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A workflow to integrate ecological monitoring data from different sources

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► **To cite this version:**

Jérémy Wicquart, Mishal Gudka, David Obura, Murray Logan, Francis Staub, et al.. A workflow to integrate ecological monitoring data from different sources. *Ecological Informatics*, 2022, 68, pp.101543. <10.1016/j.ecoinf.2021.101543>. <hal-03839113>

HAL Id: hal-03839113

<https://univ-perp.hal.science/hal-03839113v1>

Submitted on 8 Jan 2024

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21 Abstract

22 Programs and initiatives aiming to protect biodiversity and ecosystems have increased over the last
23 decades in response to their decline. Most of these are based on monitoring data to quantitatively
24 describe trends in biodiversity and ecosystems. The estimation of such trends, at large scales,
25 requires the integration of numerous data from multiple monitoring sites. However, due to the high
26 heterogeneity of data formats and the resulting lack of interoperability, the data integration remains
27 sparsely used and synthetic analyses are often limited to a restricted part of the data available.

28 Here we propose a workflow, comprising four main steps, from data gathering to quality control, to
29 better integrate ecological monitoring data and to create a synthetic dataset that will make it
30 possible to analyse larger sets of monitoring data, including unpublished data.

31 The workflow was designed and applied in the production of the *Status of Coral Reefs of the World:
32 2020* report, where more than two hundred individual datasets were integrated to assess the status
33 and trends of hard coral cover at the global scale. The workflow was applied to two case studies and
34 associated R codes, based on the experience acquired during the production of this report.

35 The proposed workflow allows for the integration of datasets with different levels of taxonomic and
36 spatial precision, with a high degree of reproducibility. It provides a conceptual and technical
37 framework for the integration of ecological monitoring data, allowing for the estimation of temporal
38 trends in biodiversity and ecosystems or to test ecological hypotheses at larger scales.

39

40 Key-words

41 Data · Homogenization · Integration · Standardization · Aggregation · Ecological synthesis · GCRMN ·

42 Meta-analysis

43

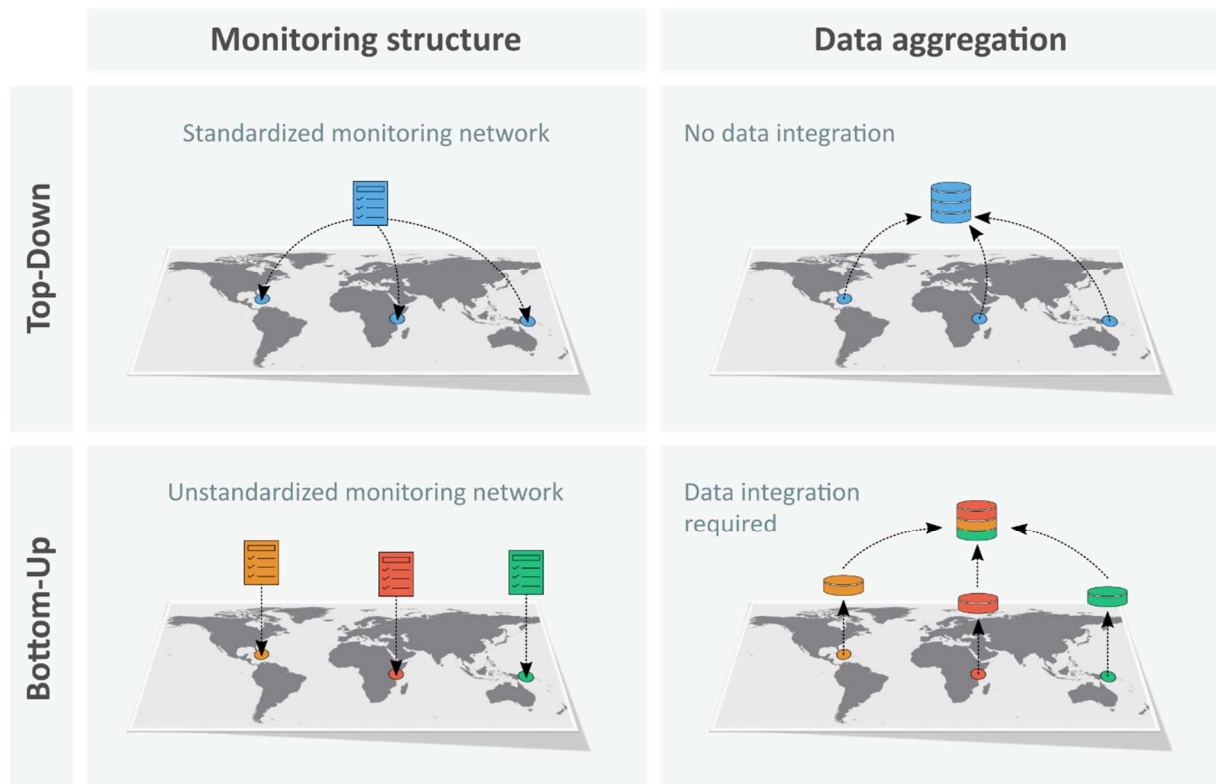
44 1. Introduction

45 Global (e.g. Aichi Biodiversity Targets of the Convention for the Biological Diversity - CBD), regional
46 (e.g. Coastal Oceans Research and Development Indian Ocean - CORDIO) and national (e.g. French
47 Coral Reef Initiative) initiatives that seek to protect biodiversity and ecosystems have multiplied over
48 the last two decades. To gauge the success of these different programs in order to inform
49 conservation policies, it is necessary to estimate changes in biodiversity and ecosystems at each of
50 these different scales. Ecological monitoring (see **Table 1** for definitions of mains terms used) is the
51 foundation on which such studies are built, yet, it is typically focused and constrained to local scales.
52 Therefore, in order to assess the broader status and trends of biodiversity and ecosystems, it is
53 necessary to group monitoring sites within a monitoring network (Balmford et al., 2005; Lindenmayer
54 & Likens, 2010; Schmeller et al., 2015; Küh et al., 2020).

