

REPORTING FORMAT FOR BIOTA DATA

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REPORTING FORMAT FOR BIOTA DATA

1 OVERVIEW OF THE BIOTA SYSTEM

The biota reporting format is used for reporting data on bio-physical characteristics, biological effects measurements, and contaminant determinations in tissues of fish, invertebrates, birds or mammals—data type ‘CF’. Although the reporting system is intended to be generally applicable for reporting data on biological effects in biota, it is, at present, only defined for reporting information for the biological effects technique ‘Mixed function oxidase (MFO) ethoxyresorufin-O-deethylase (EROD)’ measurements in fish.

Each data type has a number of record types associated with it. The record types available for biota are: The *Contaminant Analytical Methods Record* (RECID: 21), the *EROD Methods Record* (RECID: 22), the *Sample Master Record* (RECID: 01), the *Specimen/Sub-sample Data Record* (RECID: 04), the *Bird Data Record* (RECID: 05), the *Tissue Data Record* (RECID: 07), the *Parameter/Contaminant Data Record* (RECID: 10), and the *Plain Language Comment Record* (RECID: 13). Record types are combined depending on the type of biota data reported.

The biota format description includes sections explaining data file structure, short descriptions of record types, sample definitions, sections on the reporting of fish, invertebrate, mammal, bird and EROD data, tables describing layouts for each data record type, and specific examples of the use of the reporting format.

2 BIOTA DATA FILE

2.1 Data file structure

The data file consists of two parts, the methods section and the results section.

The first section, comprising a series of (one or more) *Contaminant Analytical Methods Records* and/or *EROD Methods Records*, defines the methods involved in obtaining any particular measurement of a parameter or contaminant in the biota sample(s). The ‘methods part’ of the data file generally summarizes the methods used by the various laboratories involved in the collection and analysis of the biota samples in a given year. Reporting institutes are encouraged to pay careful attention to the methods information reported each year, and should not simply assume that the information entered in the previous year’s data file can be repeated. The information reported on the various ‘*Methods Records*’ should form the basis for a historical record of changes in the procedures applied in the monitoring programmes, which is of relevance both in relation to data assessment activities and to the long-term archiving of environmental data.

The second section in the data file includes the actual results of the monitoring activity. This part of the data file is a hierarchical arrangement comprising a series of (one or more) *Sample Master Records*, each followed by a series of (one or more) *Specimen/Sub-sample Data Records*. In the case of birds, an optional *Bird Data Record* can follow the *Specimen/Sub-sample Data Record*. Otherwise, each *Specimen/Sub-sample Data Record* is followed by a series of (one or more) *Tissue Data Records*. This is also the case for the *Bird Data Record*. Finally, each *Tissue Data Record* is followed by a series of (one or more) *Parameter/Contaminant Data Records*.

Each *Sample Master Record* defines a new biota sample; each *Specimen/Sub-sample Data Record* associated with a given *Sample Master Record* defines a new sub-sample within that sample. The optional *Bird Data Record* associated with a given *Specimen/Sub-sample Data Record* gives additional information on birds in the particular sub-sample. The *Tissue Data Record(s)* associated with a given *Specimen/Sub-sample Data Record* define the tissue analysed, and each *Parameter/Contaminant Data Record* associated with a given *Tissue Data Record* reports the measurements made for a given parameter in that tissue. *Plain language Comment Records* may also be included after any record, as appropriate.

Links between the information contained on the *Parameter/Contaminant Data Records* and that contained on the *Contaminant Analytical Methods Records* and/or *EROD Methods Records* are established using link-keys as described below in Section 2.3.

Figure A is a schematic representation of the data file structure, illustrating the hierarchy in the data part of the file. The ‘Analytical methods record’ can be a *Contaminant Analytical Methods Record* or an *EROD Methods Record*.

Figure A – Biota data file structure

Please note that the second *Sample Master Record* below reflects the way in which the *Bird Data Record* (05-record) can be utilized to report length information on juvenile/adult bird specimens.

21 or 22 – Analytical methods recordMETHODS PART
13 – Plain language comment record	
:	
21 or 22 – Analytical methods record	
:	
01 – Sample master recordDATA PART
13 – Plain language comment record	
:	
04 – Specimen/Sub-sample data recordSub-sample cycle
13 – Plain language comment record	
:	
07 – Tissue data recordTissue cycle
13 – Plain language comment record	
:	
10 – Parameter/contaminant data record	
:	
07 – Tissue data recordTissue cycle
10 – Parameter/contaminant data record	
:	
07 – Tissue data recordTissue cycle
:	
04 – Specimen/Sub-sample data recordSub-sample cycle
07 – Tissue data recordTissue cycle
10 – Parameter/contaminant data record	
:	
:	
04 – Specimen/Sub-sample data recordSub-sample cycle
:	
01 – Sample master record	
13 – Plain language comment record	
:	
04 – Specimen/Sub-sample data recordSub-sample cycle
05 – Bird data recordBird data
07 – Tissue data recordTissue cycle
10 – Parameter/contaminant data record	
:	
:	
:	
01 – Sample master record	
:	
End of file	

The ordering of the records in a data file follows the general hierarchical system of the file structure as defined above. However, a number of possible arrangements exist for a given sample due to the different ways of constructing sub-samples (cf. Section 3.1). Furthermore, the arrangement of records for a given sample will depend on whether the data concern fish, invertebrates and mammals (which are reported via the same record types), or birds (which have an additional record type).

2.2 Data records included in the biota format

The format for reporting data on contaminants and/or biological effects measurements in biota utilizes the following types of data records:

