

Supplementary Information to
A trait collection of marine fish species from North Atlantic and Northeast Pacific continental shelf seas

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Background and summary

This dataset containing traits of marine fish is based on fish taxa observed during international scientific bottom-trawl surveys regularly conducted in the Northeast Atlantic, Northwest Atlantic and the Northeast Pacific. These scientific surveys target primarily demersal (bottom-dwelling) fish species, but pelagic species are also regularly recorded. The overarching aim of this dataset was to collect information on ecological traits for as many fish taxa as possible and to find area-specific trait values in order to account for intraspecific variation in traits, especially for widely distributed species. We collected traits for species, genera and families. The majority of trait values were sourced from FishBase (Froese and Pauly, 2019), and have been supplemented with values from primary literature.

Spatial coverage

The bottom-trawl surveys are performed on and along the continental shelves of the U.S. and Europe, including southern Greenland (Figure 1, Table 1). To collect area-specific trait information, we made use of the division of the world oceans into Large Marine Ecosystems (LMEs; <http://lme.edc.uri.edu/>) and FAO fishing areas (<http://www.fao.org/fishery/area/search/en>). The dataset covers 22 LMEs (Table 2) and 7 FAO areas (Table 3).

Taxonomic coverage

This data includes 1702 unique species, 801 genera, and 236 families occurring across LMEs and FAO areas, resulting in 6216 different taxa with their assigned geographic information. The collection of traits provided here is not complete. The missing information per trait and taxa is further detailed in the sections below.

Traits

We collected information on 14 traits of marine fish, among which 9 are continuous and 5 are categorical traits (Table 4). Trait information was collected by extracting trait values from an offline version of FishBase from 2015, followed by supplementing missing information with values from primary literature and the most recent version of FishBase (Froese and Pauly, 2019); or by inferring values from closely related species (within genus or family) when no trait information could be found in the literature. Each trait and the trait extraction procedure are described in more detail below. Figure 2 and Table 5 provide information on the number of trait categories per taxonomic group for the categorical traits, whereas Tables 6 and 7 demonstrate some summary statistics for the continuous traits and the availability of trait values per taxonomic group.

Maximum length

Maximum length is the maximum recorded body size in cm. The majority of measurements measure total body length (TL), i.e. from snout to tail. Other types of measurements are standard length (SL; from snout to posterior end of the last vertebra), width of disc (WD; for skates and rays) or fork length (FL; from snout to end of middle caudal fin rays). In other cases, the type of measurement of not given (NG) or is of another type (OT).

Maximum length was extracted from the FishBase table ‘Age/Size’ (Binohlan and Pauly 2000a¹) and from the species page shown on the web version of FishBase (under the heading ‘Length at first maturity / Size / Weight / Age’). Values from the ‘Age/Size’ table were preferred over the ones from the species page, since they are provided with a location specifying where the measurement was taken. Missing values were then supplemented by the ‘Species’ table, values from primary literature, or inferred from genus or family.

Table 1: Bottom-trawl surveys used to collect fish species for which traits were collected. Source of the data and information on the survey are given, if available, in the last two columns.

