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BRITISH ECOLOGICAL SOCIETY Methods in Ecology and Evolution

PRACTICAL TOOLS

CheckEM: An open-source toolkit for standardising, cleaning and visualising stereo-video fish survey data

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Abstract

1. Effective research and monitoring requires accurate, interoperable and representative data. Stereo-video based methods are commonly used to survey fish and are rapidly expanding globally due to their cost-effectiveness, ability to provide accurate body size measurements, non-destructive approach and capacity to create permanent data records. However, the representativeness of both stereo and mono-video derived data depends on standardised approaches to provide quality assurance of reliable, reproducible and error-free data. A national synthesis of both stereo and mono-video fish survey datasets identified numerous errors in data collection and annotation, many of which are also relevant to other survey methods.
2. To develop an open-source toolkit, CheckEM, for quality control checks on fish survey data.
3. The *CheckEM* web application and R package identifies errors in metadata and cross-checks annotations of fish with taxonomic databases, expected spatial distributions, and, in the case of stereo-video, maximum body sizes, and works with the outputs of a range of annotation tools (including EventMeasure and other annotation software). *CheckEM* flags species observed beyond their known range, outdated scientific names and body size outliers. *CheckEM* standardises, cleans and visualises datasets, offering interactive plots and tables in a user-friendly

interface. Downloadable summary data and error reports support iterative checks and improvement of data quality.
4. We demonstrate that *CheckEM* enhances data accuracy, confidence, interoperability and reusability, improving collaboration and cross-dataset comparisons to support robust analyses and informed marine monitoring and management.

KEYWORDS
BRUVs, data cleaning and confidence, EventMeasure, fish, quality assurance, quality control, R package, stereo-video

1 | INTRODUCTION

Documenting and addressing global environmental challenges necessitates expanding datasets and ensuring consistency across both spatial and temporal scales (Soranno et al., 2015). Exemplifying these challenges is the development of FAIR data standards (Findable, Accessible, Interoperable, Reusable) that aim to enhance the impact of datasets by increasing their ability to be easily amalgamated and synthesised (Wilkinson et al., 2016). A second related requirement for scaling-up datasets is ensuring that they are robust and reliable, by minimising errors (Tanhua et al., 2019). This can be achieved by implementing processes to proactively prevent errors from entering datasets (Quality Assurance; QA) and detecting and correcting errors in datasets once they occur (Quality Control; QC).

QC assessments and procedures are well established in many scientific fields, ensuring data reliability and reproducibility. In medicine, standardised QC protocols help maintain the accuracy of diagnostic tools and clinical trials (Plsek, 1999). Remote sensing uses rigorous validation techniques to assess spatial accuracy of predictive models (Congalton, 1991), and gene sequencing employs automated quality control pipelines to minimise errors in genomic datasets (Beissbarth et al., 2000). Similarly, in marine science, structured QA/QC processes are essential for maintaining high-quality datasets, particularly in large-scale monitoring efforts (e.g. Vandepitte et al., 2015). For instance, Australia's continental-scale acoustic tracking database includes an automated quality control system to detect and correct errors, ensuring reliable movement data for marine species (Hoenner et al., 2018). Similarly, we have seen coordinated efforts by the global oceanographic observing networks in QA through the development of best-practice documentation (Bushnell et al., 2019). Without structured QA/QC processes, datasets may contain errors that reduce confidence in the data and the analyses, potentially dramatically influencing results and interpretations. Identifying and correcting errors may be especially challenging, but particularly important, when combining datasets across research groups both nationally and internationally where differing data standards may have emerged (Chapman, 2005; O'Dea et al., 2021).

Within imagery-based methodologies, best-practice field manuals (a form of QA) have been developed for various methodologies such as diver operated stereo-video (Goetze et al., 2019), benthic observation survey systems (Langlois et al., 2025), remotely operated vehicles (Monk et al., 2024) and stereo-baited remote underwater video (stereo-BRUVs, Langlois et al., 2020). These manuals outline the QA procedures for system design, field operations and image annotations, helping to ensure that methods used to collect data are broadly comparable across studies.

Despite these safeguards, the multistep workflow, from metadata to annotations and then to data products, required for many methods using underwater imagery means that errors can easily enter datasets. Errors in one step, such as incorrectly entering metadata, can propagate through the workflow, potentially resulting in more consequential errors in later stages, such as falsely recording a species as absent when they are present. In 2018, 12 Australian academic, research and management organisations synthesised data collected from 19,939 Baited Remote Underwater Video (BRUV) deployments (Harvey et al., 2021). Despite broad adherence to an established field manual (Langlois et al., 2020), we identified various recurring errors across datasets. This provided a unique opportunity to design a process to identify and rectify common errors in fish survey datasets. Although originally designed for stereo-BRUV datasets, the QC process has been expanded to capture errors in any point count or transect fish survey dataset.

