Biological Conservation 236 (2019) 556–570

Contents lists available at ScienceDirect

Biological Conservation

journal homepage: www.elsevier.com/locate/biocon

Review

The characterization of seafood mislabeling: A global meta-analysis

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ARTICLE INFO

Keywords:
Seafood fraud
Mislabeling
Meta-analysis
Bayesian estimation
Species substitution
Convenience sampling

ABSTRACT

With the advent of DNA forensics, research on seafood fraud has increased drastically. The documentation of mislabeling has raised concern over the identity, value, and safety of seafood. However, the general characterization of mislabeling is limited. We conduct a Bayesian meta-analysis to estimate global mislabeling rates and their uncertainty across several factors. While the effort to document mislabeling is impressive, it is highly skewed toward certain taxa and geographies. For most products, including all invertebrates, there is insufficient data to produce useful estimates. For others, the uncertainty of estimates has been underappreciated. Mislabeling is commonly characterized by study-level means. Doing so often overestimates mislabeling, masks important product information, and is of limited utility—particularly given that studies often lack adequate sampling designs for parameter estimation. At the global level, overall mislabeling rates do not differ statistically across supply chain locations, product forms, or countries. Product-level estimates are the most informative. The majority of products, for which there is sufficient data, have mislabeling estimates lower than commonly reported. The most credible average mislabeling rate at the product-level is 8% (95% HDI: 4–14%). Importantly, some products have high estimates, which should be priorities for research and interventions. Estimates must be combined with other data in order to understand the extent and potential consequences of mislabeling, which is likely to vary drastically by product. Our meta-analysis, which can be updated with new data, provides a foundation for prioritizing research to inform programs and policies to reduce seafood fraud.

1. Introduction

Media outlets, governments, academics, and NGOs are increasingly documenting seafood fraud. This attention has raised public concern over the identity, value, and safety of seafood. While seafood fraud comes in a variety of forms, mislabeling is perhaps the most concerning (Reilly, 2018).[2] Misrepresenting one species, provenance, or production system as another has many potential consequences: human health risks, economic losses, natural systems impacts, and the undermining of sustainability efforts. For example, consumers may be unknowingly dining on endangered species or seafood that can pose health risks (Cohen et al., 2009; Ling et al., 2008; Palmeira et al., 2013). A seafood product that appears readily available in the marketplace through mislabeling can create a distorted public impression that there is a plentiful supply in the sea. By contrast, an accurate representation of the endangered status of a fishery can sometimes reduce consumer demand (Brownstein et al., 2003). Seafood mislabeling is also suspected of being an important enabler of illegal, unreported, and unregulated (IUU) fisheries (Gordoa et al., 2017; Helyar et al., 2014; Wu, 2017; Xiong et al., 2016). Yet, the extent of potential biological, economic, and health impacts from seafood mislabeling is unknown, with evidence largely limited to anecdotal cases (Kroetz et al., 2018).

With the advent of food forensics (e.g., DNA barcoding), research on seafood fraud has grown over the past decade: 51 papers were published on the topic in 2015 compared to four in 2005 (Fig. 1). Once dominated by environmental and media organization investigations (Boston Globe, 2011; Grogran, 1988; Warner et al., 2016), peer-reviewed studies have increased substantially in recent years (Pardo et al., 2016). The majority of research has focused on developing forensic tools and documenting mislabeling ad hoc for a particular product or geography. Consequently, our current understanding of seafood fraud is largely limited to a growing collection of idiosyncratic studies. The general characterization of seafood fraud is limited, and even less is known about its causes and consequences.

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[2] Other types of fraud include over-glazing, over-breading, and the use of undeclared water-binding agents to increase weight.

https://doi.org/10.1016/j.biocon.2019.04.006
Received 25 January 2019; Received in revised form 19 March 2019; Accepted 12 April 2019
Available online 21 June 2019

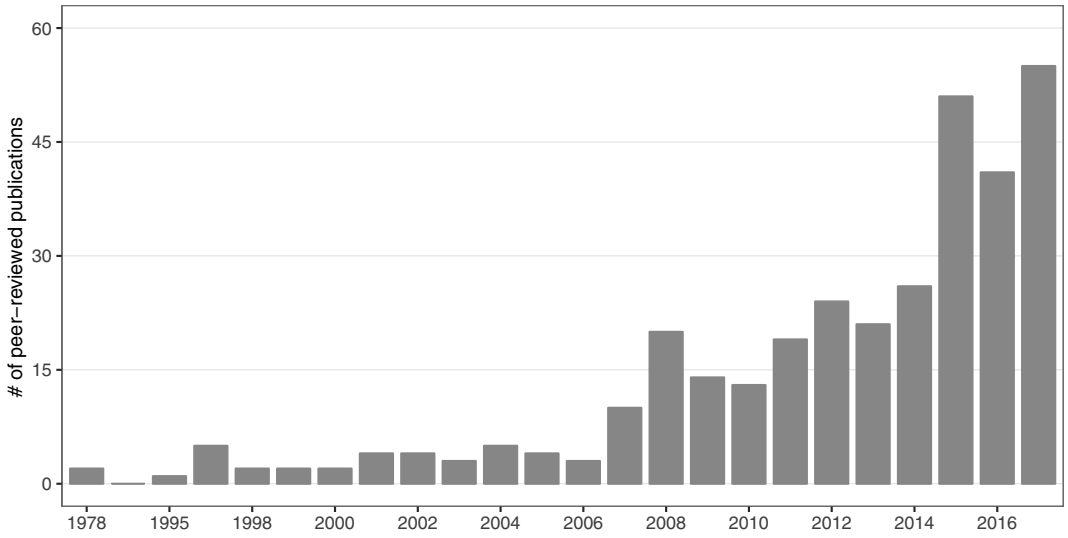

Fig. 1. Number of peer-reviewed publications involving seafood fraud over the past four decades. See Methods and Materials for details on data collection.

Due to the globalized nature and complexity of seafood markets (Anderson et al., 2018; Gephart and Pace, 2015), understanding seafood fraud is a wicked problem. Mislabeled or not, seafood products often do not comply with labeling regulations, which are often confusing (Barendse and Francis, 2015; Cawthorn and Hoffman, 2017a; Meloni et al., 2015; Towers, 2013). Diverse national policies on seafood labeling and traceability, along with weak enforcement, complicate efforts to characterize mislabeling (D'Amico et al., 2016; Hofherr et al., 2016; Meloni et al., 2015). For example, under current US policy, over 60 species can be legally labeled *rockfish* or *grouper* (FDA, 2018). Yet, even where seafood traceability regulations are progressive (e.g., European Union), mislabeling continues to be documented (Bréchon et al., 2016; Charlebois et al., 2014; Christiansen et al., 2018; Gordoa et al., 2017; Harris et al., 2016; Tantillo et al., 2015).

An accurate characterization of seafood mislabeling is a critical first step to investigating the causes and consequences of seafood fraud, as well as designing solutions to reduce it. This is particularly important as current national policies are being revised and new ones implemented (Charlebois et al., 2014; D'Amico et al., 2016; Hofherr et al., 2016). In the United States, for example, a new seafood import monitoring program was implemented in 2018 focused on reducing seafood fraud and IUU fishing (Department of Commerce, 2018). It is being rolled out in stages, with the first stage covering 16 groups of seafood products that were deemed priorities (Department of Commerce, 2016). Yet, for these products and others, little is known about mislabeling rates and the uncertainty of those rates.

Building upon several reviews (Golden and Warner, 2014; Naaum et al., 2016; Pardo et al., 2016), we conduct a meta-analysis on seafood mislabeling. We produce, for the first time, global mislabeling rate estimates and their associated uncertainty. We do so by compiling a global database and using a Bayesian approach to develop statistical models to estimate mislabeling across a suite of factors. In this paper, we present four main results from our meta-analysis. First, we synthesize efforts to document mislabeling and discuss the challenges of characterizing seafood mislabeling. Second, we produce global estimates of study-level mislabeling rates and their uncertainty. While mislabeling rates at the study-level are most commonly reported, we argue that they have limited utility for characterizing seafood fraud. Third, we produce mislabeling estimates across supply chain location (e.g., restaurant vs. port), product form (e.g., processed vs. filet), and country. Fourth, we estimate rates for specific seafood products, which we argue is the most informative for characterizing fraud. Last, we discuss our results in the broader context of seafood fraud and make recommendations on research that will inform the design of programs and policies to reduce it.

2. Methods and materials

2.1. Data collection

We conducted a literature review using the Web of Science to compile all published literature up to December 2017. Searching title, abstract, and keywords, we constrained our search with keywords related to seafood (i.e., seafood OR fish OR crab OR sushi OR shrimp OR caviar OR salmon OR trout) and fraud (i.e., mislabel* OR fraud OR misdescription). We then screened those publications to confirm a focus on seafood fraud, which excluded 37 papers. We also checked cited references within identified papers for any additional relevant papers not captured in the literature search. A total of 331 publications were identified related to seafood fraud (Fig. 1). We also conducted a review of reports and articles on mislabeling that did not undergo a formal peer-review process. Studies were identified via internet searches (i.e., Google) using the same keywords. This included publications by government agencies, media outlets, and NGOs. A total of 69 additional publications were identified related to seafood mislabeling.

We screened each publication for usable data on seafood mislabeling. Using a seafood sample tested for mislabeling with a forensic method as the replicate, we compiled and coded the following information when possible: 1) study, 2) content of the label, 3) genus reported, 4) species reported, 5) the product form (e.g., filet), 6) the location in the supply chain (e.g., restaurant), 7) country where the sample was collected, 8) year collected, and 9) the true identity (e.g., genus and species) of the sample (see Table SM1 for details). We used Fishbase and Sealifebase as taxonomic authorities and adopted common names from these sources (i.e., for species and families; Froese and Pauly, 2018; Palomares and Pauly, 2018).

