Supplement 1

The Arctic Traits Database was originally designed as an interactive tool for benthologists working in the field of (arctic) trait-based ecology, in order to facilitate the exchange and the discussion of biological trait information within the community. The final goal is to provide sound and easy accessible trait information to the entire

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scientific community. While trait information that is added to the database is immediately visible and accessible online via the public page (http://www.univie.ac.at/arctictraits/), the restricted, interactive area of the database offers several benefits solely to the registered user:

- 1) A well-structured and user-friendly interface to get trait information organized and obligatory linked to source information and to taxonomy (via the World Register of Marine Species, WoRMS).
- 2) A working environment that facilitates knowledge exchange and discussion among collaborators.
- 3) Additional options to inspect, organize, and analyze the entire dataset included in the database.
- 4) Traceable credit, as every collaborator is listed as board member on the public page and right after every trait entry performed.

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The following manual for registered users explains in detail and via screenshots how species and trait information can be entered in the Arctic Traits Database. It is also provided in the "About" section of the Arctic Traits Database (via the public access).

20 Database manual for registered users

- 1. Login
- 2. Getting started
 - 2.1. The top menu bar
- 3. Adding taxa to the Arctic Traits Database
 - 3.1. Manual entry of taxa
 - 3.2. AphiaID batch entry
- 4. Dataset management
- 5. Adding trait and source information

1 Login

30 Once a user entry is received from the editor, the restricted area of the database can be accessed via the "Login" button on the public page (Fig. S1).

* * *	*			data ei	ntry interfac	e - login
I	About	▼ Da	ata per taxon 🔻	Trait definitions	Download data 🔻 🚺	Login
user:						
pass:						
login						

Fig. S1. User entry interface.

35 2 Getting started

After signing in the user is transferred to a starting page with a top menu bar of seven headers (Fig. S2, Table S1). In addition, an alphabetic list of all taxa in the database is displayed (grouped in species/genus/family level taxa). The taxon list can be filtered for datasets (see Sect. 4) or phyla. Each taxon name links directly to the respective taxon page (see Sect. 5).

Species, genera & familie	es, alphabetically	
	The second se	
Display only taxa within the following dataset:	Display only taxa within the following phyl	
All datasets \$	All phyla 🗘	Apply filter
		urrently accepted taxon. Subjective (heterotypic) synonyms are dis
Objective (homotypic) synonyms and misspellings are normally and have their own taxon page but their curre		urrently accepted taxon. Subjective (heterotypic) synonyms are dis
		urrently accepted taxon. Subjective (heterotypic) synonyms are dis Family level taxa
normally and have their own taxon page but their curre	ently accepted name is displayed next to them.	
normally and have their own taxon page but their curre Species level taxa	ently accepted name is displayed next to them. Genus level taxa	Family level taxa

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Fig. S2. Clip of the starting page for registered users.

Header	Function			
Public site	Transfer back to the public page.			
Traits		aits included in the database. Each trait links	to all those taxa for	
		this specific trait are existing.		
Taxa	Taxa alphabetically	Alphabetic list of taxa, same than starting page.		
	Classification	Classification tree, branches can be expanded taxa selected.	l per mouse click and	
	Add new taxon	Manual entry of taxa (see 3.1).		
	Aphia batch entry	Batch entry of up to 50 taxa via their Aphia	IDs (see 3.2).	
References	List of references	Show total list of included sources (see Sect.	. 5).	
	Add new reference	Entry window for new reference or observation	ion (see Sect. 5).	
Statistics	My data	Overview of all entries of the respective user		
Tools	Dataset management	Add a new dataset.	see Sect. 5	
		Remove an existing dataset.	see Sect. 5	
		Add taxa to an existing dataset.	see Sect. 5	
		Remove taxa from an existing dataset.	see Sect. 5	
	Data with conflicts	Lists all taxa for which conflicts exist (see Se	ect. 5).	
Logout	Logs the user out of the	he system and leads back to the public site (Fig	. 1).	