Survey	Area	Source	Reference
AI	Aleutian Islands	(Batt, 2015)	(Alaska Fisheries Science Center, 2019)
EBS	Eastern Bering Sea Shelf	(Batt, 2015)	(Alaska Fisheries Science Center, 2019)
EVHOE	Bay of Biscay & Celtic Sea	(ICES, 2018)	(ICES, 1997)
FR-CGFS	English channel	(ICES, 2018)	(ICES, 2017)
FR-MEDITS	French Mediterranean coast	(IFREMER, 2018)	(MEDITS Working Group, 2012)
GMEX	Gulf of Mexico	(Batt, 2015)	(Gulf States Marine Fisheries Commission, 2015)
GOA	Gulf of Alaska	(Batt, 2015)	(Alaska Fisheries Science Center, 2019)
Gre-GFS	Greenland	H. Fock	(Fock, 2008)
Ice-GFS	Iceland	J. Sólmundsson	(Sólmundsson <i>et al.</i> , 2010)
IE-IGFS	Ireland Shelf Sea	(ICES, 2018)	(ICES, 2017)
NEUS	North East US	(Batt, 2015)	(Northeast Fisheries Science Center, 2018)
NI-GFS	Irish Sea - Ireland	(ICES, 2018)	(ICES, 2017)
NorBTS	Norwegian Sea, Barents Sea and northern North Sea	(Djupevåg, 2018)	(Mjanger <i>et al.</i> , 2006, 2017)
NS-IBTS	North Sea	(ICES, 2018)	(ICES, 2015)
PT-IBTS	Portugal Shelf Sea	(ICES, 2018)	(ICES, 2017)
ROCKALL	Rockall plateau	(ICES, 2018)	(ICES, 2017)
SA	South East US	(Batt, 2015)	
SCS	Scotian Shelf	(Batt, 2015)	(Northeast Fisheries Science Center, 2018)
SP-NORTH	North of Spain	(ICES, 2018)	(ICES, 2017)
SWC-IBTS	Scotland Shelf Sea	(ICES, 2018)	(ICES, 2017)
WCANN	West Coast US	(Batt, 2015)	(Keller <i>et al.</i> , 2017)

¹ https://fishbase.ca/manual/English/fishbasethe_popchar_table.htm

Table 2: Overview of Large Marine Ecosystem (LME) numbers covered by the dataset and corresponding names.

LME number	LME name
1	East Bering Sea
2	Gulf of Alaska
3	California Current
5	Gulf of Mexico
6	Southeast U.S. Continental Shelf
7	Northeast U.S. Continental Shelf
8	Scotian Shelf
9	Newfoundland-Labrador Shelf
18	Canadian Eastern Arctic – West Greenland
19	Greenland Sea
20	Barents Sea
21	Norwegian Sea
22	North Sea
23	Baltic Sea
24	Celtic-Biscay Shelf
25	Iberian Coastal
26	Mediterranean
53	West Bering Sea
54	Northern Bering-Chukchi Seas
59	Iceland Shelf and Sea
60	Faroe Plateau
65	Aleutian Islands

Table 3: Overview of the FAO fishing areas covered by the dataset and their corresponding name

FAO number	FAO name
21	Northwest Atlantic
27	Northeast Atlantic
31	Western Central Atlantic
37	Mediterranean and Black Sea
61	Northwest Pacific
67	Northeast Pacific
77	Eastern Central Pacific

Trophic level

Trophic level represents a species' position in the food web. Two types of trophic level values were extracted from the 'Feeding' table, found under the 'Ecology' table on FishBase (Palomares 2000²). The trophic level calculated based on the 'Diet' table (Palomares and Sa-a 2000³) was preferred over the 'Food items' table (Sa-a et al. 2000⁴), because the 'Diet' table includes information on the proportion of prey items. Data from the 'Food items' table was chosen when information from the 'Diet' was not available.

² https://fishbase.ca/manual/English/fishbasethe_ecology_table.htm

³ https://fishbase.ca/manual/English/fishbasethe_diet_table.htm

⁴ https://fishbase.ca/manual/English/fishbasethe_food_items_table.htm

Age at maturity

Age at maturity is the age at which 50% of the population is mature. In cases where this value was not available, other types of maturity estimates were used, e.g. the lowest reported age at which a mature individual has been found. Values were extracted from the ‘Maturity’ table (Binohlan 2000⁵), which provides a single value and/or a range of ages, for which an average was then calculated. Missing values for age at maturity have been supplemented with values from literature.

Maximum age

Maximum age is the maximum reported age in years. Values were extracted from the FishBase table ‘Age/Size’ and from the species page of the web version of FishBase (under the heading ‘Length at first maturity / Size / Weight / Age’). Values from the ‘Age/Size’ table were preferred over the ones from the species page, since they are provided with a location of where the measurement was taken. Missing values were supplemented by values from primary literature or inferred from genus or family.