- The *Contaminant Analytical Methods Record* (RECID: 21)
 The *Contaminant Analytical Methods Record* is a general purpose record for recording information on analytical methodologies employed in the contaminant monitoring programmes for biota, sediment and seawater. The record is used for reporting information on the method of analysis for a particular contaminant or parameter by the analytical laboratory involved, for the year concerned. In addition, it includes information on aspects of the laboratory quality assurance programme relevant to the analysis concerned, on the detection limit for the analysis, and on the laboratory's participation in relevant intercomparison exercises. A series of *Contaminant Analytical Methods Records* should be included at the beginning of the data file, describing the methods associated with any contaminant subsequently reported. Each record reports a particular combination of analytical methodologies used within a given laboratory for a single contaminant. Thus, the number of records will depend on the number of laboratory-contaminant-analysis combinations used in the data being reported. Each contaminant analysis reported later in the data file on a *Parameter/Contaminant Data Record* is unambiguously associated with a specific *Contaminant Analytical Methods Record* by means of an 'Analytical methods link' (AMLNK) identifier.
- The *EROD Methods Record* (RECID: 22)
 The *EROD Methods Record* is specifically designed for recording information on the method(s) used to obtain EROD measurements. The record is used for recording information on incubation conditions, the nature of the buffer used, the concentrations of the cofactor and substrate, etc., for the analytical laboratory involved, for the year concerned. In addition, it includes information on aspects of the laboratory quality assurance programme relevant to the EROD determination. Each EROD determination reported later in the data file on a *Parameter/Contaminant Data Record* is unambiguously associated with a specific *EROD Methods Record* by means of an 'Analytical methods link' (AMLNK) identifier.
- The *Sample Master Record* (RECID: 01)
 The *Sample Master Record* serves as the master record for the series of data deriving from a particular biota sample. The information defines a biota sample in terms of a 'sampling occasion', i.e., it locates the biota sample in space (sampling area coordinates) and time (sampling date/time), and also supplies administrative information in relation to the intended use of the data.
- The *Specimen/Sub-sample Data Record* (RECID: 04)
 The *Specimen/Sub-sample Data Record* defines a biota sub-sample as either an individual specimen or a pool of specimens. It records information on a range of biological measurements for the individual or pooled specimens concerned, and acts as a 'header' record for a series of *Tissue Data Records* (and their associated *Parameter/Contaminant Data Records*) which describe measurements made on the sub-sample defined. The concepts of 'sample' and 'sub-sample' as applied in relation to the biota data reporting formats are discussed below.
- The *Bird Data Record* (RECID: 05)
 The *Bird Data Record* records information on biological measurements specific for birds; it acts as an 'extension' of the previous *Specimen/Sub-sample Data Record*. This is in contrast to all other data records which define a new level in the hierarchical structure. The record includes information on various lengths of the specimen (or pool of specimens) concerned. The record is optional, and should only be included if the associated *Specimen/Sub-sample Data Record* concerns adult or juvenile birds. If the associated *Specimen/Sub-sample Data Record* only concerns eggs, then this record should be omitted.

- The *Tissue Data Record* (RECID: 07)
The *Tissue Data Record* defines the tissue or organ used as the matrix in which parameters reported on associated *Parameter/Contaminant Data Records* are measured; it acts as a 'header' record for a series of these *Parameter/Contaminant Data Records*. In addition, the record includes information on a number of measurements pertaining to the tissue or organ (or the homogenized pooled tissues/organs) concerned.
- The *Parameter/Contaminant Data Record* (RECID: 10)
The *Parameter/Contaminant Data Record* is used for recording data on a range of parameters in a given tissue-matrix. Each record included in the data file is associated with (i) a particular *Sample Master Record* which defines the biota sample concerned; (ii) a particular *Specimen/Sub-sample Data Record* which defines the biota sub-sample concerned; and (iii) a particular *Tissue Data Record* which defines the tissue-matrix concerned. Each *Parameter/Contaminant Data Record* includes information on a particular parameter or contaminant.
- The *Plain Language Comment Record* (RECID: 13)
Plain Language Comment Records can be inserted at any point in the data file to supply additional information or comments to aid the interpretation of the data reported on the preceding data record. If the explanatory text does not fit on a single *Plain Language Comment Record*, several of these records can be included in a block. It should be noted that, whilst information reported as plain language text will be stored at the data centre, and where possible retrieved and presented together with the data, data handling systems do not generally take account of plain language text. The comments are likely to become dissociated from the coded data, for example during exchange of data in non-ICES format for import into software packages used for data evaluation purposes. Thus, *Plain Language Comment Records* should be avoided unless they are specifically required by the reporting format.

2.3 Linking methods records to data records

The biota data reporting format involves one link-key to relate information items appearing on different data records within the data file:

- The **analytical methods link-key** associates a given measurement (as reported on a particular *Parameter/Contaminant Data Record*) with the information on the methods used to obtain that measurement, as reported on a *Contaminant Analytical Methods Record* or an *EROD Methods Record*.
The link-key is constructed by concatenating the following data fields, which appear on both the *Contaminant Analytical Methods Records/EROD Methods Record* and the *Parameter/Contaminant Data Records*:

ALABO + PARAM + AMLNK

The resulting key must be unique for each Analytical Methods Record, whether a *Contaminant Analytical Methods Record* or an *EROD Methods Record*, included in the data file. The same key can, however, appear on any number of *Parameter/Contaminant Data Records* included in the data file.

3 BIOTA SAMPLE AND SUB-SAMPLE DEFINITIONS

3.1 Definitions

For the purposes of reporting data using this format, a biota sample is considered to comprise an appropriate number of specimens of a single species, collected in a given area within a limited time period, and which are subsequently analysed/examined as a single unit, either as individual specimens or as pooled sub-samples. As the area and time period concerned are not specified in detail and a number of interpretations can be applied depending on the method of collecting organisms and the subsequent handling of the sample(s), this is not a complete specification. Additional information is to be found in relevant sets of monitoring guidelines (e.g., see GUIDE) which detail the species to be sampled, the number of specimens to be collected, length ranges to be sampled, etc., in relation to a number of defined objectives of monitoring. To ensure some degree of consistency in the use of the reporting format, the following definitions are employed:

- All data relating to the specimens collected as part of a single sample of fish, invertebrates, mammals or birds, **as defined by an appropriate set of monitoring guidelines** should be reported as a distinct sample, i.e., under a single *Sample Master Record* (RECID: 01) with a unique ‘Sample sequence number’ (data field SEQNO).
- The reporting formats can be used to report individual or pooled data depending on the type of biota reported. In some cases the specimens comprising the sample are examined/analysed individually. In other cases, the specimens comprising the sample are grouped into one or more ‘sub-samples’; analyses are then conducted on pooled material from several organisms. A third alternative is to treat a sample by a combination of both of these methods, i.e., by conducting analyses in one type of tissue individually for each specimen in the sample, and for another tissue/organ in (homogenized) pools of material from several specimens in a sub-sample. To allow the reporting format to be used for any of the above, the following sub-sample concept is employed:
 - a sub-sample can consist of a single specimen if data are reported on measurements of a contaminant/parameter in a tissue or organ deriving from that organism alone;
 - a sub-sample can consist of several specimens (up to the total number of specimens in the sample) if data are reported on measurements of a contaminant/parameter in homogenized tissue/organs deriving from all of the organisms concerned.

Each sub-sample is defined in a *Specimen/Sub-sample Data Record*. In cases where parts of the organism have been analysed individually and parts in a pool together with material from other specimens, the same organism will be a component in two sub-samples. Data for the parts of the organism analysed individually will be reported on *Parameter/Contaminant Data Record(s)* ‘belonging’ to one *Specimen/Sub-sample Data Record*, and data for the pooled parts will be reported on *Parameter/Contaminant Data Record(s)* ‘belonging’ to another *Specimen/Sub-sample Data Record*.