Table S1. Brief summary of the options behind each header in the top menu bar

3 Adding taxa to the Arctic Traits Database

45 As trait information is always connected to specific taxa, in a first step the respective taxon (Sect. 3.1) or a whole list of taxa (Sect. 3.2) hast to be entered or uploaded. Optionally, the taxa can be organized into specific datasets, e.g. linking to a specific sampling campaign and location (see Sect. 4 "Dataset management").

3.1 Manual entry of taxa

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The system allows data entry at different taxonomic levels, from species to phylum. Via the "Taxa" dropdown in the top menu and "Add new taxon" (Fig. S3, Table S1) taxon names can be entered one by one manually. In that case, the system will query the World Register of Marine Species (WoRMS Editorial Board, 2018; http://www.marinespecies.org/) for the taxon, may correct for misspellings, and then enter the taxon and its higher classification automatically. In the event that taxon names have changed ("unaccepted" in worms), we recommend to stick to the original taxon name as information might end up attached to the wrong taxon if the classification

55 changes again at any point in the future. In the database synonyms are displayed and deep-linked to WoRMS in the taxonomic tree on the taxon page (Fig. S5). If the taxon is already included in the database, a message is displayed and the taxon is not entered, thus avoiding duplicates. The user can of course still add trait information to the already existing taxon.

Public site Traits Ta	axa 🔻 References	 Statistics 	Tools 🔻	Logout
	K			
Enter new taxon	N			
Enter taxon name:	1			
Got	5			

60 Fig. S3. Screenshot of the manual taxon entry.

3.2 AphiaID batch entry

Adding of multiple taxa at once is possible via the "AphiaID batch entry" function in the "Taxa" dropdown menu (Fig. 4). This function allows to enter up to 50 AphiaIDs at the same time. The system will query WoRMS for the taxa for these AphiaIDs and enter them automatically. In this case, the taxon names have first to be matched to

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taxa for these AphiaIDs and enter them automatically. In this case, the taxon names have first to be matched to WoRMS by the user (see taxon match tutorial at http://www.marinespecies.org). In the event that AphiaIDs have changed ("unaccepted" taxa in worms), we recommend to stick to the original AphiaID (see Sect. 3.1). Again, if a taxon is already included in the database, a message is displayed and the taxon is not entered.

Public site Traits	Taxa V References V Statistics V Tools V Logout
Enter new taxon	
Enter list of AphialDs (one Aphia ID per line	
Rease restrict your list to 50 Aphia IDs per	submission to avoid server problems. The data entry for 50 Aphia IDs can take several minutes.
124934 107315 124703 106674 124966 139710 138818 140579 558 124321 138823 124441 137683 124446 140584 1839 100716 246815 107323 1337	

70 Fig. S4. Screenshot of the AphiaID batch entry. The AphiaIDs can be entered simply via copy-paste.

4 Dataset management

In the "Tools" section taxa can be allocated to one or more specific datasets via the "dataset management" function. This can be done either to organize a user's working process, to ensure a certain degree of traceability to the original data source and to the region where the taxon was sampled, or to be able to export only pre-defined subsets of data. As one specific example, the echinoderm species *Crossaster papposus* is one of 350 taxa from a dataset

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named "RUSALCA 2012" provided by Jaqueline Grebmeier, sampled on the RUSALCA cruise 2012 (Grebmeier

et al. 2015). If another dataset is uploaded including *C. papposus*, the taxon is not entered again, but also the second dataset linked to the taxon. There is no limitation in the number of datasets to which a taxon can be linked. In case the connection of a taxon to a specific dataset is no longer desired, it can – again via the "dataset

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management" function – easily be removed from the dataset ("Remove taxa from an existing dataset"), or added to another ("Add taxa to an existing dataset"). In any case, the taxon or the trait information tied to this taxon is thereby not affected.

5 Adding trait and source information

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Once a taxon is added to the database, it has its own taxon page (Fig. S5) and trait information to each of the 20 traits and 85 trait categories can be added. Below the taxon (and author) name the taxonomic tree (derived from WoRMS) is displayed. The WoRMS logo (left of the taxon name) directly links to the WoRMS taxon page of – in this example – *C. papposus*. The 20 traits are highlighted in light grey color, indicating that so far, no trait information was entered for this taxon.