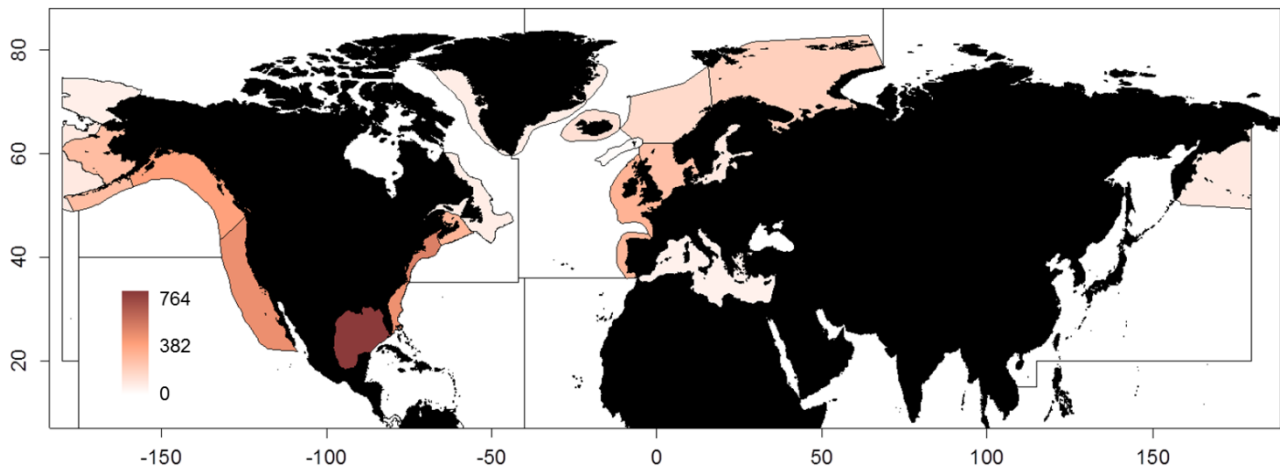


Figure 1: Global map with the number of taxa included in the trait database in each Large Marine Ecosystem (LME). The major fishing FAO areas are also indicated.

Von Bertalanffy growth coefficient K

The growth coefficient K (1/year) is a parameter in the Von Bertalanffy growth equation, describing how fast an individual reaches its asymptotic size (i.e., length infinity). Values were extracted from the FishBase table ‘Growth’ (Binohlan and Pauly 2000b⁶).

Length infinity

Length infinity (cm) is a parameter in the Von Bertalanffy growth equation and represents the maximum asymptotic size an individual can reach. Values were extracted from the FishBase table ‘Growth’.

⁵ https://fishbase.ca/manual/English/fishbasethe_maturity_table.htm

⁶ https://fishbase.ca/manual/English/fishbasethe_popgrowth_table.htm

Table 4: The traits included in the dataset classified as either continuous or categorical traits.

Continuous traits	Categorical traits
Trophic level	Habitat
Caudal fin aspect ratio	Feeding Mode
Offspring size (mm)	Body Shape
Age at maturity (year)	Caudal Fin Shape
Fecundity (number of eggs or offspring produced per year by female)	Spawning Type
Length infinity (cm)	
Von Bertalanffy growth coefficient K (1/year)	
Maximum length (cm)	
Maximum age (year)	

