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SPECIAL FEATURE: Advances in Avian Diet Methods and Applications

Current methods and future directions in avian diet analysis

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ABSTRACT

Identifying the composition of avian diets is a critical step in characterizing the roles of birds within ecosystems. However, because birds are a diverse taxonomic group with equally diverse dietary habits, gaining an accurate and thorough understanding of avian diet can be difficult. In addition to overcoming the inherent difficulties of studying birds, the field is advancing rapidly, and researchers are challenged with a myriad of methods to study avian diet, a task that has only become more difficult with the introduction of laboratory techniques to dietary studies. Because methodology drives inference, it is important that researchers are aware of the capabilities and limitations of each method to ensure the results of their study are interpreted correctly. However, few reviews exist which detail each of the traditional and laboratory techniques used in dietary studies, with even fewer framing these methods through a bird-specific lens. Here, we discuss the strengths and limitations of morphological prey identification, DNA-based techniques, stable isotope analysis, and the tracing of dietary biomolecules throughout food webs. We identify areas of improvement for each method, provide instances in which the combination of techniques can yield the most comprehensive findings, introduce potential avenues for combining results from each technique within a unified framework, and present recommendations for the future focus of avian dietary research.

Keywords: avian diet, dietary biomolecules, DNA metabarcoding, feeding ecology, prey identification, stable isotope analysis

LAY SUMMARY

- Providing accurate assessments of diet composition is an essential step in understanding the life history of birds as well as their roles within ecosystems.
- A wide array of techniques exists to study the prey composition of birds, including recently developed laboratory-based methods, but each of these methods comes with their own strengths and weaknesses.
- This review details the benefits and drawbacks of each technique, suggests pathways to overcoming methodological limitations, and demonstrates how these techniques can be leveraged to answer cutting-edge questions in avian dietary studies.
- Finally, we discuss how the use of multiple techniques within a single study can yield a more comprehensive understanding of avian diet, present novel ways to combine data from each technique within a unified framework, and suggest areas of research to advance the field of avian dietary ecology.

Métodos actuales y direcciones futuras en el análisis de la dieta aviar

RESUMEN

Identificar la composición de las dietas aviares es un paso fundamental para caracterizar los roles de las aves dentro de los ecosistemas. Sin embargo, debido a que las aves son un grupo taxonómico diverso con hábitos de dieta igualmente diversos, puede resultar difícil obtener una comprensión precisa y completa de la dieta de las aves. Además de superar las dificultades inherentes del estudio de las aves, el tema avanza rápidamente y los investigadores se enfrentan al desafío de una miríada de métodos para estudiar la dieta aviar, una tarea que se ha vuelto incluso más difícil con la introducción de técnicas de laboratorio a los estudios de la dieta. Debido a que la metodología condiciona la inferencia, es importante que los investigadores sean conscientes de las capacidades y limitaciones de cada método para garantizar que los resultados de su estudio se interpreten correctamente. Sin embargo, existen pocas revisiones que detallen cada una de las técnicas tradicionales y de laboratorio utilizadas en los estudios de dieta, y aún menos enmarcan estos métodos de modo específico para las aves. Aquí, discutimos las fortalezas y limitaciones de la identificación morfológica de presas, de las técnicas basadas en ADN, del análisis de isótopos estables y del rastreo de biomoléculas de la dieta a lo largo de las redes tróficas. Identificamos áreas de mejora para cada método, proporcionamos instancias en las que la combinación de técnicas puede producir los hallazgos más completos, presentamos posibles vías para combinar los resultados de cada técnica dentro de un marco unificado y brindamos recomendaciones para el futuro enfoque de la investigación de la dieta de las aves.

Palabras clave: análisis de isótopos estables, biomoléculas de la dieta, dieta aviar, ecología de la alimentación, identificación de presas, meta codificación de barras de ADN

INTRODUCTION

Evaluating the composition of avian diets has been a focus of ornithological inquiry for over a century (Slater 1892). Dietary studies have helped to characterize ecological interactions of birds (Burin et al. 2016) and identify prey preference as a driving force behind the evolution of the immense biodiversity across the Class Aves (Kissling et al. 2012, Barnagaud et al. 2014). Diet has long been recognized as a defining life-history trait (Eaton 1958), and characterizing the dietary niche is an important step in identifying the roles of species within ecosystems (Elton 1927). A baseline understanding of avian prey preferences has helped researchers to better identify dietary shifts caused by natural (Jaksic 2004) and anthropogenic disturbances (Murray et al. 2018, Trevelline et al. 2018a) as well as the population- (English et al. 2018) and community-wide (Spiller and Dettmers 2019) consequences of these disturbances. Studies of dietary composition also inform our understanding of biotic interactions, such as those stemming from intraspecific competition (McMahon and Marples 2017), interspecific competition (Trevelline et al. 2018b), and trophic cascade events (Mäntylä et al. 2011). Finally, studies of bird diets have been used to highlight the ecological services that birds provide (Whelan et al. 2008). In short, understanding the dietary niche of a species allows researchers to quickly describe important life-history traits (Abrahamczyk and Kessler 2015) as well as the complex interactions that birds have with their environments (O'Donnell et al. 2012) and, in turn, provides essential information for the management and conservation of avian species and their habitats (Ontiveros et al. 2005).

Early investigation of avian diet relied upon direct methods such as the observation of foraging (Croxall 1976) and provisioning events (Snyder and Wiley 1976) or morphological identification of prey retrieved from gastric lavage (Moody 1970), feces (Tucker and Powell 1999), and stomach samples from sacrificed birds (Beal 1915). While these methods provide a strong foundation, they are laborious, seldom provide taxonomically-precise prey identification (Symondson 2002), and often fail to detect relatively small prey (Culicidae; Guinan et al. 2020, Jedlicka et al. 2017), rapidly digested prey (Lepidoptera; Eaton 1958, Trevelline et al. 2016), or highly fragmented prey remains (Galimberti et al. 2016). The advent of several laboratory-based methods now allows for indirect estimation of prey composition, thus permitting increased precision in prey detection and taxonomic assignment (Taberlet et al. 2012), while adding information on nutrient assimilation (Hobson and Clark 1992a) across time scales ranging from hours to years depending on the tissue sampled (Podlesak et al. 2005). However, while these laboratory-intensive techniques have revitalized studies of avian diets and trophic dynamics, they have their own drawbacks, such as an inability to accurately quantify prey counts or biomass with DNA-based methods (Piñol et al. 2015), and the variable nature of biomolecule assimilation (Galloway and Budge 2020) potentially impacting results stemming from isotopic and lipid-based methods. Because the findings of dietary studies are methodologically sensitive (Marti 1987), it is important to understand the benefits and limitations of each technique before use.

While valuable reviews detail the most commonly used methodologies in dietary reconstruction (Schoeninger 2010, Traugott et al. 2013, Nielsen et al. 2017, Alberdi et al. 2019), few pertain specifically to birds (Rosenberg and Cooper 1990, Barrett et al. 2007), and none discuss how these methods are currently used in avian diet research

or how they can be leveraged to build on the wealth of prior research in birds, one of the best-studied taxonomic groups. Here, we review the current methods in avian dietary studies detailing the applications, limitations, and future directions of each technique. In particular, we highlight areas where additional methodological refinement is needed, the future directions for avian dietary studies, and how data from morphological, molecular, and isotopic studies can be integrated to provide a more comprehensive understanding of avian diet.

MORPHOLOGICAL IDENTIFICATION

History and Focus

Traditional methods have informed much of our understanding of avian dietary ecology (Hyslop 1980, Rosenberg and Cooper 1990, Bent 1925), and serve as the basis for comparison with more recently developed laboratory techniques. Morphological prey identification has aided in dietary descriptions of near-threatened warblers (Deloria-Sheffield et al. 2001), helped to explain how habitat structure and search tactics are related to forest bird prey choice (Robinson and Holmes 1982), and revealed how aerial insectivores recognize differences in the quality of prey provisioned to offspring (Quinney and Ankney 1985). As these methodologies have been used for well over a century (McAtee 1912), a wealth of literature already exists that describes different approaches to the collection and identification of prey from morphological samples (Duffy and Jackson 1986, Rosenberg and Cooper 1990). Here, we briefly introduce methods for morphological prey identification to understand prey composition (vs. behavioral ecology, e.g., Remsen and Robinson 1990, Ydenberg 1994).

Methodological Considerations

Sample collection, storage, and processing. Morphological prey identification techniques are diverse, and include manual identification of prey during observations of foraging (Collis et al. 2002), feeding (Fleischer et al. 2003) or provisioning events (Margalida et al. 2005) as well as monitoring nestling-provisioning attempts with nest-box cameras (Currie et al. 1996) and digital photography (Gaglio et al. 2017). Researchers have also identified prey retrieved from regurgitates collected via emetics (Prŷs-Jones et al. 1974), neck ligatures (Owen 1956), or lavage (Brensing 1977); feces collected while handling birds (Ralph et al. 1985) or from past deposits (Waugh and Hails 1983); and samples collected directly from gizzards (McAtee 1918) or stomachs (Sherry 1984, Chapman and Rosenberg 1991). Some types of direct prey collection can cause undue stress (Duffy and Jackson 1986), induce behavioral changes (Little et al. 2009), or have lethal outcomes (Zach and Falls 1976, Poulin et al. 1994, Carlisle and Holberton 2006), suggesting that some direct collection techniques are undesirable, particularly with at-risk species (Ralph et al. 1985).

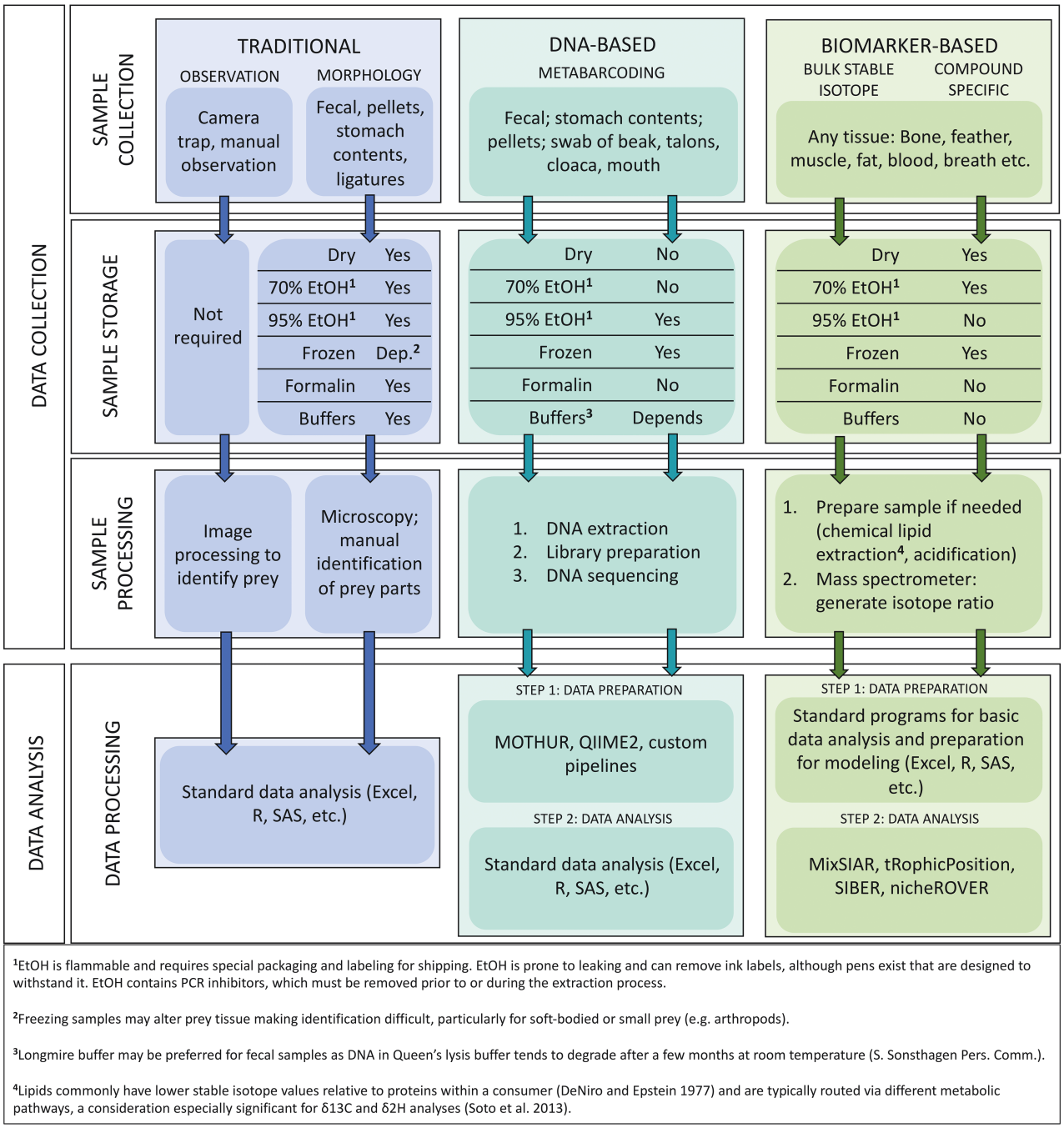
When samples must be collected, diet items should be analyzed and classified soon after collection to avoid issues caused by tissue degradation. However, if samples cannot be processed immediately, preservation via freezing or storage in high concentration ethanol or formalin enables long-term storage with minimal loss of morphological integrity (Duffy and Jackson 1986). For studies using both observational and laboratory-based techniques, storage methods must be compatible as they may influence the chemical make-up of prey tissue (Sarakinos et al. 2002) or the ability to retrieve high-quality DNA (Williams et al. 1999) (Figure 1).

Prey classification. Expertise in prey systematics or the aid of detailed taxonomic keys (Merritt and Cummins 1996, Williams and McEldowney 1990) increases prey classification accuracy (Ralph et al. 1985, Sullins et al. 2018). However, even expert taxonomists are challenged to provide complete and detailed taxonomic classifications (Ralph et al. 1985, Parrish 1997), especially if prey remains are difficult to detect in feces or stomach contents (Deagle et al. 2007, Thalinger et al. 2017). Fortunately, characteristic hard parts of prey, such as sclerotized arthropod mandibles or wing fragments (Sherry et al. 2016), chitinous beaks of cephalopods (Xavier et al. 2011), bones of vertebrate prey (Dirksen et al. 1995), and seeds from fruits (Gorchov et al. 1995) and grains (Desmond et al. 2008) often persist in both regurgitant and fecal samples.

Visual identification methods are frequently criticized for their inability to classify prey items to fine taxonomic levels (Symondson 2002, Pompanon et al. 2012). However, using vouchered reference collections of locally available prey can help to alleviate these problems and can quantify prey availability in the process (Sherry et al. 2016, Kent and Sherry 2020). Additionally, species-level prey identification is not always necessary (Sherry et al. 2020), suggesting that studies will not always benefit from increased taxonomic resolution.

Future Potential

In certain cases, morphological prey identification provides greater insights than molecular or isotopic methods. For instance, the ability to distinguish caterpillars from adult moths (Barbaro and Battisti 2011) and winged from worker ants (Herrera 1983) may be important for understanding how prey is captured and for estimating the nutrient content of prey items. DNA-based methods cannot distinguish between developmental stages of prey items (Trevelline et al. 2016) while isotopic methods can only be used to do so if life stages differ in their isotopic composition (Mihuc and Toetz 1994).



[1]EtOH is flammable and requires special packaging and labeling for shipping. EtOH is prone to leaking and can remove ink labels, although pens exist that are designed to withstand it. EtOH contains PCR inhibitors, which must be removed prior to or during the extraction process.

[2]Freezing samples may alter prey tissue making identification difficult, particularly for soft-bodied or small prey (e.g. arthropods).

[3]Longmire buffer may be preferred for fecal samples as DNA in Queen's lysis buffer tends to degrade after a few months at room temperature (S. Sonsthagen Pers. Comm.).

[4]Lipids commonly have lower stable isotope values relative to proteins within a consumer (DeNiro and Epstein 1977) and are typically routed via different metabolic pathways, a consideration especially significant for δ13C and δ2H analyses (Soto et al. 2013).

FIGURE 1. An outline of the general workflow from sample collection through data analysis for the most common methods used in avian diet studies.

Morphological techniques also provide quantitative information about prey, such as the number of distinctive prey parts and thus the number of prey individuals per sample (Sherry et al. 2016), the size of prey items (Calver and Wooller 1982), and even the estimated size of partially digested prey (Hódar 1997, Rosamond et al. 2020). Furthermore, morphological techniques are unique in that they can be used to estimate prey biomass (Lalas and McConnell 2012, Ormerod and Tyler 1991), which provides critical information on energetic fluxes through food webs and can be used in conjunction with frequency of occurrence and total count to determine the relative or absolute importance of individual prey taxa (reviewed in Duffy and Jackson 1986). Finally, as morphological identification of prey is minimally destructive, researchers can glean nutritional information on prey (Grémillet et al.

2004) as well as digestion-related information (Barton and Houston 1993) from bolus (Boyle et al. 2014), pellet (Wallick and Barrett 1976), lavage (Cherel and Ridoux 1992), or fecal samples (Varennes et al. 2015), to assess gross energy content (Karasov 1990), the caloric value of different prey sizes (Stephens and Barnard 1981) or species (Guillemette et al. 1992), as well as concentrations of prey-derived macronutrients (Albano et al. 2011).

Although researchers may turn to DNA-based methods for rapid, thorough, and precise identification of diet items or isotopic methods for information on nutrient assimilation at greater time scales, morphological prey identification will remain relevant. In addition to a list of potential prey taxa, morphological techniques can also provide the reference tissue required for laboratory-based techniques (i.e. prey DNA sequences and isotopic or lipid composition), as well as data on prey consumption, which can be used as informative priors in Bayesian stable isotope mixing models (Franco-Trecu et al. 2013). Furthermore, advances in deep learning and image processing may soon allow for computational classification and quantification of prey taxa, thus reducing the drawbacks associated with morphological identification (Høye et al. 2021) and ushering in the development of an online database of "prey part" images, akin to the DNA barcodes found in the Barcode of Life Database (BOLD; Ratnasingham and Hebert 2007).

DNA-BASED METHODS

History and Focus

DNA-based methods have been used to study the feeding habits of birds for over 20 years (Sutherland 2000, Casement 2001) with sequence-based identification, or DNA barcoding, evolving and improving dramatically in the last decade. The development of high-throughput sequencing used in combination with DNA barcoding across multiple taxa within a mixed sample (i.e. DNA metabarcoding), now allows for hundreds of complex samples to be processed in parallel (Pompanon et al. 2012). Although powerful, the greatest drawbacks associated with high-throughput techniques lie in the up-front costs and the computational complexity of analysis (Jo et al. 2016). However, the cost of sequencing continues to decrease—particularly the per-sample costs when highly multiplexed—and open-source software is available for the analysis of many prey types (Bolyen et al. 2019, Palmer et al. 2018).