Here, we describe and demonstrate an easy-to-use open-source toolkit (CheckEM V.1.0.0) designed to perform QC checks on metadata and fish survey data. This toolkit is accessible to researchers globally and includes an R package, interactive web-based app and extensive documentation and tutorials. The app allows users to drag and drop files to compare annotations against national (CAAB, Rees et al., 1999) and global (FishBase, Froese & Pauly, 2024; WORMS, Ahyong et al., 2024) open-access databases, explore interactive plots and tables in a graphical interface, and download summarised data and error reports. The toolkit streamlines the QC process and is easily integrated into existing workflows using observational or image-based methods to study fish assemblages, but is applicable to other marine organisms. CheckEM accepts outputs from annotation tools including EventMeasure, BIIGLE, StereoMorph (Olsen & Westneat, 2015) and others. *CheckEM* provides ecologists with an open-access, user-friendly toolkit to efficiently detect, correct and prevent recurring dataset errors. The development of *CheckEM* addresses a lack of standardised QC procedures in fish survey data systems and helps ensure fish datasets can be aggregated to address global environmental challenges.

2 | THE DEVELOPMENT OF '*CheckEM*'

Several common errors and inconsistencies were identified during a national synthesis of Australian BRUV data (Harvey et al., 2021; Supporting Information S1), many of which stemmed from metadata quality issues or mistakes in annotation. Such problems are widespread across workflows and are not unique to any single method or annotation tool (Thompson & Mapstone, 1997), highlighting the need for effective QC procedures irrespective of data or the source. A variety of specialist software tools are used for image annotation of fish, including EventMeasure, StereoMorph and BIIGLE. Although these tools are well designed, the annotation process remains susceptible to human error.

EventMeasure (www.seagis.com.au) is the most commonly used software for stereo-video annotation of fish which made it the logical starting point for the development of CheckEM (Gomes-Pereira et al., 2016; Whitmarsh et al., 2017). We further developed R scripts published by Langlois et al. (2015) to automate error detection from EventMeasure outputs (see Supporting Information S2 for examples). We subsequently extended the approach to outputs of other annotation tools or visual datasets (see Supporting Information S3 and S4 for examples). To support this broader use, we provide worked guides showing how outputs from other software can be converted into the generic input format required by CheckEM. For example, Supporting Information S4 demonstrates a step-by-step Excel workflow to prepare BIIGLE annotation data without requiring any coding. In addition, for the R based StereoMorph package we provide a GitHub repository (github.com/GlobalArchiveManual/StereoMorph-CheckEM-example) and workflow that illustrates a coding-based route using annotation data from García-Baciero et al. (2025). Together, these examples show how both basic tools and higher level coding approaches can be used to create data compatible with CheckEM and serve as templates for users working with other annotation software. In this way, CheckEM enables abundance and body size data from any annotation method to be rigorously checked, ensuring accessibility and consistent QC across a wide range of workflows.

To make these QC procedures more accessible, we turned the scripts into a user-friendly web-based dashboard named '*CheckEM*', (Check**E**vent**M**easure). Designed in RStudio (Posit Team, 2024) using the *shiny* (Chang, 2024) and *shinydashboard* (Chang & Borges Ribeiro, 2021) packages, the application provides an intuitive interface for users to identify and address errors. The online version is available at marine-ecology.shinyapps.io/CheckEM/, published through a subscription-based shiny server. The source code for *CheckEM* is freely available on GitHub (github.com/GlobalArchiveManual/CheckEM).

Fully automated QC has its limitations, and there is a risk that real and potentially important observations could be ignored or removed (e.g. a verified sighting of a species outside its known range being identified as an error). To ensure this does not happen, *CheckEM* is intentionally semi-automated, it only flags but does not remove or change suspicious annotations. Users are responsible for revisiting the raw annotations and imagery to verify flagged entries. If the flagged errors can be verified as correct (e.g. taxonomic expert identification of species in a new location), this feedback can be provided in a short form to be reviewed and incorporated into the life-history information used by *CheckEM* (globalarchivemanual.github.io/CheckEM/articles/community-updates). This process ensures that the information used to QC annotations remains up to date, thereby improving the process for all users. By focusing on flagging rather than automatic correction, *CheckEM* corrects both the raw annotations and the summarised data. This is important for maintaining the interoperability of annotations (e.g. for training image automation algorithms), and for preventing the recurrence of errors in future data exports.