The resulting database was organized into multiple levels, depending on the level of taxonomic resolution. We include the taxonomic level of family, which was derived either by genus-level information or inferred, when possible, from the common name declared (e.g., *Pacific Cod* can be assigned to the family Gadidae, while *crab* cannot be assigned to a family since it includes over 90 possible families). Since many seafood samples include labels with common names only, we derived a level of analysis at the resolution of seafood product, which includes all samples where the genus or species were reported and samples where the species can be confidently inferred by the common name reported (e.g., sample labeled *swordfish* are grouped with samples that reported *Xiphias gladius* to create a level of analysis based on the

common name of swordfish). This level increases the number of samples and studies, while also allowing us to estimate mislabeling rates for groups of species based on the reported label. This includes commonly consumed seafood products that are often ambiguously labeled, such as *Pacific salmon*, *tuna*, *cod*, and *snapper*. Pacific salmon, for example, encompasses several species belonging to the genus *Oncorynchus* and cod includes several species of fish belonging to the family Gadidae. These products were deemed mislabeled if their true identity is determined otherwise. In this paper, our characterization of mislabeling relies on analyses at the product and family levels. A product-level analysis aligns better with how seafood is currently traded and purchased globally.

Results of forensic testing were also organized into multiple levels, depending on the taxonomic resolution. In most cases, results were reported at the level of species, thus all four levels of analysis were recorded. However in some cases, results are reported only at the resolution of genus or family. And, in other cases, sources reported only common names or only reported that the sample was mislabeled with no information on the identification of the substitute species. Mislabeling necessarily involves two products: we refer to them as the *expected* product (e.g., the species that the product is purported to be based on a label) and the *substitute*—the true identity of a mislabeled product.

2.2. Data filters

We excluded certain data from our analyses to remove potential biases. First, we excluded any studies that reported data such that 1) a seafood product could not be identified to at least one level of analysis, 2) sample sizes of products tested could not be determined or 3) only mislabeled samples of a certain product were reported and information on correctly labeled samples were omitted. In some cases, a study is included in study-level estimates, but excluded in product-level estimates because total sample sizes were not reported for a specific expected product (e.g., Warner et al., 2012). Second, we excluded samples that were considered mislabeled because of a strict interpretation of the expected common name versus the common name reported on the label. For example, if a sample was labeled *salmon* or *crab* and it was considered mislabeled in a study despite being identified at *Salmo salar* (Atlantic Salmon) and *Portunus sanguinolentus* (Threespot swimming crab), we excluded it from our analysis. While such cases can often be considered mislabeled from a policy perspective, the focus of our meta-analysis is on one seafood product being physically substituted for another (i.e., species substitution). Third, we excluded any studies when the primary data was no longer available (e.g., certain investigative journalism efforts). Last, we excluded any samples, despite its determination of being mislabeled or not, if the source stated that the substitute was unable to be identified to any level of taxonomy (e.g., DNA did not amplify). These data filters allowed us to collate only studies that could contribute to the statistical estimation of mislabeling rates.

2.3. Meta-analysis

The basic premise of a meta-analysis is that the average of estimates provided by a group of studies is closer to the truth than the estimate provided by an individual study. While common in the medicine for decades, meta-analysis is increasingly being used in conservation science (Benayas et al., 2009; Koricheva et al., 2013). Meta-analysis often assumes that each study is a near replication of the same experiment and that observed differences in the results are solely due to chance (i.e., fixed-effects model). Like many clinical medical trials (Cornell et al., 2014), this is not the case with mislabeling studies: seafood is sampled in different ways, with different products, for different reasons, and in different locations. Thus, a random-effects model is more appropriate for characterizing seafood mislabeling, which assumes that study results are a combination of an effect common to all studies plus a component specific to that study alone (Cornell et al., 2014; Raudenbush, 2009).

A Bayesian meta-analytic approach offers a number of advantages to characterizing seafood mislabeling, including delivering easily interpretable results with fewer assumptions (Kruschke and Liddell, 2018). First, meta-analyses are a type of hierarchical model, for which Bayesian methods are particularly useful. The structure of data across multiple studies can be described by a hierarchical model: that is, each study has individual parameters and a higher-level distribution describes the variation of those parameters across studies. The top-level distribution describes the central tendency of the trend across studies, and the uncertainty of that trend. Because of the hierarchical nature, estimates of each individual study are informed by the other studies, resulting in overarching estimates as well as improved estimates of the individual studies (Kruschke, 2014; Kruschke and Vanpaemel, 2015). Second, Bayesian inference provides the exact desired information on mislabeling: the probability distribution of all possible parameter values given the actual data. Third, a Bayesian approach can allow for different variances within levels and model an exact binomial distribution, avoiding the shortcomings of a normal approximation with binary data, especially when zero counts are common (Cornell et al., 2014; Kruschke, 2014; Schmid and Mengersen, 2013). Fourth, Bayesian inferences are more informative with respective to parameter estimation because the posterior distribution reveals joint probabilities of combinations of parameter values, and therefore, there is no reliance on sampling distributions and *p*-values to interpret parameter estimates (Kruschke and Liddell, 2018). In sum, a Bayesian approach allows precision of estimation to be a main research goal more coherently than a frequentist approach.

A meta-analysis requires a set of effect size estimates with their corresponding variance. Our effect size estimates are for an individual group with a dichotomous outcome (i.e., there is no control group): the proportion of seafood samples mislabeled, along with the total number of samples tested in a study. The goal of the meta-analysis is to estimate the average true effect and the amount of heterogeneity among the true effect. Bayesian hierarchal models do so by estimating parameters easily interpreted from the posterior distribution, in particular the parameter mode and credibility intervals (i.e., 95% highest density interval, HDI). We present the mode as an estimate for the central tendency, as opposed to the mean, because it is the value of the parameter that is most credible (i.e., likely) given the data, and thus is arguably more appropriate and informative in characterizing mislabeling data, which can often have skewed distributions. However, the mode can sometimes be unstable when using a MCMC sample (Kruschke, 2014). Thus, we also report the posterior median and mean from our models. The 95% HDI is the interval that includes 95% of all values in the posterior distribution, and thus is a measure of precision or uncertainty.

First, we model mislabeling estimates at the level of the study. Study-level mean mislabeling rates are what is typically reported in the literature. We do so with a robust logistic regression model with one level of hierarchy (Fig. SM1; Kruschke, 2014). The likelihood function is

$$y_i \,|\theta_i \sim \mathrm{Bin}(\theta_i, N_i) \quad (1)$$

where, y_i represents the number of mislabeled samples by study i, out of N_i (total # samples in study i). The datum, y_i, is assumed to be a random draw from a binomial distribution with mean θ_i. The estimated mislabeling rate of study i is denoted θ_i, which can only take values between 0 and 1. There are as many θ_i as number of studies. We perform a logistic transformation of the parameters θ_i [$\alpha_i = \mathrm{logit}(\theta_i)$] for which we use a t distribution as a conjugate prior of the likelihood function, which is defined as

$$\alpha_i \,|\, \mu, \sigma, \nu \sim t(\mu, \sigma, \nu). \quad (2)$$

The estimated α_i are t-distributed random values around the central tendency μ. A t distribution is similar to a normal distribution with two parameters that control its mean μ and width σ. But, it also has a third

parameter that controls the heaviness of its tails: the normality parameter (✓), which describes the deviation from normality when there are outliers (i.e., data values that fall unusually far from a model's expected value). Thus, the *t* distribution is robust against outliers. For the three hyperparameters (μ, σ, and ✓), we use non-informative priors because little is known about the parameter values and we were interested in what the data themselves provide as inferences. The model, its parameters, and priors are explained in detail in the Supplementary materials.

We compare our model results with the study-level arithmetic mean, which ignores study effort (i.e., sample size; hereafter, referred to as the *naive mean*[3]). We do so by establishing a region of practical equivalence (ROPE) around the naive mean, which we set as ± 1%. Analogous to equivalence testing, ROPEs are a decision tool for some null value (Kruschke and Liddell, 2018). For example, when the 95% HDI falls outside the ROPE, it can be concluded that 95% of the most credible values of the parameter are not practically equivalent to the null value.

Second, we developed a series of two-level hierarchal models in order to estimate mislabeling rates for seven factors: study type, seafood type, supply chain location, product form, country, taxonomic family, and seafood product. Each two-level hierarchal model is similar to the study-level model, but each level of a factor is a different category *c* in the models (e.g., the factor seafood type has two categories of fish and invertebrate; see Fig. SM2). We estimate the mean (μ_c), scale (σ_c), and normality($\checkmark_c$) for each category within each factor separately. The likelihood function is,

$$y_{i,c} \mid \theta_{i,c} \sim \mathrm{Bin}(\theta_{i,c}, N_{i,c}) \quad (3)$$

where, $y_{i,c}$ represents the number of mislabeled samples by study *i* out of N_i within each category *c*. The datum, $y_{i,c}$, is assumed to be a random draw from a binomial distribution with mean $\theta_{i,c}$. There are as many $\theta_{i,c}$ as number of studies within each category *c*. We also perform a logistic transformation of the parameters $\theta_{i,c}$ for which we use a *t* distribution as a conjugate prior of the likelihood function. In these models, there are five types of hyperparameters: 1) estimated mislabeling rates for each category of a factor (μ_c), the precision of those rates (σ_c), the normality parameter ($\checkmark_c$), and estimated overall mislabeling rate (μ_0), and precision (σ_0) of μ_0. Like the study-level model, we use non-informative priors. The models, its parameters, and priors are explained in detail in the Supplementary materials.

Third, for the two-level hierarchical models, we explore potential differences in mislabeling estimates between different categories for each factor. The visual examination of the distributions of two parameters does not necessarily reveal whether the parameter values are different because the joint distribution of the two parameters might have positive or negative correlation that may mask any true difference (Kruschke, 2014). Rather, it is the difference between two posterior distributions that provides evidence for any difference. If the difference of two distributions includes zero, and in particular when zero is included in the 95% HDI, then there is no evidence to suggest the parameters differ. Only when a difference of zero falls outside the 95% HDI would one conclude that there is a difference between two parameters (e.g., one mislabeling estimate is greater than another). We use this comparison to test for differences between supply chain location, product form, and countries with respect to mislabeling rates. See Supplementary materials for more detail.

