Counting and Measuring Fishes: The Use of Baited Remote Underwater Video Systems (BRUVS)

Introduction

Fundamental to ecology, conservation and fisheries management is an understanding of where fish are found, how many there are and their size. Fish are more difficult to count than terrestrial animals simply by virtue of inhabiting a vast 3-dimensional realm, hidden beneath the blue curtain of the ocean's surface.

The fishes of shallow coastal waters have been counted by snorkelers and SCUBA divers for decades; many other species exist well beyond the limits of this method. Indeed, much of what we know about pelagic species is limited to those we eat, with knowledge inferred from fish catches (www.seaaroundus.org). While important, such data do not cover many species of conservation interest. Moreover, fisheries-derived data are by definition lethal, and their collection is inappropriate in highly protected marine parks.

Baited remote underwater video systems (BRUVS) deliver non-lethal sampling across a wide range of habitats and depths. First deployed on shallow reefs (Figure 1), seabed BRUVS have also been deployed at depth on mesophotic reefs (Andradi-Brown et al. 2016). Development of mid-water BRUVS (Figure 2) have extended their use into pelagic and open ocean environments (Bouchet & Meeuwig 2015, Letessier et al. 2017). BRUVS are deployed as single cameras (Cappo et al. 2004, Speed et al. 2018) or in stereo-configuration (Cappo et al. 2006, Harvey et al. 2012).

BRUVS generate records of species identifications, relative abundance and, when stereo-BRUVS are used, length (Whitmarsh et al. 2017). They can also, under some circumstances, be used to explore animal behaviour (Ryan et al. 2015, van Elden & Meeuwig 2020). Other applications include understanding individual behaviour (Sherman et al. 2018) where markings can be determined. BRUVS have been used to test benefits of marine protected areas (Espinoza et al. 2014, Malcolm et al. 2018), identify refuges of ocean wildlife (Letessier et al. 2019), determine the direct and indirect effects of fishing (Mclean et al. 2011, Langlois et al. 2012), and provide insight into the distribution and foraging behaviour of cryptic species (Letessier et al. 2014, Thompson et al. 2019).

As with all sampling methods, BRUVS have biases. Biases occur due to:

(1) the use of bait which may disproportionately attract high trophic level species (Dorman et al. 2012, Hardinge et al. 2013), and evidence that diver presence can reduce estimates of shark abundance (Langlois et al. 2010, Schramm et al. 2020);

(2) the creation of bait plumes which means that the "catchment", the area occupied by individuals, is unknown and thus numbers per unit area cannot be calculated; and

(3) the movement of individuals in and out of the camera field of view, necessitating the use of a conservative measure of abundance, MaxN, the maximum number of individuals of a given species in a given frame.

Despite these biases, multiple studies across space (Letessier et al. 2017) and through time (Forrest et al. 2021) have demonstrated that these biases are consistent and thus BRUVS-derived data can be successfully used to assess relative change in marine vertebrate assemblages.

For more information on how seabed and mid-water BRUVS are deployed and used, see Bouchet et al. (2018) and Langlois et al. (2018).

Figure 1. Seabed BRUVS.
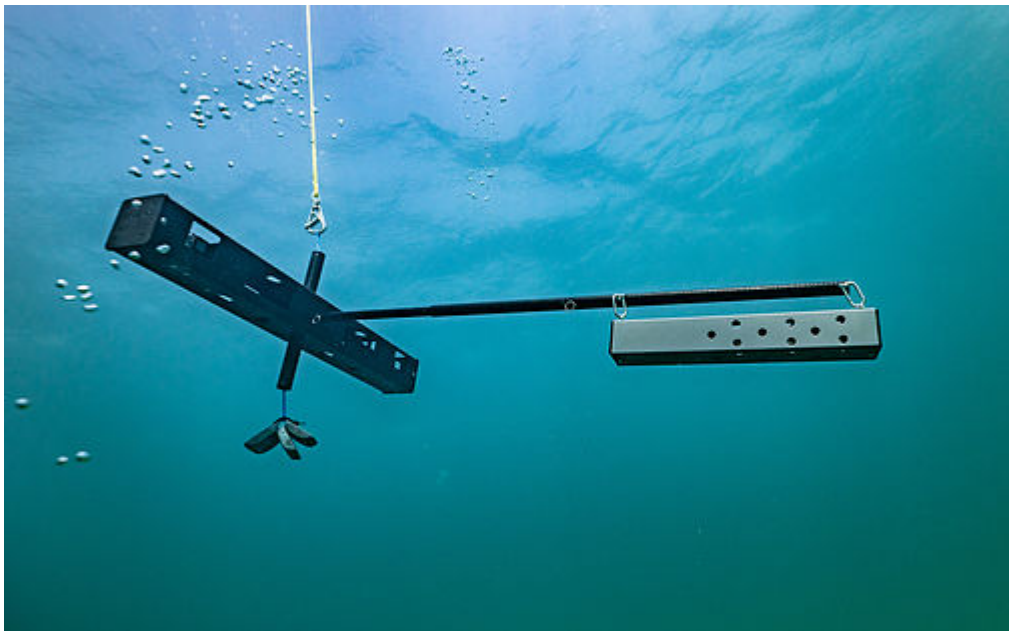
Figure 2. Mid-water BRUVS.