2.1 | Life-history information

CheckEM verifies annotations by comparing uploaded data against species-specific life-history information. This includes expected geographic distributions and maximum recorded body length, which are used to flag potential errors in species identification and measurement. Initially, *CheckEM* was designed to verify annotations for Australian species, using a collated list of life-history information (Supporting Information S5). To make *CheckEM* applicable globally, we collated life-history information for all fish species listed on FishBase (Supporting Information S6; Froese & Pauly, 2024). Due to the greater number of species, this global list contains less detail than the Australian list. The following sections describe the sources used for both life-history lists to validate annotations.

2.1.1 | Species distributions

QC checks on fish annotations need to be specific to the locations where imagery is collected, as fish exhibit spatial distribution patterns in abundance, driven by environmental conditions (Planque et al., 2011). Species-specific distribution patterns are available in Australia through 'fishmap', accessed through the Codes for Australian Aquatic Biota (CAAB, Rees et al., 1999). These distributions are based on the best validated evidence and expert knowledge. The distributions of all fish species listed on CAAB were simplified into Australia's six marine bioregions (South-east, Temperate East, South-west, North-west, North and Coral Sea, Richardson et al., 2020). Once data are uploaded to CheckEM, the metadata is spatially joined to the Australian bioregions to find species outside of their known range.

Names of all marine fishes in the world were obtained using the *load_taxa* function in *rfishbase* (35,000+ species Boettiger et al., 2012). Global distributions were acquired through the *rfishbase* package using the *distribution* function (Boettiger et al., 2012), which returned the Major Fishing Areas of the Food and Agriculture

Organization of the United Nations (FAO) where a species is present. Users can choose to use the Australian or the global list of species distributions to check their annotations. Once data are uploaded to CheckEM, the metadata is spatially joined to the FAO major fishing areas to find species outside of their known range.

2.1.2 | Scientific nomenclature and synonyms

A widespread increase in active exploration and hence the number of newly described species has resulted in a multiplicity of names, many due to scientists working independently (King et al., 1985). Taxonomic advances have clarified relations among species, resulting in changes to scientific names at the levels of family, genus and species after species were originally named (Tracy, 2022). Here, we define a synonym as an invalid scientific name, which can either be a new combination of family, genus and species, a junior synonym, a misidentification or a misspelling. Scientific names can be difficult to manually validate (Froese, 1997), yet problematic, for example, Bailly and Hureau (1995) found 14 different spellings for *Bregmaceros mcclellandi* in two databases. Synonyms were obtained from CAAB and the *rfishbase* and *worrms* packages, which include misspellings, misidentifications and name changes (Boettiger et al., 2012; Chamberlain, 2020). Some valid species names are also synonyms for other species (e.g. *Pagrus auratus* is synonym for *Sparus aurata Linnaeus, 1758*, however, both *P. auratus* and *S. aurata* are valid scientific names in their own right). We have defined these as ambiguous synonyms. When an ambiguous species name is uploaded to CheckEM, the software will not change the species name but will warn the user that the species has multiple valid names linked to it.

2.1.3 | Maximum length

Maximum length for the Australian and global life-history lists were obtained using the *species* function in the rfishbase package (Boettiger et al., 2012). For some species, the maximum length recorded was smaller than those reported from other sources. This discrepancy was important to address because the smaller recorded lengths led to an excessive number of length measurements being flagged as errors. As a result, annotators spent considerable time reviewing these flagged measurements, many of which were realistic. To address this, we collected additional maximum length data from various references, including books, websites and journal articles. This information was collected via a Google form (globalarchivemanual.github.io/CheckEM/articles/community-updates), which users could fill out. These data are included in the life-history information with a corresponding column indicating the source of the maximum length value. Standard operating manuals recommend measuring fish using fork rather than total lengths (Langlois et al., 2020), therefore, where available we have reported maximum lengths in fork length. If a maximum length was not in fork length and a length–length equation was available on FishBase (Froese & Pauly, 2024), the maximum length was transformed into fork length. The type of length measure and source used is reported for every maximum length.

2.1.4 | Length–weight relationships

Fisheries management and ecological studies often require information on body weight or estimates of biomass (Froese et al., 2014). Weight (W in g) can be calculated from length (L in cm) using the formula $W = a\ L^b$, where coefficient b indicates isometric growth in body proportions and a describes body shape and condition (Froese, 2006; Le Cren, 1951). The length–weight coefficients a and b for individual species were accessed through the *rfishbase* package (Boettiger et al., 2012). The length–weight relationship studies obtained were ranked on the number of individuals (studies with more data were preferred over those with low numbers), sex (studies with both sexes were chosen over those with just one sex or juveniles), r^2 (higher r^2 were preferred) and by country for the Australian version (studies in Australia were preferentially selected). The length–weight relationship study with the best ranking was selected for each species, where length–weight parameters were not available for an individual species the Bayesian length–weight estimates were obtained from www.fishbase.org using the package *fishflux* (Froese et al., 2014; Schiettekatte et al., 2020).