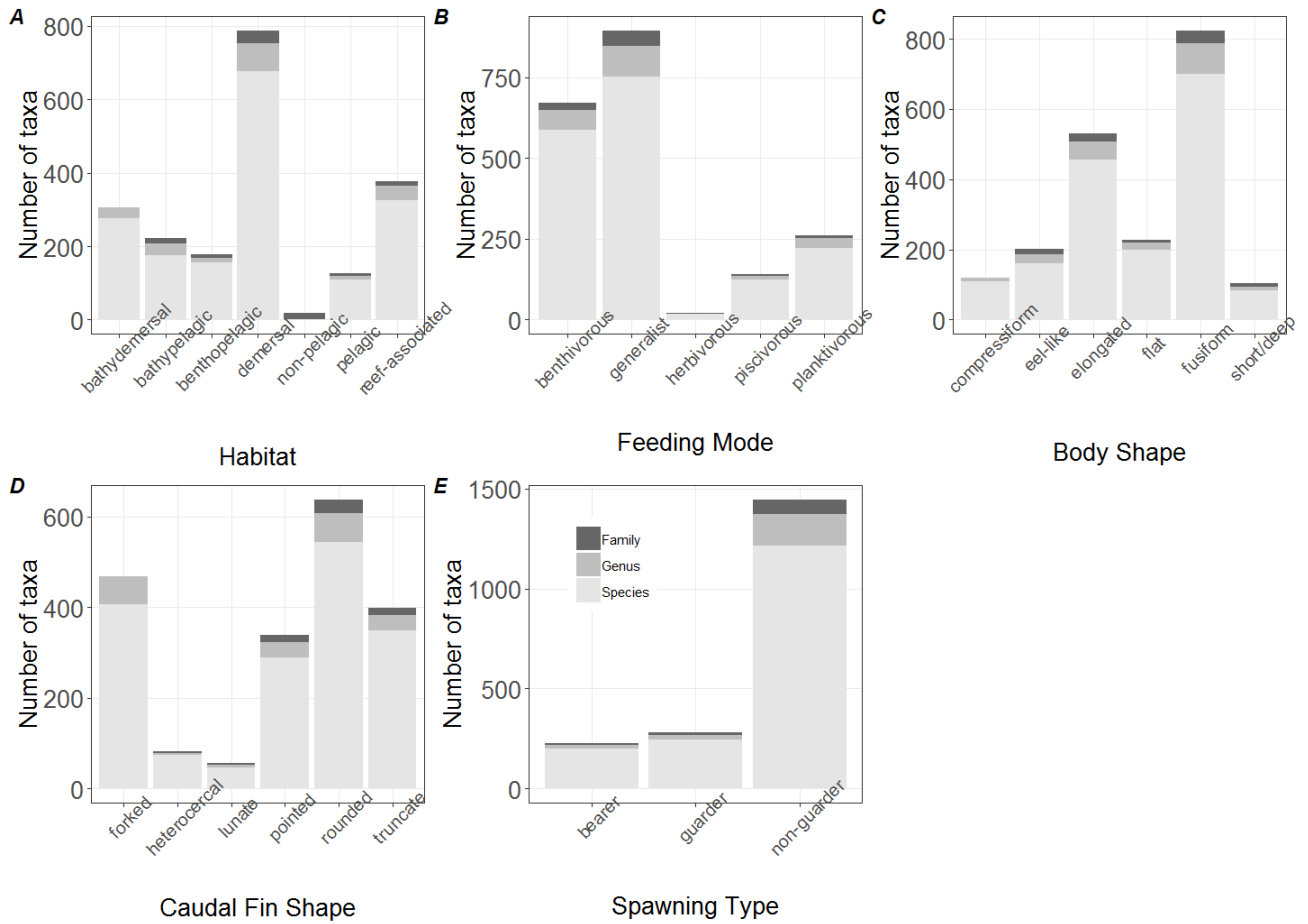


Figure 2: Distribution of the number of taxa for each categorical trait. A) Species habitat, B) Feeding mode, C) Body shape, D) Caudal fin shape, E) Spawning Type. Colors indicate the taxonomic level at which the trait value was assigned.