2.4. Model performance and diagnostics

For all of our models, we include as much data and factors as possible while still producing well-performing models. In many cases, data is excluded due to the lack of replication. We use multiple visual and numerical diagnostics to assess model performance, in particular to check whether MCMC samples from the posterior distribution of each model are representative of the true posterior distribution and whether the estimates are accurate and stable. Diagnostics include trace plots, density plots, Gelman-Rubin statistics, autocorrelation plots, effective sample sizes (ESS), and Monte Carlo standard errors (MCSE). We also explored any potential impact on our model results from our non-informative priors by re-running the models with mildly-informative priors (Gelman et al., 2008; Kruschke, 2014). Diagnostics are described and reported in detail in Supplementary materials along with the use of alternative priors. All analysis were conducted in the statistical language R and JAGs (Plummer, 2017; R Development Core Team, 2017).

3. Results

3.1. Efforts to document mislabeling

Seafood mislabeling has been evaluated in 38 countries; however, two-thirds (22) of those countries include two or less studies (Fig. 2). The United States, Italy, and Spain are the countries with the largest effort. Our review resulted in 141 studies with usable data for our meta-analysis: 117 from peer-reviewed sources and 24 from sources that were not peer reviewed (Table SM2). Most (94%) studies used DNA methodologies as the forensic tool. Other methods included isoelectric focusing (n = 2), immunological essays (n = 1), staple isotopes and fatty acids (n = 1), morphometrics and DNA (n = 1), testing for synthetic coloring (n = 1), and a combination of these methods (n = 1). While our analysis included total of 27,313 samples, study sample size is highly variable (range: 8–4656; mean = 194; median = 68; mode = 90). We documented 401 seafood products that have been tested for mislabeling, of which 222 (55%) where mislabeled at least once. This includes 138 families, 209 genera, and 301 species.

Sampling effort is highly skewed toward certain taxa. Fifty-five (42%) of the 138 families that have been tested for mislabeling consist of a single study (Fig. 3). Gadidae (cods and haddocks), Scombridae (mackerels, tunas, bonitos), and Salmonidae (salmonids) have been included the most in mislabeling studies (n > 40), while Gadidae, Acipenseridae (sturgeons and paddlefishes), and Rajidae (skates) have the most number of samples pooled across studies (Fig. 3). Effort is also heavily skewed from the perspective of seafood product (Fig. SM5). For example, 57% of all products have been tested by a single study, and 50% have ≤5 total samples. When effort is broken down by seafood product per study, average sample size is small (range: 1–2,609; mean = 19, median = 3, mode = 1). Mislabeling studies tend to sample less than a dozen different seafood products (mean = 10, median = 5, mode = 1; standard deviation = 13).

We documented 358 species that have been identified as substitute species in mislabeling studies (Fig. SM5). The majority (69%) were identified from a single study, while almost half (46%) have been identified a total of two times or less (i.e., total number of samples). Striped Catfish (*Pangasianodon hypophthalmus*) was identified by the most number of studies (n = 26), followed by Alaska Pollock (*Gadus chalcogrammus*, 19), Bigeye Tuna (*Thunnus obesus*, 14), Atlantic Cod (*Gadus morhua*, 13), Haddock (*Melanogrammus aeglefinus*, 13), and Atlantic Salmon (*Salmo salar*, 13; Fig. SM6).

3.2. Study-level mislabeling estimates

Our model predicted a posterior mode mislabeling rate of 24% with a 95% HDI spanning from 20% to 29% (Fig. 4a). The posterior mean and median were the same as the mode. The model performed well, with large ESSs, small MCMEs, and convergence for estimates of the mean and variance (Table SM4). The probability that the naive mean of the 141 study rates (30%) and the established ROPE (29–31%) is a

[3] This term is borrowed from the forecasting field, where the *naive model* is often the simplest and most cost-effective model that is compared to others using different methodologies.

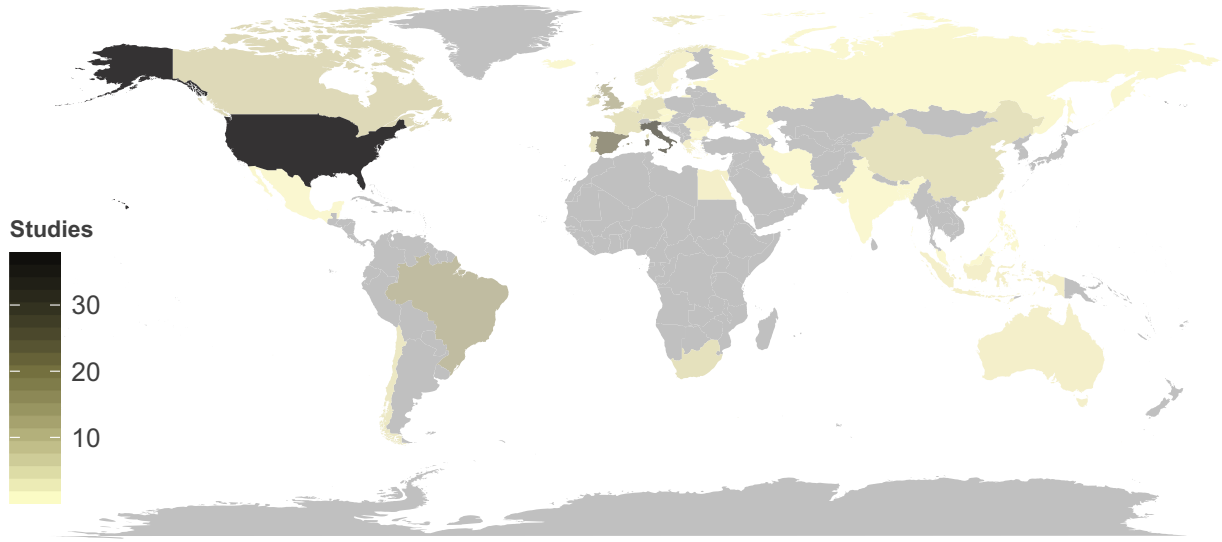

Fig. 2. Distribution of effort to document seafood mislabeling by country. The United States (37), Italy (24), and Spain (18) have the most studies, followed by Brazil (10) and the countries of the United Kingdom (10).

credible value is 1.2% (Fig. 4). Predicted study-level mislabeling rates were highly variable across studies, ranging from < 1–90%. They are also uncertain, with an average 95% HDI of 19% (Fig. 4a, Table SM2). The predicted posterior distributions for studies that underwent peer-review or not were similar (Fig. 5). Both posterior mode estimates were lower than their respective naive means. There are roughly five times as many peer-reviewed studies compared to reports that did not undergo a formal peer-review process. The posterior means and medians were similar to the modes (Table SM3). For peer-reviewed studies, the predicted distribution was similar to the overall study-level distribution (Figs. 4–5). The study-type model performed well with inclusion of all 141 studies (Table SM4).

3.3. Non-taxonomic mislabeling estimates

Most effort has focused on sampling restaurants and grocery stores. Fewer studies have tested for seafood mislabeling at wholesale venues, ports, and markets. Wholesale venues were excluded from our model because we identified only five studies that have sampled them (Armani et al., 2015; Burros, 2005; Cawthorn et al., 2012; Kappel and Schröder, 2016; Roman and Bowen, 2000). All supply chain estimates were similar (21–27%) and uncertain (Fig. 6). Using the difference between two posterior distributions to conduct pairwise contrasts, there is currently no statistical evidence that overall mislabeling rates differ across supply chain locations at the global level (Table SM5). In all cases, the posterior median and mean estimates were similar to the mode (Table SM3). With the exception of markets, predicted modes were less than the naive mean. The model performed well with the inclusion of the four supply chain locations (Table SM4).

With respect to seafood form, filet and processed products have been sampled the most (n > 50 studies), while whole, sushi, and roe forms have half as many studies (Fig. 7; Table SM3). Posterior mode estimates were similar and uncertain across supply chain locations, ranging from 20 to 22% and with overlapping 95% HDIs (Fig. 7). Using the difference between two posterior distributions to conduct pairwise contrasts, there is currently no statistical evidence that overall mislabeling rates differ across product form at the global level (Table SM5). For all forms, the posterior modes and medians are similar to the mode, and the naive means are greater than all posterior estimates (Table SM3). The model performed well with the inclusion of the five product forms (Table SM4).

We estimated mislabeling rates for five countries, which had ≥10 studies. Posterior modes and 95% HDIs were similar, with the modes ranging from 25 to 28% (Fig. 8). Using the difference between two posterior distributions to conduct pairwise contrasts, there is currently no statistical evidence that overall mislabeling rates differ across countries (Table SM5). Posterior means and medians were similar to the modes (Table SM3). For three of the five countries, the naive mean was greater than the mode (Fig. 8). Like other non-taxonomic factors, estimates were uncertain, with an average 95% HDI of 17%. The model performed well with the inclusion of the five countries (Table SM4).

3.4. Taxonomic mislabeling estimates

While five times more studies have sampled fish compared to invertebrates, the predicted posterior modes and distributions are similar, with invertebrates having a larger 95% HDI (15% vs. 9%; Fig. 9). In both cases, the posterior means and medians are similar to the modes, and all are less than the naive means (Fig. 9; Table SM3). The model performed well (Table SM4).

We estimated mislabeling rates for 23 families, which had ≥10 studies (Fig. 10). Posterior modes ranged from 3 to 61% and, with a few exceptions, estimates were uncertain (mean 95% HDI = 25%; Fig. 10; Table SM6). Twenty (and 9) of the 23 families have posterior modes (and upper 95% HDIs) less than the study-level mode of 24% (Table SM5). Serranidae (sea basses: groupers and fairy basslets) and Lutjanide (snappers) have the highest estimated mislabeling rates. Four families have estimates ≤5%: Cichlidae (cichlids), Carcharhinidae (requiem sharks), Lophiidae (goosefishes), and Xiphiidae (swordfish; Fig. 10). For most families the naive mean was greater than the posterior mode, and for some cases the posterior medians and means were also greater than the modes (Fig. 10; Table SM5). We were unable to estimate mislabeling for any invertebrate families due to lack of study replication. The model performed well with the inclusion of 23 families; however, for four families the ESS for variance estimates were < 10,000 (Table SM7).

