Fisheries
Research Institute
of Slovenia

Quality assurance, quality control and sampling protocols documentation for biological data

Version 1.0

BioS
Biological database of the
Fisheries Research Institute of Slovenia

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Spodnje Gameljne, June 2023

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Document versions

Version	Date	Author	Version summary
1.0	October 2022 to June 2023	Bojan Marčeta	Creation of first document.

Versions are 1.0, 2.0, etc.; subsequent edited versions become 1.1, 1.2 or if it's a major update 2.0.

Abbreviations and acronyms

Abbreviation	Description
ASFIS	List of Species for Fishery Statistics Purposes (FAO)
BCD	Discard and incidental by-catch survey
BIOS	Biological database of the Fisheries Research Institute of Slovenia (http://www.biosweb.org/)

Abbreviation	Description
CFR	Common fleet register (CFR) number
CV	Coefficient of variation
D96/TM	National coordinate system
DCF	The data collection framework (EU)
DCRF	Data Collection Reference Framework (GFCM)
EPSG	Geodetic Parameter Dataset (also EPSG registry)
FAO	Food and Agriculture Organization of United Nations
FRIS	Fisheries Research Institute of Slovenia (https://www.zzrs.si/; http://www.biosweb.org/)
GFCM	General Fisheries Commission for the Mediterranean
GIS	Geographic information system
GPS	Global Positioning System
HTTPS	Hypertext Transfer Protocol Secure
ID	Unique identifier
LFD	Length frequency distribution
LWR	length-weight relationship
MEDIAS	MEDiteranean International Acoustic Survey (http://www.medias-project.eu/medias/website/) or Pan-Mediterranean Acoustic Survey according Commission Implementing Decision (EU) 2021/1168
MEDITS	International Bottom Trawl Survey in the Mediterranean (https://www.sibm.it/SITO%20MEDITS/principalemedits.htm)
NIB	National Institute of Biology (https://www.nib.si/)
ODBC	Open Database Connectivity
OTB_VOL	Monitoring of catch composition with otter bottom trawl (type "volantina") in the specific stretch between 1.5 and 3 nautical miles from the coast in Slovenian waters
OTBSLO	Monitoring of fisheries resources with otter bottom trawl in the fishing sea of the Republic of Slovenia
PETS	Protected, endangered, and threatened species.

Abbreviation	Description
PostgreSQL	Relational database management system
PSU	Primary sampling unit
QA	Data quality assurance
QC	Data quality control
SOLEMON	Rapido trawl surveys in the Northern Adriatic Sea (https://www.cnr.it/sites/default/files/public/media/navi/Dallaporta2018/SOLEMON.pdf)
SQL	Structured Query Language
UTC	Coordinated Universal Time
VPN	Virtual private network
WGS84	Current version of the World Geodetic System

Definitions

Term	Definition
fisherman	Any person engaging in commercial fishing activities, as recognised by the Member State (Regulation (EU) No 508/2014).
metier	A group of fishing activities targeting a similar species or assemblage of species, using similar gear (6), during the same period of the year and/or within the same area, and which are characterised by a similar exploitation pattern (Commission Delegated Decision (EU) 2021/1167).
recreational fisherman	Any person engaging in non-commercial fishing activities exploiting marine biological resources for recreation, tourism or sport (adapted from Regulation (EU) 2017/1004).
research survey at sea	Activities involving the monitoring of fish stocks and/or marine biological resources and the ecosystem, carried out on a vessel dedicated to such scientific research and designated for this task by a Member State (Commission Delegated Decision (EU) 2021/1167).
scientific observer	Person appointed to observe fishing operations in the context of data collection for scientific purposes and designated by a body in charge of the implementation of the national work plans for data collection (Regulation (EU) 2017/1004).
sensitive species	A species whose conservation status, including its habitat, distribution, and population size or population condition is adversely affected by pressures arising from human activities, including fishing activities. Sensitive species, in particular, include species listed in Annexes II and IV to Directive 92/43/EEC, species covered by Directive 2009/147/EC and species whose protection is necessary to achieve good environmental status under Directive 2008/56/EC (Regulation (EU) 2019/1241).
small–scale coastal fishing	Fishing carried out by fishing vessels of an overall length of less than 12 metres and not using towed fishing gear as listed in Table 3 of Annex I to Commission Regulation (EC) No 26/2004 (Regulation (EU) No 508/2014).

Term	Definition
spear gun	A pneumatic or mechanically powered hand-held gun that shoots a spear for the purpose of underwater fishing (Regulation (EU) 2019/1241).

1 Introduction

Biological database of the Fisheries Research Institute of Slovenia (BIOS) has a rich history that traces back to 1995. It originated as a single-user database for fisheries biological data, developed by Bojan Marčeta during his employment at the National Institute of Biology. Over the years, BIOS underwent significant growth and evolution.

In 2003, the field of marine fisheries biology was transferred from the National Institute of Biology (NIB) to the Fisheries Research Institute of Slovenia (FRIS). This transition to a new scientific environment at the Institute played a crucial role in the continued development and advancement of BIOS. The new scientific setting provided opportunities for collaboration, expertise exchange, and dedicated resources, allowing BIOS to expand its capabilities and address the evolving needs of the fisheries research community. With the support and involvement of the FRIS, BIOS has continued to develop and mature as a comprehensive database for fisheries biological data.

The accession of Slovenia to the European Union in 2004 introduced new requirements for the collection and processing of biological data in the field of marine fisheries biology. To comply with these requirements and effectively manage the data, it became necessary to consolidate all the collected data into a single database. To address this need, the author of BIOS developed a new data model that facilitated the organization of data based on specific sampling protocols. This allowed for the segregation of data into separate data series, making it possible to store data collected from different studies while maintaining their distinct characteristics.

However, despite these advancements, BIOS remained a single-user database focused solely on marine fisheries data. In order to support the efficient functioning of expert services and accommodate the data related to freshwater fisheries, the development of a multi-user database became imperative. The expansion of BIOS to include freshwater fisheries data required the enhancement of the existing database infrastructure to support multiple users and provide a comprehensive platform for managing and analysing fisheries data from both marine and freshwater environments. This expansion aimed to ensure the seamless integration and availability of data from various sources, enabling a more comprehensive and holistic approach to fisheries research and management in Slovenia.

In 2007, the establishment of a common biological database at the FRIS became a necessity. To facilitate the growth and accessibility of the database, several key developments were undertaken. Firstly, the transition of BIOS from a PC-based system to a central server took place. This shift allowed for improved data management, increased storage capacity, and enhanced security measures. Moving BIOS to a centralized server laid the foundation for future expansion and scalability.

Subsequently, a web application was developed to facilitate data entry. This web-based interface provided a user-friendly platform for managing the database and allowed for convenient and efficient data entry. Bojan Marčeta played a vital role in designing a universal web data entry application, which facilitated the seamless adaptation of entry forms to new sampling protocols. This adaptability ensured that BIOS could accommodate evolving research requirements and efficiently incorporate data from different studies.

On 4 March 2009, BIOS made the transition from the development environment to production. By this time, the database already contained comprehensive marine fisheries data, and the web application was fully operational. Additionally, preparations were underway to incorporate freshwater fisheries data into BIOS, further expanding the scope and utility of the database.

Starting at the end of 2009, the online entry of freshwater fisheries data began, marking an expansion of BIOS to include this important dataset. In 2012, older freshwater fisheries data, previously stored in electronic spreadsheets, were also migrated to BIOS, consolidating all relevant data within the database. Over time, BIOS has grown to encompass all the data obtained from fieldwork conducted by the Institute.

The data stored in BIOS are accessible to the staff and collaborators of the Institute, facilitating their research and analysis endeavours. Additionally, a portion of the aggregate data is made publicly available through the BiosWeb[1] website, promoting transparency and the dissemination of scientific findings.

The ongoing development of BIOS is closely intertwined with the continuous improvement of quality assurance and quality control practices. Recognizing the importance of data quality, the FRIS has devoted considerable attention to refining and implementing robust procedures to ensure the accuracy, completeness, and reliability of the data stored in BIOS.

The first part of the document focuses on the description of the quality assurance and quality control measures implemented in the data collection and management processes. These measures encompass various aspects such as data validation, error detection and correction, adherence to sampling protocols, and data completeness checks. By implementing these measures, the FRIS aims to maintain high data quality standards and ensure that the collected data are fit for their intended purposes.

In parallel with the development of quality assurance and quality control, the FRIS has also been actively refining its sampling protocols and methods. These protocols define the systematic approach to collecting biological data and related information, ensuring consistency and standardization across different studies and research projects. The second part of the document provides a comprehensive

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[1] http://www.biosweb.org

overview of these sampling protocols, highlighting their importance in generating reliable and comparable data.

2 Data-quality management

The National work plans shall, among other, contain a detailed description of the quality assurance and quality control framework to ensure adequate quality of the data in accordance with Article 14 of Regulation (EU) 2017/1004[2].

Data-quality management at the FRIS is based on good data collection practice. That consists of qualified staff together with protocols and methods to ensure that data are properly collected, handled, processed, used, and maintained at all stages of the data lifecycle. In this way the systematic errors are reduced to the minimum.

2.1 Quality assurance

Data quality assurance (QA) refers to the systematic processes and activities undertaken to ensure the overall quality, reliability and usability of data. It involves setting standards, establishing procedures and implementing controls to ensure the integrity of data throughout its life cycle. This is ensured through data collection plans, sampling protocols, quality improvement of the team through training and discipline, and finally through the database, among others.

2.1.1 Data collection plans

The Slovenian Work Plan for data collection in the fisheries and aquaculture sectors (https://datacollection.jrc.ec.europa.eu/wps) serves as the fundamental framework for collecting fishery related biological data in Slovenia. By aligning with this program, the FRIS demonstrates its commitment to standardized and comprehensive data collection practices in the field of marine fisheries.

The work plan provides guidelines and procedures for data collection, ensuring that data is collected consistently and according to established protocols. By following this framework, the FRIS can contribute to the overall data quality and comparability at both the national and European levels.

Incorporating the program into the annual work plan demonstrates the Institute's dedication to upholding high standards in data collection and management. This commitment helps ensure that the collected data is reliable, accurate, and suitable for scientific analyses, policy development, and decision-making in the marine fishery sector.

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[2] https://eur-lex.europa.eu/legal-content/en/TXT/?uri=CELEX%3A32017R1004

2.1.2 Data collection protocols

As part of our collection of biological data, we use a variety of sampling protocols. We collect biological data and data related to the fishing trip and gear. Consistent adherence to sampling protocols achieves the highest possible quality criteria for the data collected. The various sampling protocols are described in Chapter 3. Each sampling protocol also consists of a specific set of protocol sheets on which mandatory data are defined. The result is clear and unambiguous field notes.

The utilization of various sampling protocols and the collection of both biological data and data related to fishing trips and gear showcase a comprehensive approach to data collection. Consistent adherence to these sampling protocols ensures that the highest quality criteria are met for the collected data.

The inclusion of specific sampling protocols in Chapter 3 provides a structured framework for conducting data collection activities. These protocols outline the standardized procedures, methodologies, and guidelines for collecting data in a consistent and reliable manner. By following these protocols, we can ensure that the data collected is comparable, accurate, and suitable for analysis.

The use of protocol sheets within each sampling protocol further enhances data consistency and completeness. These sheets specify the mandatory data fields and information that need to be recorded during the data collection process. By having clear and unambiguous field notes, we facilitate the accurate capture of essential data elements, reducing the chances of errors or missing information.

The combination of well-defined sampling protocols and protocol sheets streamlines the data collection process and helps maintain data quality and integrity. It also promotes harmonization and standardization across different sampling activities, ensuring that data collected from various sources can be effectively compared, analysed, and aggregated.

By adhering to these protocols and using the specified protocol sheets, we establish a robust foundation for collecting high-quality biological and fishing-related data. This consistency and attention to detail contribute to the reliability of the database and the subsequent analysis and reporting derived from the collected data.

2.1.3 Data collection team

A dedicated data collection team within the Marine Fisheries Department of the FRIS, consisting of biologists or individuals with training in closely related natural sciences, demonstrates the expertise and specialized knowledge required for collecting accurate and reliable biological data.

The fact that the team members have relevant educational backgrounds provides them with a solid foundation in understanding the scientific principles and concepts necessary for effective data collection. Their training and experience in the field further enhance their ability to carry out data collection activities in a precise and standardized manner.

Internal training programs play a crucial role in ensuring that the data collection team is well-equipped with the necessary skills and knowledge to collect biological data correctly. These training programs likely focus on specific protocols, methodologies, and quality control measures to ensure consistent and accurate data collection practices.

2.1.4 Quality assurance on the database and data entry forms level

At the FRIS we ensure data quality at each stage of the process, from data collection to reporting. This is crucial for maintaining the integrity and reliability of the database.

At the database level, measures are implemented to guarantee the basic quality of data. This includes the establishment of data integrity constraints, which enforce rules and requirements on the database schema. These constraints ensure that data entered into the database adheres to predefined criteria, such as mandatory fields, data types, and relationships between tables. By implementing these constraints, we prevent the insertion of erroneous or inconsistent data, contributing to the overall data quality.

Furthermore, at the data entry form level, additional quality checks are performed to maintain data accuracy and completeness. Data entry forms, whether in paper or web-based format, can include validation rules and prompts that guide data entry personnel to provide accurate and complete information. These rules may include field-level validations, data format validations, and checks for logical consistency. By incorporating these checks into the data entry process, we can minimize errors and ensure that only valid and reliable data is entered into the system.

The use of SQL views and temporary tables during the data processing phase further contributes to data quality assurance. SQL views provide a way to create virtual tables that present subsets of data or apply transformations to the underlying data. By using views, we can ensure consistent data representation and reduce the risk of errors during processing. Temporary tables, on the other hand, offer a way to store intermediate results during complex data manipulations or calculations, ensuring data integrity and accuracy throughout the processing steps.

Finally, making the read-only data available to internal users via ODBC enables further processing and reporting while maintaining data integrity. ODBC allows users to access the data in a standardized and secure manner, facilitating the extraction of data for analysis and reporting purposes. By providing read-only access, we ensure that the original data remains protected and unaltered, promoting data consistency and reliability.

By addressing data quality at both the database and data entry form levels, and implementing quality checks throughout the data workflow, we establish a robust framework for maintaining the integrity and reliability of the database. This, in turn, enhances the credibility of the data and supports informed decision-making and accurate reporting based on the available information.

2.1.4.1 Database BIOS

BIOS is a database containing all DCF and DCRF (GFCM, 2018) related biological and geographic (GIS) data. This is a single database designed to be able to store all biological data regardless of the data source (e.g. biological sampling of landing, sampling of discards, research samplings etc.). The database is hosted internally at the FRIS. It is running on a Debian virtual server. The database engine is PostgreSQL (PostgreSQL 13.1 (Debian 13.1-1.pgdg100+1) on x86_64-pc-linux-gnu, compiled by gcc (Debian 8.3.0-6) 8.3.0, 64-bit) with PostGIS extension ("POSTGIS=""3.1.0 5e2af69"" [EXTENSION] PGSQL=""130"" GEOS=""3.7.1-CAPI-1.11.1 27a5e771"" PROJ=""Rel. 5.2.0, September 15th, 2018"" LIBXML=""2.9.4"" LIBJSON=""0.12.1"" LIBPROTOBUF=""1.3.1"" WAGYU=""0.5.0 (Internal)""").

At the database level the quality of data is assured by the design of the database itself. The BIOS is a relational database. The data are organized in several tables, corresponding to entity types. Every row in each table has its own unique key (primary key). For example, each row of a sampling table corresponds to a sampling data (where, when, how, who etc.), and a sample corresponds to zero or multiple species found in a particular sampling. The tables are connected, and the referential integrity of data is respected via primary and foreign keys.

There are also constraints on columns which determine a logical set of possible values for a given attribute (e.g. length and mass of fish must be >0). On this way it restricts the entry of nonsense data.

2.1.4.1.1 One database for all projects

As mentioned in the previous chapter database BIOS is capable to store data from different data sources (e.g. sampling protocols and projects). Besides using open source software, we chose this approach to further rationalize costs and the amount of work. On the back-end level, there are many advantages: a single virtual server, database, and backup. All code lists are common and shared among various projects (e.g. list of taxa). In addition, we also have a single web application (front-end) that we can customize for each project. Such an approach significantly reduces development, testing and maintenance costs plus improve data assurance (see Chapter 2.1.4.1.8).

2.1.4.1.2 Database normalization

Database normalization is indeed a crucial process for ensuring data integrity, preventing redundancy, and improving efficiency in a relational database. By following a set of rules known as normal forms, the database structure is designed to minimize data anomalies and provide a logical and organized representation of the data.

Normalization involves breaking down a database into multiple related tables, each containing specific attributes or fields that relate to a particular entity or concept. This helps eliminate data redundancy, as information is stored only once and referenced through relationships between tables. Redundancy reduction not only saves storage space but also improves data consistency and accuracy, as updates or modifications need to be made in a single place rather than in multiple instances.

The normal forms, such as First Normal Form (1NF), Second Normal Form (2NF), Third Normal Form (3NF), and so on, provide guidelines for structuring the database tables to ensure data integrity and maintain logical relationships between entities. Each normal form builds upon the previous one, with higher levels of normalization resulting in more refined and efficient database designs.

Implementing the necessary normal forms in the BIOS database demonstrates a commitment to balancing the benefits of normalization with practical application. This means that while achieving a normalized database structure, considerations are made to ensure the design remains practical and efficient for data entry, retrieval, and analysis tasks.

By organizing the data in a structured and logical manner, the normalized database in BIOS enhances data integrity by reducing redundancy and preventing data anomalies. It also facilitates efficient querying and retrieval of information, as the data is stored in a format that optimizes performance.

2.1.4.1.3 Tracking the history of changes to data

To track the history of changes to data in a BIOS database, we have implemented a technique for capturing and storing information about insertions, updates, and deletions made to the database. For this purpose we use separate tables to store the history of changes. All changes are captured automatically using trigger-based approach. Triggers are executing code in response to specified events, such as insert, update, or delete operation. These triggers are set up to insert a record into the history table whenever a change is made to the monitored table.