The FishBase BRUVS Portal: what the data look like

The fundamental unit of the FishBase BRUVS is "survey". A survey is comprised of BRUVS deployments at a given location during a given time period (typically between 5 and 30 days, depending on the spatial extent of the location of interest). Details of each sample are provided in the "metadata" file that can be downloaded (Table 1).

Table 1: Definitions of information provided in the metadata csv provided on download of surveys.

Variable	Definition
Survey Name	Survey name typically presented as "Location_YYYY" i.e., Gracetown_2019
Sample ID	Sample id typically presented as "SURYY_XXX" i.e., GCT19_001
String	String id which is the string on which each BRUV is deployed, typically presented as "SURYY_XX" i.e., GCT19_01 which would include samples GCT19_001 to GCT19_005
Location	Main location i.e., Gracetown
Sub-location	Determined by researchers
Country	Internationally accepted country names i.e., Australia
Ecosystem Name	Ecosystem where survey was conducted; names are based on FishBase conventions
LOICZID	LOICZ ID identifies the half-degree cell that is used by the *Sea Around Us* and AquaMaps.
IUCNMPA	IUCN zone (link) at the time of survey
Sample Date	Date on which sample was collected: YYYY-MM-DD
Time In	Time when the BRUVS was deployed based on 24 hr clock as HH:MM
Time Out	Time when the BRUVS was recovered based on 24 hr clock as HH:MM
Latitude In	Latitude at which the BRUVS was deployed in decimal degrees
Latitude Out	Latitude at which the BRUVS was recovered in decimal degrees
Longitude In	Longitude at which the BRUVS was deployed in decimal degrees
Longitude Out	Longitude at which the BRUVS was recovered in decimal degrees
Gear Type	Refers to whether BRUVS are moored or drifting in longline formation and whether stereo or mono camera systems
Depth (m)	Estimated depth in metres at which the sample was collected
Data Providers	Institution or individual providing the data

Following completion of the survey, each video sample is processed. For seabed BRUVS, 60 minutes of video are analysed, starting from the time that the BRUVS settles on the seabed. For midwater BRUVS, 120 minutes of video are analysed, starting from the time that the BRUVS settles at its suspended depth. The longer length for midwater BRUVS reflects the patchier and sparser nature of pelagic species compared to demersal species. The information that is generated from image analysis and through the dynamic harvesting of ancillary data is defined in Table 2.

Table 2: Definitions of information provided in the BRUVS SURVEY LIST csv.

Variable	Definition
Survey Name	Survey name typically presented as "Location_YYYY" i.e., Gracetown_2019
Sample ID	Sample id typically presented as "SURYY_XXX" i.e., GCT19_001
Family	Taxonomic family as identified by FishBase
Genus	Taxonomic genus as identified by FishBase
Species	Taxonomic species as identified by FishBase
Common Name	Common name as identified by FishBase on species pages
MaxN	The maximum number of individuals of a given species observed in a given video frame
Time of MaxN (min)	The time in minutes at which MaxN was recorded
Biomass (g)	The total biomass for species X on a given deployment calculated as MaxN x the mean weight of individuals calculated from the length weight relationship (LRW) reported in FishBase based on mean length for that species.
Mean FL (cm)	The mean fork length for a given species used to calculate weight. See information on estimating length when a sample-specific fork length is not available for a given taxa.
FL Source	The source of the fork length
LWRa	The intercept of the Bayesian length weight relationship
LWRb	The slope of the Bayesian length weight relationship
Troph	Trophic level determined from diet composition or food items or from that of nearest relatives if no species-specific information available
seTroph	Standard error of the trophic levels extracted from FishBase
Vulnerability	Vulnerability to fisheries extracted dynamically from FishBase
PD50	Phylogenetic diversity extracted dynamically from FishBase
IUCN Status	The IUCN status of the taxa where CR=Critically Endangered; EN=Endangered; VU=Vulnerable; LC=Least Concern and DD=Data Deficient; median values are used for Family sp and Genus sp taxa.
IUCN Date Assessed	The date at which time the reported IUCN status was determined.

All animals that are visible in the field of view are identified to species when possible. When an individual can only be identified to genus, it is recorded as, for instance, *Thunnus* sp. If it can only be identified to family, it is recorded as, for instance, Scombridae sp. We estimate abundance as the maximum number of individuals of each taxa in a given frame, a relative estimate of abundance known as MaxN and used in most BRUVS-based studies (Bouchet et al. 2018; Langlois et al. 2018). The methods to estimate size are taxon-specific and summarised in Table 3. For fishes and sharks, size is measured as fork length given the difficulty of determining total length on a moving animal.