Table 5: Number of trait values available and not available (separated by a dash) for each categorical trait and taxonomic level ($n_{Family} = 347$, $n_{Genus} = 402$, $n_{Species} = 5467$)

	Habitat	Feeding mode	Body shape	Caudal fin shape	Spawning type
Family	347/0	286/61	347/0	347/0	323/24
Genus	402/0	400/2	402/0	402/0	387/15
Species	5467/0	5454/13	5467/0	5467/0	5337/130

Table 6: Summary statistics of continuous traits

Continuous trait	Minimum value	Mean value	Maximum value
Trophic level	2.00	3.67	4.65
Aspect ratio	0.08	1.39	7.05
Offspring size	0.05	24.30	1750
Age at maturity	0.20	4.54	156
Fecundity	1	132,000	300,000,000
Length infinity	2.50	57.13	1000
Growth coefficient	0.01	0.33	5.90
Maximum length	1.40	57.39	1000
Maximum age	0.30	18.00	392

Table 7: Number of trait values available and not available (separated by a dash) for each continuous trait and taxonomic level ($n_{Family} = 347$, $n_{Genus} = 402$, $n_{Species} = 5467$)

	Trophic level	Aspect ratio	Offspring size	Age at Maturity	Fecundity	Length infinity	Growth coefficient	Maximum length	Maximum age
Family	337/10	299/48	324/23	284/63	317/30	331/16	331/16	347/0	299/48
Genus	401/1	352/50	384/18	339/84	375/27	387/15	387/15	402/0	360/42
Species	5462/5	4712/755	5223/244	4890/577	5122/345	5204/263	5213/254	5467/0	5014/453

Fecundity

Fecundity is the number of eggs or offspring a female produces per year (if spawning only once) or per batch (if spawning multiple times per year). Due to limited knowledge for many species on whether they are batch spawners or not, fecundity values per batch have not been corrected to reflect the total fecundity per year.

The 'Spawning' table of FishBase (Torres 2000a⁷) provides both the absolute and relative fecundity, the latter being fecundity relative to body size. Since relative fecundity is only rarely available, absolute fecundity was chosen. When both a minimum and maximum fecundity was reported, the mean value was calculated.

Missing values were searched for in primary literature, as well as on the FishBase website under the headings 'Biology' and 'Life cycle and mating behaviour'. If unavailable, values were inferred from the genus or family.

Offspring size

Offspring size (mm) represents the egg diameter for fish, length of egg case for skates and rays or body length of a new-born pup for sharks. Values were extracted from the 'Eggs' table of FishBase (Froese 2000⁸). Missing values were searched for in primary literature, as well as on the FishBase website under the headings 'Biology' and 'Life cycle and mating behaviour'. If unavailable, values were inferred from the genus or family.

Caudal fin aspect ratio

The caudal fin aspect ratio is the squared height of the caudal fin divided by the surface area of the caudal fin. It is known to correlate with fish swimming speed, activity, metabolism and food consumption (Pauly, 1989; Sambilay, 1990).

Values were extracted from the 'Morphology' table (Froese and Reyes 2000⁹). Missing values were not supplemented with values from primary literature.

Feeding mode

Feeding mode is the type of food consumed and reflects species diet, categorized as: herbivorous (feeding on algae), benthivorous (feeding on benthos), planktivorous (feeding on plankton), piscivorous (feeding on fish) or generalist (feeding on two or more types of food, assigned when the major food type comprised no more than approximately two-thirds of the diet).

Feeding modes were assigned consulting the feeding type and feeding habit from the 'Ecology' table and the 'Diet' table of FishBase.

Body shape

Information on the lateral body shape and cross section of fish was extracted from the 'Morphology' table of FishBase. Based on these two descriptors, the following six body shape

⁷ https://fishbase.ca/manual/English/fishbasethe_spawning_table.htm

⁸ https://fishbase.ca/manual/English/fishbasethe_eggs_table.htm

⁹ https://fishbase.ca/manual/English/fishbasethe_morphology_table.htm

categories reflecting the most striking feature (either lateral or cross-sectional): fusiform (or: normal), elongated, eel-like, flat, short and/or deep and compressiform (Figure 3).