For an insert operation the new values are stored, for an update operation an updated values are stored, and for a delete operation values being deleted are stored. Additionally, in the history tables information like the timestamp of the change and the user responsible for the modification are included. A relationship between the history table and the corresponding data table is also provided. This is done by including foreign key as an identifier in the history table that links back to the primary key of the modified record in the data table.

2.1.4.1.4 Data access tables and views

For local users, a read-only data access is granted in a separate database schema, enhancing security of a database. For this purpose we are using dedicated tables and views to control the access and present the data in a structured manner. Both types of objects provide a customized representation of the data from one or multiple production table. The tables, which are in daily use, are refreshed every night, the tables that are used periodically are refreshed as needed by administrators.

This approach provides a simplified and tailored interface for users to access the data without exposing the complexity of underlying tables or database structure. The sensitive or irrelevant data is also hidden from users. In data access objects also the descriptions of the code values in the table are provided. In such a way additional information or context about the codes is provided, helping users understand their meaning.

To ensure that calculation errors are kept to a minimum, all standard calculations are available to users in the data access objects. The methodologies used for calculations are documented in SQL scripts, including the formulas, algorithms, or rules applied. Comments on the content of each column is described and accessible to users. Users can query the tables and views directly to retrieve the data using SELECT statements.

2.1.4.1.5 BIOS sandbox

To avoid compromising the production database while providing a testing or development environment, a sandbox database was set up. A sandbox database is a separate instance or copy of the production database where users can experiment, test new features, or perform development activities without affecting the live data. The sandbox can be used directly via SQL statements or via web application.

A creation of a clone of the production database that serves as the sandbox environment is performed every night and ensures the most recent state of the production data. This involves copying the schema structure and data from the production database to the sandbox database instance.

2.1.4.1.6 Security and backup

Two virtual machines are running on a dedicated physical server at the FRIS. The first virtual machine is specifically allocated to host the BIOS database and the web application for data entry and administration. The second virtual machine is dedicated to hosting the publicly accessible http://www.biosweb.org/ website and its associated database.

On the first virtual machine, there are three Docker containers: one for the production application, one for the sandbox application, and one for the PostgreSQL server where the two databases (production and sandbox) are located. Access to everything within this virtual machine is limited to local connections or through an SSL VPN connection. The passwords of the web application users are encoded with hashes, specifically using the MD5 hash algorithm. Additionally, all web communication on the production and sandbox applications is encrypted with HTTPS to ensure secure data transmission.

The application includes a separate process called the identity server, which handles user authorization and authentication. User authentication is performed using JWT Bearer Tokens, which have a limited validity period and must be renewed. PostgreSQL users used to access the databases on the PostgreSQL server are encrypted using the scram-sha-256 algorithm, adding an extra layer of security to the database.

Backup procedures are in place for the entire virtual machine. Daily backups are performed and stored locally for the past 90 days, ensuring a recent history of backups. Additionally, weekly backups for the last year are stored at a remote location, with approximately the last 50 weekly backups available. Furthermore, every time a change is committed to the source code of the web application, the source code repository is backed up to a remote location, ensuring that the full commit history can be retrieved as needed. These measures help to safeguard data and ensure its availability and recoverability in the event of any unforeseen issues or disasters.

The second virtual machine is specifically allocated for hosting the publicly accessible website. Similar to the first virtual machine, regular backups are performed for the entire virtual machine, including both the website code and the associated database. Access to this virtual machine is restricted to local connections or via an SSL VPN connection, except for the publicly accessible website which is open to external visitors.

Backup procedures for the second virtual machine involve storing the backups on a local disk. The most recent 60 daily backups are retained, ensuring a sufficient history of recent backups. Additionally, weekly backups for the past year are stored at a remote location, with approximately the last 50 weekly backups available. This backup strategy provides a level of data protection and allows for the recovery of the virtual machine, website code, and database in the event of any unexpected issues or data loss. By implementing regular backups, both locally and at a remote location, the FRIS ensures data integrity and availability for the publicly accessible website, providing a means to restore the virtual machine and its associated data if needed.

2.1.4.1.7 Data aggregation levels

Primary data

Primary data refers to original data collected directly from the source for a specific research or analysis purpose. It is typically obtained through data collection methods. Primary data is specific to a particular study and is collected first-hand by the researcher. According Regulation (EU) 2017/1004[3] this data is associated with individual vessels, natural or legal persons or individual samples. As primary data is confidential, only certain employees of the FRIS have access to it.

Metadata

Metadata refer to descriptive information about the data. It provides context and details about the characteristics, structure, and meaning of the data. Metadata helps in understanding the content, quality, and usability of the data. It includes information such as data source, data format, data dictionary, data lineage, data ownership, and data attributes. According Regulation (EU) 2017/1004[4] this data is giving qualitative and quantitative information on the collected primary data. This information is available through data access tables and views (see chapter 2.1.4.1.4) to all staff of the FRIS.

Detailed data

Detailed data, also known as granular data or transactional data, contains individual-level or event-level information. It includes all the specific data points or records captured at a fine level of detail. Detailed data provides a comprehensive view of the individual elements or events within a dataset, allowing for in-depth analysis and examination of specific cases.

According (EU) 2017/1004[5] detailed data means data based on primary data in a form which does not allow natural persons or legal entities to be identified directly or indirectly. This information is available through data access tables and views (see chapter 2.1.4.1.4) to all staff of the FRIS.

Aggregated data

Aggregated data is in the summarized form of data obtained by combining or grouping primary or detailed data into higher-level categories or units. It involves the process of summarizing or consolidating individual data points or records to derive meaningful insights or trends. Aggregated data allows for a more general or macroscopic view of the dataset, making it easier to identify patterns, trends, or statistical summaries.

According Regulation (EU) 2017/1004[6] aggregated data means the output resulting from summarising the primary or detailed data for specific analytic purposes. This information is available through data access tables and views (see chapter 2.1.4.1.4) to all staff of the FRIS. We also provide aggregated data to end-users (bodies with a research or management interest) upon their request (e.g. EU-DCF or

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[3] https://eur-lex.europa.eu/legal-content/en/TXT/?uri=CELEX%3A32017R1004
[4] https://eur-lex.europa.eu/legal-content/en/TXT/?uri=CELEX%3A32017R1004
[5] https://eur-lex.europa.eu/legal-content/en/TXT/?uri=CELEX%3A32017R1004
[6] https://eur-lex.europa.eu/legal-content/en/TXT/?uri=CELEX%3A32017R1004

GFCM-DCRF data calls). Part of the aggregated data is also publicly available on the website biosweb.org.

2.1.4.1.8 Data entry forms

At the data entry forms level the quality of data is assured by the rules which must be respected during the data entry process for each sampling protocol. The data entry forms reflect the requirements of each sampling protocol. For each sampling protocol the tables and fields that have to be filled in are specified. The administration of data input forms determines mandatory and optional fields, possible default values, and data interdependence. Mandatory data represent the minimum of data set that ensures the creation of reports for a particular project. If applicable, we set default values that also represent mandatory data.

Mandatory data

In addition to the table and field level data requirements (NOT NULL CONSTRAINTS) that apply to the whole database, we also have data requirements at the level of the web application for data entry. In the latter case, the application is customised for each sampling protocol. This means that it displays a subset of the data entry fields, which can be arbitrarily ordered and for which the data entry requirement can be specified.

Data interdependencies

At the level of the web-based data entry application, control over interdependent data is ensured. An example of two dependent pieces of information is the mass of a specimen and the scale used to measure it. The web app only allows you to enter both or neither of these data.

Drop-down and autocomplete lists

For each sampling protocol the subset of values in drop-down or autocomplete lists is determined. For example, if a sampling protocol is designed to collect data on marine fish, its autocomplete list will not include freshwater fish. Some dropdowns (e.g. gonad maturity stages) are also dependent on the taxonomical branch of the species. For example, if the individual organism belongs to cephalopods, then only a maturity scale for cephalopods will be available in the drop-down list. Such an approach significantly reduces the chances of incorrect data entries.

2.1.4.2 Biological data

2.1.4.2.1 Catch

Catches are tagged with the sampling number and photographed before sorting. This is followed by a sorting of the catches by species. In the case of research fishing, the catch is sorted by the researchers, in the case of commercial fishing, the retained part of the catch is sorted by the fishermen, and the discarded part of the catch is sorted by the scientific observers.

2.1.4.2.2 Species identification

For identification of biological entities we use the most appropriate identification keys. For each species entered in the database, we can define whether the species identification is accurate or doubtful. It is also possible to enter the identification key used and personnel who performed the identification.

2.1.4.2.3 Subsampling

Subsampling is a common method for estimating the abundance of species in trawl catches (Heales et al., 2000). Using this approach, we increase efficiency and therefore reduce the cost of sampling in commercial fishing and research fishing. In order to be able to extrapolate subsamples fractions to the whole, we use three levels of subsampling. For each level, we calculate a subsample factor, and we use it in the process of extrapolation. Different sampling protocols use different levels of subsampling. In case of sampling discard and incidental by-catch, we use three levels of subsampling (F1, F2, and F3) and in case of research surveys just two levels (F2 and F3; Figure 1).

In order to obtain all necessary data for calculation of subsample factors we need to strictly follow all the steps in a subsampling procedure. Scientific observers on board of the fishing vessel shall collect data concerning the whole fishing trip (Figure 1: **1**). In practice, it is often not possible to process all the catches from a single fishing trip. Therefore, scientific observers commonly process a single catch (Figure 1: **2**, **3**). In the exceptional circumstances that catch could be divided (Figure 1: **4**). In this case, scientific observers process one part of the catch (Figure 1: **5**) and from the second part (Figure 1: **6**) they take only information on the total mass of the representative species. Total catch or its part is then sorted by species (Figure 1: **7**, **8**). Each species can be further sorted into categories (e.g. smaller, larger; Figure 1: **9**). Each category (Figure 1: **10**) is treated separately. If there is a large number of specimens in a single category, these categories could be subsampled (Figure 1: **11**) for collection of individual biological information (e.g. length, mass, sex, etc.; Figure 1: **12**, **13**).

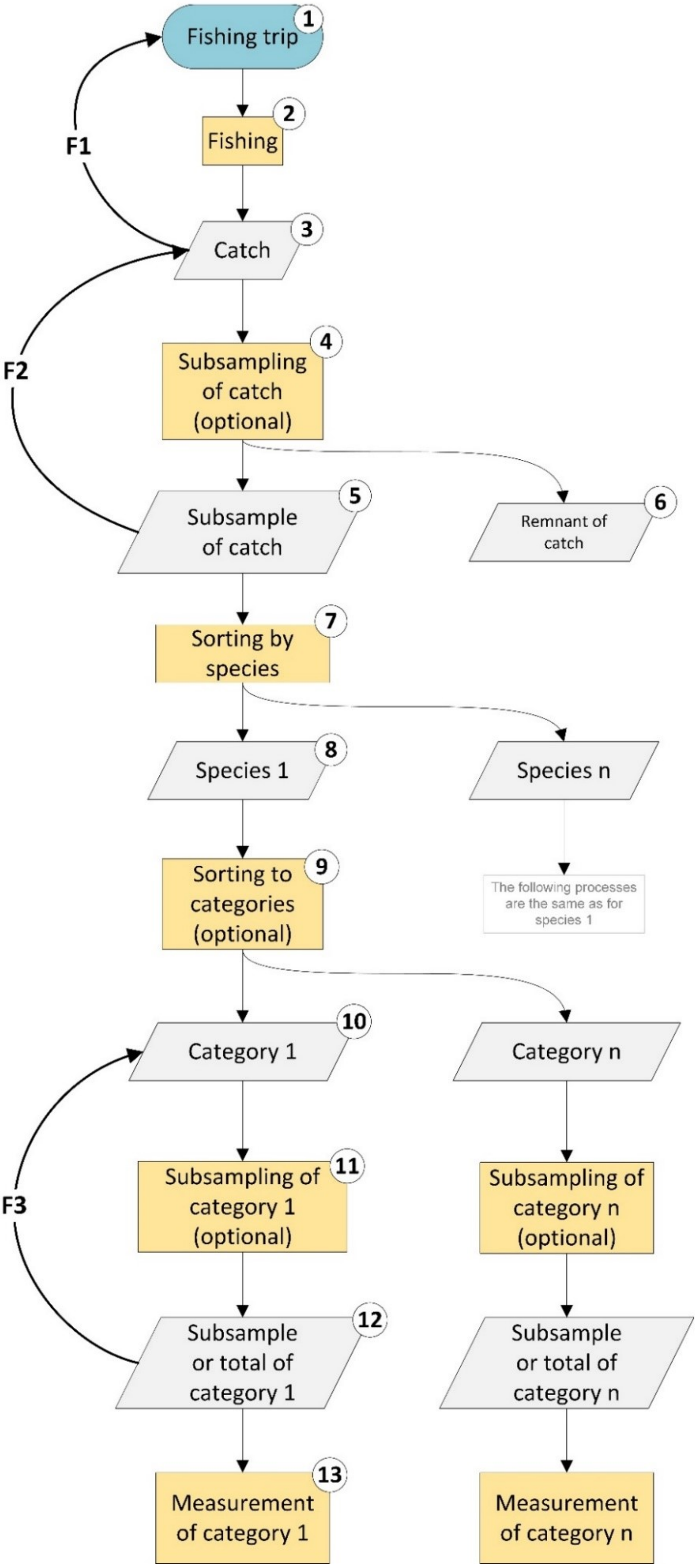

Figure 1 Subsampling procedure for biological data.

2.1.4.2.3.1 Subsampling factors

Subsampling factor F1

Subsampling factor F1 (Figure 1) allows us to raise data from a single catch or multiple catches to the level of fishing trip. F1. The factor is calculated by dividing the total length of fishing activities (e.g. length of all set nets or all hauls performed with towed gears) by the length of the fishing activity processed.

Subsampling factor F2

Subsampling factor F2 (Figure 1) allows us to raise data from a subsample of a single catch to the level of subsampled catch. F2 is applied in exceptional circumstances. An example is when a fisherman divides the catch from a single fishing activity. In Slovenia, this happened when fishing with pelagic trawl (PTM). In that case catch was divided between two fishing vessels. F2 is calculated so that the sum of mass of representative species from both vessels is divided by the mass of processed fraction of that species.

Subsampling factor F3

Subsampling factor F3 (Figure 1) allows us to raise data from a subsample of species category to the level of this category. Application of F3 is crucial to maintain the appropriate ratio of the length frequency distribution (LFD) between categories. F3 is calculated so that the total mass of the category is divided by the mass of processed subsample.

2.1.4.2.4 Morphometric

The subsampled specimens are processed morphometrically. This includes recording of basic morphometric data (e.g. individual length and weight; Table 1) and sometimes more detailed data (Table 2). The methods for carrying out the measurements are documented for the higher taxonomic groups (e.g. Actinopterygii, Cephalopoda etc.). Measurements are performed in situ on fishing vessel or later in the laboratory. For detailed measurements, individual specimen is photographed. In this case measurements are performed using computer software (e.g. ImageJ).

Table 1 Basic measurements recorded on the Specimen protocol sheet.

Scientific name	bm1	bm2	bm3	bm4	bm5
Gastropoda	SH				SL
Bivalvia	SH			SW	SL
Cephalopoda		TL		ML	
Stomatopoda		TL		CL	
Decapoda		TL	CLR	CL	
Cephalaspidomorphi		TL			
Selachimorpha	TLmax		FL	SL	BH
Batiomorpha	TLmax			DL	PS
Actinopterygii	TLmax	TL	FL	SL	BH
Testudines	CCLmax		CCLmin	CCL	CCW
Cetacea		TL	FL		

Table 2 Detailed measurements.

