**Title:** Understanding and managing fish populations: keeping the toolbox fit for purpose

**Running title:** Tools for understanding fish populations

**Authors** Paris, J.R.[1]*, Sherman, K.D.[1]*, Bell, E.[2], Boulenger, C.[3], Delord, C.[3], El-Mahdi, M.B.M.[4], Fairfield, E.A.[2], Griffiths, A.M.[1], Gutmann Roberts[5], C., Hedger, R.D.[6], Holman, L.E.[7], Hooper, L.H.[1], Humphries, N.E.[8], Katsiadaki, I.[9], King, R.A.[1], Lemopoulos, A.[10], Payne, C.J.[11], Peirson, G.[12], Richter, K.K.[13], Taylor, M.I.[2], Trueman, C.N.[7], Hayden, B.[14†] & Stevens, J.R. [1†]

* Joint first authors; † Joint senior authors

[1] Biosciences, University of Exeter, Stocker Road, Exeter, Devon EX4 4QD, UK

[2] School of Biological Science, University of East Anglia, Norwich Research Park, Norwich, UK

[3] ESE, Ecology and Ecosystem Health, Agrocampus Ouest, INRA, Rennes, France

[4] Faculty of Science, Laboratory of Molecular Genetics and Molecular Biology, Zoology Department, South Valley University, Qena 83523, Egypt

[5] Department of Life and Environmental Sciences, Faculty of Science and Technology, Bournemouth University, Bournemouth, BH12 5BB, UK

[6] Norwegian Institute for Nature Research, Trondheim, NO-7485, Norway

[7] Ocean and Earth Science, National Oceanography Centre, University of Southampton, European Way, Southampton SO14 3ZH

[8] Marine Biological Association of the United Kingdom, The Laboratory, Citadel Hill, Plymouth PL1 2PB, UK

[9] Cefas, Weymouth Laboratory, Weymouth, Dorset, DT4 8UB, UK

[10a] Department of Environmental and Biological Sciences, University of Eastern Finland, P.O. Box 111, FI-80101 Joensuu, Finland.

[10b] Department of Biology, University of Turku, FI- 20014, Turku, Finland.

[11] Institute of Aquaculture, Faculty of Natural Sciences, University of Stirling, Stirling, UK

[12] Environment Agency, Research Analysis and Evaluation, Mance House, Kidderminster, UK

[13] BioArCh, Department of Archaeology, University of York, York YO10 5DD, UK

[14] Biology Department, Canadian Rivers Institute, University of New Brunswick, Fredericton, NB, E3B 5A3, Canada

**Corresponding Author:** Jamie R. Stevens, j.r.stevens@exeter.ac.uk 01392 723 775

## Abstract

Wild fish populations are currently experiencing unprecedented pressures, which are projected to intensify in the coming decades. Developing a thorough understanding of the influences of both biotic and abiotic factors on fish populations is a salient issue in contemporary fish conservation and management. During the 50th Anniversary of the Fisheries Society of the British Isles, University of Exeter, 2017, scientists from diverse research backgrounds gathered to discuss key topics under the broad umbrella of 'Understanding Fish Populations'. Below, the output of one such discussion group is detailed, focusing on tools used to investigate natural fish populations. Five main groups of approaches were identified: (i) Tagging and telemetry; (ii) Molecular tools; (iii) Survey tools; (iv) Statistical and modelling tools; and (v) Tissue analyses. The appraisal covered current challenges and potential solutions for each of these topics. In addition, three key themes were identified as applicable across all tool-based applications. These included data management, public engagement, and fisheries policy and governance. The continued innovation of tools and capacity to integrate interdisciplinary approaches into the future assessment and management of fish populations is highlighted as an important focus for the next 50 years of fisheries research.

Key words: archaeology, genetics, modelling, surveys, stable isotopes, telemetry

## Introduction

Approximately 30% of fish species have been overexploited (FAO, 2014), representing significant losses to biodiversity, ecosystem services and socioeconomic contributions (Worm et al., 2006). In light of the increasing challenges presented by climate change and other natural and anthropogenic stressors (Gordon et al., 2017), an improved understanding of fish populations is critical to facilitate effective management and conservation initiatives. During the summer of 2017, the Fisheries Society of the British Isles (FSBI) held its 50th Anniversary Symposium under the broad umbrella of 'Understanding Fish Populations'. To highlight key knowledge gaps and opportunities, we detail the outcome of a working group convened at the symposium, which was tasked with considering the theme of 'Tools for understanding fish populations'. The scope of the discussion spanned diverse areas including spatial ecology and migration patterns, genetics and evolutionary biology, physiology, trophic ecology, and developmental and population biology. In this article, we consider major advancements in the use of tools across broad areas of fish biology, and identify knowledge gaps and potential solutions in each area in order to guide and inform future research, to better understand and protect wild fish populations.

## Tagging and telemetry

A significant problem hampering the study of marine fish is that of determining their geographical locations at fine scales, over long durations and, in particular, for benthic species. Tagging and telemetry involves the application of external and or internal tags or devices to manually or passively track fish movement (Cooke et al., 2013). Both forms can be particularly challenging in the marine environment, though manual tracking can work at feeding grounds and at spawning aggregations (e.g. Murchie et al., 2015), while passive tracking has valuable applications along known migration routes (Dahlgren et al., 2016), for example, as anadromous/catadromous species migrate in and out of river estuaries (e.g. Lauridsen et al., 2017). Suites of tools exist for such tasks (e.g. acoustic transmitters, PIT and Floy™ tags, radio, archival, etc.) and have been routinely used to understand the spatial ecology of a range of fish taxa (Bograd et al., 2010). With technological improvements in tags and tracking equipment, the field has grown vastly in recent decades (see reviews by Pine et al., 2003; Bograd et al., 2010; Jepsen et al., 2015). We briefly highlight some of the tags and telemetry options commonly used by researchers along with a discussion of some of the limitations and challenges associated with these tools.

Data storage tags (DSTs), which collect data on both the internal and/or external environments of fish are the only method available to assess internal states (e.g. bioenergetics, Cooke et al., 2016). However, DSTs currently only provide information on the environment experienced by the tagged fish if the tag is recovered, meaning these data are lost if fish recapture rates are low, often the case in fish tagging surveys. Communication History Acoustic Tags (so called 'CHATs'), which transmit data to nearby transponder receivers are a promising alternative. Since there have been relatively few uses of this tag type (Voegeli et al., 2001; Hight & Lowe, 2007), there is potential for development in this area.

Pop-up satellite archival tags (PSATs), which detach from the tagged fish after some time at sea and transmit telemetry data to overpassing satellites, are currently limited in terms of hardware, software and satellite reception. PSATs are large, so are limited in use for larger, often highly migratory individuals, and may also affect fish behaviour (Methling et al., 2011). Additionally, battery failure, antenna damage, or mechanical failure may limit registration or transmission of data (Musyl et al., 2011). PSAT technology is relatively new, so future reductions in size and weight and also improvement in reliability can be expected. In terms of software, PSATs currently only transmit limited amounts of data due to transmission costs and the short time that the receiving satellite is above the horizon. Future software development is required to reduce transmission costs, optimise data transmission and provide more flexibility for users to tailor controls to provide higher resolution data at the desired temporal scale. An increase in the number of satellite platforms that can receive PSAT data would help to improve reception issues. Interference on frequencies selected for tags at certain geographical locations (see Musyl et al., 2011) also requires consideration.

Acoustic telemetry offers autonomous, continuous monitoring (Heupel et al., 2006) and has the potential to significantly enhance our understanding of marine predator habitat use, activity patterns and resource partitioning (Hussey et al., 2015). Acoustic arrays have been used in many studies in elucidating fish movements (e.g. Papastamatiou et al., 2013; Lea et al., 2016), and transmitters have been used more innovatively to measure trophic interactions (Halfyard et al., 2017). Issues remain however, for example, in the significant cost and effort involved in deploying and maintaining acoustic arrays.

Organisations such as the Ocean Tracking Network (Whoriskey et al., 2015), (OTN; http://oceantrackingnetwork.org) and the Australian Animal Tracking Network both maintain acoustic infra-structure in the form of deployed receivers (arrays or curtains) in key ecological areas into which researchers are free to release tagged animals.

These initiatives substantially reduce the cost and risk associated with acoustic tracking projects and similar approaches can be applied globally. Furthermore, integration of data standardised repositories along with a comprehensive set of analytical tools to ensure rapid and sophisticated analysis of acoustic array data would lead to new insights into the spatial ecology of fish. Further technological developments such as the use of AUVs to perform routine data download operations, or even complement fixed acoustic receivers (Davis et al., 2016), will make acoustic telemetry increasingly affordable and accessible to more researchers. Continued collaborations with established regional and international tracking networks, together with the ever-increasing sophistication, miniaturisation, durability and cost reduction of tags promises an increasingly important role for acoustic telemetry in our understanding of fish ecology.

## Molecular tools

### *Population genetics and genomics*

Using genetic tools to understand fish genetic diversity and population structure has wide-ranging applications for evolutionary biology, and the conservation and management of fish stocks. Until recently, molecular techniques such as mitochondrial sequencing and the analysis of microsatellite loci have been used most commonly to explore intra-specific variation in fish and many other organisms (e.g. Ferguson & Danzmann 1998; Chistiakov et al., 2006; Abdul-Muneer, 2014). More recently, however, the increased availability and cost efficiency of high-throughput sequencing, which is capable of producing millions of sequencing reads (e.g. RADseq, RNAseq), has revolutionised the fields of population and conservation genetics (Allendorf et al*.,* 2010). It is however important to understand what extra information high-throughput sequencing data can provide, the biases involved in study design and data generation, and also how its usage might be optimised. Here, we seek to identify knowledge gaps in the field of fish population genetics, and contemplate how this area of research may evolve in the future.