Methodological Considerations

Sample collection, storage, and processing. Most DNA-based avian dietary analyses are performed on fecal samples (Ando et al. 2020), which can be collected directly from birds (Trevelline et al. 2018b, Jarrett et al. 2020), from holding bags (paper: Trevelline et al. 2016, Southwell 2018; or cloth: Karp et al. 2013), or even from the environment, although the risk of sample contamination is greater (Oehm et al. 2011, Gerwing et al. 2016, McClenaghan et al. 2019). Similar to fecal samples, boluses are a minimally invasive source of dietary DNA. Other sample types have been used for genomic diet analyses, but these techniques are more invasive (i.e. lavage, induced regurgitation) or otherwise hold no obvious advantage over fecal samples (cloacal or mouth swabs, Vo and Jedlicka 2014; stomach samples, Snider et al. 2021). Though not frequently used, stomach samples in natural history collections hold great potential for molecular diet analyses (Remsen et al. 1993). However, this approach may not always be suitable because many historic samples are stored in formalin, a chemical that crosslinks DNA and complicates downstream amplification and sequencing techniques. Freezing samples upon collection is ideal for most analyses (Crisol-Martínez et al. 2016, Gerwing et al. 2016, Jarrett et al. 2020), and while additional preservation media are not necessary, samples can also be placed in stabilizing buffer, silica, or ethanol before freezing for long-term storage (Figure 1). If immediate freezing is not possible, samples stored at room temperature in ethanol are useful for extended periods (Trevelline et al. 2016), although samples can degrade if ethanol concentrations fall below 70% (S. Sonsthagen, USGS, personal communication).

Studies have tested the efficacy of different DNA extraction techniques (Oehm et al. 2011, Jedlicka et al. 2013), though most DNA-based studies use commercially available kits (e.g., Qiagen or Zymo) with protocol modifications to optimize DNA yield and quality (Trevelline et al. 2016). Phenol/chloroform extractions tend to produce inferior results at the polymerase chain reaction (PCR) stage (Lee et al. 2010), likely due to inhibitors found in fecal samples (Al-Soud and Rådström 2000). Because commercial kits cannot always accommodate an entire sample, sub-sampling is common, but samples should be thoroughly homogenized before sub-sampling (e.g., Forsman et al. 2021) to minimize biases in prey detection (Figure 2). Increasing the number of extraction replicates (Lanzén et al. 2017, Mata et al. 2019), as opposed to increased sample input amount, has been shown to be more effective for capturing alpha-diversity within a sample (Brannock and Halanych 2015), while chemical lysis, physical disruption (e.g., bead-beating) and homogenization may minimize prey-specific DNA recovery bias.

DNA barcode markers. Identifying a suitable portion of the genome as the taxonomic barcode is critical. This region must be sufficiently conserved across putative diet taxa to develop generalized PCR primers, but also variable enough to distinguish prey taxa. An effective barcode is one for which the divergence of species within a genus will be lower than that of genera within a family, and so on (Hajibabaei et al. 2006, Clare et al. 2007). Thus, only a few suitable markers, such as the frequently used mitochondrial cytochrome *c*

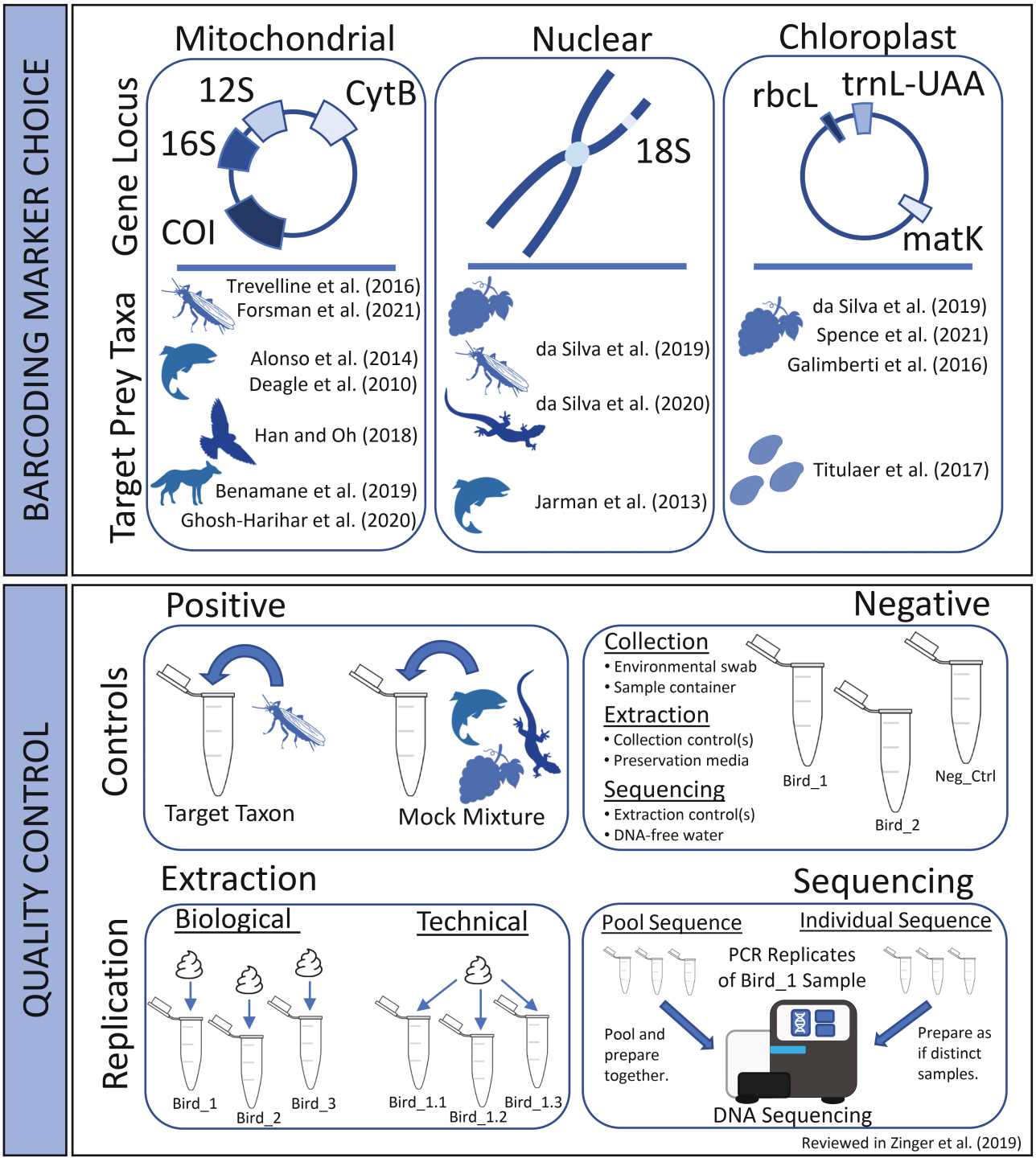


FIGURE 2. A diagram of common considerations when characterizing prey with DNA-based methods, including barcoding marker choice and quality control. While no consensus method exists for DNA-based dietary characterizations, articles further detailing each step are included.

oxidase I (COI) gene, have been identified and consistently used in avian diet studies (Figure 2). The specific primers and number of DNA barcoding loci used will depend on whether specific prey (Karp et al. 2014) or a wide range of taxa (Jusino et al. 2019) are targeted. However, no single primer set can perfectly amplify every species, therefore using multiple primer sets targeting different loci is advised (Corse et al. 2019, da Silva et al. 2019, Forsman et al. 2021).

Indexing. Before high-throughput sequencing, diet-derived DNA must be appended with oligonucleotide adapters to allow PCR amplicons to bind to the sequencing flow cell. These adapters also contain sample-specific DNA sequences (i.e. indexes) that allow for the binning of reads from each sample. Adapters can be appended directly to barcoding primers (i.e. one-step preparation) or appended to DNA barcode amplicons during a second, low-cycle PCR (i.e. two-step preparation; Zizka et al. 2019). One-step approaches are faster and reduce the costs of PCR reagents, but there is evidence that PCR efficiency may be reduced compared to the two-step approach (Zizka et al. 2019). The two-step approach is often preferred because indexes can be attached to any amplicon, as long as they have a linker sequence complementary to the indexing primer. Both approaches retain information on the sample and primer set used; therefore, researchers can use the same adapters on all of the amplicons in a single sample even if multiple primers targeting various barcoding loci are used. However, if amplicon length differs greatly between the target loci, sequencing multiple barcoding regions on the same flow cell may alter the number of expected reads for each sample/primer combination due to the preferential binding of smaller sequences to the flow cell (S. Dabydeen, Illumina Inc., personal communication).

Sequence processing. Following sequencing, a number of processing steps are required before assessing diet composition (Figure 3). Reads should be trimmed and filtered to remove low-quality sequencing reads and artifacts. However, as a consensus approach has not been reached (see Alberdi et al. 2018, O'Rourke et al. 2020), we recommend making bioinformatic pipelines open access to facilitate comparability of data across studies. Next, putative dietary taxa are delineated by clustering highly similar sequences (typically 97%) into operational taxonomic units (OTUs) and selecting a representative sequence for each cluster. Alternatively, algorithms can be used to correct sequencing errors and retain amplicon/exact sequence variants (ASVs or ESVs), which are, in effect, OTUs clustered to 100% similarity (Figure 3). Ideally, an OTU or ASV/ESV should represent a taxonomic unit corresponding to the species level (Alberdi et al. 2018).

Prey classification. Taxonomic assignment of OTUs is accomplished by comparing the representative prey-derived sequences to sequences in a reference database such as the National Center for Biotechnology Information (NCBI) nucleotide database (Benson et al. 2013) or the Barcode of Life Database (Ratnasingham and Hebert 2007) (Figure 2). Both databases tend to be biased towards areas where researchers are actively sampling biodiversity, thus representation is higher for some taxonomic groups (e.g., charismatic Lepidoptera) and for certain parts of the world (e.g., Europe, North America).

When reference libraries are incomplete, diet items may only be assignable to higher-level taxonomic ranks (e.g., Order or Family), or may be missed completely leading to false negative results (Virgilio et al. 2010). Furthermore, distinct representative prey sequences (e.g., multiple ASVs) could be assigned the same taxonomic classification, leaving open the decision whether different sequences assigned to the same taxonomic rank should be lumped or considered distinct. One approach is to aggregate diet items with the same taxonomic assignment (da Silva et al. 2020), but this can be unsatisfactory if sequencing errors cause sequences from a particular species to be assigned to the genus level instead of being aggregated with other sequences of the same species. In this case, the prey taxon would be treated as a distinct, unidentified species within the same genus. In addition to biases stemming from incomplete and erroneous reference databases or from PCR and sequencing, prey taxa may be distinguished based on genetic divergence rather than reproductive isolation. Recently diverged species may be reproductively isolated yet genetically similar at barcoding regions unaffected by the speciation event (Wiemers and Fiedler 2007), while hybridization and introgression can cause cytonuclear disequilibrium and mask distinct species when primers target organelle DNA (Funk and Omland 2003, Toews and Brelsford 2012). Conversely, prey items with large population sizes may contain substantial genetic diversity, causing their sequences to demonstrate high intraspecific divergence (Funk and Omland 2003), though using a barcoding marker with low intraspecific variation can alleviate this issue.

Finally, DNA-based methods alone cannot determine how a diet-derived sequence became present in the sample. Probabilistic cooccurrence models (Griffith et al. 2016) have been proposed to detect accidental consumption (i.e. the consumption of prey which contains the DNA of other taxa through consumption/parasitism of another taxa), though direct observation may be necessary as these models cannot definitively indicate secondary consumption (Tercel et al. 2021) nor can they determine if an avian parasite was consumed purposefully or accidentally. Detecting cannibalism also poses a unique issue as DNA-based classification techniques rely on conspecifics sharing highly similar, if not identical, barcode sequences. However, researchers can employ barcoding markers that are conserved within the predator species but exhibit high intraspecific variation, thus allowing for the differentiation of DNA sequences stemming from an individual's diet vs. its own genome.

Quality control. The degree of biological and technical replication necessary for maximizing the detectability of diet-derived sequences must be balanced with minimizing false positives caused by contamination or sequencing errors (Taberlet et al. 2018). The use

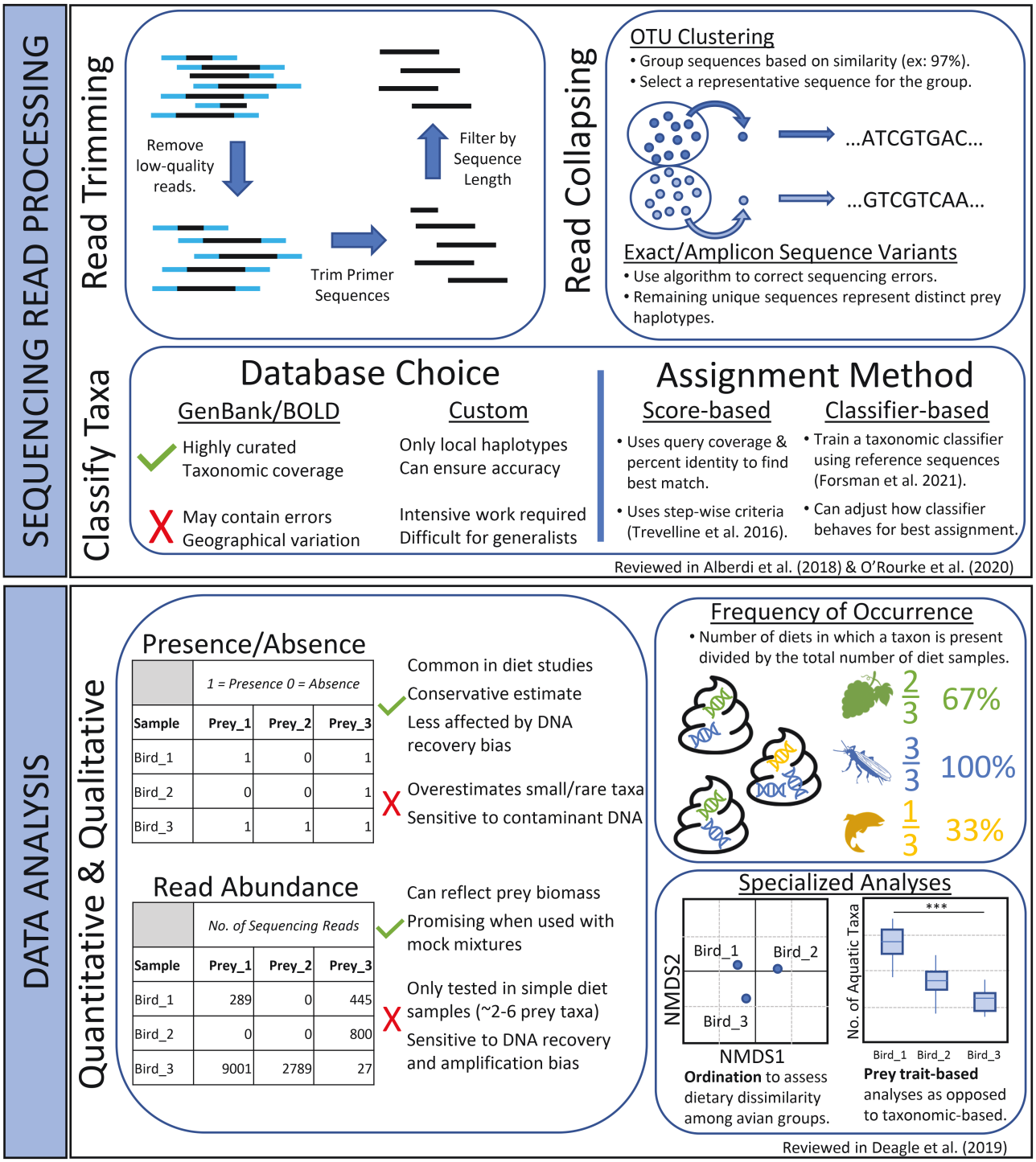


FIGURE 3. A diagram of the common considerations when characterizing prey with DNA-based methods, which includes sequencing read processing and data analysis. While no consensus method exists for DNA-based dietary characterizations, articles further detailing each step are included.

of positive and negative controls during sample collection and DNA extraction, amplification, and sequencing processes can guide how reads are filtered during the sequence analysis stage (reviewed in Zinger et al. 2019) (Figure 2). Additionally, technical replicates, in the form of multiple PCR reactions for each DNA extract, can minimize false negatives in DNA metabarcoding data, especially for diet items with low detection probabilities

(Ficetola et al. 2015) or poor DNA amplification efficiency (Jusino et al. 2019).

Data Analysis

Summary analyses. Once the taxonomic composition of the sample has been determined, data are summarized with a variety of analytical techniques (Figure 3) to create a representation of an individual's diet. Researchers frequently transform sequence data into presence-absence matrices because read abundance does not directly correlate to the biomass or frequency of corresponding prey consumed. However, this method can overestimate the importance of food consumed in small quantities (Deagle et al. 2019). Assuming the use of a presence-absence matrix of unique prey taxa or sequences, the next step is often to estimate the proportion of samples that contain a particular taxon, termed the frequency of occurrence.

Specialized analyses. More complex analytical approaches include ordination, such as principal components analysis (PCA; Crisol-Martínez et al. 2016) or non-metric multidimensional scaling (NMDS; Trevelline et al. 2018a) (Figure 3), which are statistical methods that collapse high-dimensionality data (i.e. taxonomic composition) into a smaller number of meaningful diet axes. If downstream analyses are to be implemented, such as deriving a measure of distance in niche space between two species, PCA is generally preferable to NMDS, t-SNE (Maaten and Hinton 2008), or UMAP (McInnes et al. 2018) because these methods do not preserve distances in multivariate space. Following data ordination, hypothesis testing can be implemented. For example, criteria can be developed to identify groups in multivariate space and test whether these accord with the bird species or groups in question (e.g., k-means clustering, Forgy 1965), they might derive multivariate hypervolumes (Blonder et al. 2014), and implement a randomization, null-model approach, or describe the qualitative differences in multivariate niche space among species or other groups.

Future Potential

DNA-based methods are relatively new (Hebert et al. 2003) and are advancing rapidly to overcome current limitations. For instance, recent areas of research are exploring the use of custom positive controls, such as mock mixtures of potential prey DNA, to gauge the success of the sequencing run and the ability of primers to detect prey taxa (O'Rourke et al. 2020). The inclusion of mock mixtures may become a standard feature of DNA metabarcoding diet studies, though familiarity with potential prey taxa is essential to develop an appropriate mock mixture. Custom reference libraries may be designed for particular prey taxa within the study area to verify the accuracy of representative prey barcodes; though, such an approach necessitates the collection, identification, and sequencing of all putative prey taxa.

The inability to accurately quantify the amount of each prey type consumed, either absolutely or relative to other prey taxa, is a major weakness of DNA-based methods and may be difficult to resolve due to the variety of factors: primers are inherently more efficient at amplifying some prey (reviewed in Nilsson et al. 2019); tissue types and prey taxa may have different copy numbers of marker genes (Thomas et al. 2014, Prokopowich et al. 2003); and some prey may be more difficult to digest, like those with exoskeletons (Clare et al. 2014). *In silico* analyses (Clarke et al. 2014) and controlled feeding studies (Thomas et al. 2016) have shown promise in mitigating (Piñol et al. 2019), or at least accounting for quantification biases inherent to DNA-based studies (Palmer et al. 2018). However, the limited experimental work done to associate the number of reads obtained for known amounts of specific prey taxa (Deagle et al. 2010) often uses an extremely limited diversity of prey items (approximately 2–6 taxa), suggesting that direct comparisons will be ineffective for complex dietary mixtures. Experimental designs that consider multiple consumer species, and a wider, more realistic range of diet items are necessary before its widespread application.