Public site Traits Taxa 🔻 References 🔻 Statistics 🔍 Tools 🔍 Logout
Top menu bar
Grossaster papposus (Linnaeus, 1767) Taxon & author Taxon & T
Biota (-) > Animalia (Kingdom) > Echinodermata (Phylum) > Asterozoa (Subphylum) > Asteroidea (Class) > Valvatacea (Superorder) > Valvatida (Order) > Solasteridae (Family) >
Crossaster (Genus)
Link to WoRMS taxon page
Morphology
Size
Weight (WM)
Body Form
Skeleton 20 traits
▶ Fragility
▶ Sociability
Life History
Reproduction
Larval development
▶ Longevity/Life Span
Behaviour
▶ Living habit
Adult movement
Mobility
Feeding Habit
Trophic Level
Substratum Afinity
Bioturbation
Tolerance
Environmental position
Depth Range
Zoogeography

Fig. S5. Screenshot of the taxon page of Crossaster papposus before trait information was entered.

The data in the database are organized in the format of taxon – trait – trait categories – fuzzy codes – references (Fig. S6). When moving the mouse cursor over a trait category (e.g. LD3 "benthic/direct" in Fig. S6), the trait definition is shown in a small window ("Larvae have benthic or direct development [no larval stage, eggs develop into miniature adults]"). For each trait category, a fuzzy value from 0 to 3 (see Sect. 2.4 of main text or the "About" section of the public page) can be checked per mouse click and must be supported by at least one reference. This guaranties that no trait information in the entire database is without a source information. In the example below (Fig. S6) two users checked the fuzzy code "3" and added references to the trait category LD2 ("pelagic/lecitotrophic"). Once information is added the color of the respective trait changes from light grey to

100 blue (after the page is reloaded).

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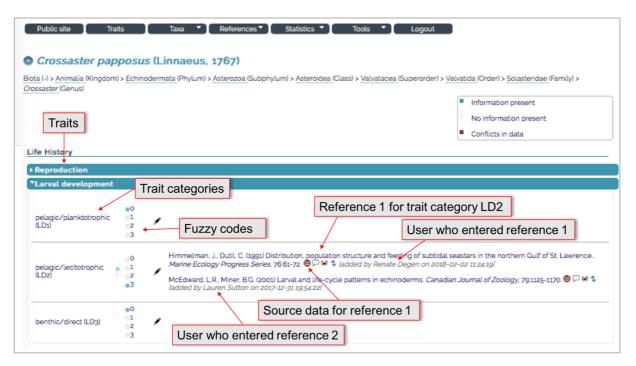


Fig. S6. Screenshot of the taxon page of the *Crossaster papposus*. Trait information for the trait "Larval development" was entered, and the trait is now highlighted in blue.

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The exact reference needs to be chosen from the database bibliography via a window that opens automatically once a fuzzy code is entered (Fig. S7, left). The search options are "author", "title", "year", "journal", "DOI", "url", and "other". The option "other" is included because trait information does not always stem from published literature, but from communication with experts. In such cases the name of the taxonomic expert that passed on the information can be entered in the "Enter new publication" window (Fig. S7, right). In such cases the

- 110 reference type "Other" needs to be selected. Also, the event of a "Personal observation", i.e. when the user personally observed or measured a certain trait, is included in the option "other". The "enter new publication" window is needed in any case when the respective reference (published or communicated) is not yet included in the database bibliography. Then the entire bibliographic information (reference type, authors, year, title, journal, ...) needs to be entered. The use of the "Lookup data from DOI" option speeds up the process, as then manual
- 115 entry is no longer required. Additional references can be added at any time via the "References" section in the top menu bar (Fig. S2, Table S1).