Taxonomic group	Biometry acronym	"bm" column	Morphometry	Accuracy
Gastropoda	SH	bm1	Shell height	1 or 0.1 mm
Gastropoda	SL	bm5	Shell length	1 or 0.1 mm
Bivalvia	SW	bm4	Shell width	1 or 0.1 mm
Bivalvia	SL	bm5	Shell length	1 or 0.1 mm
Bivalvia	SH	bm1	Shell height	1 or 0.1 mm

Taxonomic group	Biometry acronym	"bm" column	Morphometry	Accuracy
Cephalopoda - Teuthida	FinL		Fin length	1 or 0.1 mm
Cephalopoda - Teuthida	ML	bm4	Mantle length	1 or 0.1 mm
Cephalopoda - Teuthida	AR		Arm length	1 or 0.1 mm
Cephalopoda - Sepia	TL	bm2	Total length	1 or 0.1 mm
Cephalopoda - Sepia	ML	bm4	Mantle length	1 or 0.1 mm
Cephalopoda - Loliginidae	TL	bm2	Total length	1 or 0.1 mm
Cephalopoda - Loliginidae	FinL		Fin length	1 or 0.1 mm
Cephalopoda - Loliginidae	ML	bm4	Mantle length	1 or 0.1 mm
Cephalopoda - Octopodidae	ML	bm4	Mantle length	1 or 0.1 mm
Cephalopoda - Octopodidae	TL	bm2	Total length	1 or 0.1 mm
Cephalopoda	TL	bm2	Maximal length	1 or 0.1 mm
Cephalopoda - Loligo	RA1		Length of right arm 1	1 mm
Cephalopoda - Loligo	NCL		Nucal cartilage length	1 mm
Cephalopoda - Loligo	LSD		Diameter of the largest sucker on the right tentacle club	0.1 mm
Cephalopoda - Loligo	HW		Head width	1 mm
Cephalopoda - Loligo	RA4		Length of right arm 4	1 mm
Cephalopoda - Loligo	TCL		Length of the right tentacle club	1 mm
Cephalopoda - Loligo	HL		Head length	1 mm
Cephalopoda - Loligo	GL		Length of the right gill	1 mm
Cephalopoda - Loligo	TL		Length of the right tentacle	1 mm
Cephalopoda - Loligo	RA3		Length of right arm 3	1 mm
Cephalopoda - Loligo	PL		Pen length	1 mm
Cephalopoda - Loligo	PW		Pen width	1 mm
Cephalopoda - Loligo	ML	bm4	Dorsal mantle length	1 mm
Cephalopoda - Loligo	FL		Fin length	1 mm
Cephalopoda - Loligo	FW		Fin width	1 mm
Cephalopoda - Loligo	MC		Mantle circumference	1 mm
Cephalopoda - Loligo	RA2		Length of right arm 2	1 mm
Cephalopoda - Loligo	FCL		Length of the right funnel cartilage	1 mm

Taxonomic group	Biometry acronym	"bm" column	Morphometry	Accuracy
Stomatopoda	CL	bm4	Carapace length	1 or 0.1 mm
Stomatopoda	TL	bm2	Body length	1 or 0.1 mm
Decapoda - Homarus	CL	bm4	Postorbital carapace length	1 or 0.1 mm
Decapoda - Homarus	CLR	bm3	Carapace length with rostrum	1 or 0.1 mm
Decapoda - Homarus	TL	bm2	Body length	1 or 0.1 mm
Decapoda - Majidae	ANSL		Antorbital spine length	1 or 0.1 mm
Decapoda - Majidae	TL	bm2	Body length	1 or 0.1 mm
Decapoda - Majidae	CL	bm4	Carapace length	1 or 0.1 mm
Decapoda - Penaeus kerathurus	TL	bm2	Total length	1 or 0.1 mm
Decapoda - Penaeus kerathurus	CL	bm4	Postorbital carapace length	1 or 0.1 mm

Taxonomic group	Biometry acronym	"bm" column	Morphometry	Accuracy
Cephalaspidomorphi	TL	bm2	Total length	1 or 0.1 mm

Taxonomic group	Biometry acronym	"bm" column	Morphometry	Accuracy
Selachimorpha	PD1		Pre-first dorsal-fin length	1 mm
Selachimorpha	DCS		Dorsal caudal-fin space	1 mm
Selachimorpha	PAL		Preanal-fin length	1 mm
Selachimorpha	HL		Head length	1 mm
Selachimorpha	PP1		Prepectoral-fin length	1 mm
Selachimorpha	PGL		Prebranchial length	1 mm
Selachimorpha	POB		Preorbital length	1 mm
Selachimorpha	FL	bm3	Fork length	1 mm
Selachimorpha	PSP		Prespiracular length	1 mm
Selachimorpha	SVL		Snout-vent length	1 mm
Selachimorpha	PP2		Prepelvic-fin length	1 mm
Selachimorpha	PPS		Pectoral-fin pelvic-fin space	1 mm
Selachimorpha	ACS		Anal-fin caudal-fin space	1 mm
Selachimorpha	PCA		Pelvic-fin caudal-fin space	1 mm
Selachimorpha	IDS		Interdorsal space	1 mm
Selachimorpha	VCL		Vent caudal-fin length	1 mm
Selachimorpha	SL	bm4	Standard length	1 mm
Selachimorpha	PAS		Pelvic-fin anal-fin space	1 mm
Selachimorpha	PD2		Pre-second dorsal-fin length	1 mm
Selachimorpha	TLmax	bm1	Maximal length	1 mm
Selachimorpha	TAH		Tail height	1 mm
Selachimorpha	DPO		First dorsal-fin midpoint pelvic-fin origin	1 mm
Selachimorpha	DAO		Second dorsal-fin origin anal-fin origin	1 mm
Selachimorpha	PDO		Pelvic-fin midpoint second dorsal-fin origin	1 mm
Selachimorpha	ABH		Abdomen height	1 mm
Selachimorpha	BH	bm5	Body height	1 mm
Selachimorpha	HDH		Head height	1 mm
Selachimorpha	PDI		Pelvic-fin midpoint first dorsal-fin insertion	1 mm
Selachimorpha	CPH		Caudal-fin peduncle height	1 mm
Selachimorpha	DPI		First dorsal-fin midpoint pectoral-fin insertion	1 mm
Selachimorpha	DAI		Second dorsal-fin insertion anal-fin insertion	1 mm
Selachimorpha	NOW		Nostril width	1 mm
Selachimorpha	ULA		Upper labial-furrow length	1 mm
Selachimorpha	INW		Distance between nostrils	1 mm
Selachimorpha	MOW		Mouth width	1 mm
Selachimorpha	ANF		Anterior nasal-flap length	1 mm
Selachimorpha	LLA		Lower labial-furrow length	1 mm
Selachimorpha	MOL		Mouth length	1 mm
Selachimorpha	GIR		Girth	1 mm
Selachimorpha	SP2		Width of nostril operculum	1 or 0.1 mm

Taxonomic group	Biometry acronym	"bm" column	Morphometry	Accuracy
Batiomorpha	TLmax	bm1	Maximal length	1 mm
Batiomorpha	PS	bm5	Pectoral fins spread	1 mm
Batiomorpha	DL	bm4	Disc length	1 mm

Taxonomic group	Biometry acronym	"bm" column	Morphometry	Accuracy
Actinopterygii	TL	bm2	Total length	1 or 0.1 mm
Actinopterygii	TLmax	bm1	Maximal length	1 or 0.1 mm
Actinopterygii	FL	bm3	Fork length	1 or 0.1 mm
Actinopterygii	SL	bm4	Standard length	1 or 0.1 mm
Actinopterygii	BH	bm5	Body height	1 or 0.1 mm
Actinopterygii	D1L		Length of the first dorsal fin base	1 or 0.1 mm
Actinopterygii	SNL		Snouth length	1 or 0.1 mm
Actinopterygii	PreDL		Body length to the first dorsal fin base	1 or 0.1 mm
Actinopterygii	AL		Length of anal fin base	1 or 0.1 mm
Actinopterygii	CPL		Caudal peduncle length	1 or 0.1 mm
Actinopterygii	PreVL		Body length to the pelvic fin base	1 or 0.1 mm
Actinopterygii	CPH		Caudal peduncle height	1 or 0.1 mm
Actinopterygii	ED		Eye diameter	1 or 0.1 mm
Actinopterygii	PrePL		Body length to the pectoral fin base	1 or 0.1 mm
Actinopterygii	PreAL		Body length to the anal fin base	1 or 0.1 mm
Actinopterygii	HL		Head length	1 or 0.1 mm
Actinopterygii - Syngnathiformes	SH		Snouth height	0.1 mm
Actinopterygii	BB		Body width	1 or 0.1 mm
Actinopterygii - Hippocampus	TRL		Trunk length - seahorses	1 or 0.1 mm
Actinopterygii - Hippocampus	HL		Head length - seahorses	1 or 0.1 mm
Actinopterygii - Hippocampus	SL	bm4	Standard length - seahorses	1 or 0.1 mm
Actinopterygii - Hippocampus	SNL		Snouth length - seahorses	1 or 0.1 mm
Actinopterygii - Hippocampus	TAL		Tail length - seahorses	1 or 0.1 mm

Taxonomic group	Biometry acronym	"bm" column	Morphometry	Accuracy
Testudines	VTTL		Vent to tip	1 mm
Testudines	CIRCUM		Circumference	1 mm
Testudines	CPL		Plastron length	1 mm
Testudines	PVTL		Plastron to vent length	1 mm
Testudines	TTL		Total tail length	1 mm
Testudines	CCW	bm5	Carapace width	1 mm
Testudines	CCL	bm4	Curved carapace length	1 mm
Testudines	CCLmin	bm3	Minimum carapace length	1 mm
Testudines	CCLmax	bm1	Maximum carapace length	1 mm
Testudines	BD		Body depth	1 mm
Testudines	CL		Carapace length	1 mm
Testudines	HW		Maximum head width	1 mm
Testudines	HL		Maximum head length	1 mm
Testudines	SCW		Carapace width	1 mm
Testudines	SPL		Plastron length	1 mm
Testudines	SCLmin		Minimum carapace length	1 mm
Testudines	SCL		Standard carapace length	1 mm
Testudines	SCLmax		Maximum carapace length	1 mm
Testudines	SPW		Plastron width	1 mm

Taxonomic group	Biometry acronym	"bm" column	Morphometry	Accuracy
Cetacea	FL	bm3	Fork length	1 mm
Cetacea	TL	bm2	Total length	1 mm

2.1.4.2.5 Meristic

Meristic relates to counting quantitative features (e.g. number of fin rays). The methods for carrying out counting are documented for the higher taxonomic groups (e.g. Actinopterygii, Cephalopoda etc.; Table 3).

Table 3 Meristic.

Taxonomic group	Meristic acronym	Meristic
Actinopterygii - Scombridae	PNLI	Number of ventral finlets
Actinopterygii - Scombridae	PNLS	Number of dorsal finlets
Actinopterygii - Atherina	LD1D2	Number of scales between D1 and D2
Actinopterygii	D3S	Number of third dorsal fin spinous rays
Actinopterygii	D1R	Number of first dorsal fin soft rays
Actinopterygii	VR	Number of pelvic fin soft rays
Actinopterygii	A2R	Number of second anal fin soft rays
Actinopterygii	D3R	Number of third dorsal fin soft rays
Actinopterygii	A1S	Number of first anal fin spinous rays
Actinopterygii	D2S	Number of second dorsal fin spinous rays
Actinopterygii	A2S	Number of second anal fin spinous rays
Actinopterygii	D2R	Number of second dorsal fin soft rays
Actinopterygii	VS	Number of pelvic fin spinous rays
Actinopterygii	A1R	Number of first anal fin soft rays
Actinopterygii	D1S	Number of first dorsal fin spinous rays
Actinopterygii	P	Number of pectoral fin rays
Actinopterygii	C	Number of caudal fin rays
Actinopterygii	BR	Number of branchiostegal rays
Actinopterygii	LTS	Number of scales above the lateral line
Actinopterygii	LTI	Number of scales under the lateral line
Actinopterygii	LL	Number of lateral line scales
Actinopterygii	BSS	Number of gillrakers on upper limb
Actinopterygii	BSI	Number of gillrakers on lower limb
Actinopterygii - Acipenseridae	DP	Number of dorsal bony plates
Actinopterygii - Acipenseridae	VP	Number of ventral bony plates
Actinopterygii - Acipenseridae	LP	Number of lateral bony plates
Actinopterygii - Syngnathidae	SD	Number of segments under D
Actinopterygii - Syngnathidae	SC	Number of segments on the tail
Actinopterygii - Syngnathidae	ST	Number of segments on the trunk
Actinopterygii	DU	Number of mandible teeths

2.1.4.2.6 Gonad maturity

The gonad maturity stages are determined macroscopically. For this purpose, we use the scales from the latest MEDITS manual (MEDITS Working Group, 2017) for the different taxonomic groups: bony fish, oviparous and viviparous elasmobranchs, crustaceans, and cephalopods.

2.1.4.2.7 Stomach content analysis

To study the feeding habits and dietary preferences of fish we use stomach content analysis. It involves examining the contents of stomachs to identify and quantify the types of food items or prey consumed. Stomach is removed and dissected to access its contents. The contents are visually inspected under a microscope or with the naked eye to identify and classify the different food items present. This involves identifying prey remains or other identifiable fragments. The identified food items are quantified, usually by weight or volume, to determine the relative importance of different food sources in the fish's diet. This provides insights into prey preferences, seasonal variations, or dietary shifts.

2.1.4.3 Fishery related data

2.1.4.3.1 Fishing vessel

Fishing vessel administrative identifications (CFR, vessel name, registration port, external marking) and technical characteristics (length, tonnage, power) is collected from public sources: mostly Fleet Register[7] and when appropriate also national Register of Sea-going Boats[8].

2.1.4.3.2 Fishing trip and fishing activities

Geographical data (path and waypoints) are recorded with a handheld GPS device. The GPS device is switched on before the departure of the fishing vessel and switched off after returning to port. The device records the entire fishing trip track in five-second intervals. This way, we can find out the exact time of departure and return to the fishing port.

Fishing activities take place on one or several parts of the fishing trip track. The start and end of each fishing activity are marked with waypoint recorded by scientific observers. This way, we can find out the exact time of the start and end of each fishing activity. The fishing trip track is cut at waypoints and the length of the fishing activity (e.g. length of bottom trawl haul, length of set net etc.) is determined from the resulting track segments. We also record logbook number. This allows us to cross-check scientific observers and fisherman data at a later stage.

2.1.4.3.3 Fishing gear

Data on the technical characteristics of fishing gear are collected by measuring the gear on board of fishing vessel. Some measurements are also obtained from the fisherman. For each type of fishing gear, we have a specific protocol sheet to record its technical characteristics.

2.2 Quality control

Quality control (QC) of data refers to the application of methods or processes that determine whether data meet overall quality goals and defined quality criteria for individual values. Data are evaluated against a set of quality goals and specific criteria. We also use rapid data scanning methods to tag records or sets of records that meet or fail to meet a particular criterion.

The quality control process primarily focuses on two types of primary data: (1) fishery-related data, including biological stock-related data and biological metier-related data, and (2) research survey-related data. The aggregated data, which is derived from the thoroughly checked primary data, is

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[7] https://webgate.ec.europa.eu/fleet-europa/index_en;jsessionid=GL1_CkBm1JPIyokIu7qtE66x4R2nPjxUtE1DktIPz1vnNXnJ0VbY!-1111807712

[8] https://e-uprava.gov.si/javne-evidence/plovila.html

assumed to be correct. The checking process involves the assessment of qualitative and quantitative indicators, as well as other quality checks. To perform quality control, SQL scripts are utilized, allowing for efficient data analysis and validation. It's important to note that the quality indicators themselves are not stored in a database, but rather used within the QC process to assess and ensure data quality.

2.2.1 Qualitative indicators

Availability

The data follows a defined workflow where its status progresses from "data input" to "production" before it can be used for analysis and reporting. The transition to the production status is contingent upon the completion of all required data fields, ensuring that the data is comprehensive and dependable for subsequent processing.

By adhering to this workflow, the completeness criteria are enforced, guaranteeing that only fully populated and verified data is made available for analysis and reporting purposes. This systematic approach mitigates the risk of incomplete or unreliable data being used, thereby upholding the integrity and accuracy of the subsequent analyses and reports.

This workflow serves as a crucial quality control measure, providing a structured process for ensuring the data's readiness and reliability before it progresses to the production stage. It establishes a consistent standard for data completeness, enabling confident decision-making and robust reporting based on reliable information.

Accessibility

Accessibility is indeed assured for all data that has attained the production status. Once the data has successfully undergone the requisite quality checks, including the fulfilment of mandatory fields and adherence to predefined quality criteria, it becomes readily accessible for analysis and reporting purposes.

Authorized individuals or systems are then able to retrieve and utilize the data for a range of analytical or reporting activities, with the assurance that it is reliable and appropriate for their needs. The attainment of the production status signifies that the data has undergone the necessary validation and quality control measures, ensuring its suitability for access and utilization by relevant stakeholders.

This accessibility guarantee fosters efficient data utilization, enabling timely and informed decision-making processes based on reliable and verified information. It underscores the significance of maintaining a robust quality control framework, which ultimately enhances the value and trustworthiness of the data for analysis and reporting purposes.

Missing values

In the database system, measures are implemented at both the database level and the data entry form level to prevent missing values. These measures include the use of constraints and rules to enforce data integrity and completeness.

At the database level, constraints are defined during the database schema design to specify data integrity rules. These constraints ensure that required fields cannot contain null or missing values. For example, a constraint can be set to mandate that a certain field must have a non-null value.

At the data entry form level, rules are enforced to guide data entry personnel. These rules prompt users to complete all required fields before they can submit or save the data. The data entry forms may also include validation checks to ensure that specific fields have valid values or prompt users to provide necessary information.

By combining these measures, missing values are effectively prevented from being stored in the database. The constraints and rules work together to maintain data completeness, consistency, and accuracy. This helps ensure that the data remains reliable for analysis and reporting purposes, as missing values can introduce errors or bias in the results.

Duplicated records

On the database level, constraints can be implemented to prevent duplicated records from being stored. These constraints can include unique keys or indexes on specific fields, ensuring that each record in a table is unique based on the defined criteria. This helps maintain data integrity and prevents the accidental or intentional insertion of duplicate records.

However, it is important to note that there might be scenarios where duplicate records can occur during the data aggregation process. For instance, when performing joins between subqueries or combining data from multiple sources, improper join conditions or logic can lead to duplicate records in the aggregated data set.

To address this, it is a good practice to perform a thorough check on the aggregated data results before submission. This involves reviewing and validating the data to identify and eliminate any duplicate records that may have arisen during the aggregation process. By verifying the uniqueness of the data, we can ensure that only accurate and non-duplicated information is submitted for further analysis or reporting.

Coding

On the database level, internal codes, such as taxon_id, are commonly implemented to uniquely identify specific entities or concepts. These internal codes serve as references within the database and provide a consistent and efficient way to represent and link related data.

However, when preparing reports or outputs from the database, it is often necessary to translate these internal codes into codes that are suitable for the specific type of report or external system. This translation process allows the data to be presented in a format that is meaningful and compatible with the target audience or system.

For example, in our case, the internal taxon_id "910" may be translated to different codes depending on the type of report or code list being used. It could be translated to "PIL" in the FAO ASFIS 3A_CODE system or "SARDPIL" in the MEDITS species code system.

By implementing this principle across all code lists in the database, we ensure that the data can be effectively communicated and utilized in various reporting scenarios, taking into account the specific code standards or conventions required by different systems or organizations. This translation process enhances interoperability and facilitates seamless integration between our database and external systems or reporting frameworks.

Accuracy of the spatial data

The accuracy of spatial data is indeed dependent on the accuracy of the measuring instrument used. Typically, the accuracy of such instruments is within a few meters. However, when coordinates are entered manually, errors may occur due to human factors.

To ensure the accuracy of spatial data before inserting it into the geodatabase, we follow a process of plotting the data on a map to verify their locations. This visual verification allows us to identify any outliers or discrepancies, and corrections are made accordingly to rectify the data.

It's worth noting that slight discrepancies can also arise during the transformation of geodetic datum. In our case, the native measuring instrument uses the WGS84 geodetic datum (EPSG = 4326), which is an Earth-centred datum primarily used for global positioning. However, WGS84 does not provide precise length or surface calculations. To perform accurate length or surface calculations, a transformation to the local datum (D96/TM – EPSG = 3794) is required.