A semi-quantitative understanding of diet might also be possible with longer sequencing reads that are variable enough to detect and distinguish different individuals within each of the prey species present in a diet sample. However, most high-throughput sequencing methods are currently limited to short read lengths (<600 base pair paired-end reads) and, even if sequencing technology would allow for longer barcodes with sufficient sequence variation among conspecifics, it is possible that such long DNA fragments would not survive extended preservation or digestion (Symondson 2002), thus necessitating bioinformatic algorithms to identify unique contiguous prey sequences among highly similar barcode sequences. Finally, the use of internal standards for metabarcoding analyses may one day offer a method to compare absolute prey-derived molecule counts (Harrison et al. 2020), similar to the use of "housekeeping" genes as internal standards for studying gene expression across samples with qPCR methodologies (reviewed in Eisenberg and Levanon 2013).

Current DNA-based approaches are also limited by their ability to identify specific prey traits, such as age or life stage, as an organism's DNA marker remains unchanged throughout its life. However, epigenetic molecular age biomarkers (MABs; Jarman et al. 2015), such as mRNA expression levels, locus-specific DNA methylation, or telomere length, are likely to change throughout an organism's life, thus giving researchers the opportunity to glean prey life history information through the development of additional genetic tools. To date, such methods have not been implemented in dietary studies generally, let alone in avian studies. However, the development of such novel applications promises to address research

questions fundamental to our understanding of avian trophic ecology.

DNA-based metabarcoding methods excel at individual prey detection and identification, and so are particularly well-suited to answer questions that require species-level data. However, given that dietary taxa can vary greatly in resource quality, an alternative approach would be to step away from taxonomic complexities and instead focus on prey characteristics (e.g., nutrient content or life history traits), as this would dramatically simplify both the analysis and, presumably, the number of samples required to reach robust conclusions. We are aware of only one avian metabarcoding study that directly assessed prey characteristics (aquatic vs. terrestrial life stages; Trevelline et al. 2018a), and while the absence of a comprehensive prey trait database currently makes such an approach challenging, we encourage future research to consider prey traits in their analyses to better illuminate the functional characteristics of avian dietary ecology.

DNA-based dietary studies have mostly focused on the description of prey taxa and the ecosystem services of avian predators (e.g., Crisol-Martinez et al. 2016); however, we can also leverage DNA-based methods to examine diet overlap of sympatric species (Trevelline et al. 2018b), and thus address theoretical questions related to competition and resource partitioning (e.g., Spence et al. 2021). There is also considerable scope to examine whether species are dietary specialists or generalists (Jesmer et al. 2020), and how prey selection is influenced by disturbance (e.g., hurricanes, fire) or time of the annual cycle when nutrient requirements are high (e.g., breeding, pre-migration), thus clarifying responses to prey availability and physiological need. DNA-based methods are also well-suited for identifying the ecological services that birds offer, such as in seed dispersal (González-Varo et al. 2014) and pollination (Spence et al. 2021). From a conservation standpoint, DNA-based methods can help managers assess the foraging success of captive bred individuals reintroduced to the wild, thus lending an important perspective on the potential for long-term resilience (e.g., Volpe et al. 2021). Finally, there is considerable opportunity to examine how prey species communities have changed over time by taking core samples (i.e. guano at communal roosts) and extracting DNA from different layers representing different points in time. The ability to associate prey communities with climate may help to predict how climate change will affect prey availability for a range of birds.

STABLE ISOTOPE ANALYSIS

History and Focus

Elements may exist in forms that differ in atomic mass (i.e. isotopes) and are typically found overwhelmingly in one common form with lower abundances of rarer, usually heavier, forms. The relative abundance of rare to common isotopes can change as a result of numerous biogeochemical reactions, where abundance is expressed in delta (δ) notation relative to international standards in parts per thousand (‰, per mil; Hayes 1982). In biological systems, stable isotopes are incorporated at the base of food webs through fixation of inorganic compounds by primary producers (Kelly 2000), and their relative abundances are subsequently modified as they move through the food web via metabolic processes. For example, birds incorporate the isotopic values of their prey into their own tissue, and the extent of subsequent isotopic change is generally dependent upon the element, dietary quality, and tissue type (Boecklen et al. 2011). Some elements (e.g., lead or strontium) with high atomic mass show little to no isotopic change with trophic position and, thus, make for useful direct tracers of basal energy pathways to consumers (DeNiro and Epstein 1978), while the lighter elements (e.g., nitrogen) show stronger isotopic changes with trophic level and can inform trophic position (Wassenaar 2019). Thus, by characterizing the stable isotope ratios of prey sources at the base of food webs and knowing how these ratios are modified between diet and consumer through isotopic discrimination, it is possible to use the stable isotope ratios in avian tissues to infer dietary source and feeding habits.

A wealth of literature discusses the details of stable isotope analyses in ecological studies (e.g., Peterson and Fry 1987, Schmidt et al. 2007, Katzenberg 2008, Hobson 2011, Boecklen et al. 2011, Layman et al. 2012, Wiley et al. 2017), and their use in the study of bird movements (Rubenstein and Hobson 2004, Hobson and Wassenaar 2019). Here, we provide a brief overview of stable isotope analysis to investigate the diets of birds by detailing the relevant applications, considerations, and future directions of this technique.

Methodological Considerations

Sample collection, storage, and processing. Because stable isotopes are incorporated during tissue synthesis, any tissue that can be retrieved from a bird can be used for stable isotope analysis; though, selection of tissue will depend on the focus and timescale of the research question (Figure 4). To assess dietary isotopic endpoints, researchers should be sure to analyze the tissues of the main dietary items that birds consume, such as fruits (Vitz and Rodewald 2012), prey muscle tissue (Anderson et al. 2009), or even the entire body (Herrera et al. 2003) to ensure that the isotopic sources are representative of the prey pool contributing to the nutrition of the consumer. For all tissues, freezing is the preferred preservation method (Bond and Jones 2009) followed by air drying with a smokeless heat source (Bugoni et al. 2008), or storage in 70% ethanol (Hobson et al. 1997). Preservation media, such as formalin, genetic buffer solutions (Hobson et al.

1997), or high percentage ethanol (Bugoni et al. 2008) can replace isotopes within dietary or avian tissues with their own, which can be particularly problematic for carbon, nitrogen, and hydrogen stable isotope analyses. For lipid-rich tissues, chemical lipid-extraction may be needed before analysis (Bond and Jones 2009) to facilitate accurate diet reconstruction (Kojadinovic et al. 2008). Similarly, diets or avian tissues rich in carbonates often require acidification before analysis to obtain the unbiased $\delta^{13}C$ values of the organic matrix (Polito et al. 2009, Mackenzie et al. 2015). However, chemical lipid-extraction and acidification have the potential to bias tissue $\delta^{13}C$ and $\delta^{15}N$ values (Jaschinski et al. 2008, Elliott and Elliott 2016). As such, mathematical normalization for tissue lipid and/or carbonate content represents an alternative method when chemical lipid-extraction or sample acidification is not feasible or advisable (Post et al. 2007, Jaschinski et al. 2008, Oppel et al. 2010).

Isotope systems. The most common elements used in isotopic dietary studies are those of carbon ($^{13}C/^{12}C$; $\delta^{13}C$) and nitrogen ($^{15}N/^{14}N$; $\delta^{15}N$), which typically provide information on the source of feeding and trophic position, respectively (Figure 4). Stable isotopes of hydrogen ($^{2}H/^{1}H$; $\delta^{2}H$) and oxygen ($^{18}O/^{16}O$; $\delta^{18}O$) are tightly linked to the hydrological cycle and ambient temperature, and have also been used to identify nutrient inputs from terrestrial and aquatic origins (Figure 4). Sulfur ($^{34}S/^{32}S$; $\delta^{34}S$) isotope ratios have been used to identify nutrients derived from marine vs. terrestrial sources, proximity to coastlines, benthic vs. pelagic energy pathways, and use of estuarine and marsh habitats (Figure 4). Analysis of "heavy" elements can be useful for delineating source of feeding, especially those of strontium ($^{87}Sr/^{86}Sr$; $\delta^{87}Sr$), which are associated with the age of bedrock and, in North America, tend to vary along longitudinal gradients (Figure 4). While the investigation of a single element's isotopic ratio within avian tissues can provide details about diets and foraging habitat, using the stable isotopic values of multiple elements within a single study can allow researchers to differentiate among prey sources using isotopic mixing models or determining spatial origins of diets (Bowen and West 2019).

Isotopic discrimination. The change in stable isotope ratios that takes place between reactants and products or as a result of kinetic processes is known as isotopic fractionation (Tiwari et al. 2015). Isotopic fractionation is rarely measured in natural systems; instead, the isotopic discrimination that results from many individual fractionation events is measured (Schoeller 1999). Isotopic discrimination patterns between diets and consumers in animal food webs involving changes in $\delta^{15}N$ values are particularly useful once established. Processes of amination and deamination of proteins result in step-wise and fairly predictable increases in consumer tissue $\delta^{15}N$ values with each trophic transfer (Macko et al. 1986), and this has allowed researchers to use tissue $\delta^{15}N$ values to estimate consumer trophic position (DeNiro and Epstein 1981, Hobson and Welch 1992). Trophic discrimination factors (TDFs) based on $\delta^{15}N$ values, or the differences in $\delta^{15}N$ values between prey and consumer tissues, range between +2.5‰ to +5‰ with average values centered around +3‰ to +3.5‰ (Post 2002). A recent meta-analysis of factors influencing TDFs have resulted in the development of the R-package *SIDER* as a tool to predict TDFs when TDFs from controlled studies are not available (Healy et al. 2018) (Figure 5). However, researchers are encouraged when possible to conduct controlled long-term feeding trials of focal species to establish appropriate TDFs (Martínez del Rio et al. 2009).

For $\delta^{13}C$ values, it is generally assumed that TDFs are relatively low with average values centering around +0.4‰ (Post 2002). However, TDFs can vary by avian tissue type even when synthesized under the same diet due to differences in biochemical processes and macromolecule routing, which is especially apparent among lipid-rich and keratin-based tissues that may require correction factors before analysis (Hobson and Clark 1992b, Cherel et al. 2014b). Stable sulfur isotope measurements ($\delta^{34}S$) appear to also have low TDF values (~0.0‰ to +1‰) and so can be more readily linked to food web source inputs (Richards et al. 2003, Arneson and MacAvoy 2005, Florin et al. 2011). Even so, $\delta^{34}S$ TDFs can vary due to the input of endogenous sulfur from the recycling of body proteins when individuals consume low-protein diets (Richards et al. 2003). Little is currently known about TDFs associated with $\delta^{2}H$ values and whether or not patterns of trophic enrichment are due to isotopic discrimination or ambient exchange (reviewed in Vander Zanden et al. 2016).

Isotopic turnover. The residency time of elements in animal tissues varies approximately by the metabolic rate of that tissue (Figure 4). This means that metabolically active tissues will assimilate isotopic information on diet over different timescales, and thus present an opportunity to choose a tissue most appropriate for the dietary integration period of interest (Hobson 1993, reviewed by Thomas and Crowther 2015, Carter et al. 2019a). Researchers have performed stable isotope analysis on various avian tissues to understand an individual bird's diet composition at scales ranging from hours (breath and plasma; Hatch et al. 2002, Podlesak et al. 2005, Pearson et al. 2003), days and weeks, (red blood cells; Podlesak et al. 2005, Hobson and Clark 1993), to months (feathers and claws; Hedd and Montevecchi 2006, Bearhop et al. 2003) or even years (bone collagen; Stenhouse et al. 1979, Hobson and Clark 1992a, Hobson and Sealy 1991, Hedges et al. 2007). Indeed, it is possible to estimate year-round dietary patterns by examining multiple tissues from the same individual (Hobson 1993, Hobson and Bond 2012, Gòmez et al. 2018). For tissues that are metabolically inactive following

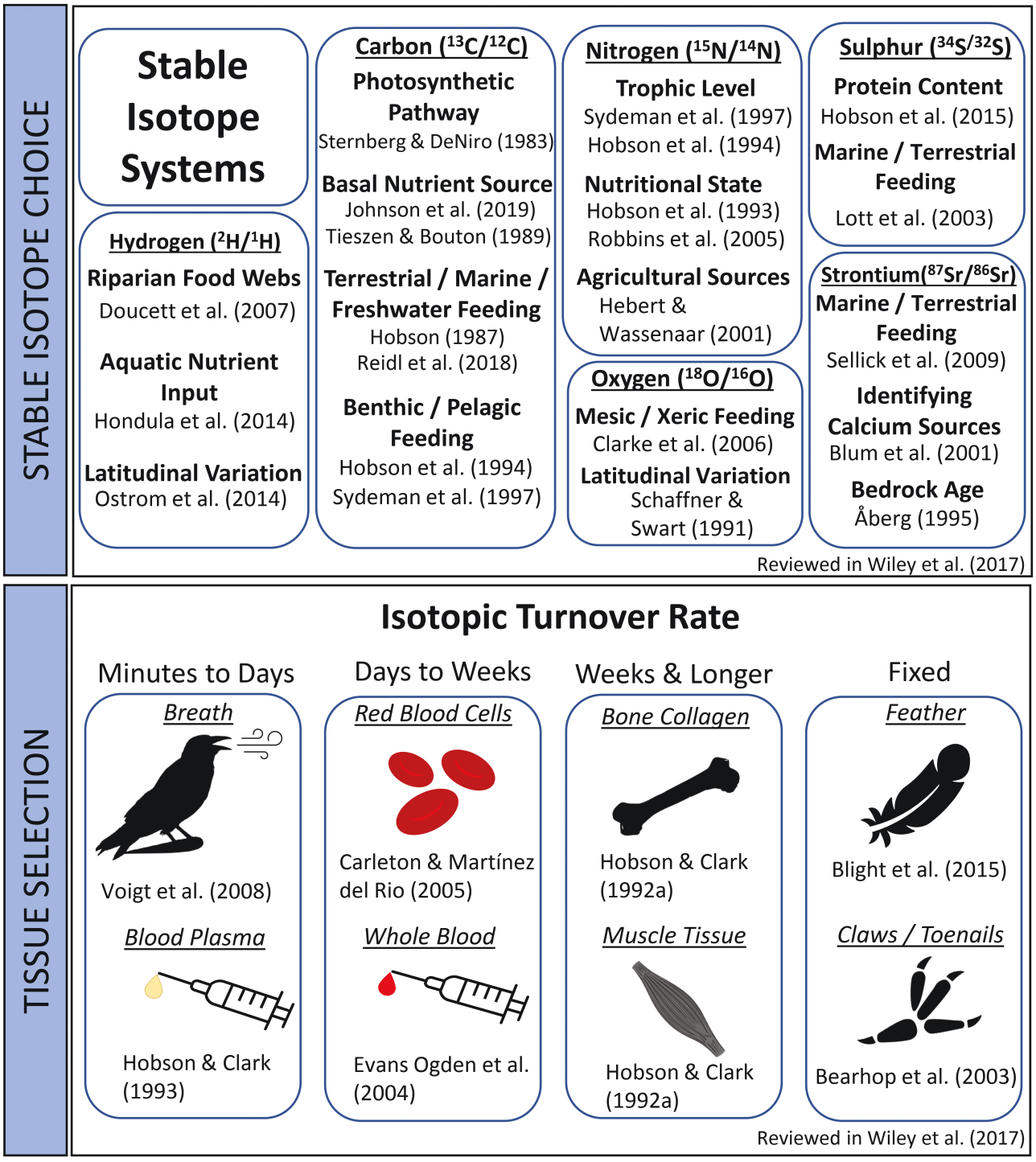


FIGURE 4. A diagram of the common considerations when characterizing prey with isotopic methods, which includes stable isotope choice and tissue selection. Citations are included to provide example studies and to highlight review articles that detail each methodological consideration.

synthesis (e.g., claws, feathers) the tissue's isotopic information is effectively "locked in", and represents only the time window over which the tissue was grown (Hobson 2005). For birds with predictable molt cycles or those stored in museum collections, this represents an opportunity to sample feathers to infer diet at a previous time (Blight et al. 2015). Additionally, claw tissue is metabolically inert once formed but claws grow continuously, thus allowing

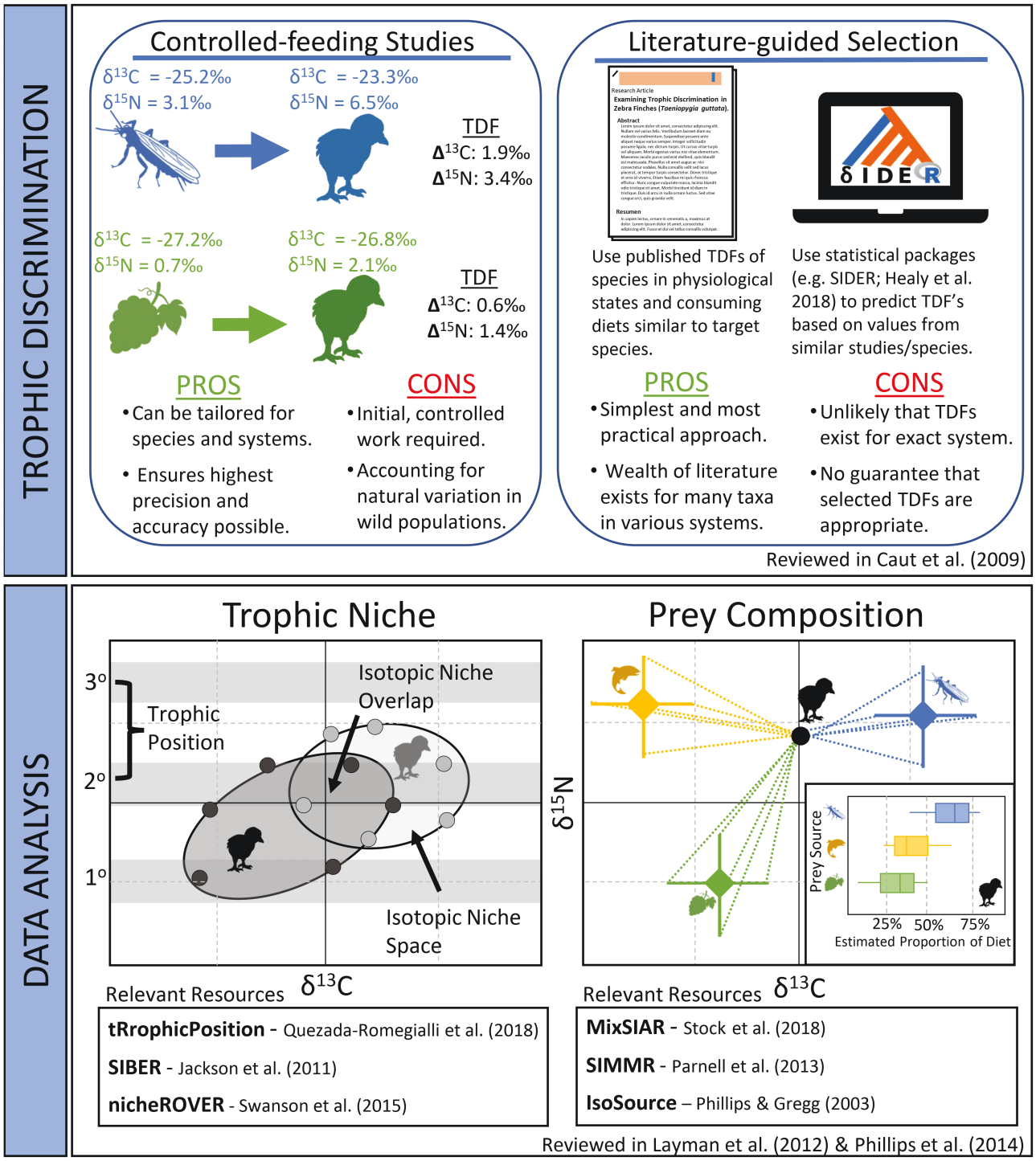


FIGURE 5. A diagram of the common considerations when characterizing prey with isotopic methods, which includes trophic discrimination and data analysis. Citations are included to provide example studies and to highlight review articles that detail each methodological consideration.

researchers to make dietary inferences on a captured bird based on previous months (Bearhop et al. 2003).

