

## 1.3 Example: Frierfjord macrofauna

The first example is from the IOC/GEEP practical workshop on biological effects of pollutants ( [Bayne, Clarke & Gray \(1988\)](#) ), held at the University of Oslo, August 1986. This attempted to contrast a range of biochemical, cellular, physiological and community analyses, applied to field samples from potentially contaminated and control sites, in a fjordic complex (Frierfjord/Langesundfjord) linked to Oslofjord ( *{F}*, Fig. 1.1). For the benthic macrofaunal component of this study ( [Gray, Aschan, Carr et al. \(1988\)](#) ), four replicate 0.1m<sup>2</sup> Day grab samples were taken at each of six sites (A-E and G, Fig 1.1) and, for each sample, organisms retained on a 1.0 mm sieve were identified and counted. Wet weights were determined for each species in each sample, by pooling individuals within species.

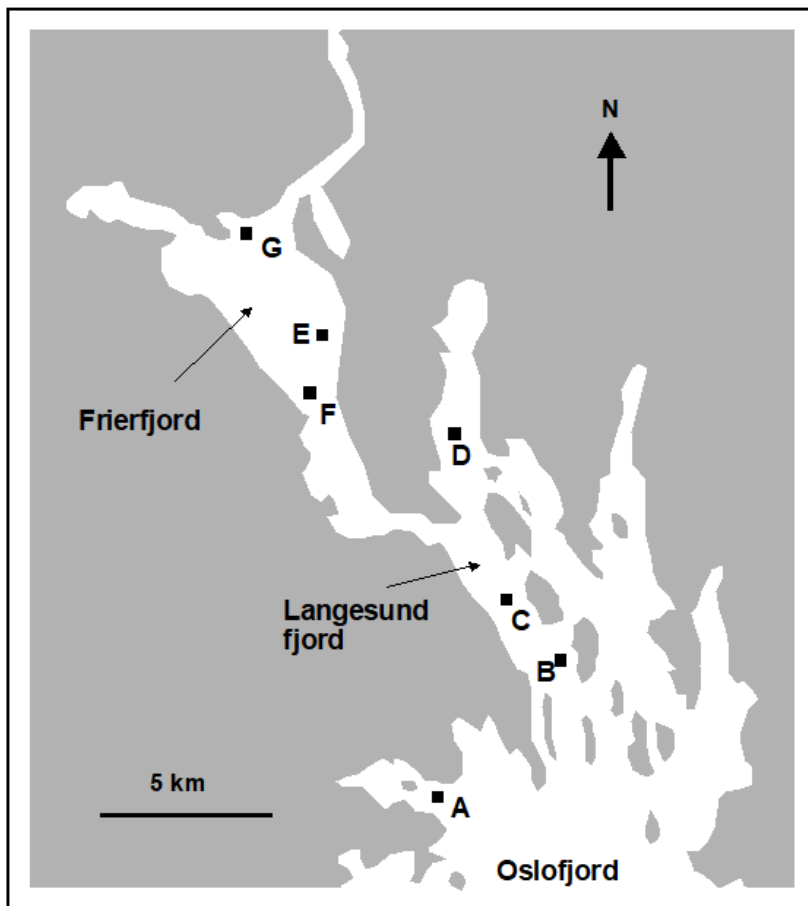


Fig. 1.1. Frierfjord, Norway *{F}*. Benthic community sampling sites (A-G) for the IOC/GEEP Oslo Workshop; site F omitted for macrobenthos.