By performing the necessary transformations, we ensure that the spatial data is correctly aligned with the local coordinate system, allowing for accurate calculations of length and surface area. This attention to spatial accuracy, verification, and appropriate transformations helps maintain the reliability and precision of the spatial data within our geodatabase.

Data anomalies

One of the most common anomalies detected in the data pertains to discrepancies between the length and mass of specimens. To address this issue, we periodically update the length-weight relationship (LWR), which helps establish the expected correlation between these two variables. During this updating process, any outliers or data points that deviate significantly from the expected relationship are identified.

These outliers are then corrected at the primary data level, ensuring that the erroneous data is rectified. It is found that the majority of these errors are due to incorrect transcription or typing errors when transferring the data from paper forms into the database. Such mistakes can lead to inconsistencies between recorded lengths and masses.

By proactively detecting and correcting these outliers, we improve the accuracy and reliability of the data. This maintenance process allows for a more robust length-weight relationship and ensures that subsequent analyses and reports based on this data are more precise.

2.2.2 Quantitative indicators

Standard deviation

The standard deviation is a widely used statistical measure that quantifies the variability or dispersion of data values within a database. It provides insights into the spread or distribution of values within a dataset and helps identify potential outliers or unusual observations.

By calculating the standard deviation for specific data fields or attributes, we can assess the consistency and reliability of the data. A low standard deviation indicates that the data values are closely clustered around the mean, suggesting a higher level of consistency and less variability. On the other hand, a high standard deviation indicates greater dispersion or variability among the data values, which may warrant further investigation to understand the potential causes or sources of variation.

Analysing the standard deviation can provide valuable information about the quality and consistency of the data. It allows us to identify data points that deviate significantly from the mean, which may be indicative of data entry errors, measurement issues, or other anomalies that require attention. By monitoring and addressing outliers or high variability, we can enhance the overall reliability and integrity of the database.

Coefficient of variation

The coefficient of variation (CV) is a statistical measure that is useful for comparing the variability of different data fields or attributes within a database. It is particularly helpful when comparing datasets that have different scales or units of measurement.

The CV is calculated by dividing the standard deviation of a dataset by its mean and then multiplying by 100 to express it as a percentage. It provides a standardized measure of variation relative to the mean. By using the CV, we can assess and compare the relative variability of different attributes.

The CV is particularly valuable in identifying areas within the database where data quality may vary significantly. A higher CV indicates a relatively larger variation compared to the mean, suggesting greater inconsistency or variability in the data. On the other hand, a lower CV implies a more stable and consistent dataset.

By examining the CV for different attributes, we can prioritize areas that may require further investigation or quality improvement efforts. It helps in identifying attributes with high variability or potential data quality issues, enabling us to focus our attention on enhancing the accuracy and reliability of those specific data points.

Sample size

The sample size is an important consideration in database quality control. It plays a role in evaluating the quality of a subset of data within a larger database, even outside the context of statistical sampling. The sample size influences the accuracy and reliability of our assessments.

When evaluating a subset of data, a larger sample size tends to provide more reliable estimates of data quality. With a larger sample size, we have a greater representation of the overall dataset, increasing the likelihood that the assessed subset is a true reflection of the entire population. This reduces the potential for sampling bias and improves the generalizability of our findings.

A larger sample size also allows for more robust statistical analysis, enabling us to draw more precise conclusions and make more accurate assessments of data quality indicators. It helps to reduce the impact of random variations and provides a more stable estimate of the quality measures we are evaluating.

However, it's important to note that the required sample size may vary depending on the specific context and objectives of the data quality evaluation. Factors such as the level of desired precision, the heterogeneity of the dataset, and the resources available for the evaluation should be considered when determining an appropriate sample size.

Sampling rate

Sampling rate plays a crucial role in evaluating the quality of data collected through sampling techniques and it is a crucial factor when evaluating the quality of data collected through sampling techniques. It refers to the proportion or percentage of the population that is included in the sample.

A higher sampling rate typically leads to a more representative sample, meaning it better reflects the characteristics of the overall population or database. When the sampling rate is high, a larger portion of the population is included in the sample, reducing the potential for sampling bias and increasing the likelihood of obtaining reliable insights about the quality of the entire database.

Response rate

The response rate is a critical factor when assessing the quality of survey data stored in a database. It quantifies the percentage of entities or individuals that have provided valid responses out of the total number of surveys planned.

A higher response rate is generally indicative of better data quality, as it implies a higher level of engagement and participation from the targeted population. A higher response rate suggests that a greater proportion of the intended respondents have actively and accurately provided their responses, leading to a more comprehensive and representative dataset.

A high response rate is desirable because it reduces the potential for non-response bias, which occurs when the characteristics of non-respondents differ significantly from those of respondents. A higher response rate increases the likelihood that the collected survey data is more representative of the entire population or target group, enhancing the reliability and validity of the conclusions drawn from the data. Monitoring and maximizing the response rate is crucial in ensuring the quality of survey data.

Coverage rate

The coverage rate is an important factor when evaluating the representativeness and quality of data in a database. It measures the percentage of the target population that is covered or represented in the database.

A higher coverage rate indicates a more comprehensive representation of the population within the database. It implies that a larger proportion of the target population is included in the dataset, increasing the likelihood of obtaining accurate and reliable insights about the entire population.

A high coverage rate is desirable because it helps mitigate potential bias and ensures that the database reflects the diversity and characteristics of the target population. It allows for more robust analysis and generalization of findings to the larger population.

A low coverage rate, on the other hand, can introduce selection bias and limit the generalizability of the findings. It may indicate underrepresentation of certain segments or groups within the population, leading to potential inaccuracies or skewed results.

2.2.3 Other quality checks

Typing errors

Typing errors are common mistakes that can occur during the data entry or data transfer processes. They encompass a range of errors, including misspellings, transpositions of characters or digits, and incorrect formatting of data.

To ensure data quality, regular data validation and cleansing procedures are performed. These processes help identify and correct typing errors and other inconsistencies within the data. Various techniques can be employed during data validation, such as automated algorithms, manual review, and comparison with external sources or known standards.

During the data validation process, potential typing errors are flagged for review and correction. This may involve cross-checking data entries against predefined rules, conducting range checks, or using data profiling techniques to identify outliers or improbable values. Data cleansing techniques, such as standardization and normalization, may also be applied to rectify common errors or inconsistencies.

By proactively detecting and rectifying typing errors, the data quality is enhanced, ensuring the accuracy and reliability of the database. This, in turn, improves the validity of any subsequent analyses, reports, or decision-making processes that rely on the data.

It's important to establish and maintain data entry protocols and quality control measures to minimize typing errors from occurring in the first place. This can include training data entry personnel, providing clear instructions and guidelines, and implementing data validation rules at the point of data entry or during the data transfer process.

Arithmetic checks

Arithmetic checks play a crucial role in database quality control by verifying the accuracy of numerical calculations and mathematical relationships within the data. These checks help ensure that calculations and formulas are correctly implemented and that the resulting values align with the expected outcomes.

Arithmetic checks involve various operations, such as summing columns or fields to validate that the total matches the expected value. In addition to sums, arithmetic checks may involve calculating averages, ratios, percentages, or other mathematical computations based on the data. These calculations are compared against pre-determined benchmarks or known formulas to ensure their accuracy.

By conducting arithmetic checks, any discrepancies or inconsistencies can be identified and investigated promptly. Discrepancies may indicate potential data entry errors, issues with data integrity, or problems with the underlying mathematical relationships or calculations. Investigating and resolving these issues is essential to maintaining the accuracy and reliability of the database.

We utilize automated scripts to perform arithmetic checks on a regular basis. These checks can be customized based on the specific requirements of the data and the mathematical relationships involved.

Logical checks

Logical checks are an important aspect of database quality control and involve assessing the consistency and coherence of data based on predefined logical rules or relationships. These checks help ensure that the data follows expected patterns, adheres to logical constraints, and is free from inconsistencies or illogical values.

Logical checks involve verifying that data values meet specific criteria or conditions. For example, in a database of individual measurements, a logical check may be applied to ensure that the length or mass of an individual is always greater than zero. If any value is zero or fall below zero or is missing, it would indicate a data quality issue that needs to be addressed.

Logical checks can be implemented through the use of constraints, validation rules, or scripts that evaluate the data against predefined logic. They help identify data inconsistencies, outliers, or missing values that do not align with the expected patterns or logical relationships within the database.

By performing logical checks, potential errors or inconsistencies can be flagged for further investigation and resolution. This ensures that the data remains coherent, reliable, and suitable for analysis or reporting purposes. Logical checks contribute to data integrity, accuracy, and the overall quality of the database.

Range checks

Range checks are an important component of database quality control, particularly for numerical data fields. These checks involve evaluating whether data values fall within expected ranges or thresholds that are considered valid or acceptable.

Range checks help identify data points that significantly deviate from the normal or expected range, which may indicate errors, anomalies, or outliers. By defining specific ranges or thresholds for each data field, we can assess the data's consistency and identify potential data quality issues.

Cross-sectional and time series analyses are useful techniques for conducting range checks. In cross-sectional analysis, we compare data points across different entities or time periods to identify outliers that are inconsistent with the overall patterns. Time series analysis focuses on detecting outliers or deviations from expected trends within a specific data series over time.

When conducting range checks, it's important to consider the context and characteristics of the data. Different data fields may have different expected ranges or thresholds based on domain knowledge, standard practices, or specific requirements.

3 Data collection methods

The chapter is covering data collection methods and data requirements for biological data on exploited biological resources caught by Union commercial and recreational fisheries in accordance with Commission Delegated Decision (EU) 2021/1167[9]. Data collection methods are taking into consideration relevant scientific advice and best practices and are suitable for the intended purpose. This means that they are suitable for collecting biological data in the frames of different sampling protocols which are described below.

3.1 Collection of biological data for certain stocks

According to the provisions in the Chapter II (Thresholds for data collection) of the Commission Implementing Decision (EU) 2021/1168[10] Slovenia is currently not obliged to collect data on biological parameters.

In the past, we have collected biological data for sardine (*Sardina pilchardus*) and anchovy (*Engraulis encrasicolus*). Data collection started in 2006, when landings of sardine and anchovy exceeded the 200 tonne threshold. In 2012, landings of both species decreased due to the scrapping of two pelagic trawlers. Although the landing threshold was no longer exceeded, we continued to sample the landings of purse seiners till 2016. After that year, there were no more active purse seiners.

3.2 Recreational Fishery

Recreational fishery means non-commercial fishing activities exploiting marine biological resources for recreation, tourism or sport (Regulation (EU) 2017/1004[11]). In the frame of recreational fishery data collection in Slovenia is covering all species caught by recreational fisherman and not only those listed in Table 4 of the Commission Delegated Decision (EU) 2021/1167[12].

Marine recreational fisheries in Mediterranean and Black Sea is in general data-poor sector (Grati et al., 2021). Slovenia is an exception in this area, in a good sense of the word. In Slovenia recreational fishery is regulated by the Rules on leisure sea Fishing (Official Journal of the RS, No 64/08[13]). Fishing licences are required for boat fishing and spearfishing, while fishing from the shore is free. Recreational fisheries can be divided into five strata, depending on the fishing licences and the way fishing: (1) sport fishing on the basis of annual licence; (2) sport fishing with a spear gun on the basis of annual licence;

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[9] https://eur-lex.europa.eu/eli/dec_del/2021/1167/oj

[10] Commission Implementing Decision (EU) 2021/1168 of 27 April 2021 establishing the list of mandatory research surveys at sea and thresholds as part of the multiannual Union programme for the collection and management of data in the fisheries and aquaculture sectors from 2022 (https://eur-lex.europa.eu/legal-content/en/TXT/?uri=CELEX%3A32021D1168)

[11] https://eur-lex.europa.eu/legal-content/en/TXT/?uri=CELEX%3A32017R1004

[12] https://eur-lex.europa.eu/eli/dec_del/2021/1167/oj

[13] http://www.pisrs.si/Pis.web/pregledPredpisa?id=PRAV8023

(3) recreational fishing on the basis of daily and weekly licences; (4) organised sport fishing competitions and (5) recreational fishing from the shore for which no licence is required. These strata are the basis for data collection.

Sport fishermen referred to stratum 1 and 2 shall be required to complete the forms for keeping a daily catch record. The completed form must be returned by the fisherman to the holder of the public authority responsible for issuing annual licences no later than 15 January for the preceding calendar year. Recreational fishermen referred to stratum 3 must also record their catches on their fishing licences and then return it to the publisher. The holder of the public authority to issue daily and weekly fishing licences shall send to the fishing register information on the number of fishing licences issued, broken down by month of issue, no later than 15 January for the preceding calendar year. The organiser of the sport fishing competition referred to stratum 4 shall keep a record of the catch. Catch data is not collected for recreational fishing from shore for which no licence is required.

Since 2017, the collection of data on recreational fishery has been under the responsibility of the Ministry of Agriculture, Forestry and Food.

The estimation of recreational fishermen population is based on the number of issued licences in stratum 1 to 3. Fishermen in stratum 4 are the same as in stratum 1 to 3. Stratum 5 is excluded since those fishermen do not need a licence.

The estimation of catches by recreational fishermen is based on the data from stratum 1 to 4 while stratum 5 is excluded. In 2017 a methodology for estimating catch data from recreational fisheries was developed in cooperation between the Statistical Office of the Republic of Slovenia and Ministry of Agriculture, Forestry and Food.

Catch estimates for strata 1 to 3 are based on information from fishermen. In case that the number of issued licences is equal to the number of return forms this is treated as census and no estimation is required, otherwise the estimation is required. The estimation of recreational fishermen's catches is based on the assumption that fishermen who did not return their forms with catch data fished at the same rate as those who did return forms. The calculation is based on the number of licences issued and the number of forms returned. The returned forms contain information on fishing days and catch quantities by species. The estimation fishing days (***FDe***) for the stratum ***i*** is calculated according the equation:

$$FDe_i = \frac{(Li_i - Fr_i) * FDr_i}{Fr_i}$$

where ***Li*** is the number of issued licences for the stratum ***i***; ***Fr*** is the number of returned forms for the stratum ***i*** and ***FDr*** is fishing days from the returned forms for the stratum ***i***.

The estimation of catch from not returned forms (***Cef***) for the stratum ***i*** is calculated according the equation:

$$Cef_i = \frac{FDe_i * Cf_i}{FDr_i}$$

where ***FDe*** is the estimated fishing days for the stratum ***i***; ***Cf*** is the catch from the returned forms for the stratum ***i*** and ***FDr*** is fishing days from the returned forms for the stratum ***i***.

The estimation of catch (***Ce***) for the stratum ***i*** is calculated according the equation:

$$Ce_i = Cf_i + Cef_i$$

where ***Cf*** is catch from the returned forms for the stratum ***i*** and ***Cef*** is the estimation of the catch from not returned forms for the stratum ***i***.

To estimate the quantities caught by species, we use a raising factor for the stratum ***i*** calculated using the equation:

$$RF_i = \frac{Ce_i}{Cf_i}$$

where ***Ce*** is estimation of catch for the stratum ***i*** and ***Cf*** is the catch from the returned forms for the stratum ***i***.

The final catch estimate is made by summing all the estimates for strata 1 to 3 and adding the data for stratum 4. Since catch data for stratum 4 is based on census no estimation is needed.

3.3 Anadromous and catadromous species

Anadromous and catadromous species data collection in fresh water is not performed due to following reasons (see comment for each species below).

Anguilla anguilla is a protected species in Slovenia (Decree on protected wild animal species, Official Journal of the RS, No 46/2004[14]) and it is not subject of any fishery. Slovenia informed the European Commission that European eel has been protected on the national level since 2004. On the basis of this Decree, the fishing of European eel in Slovenia is completely prohibited. It is also prohibited to intentionally harm, poison, kill, take from nature, catch or disturb the specimens of European eel. Because of this, Slovenia cannot collect data on European eel as specified in Commission Delegated Decision (EU) 2021/1167[15]. In cases of incidental catch of European eel during inland research samplings, the data on number and weight are regularly recorded. Incidental catches are very rare and all are recorded in a Biological database of the FRIS (publicly available on BiosWeb http://www.biosweb.org/index.php?task=map&tid=144).

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[14] http://www.pisrs.si/Pis.web/pregledPredpisa?id=URED2386

[15] https://eur-lex.europa.eu/legal-content/EN/TXT/PDF/?uri=CELEX:32021D1167&from=EN

Salmo salar is not present in Slovenian waters.

Salmo trutta - in Slovenia is represented by a subspecies *Salmo trutta fario*, which is landlocked (not anadromous).

3.4 Discard and incidental by-catch (BCD)

Discard and incidental by-catch (BCD) is a survey conducted by scientific observers aboard fishing vessels, which commenced in 2006. The survey is incorporated into the Work Plan for data collection in the fisheries and aquaculture sectors.

The primary objective of BCD is to gather data on the composition of commercial catches by species. The analysis of the catch focuses on several aspects, including target species and by-catch species, quantities retained and discarded by species, individual length and mass, size structure, and the proportion of juveniles listed in Annex III - Minimum Sizes of marine organisms of Council Regulation (EC) No 1967/2006[16]. Observers diligently monitor all species, including those that are protected, endangered, and threatened (Carpentieri et al., 2021). Additionally, observers quantify non-commercial benthic bycatch.

3.4.1 Sampling design for discard and incidental by-catch

The collection of biological data related to metiers is conducted using a combination of stratified and random sampling. Stratified sampling provides geographic and temporal coverage of data collection. Random sampling within strata provides statistical reliability.

3.4.1.1 Geographical stratification

Geographical stratification is necessary to obtain an even geographical distribution of sampling. The entire territorial sea of Slovenia is located in GFCM GSA17 and in FAO division 37.2.1. In addition, the Slovenian coast is short, which is why we treat the entire area as one stratum.

3.4.1.2 Temporal stratification

Temporal stratification is necessary to obtain an even temporal distribution of samplings. According Commission Decision 2010/93/EU[17] sampling is performed in order to evaluate the quarterly length distribution of species in the catches, and the quarterly volume of discards.