Isotopic turnover rates can also differ due to diet composition (Hobson and Clark 1993, Podlesak et al. 2005), tissue type (Vander Zanden et al. 2015), an individual's physiological state (Carleton and Martínez del Rio 2005, Cherel et al. 2005), and energy expenditure. For instance, in proteinaceous tissues, structural turnover is the main

driver of isotopic turnover (Carter et al. 2019a), but in lipids, it appears to be influenced by energy expenditure (Foglia et al. 1994, Carter et al. 2018). Though there is now a greater understanding of isotopic turnover both among individuals and tissue types, uncertainty remains for less-studied systems (Carter et al. 2019a). In addition, drivers of tissue-specific and macromolecule-specific turnover rates as well as the development of mechanistic models of isotopic turnover that can be applied across a broad diversity of taxa are needed (Carter et al. 2019a, Caut et al. 2009). The derivation of allometric relationships driving isotopic turnover rates will assist research on birds that differ in body mass (Carleton and Martinez del Rio 2005, Carter et al. 2019a).

Macromolecule routing. While isotope-based dietary reconstruction is founded on the notion that "animals are what they eat plus a few parts per mil" (DeNiro and Epstein 1976), the idea that the isotopes derived from prey tissues are dispersed throughout a bird's body uniformly (coined the "Scrambled egg theory"; Van der Merwe 1982) is an unrealistic (Martínez del Rio et al. 2009) and unsupported assumption (Ambrose and Norr 1993). Instead, stable isotopes located in macromolecular pools of diets (e.g., proteins, lipids, carbohydrates) can be differentially allocated to various consumer tissues through the process of isotopic routing (Schwarcz 1991), an effect that may be particularly important to consider when studying omnivores (Podlesak and McWilliams 2006). Thus, the selection of bulk avian tissue type for stable isotope analysis is not only based on the time scale of nutrient assimilation but also on the sources and destination of dietary macromolecules. Dietary amino acids may be preferentially routed to more proteinaceous tissues (Gannes et al. 1998, Martínez del Rio and Wolf 2005) whereas less proteinaceous tissues derive the bulk of their isotopic values from dietary carbohydrates and lipids (Gannes et al. 1998), though some mixing of isotopic assimilation between prey sources and avian tissue is expected to occur. Where possible, researchers should strive to understand the biochemical processes and routing resulting in the isotopic composition of a given tissue (Voigt et al. 2008), as known isotopic routing and discrimination will guide interpretation (Martínez del Rio and Wolf 2005).

Bulk stable isotope analysis. Stable isotope analysis of bulk tissues (e.g., muscle, blood, feather) has been the most common approach to avian dietary studies thus far. This approach has been effective because sample cost is relatively low, and analyses can be performed rapidly with high sample throughput. In addition, avian tissues used in non-lethal diet reconstruction studies, such as feathers (Kojadinovic et al. 2008) or blood (Bond and Jones 2009), will typically require little additional sample processing before bulk stable isotope analysis (but see Bond et al. 2010). When dietary sources are well characterized and isotopically distinct, and tissue-specific TDFs have been quantified, bulk stable isotope analysis can provide robust insights into the dietary history of birds (Inger and Bearhop 2008). However, when sources and/or TDFs cannot be adequately characterized, a common challenge in the interpretation of bulk tissue stable isotope values is determining whether the variation is due to changes in diet, variability in baseline food web isotope values, or some combination of these factors (Inger and Bearhop 2008). These challenges are now being overcome through more complex isotopic analyses of specific compounds (e.g., fatty acids and amino acids; Whiteman et al. 2019, Twining et al. 2020) with a method known as compound-specific isotope analysis (CSIA; Lorrain et al. 2009).

Data Analysis

Mixing models, trophic position, and isotopic niche analyses. Isotopic values of a consumer's tissue are a mixture of the isotopes derived from their prey, thus stable isotope mixing models can be used to determine the relative contributions of each prey taxon (Phillips 2012) (Figure 5). To accurately quantify prey composition, researchers must not only know the potential prey groups that birds eat, but also the isotopic values of each potential prey group, ensuring that the isotopic values of each group are distinct. If unique prey sources are not isotopically distinct, but belong to a shared functional group, researchers should consider combining these sources in downstream analyses (Phillips et al. 2005). While all mixing models work under the principle that a consumer's isotopic ratio is proportional to that of its assimilated prey, earlier iterations of these models have been improved by including the elemental concentrations of prey sources (Phillips and Koch 2002), considering isotopic routing (Martínez del Rio and Wolf 2005), and working within a Bayesian framework to allow for better propagation of uncertainty and use of informative priors (Parnell et al. 2013). Mixing models can be applied to both bulk tissue stable isotope analysis and CSIA data to reconstruct avian diets (Johnson et al. 2019), and dietary predictions can be improved through the inclusion of data from morphological or laboratory-based methods (Polito et al. 2011, Chiaradia et al. 2014, Johnson et al. 2019).

The R-package *MixSIAR* provides a Bayesian mixing model framework that can include fixed and random effects as covariates explaining variability in mixture proportions, incorporate prior data sources, and calculate relative support for multiple models via information criteria (Stock et al. 2018). Another R package applying a similar Bayesian framework, *tRophicPosition*, calculates consumer trophic positions using stable isotopes, with one or two isotopic baselines, while explicitly including individual variability and propagating sampling error in the resulting posterior estimates (Quezada-Romegialli et al. 2018). In addition,

the *SIBER* (Jackson et al. 2011) and *nicheROVER* (Swanson et al. 2015) packages allow for direct comparison of isotopic niche area (a proxy for trophic niches; Newsome et al. 2007) and overlap (Flaherty and Ben-David 2010) across consumers and/or communities (Figure 5). While sophisticated analyses continue to be published, these models are only as good as the data and study design employed, and decisions about model parameterization and source grouping can influence results (Bond and Diamond 2011). Phillips et al. (2014) provide a summary of the best practices for stable isotope mixing models in food-web studies that are broadly applicable to avian research.

Future Potential

As stable isotope analysis has been used in avian diet reconstruction for nearly 40 years (Schoeninger and DeNiro 1984), many of its limitations and future directions have been identified—or even addressed (Post 2002, Boecklen et al. 2011, Wiley et al. 2017). However, one promising new development in the field lies in CSIA or the isotopic analysis of biological macromolecule groups, such as amino acids or fatty acids. Because specific compounds are metabolized through unique pathways, CSIA is an improvement on bulk isotopic analysis as it can quantify and account for variation in isotopic baselines over time and space, and the differential routing of dietary macromolecules throughout consumer tissues (Whiteman et al. 2019). For $\delta^{15}N$, some individual amino acids (e.g., glutamic acid) undergo large isotopic fractionation during transamination/deamination providing greater sensitivity when estimating trophic position (McMahon et al. 2015, Ohkouchi et al. 2017). In contrast, other amino acids (e.g., phenylalanine) show little to no trophic fractionation between diet and consumer allowing researchers to quantify isotopic baselines (McMahon et al. 2015, Ohkouchi et al. 2017). The analysis of individual "trophic" and "source" amino acids can thus be used to infer trophic position of avian consumers even in situations where baseline food web isotopic values are not known. For example, McMahon et al. (2019) used feather glutamic acid and phenylalanine $\delta^{15}N$ values to calculate a nearly 100-year record of *Pygoscelis* spp. penguin trophic positions that explicitly accounted for variation in food web isotopic baselines over time, while Whiteman et al (2020) quantified $\delta^{13}C$ and $\delta^{15}N$ values of various amino acids to investigate nutrient allocation by birds to their eggs within the context of the capital vs. income continuum.

Animals must acquire essential amino acids from their diet, and as these amino acids undergo little to no additional isotopic change from diet to consumer (Hayes 2001, McMahon et al. 2015), $\delta^{13}C$ stable isotope analysis of amino acids (CSIA-AA) can better trace energy pathways from basal sources to upper-level consumers. For example, Johnson et al. (2019) found that while bulk stable isotope analysis and CSIA-AA of Seaside Sparrow (*Ammospiza maritima*) liver tissues predicted similar contributions of terrestrial and aquatic-derived carbon, CSIA-AA did so with greater precision. CSIA of fatty acids (CSIA-FA) have also provided a glimpse into the importance of fatty acid composition in the energy metabolism of migrating birds (Carter et al. 2019b), and novel applications of $\delta^{13}C$ CSIA-FA promise to broaden our understanding of avian food webs and address the limitations of previous applications (Twining et al. 2020).

ALTERNATIVE DIETARY BIOMOLECULE TRACING

While DNA-based and stable isotope techniques are applicable to most study systems, researchers also trace other biomolecules through food webs to address more specialized questions in avian dietary ecology. Useful dietary tracers include essential biomolecules that are not synthesized by birds (e.g., essential lipids, amino acids, vitamins; Ruess and Müller-Navarra 2019), biomolecules that undergo little or no metabolic change post-consumption (e.g., long-chain polyunsaturated fatty acids; Twining et al. 2016), and non-nutritional components indicative of environmental contamination (e.g., lead, mercury). Because alternative dietary tracers are often specific to certain environments, studies typically couple one of the previously described techniques with these tracers to draw ecological inferences about the effect of diet variation; though, continued development of mixture modeling approaches (e.g., quantitative fatty acid analysis [QFASA]; Iverson et al. 2004) and the identification of additional dietary tracers in new habitats (Hixson et al. 2015) will allow for broader application of biomolecule tracing in diet reconstruction. Analytical methods for individual dietary tracers are beyond the scope of this review, but have been discussed by others (Williams and Buck 2010, Nielsen et al. 2017, Majdi et al. 2018). Here, we focus on analyses employing multiple techniques to address objectives beyond diet identification.

Nutritional Components: A Healthy Diet

In addition to meeting energy demands and broad macronutrient requirements, birds must obtain essential biomolecules from diet to maintain optimal health and productivity (Klasing 1998). Essential polyunsaturated fatty acids have been useful as tracers because vertebrates tend to have a limited ability to convert these biomolecules, and controlled diet studies suggest that consumer fatty acid signatures resemble the fatty acid signatures of their food (Twining et al. 2016). Historically, most research in avian nutrition has focused on domesticated species, but there has been recent momentum in studying the nutritional response of wild populations to changes in food availability resulting from anthropogenic influences and

climate change (Birnie-Gauvin et al. 2017). Because diet items are not all nutritionally equivalent, the impacts of changes in food quality to avian health and fitness should be considered alongside prey identification in shifting diets through a combination of techniques. For example, morphological diet identification followed by fatty acid analysis has shown that diets containing optimal prey items correlate with greater concentrations of essential polyunsaturated fatty acids as well as metrics of survival and reproductive success in grassland (Zhang et al. 2020) and riparian songbirds (Twining et al. 2018). Combining bulk stable isotope analysis and fatty acid analysis enabled Hebert et al. (2014) to trace prey-specific fatty acids to aquatic birds foraging in benthic and pelagic locations, thus explaining how shifts in bird diet were linked to disease emergence. Similarly, combining fatty acid analysis and CSIA-FA showed that riparian songbirds derive essential long-chain polyunsaturated fatty acids from aquatic prey, even if terrestrial prey make up a greater portion of their diet (Twining et al. 2019). Furthermore, integrating morphological, stable isotope and fatty acid techniques has the potential to produce a more cohesive picture of avian feeding habits across short- and long-term scales, which has been influential in identifying patterns of foraging plasticity (Moseley et al. 2012) and niche partitioning (Connan et al. 2014). While future research will likely focus on the composition of fatty acids and amino acids, other diet-derived molecules, such as carotenoids (Witmer 1996), may also enable the examination of diet as well as the resulting consequences for avian populations.

Non-Nutritional Components: A Contaminated Diet

In addition to nutritional components, non-nutritional chemicals and debris are also consumed directly or indirectly via contaminated prey. Anthropogenically-induced environmental contamination is a major cause of avian mortality, and also generates sublethal effects that can be tied to declining populations. For example, lead and mercury exposure can both cause immune suppression and reduce reproductive output (Whitney and Cristol 2018, Williams et al. 2018, Vallverdú-Coll et al. 2019), while brominated flame retardant exposure impacts avian courtship behavior, growth, and development (Guigueno and Fernie 2017). Environmental contaminants often biomagnify at higher trophic levels, therefore, combining dietary and contaminant analyses can lead to greater insights regarding exposure risk for birds among different habitats and feeding guilds. For instance, Barn Owls (*Tyto alba*) are most heavily exposed to anticoagulant rodenticides during the fall, as estimated by diet and chemical residues in pellets (*Apodemus* spp.; Geduhn et al. 2016). Regurgitates and pellets as well as feces have also been analyzed to detect the presence of plastics ingested by wetland birds (Gil-Delgado et al. 2017, Reynolds and Ryan 2018), gulls (Lindborg et al. 2012, Furtado et al. 2016), and seabirds (Acampora et al. 2017). Although no sampling method for detecting ingested plastics is perfect (Provencher et al. 2019), tracking consumption of contaminated diet items or debris by applying morphological identification methods can support the use of avian populations as biomonitors of an increasingly polluted environment.

Future Potential

Bulk stable isotope methods have also been incorporated into studies of contaminant exposure where the effects of trophic position ($\delta^{15}N$) and dietary source ($\delta^{13}C$ and $\delta^{34}S$) influence levels of exposure. For example, positive correlations between mercury concentrations and $\delta^{15}N$ values show biomagnification of lead, mercury, and arsenic, resulting in higher contaminant loads for aquatic and terrestrial birds feeding at higher trophic levels (Cui et al. 2011, Carravieri et al. 2013, Badry et al. 2019, Tasneem et al. 2020, Costantini et al. 2020). Correlations between mercury concentrations and $\delta^{34}S$ have revealed a greater exposure risk for gulls with a marine-sourced diet (Ramos et al. 2013), and the correlation between flame retardants and $\delta^{13}C$ explain the role of a terrestrially-sourced diet on Peregrine Falcon (*Falco peregrinus*) contaminant exposure in urban environments (Fernie et al. 2017). Stable isotope reconstruction of diet over long time periods has also been useful in explaining Chimney Swift (*Chaetura pelagica*) diet shifts with respect to the historical use of DDT (Nocera et al. 2012) and in creating an accurate mercury exposure trend for Herring Gulls (*Larus argentatus*) by incorporating diet shifts (Burgess et al. 2013). These studies highlight the utility of combining diet and contaminant analyses to the source, timing, and risk of exposure to avian populations.

COMBINING DIETARY ANALYTICAL TECHNIQUES

While the vast majority of avian dietary studies use only a single method for dietary characterization, the use of multiple techniques within a single study, either independently or in concert, will mitigate some of the drawbacks of each technique and yield a more accurate understanding of the study system overall. There are four basic approaches to combining the dietary analytical techniques we have described. All have advantages and disadvantages, and all depend on assumptions related to biases inherent in any given application. First, researchers may present the results of various techniques separately and consider in depth what each suggests about diet (Sydeman et al. 1997, Lavoie et al. 2012, Alonso et al. 2014, Génier et al. 2021, Bumelis et al. 2021). For example, researchers could apply DNA-based methodologies to identify each prey taxon to the species level, morphological techniques to understand which prey life stages and sizes are often targeted, and

stable isotope analysis to quantify the assimilated nutrients that birds acquire from each prey group or life stage over a certain time period, thus gaining important information on many facets of a bird's dietary niche. Such an approach would effectively mitigate the drawbacks associated with each technique, and in many ways, would be entirely complementary as each method represents different degrees of dietary resolution and periods of assimilation. The net result of such analyses will be to provide a *weight of evidence* approach that will require a forensic reconstruction of diet similar to approaches advocated for a court of law (e.g., Ehleringer et al. 2020). This approach is appealing because all dietary evidence is presented for the reader to interpret on its own merits.

The second approach is to convert all dietary information to relative probabilities of input to a given individual or population-level diet. Once converted to probabilities, they can then be formally combined as informative priors in Bayesian mixing models (Parnell et al. 2013). For example, mixing models based on bimodal isotopic data (e.g., $\delta^{13}C$ and $\delta^{15}N$) for avian tissues and diet can be combined with morphological (Robinson et al. 2018, Johnson et al. 2020) or DNA-based data (Franco-Trecu et al. 2013, Chiaradia et al. 2014) as informative priors. In general, the formal incorporation of informative priors will improve the precision of dietary mixing models. For example, if two prey species overlap isotopically, the use of informative priors based on non-isotopic data may better resolve these inputs in the final posterior probability distributions of prey inputs. However, it is also clear that informative priors can result in misleading inferences in dietary reconstructions (Franco-Trecu et al. 2013) and considerable attention must be paid to potential biases associated with prior information. The effect of an informative prior will depend heavily on sample size and will be especially powerful with small sample sizes. As with most aspects of mixing model applications, true evaluation of the use of priors based on controlled feeding experiments (e.g., Chiaradia et al. 2014) is rare. Currently, researchers are encouraged to present results of Bayesian mixing models with and without the use of informative priors.

A third approach is to incorporate various biomarkers directly into a multidimensional Bayesian mixing model framework (i.e. without necessarily employing informative priors). Because different biomarkers have different units of measurement, they must first be transformed to the same unitless scale by subtracting the mean and dividing by the standard deviation. The mixing model is then run in the normal fashion to discern relative dietary inputs. The approach of using stable isotope measurements and fatty acid analyses has been relatively common in marine systems (Neubauer and Jensen 2015), though O'Donovan et al. (2018) used this approach to investigate diets of wolves in northern Canada using two stable isotopes ($\delta^{13}C$ and $\delta^{15}N$) and three fatty acids of wolf and prey tissue in a five-dimensional model. While the authors found the combined approach was more powerful than using stable isotopes alone, they cautioned that adding more variables (i.e. more fatty acids) will not necessarily improve resolution.

Related to the third approach, a fourth approach combines various analytical approaches into a multidimensional dietary niche space (Swanson et al. 2015). Though studies frequently derive values from the same type of assay (e.g., stable isotope analysis), axes can theoretically include other metrics such as trace element concentrations or fatty acid concentrations. As indicated above, incorporating different metrics requires that the various axes be expressed in quantities that are unitless (typically expressed as mean values divided by the standard deviation). Analytically, this approach has many advantages, though the main drawback is that it can become difficult to interpret multidimensional niche volumes and again, multidimensional niche overlap does not necessarily mean true dietary overlap. Nonetheless, if the objective is to examine the evidence for differences in diet among individuals or populations, the derivation of such multidimensional niche hypervolumes is appealing.