55 Two approaches can be adopted to achieve this objective (Henry et al., 2008). The first is a “top-
56 down” approach and corresponds to a highly standardized monitoring network where all monitoring
57 sites within the network use the same protocol (**Fig. 1**). Monitoring networks that are based on this
58 “top-down” approach are usually found within national frameworks (e.g. US National Coral Reef
59 Monitoring Program - National Oceanic and Atmospheric Administration (NOAA) CoRIS) or within
60 research groups (e.g. Service National Observation (SNO) CORAIL). However, while standardized
61 protocols are used for some monitoring networks (e.g. Hallmann et al., 2017), most monitoring sites
62 are far from being part of a real “top-down” approach due to issues around coordination and
63 standardisation between different research groups who have different objectives, interests, funding
64 streams and capacities. Moreover, the “top-down” approach does not allow for the inclusion of
65 existing monitoring sites that use different protocols. Existing monitoring sites cannot be greatly
66 modified since doing this would lead to a loss of consistency in methodology and hence
67 comparability of data over time, which is one of the main targets of long-term monitoring
68 (Lindenmayer & Likens, 2009). To resolve these issues, a second strategy, the “bottom-up” approach,

69 may be considered (Fig. 1). This strategy consists of combining data (hereafter called data
70 integration) acquired from existing monitoring sites that use different methodologies. In contrast to
71 the “top-down” approach, this strategy enables the existing condition of monitoring networks to be
72 considered for data integration, where it would otherwise be impossible.

73



74

75 **Figure 1.** Comparison of monitoring structure and data aggregation between top-down and bottom-
76 up approaches. For the top-down approach, the monitoring network is standardized and is based on
77 a unique protocol and data format. In contrast, for the bottom-up approach, the monitoring network
78 is unstandardized and is based on different protocols and data formats, making data integration
79 necessary for synthetic analyses.

80

81

82 In contrast to other scientific fields such as physics, oceanography or genetics, ecology is based on a
83 high diversity and heterogeneity of data collection methods and hence data formats (Reichman,
84 Jones, & Schildhauer, 2011; Michener & Jones, 2012; Poisot, Bruneau, Gonzalez, Gravel, & Peres-
85 Neto, 2019), and this, despite the existence of data standards (e.g. DarwinCore (Wieczorek et al.,
86 2012)). This leads to a lack of interoperability between datasets, which represents a major challenge
87 for wider data integration. This is likely one of the main reasons why data integration, which is
88 needed for the “bottom-up” approach, remains poorly developed (Henry et al. (2008) but see Miller,
89 Pacifici, Sanderlin, & Reich, 2019; O’Donnell et al., 2021) outside of large databases such as GBIF
90 (GBIF: The Global Biodiversity Information Facility, 2021) or OBIS (Ocean Biodiversity Information
91 System, OBIS (2021)). An increased use of data integration may lead to a deeper understanding of
92 status and trends in biodiversity and ecosystems, without having to acquire new data (Jones,
93 Schildhauer, Reichman, & Bowers, 2006; Carpenter et al., 2009). Moreover, as emphasized by
94 Borregaard and Hart (2016), data preparation, which includes data integration, is barely considered
95 and reported as part of data analysis and is rarely documented in code associated with published
96 articles. This represents a major issue for transparent science and reproducibility as the data
97 preparation step can also contain errors that other researchers must be able to track. Finally, this
98 also limits the ability for other researchers to rely on existing methods to conduct similar studies.

99 To address these issues, we propose a workflow which integrates ecological monitoring data from
100 different data sources into a synthetic dataset, which can then be used to perform national, regional
101 or global analyses on the status and trends of the considered ecological metric. We illustrate the
102 proposed workflow by providing an R code template for two case studies inspired from the *Status of*
103 *Coral Reefs of the World: 2020* report, where 248 datasets from contributors across the world were
104 integrated to estimate the status and trends of hard coral cover at the global scale (Souter et al.,
105 2021).

106

107

108 **Table 1.** Definitions of main terms used in the article.

Term	Definition
Dataset	A collection of related sets of information that is composed of separate elements (data files) but can be manipulated as a unit by a computer.
Data aggregator	Data analyst responsible for the data integration process.
Data integration	Process of combining, merging, or joining data together, in order to make what were distinct, multiple data objects, into a single, unified data object (Schildhauer, 2018).
Data provider	A person or an institution sharing a dataset for which they have been or are involved in the acquisition of the data contained in the dataset.
Monitoring site	Repetitive measurement of a specified set of variables at one location over an extended period of time (Vos, Meelis, & Ter Keurs, 2000).
Synthetic dataset	A dataset resulting from the integration of multiple existing datasets (Poisot et al., 2016).

109

110 2. Workflow

111 We distinguished four main data sources: databases, data papers, research articles with associated
112 data and unpublished data from data providers. Over the last decades, large databases which
113 gathered data from different monitoring sites, have emerged in ecology, such as ILTER (Vanderbilt &
114 Gaiser, 2017), GBIF (GBIF: The Global Biodiversity Information Facility, 2021) or BioTIME (Dornelas et
115 al., 2018). In addition to these databases, an increasing number of data papers are being published
116 (Shin et al., 2020), extending the availability of monitoring data. However, based on our experience
117 with the *Status of Coral Reefs of the World: 2020* report (Souter et al., 2021), the vast majority of
118 monitoring data remains unpublished, or only partially published, and thus, can only be acquired
119 from direct exchanges with data providers. For this reason, we chose to focus the proposed workflow
120 on the acquisition of unpublished data, while also making it possible to incorporate data from
121 databases, research articles and data papers.

122 We identified three main approaches which have the potential to yield a synthetic dataset: (1)
123 propose a web-based interface for data entry by data providers (e.g. Chaudhary, Walters, Bever,
124 Hoeksema, & Wilson (2010), Robertson et al. (2014)), (2) ask data providers to reformat their data