We synthesised the above life-history information into two spreadsheets (Australia and Global, herein referred to as the life-history tables). The code to create the life-history tables and the tables themselves are publicly available github.com/GlobalArchiveManual/CheckEM. The life-history tables are compared to annotations uploaded to *CheckEM* to identify species that have been observed outside of their range, update scientific names that have been changed and to convert length to weight using length–weight equations.

2.2 | Spatial management validation

Spatial areas that are closed to extractive (e.g. fishing) and destructive (e.g. dredging) practices are frequently important in research and monitoring of human impacts on the marine environment (Ballantine, 2014). CheckEM overlays the coordinates of uploaded annotations onto a database of marine protected areas. This facilitates broad checks of coordinates in the metadata and coarsely explores patterns in fish abundance and size across areas with different spatial management. For Australian datasets, *CheckEM* uses the Collaborative Australian Protected Areas Database (CAPAD), which lists the Government, indigenous and privately protected offshore protected areas in the State and Commonwealth waters of Australia (Commonwealth of Australia, 2020). For all other datasets, *CheckEM* uses marine areas from the World Database on Protected Areas (WDPA; IUCN & UNEP-WCMC, 2023). However, users should be aware that these spatial layers may not always reflect current regulations or zoning. Some areas may have temporary exemptions or policy changes that are not captured in the datasets.

3 | USING *CheckEM*—APPEARANCE AND FUNCTIONALITY

The *CheckEM* dashboard and R-workflows are organised into modules, including (1) Combine Datasets: standardising and formatting multiple annotation sets; (2) Check Metadata: flagging incorrect, suspicious or missing metadata; (3) Check Count: cross-check annotations against life-history information and known distributions; (4) Check Length Measurements: compare length measurements against known maximum sizes and flag errors in precision and accuracy; (5) Calculate Biomass: convert length measurements to biomass using length–weight equations; (6) Check Benthic Annotations: conduct basic checks on benthic habitat annotations; (7) Quality Control Scores: produce scores to easily compare the quality of datasets; and (8) Downloads: tables of all errors and summarised data are downloadable (Figure 1). A case study is also provided to represent the typical iterative usage of *CheckEM* and demonstrates the reduction in errors by using *CheckEM*. We provide extensive

