Zooplankton Taxonomy Protocol

An excel macro created by the Institute of Ocean Sciences (IOS) is used while the sample is counted to keep track of numbers of specimens. This macro uses an alphanumeric code for each species, size, and/or stage where applicable. Both cruise and event numbers are needed to enter data into the database at IOS and to retrieve it easily. These are tracked in the Event number assignment spreadsheet.

Each specimen in the sample or subsample is identified to as high of a resolution as possible by the lab technicians counting the sample. This includes genus, species, sex, size class and/or developmental stage as applicable.

Counting the microscopy sample (Net 1)

1. Pour formalin sample over sieve to remove formalin solution (sieve should be equal to or slightly finer than the mesh size of the net used to collect the sample).
2. Capture the formalin/seawater mixture in a screw cap jar for re-use when the sample is preserved again after analysis.
3. Rinse the sample in the sieve with filtered seawater (or fresh water if filtered seawater is not available) retaining the rinse water for later neutralization.
4. The sample is then processed into three size categories:
    - **s3**: ≥ 10mm
    - **s2**: ≥ 5mm <10mm
    - **s1**: <5mm
    - On occasion, s0 is used for very small/juvenile specimens (<2mm)
5. Once the sample is under the microscope, scan for unique or large specimens (≥ 10mm). All taxa identified at this stage are in a 1:1 split.
6. If there is a large number in these size classes, a folsom splitter is used to obtain a representative split. The ≥ 5mm portion is subsampled to approximately 100 individuals and the < 5mm portion is subsampled to approximately 400 individuals for a total of ~500 per sample (see note).
    - As the sample is split, periodically scan the remaining (non-enumerated) portion for any rare species that would be underrepresented by the splitting and as a general check on relative proportions of the counted side.
7. As each animal is identified, it is removed from the sample or moved to the side of the tray if using a borogov tray.
8. Any animals that are unknown (to the analyst) are set aside to be reviewed at the end of the sample sorting or for outside verification of identification.
9. After processing, all portions are returned to the original jar and preservative for archiving.

Note: Different groups of animals may be counted at different split fractions in order to maintain a representative count. For example, chaetognaths may be counted at a ¼ split (despite being >10mm) to avoid over counting, while smaller, abundant copepod species may be counted at a 1/128 split.