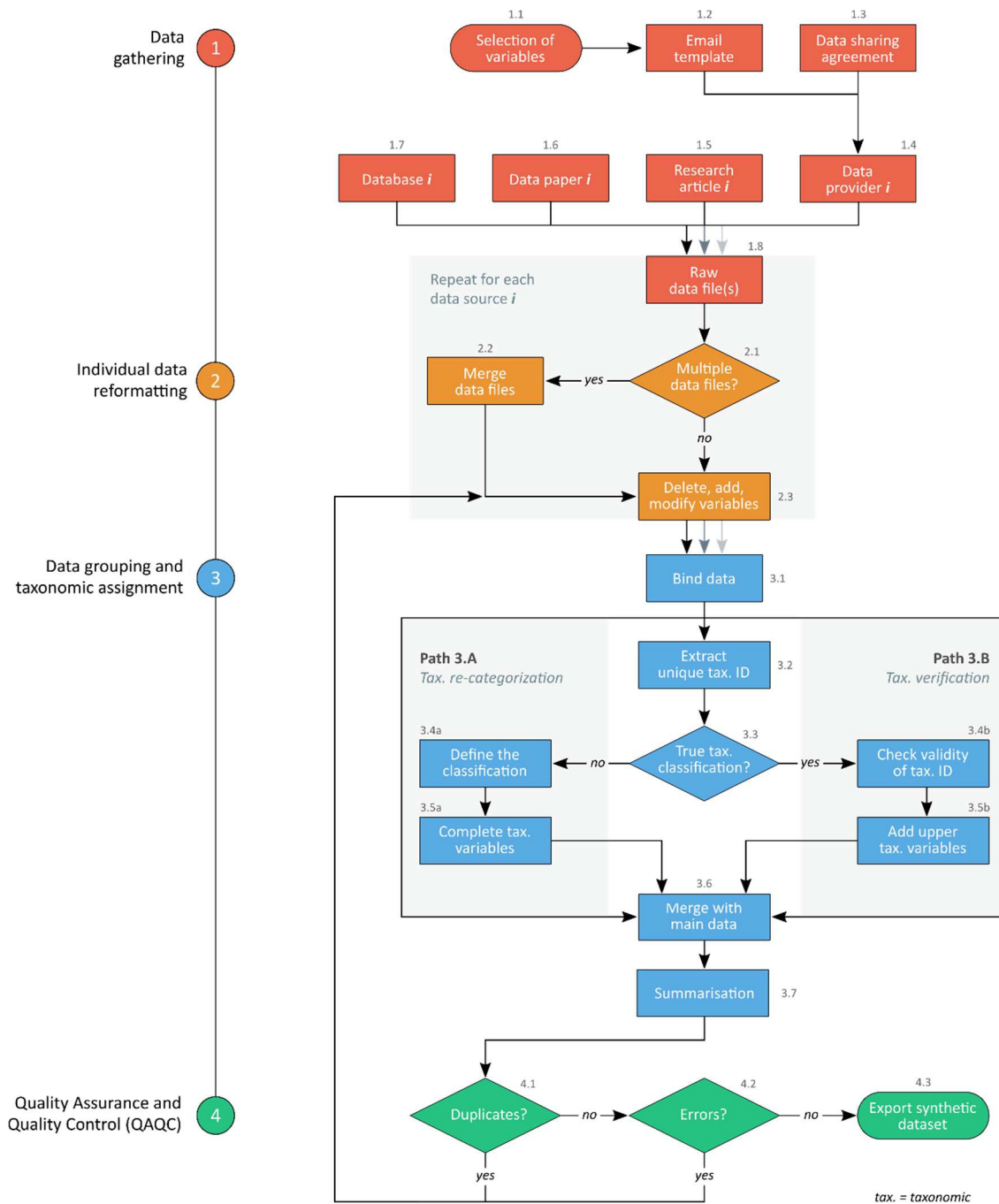
125 following a given template and (3) collect data from data providers in their original format and
126 centralize the reformatting by a data aggregator. The first approach is particularly adapted for new
127 monitoring networks but not for a “bottom-up” approach, as the entry of historical data can be
128 extremely time consuming. The second approach necessitates data wrangling skills from data
129 providers, as well as time, which can potentially discourage them from contributing. In contrast,
130 centralising the entire data homogenization procedure, allows for greater standardization of
131 homogenization, enables full tracking of changes and biases, and avoids error due to variability in
132 data wrangling skills among data providers. Moreover, the first two approaches are difficult to
133 implement for databases, data papers and research articles, as the associated data are only available
134 in a particular format, which need to be reformatted. For all of these reasons, we chose to build the
135 workflow around the third approach, centralized data reformatting where data is curated by a
136 dedicated data aggregator. This approach could interest both parties involved, as the data provider
137 could benefit from the expertise of the data aggregator on data shared, as well as providing advice
138 on metadata information or potential errors (Costello, Michener, Gahegan, Zhang, & Bourne, 2013).

139 The workflow (**Fig. 2**) is composed of four main steps: (1) data gathering, (2) individual data
140 reformatting, (3) data grouping and taxonomic assignment and (4) quality assurance and quality
141 control (QAQC). These four different steps are detailed in the following sections and are exemplified
142 by two cases studies and associated R code template.

143 The workflow was developed with the R software (version 4.1.0, R Core Team (2021)) but it can be
144 transposed into other programming languages (e.g. Python). For R users, we strongly recommend a
145 migration to the “tidyverse” meta-package (Wickham et al., 2019), as it provides a wide range of
146 functions used in data analysis, from importation of the data to their visualisation. In addition to the
147 software, we also recommend using a version control system (e.g. Git) associated to an online
148 collaborative platform (e.g. Github), particularly if the project will be maintained over time and/or if
149 it involves a team of data aggregators. Finally, we highlight that all steps which involve the

150 modification of data, must be done using code and not manually in order to reach the highest
 151 possible level of reproducibility and traceability.

152



153

154 **Figure 2.** Workflow from data gathering to exportation of the final synthetic dataset. The diamonds

155 indicate choices, rectangles indicate actions, and ellipses indicate start and end of the workflow.

156 2.1.Data gathering

157 The first step in the workflow is the selection of variables that will have to be present in the final
158 synthetic dataset (hereafter “standard variables”; **Fig. 2 - 1.1**). We propose a classification of these
159 variables into six groups: data descriptor (e.g. dataset ID, data source), spatial (e.g. latitude,
160 longitude, depth), temporal (e.g. year, date, hour of sampling), methodological (e.g. length of the
161 transect, number of quadrat), taxonomic (e.g. family, genus, species) and metric (e.g. percentage
162 cover, abundance, size). The metric(s) variable(s) correspond to the response(s) variable(s) while all
163 others correspond to potential explanatory variables or metadata. The variables selected in each of
164 these groups depends on the goal of the project and on the future analyses that will be performed.
165 Among the data descriptor variable group, a variable corresponding to the ID of each dataset must
166 be included in order to ensure the possibility of extracting or to perform sensitivity analyses on the
167 individual datasets. We emphasize that the groups of spatial and taxonomic variables are nested. For
168 example, in the case of spatial variables, we can have four variables with, for example, the country,
169 the site, the transect and the quadrat. A country may have several sites, and each site can include
170 several transects, which can then include multiple quadrats. These nested variables are very
171 important as they make it possible to integrate datasets with different spatial and taxonomic
172 precisions. Once the variables are selected, their types (e.g. character, numeric) and units (e.g.
173 meters) must be defined.