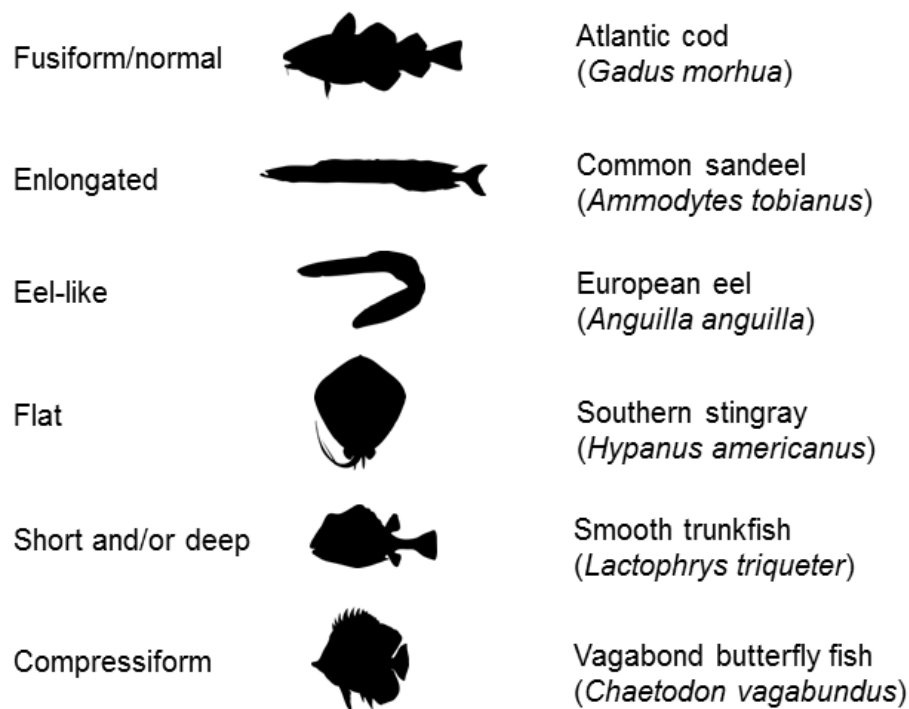


Figure 3: Body shape of fish according to six categories with species examples of each category. Pictures from www.phylopic.org under a Creative Commons Public Domain Dedication 1.0 License

Caudal fin shape

Similar to the aspect ratio, the caudal fin shape reflects differences in the mode and behaviour of swimming and locomotion. Information on the caudal fin shape was extracted from the ‘Morphology’ table of FishBase. The categories from FishBase were slightly adapted to the following six categories: forked, rounded, (more or less) truncated, lunate, pointed and heterocercal (Figure 4).

Spawning type

Spawning type reflects the reproductive guild of fish and the amount of parental care. Information was extracted from the ‘Reproduction’ table of FishBase (Torres 2000b¹⁰). We aggregated all the categories from FishBase into three categories following (Balon, 1990): ‘non-guarder’ that includes spawning in open water, on substratum and brood-hiders, ‘guarder’ that includes clutch tenders and nesters, and ‘bearer’ that includes external brooders and internal live bearers.

Habitat

The habitat trait informs the position of a fish in the water column. Information was extracted from the ‘Ecology’ table of FishBase and from the depth distribution of species on the website of the

¹⁰ https://fishbase.ca/manual/English/fishbasethe_reproduction_table.htm

Ocean Biogeographic Information System (OBIS; <http://www.iobis.org/>). Categories were classified as follows: pelagic, bathypelagic, demersal, bathydemersal, benthopelagic, reef-associated and non-pelagic. Bathypelagic and bathydemersal fish are either pelagic or demersal fish that occur in waters deeper than the continental shelf. Benthopelagic fish are those that are commonly found in both the pelagic zone and close to the bottom. Fish were classified as non-pelagic when they were clearly not pelagic but it was not possible to distinguish between demersal, bathydemersal, benthopelagic or reef-associated.