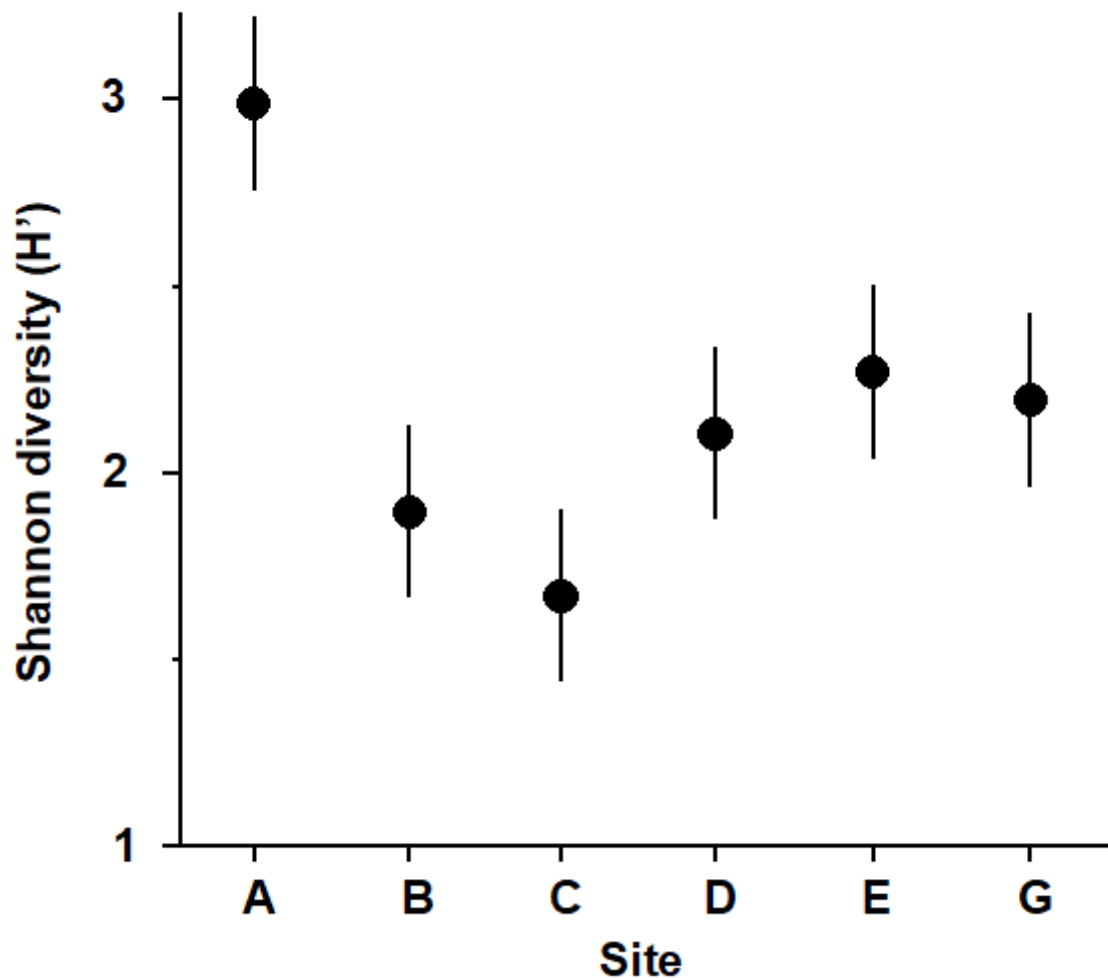


Fig. 1.2. Frierfjord macrofauna {F}. Means and 95% confidence intervals for Shannon diversity ( $H'$ ), from four replicates at each of six sites (A-E, G).

Part of the resulting data matrix can be seen in Table 1.2: in total there were 110 different taxa categorised from the 24 samples. Such matrices (abundance,  $A$ , and/or biomass,  $B$ ) are the starting point for the biotic analyses of this manual, and this example is typical in respect of the relatively high ratio of species to samples (always  $\gg 1$ ) and the prevalence of zeros. Here, as elsewhere, even an undesirable reduction to the 30 ‘most important’ species (see [Chapter 2](#)) leaves more than 50% of the matrix consisting of zeros. Standard multivariate normal analyses (e.g. [Mardia, Kent & Bibby \(1979\)](#)) of these counts are clearly ruled out; they require both that the number of species (variables) be small in relation to the number of samples, and that the abundance or biomass values are transformable to approximate normality: neither is possible.