We estimated mislabeling rates for 28 seafood products, which each had ≥10 studies (Figs. 11–13). The overall mode for all products was 8% (Fig. 4b). Posterior modes ranged from < 1–74%; many estimates are uncertain (mean 95% HDI = 26%; Table SM8). Twenty-five (and 16) out of the 28 products have posterior modes (and upper 95% HDIs) less than the study-level mode of 24% (Figs. 11–13). Nine products (32%) have posterior mode estimates greater than the overall product mode of 8% (Figs. 11–13). For many products, the naive means and posterior means and medians are greater than the posterior modes (Figs. 11–13; Table SM8). Products with the highest mislabeling rates

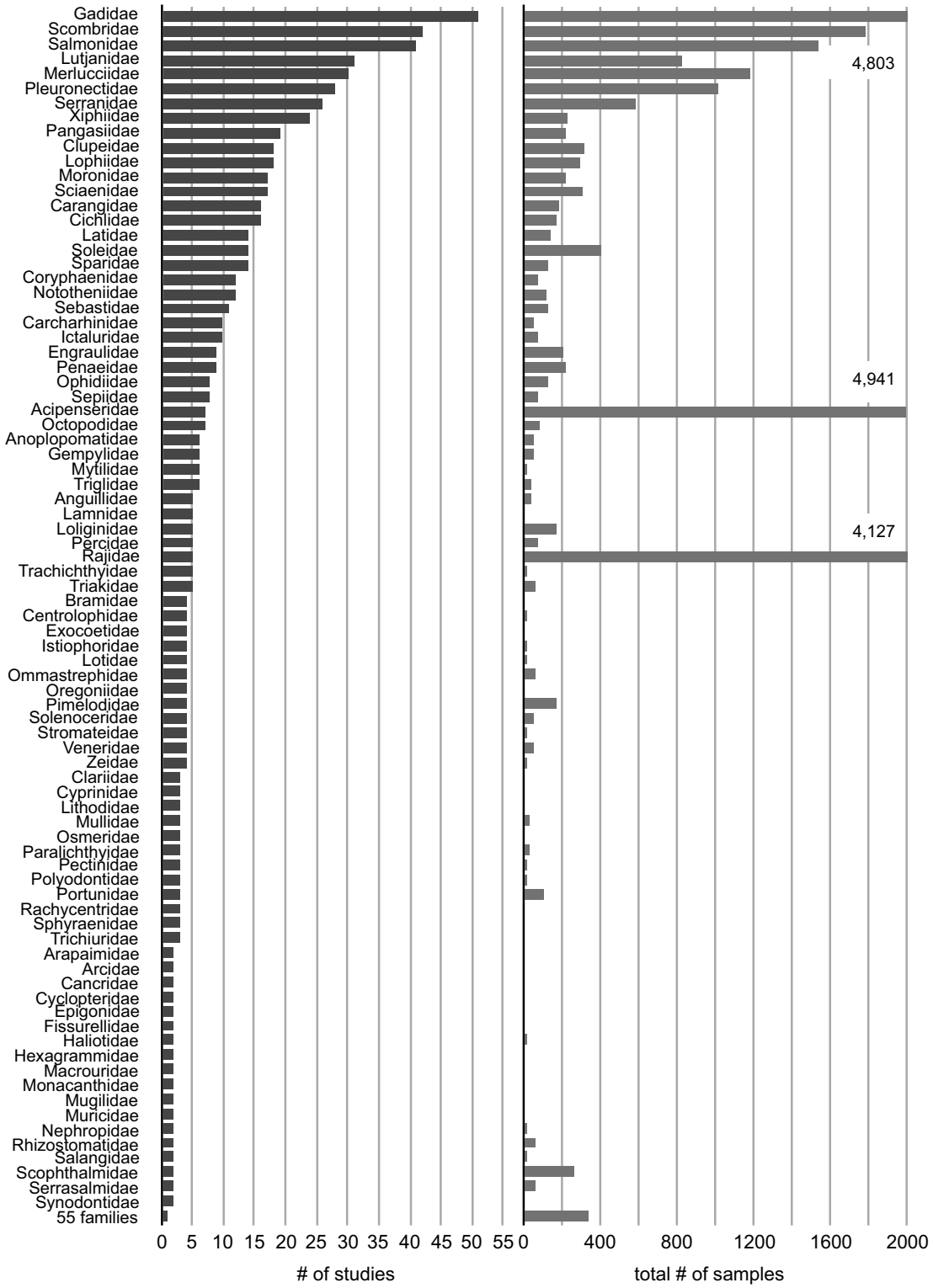

Fig. 3. Distribution of effort to document seafood mislabeling by taxonomic family (# of studies and total # of samples pooled across studies). Fifty-five families are represented by a single study.

are Northern Red Snapper (*Lutjanus campechanus*), European Hake (*Merluccius merluccius*), and fish labeled *grouper*. Fish with the lowest mislabeling rates (< 1%) are Deep-water Cape Hake (*Merluccius paradoxus*), Striped Catfish (*Pangasianodon hypophthalmus*), Blue Shark (*Prionace glauca*), Pacific Cod (*Gadus macrocephalus*), and fish labeled *salmon* (Table SM7). We were unable to estimate mislabeling for any invertebrate products due to lack of study replication. The model performed well with the inclusion of 28 products; however, for seven products the ESS for variance estimates were < 10,000 (Table SM9).

3.5. Model performance, central tendency estimates, and sampling

With very few exceptions, our Bayesian models performed well, producing robust central tendency and variance estimates. In only

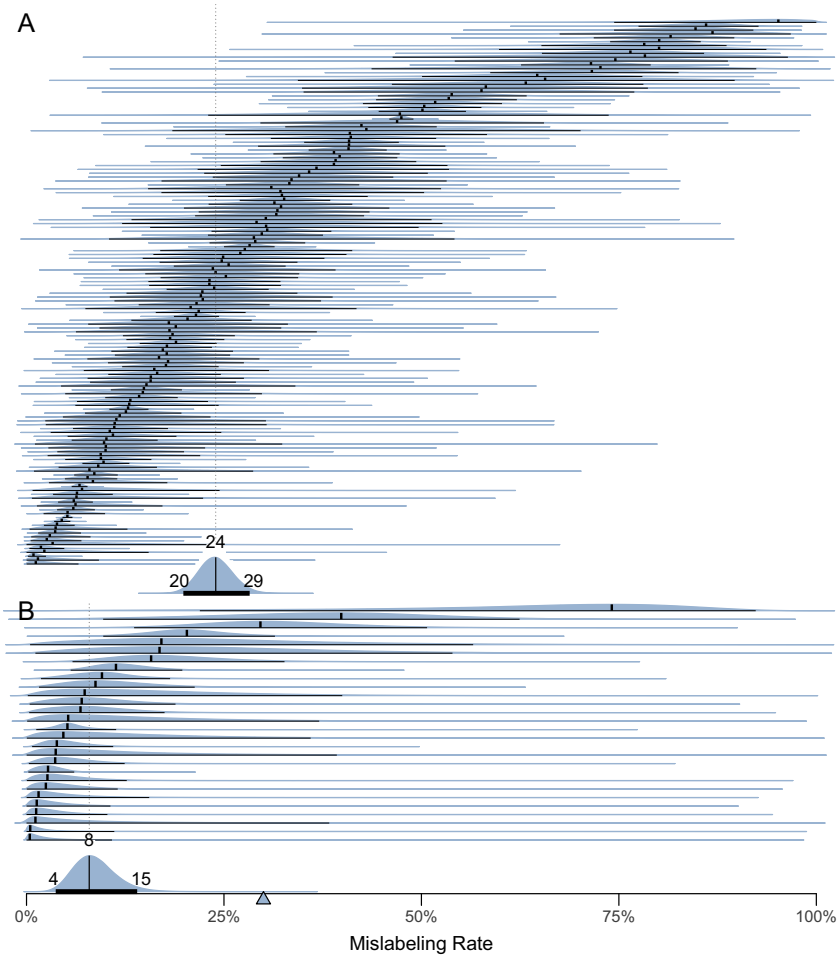

Fig. 4. A) Posterior probability density of mislabeling rates for 141 studies, along with overall probability density. The horizontal black lines mark the 95% HDI (e.g., 20–29% for the overall), while the vertical bar and black dots represent the posterior modes. B) Posterior probability density of mislabeling rates for 28 products which have ≥10 studies, along with the overall probability density. The horizontal black lines mark the 95% HDI (e.g., 4–15% for the overall), while the vertical bar represents the posterior modes (e.g., 8% for the overall). The triangle (▲) represents the overall study-level naive mean (30%). See Table SM2 for individual study-level estimates.

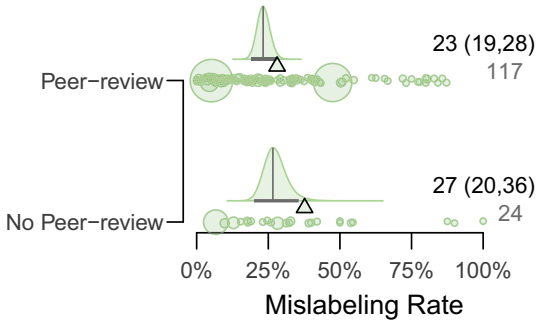

Fig. 5. Posterior probability density of mislabeling rates across study type: peer-review and no peer-review. Posterior mode (vertical line) and 95% HDI (horizontal line) are shown. Posterior mode, 95% HDI, and sample size (i.e., number of studies) are shown on the right side. Study-level mislabeling data are also shown with dot size proportional to number of samples.