Choose a reference	Enter new publication
✓ author contains: [ken searcht] title year found? Enter it.	reference Journal Article :
DOI url other Viversity Press, Oxford. 800pp.	DOI Lookup data from DOI
 □ Hayward, PJ., Ryland, J.S., Taylor, PD. (1994) Biology and Palaeobiology of Bryozoans. Olsen & Olsen, Fredensborg. 240pp. □ Bell, L., Bluhm, B., Iken, K. (2016) Influence of terrestrial organic matter in marine food webs of the Beaufort Sea shelf and slope. Marine Ecology Progress Series, 550-1-24. □ Bluhm, B., Iken, K., Hardy, S.M., Sirenko, B., Holladay, B. (2009) Community structure of epibenthic megafauna in the Chukchi Sea. Aquatic Biology, 7269- 293. □ Divine, L., Iken, K., Bluhm, B. (2015) Regional benthic food web structure on 	authors enter authors in the form. 'lastname' year title
the Alaska Beaufort Sea shelf. <i>Marine Ecology Progress Series</i> , 53115-32. Divine, L.M., Bluhm, B.A., Mueter, F.J., Iken, K. (2017) Diet analysis of Alaska	journal volume
Arctic snow crabs (Chionoecetes opilio) using stomach contents and ð 13 C and ð 15 N stable isotopes. <i>Deep Sea Research Part II: Topical Studies in</i> <i>Oceanography</i> , 135124-136.	pages
Ren, K., Bluhm, B., Dunton, K. (2010) Benthic food-web structure under Enter data Cancel & close	urt

Fig. S7. Screenshots of the reference entry interface. Once a fuzzy code is entered, a reference has to be assigned from the bibliography (left), or a new reference has to be entered (right).

120 Once a reference is selected, the exact source information (raw data, quote of the text that led to the choice of the fuzzy value, table or page number) can be entered in another popup window via the "source" symbol (book icon, Table S6) (Fig. S8). This allows other users to understand which information led to the assignment of the taxon to a specific trait category. It also provides a means for quality control and for the re-using of the information in different contexts (Faulwetter et al. 2014). This is especially helpful if a specific research question might require different trait categories than those that have been chosen in the Arctic Traits Database. In the example in Fig. S8, text information from Lambert (2000), p. 77, is entered to support the coding of the trait category LD2 ("pelagic/lecitotrophic").

Pagination	77 //	
Raw data:	The lecitotrophic larvae settles to the bottom afer 18 days and attaches by a sucker.	

130 Fig. S8. Screenshot of the source entry window.

The **"comment"** symbol (speech bladder icon, Table S2) allows to add a personal comment to the entered trait information, or to the information entered by other users.

The "taxonomy" symbol (crab icon, Table S2) allows to copy or shift the trait information to another taxon, allowing for rapid entry of characteristics and references that are valid for several taxa. In general, the information is always assigned to the most specific taxon possible. As an example, the information "Crossaster papposus is a predator and scavenger" was assigned to C. papposus, while the information "most sea stars are

predators of attached or buried animals" is assigned to the class Asteroidea.

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The "move" symbol (two arrows icon, Table S2) allows to move or copy the entered trait information and reference to another trait category. This is useful when the quote is appropriate for several categories of one trait, to avoid repeating working steps and to save time. As one specific example, the quote "15-200 m" regarding the depth distribution of *Crossaster papposus* is appropriate for the first category in the trait "depth range" which is "shallow (DR1)", as well as for the second category which is "shelf (DR2)".

If data is entered for a taxon that has child taxa (i.e. on genus level or higher), also the "child taxa" symbol (down-looking arrow icon, Table S2) is visible. It allows to copy the entered fuzzy code, reference, detailed 145 trait information and comments to all child taxa (e.g. all members of the current family) of the specific taxon. This function has to be used very carefully, as - in case the copied information proved later to be wrong - potentially dozens of wrong entries have to be deleted manually.

Once a reference is entered, a "blue flag" symbol (Table S2) shows up next to the fuzzy codes (Fig. S6). If users disagree concerning the fuzzy coding or the underlying reference, the color of the flag can be changed to 150 red (Table S2) via mouse click, indicating a "conflict" (Fig. S10). The reason for the disagreement can be entered in a window, thus enabling a discussion among users (Fig. S11). A list of all data with conflicts can be accessed via the "tools" section in the top window (Fig. S2). Conflicts can only be resolved by the editor of the database after sound evaluation of the comments and suggestions by the users. In this event, the flag will then be changed back to blue. Unsolved conflicts will keep the red flag and the respective trait will not be included in the download in order to avoid transporting disputable information.