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[16] https://eur-lex.europa.eu/legal-content/en/ALL/?uri=CELEX%3A32006R1967

[17] https://eur-lex.europa.eu/legal-content/EN/TXT/PDF/?uri=CELEX:32010D0093&from=EN

3.4.1.3 Metier selection

Metiers up to level 6 are defined in Table 5 of Commission Delegated Decision (EU) 2021/1167[18]. For sampling purpose, according Commission Decision 2010/93/EU [19], only the major metiers are considered. In order to identify the metiers to be sampled, the ranking system is used at level 6 of the matrix in Appendix IV. The metiers to be sampled are identified according cumulative share of 90% for the following parameters: the total commercial landings, total value of the commercial landings, and total effort in days-at-sea. All metiers that were within 90% of the cumulative share were selected, regardless of the parameter.

Based on data from the period 2020 to 2021, three metiers were selected for sampling: GNS_DEF_>=16_0_0, GTR_DEF_>=16_0_0, and OTB_DEF_>=40_0_0.

3.4.1.4 Species selection

Observers collect biological data for all species caught by fishing vessels. This includes the retained part of the catch and the discarded part of the catch. In addition to commercial species, this also covers non-commercial species, sensitive and protected species, as well as benthic by-catches.

3.4.1.5 Sampling unit

The primary sampling units (PSU) is fishing trip (from departure to return of the vessel to the port) of randomly select fishing vessels. During each fishing trip, the fishing vessel performs one or more of the fishing activities. The biological data should be collected from the catch of one or more fishing activities (according the possibilities).

3.4.1.6 Difficulties in data collecting

According to paragraph 2 of Article 12 of the Regulation (EU) 2017/1004[20] the masters of Union fishing vessels shall accept on board scientific observers and cooperate with them in order to allow them to discharge their duties while on board Union fishing vessels, as well as the use of alternative data collection methods, where appropriate. The masters of Union fishing vessels may refuse to accept on board the scientific observers operating under the at-sea monitoring scheme only on the basis of an obvious lack of space on the vessel or for safety reasons in accordance with national law.

Most of the problems in data collection are caused by the refusal to take scientific observers on board the fishing vessel. There are often refusals due to the small size of the fishing vessels, which is an objective reason. Non-cooperation of fishermen can also be a common reason for refusal. Difficulties

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[18] https://eur-lex.europa.eu/eli/dec_del/2021/1167/oj

[19] https://eur-lex.europa.eu/legal-content/EN/TXT/PDF/?uri=CELEX:32010D0093&from=EN

[20] https://eur-lex.europa.eu/legal-content/en/TXT/?uri=CELEX%3A32017R1004

in getting scientific observers on board fishing vessels result in fewer samplings and difficult random selection of primary sampling units. All this is affecting the quality of data.

As an alternative to on-boarding scientific observers, in case of small vessels, we also tried a self-sampling approach. The fisherman is given a container in which to collect all the unwanted organisms. We place a GPS device on the vessel to record the track throughout the fishing trip. The biggest problem with self-sampling is that fishermen do not collect all the unwanted organisms. The experience of the scientific observers on board is that they often have to warn fishermen not to throw unwanted organisms into the sea.

3.4.2 Data capture protocol for discard and incidental by-catch

Sampling of discard and incidental by-catch is conducted by scientific observers aboard fishing vessels. The sampling is performed following the protocol described below.

3.4.2.1 Fishing trip and fishing activities

Fishing trip and fishing activities are documented using a portable GPS device, protocol sheet for technical description of fishing gear and recording the number of fishing logbook. The track is recorded during the entire fishing trip. In addition also waypoints are recorded (e.g. start/end of the haul, beginning/end of set net) for each fishing activity. This data is later used for locality shape file creation, measuring the length of hauls and nets, and to obtain exact timestamps (e.g. time of start/end of the haul, start/end of fishing trip).

3.4.2.2 Division of catch and subsampling

The first division of the catch is always made by the fishermen. They divide organisms to retain and unwanted fraction. The details of both categories are later recorded by scientific observers on board the fishing vessel. In practice, it is not possible to measure all retained and discarded specimens. For this reason, we use subsampling at three levels. This allows us to extrapolate the data at the fishing trip or individual catch level (Figure 1).

3.4.2.3 Sampling protocol sheets and variables collected

Scientific observers aboard fishing vessels utilize three protocol sheets: sampling, species, specimen and extended biometry. Their content is described below.

3.4.2.3.1 Sampling

For each fishing activity, a sampling protocol sheet (Appendix 1) is used. It is divided into four sections: locality, sampling, abiotic parameters, and staff. The collected variables are listed in Table 4.

Table 4 Variables collected for discard and incidental by-catch are recorded on the protocol sheet titled "Sampling."

Division	Variables
locality	(1) locality ID, (2) locality name, (3) country ID, (4) valid from [date], (5) valid to [date], (6) notes
sampling	(1) sampling number ID, (2) project ID, (3) sampling parent number ID, (4) field work start [UTC], (5) field work end [UTC], (6) field work selectivity factor, (7) sampling start [UTC], (8) sampling end [UTC], (9) sampling is valid, (10) locality ID, (11) vessel ID, (12) sampler ID, (13) number of samplers, (14) sampling selectivity ID, (15) sampling selectivity factor, (16) length of the area sampled [m], (17) length measurement method ID, (18) height of the area sampled [m], (19) height measurement method ID, (20) width of the area sampled [m], (21) width measurement method ID, (22) document type ID, (23) document number, (24) metier ID, (25) notes, (26) record status ID
abiotic parameters	(1) ordinal number, (2) notes, (3) measurement time [UTC], (4) latitude, (5) longitude, (6) gps ID, (7) water depth [m], (8) depth gauge ID, (9) water temperature [°C], (10) water depth of temperature measurement [m], (11) thermometer (water) ID
staff	(1) ordinal number, (2) person ID, (3) person function ID, (4) notes

3.4.2.3.2 Species and categories

For each sampling (fishing activity), one or more species protocol sheets are utilized (Appendix 2). The species protocol sheets are linked to the sampling protocol sheet using a sampling ID. The species protocol sheet contains data about the species, its status (target or incidental), category, and subsample of a category. The collected variables are listed in Table 5.

Table 5 Variables collected for discard and incidental by-catch are recorded on the protocol sheets titled "Species and Categories."

Division	Variables
Species	(1) species ID, (2) original species name, (3) species status ID, (4) determination key ID, (5) determination status ID, (6) determination notes, (1) ordinal number, (2) person ID
Categories	(1) category ID, (2) category status ID, (3) mass of specimens in category [g], (4) number of specimens in subsample, (5) mass of specimens in subsample [g]

3.4.2.3.3 Specimen

For each sampling (fishing activity), one or more specimen protocol sheets are utilized (Appendix 3). The specimen protocol sheets are linked to the species protocol sheet using sampling ID, species, category, and category status. The specimen protocol sheet contains biometric and other data for each specimen. The collected variables are listed in Table 6.

Table 6 Variables collected for discard and incidental by-catch are recorded on the protocol sheet titled "Specimen".

Division	Variables
Specimen	(1) sampling number ID, (2) species ID, (3) category ID, (4) category status ID, (5) treatment date, (6) specimen ID, (7) bm1 [mm], (8) bm2 [mm], (9) bm3 [mm], (10)

	bm4 [mm], (11) bm5 [mm], (12) specimen mass [g], (13) balance (specimen) ID, (14) specimen condition ID, (15) sex ID, (16) gonad maturity ID, (17) gonad mass [g], (18) balance (gonad) ID, (19) specimen released alive

Basic biometry is recorded in columns bm1 to bm5, according to the higher taxonomic group.

3.4.2.3.4 Extended biometry

Morphometric data not included on the protocol sheet titled "Specimen," and meristic data are recorded on the protocol sheet titled "Extended biometry" (Appendix 4). This protocol sheet is also used for research surveys. The data on extended biometry protocol sheets are linked to the specimen protocol sheet using the specimen ID. The variables collected are listed in Table 7.

Table 7 Extended morphometric and meristic variables are recorded on the protocol sheet titled "Extended biometry."

Division	**Variables**
Extended biometry	**(1) specimen ID, (2) treatment date, (3) biometry category ID, (4) measurement value, (5) notes**

3.5 Research surveys

Mandatory research surveys at sea are listed in table 1 of Commission Implementing Decision (EU) 2021/1168[21]. In addition to mandatory surveys Slovenia, in the national work plan, has set out the national research surveys at sea to be carried on.

3.5.1 MEDITS

International Bottom Trawl Survey in the Mediterranean is a mandatory research survey, listed in Table 1 of the Commission Implementing Decision (EU) 2021/1168[22]. Objective of MEDITS is to produce biological data on the demersal resources in the Mediterranean Sea. The survey follows the latest sampling protocol, available on https://www.sibm.it/MEDITS%202011/principaledownload.htm.

In Slovenia, the survey is carried out using a research vessel chartered from one of the neighbouring countries. The survey is carried out at two sampling stations in the Slovenian sea (Figure 2). The net is towed parallel to the Slovenian coast so that it intersects the stations. Minor spatial variations are due to avoiding other vessels or set fishing nets.

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[21] https://eur-lex.europa.eu/eli/dec_impl/2021/1168/oj

[22] https://eur-lex.europa.eu/eli/dec_impl/2021/1168/oj

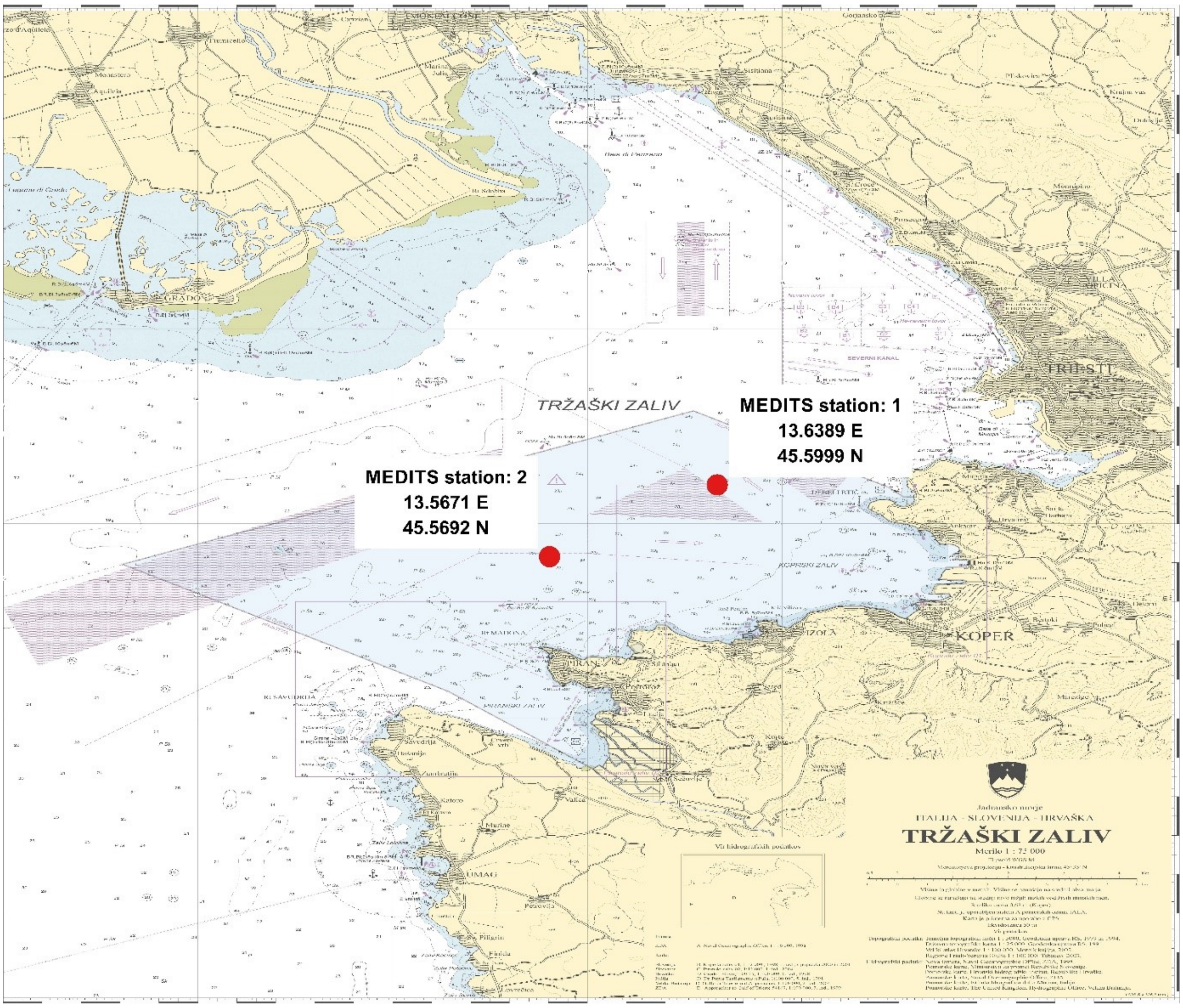


Figure 2 Sampling stations on the Slovenian sea where the MEDITS survey is carried out.

Slovenian scientists are on board the research vessel during the survey. Catches are sorted according to the species on board the vessel. Of all species, we record the total weight and number of specimens. Target species are taken to the laboratory where detailed biological data (length, weight, sex, sexual maturity) are recorded. In accordance with the sampling protocol, *sagitta* otoliths are dissected from some species for subsequent age determination. From 2023, we also take stomachs of European hake (*Merluccius merluccius*) for stomach content analysis. All data is entered into the database BIOS. This allows us to produce reports according to the MEDITS protocol.

Stomach content data are recorded on the protocol sheet titled "Stomach content analysis" (Appendix 8). This protocol sheet is also used for the OTBSLO survey. The data on the stomach content analysis protocol sheets are linked to the specimen protocol sheet using the specimen ID. The variables collected are listed in Table 8.

Table 8 All possible stomach content analysis variables collected within the framework of the MEDITS and OTBSLO surveys.

Division	**Variables**

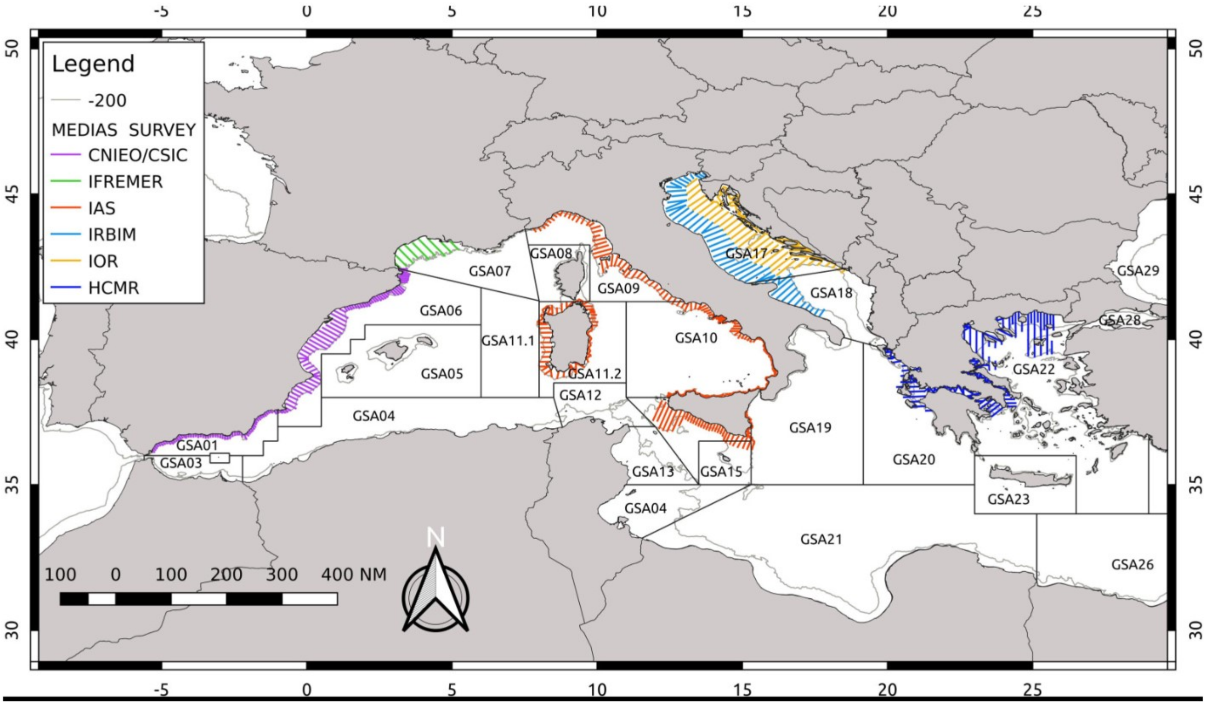
Interactions	(1) interaction type ID, (2) series number ID, (3) interaction data source, (4) specimen ID, (5) interaction data source label, (6) specimen interaction, (1) species ID, (2) original species name, (3) treatment date, (4) number of specimens, (5) wet mass [g], (6) dry mass [g], (7) volume [mL], (8) volume share [%], (9) determination status, (10) determination notes, (11) notes

3.5.2 MEDIAS

Mediterranean International Acoustic Survey or Pan-Mediterranean Acoustic Survey is a mandatory research survey, listed in Table 1 of the Commission Implementing Decision (EU) 2021/1168[23]. Objective of MEDIAS is to produce biological data on the small pelagic resources in the Mediterranean Sea. The survey follows the latest sampling protocol, available on http://www.medias-project.eu/medias/website/handbooks-menu.html.

In Slovenia, the survey is carried out using a research vessel chartered from one of the neighbouring countries. The acoustic part of the survey is performed on transects (Figure 3). Fish sampling acquired with a pelagic trawl net is required to collect representative samples to obtain biological data. Sampling intensity and sampling stations of the hauls cannot be pre-determined.

Slovenian scientists are on board the research vessel during the survey, but they are involved only in sorting of catches. The acoustic data and biological parameters are processed by scientists from a chartered research vessel. They are also contractually obliged to produce the reports.



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[23] https://eur-lex.europa.eu/eli/dec_impl/2021/1168/oj

Figure 3 Transects on which MEDIAS survey in Mediterranean is carried out.