Future dietary studies will continue to embrace ever more sophisticated forensic tools to evaluate avian nutritional ecology and these approaches will benefit from vast improvements in web-based analytical packages. Nonetheless, there are key knowledge gaps that should be urgently addressed. First, the bulk of avian studies have been focused on describing, and often re-describing, the diets of relatively few species, thus leaving gaps in our basic understanding of dietary composition for many avian taxa, particularly Neotropical species (Lees et al. 2020). While studies of most bird species will benefit from using any of the aforementioned methods, DNA-based techniques seem particularly well-suited for providing a general understanding of diet for understudied species and may help build the foundation necessary for further hypothesis-driven research. Similarly, most dietary studies have been biased toward the breeding season, and while the importance of seasonal interactions on bird populations has been known for some time (Marra et al. 1998), there has been little change in the frequency of multi-seasonal or year-round avian studies (Marra et al. 2015). While evaluating diet throughout the annual cycle may appear daunting, stable isotope techniques allow assays of different time periods based on a single capture event (Gómez et al. 2018, Cherel et al. 2014a), with sampling of migratory birds at banding stations providing such tissue samples readily (Smith et al. 2003). Finally, the combination of multiple techniques together with the recent advances in temporal and spatial analyses, such as Motus (Taylor et al. 2017) or GPS tags (Gyimesi et al. 2016), will provide additional information on foraging areas of birds, which may ultimately

lead to novel concepts, such as "nutritional landscapes or seascapes", that describe avian diets and aid in conservation efforts (Genier et al. 2021, Bumelis et al. 2021). We are, thus, in an exciting era whereby the optimization and integration of techniques and their applications for revisiting previous studies and answering novel ornithological questions will likely lead to a stronger understanding of avian trophic ecology and a greater appreciation for the roles that birds serve in changing ecosystems around the world.

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LITERATURE CITED

Åberg, G. (1995). The use of natural strontium isotopes as tracers in environmental studies. Water, Air, and Soil Pollution 79:309–322.

Abrahamczyk, S., and M. Kessler (2015). Morphological and behavioural adaptations to feed on nectar: How feeding ecology determines the diversity and composition of hummingbird assemblages. Journal of Ornithology 156:333–347.

Acampora, H., S. Newton, and I. O'Connor (2017). Opportunistic sampling to quantify plastics in the diet of unfledged Black Legged Kittiwakes (*Rissa tridactyla*), Northern Fulmars (*Fulmarus glacialis*) and Great Cormorants (*Phalacrocorax carbo*). Marine Pollution Bulletin 119:171–174.

Albano, N., J. A. Masero, J. M. Sánchez-Guzmán, A. Villegas, and F. Santiago-Quesada (2011). Effects of diet on growth-related patterns of energy and macronutrient assimilation efficiency in a semi-precocial bird, the Gull-billed Tern *Gelochelidon nilotica*. Ardea 99:93–101.

Alberdi, A., O. Aizpurua, K. Bohmann, S. Gopalakrishnan, C. Lynggaard, M. Nielsen, and M. T. P. Gilbert (2019). Promises and pitfalls of using high-throughput sequencing for diet analysis. Molecular Ecology Resources 19:327–348.

Alberdi, A., O. Aizpurua, M. T. P. Gilbert, and K. Bohmann (2018). Scrutinizing key steps for reliable metabarcoding of environmental samples. Methods in Ecology and Evolution 9:134–147.

Alonso, H., J. P. Granadeiro, S. Waap, J. Xavier, W. O. C. Symondson, J. A. Ramos, and P. Catry (2014). An holistic ecological analysis of the diet of Cory's shearwaters using prey morphological characters and DNA barcoding. Molecular Ecology 23:3719–3733.

Al-Soud, W. A., and P. Rådström (2000). Effects of amplification facilitators on diagnostic PCR in the presence of blood, feces, and meat. Journal of Clinical Microbiology 38:4463–4470.

Ambrose, S. H., and L. Norr (1993). Experimental evidence for the relationship of the carbon isotope ratios of whole diet and dietary protein to those of bone collagen and carbonate. In Prehistoric Human Bone: Archaeology at the Molecular Level (J. B. Lambert and G. Grupe, Editors). Springer, New York, NY, USA. pp. 1–37.

Anderson, O., R. Phillips, R. Shore, R. McGill, R. McDonald, and S. Bearhop (2009). Diet, individual specialisation and breeding of Brown Skuas (*Catharacta antarctica lonnbergi*): An investigation using stable isotopes. Polar Biology 32:27–33.

Ando, H., H. Mukai, T. Komura, T. Dewi, M. Ando, and Y. Isagi (2020). Methodological trends and perspectives of animal dietary studies by noninvasive fecal DNA metabarcoding. Environmental DNA 2:391–406.

Arneson, L. S., and S. E. MacAvoy (2005). Carbon, nitrogen, and sulfur diet–tissue discrimination in mouse tissues. Canadian Journal of Zoology 83:989–995.

Badry, A., L. Palma, P. Beja, T. M. Ciesielski, A. Dias, S. Lierhagen, B. M. Jenssen, N. Sturaro, I. Eulaers, and V. L. B. Jaspers (2019). Using an apex predator for large-scale monitoring of trace element contamination: Associations with environmental, anthropogenic and dietary proxies. Science of The Total Environment 676:746–755.

Barbaro, L., and A. Battisti (2011). Birds as predators of the pine processionary moth (Lepidoptera: Notodontidae). Biological Control 56:107–114.

Barnagaud, J., W. Daniel Kissling, B. Sandel, W. L. Eiserhardt, Ç. H. Şekercioğlu, B. J. Enquist, C. Tsirogiannis, and J. Svenning (2014). Ecological traits influence the phylogenetic structure of bird species co-occurrences worldwide. Ecology Letters 17:811–820.

Barrett, R. T., K. Camphuysen, T. Anker-Nilssen, J. W. Chardine, R. W. Furness, S. Garthe, O. Hüppop, M. F. Leopold, W. A. Montevecchi, and R. R. Veit (2007). Diet studies of seabirds: a review and recommendations. ICES Journal of Marine Science 64:1675–1691.

Barton, N. W., and D. C. Houston (1993). A comparison of digestive efficiency in birds of prey. Ibis 135:363–371.

Beal, F. E. L. (1915). Food of the Robins and Bluebirds of the United States. U.S. Department of Agriculture, Washington, D.C., USA.

Bearhop, S., R. Furness, G. Hilton, S. Votier, and S. Waldron (2003). A forensic approach to understanding diet and habitat use from stable isotope analysis of (avian) claw material. Functional Ecology 17:270–275.

Benamane, A. H., S. Bissati-Bouafia, K. Amrani, J. Pansu, F. Pompanon, S. Doumandji, and M. Sekour (2019). Diet of Barn Own (*Tyto alba*) determination from regurgitated pellets in southeastern Algeria, coupling the classical approach with the eDNA analysis. International Journal 75. http://dx.doi.org/10.21506/j.ponte.2019.2.5

Benson, D. A., M. Cavanaugh, K. Clark, I. Karsch-Mizrachi, D. J. Lipman, J. Ostell, and E. W. Sayers (2013). GenBank. Nucleic Acids Research 41:D36–D42.

Bent, A. C. (1925). Life histories of North American birds. U.S. Government Printing Office 107, Washington, D.C., USA.

Birnie-Gauvin, K., K. S. Peiman, D. Raubenheimer, and S. J. Cooke (2017). Nutritional physiology and ecology of wildlife in a changing world. Conservation Physiology 5:cox030.

Blight, L. K., K. A. Hobson, T. K. Kyser, and P. Arcese (2015). Changing gull diet in a changing world: A 150-year stable isotope ($\delta^{13}C$, $\delta^{15}N$) record from feathers collected in the Pacific Northwest of North America. Global Change Biology 21:1497–1507.

Blonder, B., C. Lamanna, C. Violle, and B. J. Enquist (2014). The *n*-dimensional hypervolume. Global Ecology and Biogeography 23:595–609.

Blum, J. D., E. H. Taliaferro, and R. T. Holmes (2001). Determining the sources of calcium for migratory songbirds using stable strontium isotopes. Oecologia 126:569–574.

Boecklen, W. J., C. T. Yarnes, B. A. Cook, and A. C. James (2011). On the use of stable isotopes in trophic ecology. Annual Review of Ecology, Evolution, and Systematics 42:411–440.

Bolyen, E., J. R. Rideout, M. R. Dillon, N. A. Bokulich, C. C. Abnet, G. A. Al-Ghalith, H. Alexander, E. J. Alm, M. Arumugam, and F. Asnicar (2019). Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. Nature Biotechnology 37:852–857.

Bond, A. L., and A. W. Diamond (2011). Recent Bayesian stable-isotope mixing models are highly sensitive to variation in discrimination factors. Ecological Applications 21:1017–1023.

Bond, A. L., and I. L. Jones (2009). A practical introduction to stable-isotope analysis for seabird biologists: Approaches, cautions and caveats. Marine Ornithology 37:183–188.

Bond, A. L., G. T. McClelland, I. L. Jones, J. L. Lavers, and T. K. Kyser (2010). Stable isotopes confirm community patterns in foraging among Hawaiian Procellariiformes. Waterbirds 33:50–58.

Bowen, G. J., and J. B. West (2019). Isoscapes for terrestrial migration research. In Tracking Animal Migration with Stable Isotopes (K. A. Hobson and L. I. Wassenaar, Editors). Academic Press, New York, NY, USA. pp. 53–84.

Boyle, R. A., N. J. Dorn, and M. I. Cook (2014). Importance of crayfish prey to nesting White Ibis (*Eudocimus albus*). Waterbirds 37:19–29.

Brannock, P. M., and K. M. Halanych (2015). Meiofaunal community analysis by high-throughput sequencing: Comparison of extraction, quality filtering, and clustering methods. Marine Genomics 23:67–75.

Brensing, D. (1977). Nahrungsökologische Untersuchungen an Zugvögeln in einem südwestdeutschen Durchzugsgebiet während des Wegzuges. Vogelwarte 29:44–56.

Bugoni, L., R. A. McGill, and R. W. Furness (2008). Effects of preservation methods on stable isotope signatures in bird tissues. Rapid Communications in Mass Spectrometry: An International Journal Devoted to the Rapid Dissemination of Up-to-the-Minute Research in Mass Spectrometry 22:2457–2462.

Bumelis, K. H., M. Cadman, and K. A. Hobson (2021). Endogenous biomarkers reveal diet partitioning among three sympatric species of swallows in southern Ontario. Ornithology 139:ukab000.

Burgess, N. M., A. L. Bond, C. E. Hebert, E. Neugebauer, and L. Champoux (2013). Mercury trends in Herring Gull (*Larus argentatus*) eggs from Atlantic Canada, 1972–2008: Temporal change or dietary shift? Environmental Pollution 172:216–222.

Burin, G., W. D. Kissling, P. R. Guimarães, Ç. H. Şekercioğlu, and T. B. Quental (2016). Omnivory in birds is a macroevolutionary sink. Nature Communications 7:1–10.

Calver, M., and R. Wooller (1982). A technique for assessing the taxa, length, dry weight and energy content of the arthropod prey of birds. Wildlife Research 9:293–301.

Carleton, S., and C. Martínez Del Rio (2005). The effect of cold-induced increased metabolic rate on the rate of ^{13}C and ^{15}N incorporation in House Sparrows (*Passer domesticus*). Oecologia 144:226–232.

Carlisle, J. D., and R. L. Holberton (2006). Relative efficiency of fecal versus regurgitated samples for assessing diet and the deleterious effects of a tartar emetic on migratory birds. Journal of Field Ornithology 77:126–135.

Carravieri, A., P. Bustamante, C. Churlaud, and Y. Cherel (2013). Penguins as bioindicators of mercury contamination in the Southern Ocean: Birds from the Kerguelen Islands as a case study. Science of The Total Environment 454–455:141–148.

Carter, W. A., U. Bauchinger, and S. R. McWilliams (2019a). The importance of isotopic turnover for understanding key aspects of animal ecology and nutrition. Diversity 11:84.

Carter, W. A., C. Cooper-Mullin, and S. R. McWilliams (2018). Turnover of muscle lipids and response to exercise differ between neutral and polar fractions in a model songbird, the zebra finch. Journal of Experimental Biology 221:jeb168823.

Carter, W. A., J. P. Whiteman, C. Cooper-Mullin, S. D. Newsome, and S. R. McWilliams (2019b). Dynamics of individual fatty acids in muscle fat stores and membranes of a songbird and its functional and ecological importance. Physiological and Biochemical Zoology 92:239–251.

Casement, N. (2001). Dietary niche separation of Parus major and Parus caeruleus? Evidence From Molecular Scatology.

Casement, N. (2001). Dietary Niche Separation of *Parus major* and *Parus caeruleus*? Evidence From Molecular Scatology. Doctoral dissertation, Thesis, Oxford University, UK.

Caut, S., E. Angulo, and F. Courchamp (2009). Variation in discrimination factors ($\Delta^{15}N$ and $\Delta^{13}C$): The effect of diet isotopic values and applications for diet reconstruction. Journal of Applied Ecology 46:443–453.

Chapman, A., and K. V. Rosenberg (1991). Diets of four sympatric Amazonian woodcreepers (Dendrocolaptidae). The Condor 93:904–915.

Cherel, Y., K. A. Hobson, F. Bailleul, and R. Groscolas (2005). Nutrition, physiology, and stable isotopes: new information from fasting and molting penguins. Ecology 86:2881–2888.

Cherel, Y., M. Connan, A. Jaeger, and P. Richard (2014a). Seabird year-round and historical feeding ecology: Blood and feather $\delta^{13}C$ and $\delta^{15}N$ values document foraging plasticity of small sympatric petrels. Marine Ecology Progress Series 505:267–280.

Cherel, Y., S. Jaquemet, A. Maglio, and A. Jaeger (2014b). Differences in $\delta^{13}C$ and $\delta^{15}N$ values between feathers and blood of seabird chicks: Implications for non-invasive isotopic investigations. Marine Biology 161:229–237.

Cherel, Y., and V. Ridoux (1992). Prey species and nutritive value of food fed during summer to King Penguin *Aptenodytes patagonica* chicks at Possession Island, Crozet Archipelago. Ibis 134:118–127.

Chiaradia, A., M. G. Forero, J. C. McInnes, and F. Ramírez (2014). Searching for the true diet of marine predators: Incorporating Bayesian priors into stable isotope mixing models. PLoS One 9:e92665.

Clare, E. L., B. K. Lim, M. D. Engstrom, J. L. Eger, and P. D. N. Hebert (2007). DNA barcoding of Neotropical bats: Species identification and discovery within Guyana. Molecular Ecology Notes 7:184–190

Clare, E. L. (2014). Molecular detection of trophic interactions: Emerging trends, distinct advantages, significant considerations and conservation applications. Evolutionary Applications 7:1144–1157.

Clarke, L. J., J. Soubrier, L. S. Weyrich, and A. Cooper (2014). Environmental metabarcodes for insects: In silicoPCR reveals potential for taxonomic bias. Molecular Ecology Resources 14:1160–1170.

Clarke, S. J., G. H. Miller, M. L. Fogel, A. R. Chivas, and C. V. Murray-Wallace (2006). The amino acid and stable isotope biogeochemistry of Elephant Bird (Aepyornis) eggshells from southern Madagascar. Quaternary Science Reviews 25:2343–2356.

Collis, K., D. D. Roby, D. P. Craig, S. Adamany, J. Y. Adkins, and D. E. Lyons (2002). Colony size and diet composition of piscivorous waterbirds on the lower Columbia River: Implications for losses of juvenile salmonids to avian predation. Transactions of the American Fisheries Society 131:537–550.

Connan, M., C. D. McQuaid, B. T. Bonnevie, M. J. Smale, and Y. Cherel (2014). Combined stomach content, lipid and stable isotope analyses reveal spatial and trophic partitioning among three sympatric albatrosses from the Southern Ocean. Marine Ecology Progress Series 497:259–272.

Corse, E., C. Tougard, G. Archambaud-Suard, J.-F. Agnèse, F. D. M. Mandeng, C. F. B. Bilong, D. Duneau, L. Zinger, R. Chappaz, C. C. Y. Xu, E. Meglécz, and V. Dubut (2019). One-locus-several-primers: A strategy to improve the taxonomic and haplotypic coverage in diet metabarcoding studies. Ecology and Evolution 9:4603–4620.

Costantini, D., P. Bustamante, M. Brault-Favrou, and G. Dell'Omo (2020). Patterns of mercury exposure and relationships with isotopes and markers of oxidative status in chicks of a Mediterranean seabird. Environmental Pollution 260:114095.

Crisol-Martínez, E., L. T. Moreno-Moyano, K. R. Wormington, P. H. Brown, and D. Stanley (2016). Using next-generation sequencing to contrast the diet and explore pest-reduction services of sympatric bird species in macadamia orchards in Australia. PLoS One 11:1–19.

Croxall, J. (1976). The composition and behaviour of some mixed-species bird flocks in Sarawak. Ibis 118:333–346.

Cui, B., Q. Zhang, K. Zhang, X. Liu, and H. Zhang (2011). Analyzing trophic transfer of heavy metals for food webs in the newly-formed wetlands of the Yellow River Delta, China. Environmental Pollution 159:1297–1306.

Currie, D., N. Nour, and F. Adriaensen (1996). A new technique for filming prey delivered to nestlings, making minimal alterations to the nest box. Bird Study 43:380–382.

Deagle, B. E., N. J. Gales, K. Evans, S. N. Jarman, S. Robinson, R. Trebilco, and M. A. Hindell (2007). Studying seabird diet through genetic analysis of faeces: A case study on Macaroni Penguins (*Eudyptes chrysolophus*). PLoS One 2:e831.

Deagle, B. E., A. Chiaradia, J. McInnes, and S. N. Jarman (2010). Pyrosequencing faecal DNA to determine diet of Little Penguins: Is what goes in what comes out? Conservation Genetics 11:2039–2048.

Deagle, B. E., A. C. Thomas, J. C. McInnes, L. J. Clarke, E. J. Vesterinen, E. L. Clare, T. R. Kartzinel, and J. P. Eveson (2019). Counting with DNA in metabarcoding studies: How should we convert sequence reads to dietary data? Molecular Ecology 28:391–406.

Deloria-Sheffield, C. M., K. F. Millenbah, C. I. Bocetti, P. W. Sykes Jr, and C. B. Kepler (2001). Kirtland's Warbler diet as determined through fecal analysis. The Wilson Journal of Ornithology 113:384–387.

DeNiro, M. J., and S. Epstein (1976). You are what you eat (plus a few): The carbon isotope cycle in food chains. Geological Society of America Abstract with Programs 8:834–835.

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

DeNiro, M. J., and S. Epstein (1978). Influence of diet on the distribution of carbon isotopes in animals. Geochimica et Cosmochimica Acta 42:495–506.

DeNiro, M. J., and S. Epstein (1981). Influence of diet on the distribution of nitrogen isotopes in animals. Geochimica et Cosmochimica Acta 45:341–351.

Desmond, M. J., C. Mendez-Gonzalez, and L. B. Abbott (2008). Winter diets and seed selection of granivorous birds in southwestern New Mexico. In Birds of the US-Mexico Borderlands: Distribution, Ecology, and Conservation (D. Krueper, J. Ruth, and T. Brush, Editors). Studies in Avian Biology 37:101–112.

Dirksen, S., T. J. Boudewijn, R. Noordhuis, and E. Marteijn (1995). Cormorants *Phalacrocorax carbo sinensis* in shallow eutrophic freshwater lakes: Prey choice and fish consumption in the non-breeding period and effects of large-scale fish removal. Ardea 83:167–184.

Doucett, R. R., J. C. Marks, D. W. Blinn, M. Caron, and B. A. Hungate (2007). Measuring terrestrial subsidies to aquatic food webs using stable isotopes of hydrogen. Ecology 88:1587–1592.

Duffy, D. C., and S. Jackson (1986). Diet studies of seabirds: A review of methods. Colonial Waterbirds 9:1–17.

Eaton, S. W. (1958). A life history study of the Louisiana Waterthrush. The Wilson Bulletin 70:211–236.