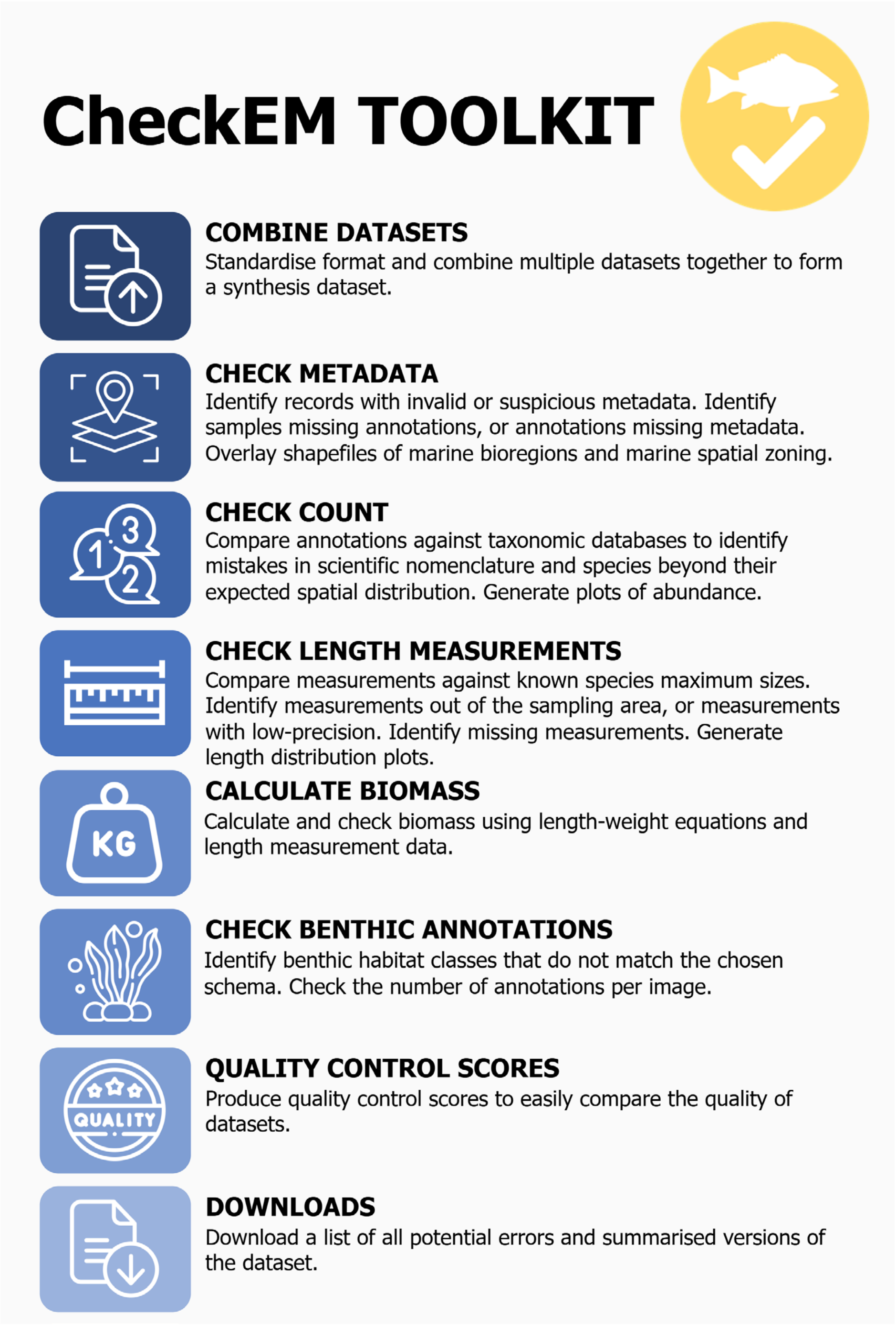

FIGURE 1 The *CheckEM* toolkit combines, standardises and checks fish survey data. The *CheckEM* package and R workflows are organised into thematic modules.

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documentation, examples and tutorials on functions on the package website (globalarchivemanual.github.io/CheckEM).

3.1 | Graphical interface

The user uploads their deployment metadata and fish annotations (EventMeasure exports or generic; see Supporting Information S2–S4 for examples). *CheckEM* conducts validations and QC rapidly (~30 s) by comparing annotations against life-history information, including expected spatial distribution, and body-size of fishes (using fork length) and suggests where species' names may have been changed historically and require updating (e.g. synonyms exist for a species). Each box within the interface represents a QC check (Figure 2). A table of all QC checks at the time of publishing are provided in Supporting Information S1.

3.2 | Error report

The user can download a list of all errors found within the annotations, ordered by deployment/sample name. This allows the user to easily check through their raw annotation files to iteratively fix errors.

3.3 | Summarised data

CheckEM provides an option to download annotation data summarised per deployment/sample name (e.g. the total number of individuals of each species in each sample) suitable for subsequent research and monitoring analysis and reporting. An option is provided to add in zeros where a sample was collected but a species was not present to ensure absence data is retained for subsequent analyses. Downloaded data are formatted to facilitate uploading to globalarchive.org, a centralised repository that allows open access and private sharing of fish image annotation data from BRUVs or similar imagery-based sampling techniques.

3.4 | Case study—Identifying data errors

Stereo-BRUV surveys of fish assemblages were performed in Exmouth Gulf, north-western Australia between the 1 and 7 May 2024 in depths ranging from 0.5 to 21.5 m, forming baseline surveys for a proposed marine protected area. The study was approved by the University of Western Australia's Animal Ethics Committee (AEC approval number RA/3/100/1671). Imagery was annotated using EventMeasure (www.seagis.com.au), following standard operating procedures outlined in Langlois et al. (2020).