3.2 Replicate analyses

The difference between the ‘Sub-sample’ (SUBNO) field and ‘Replicate number’ (REPNO) data field should be noted. The REPNO item is used to distinguish **replicate analyses** of a given contaminant in a particular ‘analytical sample’, the purpose of which is to provide information on analytical reproducibility. The SUBNO data field is used to distinguish **sub-samples**, as defined above.

4 BIOTA TYPES

4.1 Fish, Invertebrates and Mammals

For reporting data on fish, invertebrates or mammals, each sample requires a new *Sample Master Record* where the species is reported in the ‘Species’ (SPECI) data field. Otherwise, the use of *Specimen/Sub-sample Data Records*, *Tissue Data Records*, and *Parameter/Contaminant Data Record(s)* is the same for each type of organism.

4.2 Birds

The only modification to the biota data reporting format, when using it to report bird data, involves the inclusion of an (optional) additional record type. The *Bird Data Record* is used as an ‘extension’ of the *Specimen/Sub-sample Data Record*. See example in Section 7.6.

5 DATA ON BIOLOGICAL EFFECTS MEASUREMENTS IN BIOTA

5.1 EROD

Essentially, the reporting format incorporates ‘EROD’ measurements by defining ‘EROD’ parameters equivalent to, for example, the parameters defined for reporting various trace metal values in fish tissue. These parameters and their associated values are recorded on *Parameter/Contaminant Data Records*.

The only modification to the biota data reporting format, when using it to report EROD data, involves the inclusion of an additional record type to describe the methods used to obtain the EROD results. This record, the *EROD Methods Record*, is equivalent to the *Contaminant Analytical Methods Record* which is used to describe methods used for contaminants. One (or more) of these *EROD Methods Records* are placed in the ‘methods part’ of the data file together with any *Contaminant Analytical Methods Records*.

A number of items of information appearing on the various data records, which may be optional in the context of reporting contaminants data, are considered mandatory when reporting EROD data. On the *Sample Master Record*, the 'Water depth' (WADEP) should be recorded. On the *Specimen/Sub-sample Data Record*, the following data fields should be reported in addition to fish length, weight and sex information: 'Gonad weight' (GONWT) and 'Condition estimate' (CONES).

5.2 Linking biological effects data and contaminants data

An important consideration in relation to biological effects data is the ability to compare them with chemistry data in order to correlate results. To achieve this, it is necessary to consider mechanisms for 'linking' samples and sub-samples analysed for biological effects with appropriate contaminants data. Different levels of comparison can be achieved, as follows:

(i) The ideal situation occurs when the same fish are examined for both biological effects and contaminants. In such cases, the data are reported under the same *Specimen/Sub-sample Record*. See example in Section 7.8.

(ii) A second possibility is that the EROD data and the data for contaminants are measured in the same sample, but in different fish specimens collected at the same coordinates at the same time with a view to comparing the two sets of information. The data should be reported under the same *Sample Master Record*, but under separate *Specimen/Sub-sample Records*. See example in Section 7.9.

It may be the case that the two types of measurements are handled in different laboratories; the institute(s) reporting the data to ICES should ensure that the reporting of the two sub-samples is coordinated. Failure to indicate the association between the sub-samples (by separating the EROD and contaminants data under different master records) will mean that the biological effects and contaminants data will only be related if an attempt is made to 'link' data according to the procedure indicated in (iii), below.

(iii) A final possibility is that no direct association exists between a sample collected for measuring biological effects and a sample analysed for contaminants. In such cases, it may be possible to compare the EROD data with chemistry data from independent biota samples for the same species, collected in the same general area during the same general time period. For EROD measurements, this approach might involve identifying samples collected in the same 'ICES Statistical Rectangle' within the same sampling month; however, the specification of an appropriate 'window' in time and space will depend both on the types of data involved and the 'degree of comparability' required.

6 RECORD LAYOUT DESCRIPTIONS FOR BIOTA DATA

6.1 File headers

The first record of every file must be a file header, i.e., a 00-record, specifying the version numbers of the reporting format, the screening program, and the valid code list file (for example: **00 RF2.2 SV1.32 LR1**). The header numbers should coincide with the latest updates.

6.2 General field specifications

The following sections describe the layout of each record type found in the biota data reporting format. Each record is presented in the form of a table where the following are described for each data field of the record: the data field code, the data field name, the field column numbers, the valid values for the field, the format for the field, and whether the field is mandatory.

The data **field codes** and the data **field names** are described in detail in the section on Data Field Descriptions of this manual.

The **column** numbers refer to the column placement of the field in a given record.

The **valid values** for the field describe predefined values and ranges, and refer to appropriate Environmental reference codes found on the web at www.ices.dk/env/ (choose Codes).

The **format** column for the field indicates the type of variable included in the indicated data field according to one of the following:

SPC n a 'space filled' character field, consisting of n spaces.

CHAR n a character field of n characters. Character fields are formatted as left-justified, space filled.

NUM n a numeric (integer) field of width n . Integer fields are formatted as right justified, zero filled – e.g., the number 43 in a field NUM4:

0	0	4	3
---	---	---	---

NUM n m a numeric field of width n , including an **implied** decimal point; the rightmost m positions in the field are decimal positions. Values are formatted as decimal justified, zero filled – e.g., the number 3.7 in a field NUM4i2:

0	3.	7	0
---	----	---	---

NUM n m a numeric field of width n , including an **exponent**: the mantissa occupies the leftmost $n - 4$ positions, including an implied decimal point; the rightmost m positions in the mantissa are decimal positions. The exponent occupies the rightmost 4 positions ('E±dd'). Values are formatted as decimal justified, space filled – e.g. the number 56.1 in a field NUM9e4:

5	6	1			E	+	0	1
---	---	---	--	--	---	---	---	---

The **mandatory**, or 'M', column indicates those data fields which are mandatory in the context of the reporting formats, i.e., data which **must be reported**; the following codes apply:

- m mandatory;
- m? mandatory in some cases, e.g. when reporting data for a specific programme;
- mB mandatory when reporting data on birds;
- mF mandatory when reporting data on fish;
- mH mandatory when reporting data to HELCOM (BMP/COMBINE);
- mO mandatory when reporting data to OSPARCOM (JMP/JAMP);
- mM mandatory when reporting data on mammals;
- mS mandatory when reporting data on shellfish;
- x mandatory and predefined (i.e. insert the characters specified in the valid values column).