Ehleringer, J. R., S. C. Avalos, B. J. Tipple, L. O. Valenzuela, and T. E. Cerling (2020). Stable isotopes in hair reveal dietary protein sources with links to socioeconomic status and health. Proceedings of the National Academy of Sciences USA 117:20044–20051.

Eisenberg, E., and E. Y. Levanon (2013). Human housekeeping genes, revisited. Trends in Genetics 29:569–574.

Elliott, K. H., and J. E. Elliott (2016). Lipid extraction techniques for stable isotope analysis of bird eggs: Chloroform–methanol leads to more enriched ^{13}C values than extraction via petroleum ether. Journal of Experimental Marine Biology and Ecology 474:54–57.

Elton, C. (1927). Animal Ecology. Sidgwick and Jackson, London, UK.

English, P. A., D. J. Green, and J. J. Nocera (2018). Stable isotopes from museum specimens may provide evidence of long-term change in the trophic ecology of a migratory aerial insectivore. Frontiers in Ecology and Evolution 6:14.

Evans Ogden, L. J., K. A. Hobson, and D. B. Lank (2004). Blood isotopic (δ13C and δ15N) turnover and diet-tissue

fractionation factors in captive Dunlin (*Calidris alpina pacifica*). The Auk 121:170–177.

Fernie, K. J., D. Chabot, L. Champoux, S. Brimble, M. Alaee, S. Marteinson, D. Chen, V. Palace, D. M. Bird, and R. J. Letcher (2017). Spatiotemporal patterns and relationships among the diet, biochemistry, and exposure to flame retardants in an apex avian predator, the Peregrine Falcon. Environmental Research 158:43–53.

Ficetola, G. F., J. Pansu, A. Bonin, E. Coissac, C. Giguet-Covex, M. D. Barba, L. Gielly, C. M. Lopes, F. Boyer, F. Pompanon, G. Rayé, and P. Taberlet (2015). Replication levels, false presences and the estimation of the presence/absence from eDNA metabarcoding data. Molecular Ecology Resources 15:543–556.

Flaherty, E. A., and M. Ben-David (2010). Overlap and partitioning of the ecological and isotopic niches. Oikos 119:1409–1416.

Fleischer, A. L., R. Bowman, and G. E. Woolfenden (2003). Variation in foraging behavior, diet, and time of breeding of Florida scrub-jays in suburban and wildland habitats. The Condor 105:515–527.

Florin, S. T., L. A. Felicetti, and C. T. Robbins (2011). The biological basis for understanding and predicting dietary-induced variation in nitrogen and sulphur isotope ratio discrimination. Functional Ecology 25:519–526.

Foglia, T., A. Cartwright, R. Gyurik, and J. Philips (1994). Fatty acid turnover rates in the adipose tissues of the growing chicken (*Gallus domesticus*). Lipids 29:497–502.

Forgy, E. (1965). Cluster analysis of multivariate data: Efficiency vs interpretability of classifications. Biometrics 21:768–769.

Forsman, A. M., B. D. Hoenig, S. A. Gaspar, J. Fischer, J. Siegrist., and K. Fraser (2021). Evaluating the impacts of metabarcoding primer selection on DNA characterization of diet in an aerial insectivore, the Purple Martin. Ornithology 139:ukab000.

Franco-Trecu, V., M. Drago, F. G. Riet-Sapriza, A. Parnell, R. Frau, and P. Inchausti (2013). Bias in diet determination: Incorporating traditional methods in Bayesian mixing models. PLoS One 8:e80019.

Funk, D. J., and K. E. Omland (2003). Species-level paraphyly and polyphyly: Frequency, causes, and consequences, with insights from animal mitochondrial DNA. Annual Review of Ecology, Evolution, and Systematics 34:397–423.

Furtado, R., D. Menezes, C. J. Santos, and P. Catry (2016). White-faced Storm-Petrels *Pelagodroma marina* predated by gulls as biological monitors of plastic pollution in the pelagic subtropical Northeast Atlantic. Marine Pollution Bulletin 112:117–122.

Gaglio, D., T. R. Cook, M. Connan, P. G. Ryan, and R. B. Sherley (2017). Dietary studies in birds: Testing a non-invasive method using digital photography in seabirds. Methods in Ecology and Evolution 8:214–222.

Galimberti, A., S. Spinelli, A. Bruno, V. Mezzasalma, F. De Mattia, P. Cortis, and M. Labra (2016). Evaluating the efficacy of restoration plantings through DNA barcoding of frugivorous bird diets. Conservation Biology 30:763–773.

Galloway, A. W., and S. M. Budge (2020). The critical importance of experimentation in biomarker-based trophic ecology. Philosophical Transactions of the Royal Society B: Biological Sciences 375:10290638

Gannes, L. Z., C. M. Del Rio, and P. Koch (1998). Natural abundance variations in stable isotopes and their potential uses in animal physiological ecology. Comparative Biochemistry and Physiology Part A: Molecular & Integrative Physiology 119:725–737.

Geduhn, A., A. Esther, D. Schenke, D. Gabriel, and J. Jacob (2016). Prey composition modulates exposure risk to anticoagulant rodenticides in a sentinel predator, the Barn Owl. Science of the Total Environment 544:150–157.

Génier, C. S., C. G. Guglielmo, G. W. Mitchell, M. Falconer, and K. A. Hobson (2021). Nutritional consequences of breeding away from riparian habitats in Bank Swallows: New evidence from multiple endogenous markers. Conservation Physiology 9:coaa140.

Gerwing, T. G., J. H. Kim, D. J. Hamilton, M. A. Barbeau, and J. A. Addison (2016). Diet reconstruction using next-generation sequencing increases the known ecosystem usage by a shorebird. The Auk: Ornithological Advances 133:168–177.

Ghosh-Harihar, M., N. Gurung, H. Shukla, I. Sinha, A. Pandit, V. Prakash, R. E. Green, and U. Ramakrishnan (2020). Metabarcoding for parallel identification of species, sex and diet of obligate scavengers: An application to globally-threatened *Gyps* vultures. Conservation Genetics Resources 13:61–77.

Gil-Delgado, J. A., D. Guijarro, R. U. Gosálvez, G. M. López-Iborra, A. Ponz, and A. Velasco (2017). Presence of plastic particles in waterbirds faeces collected in Spanish lakes. Environmental Pollution 220:732–736.

Gómez, C., T. Larsen, B. Popp, K. A. Hobson, and C. D. Cadena (2018). Assessing seasonal changes in animal diets with stable-isotope analysis of amino acids: A migratory boreal songbird switches diet over its annual cycle. Oecologia 187:1–13.

González-Varo, J. P., J. M. Arroyo, and P. Jordano (2014). Who dispersed the seeds? The use of DNA barcoding in frugivory and seed dispersal studies. Methods in Ecology and Evolution 5:806–814.

Gorchov, D. L., F. Cornejo, C. F. Ascorra, and M. Jaramillo (1995). Dietary overlap between frugivorous birds and bats in the Peruvian Amazon. Oikos 74:235–250.

Grémillet, D., G. Kuntz, F. Delbart, M. Mellet, A. Kato, J.-P. Robin, P.-E. Chaillon, J.-P. Gendner, S.-H. Lorentsen, and Y. Le Maho (2004). Linking the foraging performance of a marine predator to local prey abundance. Functional Ecology 18:793–801.

Griffith, D. M., J. A. Veech, and C. J. Marsh (2016). Cooccur: Probabilistic species co-occurrence analysis in R. Journal of Statistical Software 69:1–17.

Guigueno, M. F., and K. J. Fernie (2017). Birds and flame retardants: A review of the toxic effects on birds of historical and novel flame retardants. Environmental Research 154:398–424.

Guillemette, M., R. C. Ydenberg, and J. H. Himmelman (1992). The role of energy intake rate in prey and habitat selection of Common Eiders *Somateria mollissima* in winter: A risk-sensitive interpretation. Journal of Animal Ecology 61:599–610.

Guinan, J. A., P. A. Gowaty, and E. K. Eltzroth (2020). Western Bluebird (*Sialia mexicana*), version 1.0. In Birds of the World (A. F. Poole, Editor). Cornell Lab of Ornithology, Ithaca, NY, USA. https://doi.org/10.2173/bow.wesblu.01

Gyimesi, A., T. J. Boudewijn, R.-J. Buijs, J. Z. Shamoun-Baranes, J. W. de Jong, R. C. Fijn, P. W. van Horssen, and M. J. Poot (2016). Lesser Black-backed Gulls *Larus fuscus* thriving on a non-marine diet. Bird Study 63:241–249.

Hajibabaei, M., D. H. Janzen, J. M. Burns, W. Hallwachs, and P. D. N. Hebert (2006). DNA barcodes distinguish species of tropical Lepidoptera. Proceedings of the National Academy of Sciences USA 103:968–971.

Han, S.-H., and H.-S. Oh (2018). Genetic identification for prey birds of the Endangered Peregrine Falcon (*Falco peregrinus*). Mitochondrial DNA Part A 29:175–180.

Harrison, J. G., W. John Calder, B. Shuman, and C. Alex Buerkle (2020). The quest for absolute abundance: The use of internal standards for DNA-based community ecology. Molecular Ecology Resources 21:30–43.

Hatch, K., B. Pinshow, and J. Speakman (2002). Carbon isotope ratios in exhaled CO_2 can be used to determine not just present, but also past diets in birds. Journal of Comparative Physiology B 172:263–268.

Hayes, J. (1982). Fractionation *et al*.: An introduction to isotopic measurements and terminology. Spectra 8:3–8.

Hayes, J. M. (2001). Fractionation of carbon and hydrogen isotopes in biosynthetic processes. Reviews in Mineralogy and Geochemistry 43:225–277.

Healy, K., T. Guillerme, S. B. Kelly, R. Inger, S. Bearhop, and A. L. Jackson (2018). SIDER: An R package for predicting trophic discrimination factors of consumers based on their ecology and phylogenetic relatedness. Ecography 41:1393–1400.

Hebert, C. E., J. Chao, D. Crump, T. B. Johnson, M. D. Rudy, E. Sverko, K. Williams, D. Zaruk, and M. T. Arts (2014). Ecological tracers track changes in bird diets and possible routes of exposure to Type E Botulism. Journal of Great Lakes Research 40:64–70.

Hebert, C. E., and L. I. Wassenaar (2001). Stable nitrogen isotopes in waterfowl feathers reflect agricultural land use in western Canada. Environmental Science & Technology 35:3482–3487.

Hebert, P. D. N., A. Cywinska, S. L. Ball, and J. R. deWaard (2003). Biological identifications through DNA barcodes. Proceedings of the Royal Society of London B: Biological Sciences 270:313–321.

Hedd, A., and W. A. Montevecchi (2006). Diet and trophic position of Leach's Storm-Petrel *Oceanodroma leucorhoa* during breeding and moult, inferred from stable isotope analysis of feathers. Marine Ecology Progress Series 322:291–301.

Hedges, R. E., J. G. Clement, C. D. L. Thomas, and T. C. O'Connell (2007). Collagen turnover in the adult femoral mid-shaft: Modeled from anthropogenic radiocarbon tracer measurements. American Journal of Physical Anthropology 133:808–816.

Herrera, C. M. (1983). Significance of ants in the diet of insectivorous birds in southern Spanish Mediterranean habitats. Ardeola 30:77–81.

Hixson, S. M., B. Sharma, M. J. Kainz, A. Wacker, and M. T. Arts (2015). Production, distribution, and abundance of long-chain omega-3 polyunsaturated fatty acids: A fundamental dichotomy between freshwater and terrestrial ecosystems. Environmental Reviews 23:414–424.

Herrera, L. G., K. A. Hobson, M. Rodríguez, and P. Hernandez (2003). Trophic partitioning in tropical rain forest birds: Insights from stable isotope analysis. Oecologia 136:439–444.

Hobson, K. A. (1987). Use of stable-carbon isotope analysis to estimate marine and terrestrial protein content in gull diets. Canadian Journal of Zoology 65:1210–1213.

Hobson, K. A. (1993). Trophic relationships among high Arctic seabirds: Insights from tissue-dependent stable-isotope models. Marine Ecology Progress Series 95:7–18.

Hobson, K. A., J. F. Piatt, and J. Pitocchelli (1994). Using stable isotopes to determine seabird trophic relationships. Journal of Animal Ecology:786–798.

Hobson, K. A. (2005). Stable isotopes and the determination of avian migratory connectivity and seasonal interactions. The Auk 122:1037–1048.

Hobson, K. A. (2011). Isotopic ornithology: A perspective. Journal of Ornithology 152:49–66.

Hobson, K. A., R. T. Alisauskas, and R. G. Clark (1993). Stable-nitrogen isotope enrichment in avian tissues due to fasting and nutritional stress: Implications for isotopic analyses of diet. The Condor 95:388–394.

Hobson, K. A., L. K. Blight, and P. Arcese (2015). Human-induced long-term shifts in gull diet from marine to terrestrial sources in North America's coastal Pacific: More evidence from more isotopes (δ^2H, δ^{34}S). Environmental Science & Technology 49:10834–10840.

Hobson, K. A., and A. L. Bond (2012). Extending an indicator: year-round information on seabird trophic ecology from multiple-tissue stable-isotope analyses. Marine Ecology Progress Series 461:233–243.

Hobson, K. A., and R. Clark (1993). Turnover of ^{13}C in cellular and plasma fractions of blood: Implications for nondestructive sampling in avian dietary studies. The Auk 110:638–641.

Hobson, K. A., and R. G. Clark (1992a). Assessing avian diets using stable isotopes I: Turnover of ^{13}C in tissues. The Condor 94:181–188.

Hobson, K. A., and R. W. Clark (1992b). Assessing avian diets using stable isotopes. II: Factors influencing diet-tissue fractionation. The Condor 94:189–197.

Hobson, K. A., and S. G. Sealy (1991). Marine protein contributions to the diet of Northern Saw-whet Owls on the Queen Charlotte Islands: A stable-isotope approach. The Auk 108:437–440.

Hobson, K. A., and L. I. Wassenaar (2019). Tracking Animal Migration with Stable Isotopes. Academic Press, London, UK.

Hobson, K. A., and H. E. Welch (1992). Determination of trophic relationships within a high Arctic marine food web using δ^{13}C and δ^{15}N analysis. Marine Ecology Progress Series 84:9–18.

Hobson, K. A., M. L. Gloutney, and H. L. Gibbs (1997). Preservation of blood and tissue samples for stable-carbon and stable-nitrogen isotope analysis. Canadian Journal of Zoology 75:1720–1723.

Hódar, J. (1997). The use of regresion equations for the estimation of prey length and biomass in diet studies of insectivore vertebrates. Miscel lània Zoològica 20:1–10.

Høye, T. T., J. Ärje, K. Bjerge, O. L. Hansen, A. Iosifidis, F. Leese, H. M. Mann, K. Meissner, C. Melvad, and J. Raitoharju (2021). Deep learning and computer vision will transform entomology. Proceedings of the National Academy of Sciences USA 118:e2002545117.

Hondula, K., M. Pace, J. Cole, and R. Batt (2014). Hydrogen isotope discrimination in aquatic primary producers: implications for aquatic food web studies. Aquatic Sciences 76:217–229.

Hyslop, E. (1980). Stomach contents analysis—A review of methods and their application. Journal of Fish Biology 17:411–429.

Inger, R., and S. Bearhop (2008). Applications of stable isotope analyses to avian ecology. Ibis 150:447–461.

Iverson, S. J., C. Field, W. D. Bowen, and W. Blanchard (2004). Quantitative fatty acid signature analysis: A new method of estimating predator diets. Ecological Monographs 74:211–235.

Jackson, A. L., R. Inger, A. C. Parnell, and S. Bearhop (2011). Comparing isotopic niche widths among and within communities: SIBER–Stable isotope Bayesian ellipses in R. Journal of Animal Ecology 80:595–602.

Jaksic, F. M. (2004). El Niño effects on avian ecology: Lessons learned from the southeastern Pacific. Ornitologia Neotropical 15:61–72.

Jarman, S. N., J. C. McInnes, C. Faux, A. M. Polanowski, J. Marthick, B. E. Deagle, C. Southwell, and L. Emmerson (2013). Adélie Penguin population diet monitoring by analysis of food DNA in scats. PLoS One 8:e82227.

Jarman, S. N., A. M. Polanowski, C. E. Faux, J. Robbins, R. De Paoli-Iseppi, M. Bravington, and B. E. Deagle (2015). Molecular biomarkers for chronological age in animal ecology. Molecular Ecology 24:4826–4847.

Jarrett, C., L. L. Powell, H. McDevitt, B. Helm, and A. J. Welch (2020). Bitter fruits of hard labour: Diet metabarcoding and telemetry reveal that urban songbirds travel further for lower-quality food. Oecologia 193:377–388.

Jaschinski, S., T. Hansen, and U. Sommer (2008). Effects of acidification in multiple stable isotope analyses. Limnology and Oceanography: Methods 6:12–15.

Jedlicka, J. A., A. M. Sharma, and R. P. P. Almeida (2013). Molecular tools reveal diets of insectivorous birds from predator fecal matter. Conservation Genetics Resources 5:879–885.

Jedlicka, J. A., A. T. E. Vo, and R. P. P. Almeida (2017). Molecular scatology and high-throughput sequencing reveal predominately herbivorous insects in the diets of adult and nestling Western Bluebirds (*Sialia mexicana*) in California vineyards. The Auk: Ornithological Advances 134:116–127.

Jesmer, B. R., M. J. Kauffman, M. A. Murphy, and J. R. Goheen (2020). A test of the niche variation hypothesis in a ruminant herbivore. Journal of Animal Ecology 89:2825–2839.

Jo, H., M. Ventura, N. Vidal, J. S. Gim, T. Buchaca, L. A. Barmuta, E. Jeppesen, and G. J. Joo (2016). Discovering hidden biodiversity: The use of complementary monitoring of fish diet based on DNA barcoding in freshwater ecosystems. Ecology and Evolution 6:219–232.

Johnson, D. L., M. T. Henderson, D. L. Anderson, T. L. Booms, and C. T. Williams (2020). Bayesian stable isotope mixing models effectively characterize the diet of an Arctic raptor. Journal of Animal Ecology 89:2972–2985.

Johnson, J. J., J. A. Olin, and M. J. Polito (2019). A multi-biomarker approach supports the use of compound-specific stable isotope analysis of amino acids to quantify basal carbon source use in a salt marsh consumer. Rapid Communications in Mass Spectrometry 33:1781–1791.

Jusino, M. A., M. T. Banik, J. M. Palmer, A. K. Wray, L. Xiao, E. Pelton, J. R. Barber, A. Y. Kawahara, C. Gratton, M. Z. Peery, and D. L. Lindner (2019). An improved method for utilizing high-throughput amplicon sequencing to determine the diets of insectivorous animals. Molecular Ecology Resources 19:176–190.

Karasov, W. H. (1990). Digestion in birds: Chemical and physiological determinants and ecological implications. In Avian Foraging: Theory, Methodology, and Applications (M. L. Morrison, C. J. Ralph, J. Verner, and J. R. Jehl, Jr., Editors). Studies in Avian Biology 13:391–415.

Karp, D. S., S. Judson, G. C. Daily, and E. A. Hadly (2014). Molecular diagnosis of bird-mediated pest consumption in tropical farmland. Springerplus 3:630.

Karp, D. S., C. D. Mendenhall, R. F. Sandí, N. Chaumont, P. R. Ehrlich, E. A. Hadly, and G. C. Daily (2013). Forest bolsters bird abundance, pest control and coffee yield. Ecology Letters 16:1139–1347.