Attaining high quality, clean DNA for large numbers of individuals is paramount for downstream sequencing processes, but in some cases can be challenging. Biological samples can often be compromised during sampling or transport, potentially rendering field efforts futile. Population genetic studies on fish frequently require sampling from river transects or remote locations at sea, and so portable laboratories for sampling, storing and extracting DNA would be welcomed. At the same time, emerging technologies, e.g. the MinION USB sequencer (https://nanoporetech.com/products/minion), have the potential to revolutionise when and where genetic data can be generated. Most new technologies are currently restricted to sequencing small genomes, such as those of bacteria, but with on-going improvements, these technologies open up the possibility of being able to sequence DNA in real-time in the field (Hayden, 2015). Recently, the MinION technology has started to be used in hybrid assemblies with Illumina short reads (Austin et al., 2017) and *de novo* eukaryotic genomes (including fish) are in progress (Jansen et al., 2017).

Alongside population genetic studies, research based on whole genome data is emerging, and the genomes of several commercially important species have now been published (e.g. Atlantic cod (*Gadus morhua*)*,* Star et al., 2011; Atlantic salmon (*Salmo salar*), Lien et al., 2016). However, while the ever-reducing cost of whole genome sequencing provides opportunities to sequence and publish more fish genomes, in our view, the key priority is not simply publishing genomes, but also high-quality genome annotation. Gene annotation and accurate knowledge of the function of different identified regions is of extreme importance if genomic tools are to be used reliably in conservation and management (Ekblom & Wolf, 2014). Therefore, projects such as the 'Functional Annotation of All Salmonid Genomes' (Macqueen et al., 2017) should be encouraged and developed. It is also important not to underestimate or neglect the computing power and bioinformatics expertise required to produce high quality genome scaffolds and annotations, and also to recognise and account for biases in next generation sequencing data (see Benestan et al., 2016).

Furthermore, population genetic approaches are usually focused on a single species. Consequently, there is a mismatch between studies of a single species genotyped at high resolution, but generally at small spatial scales (e.g. population genetics, often using hundreds to thousands of markers through GBS or GWAS) and studies of multiple species at larger spatial scales but using lower resolution markers (e.g. phylogeography or biodiversity assessments using metabarcoding or mtDNA sequencing). Nonetheless, the widespread application of molecular resources has led to the accumulation of rich datasets across a broad range of species, geographical regions and time periods (Blanchet et al., 2017). Accordingly, we anticipate that this aggregation of data may allow the underlying processes that drive genetic variability across these regions and times to be revealed, enabling a broader testing of theories in population genetics and evolution (Ellegren & Galtier, 2016; Pauls et al., 2014).

Such studies will require combining high genetic resolution markers across large spatial scales, which is a non-trivial task, especially when dealing with non-model species. Three challenges arise in such cases: firstly, the financial investment required to obtain reliable datasets for several species remains significant. Despite reductions in sequencing costs, it may be financially sensible to rely on more classical markers such as microsatellites or small subsets of single nucleotide polymorphisms (SNPs). Secondly, there is a need for a standardised framework in order to make datasets comparable across different species and regions. This standardisation must occur when collecting samples, characterising markers (e.g. Ellis et al., 2011; Helyar et al*.,* 2011) and during the subsequent data analysis to streamline user choices (Paris et al*.,* 2017), which may bias the biological interpretation of data, see Rodríguez-Ezpeleta et al*.* (2016). It is therefore important that researchers use common methods to isolate and characterise markers for entire sets of focal species, and/or provide full access to detailed analyses when datasets are generated. Finally, as multi-species approaches remain scarce, there is a need to define hypotheses at the beginning of such investigations. The integration of mathematical and statistical models with fish population genetics would be useful for revealing genotype-phenotype interactions (Ritchie et al., 2015), evolutionary signatures (Stark et al., 2007), functional DNA elements (Schrider & Kern, 2014), and spatial dynamics (Guillot et al*.,* 2009).

### *eDNA*

The use of environmental DNA, or eDNA, to identify the presence and understand the distribution of fish has expanded rapidly in the last decade. eDNA is a polydisperse mixture (Turner et al., 2014; Wilcox et al., 2015) of various biological material ranging from entire cellular fragments to extracellular DNA, which is isolated from environmental samples such as water or sediment. Such techniques are used for species identification and food security purposes. Universal primers that target mitochondrial DNA can be applied for identifying species presence (Yamamoto et al., 2016) or to gain information about species natural history (e.g. food web construction, Sousa et al. (2016)).

An important component of this work is validating the results from eDNA surveys with traditional fish survey methods. In both freshwater and marine environments, eDNA has compared favourably to traditional fish survey methods (Eichmiller et al., 2014; Sigsgaard et al., 2017). However, eDNA was found to be less effective compared to experienced snorkel surveys (Ulibarri et al., 2017). This underpins the importance of validation with traditional techniques, especially in spatially heterogeneous and complex aquatic environments (Shogren et al., 2017).

The development of effective PCR primers is central to the successful application of eDNA (e.g. Freeland, 2016; MacDonald & Sarre, 2017). As a result, a vast range of primer sets are available for fishes (e.g. Clusa et al., 2017; Gargan et al., 2017; Doi et al., 2015). Metabarcoding primers, that simultaneously amplify eDNA from many fish species, have also been developed for monitoring entire fish communities (Miya et al., 2015; Valentini et al., 2016).

Beyond inferring if a fish species is present in the sampled location, researchers have begun to investigate if eDNA can provide further information regarding fish populations. The use of eDNA to infer population level variation has been demonstrated (Sigsgaard et al., 2016; Uchii et al., 2015), but is still in its infancy.

Similarly, several attempts have been made to link eDNA concentration and fish biomass (Lacoursière-Rousse et al., 2016; Thomsen et al., 2016; Yamamoto et al., 2016), producing encouraging results. Further development is required to use this tool to more accurately estimate fish abundance and biomass.

However, for techniques utilising eDNA to be optimised, preexisting molecular information needs to be accessible. A number of publicly available databases (e.g. NCBI Genbank and BOLD - boldsystems.org) hold a vast array of molecular data but there is still a need for further mitochondrial genome sequencing to allow optimal usage of molecular identification techniques (but see Deiner et al., 2017).

### *Microbiomes*

Analysis of a microbiome can provide novel insights into the health and biology of fish populations. Traditional culture-dependent tools used to map the commensal microbiota community in teleost fish are often time-consuming, expensive and subjected to bias as only 0.1-10% of bacteria can be cultured *in vitro* (Amann et al*.,* 1995; Austin, 2006). More recently, rapid culture-independent tools such as 16S rRNA targeted sequencing have been utilised to provide detailed profiles of the structure and diversity of the microbiota residing on the mucosal surface of fish (Ghanbari et al*.,* 2015).

The gut microbiome composition has also become an important biomarker for understanding the influence of stress in fish (Llewellyn et al., 2014), as numerous stressful stimuli have been shown to alter the microbiome composition (Xia et al*.,* 2014; Gaulke et al*.,* 2016). The gut microbiome composition can provide insights into the ecology and physiology of fish in a range of areas such as ecological speciation

(Sevellec et al*.,* 2014), the biology of migratory fish (Llewellyn et al., 2016), trophic interactions within ecosystems (Ingerslev et al., 2014) and adaptation to extreme environments (Song et al*.,* 2016).

There are a number of challenges currently facing fish microbiome research. At present, the majority of data regarding the microbiome composition in wild teleost fish originates from laboratory models (Tarnecki et al*.,* 2017). More studies are required to see if captive-reared animals provide a reliable analogue for wild populations. Standardised protocols for collecting and generating microbiome data are also lacking, which could restrict progress as several processes have the potential to introduce differential bias in microbiota profiles (e.g. Salipante et al., 2014; Hart et al., 2015; Lyons et al., 2017). Adopting a framework of robust, quality-controlled protocols (e.g. similar to human microbiome research Methé et al*.,* (2012)) would be of great benefit. In addition, there is currently a lack of non-invasive protocols for conducting longitudinal or repeated sampling of the gut microbial community in individual fish over time. The application of rectal swabs (Budding et al., 2014) for sampling the vent of fish could provide a non-invasive strategy for collecting microbiome data from individuals over time. Finally, time-series data could also enhance our knowledge in terms of the functional aspects of host lifecycles and the stability and resilience of microbiota (Goodrich et al., 2014).

## Survey Tools

### *Field-based surveys*

Fish population assessments are conducted using a wide range of techniques; the advantages, limitations, personnel requirements and health and safety considerations of each are presented in Table 1. It is encouraging to note that even well-established methods such as hydro-acoustics are continually being improved, while emerging tools such as eDNA (see above) are beginning to be included in routine monitoring. We suggest that integrating methods and data series are key priorities for future research in this field.

In large and complex habitats it is often the case that a suite of survey methodologies has to be employed to sample different times, places and fish species effectively. Indeed, an advantage of field-based surveys is the ability to generate information from both fishery-independent (Nash et al., 2016) and fishery-dependent (Shin et al., 2010) data. However, this need, and the availability of a diversity of methodologies, can make the task of assessment in these habitats even more costly; issues also remain over how to use often disparate data types to develop a sound understanding of a fishery. Integrating methods represents a key means of improving data resolution from such field surveys. For instance, methods such as eDNA and hydro-acoustic sampling provide comparatively fast and non-invasive estimates of fish community structure and biomass. However, to obtain a thorough understanding of fish populations, this information must be combined with fish age, size and health data obtained via destructive sampling (e.g. gill netting). As yet, there are no structured, universally agreed guidelines on which methods should be integrated to obtain a thorough assessment of population dynamics from a specific habitat type.