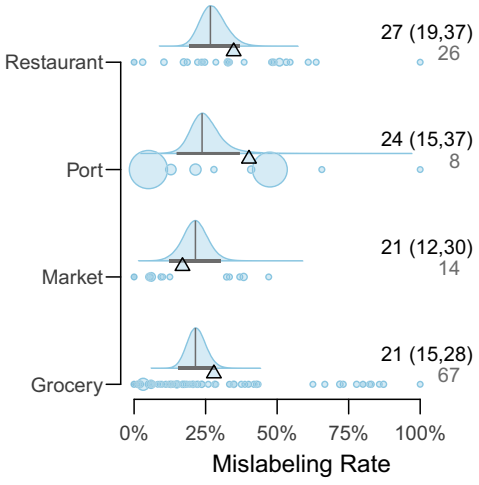

Fig. 6. Posterior probability density of mislabeling rates across supply chain location. Posterior mode (vertical line) and 95% HDI (horizontal line) are shown, along with the naive mean (▲). Products with an * represent more than one species. Sample size (N, number of studies), posterior mode, and 95% HDI are shown on the right side. Study-level mislabeling data are also shown with dot size proportional to number of samples.

eleven cases did estimates have an ESS < 10,000—all of which were variance estimates for families or products (Tables SM6, SM8). Model estimates and HDI intervals for the overall and product models did not change when we varied the priors (See Supplementary materials).

Across all over our models, the naive mean overestimated the posterior mode 87% of the time. It did so, on average, by +9% (minimum delta = −4%; maximum delta = +35%). In cases were probability distributions were skewed (i.e., some family and product estimates), the posterior means and medians were also greater than the posterior modes (Figs. 10–13; Tables SM6, SM8).

When study-level mislabeling data is segmented by seafood product, global sampling effort and naive mislabeling rates are dominated by 0% and 100%. In fact, 73% of the 1,582 product-level rates are 0% or 100%, and the pattern is similar across taxonomic families (Fig. 14). Only 27% of the naive rates are between 1 and 99%.

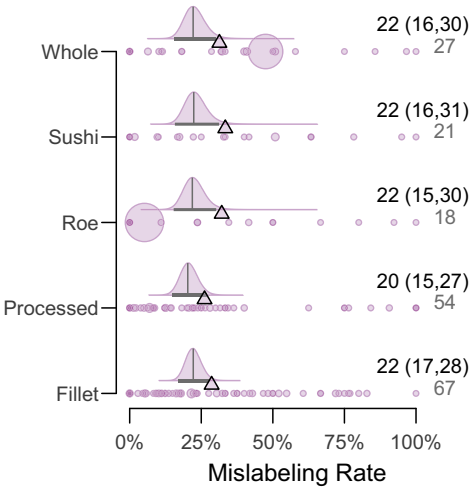

Fig. 7. Posterior probability density of mislabeling rates for product form. Posterior mode (vertical line) and 95% HDI (horizontal line) are shown, along with the naive mean (▲). Sample size (N, number of studies), posterior mode, and 95% HDI are shown on the right side. Study-level mislabeling data are also shown with dot size proportional to number of samples.

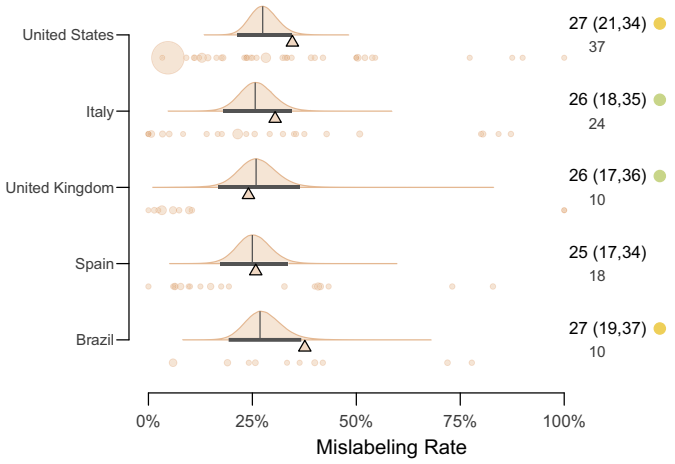

Fig. 8. Posterior probability density of mislabeling rates for countries with ≥10 studies. Posterior mode (vertical line) and 95% HDI (horizontal line) are shown, along with the naive mean (▲). Sample size (N, number of studies), posterior mode, and 95% HDI are shown on the right side. Study-level mislabeling data are also shown with dot size proportional to number of samples. The colored circles on the right represent ranking scores based on the comprehensiveness of traceability regulations for domestic and imported food products from Charlebois et al., 2014: green = superior and orange = average. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

4. Discussion

4.1. Efforts to document seafood mislabeling

Studies investigating seafood mislabeling have increased substantially over the past decade. Yet, seafood fraud is not a new phenomena: diners in New York City hotels were serving shark labeled as swordfish steaks in 1915 (Anonymous, 1915). The ability to detect seafood fraud, however, has changed dramatically, driven by the development of DNA forensics and to a lesser extent other tools (Naaum and Hanner, 2016; Rasmussen and Morrissey, 2009; Shokralla et al., 2015). The majority of research has focused on the development and testing of DNA forensic tools within the field of food science. For example, of the 331 peer-reviewed publications we identified related to

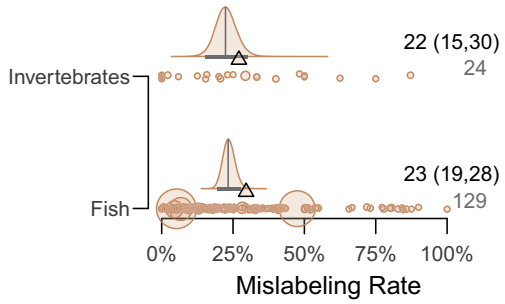

Fig. 9. Posterior probability density of mislabeling rates across seafood type: invertebrates and fish. Posterior mode (vertical line) and 95% HDI (horizontal line) are shown, along with the naive mean (▲). Sample size (N, number of studies), posterior mode, and 95% HDI are shown on the right side. Study-level mislabeling data are also shown with dot size proportional to number of samples.

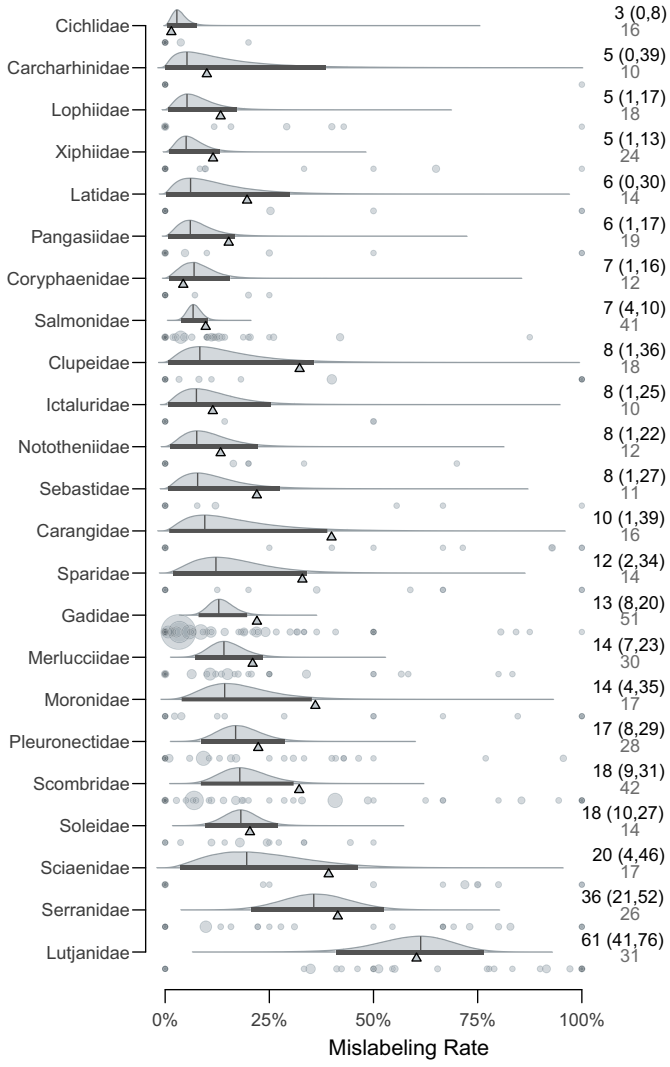

Fig. 10. Posterior probability density of mislabeling rates for 23 taxonomic families, which have ≥10 studies. Posterior mode (vertical line) and 95% HDI (horizontal line) are shown, along with the naive mean (▲). Products with an * represent more than one species. Posterior mode, 95% HDI, and sample size (N, number of studies) are shown on the right side (A 0 indicates a value < 1%). Study-level mislabeling data are also shown with dot size proportional to number of samples.

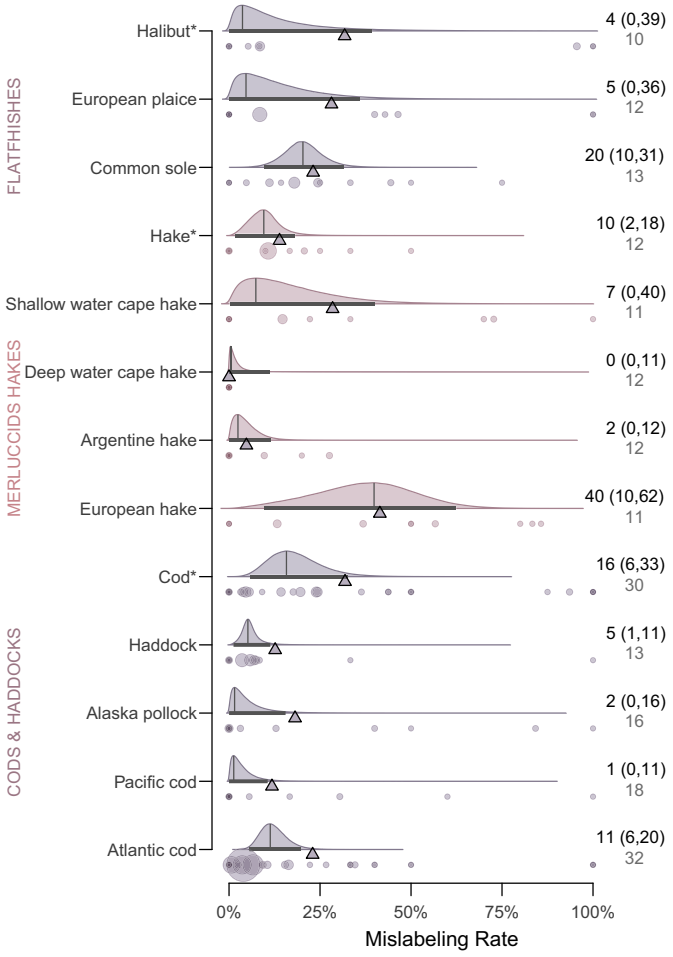

Fig. 11. Posterior probability density of mislabeling rates for 13 products belonging to three taxonomic groups: Pleuronectiformes (flatfishes), Merluccidae (Merlucid hakes), and Gadidae (cods and haddocks). Posterior mode (vertical line) and 95% HDI (horizontal line) are shown, along with the naive mean (▲). Products with an * represent more than one species. Posterior mode, 95% HDI, and sample size (N, number of studies) are shown on the right side (A 0 indicates a value < 1%). Study-level mislabeling data are also shown with dot size proportional to number of samples.

