

QA/QC of sample processing procedures using the Whole of Sample Estimate

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Introduction

The following description provides the recommended approach to assessing efficiency of sample processing procedures (live-sorting or laboratory subsampling and sorting) that should be followed when undertaking an AUSRIVAS Training and Accreditation Program. The approach is derived directly from the QA/QC procedures developed by Humphrey and Thurtell (1997) (as adapted from Davies et al 1996), which was used to assess the representativeness of the agency-sorted samples under the National River Health Program (NRHP), Phase I, 1994-96. The method involves comparing community composition (presence/absence) of agency-sorted samples with composition of a 'whole sample estimate' (WSE) derived from laboratory subsampling and sorting of sample residues.

Where live-sorting is concerned, it is important to note that the comparisons and assessments described here are *not* based upon live-sorted (LS) data appearing as similar as possible to data that would have been derived had the same sample been subsampled and sorted in the laboratory. Although this is the basis of the LS-WSE comparison (Humphrey and Thurtell 1997), only compositional (presence-absence) data are used in the formal assessments, while the assessment criteria themselves factor in the expectation that LS and WSE fractions will not be exactly the same. Rather, the use of the WSE as the benchmark for assessing live-sorting efficiency has the following advantages:

1. While the WSE is based on conventional laboratory sub-sampling and sorting, it derives a taxa list that includes the small and cryptic taxa that are often overlooked in the live-sorting procedure.
2. The approach is systematic and prescriptive which minimizes operator bias. This method will recover those taxa that are prone to live-sort operator bias.
3. The LS-WSE comparisons (*viz* WISE computer macro) has been well tested and is underpinned by research and development (see Humphrey and Thurtell 1997).
4. It will enable results to be compared over time – important if improvements in performance are to be evaluated.

Methods

Samples should be live-sorted according to the relevant state's live-sort protocols (see relevant state's AUSRIVAS Sampling and Processing Manual for details – available on the AUSRIVAS web site at <http://ausrivas.canberra.edu.au>). Retain the sample residues for further laboratory processing.

The WSE is obtained from the addition of taxa information derived from a sub-sample of the residue and a 'sub-sample' (to a similar proportion as that taken from the residue) of the Live-sort (LS) component. To obtain the WSE use the following procedure:

1. On return to the laboratory, using a multi-cell sub-sampler, take a sufficient sub-sample of animals likely to result in slightly more animals than were live-sorted (this estimate is typically derived by sorting the contents of just one or two cells of the sub-sampler). Where less than 100 animals were live-sorted, a minimum sub-sample size of 100 organisms is required.
2. Sort and identify the contents of sufficient cells giving rise to approximately 50 animals. This portion of the 'sub-sample' is used to estimate the taxa and relative abundances of animals that are 'common' in the sample.
3. Sort the remainder of the sub-sample, ignoring (leaving behind) the taxa that were recovered in step 2.
4. Scale up the raw taxa abundances derived from step 2 to the full sub-sample fraction taken in step 1. Add together taxa and relative abundances from step 2 (scaled up) and step 3, which now forms the sub-sample of the residue.
5. Enter the residue sub-sample and live-sort data into the Whole of Individual Sample Estimate (WISE) database (see details below).

Summary statistics from WISE are provided for: (a) a sample size equivalent to the LS sample size, listed under the '**Actual**' outputs (most common situation), and (b) a sample size normalised to 100 animals for situations where low live-sort sample size is encountered, listed under the '**Normalised**' outputs. Under 'Actual' and 'Normalised' outputs are the following summary statistics:

- (i) Live-Sort/Whole of Sample Estimate ('**LS/WSE**') taxa number ratio;
- (ii) Bray-Curtis dissimilarity index for presence/absence ('**Pres/Abs**') or relative abundance ('**Rel. Abund.**') data. Within each of these data categories, the dissimilarity index is provided for two situations: firstly, an unadjusted value ('**Unadjusted Bray-Curtis**'), and secondly, a value where LS taxa that are unique to LS (i.e. not found in the residue) are eliminated from the ensuing calculations (i.e. prior to WSE calculation). (This latter value, '**Bray-Curtis less taxa unique to LS**', is provided because often the live-sorting has picked out all large rare taxa so that it would not be expected that they would occur in the residue and WSE.)

WISE Database V2.2d

The Whole of Individual Sample Estimate (WISE) database is a Microsoft Access 97 database that compares the live-sorted component of a sample (LS) with an equivalent-sized component representative of the whole sample (prior to sorting) (WSE). The WISE database automatically calculates the Live-Sort/Whole of Sample Estimate (LS/WSE) taxa number ratio and various Bray-Curtis dissimilarity indices – as described above.

The WISE database has been developed to: (i) enable users to assess their performance in recovering small/cryptic taxa; and (ii) provide a standardised assessment tool of operator performance, thereby enabling performance in live-sort taxa recovery over the entire NRHP program to be validly assessed.

Details of WISE calculations

Details of the calculations performed by the WISE macro are contained in the PDF file, "AboutWise", that accompanies the WISE software.

References

Davies PE, Mitchell N & Barmuta LA 1996. *The impact of historical mining operations at Mount Lyell on the water quality and biological health of the King and Queen River catchments, Western Tasmania*. Mount Lyell Remediation and Demonstration Program. Supervising Scientist Report 118. Supervising Scientist, Canberra.

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