Fish survey methodologies are typically determined at a national level, making international comparisons of data extremely challenging. In recent years, standardised protocols initiated through the EU Water Framework Directive have facilitated Europe-wide assessments of fish community structure. Such international standardisation is essential when assessing the impact of anthropogenic effects on fish (see Gordon et al., this issue), and we recommend that efforts are made to make national datasets available using standardised metadata and biodiversity information, ideally via open sharing platforms (e.g. http://www.freshwaterplatform.eu/).

### *Historical records*

Historical records (e.g. catch records) can also be useful in helping to extrapolate population data back into the recent past. Libraries and historical societies often hold picture archives and these images can in some instances be used as a form of historical survey data to provide information on past community composition and size distributions (McClenachan, 2009). Historical records of catch data are typically held by government agencies or can be found in local archives (e.g. angling club logs) and corporate records. Such data have been used successfully to reconstruct fish populations back to the late 1800s (Thurstan & Roberts, 2010; Thurstan et al., 2010). Catch reconstruction approaches can also provide useful insights into fishery trends that may not be apparent from Food and Agriculture Organization (FAO) reported data alone (Smith & Zeller, 2015; Zeller et al., 2015). Although limited to the information that is still available and subject to the often-unidentifiable biases of the individuals who originally recorded the data, such data can provide a unique way to extrapolate population data back in time.

## Statistical and modelling tools

*Bayesian methods* - Reliable estimates of demographic parameters (e.g. abundance, survival, growth rates and fecundity) and an understanding of the processes that regulate these parameters are fundamental for sustainable management of fish populations. However, to understand the ecological processes and to truly inform policy, researchers must use multiple data sources, provide links between management actions and population responses and also estimate uncertainty as a prerequisite to making forecasts that provide useful information. Bayesian methods in ecology and conservation biology are now increasingly being used to explore these links, for example, in stable isotope analyses (see below). Indeed, the Bayesian framework provides an intuitive method for estimating parameters, expressing uncertainty in these estimates and allows for the incorporation of as much or as little existing data or prior knowledge that is available (Ellison, 2004). However, to develop the use of this specific framework in fish ecology and management, there is a need to educate and train fish biologists in the use of Bayesian principles and methods.

*Individual-based models (IBMs)* are process-based mechanistic computer models that simulate emergent properties of fish biology, behaviour, traits or group characteristics, based on simple heuristic functions, and their use has grown exponentially (e.g. DeAngelis & Mooij, 2015) as computational power has increased (DeAngelis & Grimm, 2014). Several separate individual-based models were presented at the 50th Symposium of the FSBI, and, with continued increases in computational power, IBMs look set to offer powerful new avenues for population research (DeAngelis & Grimm, 2014) in computationally challenging multifactor systems such as fish ecotoxicology (e.g. Mintram et al., 2017). Additionally, a variety of tools now exist which provide for the easier creation of new models, such as various R packages (see: http://derekogle.com/fishR/packages) and programmable environments (e.g. NetLogo; https://ccl.northwestern.edu/netlogo). However, programs such as R are sometimes not intuitive to new users, and so additional training for fisheries scientists and collaborations between scientists from different computational and statistical backgrounds would be advantageous. For more robust future application of IBMs within fisheries science, there is a need for more assessment of the relative strengths and weaknesses (and potential availability and future development) of the different models.

Integration with environmental data is a pertinent issue when modelling and is becoming easier through developments in GIS and other programming environments (such as R), which now include procedures and libraries for use in ecological work. One example is the use of food web models that integrate environmental data (e.g. Christensen & Walters, 2004) and coral reef ecosystem modelling methods (e.g. Rogers et al., 2014; Weijerman et al., 2015). A hindrance to the integration of environmental data into fisheries science is that it can be difficult to find and access data sources, although availability and accessibility of such data is improving (e.g. worldclim.org). The existence of a central node or hub with paths to these data sources would be useful.

## Tissue analysis

### *Stable isotope ecology*

Stable isotopes are now routinely used to quantify the trophic ecology (Boecklen et al., 2011) and migration history (Trueman et al., 2012) of fishes, or to identify community level patterns in food web structure and resource use (Layman et al., 2012). Although the technique is still in its relative infancy, stable isotope ecology has advanced much in recent decades. Below we outline four areas of rapid development with potential to enhance the applicability of this tool to studies of fish biology.

*Biochemical mechanism:* The relationship between the isotopic composition of a consumer's tissues and that of its prey is fundamental to all applications of stable isotopes in ecology. However, while general principles are clear (i.e. faster reaction rates and preferential incorporation of light isotopes into excretory metabolites a process termed trophic fractionation (DeNiro & Epstein, 1977)), the precise mechanisms leading to fractionation and, particularly, the extent of isotopic fractionation expected under differing physiological conditions cannot currently be predicted, primarily due to the complexity of amino acid biochemistry. Uncertainties associated with the isotopic expression of tissue composition, and relative rates of tissue growth and regeneration further complicate the interpretation of stable isotope values in ecology. However, recent information gained from compound-specific isotope analysis (i.e. assessing isotopic compositions of single amino acids) is beginning to shed light on the fractionation process (McMahon & McCarthy, 2016).

*Population-level data:* The distribution of isotopic compositions of individuals within a population (often termed the 'isotopic niche', Newsome et al., 2007) has been proposed as a powerful comparative measure of population-level ecological characters. However, in addition to individual variability in consumers, the distribution of isotopic compositions in a population is influenced by spatial and temporal variations in the isotopic composition of primary production, temporal variability within trophic linkages and differential rates of growth and isotopic assimilation. Very few studies have attempted to combine ecological and food web theory with isotope systematics to explore the sensitivity of community isotopic metrics to changes in food web structure and function.

*IsoBank:* To date, applications of stable isotopes to fish biology have predominantly focussed on analyses of specific populations or communities. The absence of a centralised, open-access repository for stable isotope data restricts the opportunity for syntheses or meta-analyses of stable isotope data (Pauli et al., 2017). Recent efforts to address this have found broad support from the stable isotope research community (Pauli et al., 2017) and would be especially beneficial to fish biologists due to the large amount of fish isotope data currently available. Defining an ontology of stable isotope metadata, information required to describe and interpret isotope data, for fish biologists is an immediate requirement in this regard.

*Marine isoscapes:* The stable isotope ratios of a consumer's tissue encode the resources (water, air, prey etc.) it was using when that tissue was formed. As such, provided one has access to a suite of isotopic baseline measurements (e.g. water, plants and primary consumers), it is possible to trace an organisms route through space and time up to the point of capture (Trueman et al., 2012). Creation of a practically useful isoscape requires relatively dense sampling of a reference organism across space (and potentially time). Bulk stable isotope analyses are now routine, commonly available globally, and relatively cheap, and regional marine isoscape models are being developed at a rapid rate (MacKenzie et al., 2014; Kurle & McWhorter, 2017). In the open ocean, sample-based isoscapes are difficult to develop, but progress is being made in isotope-enabled global biogeochemical models (Magozzi et al., 2017), offering temporal and spatial models of expected isotopic variability at global scales. Improving the precision, accuracy and availability of these baseline measurements will increase the robustness and precision of isotope based estimates animal position.

### *Archaeological material*

Archaeological material can allow an otherwise impossible snapshot into past populations. Traditional morphological approaches can provide age distributions and species ranges, and with the explosion in the past 20 years of biomolecular archaeology, many of the techniques used to explore modern populations can now be used to look into the past. From ancient DNA to proteomics, and isotopes to lipids, a wide range of biomolecules have been recovered and explored from archaeological material (Orton, 2016). For example, compound-specific isotope analysis has the potential to track trophic level changes through time (McClelland & Montoya, 2002; Naito et al., 2016). Population genetics of extinct populations have been successfully explored in terrestrial animals (Chang & Shapiro, 2016; Murray et al., 2017) and these same techniques can be used on fish bones to reconstruct past genetics (Iwamoto et al., 2012; Ólafsdóttir et al*.,* 2014). Ideally these data will be used to understand environmental and anthropogenic effects on fish populations and how modern fish populations might respond to climate change and fishing pressures.

A major barrier to the use of archaeological fish material is the fact that less than 10% of fish bones are identified to species (Wheeler & Jones, 1989; Gobalet, 2001) and much of what is identified is buried in the 'grey literature' of archaeological reports that are often not digitised and printed in small quantities (Linden & Webley, 2012). This makes the material relevant to an ecological question very difficult to find. Archaeologists are working towards ways to improve the amount of bones identified by better reference collections and education on fish bones (National

Zooarchaeological Reference Resource, Nottingham's Archaeological Fish Resource, Vertebra@UWF) and on creating searchable databases of archaeological material (Callou, 2009; Kansa, 2010). In addition, new ZooMS (Zooarchaeology by Mass Spectrometry) techniques are being explored to quickly identify even small bones and scales to species using peptide mass fingerprinting (Richter et al*.,* 2011) which will allow even more material to be identified in a useful way for those working on understanding fish populations. In the near future, it should be possible for modern fish biologists, in conjunction with archaeologists, to ask direct questions of past populations (Van Neer & Ervynck, 2010).

## General topics identified as applicable across all themes

### *Management of data: integration, calibration and standardisation*

Progression of an integrated management framework for data classification, characterisation, storage and accessibility would be a valuable resource for fish and fisheries biologists. FishBase, which at the time of writing contains information regarding 33,600 fishes, involving 2290 collaborators, and receives over 600,000 visits per month, is an example of the potential for such a resource (see: fishbase.org; Froese & Pauly, 2017). A single database for all types of fish data (for example, DNA, tagging, isotopes, diet) is probably unworkable, but the advent of application programming interfaces (API) and analytical software which allows automated querying across multiple databases represents an unprecedented opportunity to access a wealth of global data. Indeed, we suggest that more data (such as those discussed here) could be integrated into FishBase. However, such resources require significant funding and long-term commitment from governments and trans-national organisations, e.g. NASCO.

