

Revised AQEM/STAR sorting protocol

revised version, 8/4/03

This document describes a simplification of the sorting procedure according to the AQEM/STAR sampling protocol (AqemMacroinvertebrateSamplingProtocol.pdf, available from http://www.eu-star.at/tops/top_protocols.htm. It results from the discussion on www.eu-star.at over the period March/April 2003.

From the above mentioned protocol (AqemMacroinvertebrateSamplingProtocol.pdf) only the section "sample processing" (pages 11-15) is affected, in particular point 10. All other sections of the protocol remain unchanged.

To simplify sorting the following procedure can be applied as an alternative to the procedure described in the AQEM/STAR sampling protocol. Partners may use the original full protocol if they wish.

- (1) Perform the initial steps of subsampling, as described in the AQEM/STAR sampling protocol, section "sample processing", steps 1-9 (removing five grids from the subsampling tray).
- (2) Survey the material and pre-define, which of those taxa listed in Table 1 may be abundant in the material resulting from the five grids (many more than 50 or 100 individuals according to Table 1, respectively = abundant taxon). The investigators may define additional taxa, not listed in Table 1, as "abundant" in selected cases. This resulting list of abundant taxa may be revised in steps (4) and (5).
- (3) Sorting the sub-sample is generally performed by distributing a certain amount (e.g. two spoons) of material (sand, stones, debris, animals) in a white tray. From this material the specimens are to be removed.
- (4) Sorting starts with the removal of all specimens, including the abundant taxa, from the first amount of material distributed in the tray. The total number of all specimens removed should be counted and recorded as part of the process of removing the 700+ specimens required. In addition, separate counts and records should also be made for each abundant taxon that has been selected as being "abundant" in the sample.
- (5) If 50 or 100 specimens, respectively, of the abundant taxa have been removed, the remaining specimens will no longer be removed. Instead, their numbers will be extrapolated.
Example: the first tray of material is sorted until 50 *Gammarus* and 100 Baetidae have been removed; the remaining *Gammarus* and Baetidae present in the tray are counted (if there are very few more), otherwise their number is extrapolated.
From the following trays of material no further *Gammarus* and Baetidae are removed but their numbers are extrapolated. The specimens of the taxa whose numbers are now being extrapolated, remain in the sample material.
- (6) Extrapolating specimen numbers of abundant taxa can be supported by a grid separating the white sorting tray into sections (more or less the same approach as used in RIVPACS sorting). The extrapolation of the number of specimens is done by counting the number of specimens in an adequate portion (e.g. $\frac{1}{4}$ or $\frac{1}{16}$ of the tray) and projecting the result to the whole

tray. It is recommended to count the whole sub-sample if the number of the abundant taxon exceeds 50/100 specimens only marginally.

- (7) Specimens of all other taxa are completely removed from the material.
- (8) If the total number of counted plus extrapolated specimens present in the material resulting from the five grids is less than 700, remove a further grid and treat as described in (5) – (7).
- (9) Careful records of the number of specimens removed or estimated must be kept and must be supplied for audit if the sample is selected for this purpose.

Table 1: Threshold value of specimens to be removed from a sample for selected taxa. The threshold value is 100 for species-rich taxa and 50 for species-poor taxa. Investigators may define additional taxa as “abundant” in selected cases. In all such cases the threshold value should be set at 50.

Taxon	threshold value
Oligochaeta	50
Sphaeriidae	50
Asellidae	50
<i>Gammarus</i> spec.	50
Baetidae	100
Leuctridae	50
Nemouridae	50
<i>Hydropsyche</i> spec.	100
Chironomidae (larvae and pupae)	100
Simuliidae (larvae and pupae)	50