6.3 Contaminant Analytical Methods Record (21)

RECORD: Contaminant Analytical Methods Record					
Code	Field name	Columns	Valid values	Format	M
RECID	Record identifier	1–2	'21'	NUM2	x
DTYPE	Data type	3–4	'CF'	CHAR2	x
RLABO	Reporting institute code	5–8	cf. RLABO	CHAR4	m
ALABO	Analytical laboratory code	9–12	cf. RLABO	CHAR4	m
MYEAR	Monitoring year	13–14	'74' to present year	NUM2	m
PARAM	Parameter code	15–19	cf. PARAM	CHAR5	m
AMLNK	Analytical methods link	20–21	01–99	NUM2	m
METSW	<i>Field not used in biota data</i>	22–23	spaces	SPC2	x
METPT	<i>Field not used in biota data</i>	24–25	spaces	SPC2	x
METEX	<i>Field not used in biota data</i>	26–29	spaces	SPC4	x
COSED	<i>Field not used in biota data</i>	30–30	spaces	SPC1	x
METSP	<i>Field not used in biota data</i>	31–32	spaces	SPC2	x
METAN	Method of analysis of parameter/ contaminant	33–35	A–z, 0–9	CHAR3	m
DETLB	Detection limit – basis of determination	36–36	cf. BASIS	CHAR1	m
DETLI	Detection limit value	37–45	–0000 to 99999 plus 'E' plus –99 to +99	NUM9e4	m
ICCOD	Intercomparison exercise code	46–47	cf. ICCOD	CHAR2	m?
	Control chart information				
CONCH	Control chart basis	48–50	cf. CONCH and. Data Field Descriptions	CHAR3	mO
CRMCO	Control chart reference material code	51–58	cf. CRMCO and Data Field Descriptions	CHAR8	mO
CRMMB	Control chart RM mean value – basis	59–59	cf. BASIS	CHAR1	mO
CRMMV	Control chart RM mean value – value	60–68	–0000 to 99999 plus 'E' plus –99 to +99, or spaces	NUM9e4	mO
CRMSD	Control chart reference material – standard deviation	69–77	–0000 to 99999 plus 'E' plus –99 to +99, or spaces	NUM9e4	mO
CRMNM	Control chart reference material – number of measurements	78–79	01–99 or spaces	NUM2	mO
CRMPE	Control chart reference material – period	80–81	01–99 or spaces	NUM2	mO
RBMEA	Robust mean	82–90	–0000 to 99999 plus 'E' plus –99 to +99, or spaces	NUM9e4	
ZSCOR	Z-score	91–99	–0000 to 99999 plus 'E' plus –99 to +99, or spaces	NUM9e4	
PSCOR	P-score	100–108	–0000 to 99999 plus 'E' plus –99 to +99, or spaces	NUM9e4	
		109–120	spaces	SPC	x

6.4 EROD Methods Record (22)

RECORD: EROD Methods Record					
Code	Field name	Columns	Valid values	Format	M
RECID	Record identifier	1–2	'22'	NUM2	x
DTYPE	Data type	3–4	'CF'	CHAR2	x
RLABO	Reporting institute code	5–8	cf. RLABO	CHAR4	m
ALABO	Analytical laboratory code	9–12	cf. RLABO	CHAR4	m
MYEAR	Monitoring year	13–14	'74' to present year	NUM2	m
PARAM	Parameter code	15–19	cf. PARAM	CHAR5	m
AMLNK	Analytical methods link	20–21	01–99	NUM2	m
INCTE	Incubation temperature	22–23	10–30	NUM2	m
INCPH	Incubation pH	24–25	00–99	NUM2i1	m
PROTC	Protein content of incubation mixture	26–28	001–999	NUM3i1	m
NABUF	Nature of buffer	29–35	A–z, 0–9	CHAR7	m
COFCO	Cofactor concentration	36–38	001–999	NUM3	m
SUBCO	Substrate concentration	39–41	001–999	NUM3	m
EXTCO	Extinction coefficient	42–45	0001–9999	NUM4i1	m
		46–120	spaces	SPC	x

6.5 Sample Master Record (01)

RECORD: Sample Master Record					
Code	Field name	Columns	Valid values	Format	M
RECID	Record identifier	1–2	'01'	NUM2	x
DTYPE	Data type	3–4	'CF'	CHAR2	x
RLABO	Reporting institute code	5–8	cf. RLABO	CHAR4	m
MYEAR	Monitoring year	9–10	'74' to present year	NUM2	m
SEQNO	Sample sequence number	11–14	0001–9999	NUM4	m
CNTRY	Country code	15–16	cf. CNTRY	CHAR2	m
SHIPC	Ship code	17–18	cf. SHIPC	CHAR2	m
CRUIS	Cruise identifier	19–22	A–z, 0–9	CHAR4	m
SDATE	Sampling date	23–28	000000–999999	CHAR6	m
STIME	Sampling time	29–32	0000–2359 or spaces	CHAR4	
	Sampling area coordinates				
LATDG	Latitude degrees	33–34	00–90 (north)	NUM2	m
LATMI	Latitude minutes	35–36	00–59	NUM2	m
LATMF	Latitude decimal minutes	37–38	00–99	NUM2	m
LONDG	Longitude degrees	39–40	00–99	NUM2	m
LONMI	Longitude minutes	41–42	00–59	NUM2	m
LONMF	Longitude decimal minutes	43–44	00–99	NUM2	m
QEORW	Quadrant	45–45	'E', 'e', 'W' or 'w' (cf. Data Field Descriptions)	CHAR1	m
JMPAR	JMP area code	46–54	cf. JMPAR and Data Field Descriptions, or spaces	CHAR9	mO
ICEAR	ICES statistical rectangle	55–59	cf. ICEAR	CHAR5	m
OTHAR	Other area or station code	60–64	A–z, 0–9 or spaces	CHAR5	mH
SPECI	Species (RUBIN) code	65–72	cf. SPECI	CHAR8	m
NOINS	Number of specimens in sample (total)	73–75	001–999	NUM3	m
WADEP	Water depth	76–79	0000–9999 or spaces	NUM4	m?
COREL	<i>Field not used in biota data</i>	80–82	spaces	SPC3	x
ESTSR	<i>Field not used in biota data</i>	83–85	spaces	SPC3	x
SMLNK	<i>Field not used in biota data</i>	86–87	spaces	SPC2	x
ORGNZ	Organization codes	88–92	cf. ORGNZ	CHAR5	m
PURPM	Purpose of monitoring codes	93–97	cf. PURPM	CHAR5	m
RLIST	RUBIN code list	98–99	cf. RLIST	CHAR2	m
VESSL	Vessel type	100–100	cf. VESSL	CHAR1	m
GEART	Gear type used	101–103	cf. GEART	CHAR3	m
NOHAU	<i>Field not used in biota data</i>	104–105	spaces	SPC2	x
SPSEA	Spawning season code	106–106	'Y' or 'N'	CHAR1	m
TOTIN	<i>Field not used in biota data</i>	107–110	spaces	SPC4	x
ASTSA	Animal state at time of sampling	111–111	cf. ASTSA	CHAR1	mM
STTYP	Station type	112–112	cf. STTYP	CHAR1	m
PTSRC	Point source of contamination	113–113	cf. PTSRC	CHAR1	