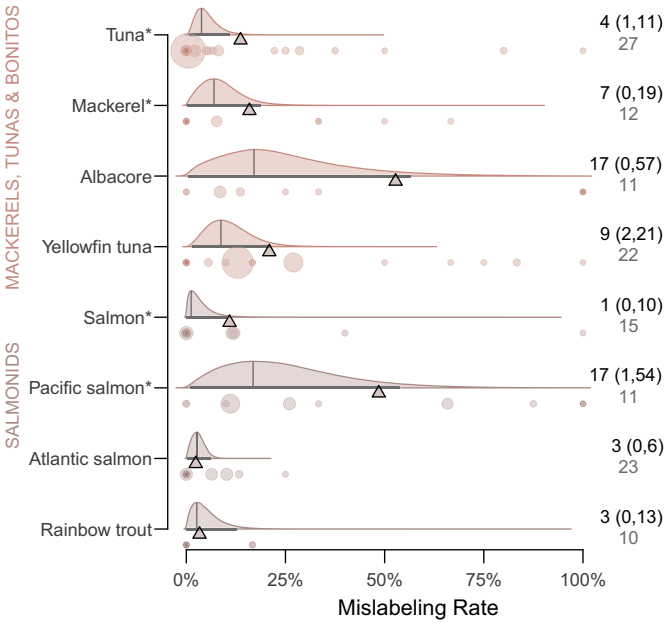

Fig. 12. Posterior probability density of mislabeling rates for eight products belonging to two taxonomic groups: Scombridae (mackerels, tunas, and bonitos) and Salmonidae (salmonids). Posterior mode (vertical line) and 95% HDI (horizontal line) are shown, along with the naive mean (▲). Posterior mode, 95% HDI, and sample size (N, number of studies) are shown on the right side (A 0 indicates a value < 1%). Study-level mislabeling data are also shown with dot size proportional to number of samples.

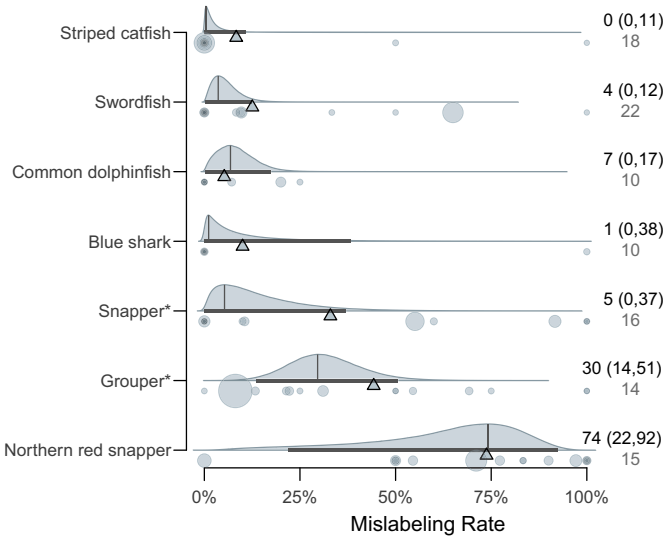

Fig. 13. Posterior probability density of mislabeling rates for seven seafood products. Posterior mode (vertical line) and 95% HDI (horizontal line) are shown, along with the naive mean (▲). Posterior mode, 95% HDI, and sample size (N, number of studies) are shown on the right side (A 0 indicates a value < 1%). Study-level mislabeling data are also shown with dot size proportional to number of samples.

seafood fraud, 40% were published in five journals: *Food Control*, *Food Chemistry*, *Journal of Agricultural and Food Chemistry*, *Food Research International*, and *European Food Research and Technology*. The growing number of studies has resulted in greater geographic coverage. However, effort is still strongly skewed toward a few countries: ≥10 studies have been conducted in only five countries. Few or no studies have been conducted in countries that are among the top seafood producers, exporters, or importers, such as China (4 studies), India (1), Indonesia (2), Japan (0), Norway (3), Peru (0), Russia (1), Thailand (0), and Vietnam (0; FAO, 2016). Nonetheless, the accumulation of information on seafood mislabeling over the past decade is impressive. There were 15 studies published prior to 2008 (covering 12 countries and containing 6,151 total samples) compared to an additional 126 studies published between 2008 and 2017, covering 37 countries and 21,163 total samples. Similarly, evidence suggests that seafood mislabeling has also increased as a topic in the popular media over the past decade (Van Holt et al., 2018).

Despite the growing number of studies, there has been few attempts to characterize the current evidence on seafood mislabeling. The NGO Oceana reviewed seafood fraud in 2014 and 2016, reporting weighted mean study mislabeling rates of 22% and 19%, respectively (Golden and Warner, 2014; Warner et al., 2016). Another 2016 review, published in the journal *Food Control*, reported a mean study mislabel rate of 30% (Pardo et al., 2016). While previous reviews provide a foundation into synthesizing seafood mislabeling, they are largely narrative in scope, reporting on commonly mislabeled species and their substitutes, as well as anecdotal cases of economic and health impacts (e.g., Naaum et al., 2016). Another study reported a median mislabeling rate of 13% for marine finfish using a bootstrapping approach (Stawitz et al., 2017); however, the authors pooled samples across studies not

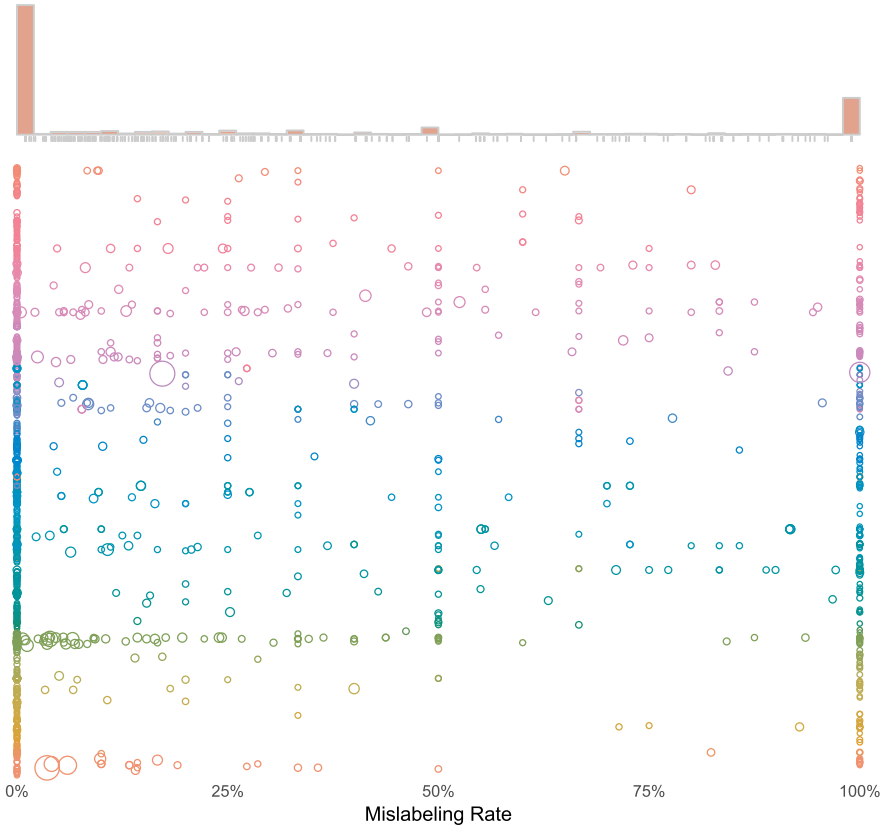

Fig. 14. Global sampling effort and naive mislabeling rates of seafood products. Circles represent the naive mislabeling rate for products by study (N = 1582 study-product combinations). Dot size is proportional to sample size, and colors represent different taxonomic families. As shown in the histogram, the majority of sampling effort has a naive mislabeling rate of 0% (57%; n = 900) and 100% (16%; n = 257). Only 27% (n = 425) of the data falls between 1 and 99%. Given that it is unlikely that true mislabeling rates are commonly 0 or 100%, under-sampling appears to be common for mislabeling studies.

taking into account sampling effort. Importantly, all of the previous reviews rarely report on the uncertainty of mislabeling estimates nor take into account sampling effort, and none estimate the uncertainty of product-specific mislabeling estimates.

With respect to characterizing mislabeling, there are two main challenges with available studies with respect to parameter estimation. First, studies tend to report the arithmetic mean pooled across studies or products without any measure of uncertainty (but see Bénard-Capelle et al., 2015). This may be partially due to the low sample sizes that are common, especially when grouped by seafood product. Also, the purpose of many mislabeling studies is to test forensic tools as opposed to estimate mislabeling rates. The mean as a measure of central tendency, however, is highly sensitive to skewed data, which is common with mislabeling data with small sample sizes. Further, the simple pooled mean is unreliable because it lacks an estimate of variance, as well as the problems associated with simply pooling data across studies (Bravata and Olkin, 2001). Our results suggest that mislabeling data is often highly skewed and the uncertainty in central tendency estimates is significant—suggesting that reporting the naive mean and ignoring measures of uncertainty will often lead to an inaccurate characterization of mislabeling.