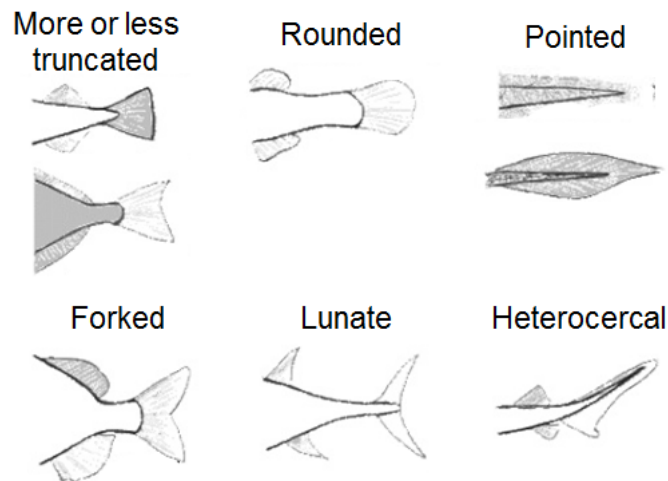


Figure 4: Caudal fin shape categories. Figure redrawn from <https://www.slideshare.net/skyearth/fish-morphology-75412494>.

Trait extraction procedure

A Microsoft Access database version of FishBase was provided by M.L. Deng Palomares. The Access database stores, whenever available, information on the location of where the trait value was measured or estimated. We assigned all taxa from the bottom-trawl survey data to the LME and FAO fishing area where they were sampled. Taxa were either recorded at the species, genus or family level.

Species trait values for continuous traits were extracted from the Access database as follows:

- 1.1 Extract the trait value from the LME that corresponds to the area where the species was recorded, and calculate an average value in the cases where multiple trait values are available.
- 1.2 If unavailable, extract the trait value from the FAO area where the species was recorded, and calculate an average value in the cases where multiple trait values are available.
- 1.3 If unavailable, extract the trait value from any ocean basin, and calculate an average value in the cases where multiple trait values are available.
- 1.4 If unavailable, extract the trait value without geographic information.
- 1.5 If unavailable, calculate the average trait value based on all other species in FishBase from the genus that the species belongs to, and that are also present in the LME where the species has been recorded.

- 1.6 If unavailable, calculate the average trait value based on all other species in FishBase from the genus that the species belongs to, and that are also present in the FAO area where the species has been recorded.
- 1.7 If unavailable, calculate the average trait value based on all other species in FishBase from the genus that the species belongs to, and that are also present in any ocean basin where the species has been recorded.
- 1.8 If unavailable, extract the trait value without geographic information.
- 1.9 If unavailable, repeat steps 1.5-1.8 above by calculating average trait values based on other species that are members of the same family as the species recorded.

When the taxon of interest was specified at the genus or family level, steps 1.4-1.9 were followed. For categorical traits where no information on the location of origin of the trait category was available the following procedure was followed:

- 2.1 Extract the trait value for the species.
- 2.2 If unavailable, extract the trait value from members of the same genus.
- 2.3 If unavailable, extract the trait value from members of the same family.

Missing trait values

When all previous steps 1.1-1.9 for continuous traits or 2.1-2.3 for categorical traits led to no trait data, we searched for missing trait values in primary literature, preferably for the species of interest, but if unavailable, a trait value was taken from a species that belongs to the same genus or family. If a value was found for a species and, at the same time, another member of the same genus was assigned a family-level value from FishBase, we replaced this value by the species-specific value of the other species of the same genus. In other words, genus-level values were preferred for species or genera over family-level values.

While searching for trait values in primary literature, we did not attempt to find LME or FAO-specific values. One exception is the high-quality trait dataset by Wiedmann *et al.* (2014), that contains trait values specifically for Barents Sea.

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