3.5.3 SOLEMON

Rapido trawl surveys in the Northern Adriatic Sea or Beam Trawl Survey (GSA 17) is a mandatory research survey, listed in Table 1 of the Commission Implementing Decision (EU) 2021/1168[24]. Objective of SOLEMON is to produce distribution, relative abundance and biological data on benthic commercial marine species in GSA 17 for use in stock assessment and fishery management. The primary target species is the common sole (*Solea solea*). Further target species include spottail mantis squillid (*Squilla mantis*), common cuttlefish (*Sepia officinalis*), great Mediterranean scallop (*Pecten jacobaeus*), queen scallop (*Aequipecten opercularis*), turbot (*Scophthalmus maximus*), brill (*Scophthalmus rhombus*), European hake (*Merluccius merluccius*), red mullet (*Mullus barbatus*), skates (Rajdae) and the caramote prawn (*Penaeus kerathurus*). The survey follows the latest sampling protocol, available on https://dcf-italia.cnr.it/#/documenti/linee-guida.

In Slovenia, the survey is carried out using a research vessel chartered from one of the neighboring countries. The survey is carried out at one sampling station in the Slovenian sea (Figure 4). The beam trawl net (rapido) is towed parallel to the Slovenian coast so that it intersects the station. Minor spatial variations are due to avoiding other vessels or set fishing nets. Due to the large quantities of macro benthos, the towing time in Slovenia is reduced to five minutes. In this case, the haul is repeated and the catches are pooled together.

Slovenian scientists are on board the research vessel during the survey, but they are involved only in sorting of catches. The biological parameters are processed by scientists from a chartered research vessel. They are also contractually obliged to produce the reports.

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[24] https://eur-lex.europa.eu/eli/dec_impl/2021/1168/oj

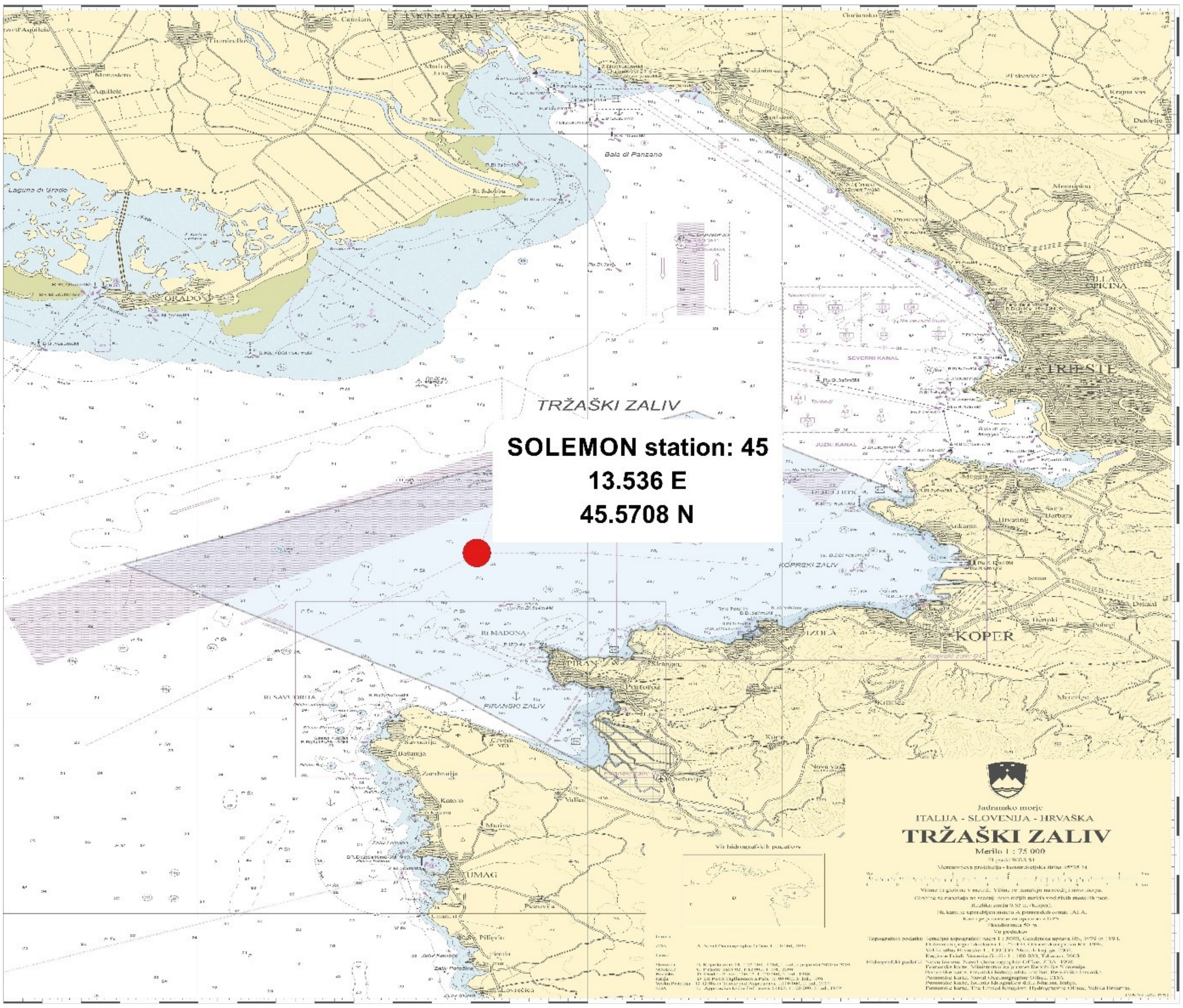

Figure 4 Sampling station on the Slovenian sea where the SOLEMON survey is carried out.

3.5.4 OTBSLO

Monitoring of fisheries resources with otter bottom trawl in the fishing sea of the Republic of Slovenia (OTBSLO) is the national research survey started in 1995. From 1995 to 2017, the survey was financed by the budget of the Republic of Slovenia. In 2018, the survey was included in the Work Plan for data collection in the fisheries and aquaculture sectors for the first time.

The main objective of the survey is to collect biological data on all species, with a particular focus on demersal species, caught by otter bottom trawl that are of commercial interest. The survey is conducted four times a year (quarterly), providing more detailed biological data, especially regarding gonad maturity and the spawning period.

The sampling design primarily follows the sampling design outlined in the MEDITS survey protocol (see Paragraph 3.5.1), with some deviations. The survey is conducted using a chartered fishing vessel and a commercial bottom trawl at three systematically defined stations (Figure 5Figure 5 Sampling stations in the Slovenian Sea where the OTBSLO survey is conducted.), with quarterly sampling carried out four times a year. The hauling time for each trawl is 40 minutes. While there is no specific target species list for the survey, it encompasses all species of fish, cephalopods, and commercial crustaceans. Furthermore, information on benthic organisms is also recorded during the survey. From 2023, we also take stomachs of European hake (*Merluccius merluccius*) for stomach content analysis.

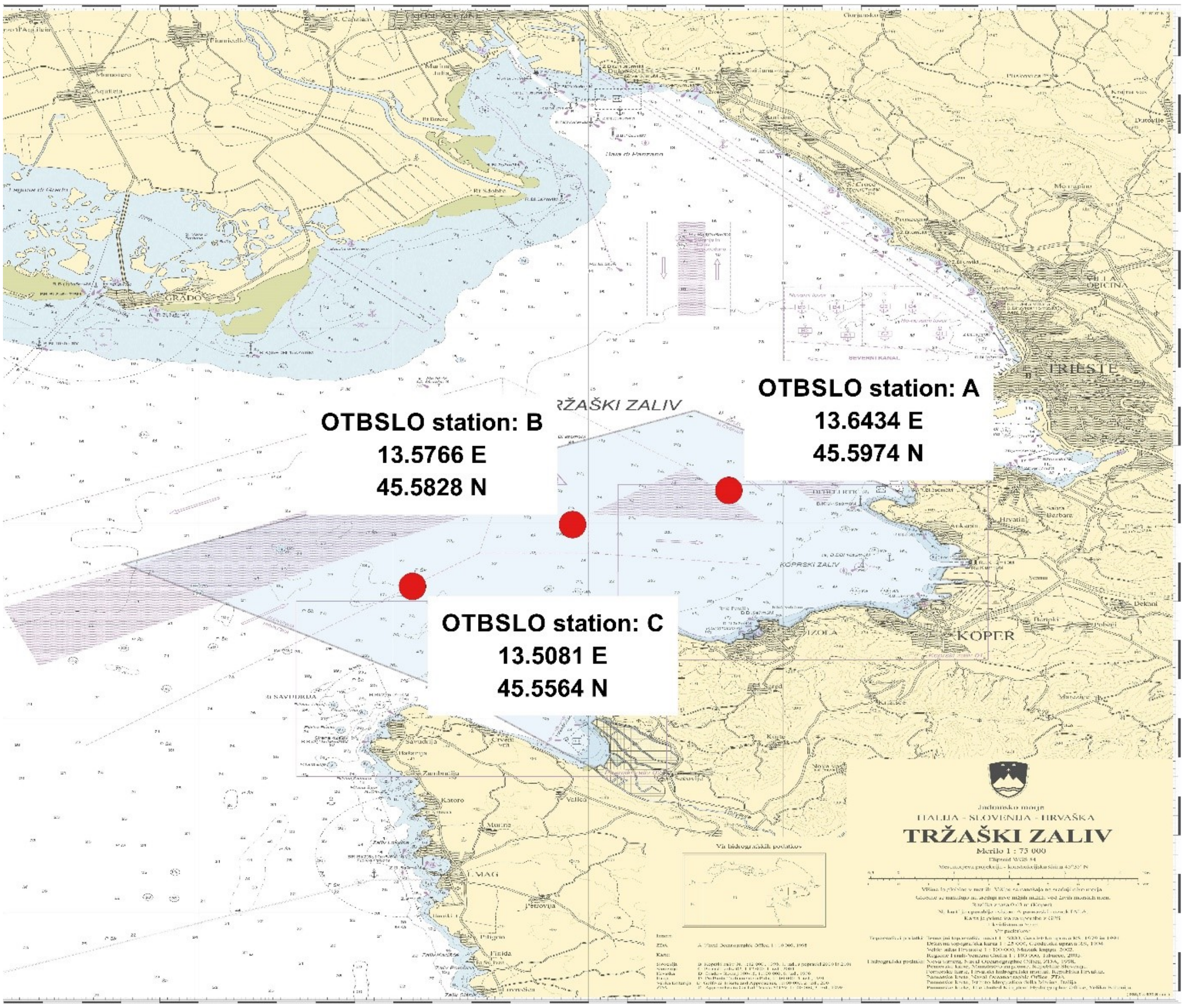

Figure 5 Sampling stations in the Slovenian Sea where the OTBSLO survey is conducted.

3.5.5 OTB_VOL

Monitoring of catch composition with otter bottom trawl (type "volantina") in the specific stretch between 1.5 and 3 nautical miles from the coast in Slovenian waters (OTB_VOL) is the national research survey started in 2016. From 2016 to 2017, the survey was financed by the budget of the Republic of Slovenia. In 2018, the survey was included in the Work Plan for data collection in the fisheries and aquaculture sectors for the first time.

The survey was designed to collect data for Slovenia to request a derogation from the first subparagraph of Article 13(1) of Regulation (EC) no. 1967/2006[25]. This derogation pertains to the use of "volantina" type trawlers in Slovenia's territorial waters at depths of less than 50 meters within the stretch between 1.5 and 3 nautical miles from the coast (Figure 6). Slovenia initially submitted a request for derogation on February 8, 2013. The request was approved by Commission Implementing Regulation (EU) No 277/2014 on March 19, 2014, which granted the derogation concerning the minimum distance from the coast and the minimum sea depth for trawlers using "volantina" in Slovenia's territorial waters. Any subsequent requests for derogations must be supported by catch structure survey data.

The sampling design primarily follows the sampling design outlined in the "Discard and incidental by-catch" (BCD) paragraph (see Paragraph 3.4), with some deviations. The survey is conducted aboard 12 fishing vessels that hold a special permit, in accordance with the derogation, to fish within a stretch of 1.5 to 3.0 nautical miles from the coast. The fishing gear used must always be the "volantina" type of otter bottom trawl, and the fishing activity is limited to the same stretch of 1.5 to 3.0 nautical miles from the coast. The temporal stratification of the sampling entails conducting two samples every two months, resulting in a total of 12 samples per year.

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[25] https://eur-lex.europa.eu/legal-content/en/ALL/?uri=CELEX%3A32006R1967

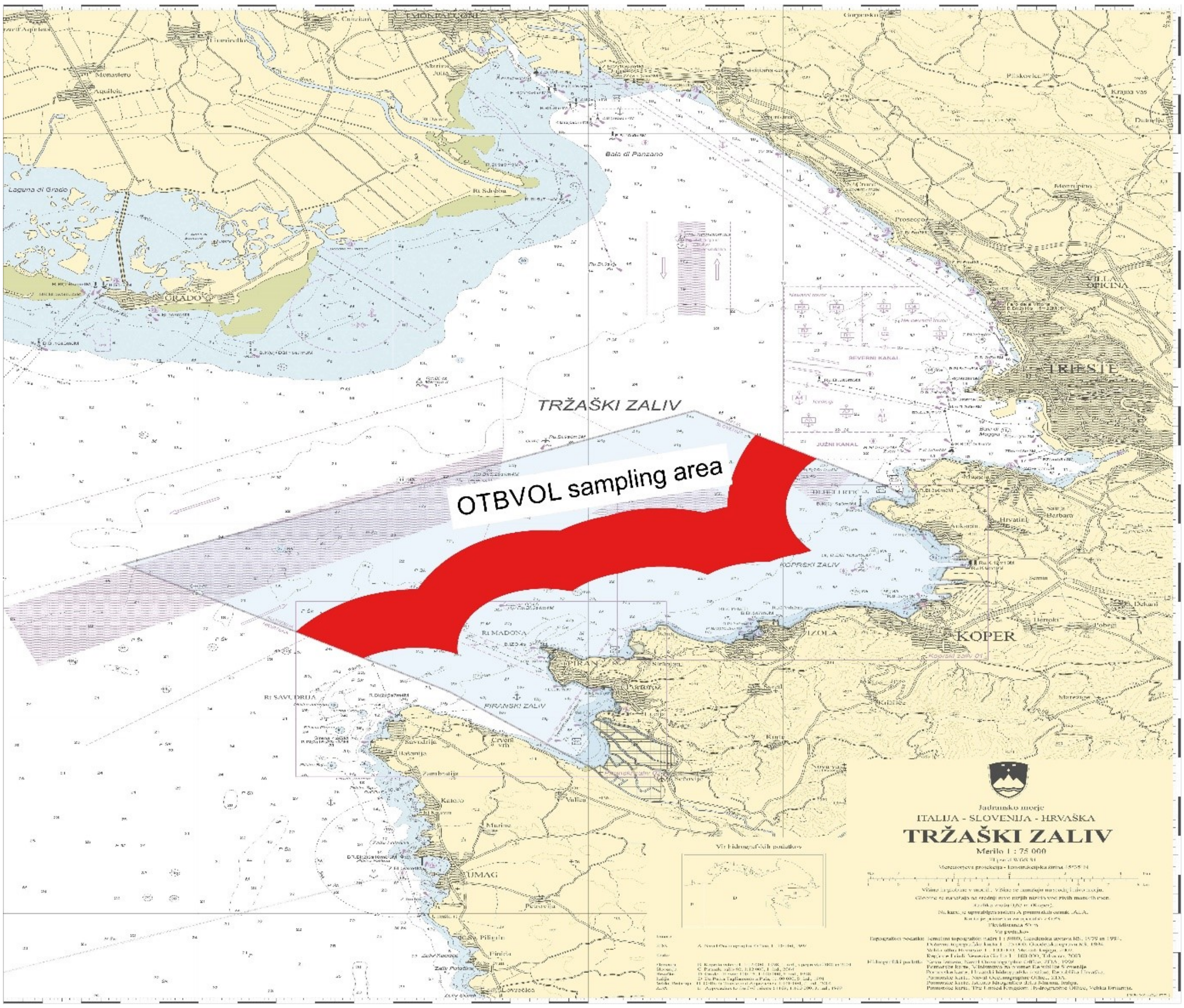

Figure 6 The sampling area in the Slovenian Sea where the OTB_VOL survey is conducted.

3.6 Stomach content analysis

Stomach content analysis was included for hake (*Merluccius merluccius*) for the first time in the 2023 Work Plan for data collection in the fisheries and aquaculture sectors[26]. The work plan was approved by the European Commission on December 18, 2022 (C(2022) 9879 final)[27].

In general the sampling protocol is following methodology and guidelines described in Guijarro (2016) and Guijarro et al. (2019). The analysis of stomach contents begins in the laboratory with the dissection of the fish and isolation of the stomach. The stomach contents are either processed immediately or the stomachs are stored for later processing in deep freeze.

For the analysis of stomach contents, the BIOS database includes the collection of various parameters. Some parameters are recorded at the specimen level, representing the predator (e.g., total stomach

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[26] SLOVENIAN Work Plan for data collection in the fisheries and aquaculture sectors 2022-2024.

[27] IZVEDBENI SKLEP KOMISIJE z dne 18.12.2022 o spremembi Izvedbenega sklepa C(2022) 696 o odobritvi delovnega načrta Slovenije za zbiranje podatkov v sektorjih ribištva in akvakulture za leta 2022–2024.

content mass, stomach fullness). More detailed data on prey are recorded in a linked table at the level of preyed taxa. In the linked table, we record the identified taxa found in the stomach contents along with their quantities (e.g., number of individuals, their mass).

3.6.1 Sampling protocol sheets and variables collected

Parameters for stomach content analysis are collected in the laboratory and recorded on protocol sheets (Appendix 8).

Parameters at the level of the specimen (predator)

The mass of the stomach content (column: stomach_content_mass). This is total mass of the stomach content in grams.

The stomach contents condition (column: stomach_content_condition_id). As the mass can vary depending on the storage method of the stomach contents, the mass measurements are labelled with the corresponding storage method (e.g., fresh, defrosted, preserved in alcohol, etc.).