6.6 Specimen/Sub-sample Data Record (04)

RECORD: Specimen/Sub-sample Data Record					
Code	Field name	Columns	Valid values	Format	M
RECID	Record identifier	1–2	'04'	NUM2	x
DTYPE	Data type	3–4	'CF'	CHAR2	x
RLABO	Reporting institute code	5–8	cf. RLABO	CHAR4	m
MYEAR	Monitoring year	9–10	'74' to present year	NUM2	m
SEQNO	Sample sequence number	11–14	0001–9999	NUM4	m
INORB	Individual or bulk code	15–15	cf. INORB	CHAR1	m
SUBNO	Sub-sample number	16–17	01–99	NUM2	m
	<i>Field reserved</i>	18–25	spaces	SPC8	x
NOINP	Number of individuals in pooled sub-sample	26–28	001–999	NUM3	m
LNMIN	Length – minimum (mm)	29–33	00001–99999 or spaces	NUM5	
LNMAX	Length – maximum (mm)	34–38	00001–99999 or spaces	NUM5	
LNMEA	Length – mean (mm)	39–43	00001–99999 or spaces	NUM5	
LNSTD	Length – standard deviation (mm)	44–48	00000–99999 or spaces	NUM5	
WTMIN	Weight – minimum (g)	49–54	000001–999999 or spaces	NUM6i1	
WTMAX	Weight – maximum (g)	55–60	000001–999999 or spaces	NUM6i1	
WTMEA	Weight – mean (g)(kg)	61–66	000001–999999 or spaces (cf. Data Field Descriptions)	NUM6i1	
WTSTD	Weight – standard deviation (g)	67–72	000000–999999 or spaces	NUM6i1	
SEXCO	Sex code	73–73	cf. SEXCO	CHAR1	
AGMIN	Age – minimum	74–75	00–99 or spaces	NUM2	
AGMAX	Age – maximum	76–77	00–99 or spaces	NUM2	
AGMEA	Age – mean	78–79	00–99 or spaces	NUM2	
CONES	Condition estimate	80–80	cf. CONES	CHAR1	m?
GONWT	Gonad weight (g)	81–85	00001–99999 or spaces	NUM5i2	m?
SHLWT	Shell weight of molluscs (g)	86–89	0001–9999 or spaces	NUM4i1	mS
AGDET	Age determination	90–90	cf. AGDET	CHAR1	m?
SEORB	Bird specimens, bird eggs or both	91–91	cf. SEORB	CHAR1	mB
		92–120	spaces	SPC	x

6.7 Bird Data Record (05)

RECORD: Bird Data Record					
Code	Field name	Columns	Valid values	Format	M
RECID	Record identifier	1–2	'05'	NUM2	x
DTYPE	Data type	3–4	'CF'	CHAR2	x
RLABO	Reporting institute code	5–8	cf. RLABO	CHAR4	m
MYEAR	Monitoring year	9–10	'74' to present year	NUM2	m
SEQNO	Sample sequence number	11–14	0001–9999	NUM4	m
INORB	Individual or bulk code	15–15	cf. INORB	CHAR1	m
SUBNO	Sub-sample number	16–17	01–99	NUM2	m
	<i>Field reserved</i>	18–25	spaces	SPC8	x
NOINP	Number of individuals in pooled sub-sample	26–28	001–999	NUM3	m
TLMIN	Total length – minimum (mm)	29–33	00001–99999 or spaces	NUM5	
TLMAX	Total length – maximum (mm)	34–38	00001–99999 or spaces	NUM5	
TLMEA	Total length – mean (mm)	39–43	00001–99999 or spaces	NUM5	
TLSTD	Total length – standard deviation (mm)	44–48	00000–99999 or spaces	NUM5	
BLMIN	Bill length – minimum (mm)	49–53	00001–99999 or spaces	NUM5i1	
BLMAX	Bill length – maximum (mm)	54–58	00001–99999 or spaces	NUM5i1	
BLMEA	Bill length – mean (mm)	59–63	00001–99999 or spaces	NUM5i1	
BLSTD	Bill length – standard deviation (mm)	64–68	00000–99999 or spaces	NUM5i1	
TAMIN	Tail length – minimum (mm)	69–73	00001–99999 or spaces	NUM5	
TAMAX	Tail length – maximum (mm)	74–78	00001–99999 or spaces	NUM5	
TAMEA	Tail length – mean (mm)	79–83	00001–99999 or spaces	NUM5	
TASTD	Tail length – standard deviation (mm)	84–88	00000–99999 or spaces	NUM5	
WLMIN	Wing length – minimum (mm)	89–93	00001–99999 or spaces	NUM5	
WLMAX	Wing length – maximum (mm)	94–98	00001–99999 or spaces	NUM5	
WLMEA	Wing length – mean (mm)	99–103	00001–99999 or spaces	NUM5	
WLSTD	Wing length – standard deviation (mm)	104–108	00000–99999 or spaces	NUM5	
		109–120	spaces	SPC	x

6.8 Tissue Data Record (07)

RECORD: (Fish, invertebrates, mammals, and birds) Tissue Data Record					
Code	Field name	Columns	Valid values	Format	M
RECID	Record identifier	1–2	'07'	NUM2	x
DTYPE	Data type	3–4	'CF'	CHAR2	x
RLABO	Reporting institute code	5–8	cf. RLABO	CHAR4	m
MYEAR	Monitoring year	9–10	'74' to present year	NUM2	m
SEQNO	Sample sequence number	11–14	0001–9999	NUM4	m
INORB	Individual or bulk code	15–15	cf. INORB	CHAR1	m
SUBNO	Sub-sample number	16–17	01–99	NUM2	m
	<i>Field reserved</i>	18–25	spaces	SPC8	x
TISSU	Tissue analysed	26–27	cf. TISSU	CHAR2	m
TISWT	Tissue weight/total organ weight (g)	28–33	000001–999999 or spaces	NUM6i2	
DRYWT	Dry weight %	34–37	0001–9999 or spaces	NUM4i2	
EXLIP	Extractable lipids %	38–41	0001–9999 or spaces	NUM4i2	
EXLIM	Extractable lipids method code	42–42	A–z, 0–9 or space	CHAR1	
FATWT	Fat weight % – total lipids	43–46	0001–9999 or spaces	NUM4i2	
BEGWT	Bird egg weight (g)	47–51	00001–99999 or spaces	NUM5i2	
BEGLN	Bird egg length (mm)	52–55	0001–9999 or spaces	NUM4i1	
BEGBR	Bird egg breadth (mm)	56–59	0001–9999 or spaces	NUM4i1	
BESWT	Bird egg shell weight (g)	60–63	0001–9999 or spaces	NUM4i2	
BESTH	Bird egg shell thickness (mm)	64–66	001–999 or spaces	NUM3i2	
BEOCA	Bird egg component analysed	67–67	cf. BEOCA	CHAR1	m?
BLUTH	Blubber thickness (cm)	68–70	001–999 or spaces	NUM3i1	
		71–120	spaces	SPC	x