174 As previously mentioned, data can originate from four main sources: databases, data papers,
175 research articles with associated data and unpublished raw data from data providers. The acquisition
176 of data from the first three sources (**Fig. 2 - 1.5 to 1.7**) can be achieved through internet literature
177 reviews and institutional or public repositories (Michener, 2018a). In addition to these approaches,
178 the fourth source of data may necessitate a call for contribution using existing mailing lists or social
179 networks. For this last data source, once the list of potential data providers is established, an email
180 template is written (**Fig. 2 - 1.2**) to describe the context and the goal of the project, as well as the

181 required data (by describing the standard variables). The way that people will be cited and
182 acknowledged in the documents that will be produced by the project (e.g. publication, reports) must
183 also be addressed and should be transformed into a Data Sharing Agreement (DSA). This document
184 (see Supplementary material; **Fig. 2 - 1.3**) defines the terms of the agreement between the data
185 provider and the person or organization responsible for the project. While the DSA may not be part
186 of a legal framework, it seeks to establish a mutual agreement and terms of use for the data, building
187 the confidence and trust between the data providers and users. Emails and DSA are then sent to all
188 of the potential data providers based on the created list (**Fig. 2 - 1.4**). When received, the original raw
189 data files are then stored with the signed DSA.

190

191 2.2. Individual data reformatting

192 The next step is the individual dataset reformatting which corresponds to a standardization of the
193 variables of each dataset gathered from the four data sources. The raw data are first imported into
194 the software, either from their format of origin or by an intermediate step, where they are first
195 exported in a plain text format (e.g. csv, txt). The importation of raw data in their format of origin
196 ensures a complete reproducibility but requires the use of specific packages (e.g. “readxl” on R
197 (Wickham & Bryan, 2019)) in order to work with all of the different raw data formats. If the
198 intermediate step, where the raw data files are exported in plain text format, is chosen, all of the file
199 paths and spreadsheet names must be written to ensure the traceability of the data.

200 If the data are separated into multiple data files, usually with one main data file, and one or more
201 supplementary data files (e.g. file with sites coordinates, file with equivalence of taxonomic codes),
202 they must all be merged together (**Fig. 2 - 2.2**). Particular attention must be paid to the factor levels
203 of the grouping variable (i.e. the variable present in both files by which the merging is done) in order
204 to avoid any loss of information. Factors are a type of variable characterized by a fixed and known set
205 of possible values, that are named levels (e.g. the variable “Site” contained the levels of factors

206 “Station A” and “Station B”). A slight difference in factor levels (e.g. first letter of one in uppercase
207 and the first letter of the second in lowercase) can lead to non-matching. Multiple data files can also
208 occur when data are stored in one file but are divided into several spreadsheets. This division is
209 usually done to separate the different years or sites within the monitoring programs. Two cases can
210 be considered to address such formatting. If the data in the different spreadsheets share the exact
211 same formatting (i.e. same columns names) they can be bound together using a loop into a single,
212 long dataset. Otherwise, each spreadsheet must be treated as a different dataset.

213 Variables corresponding to the standard variables (see part 2.1 Data gathering) are first selected.
214 Then, if the data are presented in wide format (i.e. one variable divided into several columns) they
215 must be transformed into long format (i.e. one variable by column). Next, the variable corresponding
216 to the ID of the dataset is added. Here we propose a code of several letters associated with one (e.g.
217 DATA1) or more numbers if the data comes from multiple spreadsheets within a single file (e.g.
218 DATA1.1, DATA1.2, etc.). Then, all variables selected for the synthetic dataset but absent in the raw
219 data or associated metadata files, are added (**Fig. 2 - 2.3**). For example, these variables may have
220 been created specifically for the project purpose or may correspond to information given by the data
221 provider. To ensure reproducibility, we recommend that any correspondences with data providers
222 are tracked and that they are referenced by adding comments in the code. The variables are then
223 renamed to match the standard variable names. All variables containing information on the
224 taxonomic level are grouped together in a temporary variable named “Tax_ID”. The taxonomy will be
225 resolved during the following step. Next, the variables are modified to fit with the units defined. The
226 transformation involves variables such as latitude and longitude (e.g. from one coordinate reference
227 system (CRS) to another), the altitude or the depth (e.g. feet to meters), the date (e.g. DD-MM-YY to
228 YYYY-MM-DD) or the metric variable (e.g. size from mm to cm, number of individuals on the transect
229 to number of individuals on 100 m²). When possible, we recommend that the International System of
230 Units be used. Particular attention must be given to the variable types (e.g character, numeric) of
231 each variable, as multiple data types may occur within the same variable. For example, some data

232 providers may have used both numeric values (e.g. "5") and intervals (e.g. "> 5 meters") for the
233 depth.

234 Finally, once the individual data reformatting is completed, each reformatted dataset is exported in
235 plain text format using a consistent file name nomenclature (e.g. 02_reformatted_datasetID).

236

237 2.3. Data grouping and taxonomic assignment

238 Once all data files are individually reformatted, they are all bound together (**Fig. 2 - 3.1**). This can be
239 done automatically by retrieving all files with a specific naming structure in the storage folder and
240 binding them using a loop. Some error messages can occur when the variable types differ between
241 the individual reformatted files. While such errors can be avoided by converting all variables in
242 character string, we argue that these error messages are useful to identify mistakes in variable types.
243 If such errors happen, a modification of the code for individual datasets concerned in the previous
244 step is necessary (**Fig. 2 - 2.3**).

245 As mentioned above, all information related to the taxonomy is, at this stage, stored in the unique
246 variable ("Tax_ID"). This variable is extracted from the main data and duplicates are removed to only
247 keep unique levels of factor (**Fig. 2 - 3.2**). Then, depending on the variables selected at the beginning
248 of the workflow, two pathways exist: the taxonomic re-categorization (path 3A) and the taxonomic
249 verification (path 3B).