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Other conflicts may appear due to bias in entering data. Cases where a reference is present but all fuzzy codes are "0" will be marked by the "zero" symbol (Table S2). Cases where the entered fuzzy codes are conflicting (e.g. "3" is entered twice for one trait, or a "2" and a "3" are entered, see Sect. 2.4 in main text) will be marked by the "crash" symbol (meeting arrows icon, Table S2). Such conflicts can be filtered for from the total dataset in the "Tools" section and resolved by the editor or registered users.

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Table S2. Explanations of icons in the interface for registered users.

Symbol	Action/Interpretation	
	Source – original quote from reference, page number.	
	Comment – e.g. to explain your choice of coding (not mandatory).	
	Taxonomy – Move or copy trait information to other taxa.	
	Move or copy trait information to another trait or trait category.	
Å	Copy trait information to all child taxa.	
	Trait information is present and not conflicting	
	Conflict – disagreement among users.	
0	Conflict – All fuzzy codes are set to "0".	
	Conflict – Fuzzy codes are conflicting (e.g. codes "2" and "3" in one category)	

Once trait information and references have been entered, the appearance of the respective taxon page changes (Fig. S9). Registered users will see that traits where no information is currently present are highlighted in light grey, traits with information are highlighted in blue, and traits where any of the conflicts mentioned above exist are now highlighted in brown. Once a conflict is resolved, the color will change from brown to blue after the page is reloaded. The taxon page visible via the public access shows only those traits that have complete information in blue, while absent traits are highlighted in light grey and conflicts are not visible at all.

Public site Traits Taxa 🔻 References 🗨 Statis	stics 🔻 Tools 🔻 Logout
Ashalashasha maniasi/Caist Jacash (Ost)	
Aphelochaeta marioni (Saint-Joseph, 1894)	
Biota (-) > Animalia (Kingdom) > Annelida (Phylum) > Polychaeta (Class) > Sedentaria (Subclass) > Canalipalpata (Infra Cirratulidae (Family) > Aphelochaeta (Cenus)	class) > Terebellida (Order) > Cirratuliformia (Suborder) >
Ciriadadae y army > Abretocriaeta Genas	Information present
	No information present
	Conflicts in data
Morphology	
▶ Size	
Weight (WM)	
Body Form	
▶ Skeleton	
• Fragility	
• Sociability	
Life History	
Reproduction	
Larval development	
Longevity/Life Span	
Behaviour	
Living habit	
Adult movement	
Mobility	
Feeding Habit	
Trophic Level	
Substratum Affinity	
▶ Bioturbation	
Tolerance	
Environmental position	
Depth Range	
Zoogeography	

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Fig S9. Screenshot of the taxon page of the polychaete *Aphelochaeta marioni*. Eight traits contain information (highlighted blue), one conflict is indicated for the trait "Mobility" (highlighted in brown).

Mobility	
none (MO1)	 Polychaeta_IOPAN Project Webpage. http://www.iopan.gda.pl/projects/Polychaeta/ (20) / (added by Renate Degen on 2017-12-21 10:4131) 3
low (MO2)	 Morata, N., Michaud, E. (2013) Impact of early food input on the Arctic benthos activities during the polar night. Polar Biology, 38:99-114. Discrete Degen on 2018-04-16 15:14:08/
medium (MO3)	0 0 1 0 ² 0 ³
high (MO4)	● 0 0 1 2 3

Fig. S10. Detail on the conflicting trait "Mobility" in the polychaete *A. marioni*. The first literature reference led to the coding of 3 for the trait category "none (MO1)", the second reference led to a coding of 3 for the category "low (MO2)".

	univie.ac.at
	Flag for taxon 'Aphelochaeta marioni', modality 'none' and fuzzy value '3'
Reason	for flag:
	According to Morata et al. (2013) A. marioni is mobile.
added / m	odified by Renate Degen on 2018-04-16 15:14:51
Edit/Add	

Fig. S11. Reason for the red flag/conflict in the trait category "none (MO1)".