6.9 Parameter/Contaminant Data Record (10)

RECORD: Parameter/Contaminant Data Record					
Code	Field name	Columns	Valid values	Format	M
RECID	Record identifier	1–2	'10'	NUM2	x
DTYPE	Data type	3–4	'CF'	CHAR2	x
RLABO	Reporting institute code	5–8	cf. RLABO	CHAR4	m
MYEAR	Monitoring year	9–10	'74' to present year	NUM2	m
SEQNO	Sample sequence number	11–14	0001–9999	NUM4	m
INORB	Individual or bulk code	15–15	cf. INORB	CHAR1	m
SUBNO	Sub-sample number	16–17	01–99	NUM2	m
	<i>Field reserved</i>	18–25	spaces	SPC8	x
MATRX	Matrix analysed	26–27	cf. TISSU	CHAR2	m
PARAM	Parameter code	28–32	cf. PARAM	CHAR5	m
VFLAG	Validity flag	33–33	cf. VFLAG	CHAR1	
QFLAG	Qualifier flag	34–34	'<' or space	CHAR1	
VALSN	Value in scientific notation	35–43	–0000 to 99999 plus 'E' plus –99 to +99	NUM9e4	m
BASIS	Basis of determination	44–44	cf. BASIS	CHAR1	m
SFRAC	<i>Field not used in biota data</i>	45–48	spaces	SPC4	x
REPNO	Replicate number	49–50	01–99 or spaces	NUM2	
PERCR	Percentage recovery of standard	51–54	0000–9999 or spaces	NUM4i1	
AMLNK	Analytical methods link	55–56	01–99	NUM2	m
ALABO	Analytical laboratory code	57–60	cf. RLABO	CHAR4	m
		61–120	spaces	SPC	x

6.10 Plain Language Comment Record (13)

RECORD: Plain Language Comment Record					
Code	Field name	Columns	Valid values	Format	M
RECID	Record identifier	1-2	'13'	NUM2	x
PTEXT	Plain text	3-87		CHAR85	
		88-120	spaces	SPC	x

7 BIOTA EXAMPLES

7.1 Example 1 – Single pool

A sample of 100 shrimps, collected for the purpose of assessing possible hazards to human health: The tails of the shrimps are removed and combined in a single pool of the tissues from the 100 shrimps; the material is homogenized and analysed in 3 replicates for each of 5 contaminants (P1–P5). The sample is reported as follows (with entries for selected data fields included in parentheses):

01 – Sample master record	(NOINS = 100;)
04 – Specimen/Sub-sample record, defines the single sub-sample	(INORB = H; NOINP = 100)
07 – Tissue data record, defines the single tissue analysed	(TISSU = TM)
10 – Data record	(PARAM = P1; REPNO = 1)
10 – Data record	(PARAM = P1; REPNO = 2)
10 – Data record	(PARAM = P1; REPNO = 3)
10 – Data record	(PARAM = P2; REPNO = 1)
:	
10 – Data record	(PARAM = P5; REPNO = 3)

A total of fifteen *Parameter/Contaminant Data Records* are reported, three for each of the five contaminants; the replicate analyses are identified using the ‘Replicate analysis’ (REPNO) data field.

7.2 Example 2 – Multiple pools

A sample of 75 mussels, collected for the purpose of establishing geographical distributions of contaminant levels in biota: The soft-body tissue of the mussels is combined in three pools, each comprising the tissues from 25 mussels; the material in each pool is homogenized and analysed in 2 replicates for each of 2 contaminants (P1–P2). The sample is reported as follows:

01 – Sample master record	(NOINS = 75)
04 – Specimen/Sub-sample record, defines sub-sample #1	(INORB = B; NOINP = 25; SUBNO = 1)
07 – Tissue data record, defines the tissue analysed	(TISSU = SB)
10 – Data record	(PARAM = P1; REPNO = 1)
10 – Data record	(PARAM = P1; REPNO = 2)
10 – Data record	(PARAM = P2; REPNO = 1)
10 – Data record	(PARAM = P2; REPNO = 2)
04 – Specimen/Sub-sample record, defines sub-sample #2	(INORB = B; NOINP = 25; SUBNO = 2)
07 – Tissue data record, defines the tissue analysed	(TISSU = SB)
10 – Data record	(PARAM = P1; REPNO = 1)
:	
10 – Data record	(PARAM = P2; REPNO = 2)
04 – Specimen/Sub-sample record, defines sub-sample #3	(INORB = B; NOINP = 25; SUBNO = 3)
07 – Tissue data record, defines the tissue analysed	(TISSU = SB)
10 – Data record	(PARAM = P1; REPNO = 1)
:	
10 – Data record	(PARAM = P2; REPNO = 2)

7.3 Example 3 – Individual samples

A sample of 25 fish, collected for the purpose of establishing temporal trends of contaminant levels in biota: The muscle tissue of each fish is analysed individually for 1 contaminant (P1). The sample is reported as follows:

01 – Sample master record	(NOINS = 25)
04 – Specimen/Sub-sample record, defines sub-sample #1	(INORB = I; NOINP = 1; SUBNO = 1)
07 – Tissue data record, defines the tissue analysed	(TISSU = MU)
10 – Data record	(PARAM = P1)
04 – Specimen/Sub-sample record, defines sub-sample #2	(INORB = I; NOINP = 1; SUBNO = 2)
07 – Tissue data record, defines the tissue analysed	(TISSU = MU)
10 – Data record	(PARAM = P1)
:	
:	
04 – Specimen/Sub-sample record, defines sub-sample #25	(INORB = I; NOINP = 1; SUBNO = 25)
07 – Tissue data record, defines the tissue analysed	(TISSU = MU)
10 – Data record	(PARAM = P1)

A total of twenty-five *Specimen/Sub-sample Data Records* are reported, one for each of the twenty-five fish; each *Specimen/Sub-sample Data Record* ‘heads’ one *Tissue Data Record* and one *Parameter/Contaminant Data Record*.