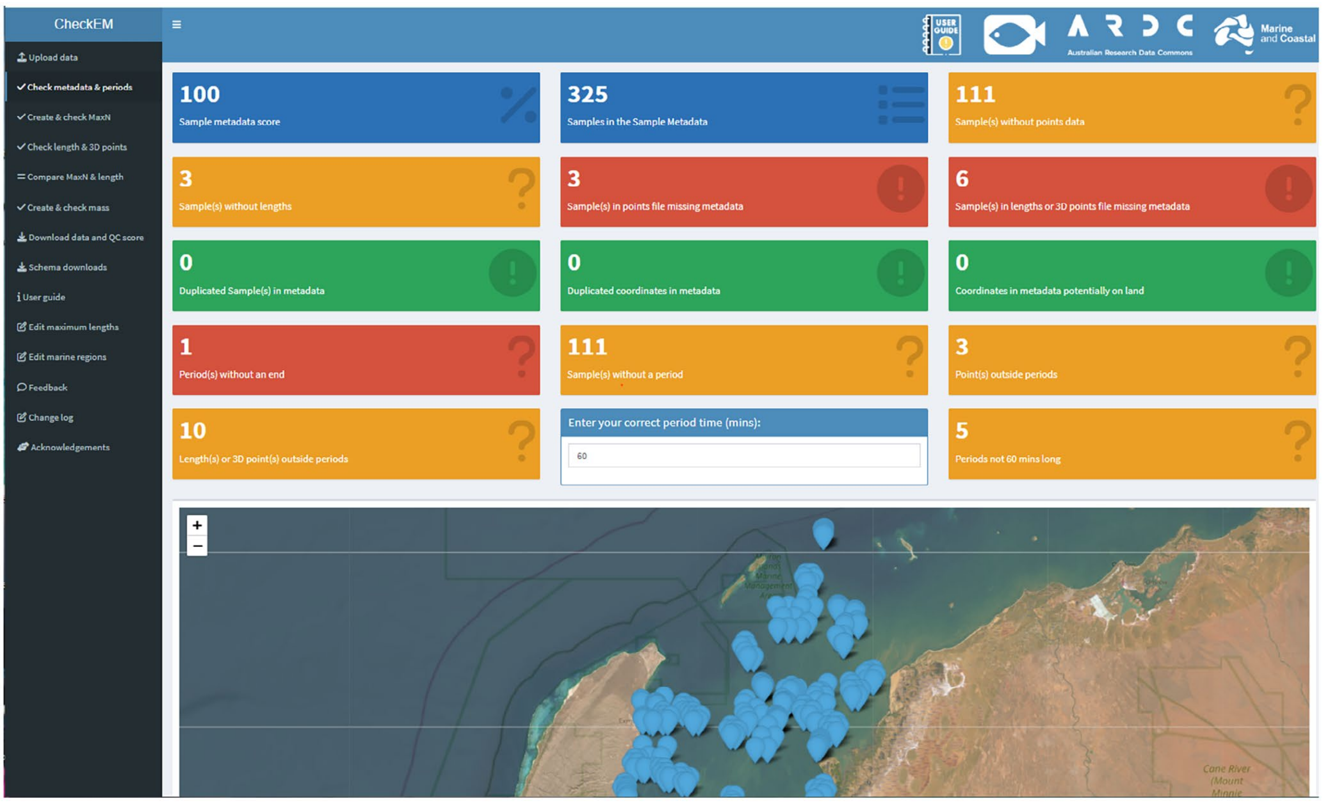

FIGURE 2 Graphical interface of the *CheckEM* web-based application, showing an example stereo-BRUV survey dataset of fish in Exmouth Gulf, north-western Australia—see case study. Each QC check is represented by a box, the colour of the box indicates if the data uploaded have passed (blue = statistic, green = no errors, yellow = potential issue to investigate and red = an error to be changed).

The database export generated from EventMeasure included .txt files (Points, 3D points, Lengths and Periods), which were uploaded into *CheckEM* with the campaign metadata (.csv) for QC checks.

CheckEM flagged 376 incorrect, misspecified, or missing metadata and potentially incorrect annotations and measurements, with a summary of these errors presented in Figure 3. The most common types of errors flagged were body-size measurements that are larger than the maximum known size, smaller than their expected size or species that were not expected to be in that region. The errors identified were corrected iteratively within the raw annotations in EventMeasure, not in the output files. Each time corrections were made in EventMeasure, new exports were generated and re-checked in *CheckEM*. This iterative process ensured the integrity of the data and prevented future exports from containing erroneous metadata and annotations. After three iterations, *CheckEM* reduced the number of metadata errors by 97%, annotation errors by 18% and measurement errors by 16%, relative to the initial error counts (Figure 3). Errors in metadata usually have flow-on effects to further checks, and in this example, the annotators fixed the metadata errors in the first iteration, before moving on to fix issues with the annotations and measurements. By the third iteration, errors have been substantially minimised, resulting in a cleaner and more reliable dataset. The final clean dataset could then be used for analyses and uploaded into GlobalArchive, where it is accessible to the broader community (Goetze, 2026).

It is important to note that some errors are left in the dataset after the QC process, for example, unexpected sampling duration; this is because the user reviewed them and decided they are not an error (here a stereo-BRUV was pulled earlier than the intended sampling duration). In this example, there are a high number of measurements that are flagged as being larger than expected. This is potentially due to the documented maximum sizes of certain fish species being smaller than their actual maximum sizes, which are not accurately represented in published life-history information. Alternatively, it could be due to a calibration error and should be inspected further. After the QC process is complete, if users believe that the species that they have observed should be listed as occurring in that region or that the maximum size should be increased, they can update the life-history and spatial distribution information used by CheckEM in a short form (globalarchivemanual.github.io/CheckEM/articles/community-updates).