### *Public engagement, education and outreach*

Scientific engagement with the public is essential to effect meaningful societal change or to ensure a wider consensus is made around new discoveries or ethical considerations. Additionally, however, the power of the public as a “tool” in science is also being increasingly recognised. ‘Crowdfunding’, whereby a scientist requests small amounts of money from a large number of interested individuals to successfully launch a project, potentially provides a powerful new way to raise funds, overcoming some of the difficulties of raising money from traditional grant bodies, especially for early career researchers or those in developing countries (Wheat et al., 2013).

In addition to funding science, the public can also actively engage in the process of research directly through citizen science projects. Whilst research conducted by non-professionals is certainly not a new concept, the numbers of projects involving citizen scientists are growing, especially in the fields of environmental science and ecology (Silverton, 2009). Through catch records of amateur anglers and commercial net fishery data extending back many years, research into fish and fisheries is uniquely placed to benefit from citizen science projects (Stuart-Smith et al., 2013), which have effectively spanned generations of contributors. Similarly, REEF (reef.org) has been collecting reef fish diversity and abundance data from trained volunteer divers for 27 years, and the data have been successfully leveraged in hundreds of publications (e.g. Stallings, 2009; Serafy et al., 2015). Citizen science can also help achieve important social outcomes, e.g. in establishing sustainable fisheries and marine protected areas, MPAs (Bonney et al., 2014). And, as with crowdfunding, the best examples of citizen science typically encourage deeper engagement with the public, and offer a pathway to the democratisation of science.

### *Fisheries policy and governance*

Conserving critical habitats is central to the sustainable management of fish species and populations. Marine Protected Areas (MPAs), networks of MPAs and Marine Conservation Zones (MCZs) are widely accepted management tools for fish and other marine organisms that have been established in many countries (Harborne et al., 2008; OSPAR, 2013). However, the design of MPA networks could benefit greatly from the integration of traditional survey data, along with modelling and connectivity data (Botsford et al., 2009; Grüss et al., 2014). From a social science perspective, there is a need to better understand public perceptions of marine-related conservation issues, e.g. fishery regulations, MPAs and MCZs, and to incorporate these data into fisheries policy and governance frameworks. For example, there is high public support for MPAs, with surveys showing that people desire around 40% of the UK's marine waters to be protected (Hawkins et al., 2016). But, while the public appears to realise that in reality levels of coverage are well below 40%, there is still a substantial disconnect between perceived coverage of highly protected UK MPAs (11%) and actual MPA coverage (<0.1%); ultimately, this means that people believe the UK oceans receive a higher level of conservation than in reality they do (Hawkins et al., 2016). Developing and implementing effective policies for fisheries management remains challenging because of the complexities of fisheries and the socio-political landscape under which they typically operate (Jentoft & Chuenpagdee, 2009). However, the establishment of guidelines or frameworks for fisheries policy and governance (e.g. FAO Voluntary Guidelines for Securing Sustainable Small-Scale Fisheries) have the potential to better address these challenges and provide appropriate implementable solutions.

## Conclusions

Across all five of the research themes identified here, it is clear that innovative and novel tools are being employed to understand all aspects of the biology of fish populations. Notwithstanding, the authors call for the continued development of these new and emerging techniques. In particular, there is a need for better integration of these methods and resulting data, to inform scientifically sound management and conservation of fish populations.

However, it should be noted that, not infrequently, revolutionary methods have been pedestalled as providing the ability to offer unprecedented novel answers to long-standing practical problems. Unfortunately, the danger is that such methods can (by their novelty and the excitement surrounding them), blinker scientists into posing questions that showcase the methodology, rather than the biology (for example, the plethora of papers that emerged in the early 1990s extolling the virtues of the random amplified polymorphic DNA (RAPD) technique). The potentially reduced power of using any technique on its own (new or otherwise), in isolation of other apparently ‘antiquated’ methods can turn out to be unnecessarily restrictive. Every technique has its limitations, but often the restrictions of one tool can be substantially alleviated by the inclusion of another approach (e.g. Godwin et al., 2016), the marriage of which can provide a new angle for researching challenging biological problems. It is important that both traditional and emerging tools remain in the toolbox of fish biology research.

Likewise, when genetic-based assignment became popular, many researchers naively believed the days of tagging fish were over. It is now realised that due to the many stochastic drivers of population structure, genetic stock identification-based methodologies such as genetic assignment, do not always succeed. In such cases, there remains a significant role for tagging in fisheries research. As tag sizes decrease, and the deleterious effects of tag insertions on fish also decrease, we can anticipate that genetics and tagging will both continue to have a role to play. The importance of the relative roles of each technique will depend on the questions being addressed, the population structure of the study species, and the scale of the questions being assessed.

A final example, which highlights the importance of applying inter-disciplinary and complimentary tools for understanding fish populations, was a five-year, multi-agency, EU-funded project investigating the migration and distribution of Atlantic salmon (*Salmo salar* L.) in the north-east Atlantic (the SALSEA project; NASCO 2008). The purpose was to understand not just where salmon go, but what they eat, migration routes to feeding grounds, and which waters and regions they pass through. The SALSEA project used a combination of genetics (microsatellites), stable isotope analysis, at-sea trawls, tagging and gut contents analysis to assess the movements and diet of Atlantic salmon across the north-east Atlantic Ocean. As a result of applying these combined approaches, salmon post-smolt movements have been confidently ascertained (Gilbey et al., 2017). Nonetheless, even while this comprehensive study was being finalised, a similarly broad-ranging study was also being undertaken using SNPs (Bourret et al., 2013). Arguably, this method offers both the potential for finer levels of stock discrimination and the ability to better explore patterns among functional loci, which may make microsatellite-based analysis redundant within a short period of time (though see Narum et al., 2008).

Thus, the authors consider the continued development of emerging tools, together with the use of multiple methodologies and inter-disciplinary approaches, to represent the best avenues for further improving our understanding of fish populations. We implore scientists from unrelated fields to collaborate on such projects. The FSBI 50th Anniversary Symposium represented one such event, where fish-focused researchers across diverse fields, came together to advance the state of fish biology.

## Acknowledgements

We thank the organising committee of the 50th Anniversary Fisheries Society of the British Isles Symposium, for enabling the working group discussion that led to the development of this review. Thank you also to the University of Exeter for hosting the 50th Anniversary Symposium and to the numerous sponsors for funding its success.

## References

Abdul-Muneer, P. M. (2014). Application of microsatellite markers in conservation genetics and fisheries management: recent advances in population structure analysis. *Genetics Research International* **2014**, 1-11. doi: 10.1155/2014/691759.

Allendorf, F. W., Hohenlohe, P. A. & Luikart, G. (2010). Genomics and the future of conservation genetics. *Nature Reviews Genetics,* **11**, 697–709. doi:10.1038/nrg2844

Amann, R. I., Ludwig, W. & Schleifer, K. H. (1995). Phylogenetic identification and in situ detection of individual microbial cells without cultivation*. Microbiological Reviews*, **59** 143-169.

Austin, B. (2006). The bacterial microflora of fish, revised. *The Scientific World Journal* **6**, 931-945. doi: 10.1100/tsw.2006.181.

Austin, C. B., Hua Tan, M., Harrisson, K. A., Peng Lee, Y., Croft, L. J., Sunnucks, P., Pavlova, A. & Ming Gan, H. (2017). *De novo* genome assembly and annotation of Australia's largest freshwater fish, the Murray cod (*Maccullochella peelii*) from Illumina and Nanopore sequencing reads. *Gigascience* gix063. doi: 10.1093/gigascience/gix063.

Benestan L*,* Moore J-S*,* Sutherland BJG*, et al.* (2017). Sex matters in massive parallel sequencing: Evidence for biases in genetic parameter estimation and investigation of sex determination systems*. Molecular Ecology,* 00*:*1–17. https://doi.org/10.1111/mec.14217*.*

Blanchet, S., Prunier, J. G. & De Kort, H. (2017). Time to go bigger: emerging patterns in macrogenetics. *Trends in Genetics*, (Online) doi: 10.1016/j.tig.2017.06.007

Boecklen, W. J., Yarnes, C. T., Cook, B. A., & James, A. C. (2011). On the Use of Stable Isotopes in Trophic Ecology. *Annual Review of Ecology, Evolution, and Systematics*, **42**, 411–440. https://doi.org/10.1146/annurev-ecolsys-102209-144726.

Bograd, S. J., Block, B. A., Costa, D. P. & Godley, B. J. (2010). Biologging technologies: New tools for conservation. Introduction. *Endangered Species Research* **10**, 1-7. doi: 10.3354/esr00269.

Bonney, R., Shirk, J. L., Phillips, T. B., Wiggins, A., Ballard, H. L., Miller-Rushing, A. J. & Parrish, J. K. (2014). Next steps for citizen science. *Science* **343**, 1436-1437. doi: 10.1126/science.1251554.

Botsford, L. W., Brumbaugh, D. R., Grimes, C., Kellner, J. B. Largier, J., O'Farell, M. R., Ralston, S., Soulanile, E. & Wespestad, V. (2009). Connectivity, sustainability, and yield: bridging the gap between conventional fisheries management and marine protected areas. *Reviews in Fish Biology Fisheries* **19,** 69−95. doi: 10.1007/s11160-008-9092-z.

Bourret, V., Kent, M.P., Primmer, C. R. et al. (2013). SNP-array reveals genome-wide patterns of geographical and potential adaptive divergence across the natural range of Atlantic salmon (*Salmo salar*). *Molecular Ecology*, **22**, 532–551.

