Loading and initial formatting of Type 2 data

Data preparation for RBS recovery rate

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1 Loading Type 2 data

1.1 Metadata, stations and biological data

1.1.1 Stations Stn_dt

The stations were loaded from the respective station worksheets and pooled into one datatable. There are four pressure types (Table 1), which were sampled with a range of grabs or trawls (Table 2) that were categorized as grab and trawls (Table 3).

Table 1: Pressure types by input files

	O2_depl	Sand extraction + fishery	SAR	trawl_index
BoBIC_GulfofCadizmud_btrawling	0	0	51	0
BoBIC_GulfofCadizsand_btrawling	0	0	16	0
BS_gotland_btrawling	0	0	8	0
BS_southernbaltic_btrawling	0	0	11	0
BS_southernbaltic_oxygendepletion	9	0	0	0
NS_BfN_beam_btrawling	0	0	50	0
NS_BfN_grab_btrawling	0	0	50	0
NS_doggerbank_btrawling	0	0	7	0
NS_fladenground_btrawling	0	0	14	0
NS_Hinderbanken_btrawling	0	0	21	0
NS_Hinderbanken_sandextr_and_btrawling	0	156	0	0
NS_Kattegat_btrawling	0	0	112	0
NS_LongForties_btrawling	0	0	5	0
NS_Oostdyck_sandextr_and_btrawling	0	70	0	0
NS_SilverPit_btrawling	0	0	0	6
NS_Thornton_sandextr_and_btrawling	0	163	0	0
WMS_IMPEC_btrawling	0	0	10	0

Table 2: Pressure types by input files

	beam trawl	box_corer	boxcore	Day grab	day_grab	hamon_grab	otter_trawl	SM	Van Veen	van Veen grab	vanVeen_grab
BoBIC_GulfofCadizmud_btrawling	0	0	0	0	0	0	51	0	0	0	0
BoBIC_GulfofCadizsand_btrawling	0	0	0	0	0	0	16	0	0	0	0
BS_gotland_btrawling	0	0	0	0	0	0	0	0	0	0	8
BS_southernbaltic_btrawling	0	0	11	0	0	0	0	0	0	0	0
BS_southernbaltic_oxygendepletion	0	0	9	0	0	0	0	0	0	0	0
NS_BfN_beam_btrawling	50	0	0	0	0	0	0	0	0	0	0
NS_BfN_grab_btrawling	0	0	0	0	0	0	0	0	0	50	0
NS_doggerbank_btrawling	0	0	0	0	0	7	0	0	0	0	0
NS_fladenground_btrawling	0	0	0	0	14	0	0	0	0	0	0
NS_Hinderbanken_btrawling	0	0	0	0	0	0	0	0	21	0	0
NS_Hinderbanken_sandextr_and_btrawling	0	0	0	0	0	0	0	0	156	0	0
NS_Kattegat_btrawling	0	0	0	0	0	0	0	112	0	0	0
NS_LongForties_btrawling	0	0	0	0	0	5	0	0	0	0	0
NS_Oostdyck_sandextr_and_btrawling	0	0	0	0	0	0	0	0	70	0	0
NS_SilverPit_btrawling	0	6	0	0	0	0	0	0	0	0	0
NS_Thornton_sandextr_and_btrawling	0	0	0	0	0	0	0	0	163	0	0
WMS_IMPEC_btrawling	0	0	0	10	0	0	0	0	0	0	0

Table 3: Pressure types by input files

	grab	trawl
BoBIC_GulfofCadizmud_btrawling	0	51
BoBIC_GulfofCadizsand_btrawling	0	16
BS_gotland_btrawling	8	0
BS_southernbaltic_btrawling	11	0
BS_southernbaltic_oxygendepletion	9	0
NS_BfN_beam_btrawling	0	50
NS_BfN_grab_btrawling	50	0
NS_doggerbank_btrawling	7	0
NS_fladenground_btrawling	14	0
NS_Hinderbanken_btrawling	21	0
NS_Hinderbanken_sandextr_and_btrawling	156	0
NS_Kattegat_btrawling	112	0
NS_LongForties_btrawling	5	0
NS_Oostdyck_sandextr_and_btrawling	70	0
NS_SilverPit_btrawling	6	0
NS_Thornton_sandextr_and_btrawling	163	0
WMS_IMPEC_btrawling	10	0

Table 4: Sampled area by input Excel file

.id	cl_description
BoBIC_GulfofCadizmud_btrawling	Gram wet weight per km2
BoBIC_GulfofCadizsand_btrawling	Gram wet weight per km2
BS_gotland_btrawling	Gram wet weight per 0.1 m2
BS_southernbaltic_btrawling	Gram wet weight per 0.3 m2
BS_southernbaltic_oxygendepletion	Gram wet weight per 0.06 m2
NS_BfN_beam_btrawling	Beam trawl: gram wet weight per ha NA = not assessed
NS_BfN_grab_btrawling	Grab samples: gram wet weight per 0.1 m²
NS_doggerbank_btrawling	Gram wet weight per 0.5 m2
NS_fladenground_btrawling	Gram wet weight per 0.5 m2
NS_Hinderbanken_btrawling	Gram wet weight per 1m2
NS_Hinderbanken_sandextr_and_btrawling	Gram wet weight per 1 m2
NS_Kattegat_btrawling	Gram wet weight per 0.1 m2
NS_LongForties_btrawling	Gram wet weight per 0.5 m2
NS_Oostdyck_sandextr_and_btrawling	Gram wet weight per 1 m2
NS_SilverPit_btrawling	Gram wet weight per 0.31 m2
NS_Thornton_sandextr_and_btrawling	Gram wet weight per 1 m2

1.1.2 Biological data B_dt

Biological data are extracted from the third excel sheet from the respective Excel files in the Type 2 data folder. Records which did not included biomass data were excluded, which was the case for all or some records from two datasets: NS_BfN_beam_btrawling, WMS_IMPEC_btrawling. Biomass data were converted to the same units using the *cl_description* from the metadata worksheet (Table 4). There were several input Excel files which did not have an Aphia-ID but only a taxon description. The taxon description was used with the `worrms` package to extract an accepted Aphia-ID using the highest to the lowest taxonomic rank. The taxon *Opisthobranchia* was replaced by *Heterobranchia*, and the Family rank of *Pseudocuma* was added manually.

1.2 Biological traits

Four biological traits databases were loaded: Foveau et al (2020), Beauchard et al (2022), Clare et al (2022) and Vaz et al (2022.) Foveau et al (2020) did not include longevity as a trait. Three missing Aphia-IDs were added to Vaz et al (2022), for the Families Rissoidae and Terebellidae, and for the Genus Hoplostethus. Aphia-IDs were added to Beauchard et al (2022). All three databases had the four same trait modalities for longevity: longevity ≤ 1, 1-3, 3-10 and ≥ 10. All data were pooled into one datatable, and records without Aphia-ID were excluded. Trait scores were averaged over the records at species level (which is in principle redundant as it only comprises the database from Beauchard et al 2022), and then at genus level. For some records the Genera matched, but the lower taxonomic rank did not, e.g. the genus Calliactis was either categorized as the class Anthozoa, or Octocorallia. Both names were merged, and the duplicated records were replaced using the merged taxonomic name. Biological trait modalities from the combined longevity database were added to the biological biomass data.