that do not guarantee long-term persistence. There are repositories available for sharing almost any type of biological or environmental data. Repositories that host specific data types, such as molecular sequences (e.g., DDBJ, GenBank, MG-RAST), are often highly standardized in data type, format, and quality control. Other repositories host a wide array of data types and are less standardized (e.g., Dryad, KNB, PANGAEA). In addition to the repositories focused on the natural sciences there are also all-purpose repositories where data of any kind can be shared (e.g., figshare).

When choosing a repository you should consider where other researchers in your discipline are sharing their data. This helps to quickly identify the community's standard approach to sharing and increases the likelihood that other scientists will discover your data. In particular, if there is a centralized repository for a specific kind of data (e.g., GenBank for sequence data) then it should be used.q

In cases where there is no *de facto* standard, it is worth considering differences among repositories in terms of use, data rights, and licensing (Table 3) and whether your funding agency or journal has explicit requirements or restrictions related to repositories. We also recommend that you use a repository that allows your dataset to be easily cited. Most repositories will describe how this works, but an easy way to guarantee that your data are citable is to confirm that the repository associates it with a persistent identifier, the most popular of which is the digital object identifier (DOI). DOIs are permanent unique identifiers that are independent of physical location and site ownership. There are also online tools for finding good repositories for your data including http://databib.org and http://re3data.org.

Repository	License	DOI	Metadata	Access	Notes
Dryad	CC0	Yes	Suggested	Open	Ecology & evolution data associated with publications
Ecological Archives	No	Yes	Required	Open	Publishes supplemental data for ESA journals and stand alone data papers
Knowledge Network for Biocomplexity	No	Yes	Required	Variable	Partners with ESA, NCEAS, DataONE
Paleobiology Database	Various CC	No	Optional	Variable	Paleontology specific
Data Basin	Various CC	No	Optional	Open	GIS data in ESRI files, limited free space
Pangaea	Various CC	Yes	Required	Variable	Editors participate in QA/QC
figshare	CC0	Yes	Optional	Open	Also allows deposition of other research outputs and private datasets

Table 2: Popular repositories for scientific datasets. This table does not include well-known molecular repositories (e.g. GenBank, EMBL, MG-RAST) that have become *de facto* standards in molecular and evolutionary biology. Consequently, several of these primarily serve the ecological community. These repositories are not exclusively used by members of specific institutions or museums, but accept data from the general scientific community.

9. Use an established and open license

Including an explicit license with your data is the best way to let others know exactly what they can and cannot do with the data you shared. Following the Panton Principles http://pantonprinciples.org we recommend:

1. Using well established licenses (or waivers) in order to clearly communicate the rights and responsibilities of both the people providing the data and the people using it.
2. Using the most open license (or waiver) possible, because even minor restrictions on data use can have unintended consequences for the reuse of the data (Schofield et al. 2009, Poisot et al. 2013).

The Creative Commons Zero (CC0) public domain dedication places no restrictions on data use and is considered by many to be one of the best ways to share data (e.g., (Schofield et al. 2009, Poisot et al. 2013), http://blog.datadryad.org/2011/10/05/why-does-dryad-use-cc0/). Several other licenses and waivers also accomplish these same goals http://opendefinition.org/licenses/#Data. Having a clear and open license (or waiver) will increase the chance that other scientists will be comfortable using your data.

Concluding remarks

Data sharing has the potential to transform the way we conduct ecological and evolutionary research (Fienberg and Martin 1985, Whitlock et al. 2010, Poisot et al. 2013). As a result, there are an increasing number of initiatives at the federal, funding agency, and journal levels to encourage or require the sharing of the data associated with scientific research (Piwowar and Chapman 2008, Whitlock et al. 2010, Poisot et al. 2013). However, making your data available is only the first step. To make data sharing as useful as possible it is necessary to make the data (re)usable with as little effort as possible (Jones et al. 2006, Reichman et al. 2011). This allows scientists to spend their time doing science rather than deciphering and cleaning up data.

We have provided a list of 9 practices that require only a small additional time investment but substantially improve the usability of data. These practices can be broken down into three major groups.

1. Well documented data are easier to understand.
2. Properly formatted data are easier to use in a variety of software.
3. Data that is shared in established repositories with open licenses is easier for others to find and use.

Most of these recommendations are simply good practice for working with data regardless of whether that data are shared or not. This means that following these recommendations (2-7) make the data easier to work with for anyone, including you. This is particularly true when returning to your own data for further analysis months or years after you originally collected or analyzed it. In addition, data sharing often occurs within a lab or research group. Good data sharing practices make these in-house collaborations faster, easier, and less dependent on lab members who may have graduated or moved on to other endeavors. Following the other recommendations (1, 8, and 9) provides broader benefits including academic credit in the form of published datasets and increased citation metrics (Piwowar et al. 2007, Piwowar and Vision 2013, Poisot et al. 2013).

Many of these recommendations can be implemented at any point during a project, but the best time to think about how to handle your data is before the project even starts (Michener and Jones 2012). A few hours of thought about how the data will be documented, structured, and shared at the beginning of a project can prevent the need to restructure data or recall old information. This will make it faster and easier to share your data when you are ready. By following these practices we can assure that the data collected in ecology and evolution can be used to its full potential to improve our understanding of biological systems.

Acknowledgments

Thanks to Karthik Ram for organizing this special section and inviting us to contribute. Carly Strasser and Kara Woo recommended important references and David Harris and Carly Strasser provided valuable feedback on null values, all via Twitter. Carl Boettiger, Matt Davis, Daniel Hocking, Heinz Pampel, Karthik Ram, Thiago Silva, Carly Strasser, Tom Webb, and @beroe (Twitter handle) provided valuable comments on the manuscript. Many of these comments were part of the informal review process facilitated by posting this manuscript as a preprint to PeerJ Preprints. The writing of this paper was supported by a CAREER grant from the U.S. National Science Foundation (DEB 0953694) to EPW.

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