Broitman, B. R., Halpern, B. S., Gelcich, S., Lardies, M. A., Vargas, C. A., Vásquez-Lavín, F., Widdicombe, S. & Birchenough, S. N. (2017). Dynamic interactions among boundaries and the expansion of sustainable aquaculture. *Frontiers in Marine Science* **4**, 1-4. doi: 10.3389/fmars.2017.00015.

Budding, A. E., Grasman, M. E., Eck, A., Bogaards, J. A., Vandenbroucke-Grauls, C. M., van Bodegraven, A. A. & Savelkoul, P. H. (2014). Rectal swabs for analysis of the intestinal microbiota. *PLoS One* **9**(7): e101344. https://doi.org/10.1371/journal.pone.0101344.

Callou, C. (2009). Inventaires archéozoologiques et archéobotaniques de France (Inventaire National Du Patrimoine Naturel). *Muséum National d'Histoire Naturelle*.

Chang, D., and Shapiro, B. (2016). Using ancient DNA and coalescent-based methods to infer extinction. *Biology Letters*, **12**(2), 20150822.

Chistiakov, D. A., Hellemans, B. & Volckaert, F.A.M. (2006). Microsatellites and their genomic distribution, evolution, function and applications: A review with special reference to fish genetics. *Aquaculture*, **255**, 1–29.

Christensen, V. & Walters, C.J. (2004) Ecopath with Ecosim: methods, capabilities and limitations. *Ecological Modelling*, **172**, 109-139.

Clusa, L., Ardura, A., Fernández, S., Roca, A. A. & García-Vázquez, E. (2017). An extremely sensitive nested PCR-RFLP mitochondrial marker for detection and identification of salmonids in eDNA from water samples. *PeerJ* **5**, p.e3045.

Cooke, S. J., Midwood, J. D., Thiem, J. D., Klimley, P., Lucas, M. C., Thorstad, E. B., Eiler, J., Holbrook, C. & Ebner, B. C. (2013). Tracking animals in freshwater with electronic tags: past, present and future. *Animal Biotelemetry*, **1**, 5.

Dahlgren, C. P., Buch, K., Rechisky E. & Hixon M. A. (2016). Multiyear tracking of Nassau grouper spawning migrations. *Marine and Coastal Fisheries: Dynamics, Management, and Ecosystem Science*, **8**, 522–535. DOI: 10.1080/19425120.2016.1223233.

Davis, R. M., Baumgartner, A. Comeau, D. Cunningham, K. Davies, A. Furlong, H. Johnson, S. L'Orsa, T. Ross, C. Taggart, F. Whoriskey & Ieee. (2016). Tracking whales on the Scotian Shelf using passive acoustic monitoring on ocean gliders. Oceans 2016 Mts/Ieee Monterey.

DeAngelis D. L. & Grimm, V. (2014). Individual-based models in ecology after four decades. *F1000Prime Reports*, **6**, 39 (doi:10.12703/P6-39)

DeAngelis, D. L. & Mooij, W. M. (2005). Individual-based modelling of ecological and evolutionary processes. 1. *Annual Review of Ecology, Evolution, and Systematics*, **36**, 147–168.

Deiner, K.*,* Renshaw, M. A.*,* Li, Y.*,* Olds, B. P.*,* Lodge, D. M. *&* Pfrender, M. E*.* (2017). Long-range PCR allows sequencing of mitochondrial genomes from environmental DNA*. Methods Ecology and Evolution (Online)* doi: 10.1111/2041-210X.12836.

DeNiro, M. J. & Epstein, S. (1977). Mechanism of carbon isotope fractionation associated with lipid synthesis. *Science,* **197**, 261–263.

Doi, H., Uchii, K., Takahara, T., Matsuhashi, S., Yamanaka, H. & Minamoto, T., (2015). Use of droplet digital PCR for estimation of fish abundance and biomass in environmental DNA surveys. *PLoS One* **10**, p.e0122763.

Eichmiller, J. J., Bajer, P. G. & Sorensen, P. W. (2014). The relationship between the distribution of common carp and their environmental DNA in a small lake. *PloS one*, **9**, p.e112611

Ekblom, R. & Wolf, J. B. W. (2014). A field guide to whole-genome sequencing, assembly and annotation. *Evolutionary Applications,* **7**, 1026–1042.

Ellegren, H. & Galtier, N. (2016). Determinants of genetic diversity. *Nature Reviews Genetics,* **17**, 422–433. https://doi.org/10.1038/nrg.2016.58.

Ellis, J. S., Gilbey, J., Armstrong, A., Balstad, T., Cauwelier, E., Cherbonnel, C., Consuegra, S. et al. (2011). Microsatellite standardization and evaluation of genotyping error in a large multi-partner research programme for conservation of Atlantic salmon (*Salmo salar* L.). *Genetica*, **139**, 353–367.

Ellison, A. M. (2004). Bayesian Inference in Ecology. *Ecology Letters,* **7**, 509–520.

FAO. (2014). The state of world fisheries and aquaculture opportunities and challenges FAO, Rome. p. 7.

FAO. (2016). The state of world fisheries and aquaculture 2016. Contributing to food security and nutrition for all. Rome. p.18.

Faulkes, Z. (2014). #SciFund round 4 analysis. http://scifundchallenge.org/blog/2014/03/18/scifund-round-4-analysis/.

Ferguson, M.M. & Danzmann, R.G. (1998). Role of genetic markers in fisheries and aquaculture: useful tools or stamp collecting? *Canadian Journal of Fisheries and Aquatic Sciences*, **55**, 1553-1563.

Ford JS & Myers RA (2008). A global assessment of salmon aquaculture impacts on wild salmonids. *PLOS Biology*, **6**, e33. https://doi.org/10.1371/journal.pbio.0060033

Freeland, J. R. (2016). The importance of molecular markers and primer design when characterizing biodiversity from environmental DNA. *Genome,* **60**, 358-374.

Froese, R. & Pauly, D. (2017) Editors. FishBase. World Wide Web electronic publication: www.fishbase.org, (06/2017).

Gargan, L. M., Morato, T., Pham, C. K., Finarelli, J. A., Carlsson, J. E. & Carlsson, J., (2017). Development of a sensitive detection method to survey pelagic biodiversity using eDNA and quantitative PCR: a case study of devil ray at seamounts. *Marine Biology,* **164**, 112.

Gaulke, C. A., Barton, C. L., Proffitt, S., Tanguay, R. L. & Sharpton, T. J. (2016). Triclosan exposure is associated with rapid restructuring of the microbiome in adult zebrafish. *PloS One*, **11**. doi: 10.1371/journal.pone.0154632

Ghanbari, M., Kneifel, W. & Domig, K. J. (2015). A new view of the fish gut microbiome: advances from next-generation sequencing. *Aquaculture,* **448**, 464-475. doi: 10.1016/j.aquaculture.2015.06.033

Gilbey J., Coughlan, J., Wennevik, V., Prodöhl, P. Stevens, J. R., Garcia de Leaniz, C., Ensing, D., Cauwelier, E., Cherbonnel, C., Consuegra, S., Coulson, M. W., Cross,

T. F., Crozier, W., Dillane, E., Ellis, J. S., García-Vázquez, E., Griffiths, A. M., Gudjonsson, S., Hindar, K., Karlsson, S., Knox, D., Machado-Schiaffino, G., Meldrup, D., Nielsen, E. E., Ólafsson, K., Primmer, C. R., Prusov, S., Stradmeyer, L., Vähä, J.-P., Veselov, A. J., Webster, L. M. I., McGinnity, P. & Verspoor, E. (2017) A microsatellite baseline for genetic stock identification of European Atlantic salmon (*Salmo salar* L.). *ICES journal of Marine Science*, fsx184, https://doi.org/10.1093/icesjms/fsx184.

Gobalet, K.W. (2001). A critique of faunal analysis; inconsistency among experts in blind tests. *Journal of Archaeological Science*, **28**, 377e386.

Goodrich, J. K., Di Rienzi, S. C., Poole, A. C., Koren, O., Walters, W. A., Caporaso, J. G., Knight, R. & Ley, R. E. (2014). Conducting a microbiome study. *Cell* **158**, 250-262. doi: 10.1016/j.cell.2014.06.037.

Goodwin, J. C. A., Andrew King, R., Iwan Jones, J., Ibbotson, A. & Stevens, J. R. (2016). A small number of anadromous females drive reproduction in a brown trout (*Salmo trutta*) population in an English chalk stream. *Freshwater Biology,* **61**, 1075–1089.

Gordon, T.A.C., Harding, H.R., Clever, F.K., Davidson, I.K., Davison, W., Montgomery, D.W., Nedelec, S.L., Weatherhead, R.C., Windsor, F.M., Armstrong, J.D., Bardonnet, A., Bergman, E., Britton, J.R., Côté, I.M., D'Agostino, D., Greenberg, L.A., Harborne, A.R., Kahilainen, K.K., Metcalfe, N.B., Mills, S.C., Milner, N.J., Mittermayer, F.H., Montorio, L., Prokkola, L.A., Rutterford, L.A., Salvanes, A.G.V., Simpson, S.D., Vainikka, A., Pinnegar, J.K., Santos, E.M. (2018). Fishes in a changing world: learning from the past to promote sustainability of fish populations. *Journal of Fish Biology,* (In review, this issue).

Grealis, E., Hynes, S., O'Donoghue, C., Vega, A., Van Osch, S. & Twomey, C. (2017). The economic impact of aquaculture expansion: An input-output approach. *Marine Policy,* **81**, 29-36. doi: 10.1016/j.marpol.2017.03.014

Gruss, A., Robinson, J., Heppell, S. S., Heppell, S. A., & Semmens, B. X. (2014). Conservation and fisheries effects of spawning aggregation marine protected areas: What we know, where we should go, and what we need to get there. *ICES Journal of Marine Science*, **71**, 1515–1534. https://doi.org/10.1093/icesjms/fsu038

Guillot, G., Leblois, R., Coulon, A. & Frantz, A. C. (2009). Statistical methods in spatial genetics. *Molecular Ecology,* **18***, 4734–4756.* doi:10.1111/j.1365-294X.2009.04410.x.