250

251 2.3.1. Taxonomic re-categorization

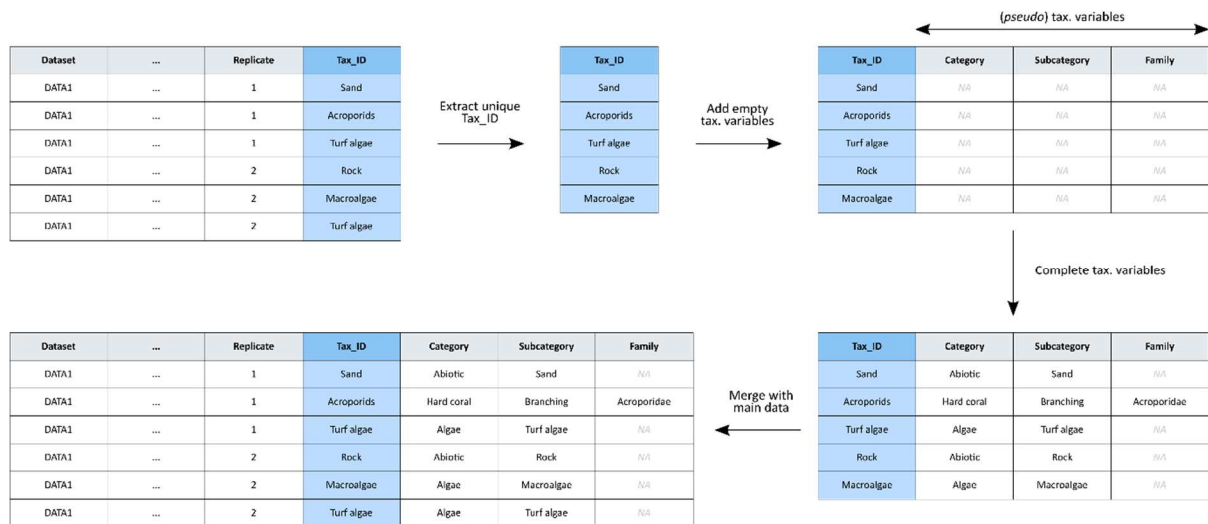
252 The first pathway (**Fig. 2 - path 3.A**) corresponds to the case where the selected variables are not (or
253 partially) included within the taxonomic classification system. Such cases can arise when the
254 taxonomic identification in the field is difficult and therefore invokes the use of broad categories

255 instead of species or genus level ID. This is the case for coral reef benthic monitoring data with
256 categories such as algae, rock or hard coral. In this situation, levels of factor (i.e. names of categories)
257 are likely to vary greatly among data providers. To achieve a homogeneous classification within the
258 synthetic dataset it is thus necessary to perform a re-categorization of the levels of factor used by
259 each data provider. To do so, a classification is first defined by choosing standardized levels of factor,
260 which should make it possible to re-categorize all cases. This homogeneous classification can be
261 based on more than one variable or a set of nested variables if necessary (see part 2.1). Then, if the
262 number of factor levels is low, the re-categorization can be done directly within the software, else a
263 file (e.g. in csv format) containing the unique "Tax_ID" levels must be exported and the re-
264 categorization variables must be completed manually. In the second case, the levels of factor of the
265 "Tax_ID" variable must not be modified because they will be used to merge the re-categorization file
266 with the main data (**Fig. 3**). The re-categorization is the most critical and the least reproducible part
267 of the workflow and thus it must be both rigorous and consistent. Re-categorization by multiple
268 individuals (i.e. cross-validation) would likely help to improve the reliability of this step. The following
269 is a list of particular cases that may result for a given level of factor of "Tax_ID":

- 270 • Mixed categories. Here, the lowest common category is used. For example, if the "Tax_ID" is
271 "Macroalgae and turf algae", the category "Algae" can be retained.
- 272 • Stacked categories. Here, the upper category can be used. For example, if the "Tax_ID" is
273 "Algae on rock", the category "Algae" can be used.
- 274 • Homonym taxa names (e.g. "Turbinaria" which is a genus of Scleractinia but also of Fucales).
275 In this case, it is necessary to contact the data provider and to modify the level of factor by
276 an unambiguous one (e.g. "Algae - Turbinaria").
- 277 • Not required categories (e.g. "Shadow"). Here, the taxonomic variables remain empty, the
278 rows which are not filled will later be removed.

279 Once the re-categorization is finished, the file is imported into the software and merged with the
 280 main data (Fig. 2 - 3.6). Fig. 3 illustrates the taxonomic assignment for path 3.A.

281



282

283

284 **Figure 3.** Example of taxonomic assignment for path 3.A (taxonomic re-categorization). NA = Not
 285 Available, tax. = taxonomic.

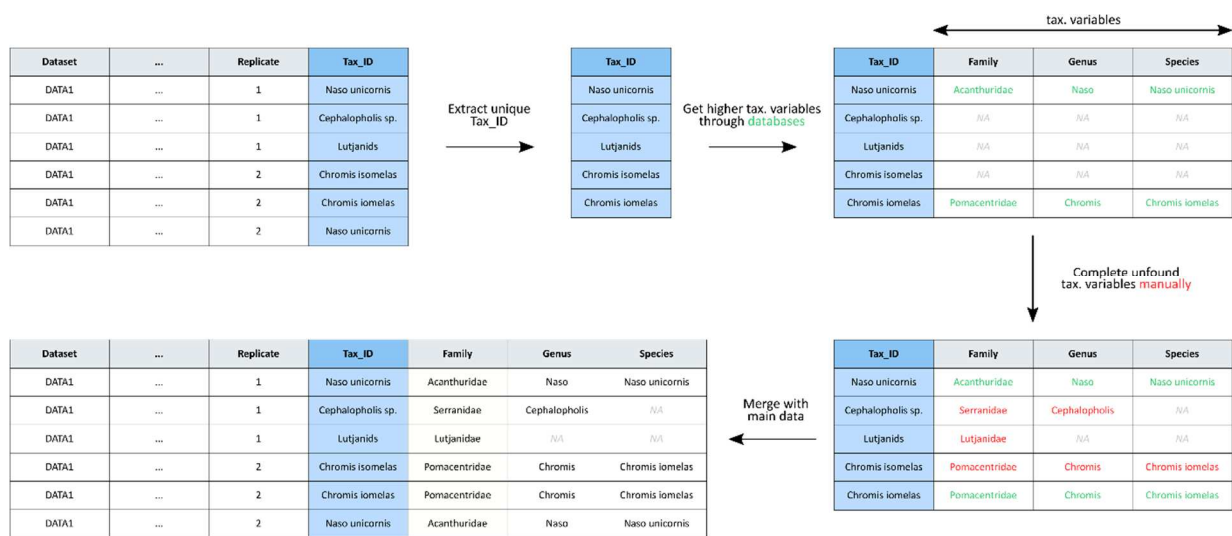
286

287 2.3.2. Taxonomic verification

288 The second pathway (Fig. 2 - path 3.B) corresponds to the case where the selected variables are part
 289 of the taxonomic classification system (e.g. family, genus, species). First, an API (*Application*
 290 *Programming Interface*, i.e. a service which allows for the query and/or upload of data from the web
 291 in a standardized format) of an online taxonomic database (e.g. “rfishbase” (Boettiger, Lang, &
 292 Wainwright, 2012) and “taxize” (Chamberlain et al., 2020) packages on R) is used to add the higher
 293 taxonomic variables for each level of the “Tax_ID” variable. The levels of factor of the “Tax_ID”
 294 variable for which upper taxonomic variables were completed through the database correspond to
 295 correct species names, while those which remained filled with NA correspond to incorrect species