Second, mislabeling studies often lack attention to sampling design (Pardo et al., 2016). Under-sampling and convenience sampling appear to be common. True product-level mislabeling rates are unlikely to be commonly 0% and 100%. Yet, these rates dominate product-level naive estimates (Fig. 14), suggesting under-sampling is widespread. While some studies claim to sample seafood *randomly*, we identified a single study that presented sufficient information to assess its sampling regime (Wu, 2017). Most give little or no information on how seafood is sampled, either at the level of venue (e.g., restaurant) or product (i.e., how a product and its sample size are selected). Further, some studies may be sampling products with a goal of seeking out mislabeling (Cheney, 2018), which is even more problematic with respect to estimating true mislabeling rates. While convenience sampling has its advantages (e.g., cost effective, expedited data collection), the potential for unmeasurable bias limits inferences. While larger samples sizes reduce the chance of sampling error with convenience sampling, this is often not the case with mislabeling studies. In general, convenience sampling reduces power to detect differences among groups, increases variation that cannot be accounted for, and limits generalizability to the actual sample studied (Bornstein et al., 2013). Across several disciplines, researchers have demonstrated that probability sampling can produce different results and inferences compared to convenience sampling (Hedt and Pagano, 2011; Hultsch et al., 2002; Özdemir et al., 2011; Pruchno et al., 2008). The observed uncertainty and inability to discern differences across factors in the results of our meta-analysis may be influenced by the convenience sampling conducted by mislabeling studies. While our Bayesian approach does not correct for any potential sample selection bias resulting from convenience sampling, it does produce improved central tendency estimates and their uncertainty—using all available data. Further, it produces probability distributions of mislabeling rates independent of assumptions associated with frequentist approaches (e.g., chi-square test, 95% confidence intervals; Kruschke and Liddell, 2018), which are likely not met for many mislabeling studies.

4.2. Study-level mislabeling estimates

The posterior mode of the study-level mislabeling rate differs from the naive mean: 24% versus 30%. Given the current data, there is a 1.2% probability that global study-level mislabeling rate is 30%. Yet, the estimated mode is uncertain, with a 95% HDI between 20% and 29%, which overlaps with one previous review that reported a weighted mean rate (Golden and Warner, 2014). Our hierarchal model, however, has several advantages in estimating study-level mislabeling rates compared to using the naive mean or weighted approaches. First, it estimates the entire probability distribution given the current data, accounting for different sampling effort across studies. Second, it

provides informative measures of variability or uncertainty of central tendency estimates. Third, it improves study-level estimates by individual studies acting as simultaneous prior information to shrink extreme cases (Kruschke, 2014). Given the observed variability, both within and across studies, the observed shrinkage between the naive and posterior means was minimal at the study-level (Table SM2). Given the diversity of seafood tested (i.e., 401 and 301 seafood products and species, respectively) along with other factors, the observed uncertainty should not be surprising. Yet, this uncertainty has been under-appreciated, and largely ignored, in the literature.

Despite a more robust central tendency estimate (and measure of uncertainty), study-level estimates are of limited utility for characterizing seafood mislabeling. They can also be misleading. First, the goal of many mislabeling studies is not to estimate rates. Second, a mislabeling study is, on average, a collection of idiosyncratic seafood products collected at different locations by different motivations and then tested for authenticity. This is likely an underlying reason for the observed variability and subsequent uncertainty across studies. It is the underlying characteristics of specific seafood products that are likely driving mislabeling patterns (Donlan and Luque, 2019), which are masked by study-level mislabeling estimates that often include multiple products, as well as multiple locations and forms. Third, study-level estimates have little generalizability beyond characterizing mislabeling studies themselves. This issue is exacerbated with potential issues associated to convenience sampling. Yet, study-level estimates often result in misleading statements: such as *30% of seafood is mislabeled* — using our naive mean as an example. Such statements in the media are not uncommon (Begley, 2014; Blank, 2017; Fraser, 2018; Oaklander, 2015; Sifferlin, 2016). Irrespective of the need to take into account production with such statements (e.g., apparent consumption; Kroetz et al., 2018), reporting the study-level naive mean is almost certainly overestimating mislabeling in many cases, and may be misleading the public even when qualifications are included (e.g., *30% of the seafood samples tested were mislabeled*), particularly given the current sampling practices and that uncertainty in estimates is rarely reported. Accurate reporting, including variability in estimates, is important given that some studies have been criticized for inflating mislabeling rates and problematic study design (Cheney, 2018; Sackton, 2014).

4.3. Non-taxonomic mislabeling rates

Teasing apart where mislabeling occurs along the supply chain and if differences exist is a challenging endeavor. Many studies focus on multiple retail venues and do not report on the locations of individual samples. The majority of available effort has focused on restaurants and grocery stores. While some have claimed wholesale distributors have the highest probability mislabeled seafood (Stawitz et al., 2017), insufficient and variable data preclude useful estimations, let alone any statistical comparison (also see Donlan et al., 2017). Some researchers have suggested that mislabeling is more prevalent at retail outlets compared to locations more upstream in the supply chain, while other have suggested rates are higher in restaurants compared to other retailers (e.g., grocery stores; Khaksar et al., 2015b; Muñoz-Colmenero et al., 2016; Stawitz et al., 2017). Results from available data provide no evidence for differences in mislabeling rates along the supply chain—at least at the global level where there is sufficient data to conduct a valid comparison (Fig. SM5). More effort and attention to sampling is needed across the seafood supply chain in order to reduce the observed uncertainty and improve estimates. Further, incentives and opportunities to mislabel products at certain supply chain locations (e.g., port versus restaurant) are likely to differ depending on the product (e.g., Atlantic Bluefin Tuna versus Pacific salmon), suggesting that multi-species, study-level analyses could mask important patterns (Cline, 2012; Gordoa et al., 2017). Where mislabeling is occurring is an important unanswered question, and it is likely influencing any potential natural system impacts of seafood fraud. Products that are mislabeled at sea or port-of-entry are more likely to manifest into population-level impacts of substitute species, particularly if it is poorly managed, for a variety of potential reasons (e.g., over-quota harvesting, under-size harvesting, and under-reporting catch). High-effort studies that focus on specific products in specific countries across the entire supply chain should be a priority and could reveal important insights into seafood fraud.

Like supply chain location, current evidence suggests there are no differences in mislabeling estimates with respect to form, at least globally and when pooled across all seafood products. Estimates and their uncertainty are similar, and all forms are likely overestimated with the naive mean. Studies focused on sushi have varied widely, with mode mislabeling rates ranging from 3 to 90% (Armani et al., 2017; Fuller, 2007; Khaksar et al., 2015b; Lowenstein et al., 2009; Stern et al., 2017; Vandamme et al., 2016; Willette et al., 2017). Some researchers have observed and hypothesized that processed products (e.g., smoked, canned) are mislabeled more frequently than other forms, while others have observed no differences (Bréchon et al., 2016; Carvalho et al., 2017b; Miller and Mariani, 2010; Muñoz-Colmenero et al., 2016). We hypothesize the difference across product forms may exist, but are being masked due to multiple seafood products, along with high levels of under-sampling. Greater effort using probabilistic sampling and targeting specific products could reveal such differences.

There is currently little evidence that overall mislabeling rates differ by country. Additional sampling might prove otherwise, which could reduce the uncertainty of estimates. Further, additional sampling targeting products of interest (e.g., products with high consumption or mislabeling rates) could reveal important insights. Mislabeling estimates for countries with progressive traceability regulations (i.e., superior; Italy and United Kingdom) do not differ from the United States and Brazil, whose regulations are considered average, at least when viewed across all studies and products (Charlebois et al., 2014). Some have claimed that progressive seafood regulations, along with media and outreach, are contributing to a reduction in seafood mislabeling in European Union (EU) countries (Mariani et al., 2015; Warner et al., 2016). These claims, however, were made without any statistical analysis and lack any measures of uncertainty. In contrast, some policy analysis have concluded that EU seafood controls are non-effective due to flaws in policy design, such as a decentralized catch verification system and the lack of unique identifiers for products at the lot level (Borit and Santos, 2015; Hosch, 2016). When we estimate annual mislabeling rates for the European Union (2006–2015), there is not any statistical evidence of a decline after 2010—when the new EU regulations were implemented (Fig. SM7). The impact of seafood labeling and traceability regulations on mislabeling remains unknown. Similar to how many governmental import inspection programs (e.g., US Compliance Measurement Program) are insufficient in effort to undercover many types of seafood fraud (GAO, 2009), any effort to properly measure regulatory impacts on mislabeling through time and space will require in-depth, targeted, and high-effort investigations.

4.4. Taxonomic mislabeling estimates

Family-level estimates provide some insights into characterizing seafood mislabeling. The seabass and snapper families have relative high and uncertain mislabeling rates, which is driven by the mislabeling of groupers and snappers, respectively. While documented mislabeling for both families is most frequent in the United States, it occurs across seven countries—suggesting that these two families are vulnerable to mislabeling globally (Armani et al., 2016; Asensio et al., 2008; Carvalho et al., 2017a; Cawthorn et al., 2015; Cox et al., 2013; Cutarelli et al., 2014; Di Pinto et al., 2015; European Comission, 2015; FDA, 2013; Filonzi et al., 2010; Guardone et al., 2017; Nagalakshmi et al., 2016; Nolhgran and Tomalin, 2006; Staffen et al., 2017; Vandamme et al., 2016; von der Heyden et al., 2010; Warner et al., 2013; Wong and Hanner, 2008). Other families have relatively low mislabeling rates

Table 1
Characteristics of expected species that have relatively high global mislabeling rates. The posterior mode mislabeling rate is shown, along with the dominant substitutes, global production (2016 in thousands of tonnes; FAO, 2016), and the main geographies where mislabeling has been documented according the compiled database. Pacific salmon production includes Chinook, Chum, Coho, Sockeye, and Pacific salmons (nei).