Halfyard, E. A., Webber, D., Del Papa, J., Leadley, T., Kessel, S. T., Colborne, S. F. and Fisk, A. T. (2017), Evaluation of an acoustic telemetry transmitter designed to identify predation events. *Methods Ecol Evol*. doi:10.1111/2041-210X.12726.

Harborne, A. R., Mumby, P. J., Cappel, C. V., Dahlgren, C. P., Micheli, F., Holmes, K. E., Sanchirico, J. E., Broad, K., Elliot, I. A., Brumbaugh, D. R. (2008) Reserve effects and natural variation in coral reef communities. *Journal of Applied Ecology* **45**, 1010–1018.

Hart, M. L., Meyer, A., Johnson, P. J. & Ericsson, A. C. (2015). Comparative evaluation of DNA extraction methods from feces of multiple host species for downstream next-generation sequencing. *PloS ONE*, **10**, e0143334. doi: 10.1371/journal.pone.0143334.

Hawkins, J. P., O'Leary, B. C., Bassett, N., Peters, H., Rakowski, S., Reeve, G., and Roberts, C. M. (2016). Public awareness and attitudes towards marine protection in the United Kingdom. *Marine Pollution Bulletin*, **111**, 231–236.

Hayden, E. C. (2015). Pint-sized DNA sequencer impresses first users. *Nature,* **521**, 15-16.

Helyar, S. J., Hemmer-Hansen, J., Bekkevold, D., Taylor, M. I., Ogden, R., Limborg, M. T., Cariani, A., Maes, G. E., Dopere, E., Carvalho, G. & Nielsen, E. E. (2011). Application of SNPs for population genetics of nonmodel organisms: new opportunities and challenges: analytical approaches. *Molecular Ecology Resources* **11**, 123–136.

Heupel, M.R., Semmens, J.M. & Hobday, A.J. (2006) Automated acoustic tracking of aquatic animals: scales, design and deployment of listening station arrays. *Marine and Freshwater Research*, **57**, 1-13.

Hight, B. V. & Lowe, C. G. (2007). Elevated body temperatures of adult female leopard sharks, Triakis semifasciata, while aggregating in shallow nearshore embayments: Evidence for behavioral thermoregulation? *Journal of Experimental Marine Biology and Ecology* **352**, 114-128.

Hobson, K. A. & Wassenaar, L. I. (2008) *Tracking Animal Migration with Stable Isotopes*, 1st ed. The Trerrestrial Ecology Series. Oxford, UK: Elsevier Acadmenic Press. Vol. 2.

Hussey, N. E., Kessel, S. T., Aarestrup, K., Cooke, S. J., Cowley, P. D., Fisk, A. T., Harcourt, R. G., Holland, K. N., Iverson, S. J., Kocik, J. F., Flemming, J. E. M. & Whoriskey, F. G. (2015). Aquatic animal telemetry: A panoramic window into the underwater world. *Science* **348**, 1221- 1255642. doi: 10.1126/science.1255642.

Ingerslev, H. C., von Gersdorff Jørgensen, L., Strube, M. L., Larsen, N., Dalsgaard, I., Boye, M. & Madsen, L. (2014). The development of the gut microbiota in rainbow trout (*Oncorhynchus mykiss*) is affected by first feeding and diet type. *Aquaculture*, **424**, 24-34. doi: 10.1016/j.aquaculture.2013.12.032

Iwamoto, E. M., Myers, J. M., and Gustafson, R. G. (2012). Resurrecting an extinct salmon evolutionary significant unit: archived scales, historical DNA and implication for restoration. *Molecular Ecology*, **21**, 1567-1582.

Jansen, H.J., M., Liem, S. A., Jong-Raadsen, S., Dufour, F-A., Weltzien, W., Swinkels, A., Koelewijn, A. P., Palstra, B., Pelster, H. P., Spaink, G. E., Van den Thillart, Dirks, R. P. & Henkel, C. V. (2017). Rapid de novo assembly of the European eel genome from nanopore sequencing reads. *bioRxiv* 101907. doi: 10.1101/101907.

Jentoft, S., & Chuenpagdee, R. (2009). Fisheries and coastal governance as a wicked problem. *Marine Policy,* **33**, 553-560. doi: 10.1016/j.marpol.2008.12.002.

Jepsen, N., Thorstad, E. B., Havn, T. & Lucas, M. C. (2015). The use of external electronic tags on fish: an evaluation of tag retention and tagging effects. *Animal Biotelemetry,* **3**, 49. 10.1186/s40317-015-0086-z.

Jennings, S., Stentiford, G. D., Leocadio, A. M., Jeffery, K. R., Metcalfe, J. D., Katsiadaki, I., Auchterlonie, N. A., Mangi, S. C., Pinnegar, J. K., Ellis, T. & Peeler, E. J. (2016). Aquatic food security: insights into challenges and solutions from an analysis of interactions between fisheries, aquaculture, food safety, human health, fish and human welfare, economy and environment. *Fish and Fisheries* **17**, 893-938. doi: 10.1111/faf.12152.

Kansa, E. C. (2010). Open context in context: Cyberinfrastructure and distributed approaches to publish and preserve archaeological data. *The SAA Archaeological Record*, **10**, 12–16.

Karlsson, S., Diserud, O. H., Fiske, P., & Hindar, K. (2016). Widespread genetic introgression of escaped farmed Atlantic salmon in wild salmon populations. *ICES Journal of Marine Science: Journal Du Conseil*, **73**, 2488–2498. https://doi.org/10.1093/icesjms/fsw121

Kurle, C. M. & McWhorter, J. (2017) Spatial and temporal variability within marine isoscaes: implications for interpreting stable isotope data from marine systems. *Marine Ecology Progress Series,* **568**, 31-45. doi 10.3354/meps12045.

Lacoursière-Roussel, A., Rosabal, M. & Bernatchez, L. (2016). Estimating fish abundance and biomass from eDNA concentrations: variability among capture methods and environmental conditions. *Molecular Ecology Resources*, **16**, 1401-1414.

Lauridsen, R. B., Moore, A., Privitera, L. Gregory, S. D., Beaumont, W. R. C. & Kavanagh, A. J. (2017). Migration behaviour and loss rate of trout smolts in the transitional zone between freshwater and saltwater In: *Sea Trout: Science & Management*. (Graeme Harris, *Ed*.). *Proceedings of the 2nd International Sea Trout Symposium, October 2015*, *Dundalk, Ireland*, 292-307.

Layman, C. A., Araujo, M. S., Boucek, R., Hammerschlag-Peyer, C. M., Harrison, E., Jud, Z. R., Matich, P., Rosenblatt, A. E., Vaudo, J. J., Yeager, L. A., Post, D. M. & Bearhop, S. (2012), Applying stable isotopes to examine food-web structure: an overview of analytical tools. *Biological Reviews* **87**, 545–562. doi:10.1111/j.1469-185X.2011.00208.x.

Lea, J. S. E., N. E. Humphries, R. G. von Brandis, C. R. Clarke & D. W. Sims. (2016). Acoustic telemetry and network analysis reveal the space use of multiple reef predators and enhance marine protected area design. *Proceedings of the Royal Society of London B: Biological Sciences* **283.**

Lien, S., Koop, B. F., Sandve, S. R., Miller, J. R., Matthew, P., Leong, J. S., Minkley, D. R., Zimin, A., Grammes, F., Grove, H. et al. (2016) The Atlantic salmon genome provides insights into rediploidization. *Nature,* **533**, 200–205.

Linden, M. V. & Webley, L. (2012). Introduction: Development-led Archaeology in North-West Europe. In R. Bradley, C. Haselgrove, M. V. Linden & L. Webley (Eds.), *Development-led Archaeology in North-West Europe*. Oxbow Books.

Little, D. C., Newton, R. W. & Beveridge, M. C. M. (2016). Aquaculture: a rapidly growing and significant source of sustainable food? Status, transitions and potential. *Proceedings of the Nutrition Society,* **75**, 274-286. doi: 10.1017/S0029665116000665.

Llewellyn, M. S., Boutin, S., Hoseinifar, S. H. & Derome, N. (2014). Teleost microbiomes: the state of the art in their characterization, manipulation and importance in aquaculture and fisheries. *Frontiers in Microbiology,* **5**. doi: 10.3389/fmicb.2014.00207.

Llewellyn, M. S., McGinnity, P., Dionne, M., Letourneau, J., Thonier, F., Carvalho, G. R., Creer, S. & Derome, N. (2016). The biogeography of the Atlantic salmon (*Salmo salar*) gut microbiome. *The ISME journal* **10**, 1280-1284. doi: 10.1038/ismej.2015.189.

Lyons, P. P., Turnbull, J. F., Dawson, K. A. & Crumlish, M. (2017). Exploring the microbial diversity of the distal intestinal lumen and mucosa of farmed rainbow trout *Oncorhynchus mykiss* (Walbaum) using next generation sequencing (NGS). *Aquaculture Research,* **48**, 77-91. doi: 10.1111/are.12863.

MacDonald, A. J. & Sarre, S. D. (2017). A framework for developing and validating taxon-specific primers for specimen identification from environmental DNA. *Molecular Ecology Resources,* **17**, 708-720.

MacKenzie, K. M., Longmore, C., Preece, C., Lucas, C. H., Trueman, C. N. (2014). Testing the long-term stability of marine isoscapes in shelf seas using jellyfish tissues. *Biogeochemistry,* **121**, 441-454. doi: 10.1007/s10533-014-0011-1.