296 names. The levels of factor with incorrect species names may be due to data entry spelling errors,
 297 changes in taxonomic classification, vernacular species names (e.g. honeycomb grouper) and
 298 incomplete (e.g. *Cephalopholis* sp.) or upper taxonomic names (e.g. Lutjanidae). Thereafter, all rows
 299 that have not been completed automatically through the API, must be manually filled. To this end, a
 300 file containing all incorrect species names is exported in a plain text format file (e.g. csv) and the
 301 higher taxonomic variables are completed for each row. When it is not possible to find the
 302 equivalence for the incorrect species name, the higher taxonomic variables are left empty (the rows
 303 which are not filled will be removed afterwards). Once finished, the file is imported into the
 304 software, bound with the table of correct species names and then merged with the main data (**Fig. 2**
 305 - **3.6**). **Fig. 4** illustrates the taxonomic assignment for path 3.B.

306



307

308

309 **Figure 4.** Example of taxonomic assignment for path 3.B (taxonomic verification). NA = Not Available,

310 tax. = taxonomic.

311

312 Following the taxonomic assignment, it is possible that some rows for the taxonomic variables were
313 left empty (i.e. fill with NA) because they corresponded either to not required (e.g. “Shadow”) or
314 non-categorizable categories (e.g. “juvenile fish”). We recommend that the levels of factor of
315 “Tax_ID” for which taxonomic variables were left empty be verified, and the corresponding rows
316 then be deleted.

317 Rows that had different levels of factor for “Tax_ID” before the taxonomic assignment (e.g. “Red
318 algae” and “Brown algae”) may have been re-categorized with a common level of factor for
319 taxonomic variable (e.g. “Algae”) after the taxonomic assignment. Hence, it is necessary to aggregate
320 these rows (on the metric(s) variable(s)) to avoid having multiple rows which correspond to the same
321 category in the same sampling unit, which unnecessarily increases the size of the dataset (**Fig. 2 –**
322 **3.7**).

323 Finally, the “Tax_ID” variable, that was used for the taxonomic assignment but which is useless for
324 the final synthetic dataset, is then deleted.

325

326 2.4. Quality Assurance and Quality Control

327 The final step of the workflow is the Quality Assurance and Quality Control (QAQC). First, duplicates
328 are identified within the data (**Fig. 2 - 4.1**) to make sure that the same data file, or row, was not
329 included more than once. Any duplicates found, should be removed.

330 Next, errors should be identified and corrected, or removed, if the error cannot be corrected (**Fig. 2 -**
331 **4.2**). Within the term “errors” we mean (1) any incorrect levels of factor for qualitative variables, (2)
332 any incorrect values for quantitative variables and (3) any invalid site coordinates (through latitude
333 and longitude variables). We detail these three points in the following paragraphs but more
334 information about QAQC can be found in Michener (2018b) and Vandepitte et al. (2015).

335

336 2.4.1. Qualitative variables

337 The identification of incorrect levels of factor can be done visually by checking the list of unique
338 levels of each qualitative variable. If the number of levels of factor is too high for a full visual
339 inspection, a list of selected levels can be created for each qualitative variable and compared with
340 the actual levels of factor present in each. Once identified, levels must be corrected during the
341 individual data reformatting step (**Fig. 2 - 2.3**).

342

343 2.4.2. Quantitative variables

344 For quantitative variables, we distinguish incorrect values which are values that are outside of the
345 normal range (e.g. a negative abundance) from outliers which are extreme values (e.g. a value of 100
346 while the mean is 1). Incorrect values are easily identifiable for variables whose values fall within an
347 interval of one (e.g. $[0 ; +\infty]$) or two limits (e.g. $[0 ; 100]$). A process can be put in place to
348 automatically remove incorrect values (i.e. those below or above the limit(s)) but we recommend
349 that each value be checked individually in order to correct for any errors that may have resulted from
350 the individual reformatting step. Outliers, however, are more difficult to treat. While their
351 identification through graphical (e.g. boxplot) or statistical (e.g. Grubbs' test, Dixon's Q-test) methods
352 is easy, it is generally difficult to know if their values result from natural variability or from an error
353 made during or following the acquisition of the data. Thus, these outliers must not be arbitrarily
354 removed from the data, without evidence which proves that they actually resulted from an error. To
355 this end, we recommend that the data provider be contacted in order to benefit from his/her
356 expertise. Among the errors which can be committed during the individual data reformatting step
357 (**Fig. 2 - 2.3**), unit conversion mistakes are the most common. Particular attention must be given to
358 the metric variable(s) (i.e. response variable) and the QAQC method must be specifically developed
359 for each of them. For example, for data expressed in percentage of cover, a quadrat can be divided

360 into multiple rows where each corresponds to the cover of a given taxa. Hence, it is necessary to
361 aggregate the cover percentage of these rows to verify that the total cover of the quadrat remains
362 above 0 % and below 100 %. We highly recommend the use of interactive data visualisation tools,
363 such as HTML tables (e.g. “DT” on R (Xie, Cheng, & Tan, 2020)) or interactive plots (e.g. “plotly” on R
364 (Sievert, 2020)), to help identify incorrect values (see Supplementary material).

