



**The National Marine Biological
Analytical Quality Control Scheme**

**Description of Scheme Standards for the Benthic Invertebrate Component
From Scheme Year 8 (2001/02)**

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Description of Scheme Standards for the Benthic Invertebrate Component

In the third year of the NMBAQC Scheme (1996/97) required levels of performance were set by the NMBAQC steering committee for the Own Sample (OS) exercise and flags were placed upon the results. The flags applied are based on a comparison of the results from sample analysis by Unicmarine Ltd. with those from the participating laboratories. The Own Sample flagging criteria were reviewed during the seventh Scheme year (2000/01). A new set of NMBAQC standards and exercise protocols was devised (Unicmarine, 2001) and introduced in Scheme year eight (2001/02).

The OS exercise has several aspects, each with a separate standard. Each of the standards has been calculated independently for the three Own Samples received from each laboratory.

The process of assigning the flags is described below. The target standards and recommended protocols may be modified in the future. A single standard 'averaged' value calculated across several components was found to be impracticable.

1. Own Sample Standards

Protocol changes introduced in Scheme year eight (2001/02):

- CSEMP (formerly NMMP) data to be audited one year in arrears.
- Own Samples to be selected from completed data matrices.
- Remedial Action to be encouraged to improve upon 'fail' flags.

1.1 Primary Performance Targets

These targets are stated for all Own Samples and give a clear indication of the samples performance.

1.1.1 Extraction/Sorting efficiency - Total taxa target

This flag relates to the performance of the laboratory with respect to the efficiency with which the animals were extracted and sorted from the OS samples. The 'correct' total number of taxa is assumed to be that resulting from re-analysis of the samples by Unicmarine Ltd. To achieve a pass the total number of taxa recorded should be within $\pm 10\%$ or ± 2 taxa (whichever is greater) of this total.

1.1.2 Extraction/Sorting/Enumeration efficiency - Total individuals target

This flag reflects the efficiency with which the laboratory estimated the total number of individuals in the sample. The total should be within $\pm 10\%$ or ± 2 individuals (whichever is greater) of the total resulting from re-analysis of the samples by Unicmarine Ltd.

1.1.3 Biomass estimation accuracy - Total biomass target

The total value should be within $\pm 20\%$ of the value obtained from re-analysis of the sample.

1.1.4 **Bray-Curtis comparison target**

Comparison of the two data sets, from re-analysis by Unicomarine Ltd. and by the participating laboratory, should result in a Bray-Curtis similarity index of $\geq 90\%$.

1.2 **Secondary Performance Targets**

These targets are analysed to determine specific areas of processing for remedial action.

1.2.1 **Extraction efficiency - Taxa in residue target**

This flag relates to the performance of the laboratory with respect to the efficiency with which the animals were extracted from the sample residue. The total number of taxa is assumed to be that resulting from re-analysis of the fauna and residue by Unicomarine Ltd. To achieve a 'pass' the number of taxa not extracted should be $<10\%$ or <2 taxa (whichever is greater) of this total.

1.2.2 **Identification accuracy – Taxonomic errors target**

This flag relates to the performance of the laboratory with respect to the identification of the animals extracted from the sample residue by the participating laboratory. The 'correct' identification is assumed to be that resulting from re-analysis of the sample by Unicomarine Ltd. (following any appeals). To achieve a 'pass' the number of taxa incorrectly identified should be $<10\%$ or <2 taxa (whichever is greater) of the number of taxa extracted by the participating laboratory.

1.2.3 **Extraction efficiency - Individuals in residue target**

This flag reflects the efficiency with which the laboratory extracted the individuals from the sample residue. The number of individuals not extracted from the residue should be $<10\%$ or <2 individuals (whichever is greater) of the total resulting from re-analysis of the fauna and residue by Unicomarine Ltd.

1.2.4 **Enumeration efficiency – Enumeration of extracted individuals target**

This flag reflects the efficiency with which the laboratory has enumerated the individuals extracted by the participating laboratory. The count variance should be $\pm 10\%$ or 2 individuals (whichever is greater) of the total resulting from re-enumeration of the fauna by Unicomarine Ltd.

1.3 **Overall Sample Flag**

Each Own Sample is assigned an individual flag based upon their Bray-Curtis similarity indices. A five tier system of classifying individual Own Samples is used:

100% BCSI	Excellent
95 - <100	Good
90 - <95	Acceptable
85 - <90	Fail - Poor – Remedial Action Suggested
<85	Fail – Bad - Remedial Action Required

If an Own Sample achieves a BCSI of less than 90% remedial action is required. The nature of this remedial action can be ascertained by examining the secondary performance targets (See 1.1.2). A remedial action guidance table is utilised to structure any resultant action:

	<5%	5-10%	>10% & ≤ 2 units	>10% & >2 units
Individual missed in residue	No action required.	Review methods/protocols extraction, possible errors include: floating & blasting methods, petri dish searching methods, tray extraction procedures, quality assurance mechanisms.	Review methods/protocols extraction, possible errors include: floating & blasting methods, petri dish searching methods, tray extraction procedures, quality assurance mechanisms.	Reprocess 'associated' samples - resort residues for all samples processed by a particular member of staff or isolated by cluster analysis of the original data.
Taxa missed in residue	No action required.	Review methods/protocols extraction, possible errors include: floating & blasting methods, petri dish searching methods, tray extraction procedures, quality assurance mechanisms.	Review methods/protocols extraction, possible errors include: floating & blasting methods, petri dish searching methods, tray extraction procedures, quality assurance mechanisms.	Reprocess 'associated' samples - resort residues for all samples processed by a particular member of staff or isolated by cluster analysis of the original data.
Taxonomic errors in extracted fauna	No action required.	Review methods/protocols identification, possible errors include: literature, reference collection, staff training/contractor, quality assurance mechanisms.	Review methods/protocols identification, possible errors include: literature, reference collection, staff training/contractor, quality assurance mechanisms.	Reprocess 'associated' samples - reanalyse fauna for all samples processed by a particular member of staff or isolated by cluster analysis of the original data.
Count variance	No action required.	Review methods/protocols enumeration, possible errors include: counter malfunction, biomass loss/damage, handling care, 'countable' recording policy, <i>in situ</i> approximation.	Review methods/protocols enumeration, possible errors include: counter malfunction, biomass loss/damage, handling care, 'countable' recording policy, <i>in situ</i> approximation.	Reprocess 'associated' samples - recount fauna for all samples processed by a particular member of staff or isolated by cluster analysis of the original data.

Revised from: Version 1.1 Remedial Action Protocol August 2002

Considerable variation in the estimation of biomass (as discussed in earlier reports; NMBAQC Scheme Annual report, 1996/97, Section 3.2.5) has led to the flag for this component being excluded from the determination of the overall sample flag for the OS exercises. Laboratories failing to supply OS data have automatically been assigned a fail flag by default.