Table 3: Size measurements for key taxa observed on BRUVS; all measurements are reported in centimetres.

Taxa	Measurement
fishes and sharks	fork length; excludes for instance, rostrums
rays	disc width
marine mammals	fork length
turtles	carapace length
squids, cuttlefish	mantle length
crabs	mantle width

Length (L) is used to estimate weight (W) based on published length weight relationships (LWR where $W=aL^b$) as reported in FishBase. Ideally, weight would be calculated for each individual. However, lengths are not measured for all individuals as some individuals are partially obscured, poorly positioned relative to the cameras, or too distant to obtain an accurate measurement. Additionally, if either the left or right camera has failed, stereo measurements are not possible. As such, the following length estimates are used as an input to the LWR.

1) Mean fork length of all measured individuals of the xth taxa on the ith sample. *If not available =>*

2) Mean fork length of all measured individuals of the xth taxa on the jth string on which the ith sample was found (midwater BRUVS) or the spatially closest sample on which that taxa was measured (seabed BRUVS). *If not available =>*

3) Mean fork length of all measured individuals of the xth taxa on that survey. *If not available =>*

4) Mean fork length of all measured individuals of the xth taxa on previous surveys from that location. *If not available =>*

5) Mean fork length of all measured individuals of the xth taxa from other locations in the region. *If not available =>*

6) Common fork length or common total length of the xth taxa from FishBase.

Mean weight is then calculated from the mean fork length using the fork length based LWR with the highest rating in FishBase. If no LWR based on fork length is available, the best LWR based on total length is used, with fork length converted to total length based on reported FL:TL relationships. Finally, if no taxa-specific LWR is available, the Bayesian relationship based on total length is used, with fork length again converted to total length (Froese et al. 2014). For individuals identified to genus or family rather than species, a median Bayesian relationship is used for the genus or family, with fork lengths converted to TL. Once weight has been estimated, it is multiplied by MaxN to calculate the biomass of each taxa on a given sample.

Dynamic updating of taxonomy and ancillary data

Taxonomic updates can lead to the presence of "zombie" data that are incorrect but nevertheless persist within the datasets. Taxonomic updates may include reassignment of a species to a different family or genus or the lumping/splitting of species. Recent examples include the reassignment of manta rays from the Myliobatidae to the Mobulidae and the lumping of the Indo-Pacific blue marlin (*Makaira mazara*) and the blue marlin (*Makaira nigricans*) into the single species *M. nigricans.* The dynamic updating of taxonomy means that all taxonomic data in the BRUVS datasets will be current.

Ancillary data such as trophic level (Froese et al. 2000), phylogenetic diversity index (Faith et al. 2004), fisheries vulnerability (Cheung et al. 2005) and conservation status as per the IUCN Red List (www.iucnredlist.org) are reported on FishBase for each species. These species attributes can be combined by the user with abundance and biomass data to quantify community level characteristics. For instance, we can calculate the trophic level of an assemblage, weighted for species abundance or biomass, and consequently determine the degree to which assemblages are characterised by low or high trophic level species. An example of such a calculation is:

$$TL_A = \frac{\sum_i (TL \times A)}{\sum_i A}$$

Where TL refers to trophic level, weighted for abundance (A) calculated across the *i* species observed on a sample. Similar calculations can be completed to determine whether, weighted for abundance or biomass, a community is phylogenetically diverse, vulnerable to fishing or the degree to which it is characterised by threatened species. Such analyses provide a common currency that can be used to compare locations regardless of the composition of species, and also provide important insights into ecological function and human impact.

To support such analyses, the FishBase BRUVS tool dynamically harvests the most up-to-date values for these attributes, thereby avoiding the presence of zombie data in the downloaded .csv files. Such updating may be important because new species-specific estimates may be available for taxa for which no estimates were previously available and improved Bayesian estimates across the genus or family. IUCN Red List status is another key example: the dynamic harvesting of Red List status means that as the status of a given species changes, it is reflected in the "live" data.

Accessing data and guidelines on analysis

The BRUVS data are accessed from the FishBase home page by going to "Tools" and choosing the BRUVS button. At this point, you can choose to select data by taxa or by geography. Taxa choices include by common name, family, genus or species. The map then shows which surveys included the chosen taxa and provides the specific surveys for download, with the opportunity to download "all". Note, the downloaded data include all taxa observed on those surveys such that the community data are also provided. If the user is only interested in the specified taxon, they will need to filter the provided data for that taxon. If the user chooses by geography, three different options exist: FAO Area, Ecosystem and Location. Depending on the spatial option chosen, different surveys will load and the user has the option to further refine these choices. As with the taxonomic data, all data are provided to the user to be filtered as per their question.

We provide the following guidelines for data analysis:

(1) For seabed BRUVS, each deployment can be considered an independent sample.

(2) For midwater BRUVS, deployments are allocated to "strings" as they are deployed in a longline formation. To that end, the appropriate sampling unit is a "string" and as such individual sample values should be averaged by string.

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