Table 1.2. Frierfjord macrofauna {F}. Abundance and biomass matrices (part only) for the 110 species in 24 samples (four replicates at each of six sites A-E, G); abundance in numbers per  $0.1\text{m}^2$ , biomass in mg per  $0.1\text{m}^2$ .

| Species | Samples |
|---------|---------|
|---------|---------|

|                            | A1 | A2 | A3 | A4 | B1 | B2 | B3 | B4 |
|----------------------------|----|----|----|----|----|----|----|----|
| <b>Abundance</b>           |    |    |    |    |    |    |    |    |
| <i>Cerianthus lloydi</i>   | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  |
| <i>Halicryptus</i> sp.     | 0  | 0  | 0  | 1  | 0  | 0  | 0  | 0  |
| <i>Onchnesoma</i>          | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  |
| <i>Phascolion strombi</i>  | 0  | 0  | 0  | 1  | 0  | 0  | 1  | 0  |
| <i>Golfingia</i> sp.       | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  |
| <i>Holothuroidea</i>       | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  |
| <i>Nemertina</i> , indet.  | 12 | 6  | 8  | 6  | 40 | 6  | 19 | 7  |
| <i>Polychaeta</i> , indet. | 5  | 0  | 0  | 0  | 0  | 0  | 1  | 0  |
| <i>Amaena trilobata</i>    | 1  | 1  | 1  | 0  | 0  | 0  | 0  | 0  |
| <i>Amphictetes gunneri</i> | 0  | 0  | 0  | 0  | 4  | 0  | 0  | 0  |
| <i>Ampharetidae</i>        | 0  | 0  | 0  | 0  | 1  | 0  | 0  | 0  |
| <i>Anaitides groenl.</i>   | 0  | 0  | 0  | 1  | 1  | 0  | 0  | 0  |
| <i>Anaitides</i> sp.       | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  |
| ....                       |    |    |    |    |    |    |    |    |
| <b>Biomass</b>             |    |    |    |    |    |    |    |    |
| <i>Cerianthus lloydi</i>   | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  |
| <i>Halicryptus</i> sp.     | 0  | 0  | 0  | 26 | 0  | 0  | 0  | 0  |
| <i>Onchnesoma</i>          | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  |
| <i>Phascolion strombi</i>  | 0  | 0  | 0  | 6  | 0  | 0  | 2  | 0  |
| <i>Golfingia</i> sp.       | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  |

|                                      | A1  | A2 | A3  | A4 | B1 | B2 | B3 | B4 |
|--------------------------------------|-----|----|-----|----|----|----|----|----|
| <i>Holothuroi dea</i>                | 0   | 0  | 0   | 0  | 0  | 0  | 0  | 0  |
| <i>Nemertina</i> ,<br><i>indet.</i>  | 1   | 41 | 391 | 1  | 5  | 1  | 2  | 1  |
| <i>Polychaeta</i> ,<br><i>indet.</i> | 9   | 0  | 0   | 0  | 0  | 0  | 0  | 0  |
| <i>Amaena trilobata</i>              | 144 | 14 | 234 | 0  | 0  | 0  | 0  | 0  |
| <i>Amphicteis gunneri</i>            | 0   | 0  | 0   | 0  | 45 | 0  | 0  | 0  |
| <i>Amphareti dae</i>                 | 0   | 0  | 0   | 0  | 0  | 0  | 0  | 0  |
| <i>Anaitides groenl.</i>             | 0   | 0  | 0   | 7  | 11 | 0  | 0  | 0  |
| <i>Anaitides sp.</i>                 | 0   | 0  | 0   | 0  | 0  | 0  | 0  | 0  |
| ....                                 |     |    |     |    |    |    |    |    |

As discussed above, one easy route to simplification of this *high-dimensional* (multi-species) complexity is to reduce each matrix column (sample) to a single univariate description. Fig. 1.2 shows the results of computing the Shannon diversity ( $H'$ , see [Chapter 8](#)) of each sample<sup>¶</sup>, and plotting for each site the mean diversity and its 95% confidence interval, based on a pooled estimate of variance across all sites from the ANOVA table, [Chapter 6](#). (An analysis of the type outlined in [Chapter 9](#) shows that prior transformation of  $H'$  is not required; it already has approximately constant variance across the sites, a necessary prerequisite for standard ANOVA). The most obvious feature of Fig. 1.2 is the relatively higher diversity at the *control/reference* location, A.

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<sup>¶</sup> Using the *PRIMER DIVERSE* routine.

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