The degree of fullness of the stomach (column: stomach_fullness_id). For each stomach, we also record an assessment of its fullness (e.g., empty, full, everted).

Parameters at the level of preyed taxa

Taxon (column: taxon_id). The ID of the taxon is recorded at the lowest possible taxonomic level that we have identified.

Treatment date (column: treatement_date). The date of processing the biological material is recorded.

Number of specimens (column: specimen_no). The number of specimens belonging to a specific taxon is recorded.

Wet mass (column: wet_mass). The wet mass in grams of specimens belonging to a specific taxon is recorded.

Taxon determination status code (column: determination_status_id): determination correct or determination doubtful.

Notes on taxon determination (column: determination_notes).

General notes (column: notes).

4 References

Carpentieri, P., Nastasi, A., Sessa, M. & Srour, A., eds. 2021. Incidental catch of vulnerable species in Mediterranean and Black Sea fisheries – A review. Studies and Reviews No. 101 (General Fisheries Commission for the Mediterranean). Rome, FAO. https://doi.org/10.4060/cb5405en

GFCM, 2018, GFCM Data Collection Reference Framework (DCRF). Version: 23, Rome, 171 pp.

Grati, F., Carlson, A., Carpentieri, P. & Cerri, J. 2021. Handbook for data collection on recreational fisheries in the Mediterranean and the Black Sea. FAO Fisheries and Aquaculture Technical Paper No. 669. Rome, FAO. https://doi.org/10.4060/cb5403en

Guijarro B., 2016, Deliverable 3.3. Protocols and guidelines for sampling, processing and analysing the stomach contents (MARE/2014/19), 21 pp.

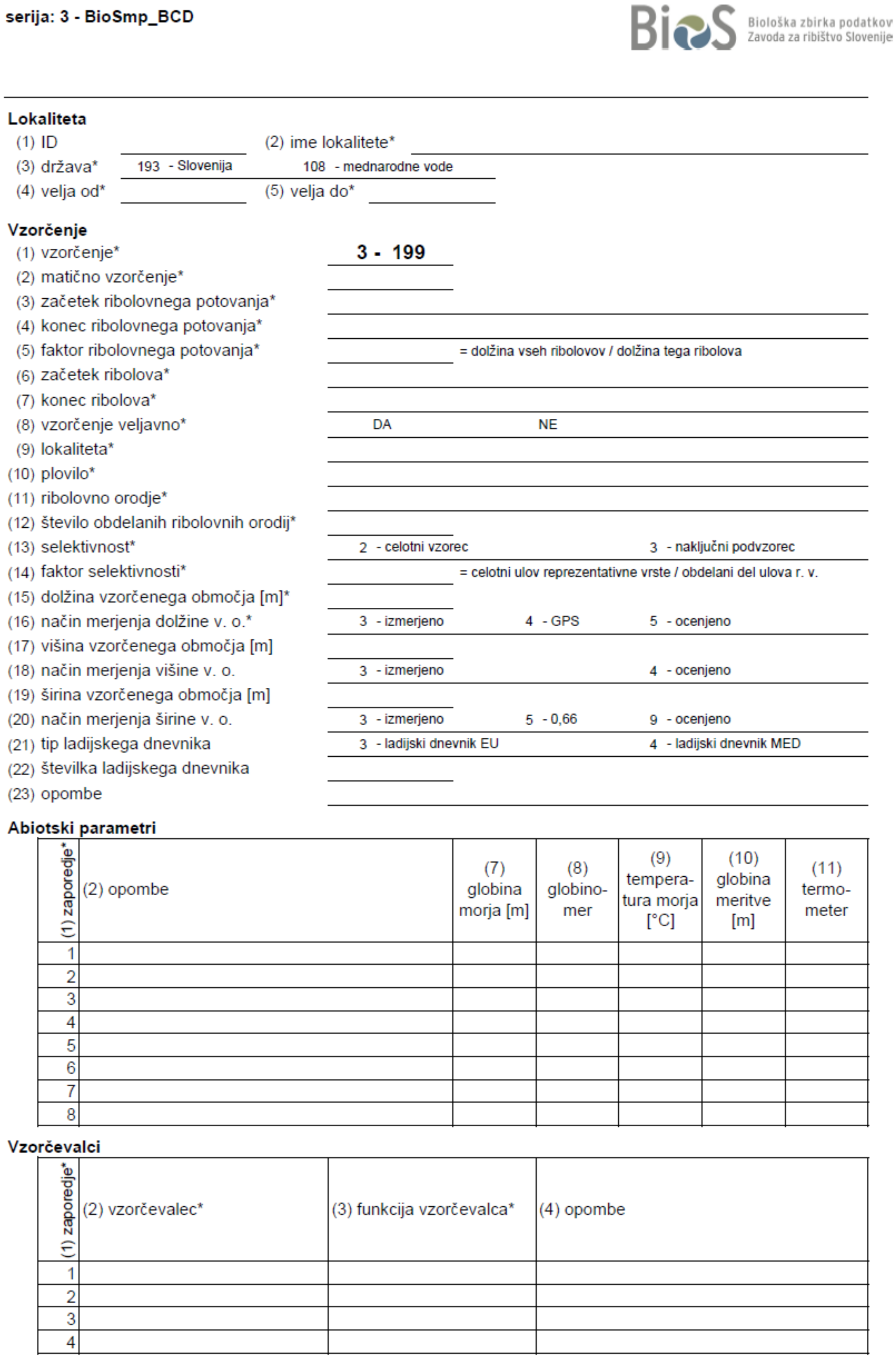
Guijarro, B., Sartor, P., Daskalov, G., Georgieva, I., Panayotova, M. & Rajkov, V., 2019, Deliverable D. 4.1 - Updated protocols and guidelines for collection, processing and analysis of stomach contents (MARE/2016/22), 28 pp.

Heales, D. S., Brewer, D. T. & Wang, Y., 2000, Subsampling multi-species trawl catches from tropical northern Australia: Does it matter which part of the catch is sampled?, Fisheries Research, 48, 117-126, https://doi.org/10.1016/S0165-7836(00)00182-X

MEDITS Working Group, 2017, International bottom trawl survey in the Mediterranean. Instruction manual. Version 9, 106 pp.

5 Appendices

Appendix 1 Discard and incidental by-catch – sampling protocol sheet.



serija: 3 - BioSmp_BCD

Biološka zbirka podatkov
Zavoda za ribištvo Slovenije

Lokaliteta

(1) ID ______ (2) ime lokalitete* ______
(3) država* 193 - Slovenija 108 - mednarodne vode
(4) velja od* ______ (5) velja do* ______

Vzorčenje

(1) vzorčenje* **3 - 199**
(2) matično vzorčenje* ______
(3) začetek ribolovnega potovanja* ______
(4) konec ribolovnega potovanja* ______
(5) faktor ribolovnega potovanja* ______ = dolžina vseh ribolovov / dolžina tega ribolova
(6) začetek ribolova* ______
(7) konec ribolova* ______
(8) vzorčenje veljavno* DA NE
(9) lokaliteta* ______
(10) plovilo* ______
(11) ribolovno orodje* ______
(12) število obdelanih ribolovnih orodij* ______
(13) selektivnost* 2 - celotni vzorec 3 - naključni podvzorec
(14) faktor selektivnosti* ______ = celotni ulov reprezentativne vrste / obdelani del ulova r. v.
(15) dolžina vzorčenega območja [m]* ______
(16) način merjenja dolžine v. o.* 3 - izmerjeno 4 - GPS 5 - ocenjeno
(17) višina vzorčenega območja [m] ______
(18) način merjenja višine v. o. 3 - izmerjeno 4 - ocenjeno
(19) širina vzorčenega območja [m] ______
(20) način merjenja širine v. o. 3 - izmerjeno 5 - 0,66 9 - ocenjeno
(21) tip ladijskega dnevnika 3 - ladijski dnevnik EU 4 - ladijski dnevnik MED
(22) številka ladijskega dnevnika ______
(23) opombe ______

Abiotski parametri

(1) zaporedje*	(2) opombe	(7) globina morja [m]	(8) globino-mer	(9) tempera-tura morja [°C]	(10) globina meritve [m]	(11) termo-meter
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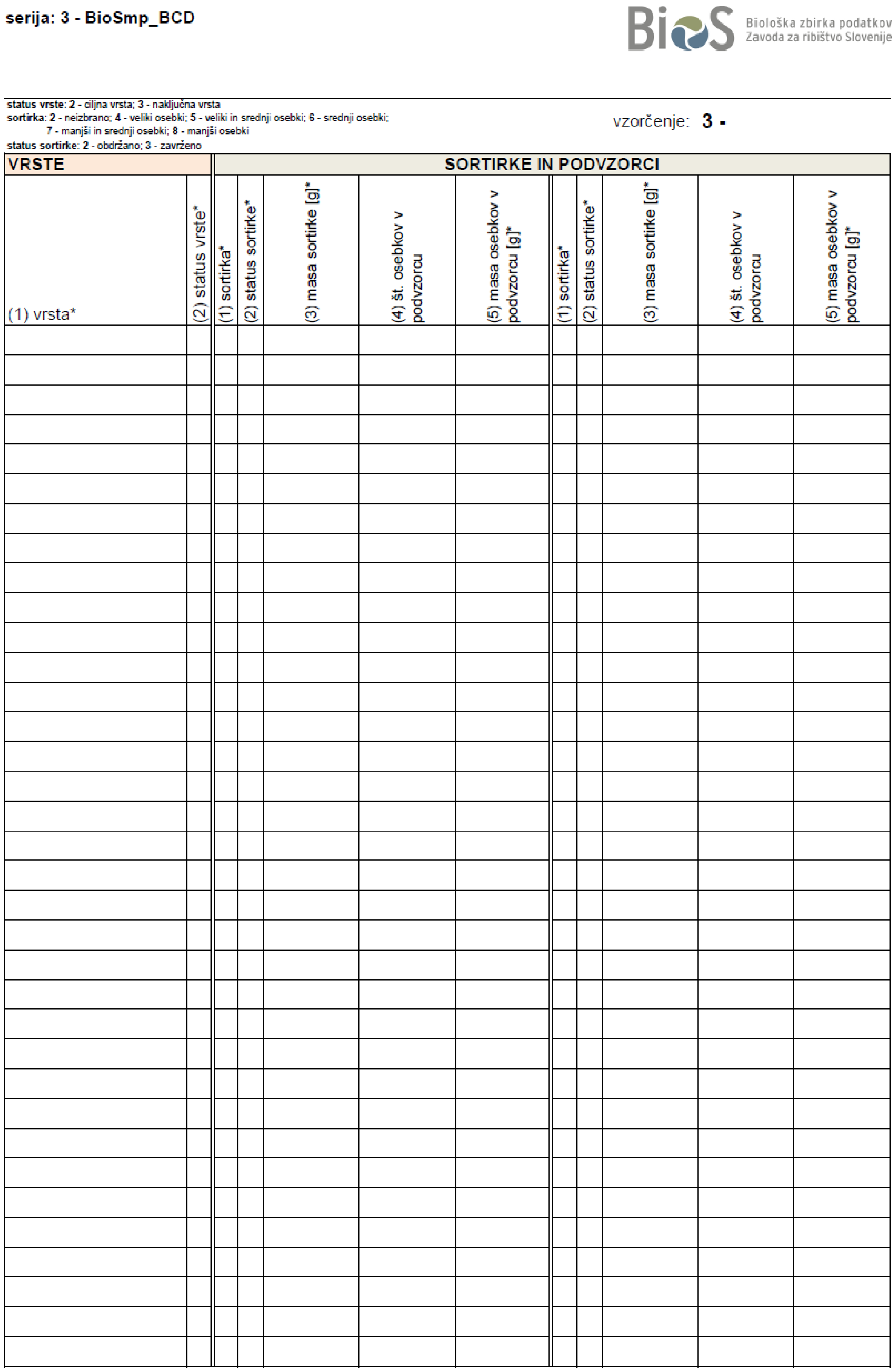
8						

Vzorčevalci

(1) zaporedje*	(2) vzorčevalec*	(3) funkcija vzorčevalca*	(4) opombe
1			
2			
3			
4			

Appendix 2 Discard and incidental by-catch – species protocol sheet.



serija: 3 - BioSmp_BCD

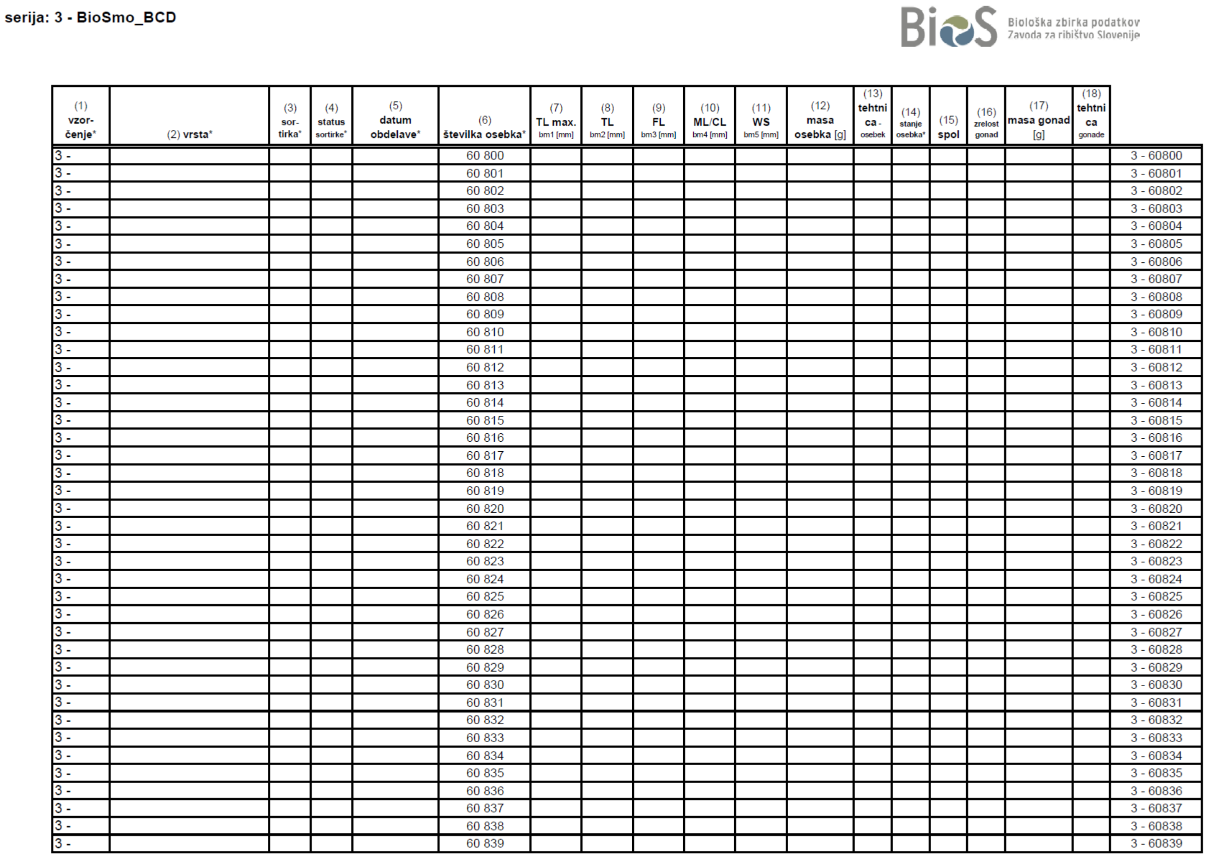
Biološka zbirka podatkov
Zavoda za ribištvo Slovenije

status vrste: **2** - ciljna vrsta; **3** - naključna vrsta
sortirka: **2** - neizbrano; **4** - veliki osebki; **5** - veliki in srednji osebki; **6** - srednji osebki;
7 - manjši in srednji osebki; **8** - manjši osebki
status sortirke: **2** - obdržano; **3** - zavrženo

vzorčenje: **3 -**

VRSTE		**SORTIRKE IN PODVZORCI**									
(1) vrsta*	(2) status vrste*	(1) sortirka*	(2) status sortirke*	(3) masa sortirke [g]*	(4) št. osebkov v podvzorcu	(5) masa osebkov v podvzorcu [g]*	(1) sortirka*	(2) status sortirke*	(3) masa sortirke [g]*	(4) št. osebkov v podvzorcu	(5) masa osebkov v podvzorcu [g]*

Appendix 3 Discard and incidental by-catch – specimen protocol sheet.