365

366 2.4.3. Site coordinates

367 Errors in data entry or an incorrect transformation of coordinates (e.g. non-homogenized coordinate
368 reference systems) may cause the presence of invalid site coordinates. The identification of some
369 invalid positions can be assessed through visual inspection, such as by using an interactive map (e.g.
370 R package “leaflet”, (Cheng, Karambelkar, & Xie, 2019)). However, the response time of interactive
371 maps tends to increase with the number of site coordinates. Thus, an alternative is to perform this
372 verification for each individual dataset (**Fig. 2 - 2.3**), when the number of coordinates is still
373 manageable. The advantage of this method is that it allows for site positions to be confirmed to
374 ensure that they are consistent within the geographic extent of each dataset. While some invalid site
375 coordinates are easily identifiable (e.g. located on land while the data come from marine monitoring
376 programs) others can be more difficult to identify, for example when the error in latitude and
377 longitude is so small that it leads to a slight modification of the site position. Finally, a broad
378 automatic identification can be done using a polygon shapefile representing the area in which the
379 sites are supposed to be present, at which point sites that do not fall inside this polygon can then be
380 identified. Unfortunately, this method cannot totally replace a visual inspection. Once identified, the
381 correction of invalid site coordinates must be done during the individual data reformatting step (**Fig.**
382 **2 - 2.3**).

383 In addition to the QAQC step, we strongly encourage the data aggregator to send basic data
384 visualisation and identified errors of individually integrated datasets to data providers and to ask for
385 their feedback in order to ensure accuracy.

386

387

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389

390 2.4.4. Export of the synthetic dataset

391 Finally, when all of the errors are corrected, the final synthetic dataset is exported (**Fig. 2 - 4.3**). We
392 strongly recommend associating a metadata file to the synthetic dataset, where at least a description
393 of the variables and their units are provided. However, if the synthetic dataset is to be shared, a
394 more complete description of the data is required and the use of the Ecological Metadata Language
395 (EML) can be considered for this purpose (Fegraus, Andelman, Jones, & Schildhauer, 2005). Metadata
396 can include the name and contact of data aggregator(s), the link for the code repository used for data
397 integration, a full description of individual datasets integrated, as well an appropriate reference to
398 cite the synthetic dataset.

399

400 3. Case studies

401 To illustrate our workflow and to facilitate its use, we have provided an R code template for two case
402 studies. These case studies are inspired by the *Status of Coral Reefs of the World: 2020* report for
403 which 248 datasets of coral reef benthic monitoring data were integrated to assess the global status
404 and trends of hard coral cover over a period of more than three decades (Souter et al., 2021).
405 However, as the data used in the frame of this report were gathered through DSA and were

406 restricted in their use, we created example datasets that do not correspond to real datasets but
407 illustrate the main types of data formats encountered in this project. The first case study illustrates
408 the integration of data from the monitoring of benthic communities (sessile organisms) in coral reefs.
409 It corresponds to path 3A of the workflow, with a taxonomic re-categorization. The second case
410 study illustrates the integration of data from the monitoring of coral reef fish communities (mobile
411 organisms). It corresponds to path 3B of the workflow, with a taxonomic verification. The code
412 template provided illustrates steps 2 (individual data reformatting), 3 (data grouping and taxonomic
413 assignment) and 4 (QAQC) of the workflow, as the first step doesn't involve code. Each of these three
414 steps are associated with an R script. The *.Rmd* format (rmarkdown (Xie, Allaire, & Golemund,
415 2018)) was selected for the different R scripts because it allows for a better segmentation and
416 annotation of the code and process (necessary for the second step) and for the exportation of code
417 and output to an HTML file which may include interactive tables, plots and maps (necessary for the
418 last two steps, see Supplementary material). The code template for these two case studies and
419 associated information are available at https://github.com/JWicquart/monitoring_workflow.

420

421 4. Discussion

422 4.1. Lessons learned and limits of the workflow

423 The workflow design was possible thanks to the development of recent packages in R which make
424 data wrangling easier, and which facilitate the access to online taxonomic databases and promote
425 interactive data visualisation. Despite these technical improvements, data integration remains a time
426 consuming task, as some steps are difficult to automate, and a full reproducibility can sometimes be
427 hard to achieve.

428 Within the context of the *Status of Coral Reefs of the World: 2020* report (Souter et al., 2021), the
429 vast majority of the 248 datasets that were integrated were unpublished data which came from

430 numerous data providers. For this reason, over the entire year that was necessary to one person to
431 complete the data integration, the data gathering has represented the longest step in the workflow,
432 involving the identification and contact of potential contributors, signing DSAs, and finally engaging
433 in discussions with contributors to ensure that their data was properly reformatted. Despite their
434 financial cost, the organization of several workshops in different countries increased the visibility of
435 the project, which significantly increased the number of data providers and facilitated the individual
436 data reformatting step. However, in contrast to data publication, data sharing, on which the *Status of*
437 *Coral Reefs of the World: 2020* report (Souter et al., 2021) was mainly built, limits the traceability of
438 integrated individual datasets (as they are not associated with a DOI), reducing the reproducibility of
439 the workflow. The trend towards increased data publication should nevertheless help to reduce this
440 problem in the coming years (Costello et al., 2013; Shin et al., 2020).

441 The reformatting of individual data has also constituted a time-consuming step, requiring between
442 thirty minutes to several hours per dataset, depending on the complexity and machine readability of
443 the data format as well as the completeness of the metadata provided. Lack of data standards (e.g.
444 Darwin Core) and appropriate data management practices are thus the main factors which explain
445 the time required for this step and the difficulty for a complete automation. With regards to the
446 reproducibility of this step, it can be improved by describing decisions taken to correct errors for
447 each individual dataset, either directly in the code, or in metadata associated with the synthetic
448 dataset.

449 Given the difficulty of identifying benthic organisms on coral reefs, each monitoring program defined
450 and used its own nomenclature, using broad benthic categories instead of the taxonomic
451 classification system. For that reason, in the context of the *Status of Coral Reefs of the World: 2020*
452 report (Souter et al., 2021), and for the third step of the workflow (path 3.A), we defined a nested
453 classification which allowed for the re-categorization all the broad benthic categories used in the
454 individual datasets. This process required an ecological expertise and was iterative, as the chosen

455 nested classification was updated several times, when new cases were encountered. Once the
456 nested classification was defined, a manual stage was necessary to re-categorize categories used in
457 the individual datasets into the categories selected. This operation can be more or less laborious
458 depending on the number or categories to re-categorize. However, the taxonomic assignment step
459 can be quick and almost fully automated in cases where taxonomic verification is used (path 3.B, true
460 taxonomic categories) instead of taxonomic re-categorisation (path 3.A, non-taxonomic categories).