7.4 Example 4 – Individual samples + pools

A sample of 25 fish, collected for the purpose of establishing temporal trends of contaminant levels in biota: The muscle tissue of each fish is analysed individually for 1 contaminant (P1). The livers of each fish are removed and combined in five pools, each comprising the organs from 5 fish; the material in each pool is homogenized and analysed for each of 3 contaminants (P2–P4). The sample is reported as follows:

01 – Sample master record	(NOINS = 25)
04 – Specimen/Sub-sample record, defines sub-sample #1	(INORB = I; NOINP = 1; SUBNO = 1)
07 – Tissue data record, defines the muscle analysed	(TISSU = MU)
10 – Data record	(PARAM = P1)
04 – Specimen/Sub-sample record, defines sub-sample #2	(INORB = I; NOINP = 1; SUBNO = 2)
07 – Tissue data record, defines the muscle analysed	(TISSU = MU)
10 – Data record	(PARAM = P1)
:	
:	
04 – Specimen/Sub-sample record, defines sub-sample #25	(INORB = I; NOINP = 1; SUBNO = 25)
07 – Tissue data record, defines the muscle analysed	(TISSU = MU)
10 – Data record	(PARAM = P1)
04 – Specimen/Sub-sample record, defines sub-sample #26	(INORB = B; NOINP = 5; SUBNO = 26)
07 – Tissue data record, defines the liver analysed	(TISSU = LI)
10 – Data record	(PARAM = P2)
10 – Data record	(PARAM = P3)
10 – Data record	(PARAM = P4)
04 – Specimen/Sub-sample record, defines sub-sample #27	(INORB = B; NOINP = 5; SUBNO = 27)
07 – Tissue data record, defines the liver analysed	(TISSU = LI)
10 – Data record	(PARAM = P2)

10 – Data record	(PARAM = P3)
10 – Data record	(PARAM = P4)
:	
:	
04 – Specimen/Sub-sample record, defines sub-sample #30	(INORB = B; NOINP = 5; SUBNO = 30)
07 – Tissue data record, defines the liver analysed	(TISSU = LI)
10 – Data record	(PARAM = P2)
10 – Data record	(PARAM = P3)
10 – Data record	(PARAM = P4)

A total of thirty *Specimen/Sub-sample Data Records* are reported, one for each of the twenty-five fish analysed individually and one for each of the five sub-samples of pooled liver tissue; each *Specimen/Sub-sample Data Record* ‘heads’ one *Tissue Data Record*, and one *Parameter/Contaminant Data Record* if the sub-sample concerns an individual fish or three *Parameter/Contaminant Data Records* if the sub-sample concerns a pool.

7.5 Example 5 – Individual samples + bulks + homogenates

A sample of 25 fish, collected for the purpose of establishing temporal trends of contaminant levels in biota: The muscle tissue of each fish is analysed individually for 1 contaminant (P1). The livers of 15 (large) fish are analysed individually; however, to obtain sufficient material for analysis, the livers of the remaining 10 fish are removed and combined in two pools, each comprising the organs from 5 fish; the liver tissues are analysed for 2 contaminants (P2–P3). Finally, the kidneys of all 25 fish are homogenized in a single pool and analysed in replicate for 1 contaminant (P4). The sample is reported as follows:

01 – Sample master record	(NOINS = 25)
04 – Specimen/Sub-sample record, defines sub-sample #1	(INORB = I; NOINP = 1; SUBNO = 1)
07 – Tissue data record, defines the muscle analysed	(TISSU = MU)
10 – Data record	(PARAM = P1)
07 – Tissue data record, defines the liver analysed	(TISSU = LI)
10 – Data record	(PARAM = P2)
10 – Data record	(PARAM = P3)
04 – Specimen/Sub-sample record, defines sub-sample #2	(INORB = I; NOINP = 1; SUBNO = 2)
07 – Tissue data record, defines the muscle analysed	(TISSU = MU)
10 – Data record	(PARAM = P1)
07 – Tissue data record, defines the liver analysed	(TISSU = LI)
10 – Data record	(PARAM = P2)
10 – Data record	(PARAM = P3)
:	
04 – Specimen/Sub-sample record, defines sub-sample #15	(INORB = I; NOINP = 1; SUBNO = 15)
07 – Tissue data record, defines the muscle analysed	(TISSU = MU)
10 – Data record	(PARAM = P1)
07 – Tissue data record, defines the liver analysed	(TISSU = LI)
10 – Data record	(PARAM = P2)
10 – Data record	(PARAM = P3)
04 – Specimen/Sub-sample record, defines sub-sample #16	(INORB = I; NOINP = 1; SUBNO = 16)
07 – Tissue data record, defines the muscle analysed	(TISSU = MU)
10 – Data record	(PARAM = P1)
:	
04 – Specimen/Sub-sample record, defines sub-sample #25	(INORB = I; NOINP = 1; SUBNO = 25)

07 – Tissue data record, defines the muscle analysed	(TISSU = MU)
10 – Data record	(PARAM = P1)
04 – Specimen/Sub-sample record, defines sub-sample #26	(INORB = B; NOINP = 5; SUBNO = 26)
07 – Tissue data record, defines the liver analysed	(TISSU = LI)
10 – Data record	(PARAM = P2)
10 – Data record	(PARAM = P3)
04 – Specimen/Sub-sample record, defines sub-sample #27	(INORB = B; NOINP = 5; SUBNO = 27)
07 – Tissue data record, defines the liver analysed	(TISSU = LI)
10 – Data record	(PARAM = P2)
10 – Data record	(PARAM = P3)
04 – Specimen/Sub-sample record, defines sub-sample #28	(INORB = H; NOINP = 25; SUBNO = 28)
07 – Tissue data record, defines the kidney analysed	(TISSU = KI)
10 – Data record	(PARAM = P4; REPNO = 1)
10 – Data record	(PARAM = P4; REPNO = 2)

A total of twenty-eight *Specimen/Sub-sample Data Records* are reported, one for each of the twenty-five fish analysed individually, one for each of the two sub-samples of pooled liver tissue, and one for the pooled kidney sub-sample. The first fifteen *Specimen/Sub-sample Data Records* ‘head’ two *Tissue Data Records* (one defining the individual muscle tissue analyses and one the individual liver tissue analyses). The next ten *Specimen/Sub-sample Data Records* ‘head’ a single *Tissue Data Record* (defining individual muscle tissue analyses). The following two *Specimen/Sub-sample Data Records* ‘head’ single *Tissue Data Records* (defining the pooled liver tissue analyses). Finally, one *Specimen/Sub-sample Data Record* ‘heads’ a single *Tissue Data Record* defining the pooled kidney tissue analyses. The replicate analyses of the kidney tissue are identified using the ‘Replicate analysis’ (REPNO) data field.