3.5 | Uptake of *CheckEM*

The *CheckEM* vignette has attracted over 800 unique users and received more than 2700 views between 1 December 2023 and 1 December 2024, across six continents. The global distribution of users highlights Australia as the primary hub, followed by the United States. This growing global engagement underscores *CheckEM's* relevance and adoption within the broader community.

4 | CONCLUSIONS

Accurate, interoperable and representative data are required for robust analyses and informed management of marine resources. *CheckEM* addresses this need by offering a rapid and standardised approach to perform QC checks on metadata and image annotations in ~30 s. By efficiently identifying issues without altering the original data, *CheckEM* saves time spent on manual data wrangling, improves data accuracy and increases confidence in results. This facilitates data sharing, reuse, integration into spatiotemporal research and monitoring programmes, while also enabling reliable aggregation of datasets to tackle challenges of national or global significance.

Misspellings of scientific names and taxonomic inconsistencies are a common source of error in ecological datasets, particularly when combining datasets over extended periods of time or by different research groups. Accurate taxonomic information is essential for synthesising data over time. *CheckEM* automatically detects and updates synonyms, and crosschecks nomenclature against taxonomic databases. This ensures taxonomic naming is consistent and reduces errors when synthesising datasets and facilitates extended time series analysis.

Stereo-video methods have become increasingly popular due to their ability to precisely measure body size (Whitmarsh et al., 2017). Accurate body size data are integral to ecological studies, and can be used for many applications, for example, calculating metrics such as biomass or productivity (Aston et al., 2024; Langlois et al., 2012; Morais & Bellwood, 2020), and if applicable, for use in length-based stock assessments (Pauly & Morgan, 1987). Measurements of fish greater than their maximum recorded size could indicate measurement errors, misidentification or potentially a new maximum size. *CheckEM* automatically finds annotations that are over the maximum size, enabling the annotator to review and correct the raw annotation before data analysis. This ensures that incorrect body size measurements are not used to calculate other metrics where they could have a large and disproportionate influence of analytical variables (e.g. biomass estimation; Harvey et al., 2002).

CheckEM's QC checks are broadly applicable beyond video-based methods, and can be applied to fish abundance and body-size information collected using other methods such as visual sampling (e.g. Bohnsack & Bannerot, 1986) or environmental DNA (e.g. Stat et al., 2019). More broadly, the framework underpinning *CheckEM* has potential applications in fisheries-related monitoring and research, including data collected from commercial trawls, seine nets and other sampling techniques. Ensuring data quality across all methods is critical for reliable methodological comparisons and synthesis in ecological studies.

Effective research and monitoring rely on accurate, interoperable and representative data but also on data quality assessment procedures (Klein et al., 2019). *CheckEM* provides a framework for improving data accuracy and providing a quality assessment. It was developed through the joint efforts of a national coalition of research groups, which helped refine and expand its capabilities, and