Macqueen, D. J., Primmer, C. R., Houston, R. D., Nowak, B. F., Bernatchez, L., Bergseth, S., Davidson, W. S., Gallardo-escárate, C., Goldammer, T., Guiguen, Y., et al. (2017). Functional Annotation of All Salmonid Genomes ( FAASG ): An International Initiative Supporting Future Salmonid Research, Conservation and Aquaculture. *BMC Genomics,* **18**, 1–9.

Magozzi, S. Yool, A., VanderZanden, H.B., Wunder, M.B., Trueman, C.N. (2017). Using ocean models to predict spatial and temporal variation in marine carbon isotopes. *Ecosphere,* **8**, e01763. doi: 10.1002/ecs2.1763.

McClelland, J. W., and Montoya, J. P. (2002). Trophic relationships and the nitrogen isotopic composition of amino acids in plankton. *Ecology*, **83**(8), 2173-2180.

McClenachan, L. (2009). Documenting Loss of Large Trophy Fish from the Florida Keys with Historical Photographs. *Conservation Biology*, **23**(3), 636–643.

McMahon, K. W. & McCarthy, M. D. (2016). Embracing variability in amino acid $\delta^{15}$N fractionation: mechanisms, implications, and applications for trophic tcology. *Ecosphere* **7**, e01511.

Methé, B. A., Nelson, K. E., Pop, M., Creasy, H. H., Giglio, M. G., Huttenhower, C., Gevers, D., Petrosino, J. F., Abubucker, S., Badger, J. H. & Chinwalla, A.T. (2012). A framework for human microbiome research. *Nature,* **486**, 215-221. doi: 10.1038/nature11209.

Methling, C., Tudorache, C., Skov, P. V. & Steffensen, J. F. (2011). Pop Up Satellite Tags Impair Swimming Performance and Energetics of the European Eel (*Anguilla anguilla*). *Plos One,* **6**, e20797. doi: 10.1371/journal.pone.0020797.

Mintram, K. S., Brown, A. R., Maynard, S. K., Thorbek, P. & Tyler, C. R. (2017). Capturing ecology in modeling approaches applied to environmental risk assessment of endocrine active chemicals in fish. *Critical Reviews in Toxicology*, DOI: 10.1080/10408444.2017.1367756

Miya, M., Sato, Y., Fukunaga, T., Sado, T., Poulsen, J.Y., Sato, K., Minamoto, T., Yamamoto, S., Yamanaka, H., Araki, H. & Kondoh, M. (2015). MiFish, a set of universal PCR primers for metabarcoding environmental DNA from fishes: detection of more than 230 subtropical marine species. *Open Science* ***2***, 150088. DOI: 10.1098/rsos.150088.

Moffitt, C.M. & Cajas-Cano, L. (2014). Blue growth: the 2014 FAO state of world fisheries and aquaculture. *Fisheries*, **39**, 552-553. doi: 10.1080/03632415.2014.966265.

Murchie, K.J., Shultz, A.D., Stein, J.A. et al. (2015). Defining adult bonefish (*Albula vulpes*) movement corridors around Grand Bahama in the Bahamian Archipelago *Environmental Biology of Fishes*, **98**, 2203–2212. https://doi.org/10.1007/s10641-015-0422-4

Murray, G. G. R., Soares, A. E. R., Novak, B. J., Schaefer, N. K., Cahill, J. A., Baker, A. J., Shapiro, B. (2017). Natural selection shaped the rise and fall of passenger pigeon genomic diversity. *bioRxiv*. https://doi.org/10.1101/154294.

Naito, Y. I., Chikaraishi, Y., Drucker, D. G., Ohkouchi, N., Semal, P., Wißing, C., and Bocherens, H. (2016). Ecological niche of Neanderthals from Spy Cave revealed by nitrogen isotopes of individual amino acids in collagen. *Journal of Human Evolution*, **93**, 82–90.

Narum, S. R., Banks, M., Beacham, T. D., Bellinger, M. R., Campbell, M. R., DeKoning, J., Elz, A., Guthrie III, C. M., Kozfkay, C., Miller, K. M., Moran, P., Phillips, R., Seeb, L. W., Smith, C. T., Warheit, K., Young, S. F. & Garza, J. C. (2008). Differentiating salmon populations at broad and fine geographic scales with microsatellites and SNPs. *Molecular Ecology,* **17**, 3464–3477.

NASCO (2008) *Salmon at Sea – SALSEA – An International Cooperative Research Programme on Salmon at Sea*. NASCO Report: SAL 04(5). http://www.nasco.int/sas/pdf/archive/other_reports/salsea_programme.pdf (accessed 31st October 2017).

Nash, K.L., Bijoux, J., Robinson, J., Wilson, S.K. & Graham, N.A.J. (2016) Harnessing fishery-independent indicators to aid management of data-poor fisheries: weighing habitat and fishing effects. *Ecosphere*, **7**, e01362.

Newsome, S. D., del Rio, C. M., Bearhop, S. & Philiips D. L. (2007) A niche for isotopic ecology. *Frontiers in Ecology and the Environment*, **5**, 429-436.

Ólafsdóttir, G. Á., Westfall, K. M., Edvardsson, R. & Pálsson, S. (2014). Historical DNA reveals the demographic history of Atlantic cod (*Gadus morhua*) in medieval and early modern Iceland. *Proceedings of the Royal Society B*, **281**, 20132976.

Orton, D. C. (2016). Archaeology as a tool for understanding past marine resource use and its impact. In *Perspectives on Oceans Past* (pp. 47–69). Springer, Dordrecht.

OSPAR Convention. (2013). An assessment of the Ecological coherence of the OSPAR Network of Marine Protected Areas in 2012. OSPAR Commission, London, UK, ISBN 978-1-909159-52-5.

Papastamatiou, Y. P., C. G. Meyer, F. Carvalho, J. J. Dale, M. R. Hutchinson & K. N. Holland. (2013). Telemetry and random-walk models reveal complex patterns of partial migration in a large marine predator. *Ecology,* **94**, 2595-2606.

Paris, J. R., Stevens, J. R. & Catchen, J. M. (2017). Lost in parameter space: a road map for stacks. *Methods in Ecology and Evolution,* **8**, 1360–1373. doi.org/10.1111/2041-210X.12775

Pauli, J. N., Newsome, S. D., Cook, J. A., Harrod, C., Steffan, S. A., Baker, C. J. O., Ben-David, M., Bloom, D., Bowen, G. J., Cerling, T. E. et al. (2017). Opinion: why we need a centralized repository for isotopic data. *Proceedings of the National Academy of Sciences* **114**, 2997–3001. doi: 10.1073/pnas.1701742114.

Pauls, S. U., Alp, M., Bálint, M., Bernabò, P., Čiampor, F., Čiamporová-Zaťovičová, Z., Finn, D. S., Kohout, J., Leese, F., Lencioni, V., Paz-Vinas, I., Monaghan, M. T. (2014). Integrating molecular tools into freshwater ecology: developments and opportunities. *Freshwater Biology,* **59**, 1559–1576. https://doi.org/10.1111/fwb.12381.

Pine, W. E., Pollock, K. H., Hightower, J. E., Kwak, T. J., Rice, J. A. (2003) A Review of Tagging Methods for Estimating Fish Population Size and Components of Mortality. *Fisheries,* **28**, 10-3, doi: 10.1577/1548-8446(2003)28.

Poikane, S., Ritterbusch, D., Argillier, C., Białokoz, W., Blabolil, P., Breine, J., Jaarsma, N. G., Krause, T., Kubečka J., Lauridsen T. L., Nõges P., Peirson, G. & Virbickas, T. (2017). Response of fish communities to multiple pressures: development of a total anthropogenic pressure intensity index. *Science of the Total Environment*, **586**, 502–511.

Richter, K. K., Wilson, J., Jones, A. K. G., Buckley, M., van Doorn, N., and Collins, M. J. (2011). Fish 'n chips: ZooMS peptide mass fingerprinting in a 96 well plate format to identify fish bone fragments. *Journal of Archaeological Science*, **38**, 1502–1510.

Ritchie, M. D., Holzinger, E. R., Li, R., Pendergrass, S. A. & Kim, D. (2015). Methods of integrating data to uncover genotype-phenotype interactions. *Nature Reviews Genetics*, **16**, 85–97. doi:10.1038/nrg3868

Rodríguez-Ezpeleta, N., Bradbury, I. R., Mendibil, I., Álvarez, P., Cotano, U. & Irigoien, X. (2016). Population structure of Atlantic mackerel inferred from RAD-seq-derived SNP markers: effects of sequence clustering parameters and hierarchical SNP selection. *Molecular Ecology Resources,* **16**, 991–1001. doi: 10.1111/1755-0998.12518.

Rogers, A., Blanchard, J.L. & Mumby, P.J. (2014) Vulnerability of coral reef fisheries to a loss of structural complexity. *Current Biology*, **24**, 1000-1005.

Salipante, S. J., Kawashima, T., Rosenthal, C., Hoogestraat, D. R., Cummings, L. A., Sengupta, D. J., Harkins, T. T., Cookson, B. T. & Hoffman, N. G. (2014). Performance comparison of Illumina and ion torrent next-generation sequencing platforms for 16S rRNA-based bacterial community profiling. *Applied and Environmental Microbiology,* **80**, 7583-7591. doi: 10.1128/AEM.02206-14.

Schrider, D. R. & Kern, A. D. (2014). Discovering functional DNA elements using population genomic information: A proof of concept using human mtDNA. *Genome Biology and Evolution*, **6**, 1542–1548. http://doi.org/10.1093/gbe/evu116.

Serafy J.E., Shideler G.S., Araújo R.J., Nagelkerken I. (2015). Mangroves enhance reef fish abundance at the Caribbean regional scale. *PLOS ONE*, **10**, e0142022. https://doi.org/10.1371/journal.pone.0142022.