461 Finally, for the QAQC step, as the data integration process used for the *Status of Coral Reefs of the*
462 *World: 2020* report (Souter et al., 2021) aimed to provide a ready-to-use synthetic dataset for data
463 analysis, we deleted all data that could not have been corrected, which sometimes led to a loss up to
464 10% of an individual dataset. Our first case study can be easily adapted for the data integration of
465 sessile communities (with metrics such as percentage cover) in the marine and terrestrial realms.
466 However, we caution that for mobile communities (with metrics such as abundance or size), like fish
467 or birds, the QAQC process is more difficult to perform as the data quality depends heavily on the
468 sampling strategy. Nonetheless, it is important to note that all issues raised by the data
469 heterogeneity cannot be fully resolved during the data integration process but that some of them
470 may be addressed during the analysis itself. Analytical methods of synthetic datasets are beyond the
471 scope of this article and information on this subject can be found in Recknagel and Michener (2018).
472 Furthermore, different analytical methods can be used to limit bias relative to data heterogeneity,
473 such as the sensitivity analysis which allows for the identification of datasets which have a greater
474 influence on observed trends.

475

476 4.2. Advantages and comparison with existing approaches

477 In spite of the limitations mentioned, which mainly concern the time-consuming nature of the
478 process, this workflow presents several advantages. First, because it is founded on the direct

479 acquisition of the data from people in charge of their collection, it widens the scope for data that can
480 be integrated to those that have not been published and enhances the quality of the data integration
481 by benefiting from the expertise of data providers. Second, the workflow allows for the integration of
482 different levels of precision of taxonomic and spatial data, elements that generally vary between
483 monitoring programs. Because this method allows for raw data to be integrated, changes can be
484 directly assessed in the unit of the considered metric (i.e. full-data analysis (Spake et al., 2020))
485 instead of using effect-size, which is usually used in ecological syntheses through meta-analyses (e.g.
486 Côté, Gill, Gardner, & Watkinson (2005)). Finally, this method guarantees a high level of
487 reproducibility in facilitating the identification and correction of errors committed during the data
488 integration process. Workflows are particularly relevant for reproducibility (Poisot et al., 2016;
489 Cohen-Boulakia et al., 2017; Botvinik-Nezer et al., 2020) as they provide a visual representation of
490 the different steps, and the possibility to adapt each step depending on the goals of the project
491 (Jones et al., 2006).

492 Until now, a vast majority of bottom-up approaches for data integration were developed by large
493 databases, in particular GBIF (GBIF: The Global Biodiversity Information Facility, 2021) or OBIS (OBIS,
494 2021). These databases typically include a web-based interface to allow data providers to publish
495 their datasets, such as the Integrated Publishing Toolkit (IPT) developed by GBIF (Robertson et al.,
496 2014), and are based on data standards, such as the DarwinCore (Wieczorek et al., 2012). Unlike
497 these databases, which seek to increase the accessibility and standardization of biodiversity datasets,
498 the workflow presented here aims to produce a ready-to-use synthetic dataset, adapted to the
499 analyses that will be performed, but also to integrate datasets whose formats are not yet suited for
500 incorporation into existing databases.

501 Outside of large databases, the number of studies related to data integration remains limited and
502 have been mainly focused on quality control (e.g. (Dou et al., 2012; Belitz et al., 2018)). Most have
503 used similar steps to the one presented here to control data quality, and to check geography,

504 taxonomy and the completeness of data or to investigate outliers (Dou et al., 2012; Vandepitte et al.,
505 2015). These studies also tended to explicitly state quality checks in the form of a series of questions
506 or items to review (Vandepitte et al., 2015; O'Donnell et al., 2021). As these items must be
507 specifically tailored to the data and the analyses that follow, we did not explicitly present a list of
508 quality checks here, but we strongly recommend the implementation of this approach. Several
509 studies have highlighted the requirement of manual step(s) during quality control, where the
510 knowledge of the data aggregator is essential to verify the consistency and ecological relevance of
511 modifications applied (Jones et al., 2006). Overall, the individual data reformatting step is not
512 mentioned in studies related to data integration mainly because the approaches developed are built
513 on web-based interfaces (Chaudhary et al., 2010; Robertson et al., 2014) where the data providers
514 are left with the responsibility of reformatting their data. Finally, O'Donnell et al., (2021) presented a
515 similar approach to the one presented here, where they developed a framework and a custom open-
516 source software to integrate long-term monitoring data of the greater sage-grouse population. While
517 this framework and resulting considerations could be applied to other studies (O'Donnell et al.,
518 2021), the software they developed was tailored to their specific scenario and could be difficult to
519 reuse. Based on the R code associated with the two case studies, we hope that the workflow
520 presented here can bridge this gap, through a more versatile approach.

521

522 5. Conclusion

523 The purpose of the workflow presented in this study is to encourage researchers to integrate
524 multiple ecological monitoring data into a single synthetic dataset in order to perform analyses on
525 the status and trends in biodiversity and ecosystems at larger scales. The results of these analyses
526 are essential to inform policy makers and to measure the effectiveness of global (e.g. CBD Post-2020
527 Biodiversity Framework), regional or national programs, that aim to protect biodiversity and
528 ecosystems (Balmford, Green, & Jenkins, 2003). Data integration could also be of great interest for

529 research topics, such as macroecology and biogeography, by testing ecological hypotheses at larger
530 scales (Carpenter et al., 2009; Poisot et al., 2016; König et al., 2019). The need for data integration
531 will likely increase in the coming years (Miller et al., 2019), due to the emergence of new standards
532 on data interoperability (e.g. FAIR data principles, (Wilkinson et al., 2016)) and a trend towards
533 further data sharing (Michener, 2015) or data publication (Costello et al., 2013; Shin et al., 2020),
534 which together sharply increase the volume of accessible data available to the scientific community
535 (Hampton et al., 2013). In this context, the publication of code and workflow are essential to increase
536 the reproducibility of results and to drive ecology toward a more transparent science.

537

538

539 Acknowledgments

540 We thank the International Coral Reef Initiative (ICRI) and the Prince Albert II of Monaco Foundation
541 for the funding. We thank Claire Bissery, Charlotte Moritz, Jason Vii, Mary Donovan and all the
542 people involved in the *Status of Coral Reefs of the World: 2020* report for the valuable discussions we
543 had during the design of the workflow. We thank two anonymous reviewers for their helpful
544 comments.

545

546 Authors' contributions

547 JW designed the workflow, made the figures and wrote the code template for the two case studies.
548 JW and SP led the writing of the manuscript. All authors contributed critically to the drafts and gave
549 final approval for publication.

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551

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