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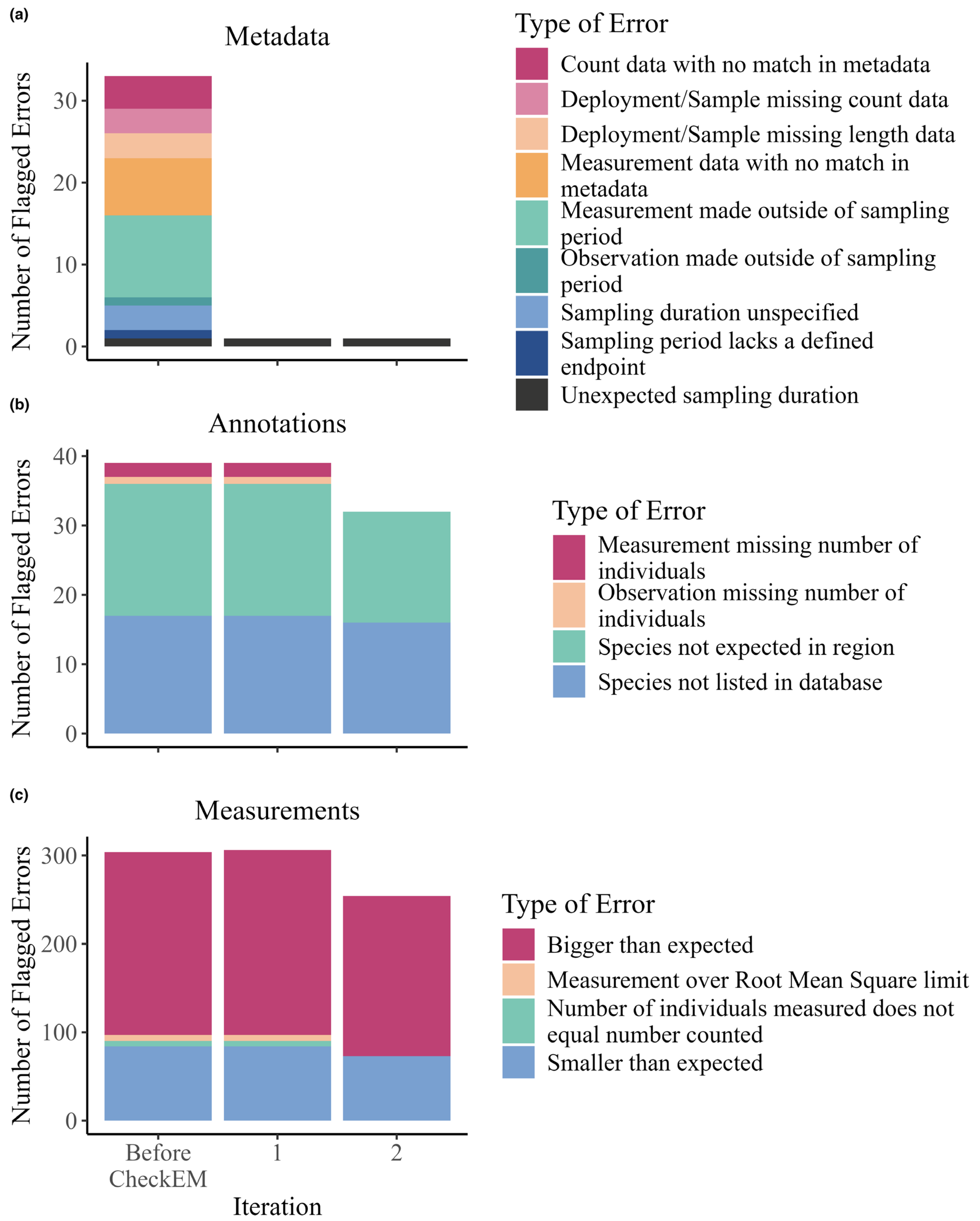

FIGURE 3 The number of flagged errors across three categories: (a) metadata, (b) annotations and (c) measurements, from the first export from EventMeasure and over two iterations of QC using *CheckEM*. The sampling period/duration and Root Mean Square (RMS) checks are unique to EventMeasure outputs. The RMS is the largest RMS of all points in a length measurement, the recommended limit is 20 mm (consistently high RMS values can indicate a calibration problem).

it provides an efficient QC solution for surveys of marine fish more broadly.

AUTHOR CONTRIBUTIONS

Brooke A. Gibbons led the writing of the manuscript and coding of the *CheckEM* shiny app. Brooke A. Gibbons and Tim Langlois conceived the project. Tim Langlois supervised the project. Brooke A. Gibbons and Claude Spencer built the CheckEM R package, examples and documentation. Brooke Gibbons, Claude Spencer, Todd Bond, Jordan Goetze, Tim Langlois and Daniel Agnello contributed conceptual input and suggestions for functionality. Dianne Mclean, Matthew Navarro, Jordan Goetze and Jac Monk contributed to the writing of the manuscript. Todd Bond, Daniel Agnello, Charlotte Aston, Charlie Huveneers, Stephen J. Newman, Shaun Wilson, Andrew Hoey, Ben Radford, Conrad W. Speed and Daniel Ierodiaconou contributed to a revision of the manuscript.

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CONFLICT OF INTEREST STATEMENT

The authors declare no conflicts of interest.

PEER REVIEW

The peer review history for this article is available at https://www.webofscience.com/api/gateway/wos/peer-review/10.1111/2041-210x.70287.

DATA AVAILABILITY STATEMENT

The code for CheckEM is available at github.com/GlobalArchiveManual/CheckEM, archived at https://doi.org/10.5281/zenodo.18677708 (Gibbons & Spencer, 2026). The package documentation is available at globalarchivemanual.github.io/CheckEM/. Data used in the case study are available at dev.globalarchive.org/ui/main/syntheses/25, archived at https://doi.org/10.60509/5sdc-rr37 (Goetze, 2026). The StereoMorph case study is available at github.com/GlobalArchiveManual/StereoMorph-CheckEM-example, archived at https://doi.org/10.5281/zenodo.18677717 (Gibbons, 2026).

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SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

Table S1. A table of all QC checks at the time of publishing.

Data S2. Example EventMeasure Database Exports.

Data S3. Example 'Generic' Data.

Text S4. Workflows to turn BIIGLE exports into 'Generic' data.

Table S5. Australian Life-history information and sources.

Table S6. Global life-history information and sources.

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