Sevellec, M., Pavey, S. A., Boutin, S., Filteau, M., Derome, N. & Bernatchez, L. (2014). Microbiome investigation in the ecological speciation context of lake whitefish (*Coregonus clupeaformis*) using next-generation sequencing. *Journal of Evolutionary Biology,* **27**, 1029-1046. doi: 10.1111/jeb.12374.

Silvertown, J. (2009). A new dawn for citizen science. *Trends in Ecology & Evolution*, **24**, 467–471. https://doi.org/10.1016/j.tree.2009.03.017.

Shin, Y.-J., Shannon, L.J., Bundy, A., Coll, M., Aydin, K., Bez, N., Blanchard, J.L., Borges, M.d.F., Diallo, I., Diaz, E., Heymans, J.J., Hill, L., Johannesen, E., Jouffre, D., Kifani, S., Labrosse, P., Link, J.S., Mackinson, S., Masski, H., Möllmann, C., Neira, S., Ojaveer, H., Abdallahi, K.O.M., Perry, I., Thiao, D., Yemane, D. & Cury, P.M. (2010) Using indicators for evaluating, comparing, and communicating the ecological status of exploited marine ecosystems. 2. Setting the scene. *ICES Journal of Marine Science*, **67**, 692-716.

Shogren, A. J., Tank, J. L., Andruszkiewicz, E., Olds, B., Mahon, A. R., Jerde, C. L. & Bolster, D. (2017). Controls on eDNA movement in streams: transport, retention, and resuspension. *Scientific Reports,* **7**, 5065. doi: 10.1038/s41598-017-05223-1.

Sigsgaard, E. E., Nielsen, I. B., Bach, S. S., Lorenzen, E. D., Robinson, D. P., Knudsen, S. W., Pedersen, M. W., Al Jaidah, M., Orlando, L., Willerslev, E. & Møller, P.R. (2016). Population characteristics of a large whale shark aggregation inferred from seawater environmental DNA. *Nature Ecology & Evolution,* **1**,0004.

Sigsgaard, E.E., Nielsen, I.B., Carl, H., Krag, M.A., Knudsen, S.W., Xing, Y., Holm-Hansen, T.H., Møller, P.R. and Thomsen, P.F., 2017. Seawater environmental DNA reflects seasonality of a coastal fish community. *Marine Biology*, **164**, 128.

Smith, N. S. & Zeller, D. K. (2015) Unreported catch and tourist demand on local fisheries of small island states: these case of The Bahamas, 1950-2010. *Fishery Bulletin,* **114**, 117-131. doi: 10.7755FB.114.1.10.

Song, W., Li, L., Huang, H., Jiang, K., Zhang, F., Chen, X., Zhao, M. & Ma, L. (2016). The Gut Microbial Community of Antarctic Fish Detected by 16S rRNA Gene Sequence Analysis. *BioMedical Research International*, doi: 10.1155/2016/3241529.

Sousa, L. L., Xavier, R., Costa, V., Humphries, N. E., Trueman, C., Rosa, R., Sims, D.W. & Queiroz, N. (2016). DNA barcoding identifies a cosmopolitan diet in the ocean sunfish. *Scientific Reports*, **6**, 1–9.

Stallings, C.D. (2009). Fishery-independent data reveal negative effect of human population density on Caribbean predatory fish communities. *PLOS ONE,* **4**, e5333. https://doi.org/10.1371/journal.pone.0005333.

Star, B., Nederbragt, A. J., Jentoft, S., Grimholt, U., Malmstrom, M., Greger, T. F., Rounge, T. B., Paulsen, J., Solbakken, M. H., Sharma, A. et al. (2011). The genome sequence of Atlantic cod reveals a unique immune system. *Nature,* **477**, 207–210.

Stark, A., Lin, M. F., Kheradpour, P., Pedersen, J. S., Parts, L., Carlson, J. W. et al. (2007). Discovery of functional elements in 12 Drosophila genomes using evolutionary signatures. *Nature*, **450**, 219–232. https://doi.org/10.1038/nature06340.

Stuart-Smith, R. D., Bates, A. E., Lefcheck, J. S., Duffy, J. E., Baker, S. C., Thomson, R. J., Stuart-Smith, J. F., Hill, N. A., Kininmonth, S. J., Airoldi, L. et al. (2013) Integrating Abundance and Functional Traits Reveals New Global Hotspots of Fish Diversity. *Nature* **501**, 539–542.

Tautz, D. (1989). Hypervariability of simple sequences as a general source for polymorphic DNA markers. *Nucleic Acids Research*, **17**, 6463-6471.

Tarnecki, A.M., Burgos, F.A., Ray, C.L. and Arias, C.R. (2017). Fish intestinal microbiome: diversity and symbiosis unravelled by metagenomics. *Journal of Applied Microbiology,* **123**. doi: 10.1111/jam.13415

Thurstan, R. H., Brockington, S. & Roberts, C. M. (2010). The effects of 118 years of industrial fishing on UK bottom trawl fisheries. *Nature Communications*, **1**, 15.

Thurstan, R. H. & Roberts, C. M. (2010). Ecological meltdown in the Firth of Clyde, Scotland: two centuries of change in a coastal marine ecosystem. *PloS One*, **5**, e11767.

Trueman, C. N., MacKenzie, K. M. & Palmer, M. R. (2012) Identifying migrations in marine fishes through stable-isotope analysis. *Journal of Fish Biology* **81**, 826–847.

Trumbull, D. J., Bonney, R., Bascom, D., & Cabral, A. (2000). Thinking scientifically during participation in a citizen-science project. *Science Education*, **84**, 265-275.

Turner, C. R., Barnes, M. A., Xu, C. C., Jones, S. E., Jerde, C. L. & Lodge, D. M. (2014). Particle size distribution and optimal capture of aqueous macrobial eDNA. *Methods in Ecology and Evolution,* **5**, 676-684.

Uchii, K., Doi, H. & Minamoto, T. (2016). A novel environmental DNA approach to quantify the cryptic invasion of non-native genotypes. *Molecular Ecology Resources,* **16**, 415-422.

Ulibarri, R. M., Bonar, S. A., Rees, C., Amberg, J., Ladell, B. & Jackson, C. (2017). comparing efficiency of American Fisheries Society standard snorkeling techniques to environmental DNA sampling techniques. *North American Journal of Fisheries Management* **37**, 644-651.

Vachelard, J., Gambarra-Soares, T., Augustini, G., Riul, P. & Maracaja-Coutinho, V. (2016). A guide to scientific crowdfunding. *PLOS Biology* **14**, e1002373.

Valentini, A., Taberlet, P., Miaud, C., Civade, R., Herder, J., Thomsen, P.F., Bellemain, E., Besnard, A., Coissac, E., Boyer, F. & Gaboriaud, C. (2016). Next-generation monitoring of aquatic biodiversity using environmental DNA metabarcoding. *Molecular Ecology,* **25**, 929-942.

Van Neer, W. & Ervynck, A. (2010). Defining “natural” fish communities for fishery management purposes: biological, historical, and archaeological approaches. In *Ecologies and Economies in Medieval and Early Modern Europe* (pp. 188–218). Brill.

Voegeli, F. A., Smale, M. J., Webber, D. M., Andrade, Y. & O'Dor, R. K. (2001). Ultrasonic telemetry, tracking and automated monitoring technology for sharks. *Environmental Biology of Fishes,* **60**, 267-281.

Weijerman, M., Fulton, E.A., Kaplan, I.C., Gorton, R., Leemans, R., Mooij, W.M. & Brainard, R.E. (2015) An integrated coral reef ecosystem model to support resource management under a changing climate. *PLoS ONE*, **10**, e0144165.

Wheat, R. E., Wang, Y., Byrnes, J. E. & Ranganathan, J. (2013). Raising money for scientific research through crowdfunding. *Trends in Ecology & Evolution* **28**, 71–2. doi: 10.1016/j.tree.2012.11.001.

Wheeler, A. & Jones, A.K.G. (1989). *Fishes*. *Cambridge Manuals in Archaeology*. Cambridge University Press, Cambridge, UK.

Whoriskey, F. G. (2015). The Ocean Tracking Network: A global partnership uses electronic tagging technologies to track the movements of aquatic animals, answer science questions, stimulate new technology development and assist with sustainable development of the ocean. *Oceans 2015* - Mts/Ieee Washington. Ieee, New York. Development and International Law **47**, 221-232.

Wilcox, T. M., McKelvey, K. S., Young, M. K., Lowe, W. H. & Schwartz, M. K. (2015). Environmental DNA particle size distribution from Brook Trout (*Salvelinus fontinalis*). *Conservation Genetics Resources,* **7**, 639-641.

Worm, B., Hilborn, R., Baum, J. K., Branch, T. A., Collie, J. S., Costello, C. et al. (2009). Rebuilding Global Fisheries. *Science*, **325**, 578–585. https://doi.org/10.1126/science.1173146

Xia, J. H., Lin, G., Fu, G. H., Wan, Z. Y., Lee, M., Wang, L., Liu, X. J. & Yue, G. H. (2014). The intestinal microbiome of fish under starvation. *BMC Genomics*, **15**, doi: 10.1186/1471-2164-15-266.

Yamamoto, S., Minami, K., Fukaya, K., Takahashi, K., Sawada, H., Murakami, H., Tsuji, S., Hashizume, H., Kubonaga, S., Horiuchi, T. & Hongo, M. (2016). Environmental DNA as a ‘snapshot’ of fish distribution: A case study of Japanese jack mackerel in Maizuru Bay, Sea of Japan. *PloS One,* **11**, p.e0149786.

Zeller, D., Harper, S., Zylich, K., and Pauly, D. (2015). Synthesis of underreported small -scale fisheries catch in Pacific island waters. *Coral Reefs*, **34**, 25-39.