serija: 3 - BioSmo_BCD

Biološka zbirka podatkov
Zavoda za ribištvo Slovenije

(1) **vzor-čenje***	(2) **vrsta***	(3) **sor-tirka***	(4) **status** sortirke*	(5) **datum obdelave***	(6) **številka osebka***	(7) **TL max.** bm1 [mm]	(8) **TL** bm2 [mm]	(9) **FL** bm3 [mm]	(10) **ML/CL** bm4 [mm]	(11) **WS** bm5 [mm]	(12) **masa osebka** [g]	(13) **tehtnica -** osebek	(14) stanje osebka*	(15) **spol**	(16) zrelost gonad	(17) **masa gonad** [g]	(18) **tehtnica** gonade	
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3 -					60 803													3 - 60803
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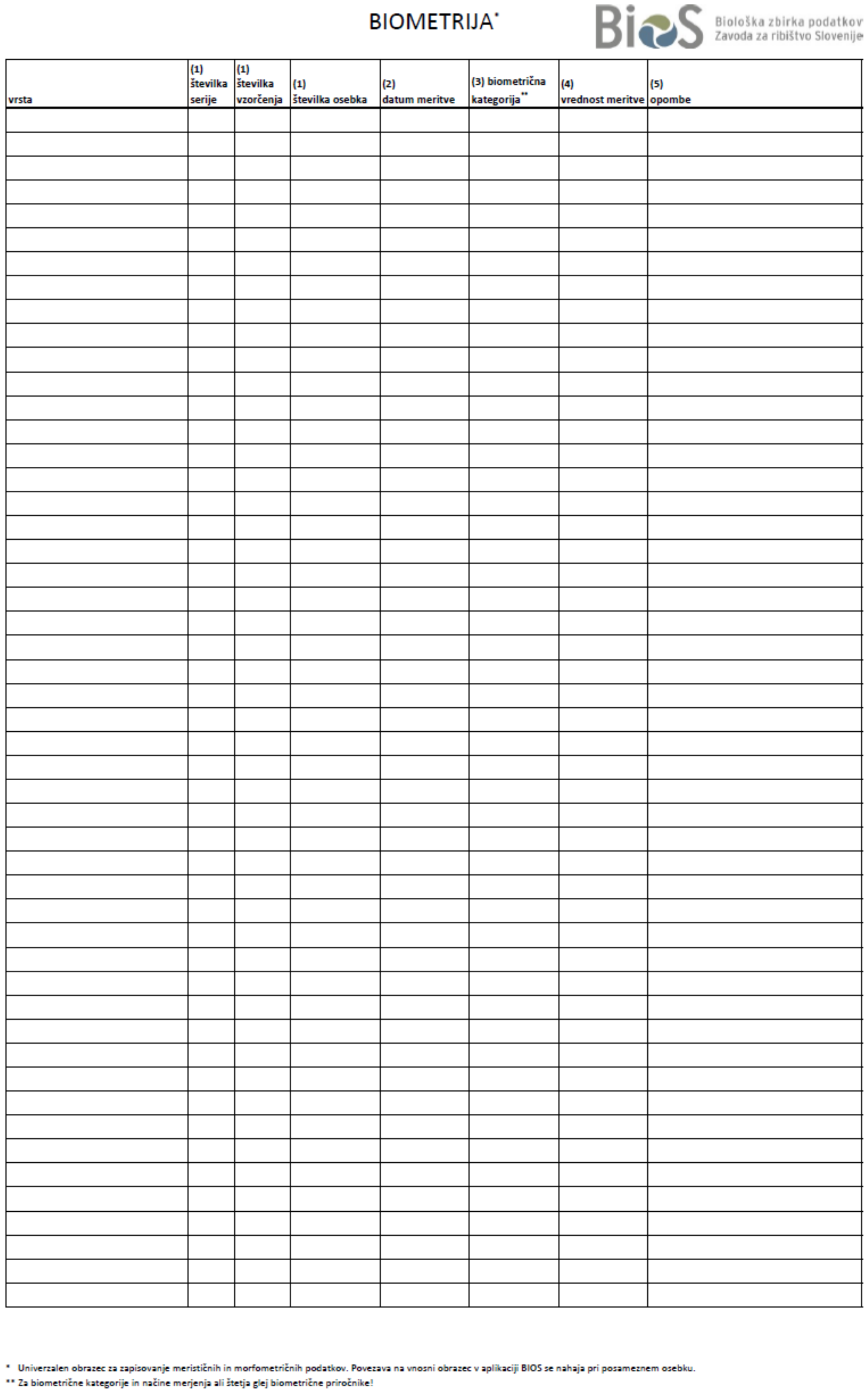
3 -					60 834													3 - 60834
3 -					60 835													3 - 60835
3 -					60 836													3 - 60836
3 -					60 837													3 - 60837
3 -					60 838													3 - 60838
3 -					60 839													3 - 60839

Appendix 4 Discard and incidental by-catch – extended biometry protocol sheet.



BIOMETRIJA*

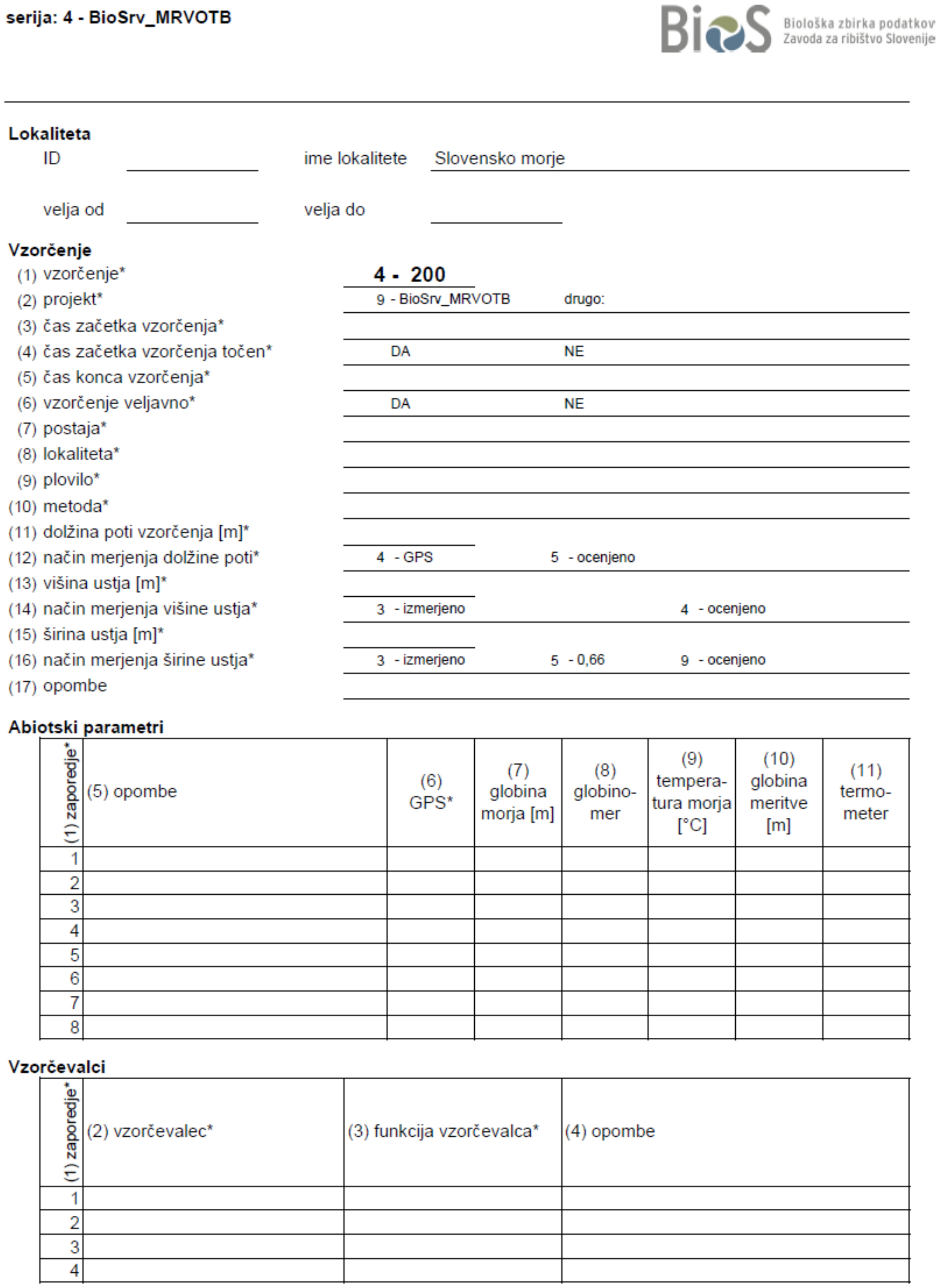
Biološka zbirka podatkov
Zavoda za ribištvo Slovenije

vrsta	(1) številka serije	(1) številka vzorčenja	(1) številka osebka	(2) datum meritve	(3) biometrična kategorija**	(4) vrednost meritve	(5) opombe

* Univerzalen obrazec za zapisovanje merističnih in morfometričnih podatkov. Povezava na vnosni obrazec v aplikaciji BIOS se nahaja pri posameznem osebku.

** Za biometrične kategorije in načine merjenja ali štetja glej biometrične priročnike!

Appendix 5 Research surveys – OTBSLO – sampling protocol sheet.



serija: 4 - BioSrv_MRVOTB

Biološka zbirka podatkov
Zavoda za ribištvo Slovenije

Lokaliteta

ID ____________ ime lokalitete Slovensko morje

velja od ____________ velja do ____________

Vzorčenje

(1) vzorčenje* **4 - 200**
(2) projekt* 9 - BioSrv_MRVOTB drugo:
(3) čas začetka vzorčenja*
(4) čas začetka vzorčenja točen* DA NE
(5) čas konca vzorčenja*
(6) vzorčenje veljavno* DA NE
(7) postaja*
(8) lokaliteta*
(9) plovilo*
(10) metoda*
(11) dolžina poti vzorčenja [m]*
(12) način merjenja dolžine poti* 4 - GPS 5 - ocenjeno
(13) višina ustja [m]*
(14) način merjenja višine ustja* 3 - izmerjeno 4 - ocenjeno
(15) širina ustja [m]*
(16) način merjenja širine ustja* 3 - izmerjeno 5 - 0,66 9 - ocenjeno
(17) opombe

Abiotski parametri

(1) zaporedje*	(5) opombe	(6) GPS*	(7) globina morja [m]	(8) globinomer	(9) temperatura morja [°C]	(10) globina meritve [m]	(11) termometer
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Vzorčevalci

(1) zaporedje*	(2) vzorčevalec*	(3) funkcija vzorčevalca*	(4) opombe
1			
2			
3			
4			

Appendix 6 Research surveys – OTBSLO – species protocol sheet.

serija: 4 - BioSrv_MRVOTB

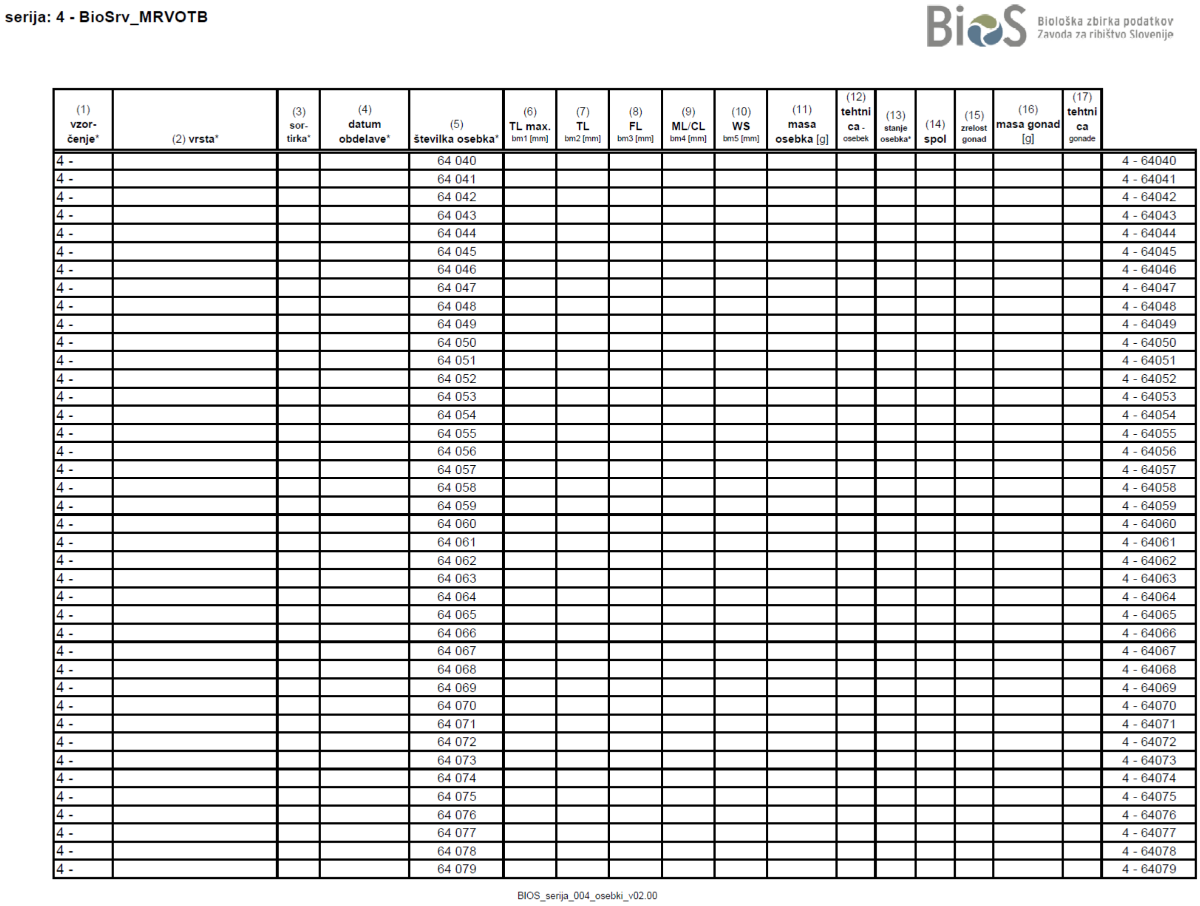
Biološka zbirka podatkov
Zavoda za ribištvo Slovenije

vzorčenje* **4 -**

Vrste	**Podvzorci**							
(1) vrsta*	(1) sortirka*	(2) masa sortirke [g]*	(3) št. osebkov v podvzorcu	(4) masa osebkov v podvzorcu [g]*	(1) sortirka*	(2) masa sortirke [g]*	(3) št. osebkov v podvzorcu	(4) masa osebkov v podvzorcu [g]*

BIOS_serija_004_vrste_v02.00

Appendix 7 Research surveys – OTBSLO – specimen protocol sheet.



serija: 4 - BioSrv_MRVOTB

Biološka zbirka podatkov Zavoda za ribištvo Slovenije

(1) **vzorčenje***	(2) vrsta*	(3) **sortirka***	(4) **datum obdelave***	(5) **številka osebka***	(6) **TL max.** bm1 [mm]	(7) **TL** bm2 [mm]	(8) **FL** bm3 [mm]	(9) **ML/CL** bm4 [mm]	(10) **WS** bm5 [mm]	(11) **masa osebka** [g]	(12) **tehtnica -** osebek	(13) stanje osebka*	(14) **spol**	(15) zrelost gonad	(16) **masa gonad** [g]	(17) **tehtnica** gonade	
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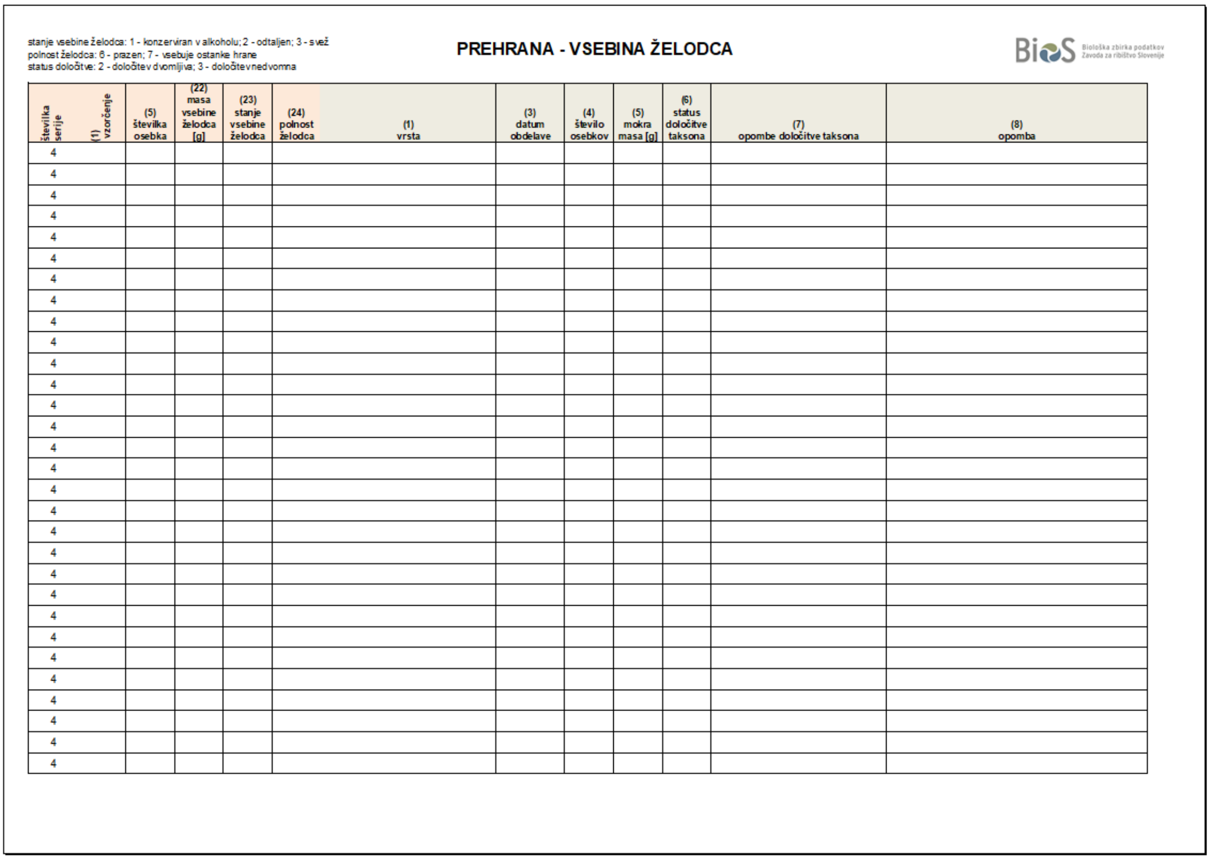
BIOS_serija_004_osebki_v02.00

Appendix 8 Research surveys – OTBSLO + MEDITS– stomach content analysis protocol sheet.



stanje vsebine želodca: 1 - konzerviran v alkoholu; 2 - odtaljen; 3 - svež
polnost želodca: 6 - prazen; 7 - vsebuje ostanke hrane
status določitve: 2 - določitev dvomljiva; 3 - določitev nedvomna

PREHRANA - VSEBINA ŽELODCA

Biološka zbirka podatkov Zavoda za ribištvo Slovenije

številka serije	(1) vzorčenje	(5) številka osebka	(22) masa vsebine želodca [g]	(23) stanje vsebine želodca	(24) polnost želodca	(1) vrsta	(3) datum obdelave	(4) število osebkov	(5) mokra masa [g]	(6) status določitve taksona	(7) opombe določitve taksona	(8) opomba
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