7.6 Example 6 – Juvenile/adult bird data

Three birds are sampled, the liver from each bird is analysed individually for 1 contaminant (P1). Various length measurements were taken.

01 – Sample master record	(NOINS = 3)
04 – Specimen/Sub-sample record, sub-sample #1	(INORB = I;NOINP = 1;SUBNO = 1;SEORB = S)
05 – Bird data record	
07 – Tissue data record, the liver tissue analysed	(TISSU = LI)
10 – Data record	(PARAM = P1)
04 – Specimen/Sub-sample record, sub-sample #2	(INORB = I;NOINP = 1;SUBNO = 2;SEORB = S)
05 – Bird data record	
07 – Tissue data record, the liver tissue analysed	(TISSU = LI)
10 – Data record	(PARAM = P1)
04 – Specimen/Sub-sample record, sub-sample #3	(INORB = I;NOINP = 1;SUBNO = 3;SEORB = S)
05 – Bird data record	
07 – Tissue data record, the liver tissue analysed	(TISSU = LI)
10 – Data record	(PARAM = P1)

A total of three *Specimen/Sub-sample Data Records* are reported, one for each of the three birds. Each *Specimen/Sub-sample Data Record* is followed by a *Bird Data Record*, that gives additional information on the length measurements of the individual specimens. Each *Specimen/Sub-sample/Bird Data Record* ‘heads’ one *Tissue Data Record*; each *Tissue Data Record* ‘heads’ one *Parameter/Contaminant Data Record*.

7.7 Example 7 – Bird egg data

From a single nest, a sample consisting of 3 bird eggs is collected. The eggs are analysed individually for 3 contaminants (P1, P2, and P3). Each egg is reported as a ‘tissue’ belonging to the same (absent) adult specimen. Since there is no information on this specimen, no *Bird Data Record* is included. The sample is reported as follows:

01 – Sample master record	(NOINS = 1)
04 – Specimen/Sub-sample record, sub-sample #1	(INORB = I;NOINP = 1;SUBNO = 1;SEORB = E)
07 – Tissue data record, defines the first egg analysed	(TISSU = EG)
10 – Data record	(PARAM = P1)
10 – Data record	(PARAM = P2)
10 – Data record	(PARAM = P3)
07 – Tissue data record, defines the second egg analysed	(TISSU = EG)
10 – Data record	(PARAM = P1)
10 – Data record	(PARAM = P2)
10 – Data record	(PARAM = P3)
07 – Tissue data record, defines the third egg analysed	(TISSU = EG)
10 – Data record	(PARAM = P1)
10 – Data record	(PARAM = P2)
10 – Data record	(PARAM = P3)

A single *Specimen/Sub-sample Data Record* is reported to reflect that the eggs are collected from the same nest. Each egg is reported under a separate *Tissue Data Record*.

7.8 Example 8 – EROD + contaminant data in same fish

A sample of 25 fish, the livers of each are removed and combined in five pools, each comprising the organs from 5 fish; the material in each pool is analysed for EROD and 2 contaminants (P1 and P2). The sample is reported as follows:

01 – Sample master record	(NOINS = 25)
04 – Specimen/Sub-sample record, sub-sample #1	(INORB = B; NOINP = 5; SUBNO = 1)
07 – Tissue data record, defines the liver analysed	(TISSU = LI)
10 – Data record	(PARAM = EROD)
10 – Data record	(PARAM = P1)
10 – Data record	(PARAM = P2)
04 – Specimen/Sub-sample record, sub-sample #2	(INORB = B; NOINP = 5; SUBNO = 2)
07 – Tissue data record, defines the liver analysed	(TISSU = LI)
10 – Data record	(PARAM = EROD)
10 – Data record	(PARAM = P1)
10 – Data record	(PARAM = P2)
:	
04 – Specimen/Sub-sample record, sub-sample #5	(INORB = B; NOINP = 5; SUBNO = 5)
07 – Tissue data record, defines the liver analysed	(TISSU = LI)
10 – Data record	(PARAM = EROD)
10 – Data record	(PARAM = P1)
10 – Data record	(PARAM = P2)

A total of five *Specimen/Sub-sample Data Records* are reported, one for each of the five sub-samples of pooled liver tissue; each *Specimen/Sub-sample Data Record* ‘heads’ one *Tissue Data Record*, and three *Parameter/Contaminant*

Data Records. The ‘methods part’ of the data file includes both *EROD Methods Record(s)* and *Contaminant Analytical Methods Records*.

7.9 Example 9 – EROD + contaminant data at same place but different fish

Fifty fish are collected at the same sampling location at the same time. The livers of the first 25 fish are analysed individually for EROD. The livers of the next 25 fish are analysed individually for contaminants P1 and P2. The data are reported as follows:

01 – Sample master record	(NOINS = 50)	
04 – Specimen/Sub-sample record, sub-sample #1		(INORB = I; NOINP = 1; SUBNO = 1)
07 – Tissue data record, defines the liver analysed		(TISSU = LI)
10 – Data record		(PARAM = EROD)
04 – Specimen/Sub-sample record, sub-sample #2		(INORB = I; NOINP = 1; SUBNO = 2)
07 – Tissue data record, defines the liver analysed		(TISSU = LI)
10 – Data record		(PARAM = EROD)
:		
04 – Specimen/Sub-sample record, sub-sample #25		(INORB = I; NOINP = 1; SUBNO = 25)
07 – Tissue data record, defines the liver analysed		(TISSU = LI)
10 – Data record		(PARAM = EROD)
04 – Specimen/Sub-sample record, sub-sample #26		(INORB = I; NOINP = 1; SUBNO = 26)
07 – Tissue data record, defines the liver analysed		(TISSU = LI)
10 – Data record		(PARAM = P1)
10 – Data record		(PARAM = P2)
:		
04 – Specimen/Sub-sample record, sub-sample #50		(INORB = I; NOINP = 1; SUBNO = 50)
07 – Tissue data record, defines the single tissue analysed		(TISSU = LI)
10 – Data record		(PARAM = P1)
10 – Data record		(PARAM = P2)
:		

A total of 50 Specimen/Sub-sample Data Records are reported under one Sample Master Record. The ‘methods part’ of the data file includes both EROD Methods Record(s), ‘linked’ to the Parameter/Contaminant Data Records, and Contaminant Analytical Methods Records, ‘linked’ to the Parameter/Contaminant Data Records.