

## MEIOFAUNA INVESTIGATION

*Adapted from D.B. Carlton's Biology of Marine Organisms Laboratory Manual*

### **Experimental Design: Testing the effects of wave energy on meiofauna abundance/diversity**

Sand collected from:

- Protected and wave exposed sections at Sandy Beach and Makapu'u Beach.
  - 2 samples from each protected site and 2 samples from each wave exposed site=4 samples from each beach=8 samples total
  - Collected from 5cm depth at tide line in each location
  - At least two sub-samples (# depends on time) should be processed for each sample so an average can be obtained for each beach x exposure treatment

### **Sample Key:**

Site	Exposure	Replicate	Subsample	Code	Processed by
Makapu'u	Exposed	1	a	ME-1a	
Makapu'u	Exposed	1	b	ME-1b	
Makapu'u	Exposed	2	a	ME-2a	
Makapu'u	Exposed	2	b	ME-2b	
Makapu'u	Protected	1	a	MP-1a	
Makapu'u	Protected	1	b	MP-1b	
Makapu'u	Protected	2	a	MP-2a	
Makapu'u	Protected	2	b	MP-2b	
Sandy's	Exposed	1	a	SE-1a	
Sandy's	Exposed	1	b	SE-1b	
Sandy's	Exposed	2	a	SE-2a	
Sandy's	Exposed	2	b	SE-2b	
Sandy's	Protected	1	a	SP-1a	
Sandy's	Protected	1	b	SP-1b	
Sandy's	Protected	2	a	SP-2a	
Sandy's	Protected	2	b	SP-2b	

### **Extracting Meiofauna**

Meiofaunal animals hold on tight to sand grains, and must be slightly stressed to get them to release. To do this we will subject them to a low concentration of salt, filter them out from the sand particles, and return them to normal salinity for observation, identification, and counting.

1. Each student will should process as many samples as time permits. Think about what samples you should process. Should one student measure all of the samples from the Sandys protected site? How might this affect the data? For each sample you process, repeat the following steps.
2. In a 250 ml plastic flask add 100 ml of sand (sample) and bring the total volume to 200 ml with 0.39 M MgCl<sub>2</sub>.
3. Stir with vigor using a spoon. Be sure to stir all the way to the bottom so that all the sand gets mixed.
4. Let stand for 10 minutes, stirring occasionally.

5. Decant off top layer of water (not sand) through a 500 $\mu$ m sieve stacked on a 62 $\mu$ m sieve. Allow the water that passes through the sieve to flow into the sink.
6. Rinse all organisms off the 62 $\mu$ m mesh into a Petri dish using a squirt bottle filled with seawater.
7. Observe the sample through a dissecting microscope. On your first sample, spend some time becoming familiar with the different organisms. You should be able to reliably identify the groups listed in Table 1.
8. When you are comfortable with the identifications, count the total number of organisms in each group as carefully as possible, and enter your data into Data Sheet 1.
9. Repeat for all samples assigned to you.
10. Dispose of all processed sand into the designated bucket.

### **Groups and Identification**

You should become familiar with the following animal groups. You are also likely to encounter other animals as well. Spend some time looking through your scope and get comfortable with identifying these animals. Consult the keys in the lab for help with identification. If you find something unusual let your TA know.

Table 1. Common groups of meiofauna

<b>Group</b>	<b>Phylum</b>
Copepods	<b>Crustacea</b> Copepoda Harpacticoidea
Other crustaceans	<b>Crustacea</b>
Nematodes-round worms	<b>Nematoda</b>
Polychaetes-segmented worms	<b>Polychaeta</b>
Flatworms	<b>Platyhelminthes</b>
Forams	<b>Foraminifera</b>
Gastrotrichs	<b>Gastrotricha</b>
Mollusks	<b>Mollusca</b>



## Calculating the Shannon-Weaver Diversity Index

Diversity contains two elements. First there is the total number of types of groups in the set. Then there is the relative abundance of each group. The **Shannon-Weaver index ( $H'$ )** and the inverse logarithm of  $H'$  ( $e^{H'}$ ) takes both these facets of diversity and combines them into one measure for each sample, by weighting the abundance of a group as well as its presence in the sample. A rare group will make a smaller contribution than a common group to the index. The formula is as follows:

$$H' = -\sum p_i \ln(p_i),$$

where  $H'$  is the Shannon-Weaver Diversity index,  $p_i$  is the proportional (relative) abundance of each group, and  $\ln$  is the natural logarithm. Table 2 illustrates relative abundance for a hypothetical sub-sample.

Table 2. Counts of meiofauna groups in a sample.

Group	Number in sample	Relative abundance
Nematodes	8	8/16 = 0.50
Copepods	4	4/16 = 0.25
Polychaetes	2	2/16 = 0.125
Gastrotrichs	2	2/16 = 0.125
Total	16	1.00

Using these data, the Shannon-Weaver Index is calculated as follows:

$$H' = - [0.50 \ln(0.50) + 0.25 \ln(0.25) + 0.125 \ln(0.125) + 0.125 \ln(0.125)] = \mathbf{1.21}$$

*Note: Groups that are absent from a sample are not used in the calculation. Example: if there were no Gastrotrichs in the sample, calculate  $H'$  based on a total sample that includes Nematodes, Copepods, and Polychaetes.*

When the Shannon-Weaver Index is expressed as the inverse logarithm  $e^{H'}$  where  $e$  (natural logarithm) is raised to the  $H'$  power, it has the following useful properties:

- It can range from 0 to the species richness (s).
- It is equal to species richness if all species are equally represented.

For our example above:  $e^{1.21} = \mathbf{3.36}$