Katzenberg, M. A. (2008). Stable isotope analysis: A tool for studying past diet, demography, and life history. Biological Anthropology of the Human Skeleton 2:413–441.

Kelly, J. F. (2000). Stable isotopes of carbon and nitrogen in the study of avian and mammalian trophic ecology. Canadian Journal of Zoology 78:1–27.

Kent, C. M., and T. W. Sherry (2020). Behavioral niche partitioning reexamined: Do behavioral differences predict dietary differences in warblers? Ecology 101:e03077.

Kissling, W. D., C. H. Sekercioglu, and W. Jetz (2012). Bird dietary guild richness across latitudes, environments and biogeographic regions. Global Ecology and Biogeography 21:328–340.

Klasing, K. C. (1998). Comparative Avian Nutrition. CAB International, Wallingford, UK.

Kojadinovic, J., P. Richard, M. Le Corre, R. P. Cosson, and P. Bustamante (2008). Effects of lipid extraction on $\delta^{13}C$ and $\delta^{15}N$ values in seabird muscle, liver and feathers. Waterbirds 31:169–178.

Lalas, C., and H. McConnell (2012). Prey of Auckland Island shags (*Leucocarbo colensoi*) in winter. Notornis 59:130–137.

Lanzén, A., K. Lekang, I. Jonassen, E. M. Thompson, and C. Troedsson (2017). DNA extraction replicates improve diversity and compositional dissimilarity in metabarcoding of eukaryotes in marine sediments. PLoS One 12:e0179443.

Lavoie, R. A., J.-F. Rail, and D. R. Lean (2012). Diet composition of seabirds from Corossol Island, Canada, using direct dietary and stable isotope analyses. Waterbirds 35:402–419.

Layman, C. A., M. S. Araujo, R. Boucek, C. M. Hammerschlag-Peyer, E. Harrison, Z. R. Jud, P. Matich, A. E. Rosenblatt, J. J. Vaudo, and L. A. Yeager (2012). Applying stable isotopes to examine food-web structure: An overview of analytical tools. Biological Reviews 87:545–562.

Lee, H. Y., M. J. Park, N. Y. Kim, J. E. Sim, W. I. Yang, and K.-J. Shin (2010). Simple and highly effective DNA extraction methods from old skeletal remains using silica columns. Forensic Science International: Genetics 4:275–280.

Lees, A. C., K. V. Rosenberg, V. Ruiz-Gutierrez, S. Marsden, T. S. Schulenberg, and A. D. Rodewald (2020). A roadmap to identifying and filling shortfalls in Neotropical ornithology. The Auk: Ornithological Advances 137:ukaa048.

Lindborg, V. A., J. F. Ledbetter, J. M. Walat, and C. Moffett (2012). Plastic consumption and diet of Glaucous-winged Gulls (*Larus glaucescens*). Marine Pollution Bulletin 64:2351–2356.

Little, L. P., A. M. Strong, and N. G. Perlut (2009). Aggressive response of adult Bobolinks to neck ligatures on nestlings. The Wilson Journal of Ornithology 121:441–444.

Lorrain, A., B. Graham, F. Ménard, B. Popp, S. Bouillon, P. Van Breugel, and Y. Cherel (2009). Nitrogen and carbon isotope values of individual amino acids: A tool to study foraging ecology of penguins in the Southern Ocean. Marine Ecology Progress Series 391:293–306.

Lott, C. A., T. D. Meehan, and J. A. Heath (2003). Estimating the latitudinal origins of migratory birds using hydrogen and sulfur stable isotopes in feathers: Influence of marine prey base. Oecologia 134:505–510.

Maaten, L. van der, and G. Hinton (2008). Visualizing Data using t-SNE. Journal of Machine Learning Research 9:2579–2605.

Mackenzie, G., F. Schaffner, and P. K. Swart (2015). The stable isotopic composition of carbonate (C & O) and the organic matrix (C & N) in waterbird eggshells from South Florida: insights into feeding ecology, timing of egg formation, and geographic range. Hydrobiologia 743:89–108.

Macko, S. A., M. L. F. Estep, M. H. Engel, and P. Hare (1986). Kinetic fractionation of stable nitrogen isotopes during amino acid transamination. Geochimica et Cosmochimica Acta 50:2143–2146.

Majdi, N., N. Hette-Tronquart, E. Auclair, A. Bec, T. Chouvelon, B. Cognie, M. Danger, P. Decottignies, A. Dessier, C. Desvilettes, S. Dubois, et al. (2018). There's no harm in having too much: A comprehensive toolbox of methods in trophic ecology. Food Webs 17:e00100.

Mäntylä, E., T. Klemola, and T. Laaksonen (2011). Birds help plants: A meta-analysis of top-down trophic cascades caused by avian predators. Oecologia 165:143–151.

Margalida, A., J. Bertran, and J. Boudet (2005). Assessing the diet of nestling Bearded Vultures: A comparison between direct observation methods. Journal of Field Ornithology 76:40–45.

Marra, P. P., E. B. Cohen, S. R. Loss, J. E. Rutter, and C. M. Tonra (2015). A call for full annual cycle research in animal ecology. Biology letters 11:20150552.

Marra, P. P., K. A. Hobson, and R. T. Holmes (1998). Linking winter and summer events in a migratory bird by using stable-carbon isotopes. Science 282:1884–1886.

Marti, C. (1987). Raptor food habit studies. In Raptor Management Techniques Manual (B. A. G. Pendleton, Editor). Institute for Wildlife Research, National Wildlife Federation, National Wildlife Federation Scientific Technical Service, Reston, VA, USA. pp. 67–79.

Martínez del Rio, C., and B. O. Wolf (2005). Mass-balance models for animal isotopic ecology. In Physiological and Ecological Adaptations to Feeding in Vertebrates (J. Matthias Starck and T. Wang, Editors). Science Publishers, Enfield, NH, USA. pp. 141–174.

Martínez del Rio, C., N. Wolf, S. A. Carleton, and L. Z. Gannes (2009). Isotopic ecology ten years after a call for more laboratory experiments. Biological Reviews 84:91–111.

Mata, V. A., H. Rebelo, F. Amorim, G. F. McCracken, S. Jarman, and P. Beja (2019). How much is enough? Effects of technical and biological replication on metabarcoding dietary analysis. Molecular Ecology 28:165–175.

McAtee, W. L. (1912). Methods of estimating the contents of bird stomachs. The Auk 29:449–464.

McAtee, W. L. (1918). Food Habits of the Mallard Ducks of the United States. U.S. Department of Agriculture, U.S. Government Printing Office, Washington, D.C., USA.

McClenaghan, B., E. Nol, and K. C. R. Kerr (2019). DNA metabarcoding reveals the broad and flexible diet of a declining aerial insectivore. The Auk: Ornithological Applications 136:uky003.

McInnes, L., J. Healy, and J. Melville (2018). UMAP: Uniform manifold approximation and projection for dimension reduction. arXiv:1802.03426 [cs, stat].

McMahon, K., and N. Marples (2017). Reduced dietary conservatism in a wild bird in the presence of intraspecific competition. Journal of Avian Biology 48:448–454.

McMahon, K. W., C. I. Michelson, T. Hart, M. D. McCarthy, W. P. Patterson, and M. J. Polito (2019). Divergent trophic responses of sympatric penguin species to historic anthropogenic exploitation and recent climate change. Proceedings of the National Academy of Sciences USA 116:25721–25727.

McMahon, K. W., M. J. Polito, S. Abel, M. D. McCarthy, and S. R. Thorrold (2015). Carbon and nitrogen isotope fractionation of amino acids in an avian marine predator, the Gentoo Penguin (*Pygoscelis papua*). Ecology and Evolution 5:1278–1290.

Merritt, R. W., and K. W. Cummins (1996). An Introduction to the Aquatic Insects of North America. Kendall Hunt, Dubuque, IA, USA.

Mihuc, T., and D. Toetz (1994). Determination of diets of alpine aquatic insects using stable isotopes and gut analysis. American Midland Naturalist 131:146–155.

Moody, D. T. (1970). A method for obtaining food samples from insectivorous birds. The Auk 87:579–579.

Moseley, C., D. Grémillet, M. Connan, P. G. Ryan, R. H. E. Mullers, C. D. van der Lingen, T. W. Miller, J. C. Coetzee, R. J. M. Crawford, P. Sabarros, C. D. McQuaid, and L. Pichegru (2012). Foraging ecology and ecophysiology of Cape Gannets from colonies in contrasting feeding environments. Journal of Experimental Marine Biology and Ecology 422–423:29–38.

Murray, M. H., A. D. Kidd, S. E. Curry, J. Hepinstall-Cymerman, M. J. Yabsley, H. C. Adams, T. Ellison, C. N. Welch, and S. M. Hernandez (2018). From wetland specialist to hand-fed generalist: Shifts in diet and condition with provisioning for a recently urbanized wading bird. Philosophical Transactions of the Royal Society B: Biological Sciences 373:20170100.

Neubauer, P., and O. P. Jensen (2015). Bayesian estimation of predator diet composition from fatty acids and stable isotopes. PeerJ 3:e920.

Newsome, S. D., C. Martinez del Rio, S. Bearhop, and D. L. Phillips (2007). A niche for isotopic ecology. Frontiers in Ecology and the Environment 5:429–436.

Nielsen, J. M., E. L. Clare, B. Hayden, M. T. Brett, and P. Kratina (2017). Diet tracing in ecology: Method comparison and selection. Methods in Ecology and Evolution 9:278–291.

Nilsson, R. H., S. Anslan, M. Bahram, C. Wurzbacher, P. Baldrian, and L. Tedersoo (2019). Mycobiome diversity: High-throughput sequencing and identification of fungi. Nature Reviews Microbiology 17:95–109.

Nocera, J. J., J. M. Blais, D. V. Beresford, L. K. Finity, C. Grooms, L. E. Kimpe, K. Kyser, N. Michelutti, M. W. Reudink, and J. P. Smol (2012). Historical pesticide applications coincided with an altered diet of aerially foraging insectivorous chimney swifts. Proceedings of the Royal Society B: Biological Sciences 279:3114–3120.

O'Donnell, S., C. J. Logan, and N. S. Clayton (2012). Specializations of birds that attend army ant raids: An ecological approach to cognitive and behavioral studies. Behavioural Processes 91:267–274.

O'Donovan, S. A., S. M. Budge, K. A. Hobson, A. P. Kelly, and A. E. Derocher (2018). Intrapopulation variability in wolf diet revealed using a combined stable isotope and fatty acid approach. Ecosphere 9:e02420.

Oehm, J., A. Juen, K. Nagiller, S. Neuhauser, and M. Traugott (2011). Molecular scatology: How to improve prey DNA detection

success in avian faeces? Molecular Ecology Resources 11:620–628.
Ohkouchi, N., Y. Chikaraishi, H. G. Close, B. Fry, T. Larsen, D. J. Madigan, M. D. McCarthy, K. W. McMahon, T. Nagata, and Y. I. Naito (2017). Advances in the application of amino acid nitrogen isotopic analysis in ecological and biogeochemical studies. Organic Geochemistry 113:150–174.
Ontiveros, D., J. M. Pleguezuelos, and J. Caro (2005). Prey density, prey detectability and food habits: The case of Bonelli's Eagle and the conservation measures. Biological Conservation 123:19–25.
Oppel, S., R. N. Federer, D. M. O'Brien, A. N. Powell, and T. E. Hollmén (2010). Effects of lipid extraction on stable isotope ratios in avian egg yolk: Is arithmetic correction a reliable alternative? The Auk 127:72–78.
Ormerod, S., and S. J. Tyler (1991). Exploitation of prey by a river bird, the Dipper *Cinclus cinclus* (L.), along acidic and circumneutral streams in upland Wales. Freshwater Biology 25:105–116.
O'Rourke, D. R., N. A. Bokulich, M. A. Jusino, M. D. MacManes, and J. T. Foster (2020). A total crapshoot? Evaluating bioinformatic decisions in animal diet metabarcoding analyses. Ecology and Evolution 10:9721–9739.
Ostrom, P. H., A. E. Wiley, S. Rossman, C. A. Stricker, and H. F. James (2014). Unexpected hydrogen isotope variation in oceanic pelagic seabirds. Oecologia 175:1227–1235.
Owen, D. (1956). The food of nestling jays and magpies. Bird Study 3:257–265.
Palmer, J. M., M. A. Jusino, M. T. Banik, and D. L. Lindner (2018). Non-biological synthetic spike-in controls and the AMPtk software pipeline improve mycobiome data. PeerJ 6:e4925.
Parnell, A. C., D. L. Phillips, S. Bearhop, B. X. Semmens, E. J. Ward, J. W. Moore, A. L. Jackson, J. Grey, D. J. Kelly, and R. Inger (2013). Bayesian stable isotope mixing models. Environmetrics 24:387–399.
Parrish, J. D. (1997). Patterns of frugivory and energetic condition in Nearctic landbirds during autumn migration. The Condor 99:681–697.
Pearson, S. F., D. J. Levey, C. H. Greenberg, and C. M. Del Rio (2003). Effects of elemental composition on the incorporation of dietary nitrogen and carbon isotopic signatures in an omnivorous songbird. Oecologia 135:516–523.
Peterson, B. J., and B. Fry (1987). Stable isotopes in ecosystem studies. Annual Review of Ecology and Systematics 18:293–320.
Phillips, D. L. (2012). Converting isotope values to diet composition: The use of mixing models. Journal of Mammalogy 93:342–352.
Phillips, D. L., and J. W. Gregg (2003). Source partitioning using stable isotopes: Coping with too many sources. Oecologia 136:261–269.
Phillips, D. L., R. Inger, S. Bearhop, A. L. Jackson, J. W. Moore, A. C. Parnell, B. X. Semmens, and E. J. Ward (2014). Best practices for use of stable isotope mixing models in food-web studies. Canadian Journal of Zoology 92:823–835.
Phillips, D. L., and P. L. Koch (2002). Incorporating concentration dependence in stable isotope mixing models. Oecologia 130:114–125.
Phillips, D. L., S. D. Newsome, and J. W. Gregg (2005). Combining sources in stable isotope mixing models: Alternative methods. Oecologia 144:520–527.
Piñol, J., G. Mir, P. Gomez-Polo, and N. Agustí (2015). Universal and blocking primer mismatches limit the use of high-throughput DNA sequencing for the quantitative metabarcoding of arthropods. Molecular Ecology Resources 15:819–830.
Piñol, J., M. A. Senar, and W. O. Symondson (2019). The choice of universal primers and the characteristics of the species mixture determine when DNA metabarcoding can be quantitative. Molecular Ecology 28:407–419.
Podlesak, D. W., and S. R. McWilliams (2006). Metabolic routing of dietary nutrients in birds: Effects of diet quality and macronutrient composition revealed using stable isotopes. Physiological and Biochemical Zoology 79:534–549.
Podlesak, D. W., S. R. McWilliams, and K. A. Hatch (2005). Stable isotopes in breath, blood, feces and feathers can indicate intra-individual changes in the diet of migratory songbirds. Oecologia 142:501–510.
Polito, M. J., S. Fisher, C. R. Tobias, and S. D. Emslie (2009). Tissue-specific isotopic discrimination factors in Gentoo Penguin (*Pygoscelis papua*) egg components: Implications for dietary reconstruction using stable isotopes. Journal of Experimental Marine Biology and Ecology 372:106–112.
Polito, M. J., W. Z. Trivelpiece, N. J. Karnovsky, E. Ng, W. P. Patterson, and S. D. Emslie (2011). Integrating stomach content and stable isotope analyses to quantify the diets of pygoscelid penguins. PLoS One 6:e26642.
Pompanon, F., B. E. Deagle, W. O. Symondson, D. S. Brown, S. N. Jarman, and P. Taberlet (2012). Who is eating what: Diet assessment using next generation sequencing. Molecular Ecology 21:1931–1950.
Post, D. M. (2002). Using stable isotopes to estimate trophic position: Models, methods, and assumptions. Ecology 83:703–718.
Post, D. M., C. A. Layman, D. A. Arrington, G. Takimoto, J. Quattrochi, and C. G. Montana (2007). Getting to the fat of the matter: Models, methods and assumptions for dealing with lipids in stable isotope analyses. Oecologia 152:179–189.
Poulin, B., G. Lefebvre, and R. McNeil (1994). Effect and efficiency of tartar emetic in determining the diet of tropical land birds. The Condor 96:98–104.
Prokopowich, C. D., T. R. Gregory, and T. J. Crease (2003). The correlation between rDNA copy number and genome size in eukaryotes. Genome 46:48–50.
Provencher, J. F., S. B. Borrelle, A. L. Bond, J. L. Lavers, J. A. van Franeker, S. Kühn, S. Hammer, S. Avery-Gomm, and M. L. Mallory (2019). Recommended best practices for plastic and litter ingestion studies in marine birds: Collection, processing, and reporting. FACETS 4. https://doi.org/10.1139/facets-2018-0043
Prŷs-Jones, R., L. Schifferli, and D. Macdonald (1974). The use of an emetic in obtaining food samples from passerines. Ibis 116:90–94.
Quezada-Romegialli, C., A. L. Jackson, B. Hayden, K. K. Kahilainen, C. Lopes, and C. Harrod (2018). tRophicPosition, an R package for the Bayesian estimation of trophic position from consumer stable isotope ratios. Methods in Ecology and Evolution 9:1592–1599.
Quinney, T. E., and C. D. Ankney (1985). Prey size selection by tree swallows. The Auk 102:245–250.
Ralph, C. P., S. E. Nagata, and C. J. Ralph (1985). Analysis of droppings to describe diets of small birds. Journal of Field Ornithology165–174.

Ramos, R., F. Ramírez, and L. Jover (2013). Trophodynamics of inorganic pollutants in a wide-range feeder: The relevance of dietary inputs and biomagnification in the yellow-legged gull (Larus michahellis). Environmental Pollution 172:235–242.

Ratnasingham, S., and P. D. N. Hebert (2007). bold: The barcode of life data system (http://www.barcodinglife.org). Molecular Ecology Notes 7:355–364.

Remsen, J., and S. K. Robinson (1990). A classification scheme for foraging behavior of birds in terrestrial habitats. In Avian Foraging: Theory, Methodology, and Applications (M. L. Morrison, C. J. Ralph, J. Verner, and J. R. Jehl, Jr., Editors). Studies in Avian Biology 13:144–160.

Remsen, J. V., M. A. Hyde, and A. Chapman (1993). The diets of Neotropical trogons, motmots, barbets and toucans. The Condor 95:178–192.

Reynolds, C., and P. G. Ryan (2018). Micro-plastic ingestion by waterbirds from contaminated wetlands in South Africa. Marine Pollution Bulletin 126:330–333.

Richards, M. P., B. T. Fuller, M. Sponheimer, T. Robinson, and L. Ayliffe (2003). Sulphur isotopes in palaeodietary studies: A review and results from a controlled feeding experiment. International Journal of Osteoarchaeology 13:37–45.

Riedl, H. L., L. Stinson, L. Pejchar, and W. H. Clements (2018). An introduced plant affects aquatic-derived carbon in the diets of riparian birds. PLoS One 13:e0207389.

Robbins, C. T., L. A. Felicetti, and M. Sponheimer (2005). The effect of dietary protein quality on nitrogen isotope discrimination in mammals and birds. Oecologia 144:534–540.

Robinson, B. G., A. Franke, and A. E. Derocher (2018). Stable isotope mixing models fail to estimate the diet of an avian predator. The Auk: Ornithological Advances 135:60–70.