Expected species	Mislabeling rate	Dominant substitutes	Global production	Geographic scope of mislabeling
Northern Red Snapper (*Lutjanus campechanus*)	74%	Other Lutjanidae snappers; Aquaculture species	N/A	USA
European hake (*Merluccius merluccius*)	40%	Other Merluccid hakes	142	EU
Common Sole (*Solea solea*)	20%	Other soles (Soleidae) species, Aquaculture species	32	EU
Albacore (*Thunnus alalunga*)	17%	Other Scombridae tunas	208	EU, USA, ZAF
Pacific salmon (*Oncorhynchus* spp.)	17%	Aquaculture Salmonidae species (Atlantic Salmon, Rainbow Trout)	655	CAN, USA
Atlantic Cod (*Gadus morhua*)	11%	Other Gadidae species (Haddock, Pacific Cod, Saithe, Alaska Pollock)	1329	BRA, CAN, EU, USA

(e.g., < 10%). Some of these families include products that are often substitute species, and thus, the low rates are not surprising, such as lower-valued aquaculture species like Tilapia (Cichlids) and Striped Catfish (Shark Catfish). Yet, other families with low mislabeling rates include higher-value products that are commonly sampled for mislabeling, such as the swordfish and dolphinfishes families. Family-level estimates, however, do have limitations with respect to characterizing seafood mislabeling because product-level patterns can be masked. The salmonid (Salmonidae) family, for example, has a relatively low mislabeling rate (8%); however, Pacific salmon species (*Oncorhynchus* spp.) are mislabeled at a higher rate, while aquaculture salmonid products are often substitutes (i.e., Atlantic Salmon and Rainbow Trout).

Product mislabeling estimates, and their uncertainty, are the most useful for characterizing seafood fraud. Our results suggest that many seafood products have relatively lower global mislabeling rates than commonly reported, much lower than the study-level mode (24%) and often much lower than the naive mean. More than half of the 28 products have estimates of ≤5%. This includes products that are common substitute species (e.g., Atlantic Salmon and Alaska Pollock), but also includes species that are considered priorities within mislabeling policies, such as Swordfish under the U.S. Seafood Import Monitoring Program (Department of Commerce, 2016). Products with relatively low mislabeling estimates are as informative as products with high rates with respect to informing policies and programs to reduce seafood fraud. For example, traceability systems come at a cost to governments and producers, and can pose a significant burden to small producers (Kher et al., 2010). For products with low mislabeling rates (and uncertainty), the costs of implementing a traceability program may outweigh the potential benefits, especially given the limited resources available for enforcement (Friedman, 2017; Wagner, 2015). Importantly, mislabeling rates must be viewed through the lens of production in order to gauge their importance and potential socio-ecological impacts (Kroetz et al., 2018). For example, a product with relatively low mislabeling rate but high production could be precipitating greater impacts compared to a species with a higher mislabeling rate, but low production.

Products with relatively high mislabeling rates provide insights into seafood fraud, particularly when coupled with additional data (Table 1). Northern Red Snapper was one of the first products for which mislabeling was documented, and subsequently has been relatively well-studied (Cawthorn and Mariani, 2017; Cawthorn et al., 2018; Grogran, 1988, 1989). It is commonly mislabeled by other snapper species belonging to the same family, followed by farmed Tilapia (*Oreochromis spp*). Mislabeling has been documented largely within the United States (but see Cawthorn et al., 2018). For this species, uncovering specific patterns of mislabeling is particularly challenging because trade data and labeling policies lack sufficient taxonomic granularity (Cawthorn and Mariani, 2017; Cawthorn et al., 2018). Similarly, Common Sole is most commonly mislabeled by other species of sole (e.g., Sengealese and Lemon Sole) and farmed Striped Catfish. Evidence for Common Sole mislabeling is restricted to the European Union, as is European Hake, which is most commonly mislabeled by other wild-caught species of hakes (e.g., Argentine Hake, Deep-water Cape Hake). While the Albacore mislabeling rate is less than the above-mentioned species, its global production is greater—raising the point that the amount of mislabeled seafood consumed is influenced by production (Kroetz et al., 2018). This point is particularly illustrated with Atlantic Cod (Table 1). Our estimated mislabeling rates for specific seafood products can allow for the construction of mislabeling profiles by combining them with other types of data, which is likely necessary to uncover product-specific patterns of mislabeling that are needed to explore the incentives, causes, and consequences of seafood mislabeling, which are likely to differ drastically by product (Donlan and Luque, 2019). These characteristics in combination (e.g., productions, substitutes, geographic scope) will be necessary to design targeted and cost-effective solutions to reduce mislabeling.

Our analysis revealed important seafood products where data is severely lacking with respect to mislabeling. For example, only nine studies have sampled the shrimp family (Penaeidae). Yet, global shrimp production in 2016 was 8.6 million tonnes (FAO, 2018). This includes a single sample from a single study from the United States, where shrimp is one the most consumed seafood products (Khaksar et al., 2015a; NMFS, 2016).[4] In fact, we were unable to estimate mislabeling rates for any invertebrates species. Yet, mislabeling for high-value invertebrate species has been documented, such as various species of lobster, squid, octopus, abalone, cuttlefish, shrimp, and crab (Aranceta-Garza et al., 2011; Armani et al., 2015; Cawthorn and Hoffman, 2017b; Guardone et al., 2017; Nicole et al., 2012; Warner et al., 2014; Warner et al., 2015). While the overall mislabeling rate for invertebrates appears similar to fish, data is currently insufficient to produce useful estimate global rates for specific invertebrate seafood products.

4.5. Conclusions and recommendations

Given the global nature of seafood markets and supply chains, the results of our global meta-analysis provide a first step into the characterization of mislabeling. Important geographic and taxonomic gaps exist in terms of characterizing seafood fraud. Study-level rates and naive means are sometimes overestimating the true extent of seafood mislabeling and are likely masking important product-level information and patterns. For most products for which there is sufficient data, mislabeling rates are below the global study-level estimate of 24%, with the majority much lower. When including only products that have been sampled sufficiently, the global mislabeling rate is 8% (95% HDI: 4–14%), which is a more appropriate estimate given the current data

[4] An unpublished report also sampled shrimp (n = 143 samples) in the United States (Warner et al., 2014). While mislabeling was documented, we were unable to extract the information needed to include it in our meta-analysis.

Box 1
Some research recommendations to improve the ability to estimate and characterize seafood mislabeling rates.

- Study-level and naive means without measures of uncertainty, particularly from studies that include multiple species, are of limited utility and will often overestimate true mislabeling rates. More focus on products of concern, particularly in specific settings, are likely to be more insightful.
- Convenience sampling should be avoided if possible. Probabilistic sampling strategies that take into account products and venues will result in estimates with more utility and generalizability.
- Tools such as power analyses can inform sampling strategies, as well as any monitoring effort interested in detecting changes in mislabeling through time and space. Attention a priori to how seafood is sampled can help avoid under sampling, increase the ability to detect differences, and maximize the value of mislabeling studies.
- High-effort studies that focus on specific products in specific countries across the entire supply chain should be a priority and could reveal important insights into seafood fraud. This is particularly true for invertebrates and wholesale venues, which are both major information gaps for seafood mislabeling.
- While important, product mislabeling estimates alone cannot inform solutions to reduce seafood fraud. Rather, estimates must be combined with other data (e.g., production and prices) in order to understand the extent of mislabeling, as well as the potential causes and consequences.

and the presence of widespread under sampling. Importantly, several products have higher mislabeling rates and should be priorities for research and interventions.

The majority of mislabeling studies have under-sampled seafood products and have not sampled probabilistically. Both issues are understandable given the goal of many mislabeling studies is to develop and test forensic tools. Yet, these issues present challenges with respect to producing useful estimates of mislabeling rates, which are needed to understand seafood fraud. Research that targets certain products and supply chain locations with high-levels of effort are likely to produce the most useful information (e.g., Bréchon et al., 2016; Gordoa et al., 2017). While useful as a rapid assessment, studies with low-effort sampling regime across many species are of little utility with respect to estimating true rates (e.g., five samples of ten different products). Targeted mislabeling research with more attention to sampling design will improve our understanding of seafood fraud. But, in order to begin to document its causes and consequences, mislabeling data must be combined with other data in order to provide a systems perspective. We suggest a number of broad research recommendations that will help improve mislabeling estimates, which are a challenging, but critical factor, in informing programs and policies to reduce seafood fraud (Box 1).

There has been little theoretical or empirical work on the potential impacts of seafood mislabeling (however, see Ugochukwu et al., 2015). A variety of impacts are possible, including socio-economic, human health, and natural system impacts (Cohen et al., 2009; Doukakis et al., 2012b; Gordoa et al., 2017; Lowenstein et al., 2010; Naaum et al., 2016; Palmeira et al., 2013). Yet, evidence for impacts are largely anecdotal, and the scale and scope of different types of impacts remain unknown. Estimating natural system impacts will require integrating mislabeling and substitution rates with fisheries management and production data. It is the substitute species, not the expected species, that is likely to be important in most cases. For example, it is the substitutes that are responsible for any potential human health impacts or could be suffering from over-harvesting, in the case of capture fisheries, driven by the opportunity to mislabel. Some common substitutes are aquaculture products, such as Striped Catfish, Atlantic Salmon, and Tilapia. While some impacts from aquaculture are well documented and have been shown to be geographically variable (Burridge et al., 2010; Ford and Myers, 2008), the net environmental impact of aquaculture substitutes in seafood fraud is unknown. In cases where a lesser-value product is labeled as a higher-value one, market and consumer impacts are possible (Cline, 2012; Doukakis et al., 2012a; Gordoa et al., 2017). But, other incentives and drivers of mislabeling are likely playing equally important roles (market access; accidental; regulation avoidance; Donlan and Luque, 2019). The prevalence of these multiple incentives and drivers remain unknown. Global mislabeling estimates (and their uncertainty) of taxonomic and non-taxonomic factors provide a foundation for prioritizing more research to inform programs and policies to reduce seafood fraud.

Acknowledgments

This work was supported by the Paul M. Angell Family Foundation. We thank K. Kroetz, V. Ruiz-Gutierrez, and C. Wilcox for input and feedback on the manuscript, including statistical analyses. We also thank two anonymous reviewers for their input, and J. Kruschke for his insights and scripts on Bayesian analyses.

Declaration of interest statement

None.

Appendix A. Supplementary data and analyes

Supplementary data to this article can be found online at https://doi.org/10.1016/j.biocon.2019.04.006.

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