Robinson, S. K., and R. T. Holmes (1982). Foraging behavior of forest birds: The relationships among search tactics, diet, and habitat structure. Ecology 63:1918–1931.

Rosamond, K. M., C. M. Kent, S. C. Hunter, and T. W. Sherry (2020). Morphological traits influence prey selection by coexisting species of New World warblers (Parulidae). Journal of Field Ornithology 91:393–408.

Rosenberg, K. V., and R. J. Cooper (1990). Approaches to Avian Diet Analysis. In Avian Foraging: Theory, Methodology, and Applications (M. L. Morrison, C. J. Ralph, J. Verner, and J. R. Jehl, Jr., Editors). Studies in Avian Biology 13:80–90.

Rubenstein, D. R., and K. A. Hobson (2004). From birds to butterflies: Animal movement patterns and stable isotopes. Trends in Ecology & Evolution 19:256–263.

Ruess, L., and D. C. Müller-Navarra (2019). Essential biomolecules in food webs. Frontiers in Ecology and Evolution 7. https://doi.org/10.3389/fevo.2019.00269

Sarakinos, H. C., M. L. Johnson, and M. J. V. Zanden (2002). A synthesis of tissue-preservation effects on carbon and nitrogen stable isotope signatures. Canadian Journal of Zoology 80:381–387.

Schaffner, F. C., and P. K. Swart (1991). Influence of diet and environmental water on the carbon and oxygen isotopic signatures of seabird eggshell carbonate. Bulletin of Marine Science 48:23–38.

Schmidt, S. N., J. D. Olden, C. T. Solomon, and M. J. V. Zanden (2007). Quantitative approaches to the analysis of stable isotope food web data. Ecology 88:2793–2802.

Schoeller, D. A. (1999). Isotope fractionation: Why aren't we what we eat? Journal of Archaeological Science 26:667–673.

Schoeninger, M. J. (2010). Diet reconstruction and ecology using stable isotope ratios. In A Companion to Biological Anthropology (C. S. Larsen, Editor). Wiley-Blackwell, John Wiley & Sons Ltd, Chichester, West Sussex, UK. pp. 445–464.

Schoeninger, M. J., and M. J. DeNiro (1984). Nitrogen and carbon isotopic composition of bone collagen from marine and terrestrial animals. Geochimica et Cosmochimica Acta 48:625–639.

Schwarcz, H. P. (1991). Some theoretical aspects of isotope paleodiet studies. Journal of Archaeological Science 18:261–275.

Sellick, M. J., T. K. Kyser, M. B. Wunder, D. Chipley, and D. R. Norris (2009). Geographic variation of strontium and hydrogen isotopes in avian tissue: Implications for tracking migration and dispersal. PLoS One 4:e4735.

Sherry, T. W. (1984). Comparative dietary ecology of sympatric, insectivorous Neotropical flycatchers (Tyrannidae). Ecological Monographs 54:313–338.

Sherry, T. W., M. D. Johnson, K. A. Williams, J. D. Kaban, C. K. McAvoy, A. M. Hallauer, S. Rainey, and S. Xu (2016). Dietary opportunism, resource partitioning, and consumption of coffee berry borers by five species of migratory wood warblers (Parulidae) wintering in Jamaican shade coffee plantations. Journal of Field Ornithology 87:273–292.

Sherry, T. W., C. M. Kent, N. V. Sánchez, and Ç. H. Şekercioğlu (2020). Insectivorous birds in the Neotropics: Ecological radiations, specialization, and coexistence in species-rich communities. The Auk 137:ukaa049.

da Silva, L. P., V. A. Mata, P. B. Lopes, R. J. Lopes, and P. Beja (2020). High-resolution multi-marker DNA metabarcoding reveals sexual dietary differentiation in a bird with minor dimorphism. Ecology and Evolution 10:10364–10373.

da Silva, L. P., V. A. Mata, P. B. Lopes, P. Pereira, S. N. Jarman, R. J. Lopes, and P. Beja (2019). Advancing the integration of multi-marker metabarcoding data in dietary analysis of trophic generalists. Molecular Ecology Resources 19:1420–1432.

Slater, W. (1892). Change of diet in birds. Science 221–221.

Smith, R. B., T. D. Meehan, and B. O. Wolf (2003). Assessing migration patterns of Sharp-shinned Hawks *Accipiter striatus* using stable-isotope and band encounter analysis. Journal of Avian Biology 34:387–392.

Snider, A. M., A. A. Bonisoli Alquati, A. A. Perez-Umphrey, P. C. Stouffer, and S. S. Taylor (2021). Metabarcoding of stomach contents and fecal samples provide similar insights about Seaside Sparrow diet. Ornithological Applications 124:in press.

Snyder, N. F., and J. W. Wiley (1976). Sexual size dimorphism in hawks and owls of North America. Ornithological Monographs, No. 20, American Ornithologists' Union, Washington, D.C., USA.

Soto, D. X., K. A. Hobson, and L. I. Wassenaar (2013). The influence of metabolic effects on stable hydrogen isotopes in tissues of aquatic organisms. Isotopes in Environmental and Health Studies 49:305–311.

Southwell, E. (2018). Dietary Niche Partitioning in American Redstarts (*Setophaga ruticilla*) and Yellow Warblers (*Setophaga petechia*): A Dietary Analysis Based on PCR Metabarcoding, Master's Thesis, Durham University, Durham, UK.

Spence, A. R., E. E. Wilson Rankin, and M. W. Tingley (2021). DNA metabarcoding reveals broadly overlapping diets in three sympatric North American hummingbirds. Ornithology 139:ukab000.

Spiller, K. J., and R. Dettmers (2019). Evidence for multiple drivers of aerial insectivore declines in North America. The Condor 121:duz010.

Stenhouse, M., M. Baxter, R. Berger, and H. Suess (1979). Radiocarbon Dating. University of California Press, Berkeley, CA, USA.

Stephens, H., and C. Barnard (1981). Prey size selection by lapwings in lapwing/gull associations. Behaviour 77:1–22.

Sternberg, L., and M. J. DeNiro (1983). Isotopic composition of cellulose from C3, C4, and CAM plants growing near one another. Science 220:947–949.

Stock, B. C., A. L. Jackson, E. J. Ward, A. C. Parnell, D. L. Phillips, and B. X. Semmens (2018). Analyzing mixing systems using a new generation of Bayesian tracer mixing models. PeerJ 6:e5096.

Sullins, D. S., D. A. Haukos, J. M. Craine, J. M. Lautenbach, S. G. Robinson, J. D. Lautenbach, J. D. Kraft, R. T. Plumb, J. H. Reitz, B. K. Sandercock, and N. Fierer (2018). Identifying the diet of a declining prairie grouse using DNA metabarcoding. The Auk: Ornithological Advances 135:583–608.

Sutherland, R. M. (2000). Molecular Analysis of Avian Diets. Doctoral dissertation, Oxford University Press, Oxford, UK.

Swanson, H. K., M. Lysy, M. Power, A. D. Stasko, J. D. Johnson, and J. D. Reist (2015). A new probabilistic method for quantifying n-dimensional ecological niches and niche overlap. Ecology 96:318–324.

Sydeman, W. J., K. A. Hobson, P. Pyle, and E. B. McLaren (1997). Trophic relationships among seabirds in central California: Combined stable isotope and conventional dietary approach. The Condor 99:327–336.

Symondson, W. O. C. (2002). Molecular identification of prey in predator diets. Molecular Ecology 11:627–641.

Taberlet, P., A. Bonin, L. Zinger, and E. Coissac (2018). Environmental DNA: For Biodiversity Research and Monitoring. Oxford University Press, Oxford, UK.

Taberlet, P., E. Coissac, F. Pompanon, C. Brochmann, and E. Willerslev (2012). Towards next-generation biodiversity assessment using DNA metabarcoding. Molecular Ecology 21:2045–2050.

Tasneem, F., N. A. Abbasi, M. J. Iqbal Chaudhry, A. Mashiatullah, S. R. Ahmad, A. Qadir, and R. N. Malik (2020). Dietary proxies ($\delta^{15}N$, $\delta^{13}C$) as signature of metals and arsenic exposure in birds from aquatic and terrestrial food chains. Environmental Research 183:109191.

Taylor, P., T. Crewe, S. Mackenzie, D. Lepage, Y. Aubry, Z. Crysler, G. Finney, C. Francis, C. Guglielmo, and D. Hamilton (2017). The Motus Wildlife Tracking System: A collaborative research network to enhance the understanding of wildlife movement. Avian Conservation and Ecology 12:8.

Tercel, M. P., W. O. Symondson, and J. P. Cuff (2021). The problem of omnivory: A synthesis on omnivory and DNA metabarcoding. Molecular Ecology 30:2199–2206.

Thalinger, B., J. Oehm, A. Obwexer, and M. Traugott (2017). The influence of meal size on prey DNA detectability in piscivorous birds. Molecular Ecology Resources 17:e174–e186.

Thomas, A. C., S. N. Jarman, K. H. Haman, A. W. Trites, and B. E. Deagle (2014). Improving accuracy of DNA diet estimates using food tissue control materials and an evaluation of proxies for digestion bias. Molecular Ecology 23:3706–3718.

Thomas, S. M., and T. W. Crowther (2015). Predicting rates of isotopic turnover across the animal kingdom: A synthesis of existing data. Journal of Animal Ecology 84:861–870.

Thomas, A. C., B. E. Deagle, J. P. Eveson, C. H. Harsch, and A. W. Trites (2016). Quantitative DNA metabarcoding: Improved estimates of species proportional biomass using correction factors derived from control material. Molecular Ecology Resources 16:714–726.

Tieszen, L. L., and T. W. Boutton (1989). Stable carbon isotopes in terrestrial ecosystem research. In Stable Isotopes in Ecological Research (P. Rundel, J. R. Ehleringer, and K. A. Nagy, Editors). Springer-Verlag, New York, NY, USA. pp. 167–195.

Titulaer, M., A. Melgoza-Castillo, A. O. Panjabi, A. Sanchez-Flores, J. H. Martínez-Guerrero, A. Macías-Duarte, and J. A. Fernandez (2017). Molecular analysis of stomach contents reveals important grass seeds in the winter diet of Baird's and Grasshopper sparrows, two declining grassland bird species. PLoS One 12:e0189695.

Tiwari, M., A. K. Singh, and D. K. Sinha (2015). Stable isotopes: Tools for understanding past climatic conditions and their applications in chemostratigraphy. In Chemostratigraphy (Mu. Ramkumar, Editor). Elsevier, Amsterdam, The Netherlands. pp. 65–92.

Toews, D. P. L., and A. Brelsford (2012). The biogeography of mitochondrial and nuclear discordance in animals. Molecular Ecology 21:3907–3930.

Traugott, M., S. Kamenova, L. Ruess, J. Seeber, and M. Plantegenest (2013). Empirically characterising trophic networks: What emerging DNA-based methods, stable isotope and fatty acid analyses can offer. Advances in Ecological Research 49:177–224.

Trevelline, B. K., S. C. Latta, L. C. Marshall, T. Nuttle, and B. A. Porter (2016). Molecular analysis of nestling diet in a long-distance Neotropical migrant, the Louisiana Waterthrush (*Parkesia motacilla*). The Auk: Ornithological Advances 133:415–428.

Trevelline, B. K., T. Nuttle, B. A. Porter, N. L. Brouwer, B. D. Hoenig, Z. D. Steffensmeier, and S. C. Latta (2018a). Stream acidification and reduced aquatic prey availability are associated with dietary shifts in an obligate riparian Neotropical migratory songbird. PeerJ 6:e5141.

Trevelline, B. K., T. Nuttle, B. D. Hoenig, N. L. Brouwer, B. A. Porter, and S. C. Latta (2018b). DNA metabarcoding of nestling feces reveals provisioning of aquatic prey and resource partitioning among Neotropical migratory songbirds in a riparian habitat. Oecologia 187:85–98.

Tucker, M. A., and A. N. Powell (1999). Snowy plover diets in 1995 at a coastal southern California breeding site. Western Birds 30:44–48.

Twining, C. W., J. T. Brenna, N. G. Hairston, and A. S. Flecker (2016). Highly unsaturated fatty acids in nature: What we know and what we need to learn. Oikos 125:749–760.

Twining, C. W., J. T. Brenna, P. Lawrence, D. W. Winkler, A. S. Flecker, and N. G. Hairston (2019). Aquatic and terrestrial resources are not nutritionally reciprocal for consumers. Functional Ecology 33:2042–2052.

Twining, C. W., J. R. Shipley, and D. W. Winkler (2018). Aquatic insects rich in omega-3 fatty acids drive breeding success in a widespread bird. Ecology Letters 21:1812–1820.

Twining, C. W., S. J. Taipale, L. Ruess, A. Bec, D. Martin-Creuzburg, and M. J. Kainz (2020). Stable isotopes of fatty acids: Current and future perspectives for advancing trophic ecology. Philosophical Transactions of the Royal Society B 375:20190641.

Vallverdú-Coll, N., R. Mateo, F. Mougeot, and M. E. Ortiz-Santaliestra (2019). Immunotoxic effects of lead on birds. Science of The Total Environment 689:505–515.

Van der Merwe, N. J. (1982). Carbon isotopes, photosynthesis, and archaeology: Different pathways of photosynthesis cause characteristic changes in carbon isotope ratios that make possible the study of prehistoric human diets. American Scientist 70:596–606.

Vander Zanden, H. B., D. X. Soto, G. J. Bowen, and K. A. Hobson (2016). Expanding the isotopic toolbox: applications of hydrogen and oxygen stable isotope ratios to food web studies. Frontiers in Ecology and Evolution 4:20.

Vander Zanden, M. J., M. K. Clayton, E. K. Moody, C. T. Solomon, and B. C. Weidel (2015). Stable isotope turnover and half-life in animal tissues: A literature synthesis. PLoS One 10:e0116182.

Varennes, E., S. A. Hanssen, J. C. Bonardelli, and M. Guillemette (2015). Blue mussel (*Mytilus edulis*) quality of preferred prey improves digestion in a molluscivore bird (Common Eider, *Somateria mollissima*). Canadian Journal of Zoology 93:783–789.

Virgilio, M., T. Backeljau, B. Nevado, and M. De Meyer (2010). Comparative performances of DNA barcoding across insect orders. BMC Bioinformatics 11:206.

Vitz, A. C., and A. D. Rodewald (2012). Using stable isotopes to investigate the dietary trophic level of fledgling songbirds. Journal of Field Ornithology 83:73–84.

Vo, A-T., and J. A. Jedlicka (2014). Protocols for metagenomic DNA extraction and Illumina amplicon library preparation for faecal and swab samples. Molecular Ecology Resources 14:1183–1197.

Voigt, C. C., K. Rex, R. H. Michener, and J. R. Speakman (2008). Nutrient routing in omnivorous animals tracked by stable carbon isotopes in tissue and exhaled breath. Oecologia 157:31–40.

Volpe, N. L., B. Thalinger, E. Vilacoba, T. W. A. Braukmann, A. S. Di Giacomo, I. Berkunsky, D. A. Lijtmaer, D. Steinke, and C. Kopuchian (2021). Diet composition of reintroduced Red-and-Green Macaws (*Ara chloropterus*) reflects gradual adaptation to life in the wild. Ornithological Applications 124:in press.

Wallick, L. G., and G. W. Barrett (1976). Bioenergetics and prey selection of captive Barn Owls. The Condor 78:139–141.

Wassenaar, L. I. (2019). Introduction to conducting stable isotope measurements for animal migration studies. In Tracking Animal Migration with Stable Isotopes (K. A. Hobson and L. I. Wassenaar, Editors). Academic Press, London, UK. pp. 25–52.

Waugh, D., and C. J. Hails (1983). Foraging ecology of a tropical aerial feeding bird guild. Ibis 125:200–217.

Whelan, C. J., D. G. Wenny, and R. J. Marquis (2008). Ecosystem services provided by birds. Annals of the New York Academy of Sciences 1134:25–60.

Whiteman, J. P., E. A. Elliott Smith, A. C. Besser, and S. D. Newsome (2019). A guide to using compound-specific stable isotope analysis to study the fates of molecules in organisms and ecosystems. Diversity 11:8.

Whiteman, J., S. Newsome, P. Bustamante, Y. Cherel, and K. A. Hobson (2020). Quantifying capital vs. income breeding: New promise with stable isotope measurements of individual amino acids. Journal of Animal Ecology 90:1408–1418.

Whitney, M. C., and D. A. Cristol (2018). Impacts of sublethal mercury exposure on birds: A detailed review. In Reviews of Environmental Contamination and Toxicology, Vol. 244 (P. de Voogt, Editor). Springer International Publishing, Cham, Switzerland. pp. 113–163.

Wiemers, M., and K. Fiedler (2007). Does the DNA barcoding gap exist? A case study in blue butterflies (Lepidoptera: Lycaenidae). Frontiers in Zoology 4:8.

Wiley, A. E., H. F. James, and P. H. Ostrom (2017). Emerging techniques for isotope studies of avian ecology. In The Extended Specimen: Emerging Frontiers in Collections-based Ornithological Research (M. S. Webster, Editor). Studies in Avian Biology, No. 50, CRC Press, Boca Raton, FL, USA. pp. 89–109.

Williams, C., F. Pontén, C. Moberg, P. Söderkvist, M. Uhlén, J. Pontén, G. Sitbon, and J. Lundeberg (1999). A high frequency of sequence alterations is due to formalin fixation of archival specimens. The American Journal of Pathology 155:1467–1471.

Williams, C. T., and C. L. Buck (2010). Using fatty acids as dietary tracers in seabird trophic ecology: Theory, application and limitations. Journal of Ornithology 151:531–543.

Williams, R. J., S. D. Holladay, S. M. Williams, and R. M. Gogal (2018). Environmental lead and wild birds: A review. In Reviews of Environmental Contamination and Toxicology, Volume 245 (P. de Voogt, Editor). Springer International Publishing, Cham, Switzerland. pp. 157–180.

Williams, R., and A. McEldowney (1990). A guide to the fish otoliths from waters off the Australian Antarctic Territory, Heard and Macquarie Islands. ANARE Research Notes, 75:1–173.

Witmer, M. C (1996). Consequences of an alien shrub on the plumage coloration and ecology of cedar waxwings. The Auk 113:735–743.

Ydenberg, R. C. (1994). The behavioral ecology of provisioning in birds. Ecoscience 1:1–14.

Xavier, J. C., R. A. Phillips, and Y. Cherel. (2011). Cephalopods in marine predator diet assessments: Why identifying upper and lower beaks is important. ICES Journal of Marine Science 68:1857.

Zach, R., and J. Falls (1976). Bias and mortality in the use of tartar emetic to determine the diet of Ovenbirds (Aves: Parulidae). Canadian Journal of Zoology 54:1599–1603.

Zhang, S., L. Zhao, X. Zhang, and W. Liang (2020). Predicting the vulnerability of birds to trophic threat posed by phenological mismatch based on nutritional and physiological status of nestlings. Conservation Physiology 7.

Zinger, L., A. Bonin, I. G. Alsos, M. Bálint, H. Bik, F. Boyer, A. A. Chariton, S. Creer, E. Coissac, B. E. Deagle, M. D. Barba, et al. (2019). DNA metabarcoding—Need for robust experimental designs to draw sound ecological conclusions. Molecular Ecology 28:1857–1862.

Zizka, V. M., V. Elbrecht, J. N. Macher, and F. Leese (2019). Assessing the influence of sample tagging and library preparation on DNA metabarcoding. Molecular Ecology Resources 19:893–899.