

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 0.1m² 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.

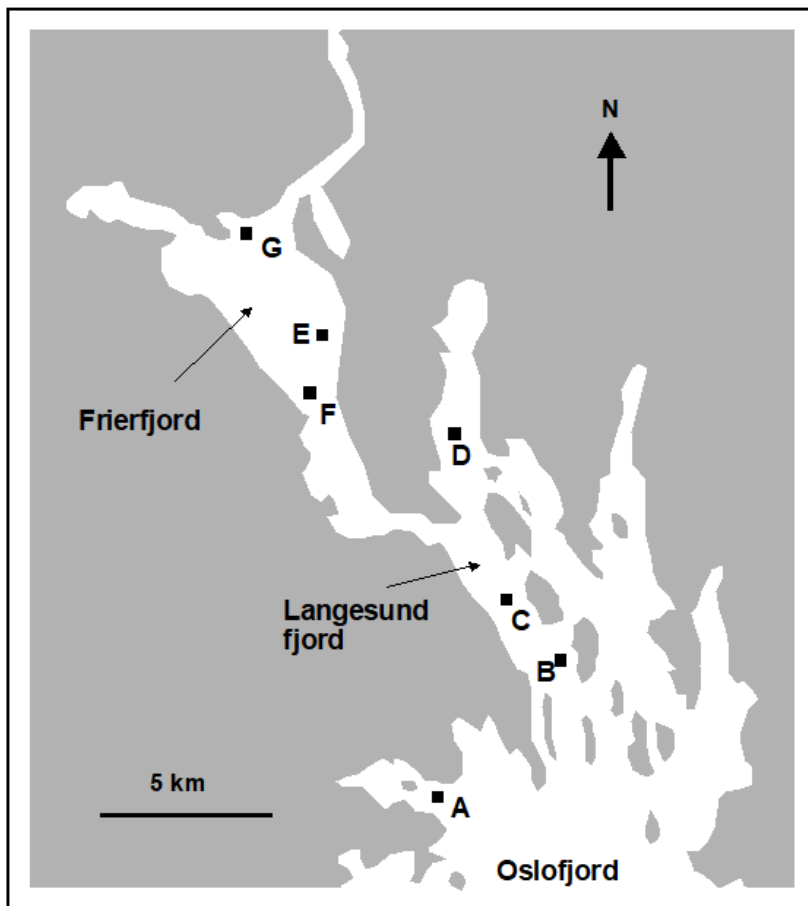


Fig. 1.1. Frierfjord, Norway {F}. Benthic community sampling sites (A-G) for the IOC/GEEP Oslo Workshop; site F omitted for macrobenthos.

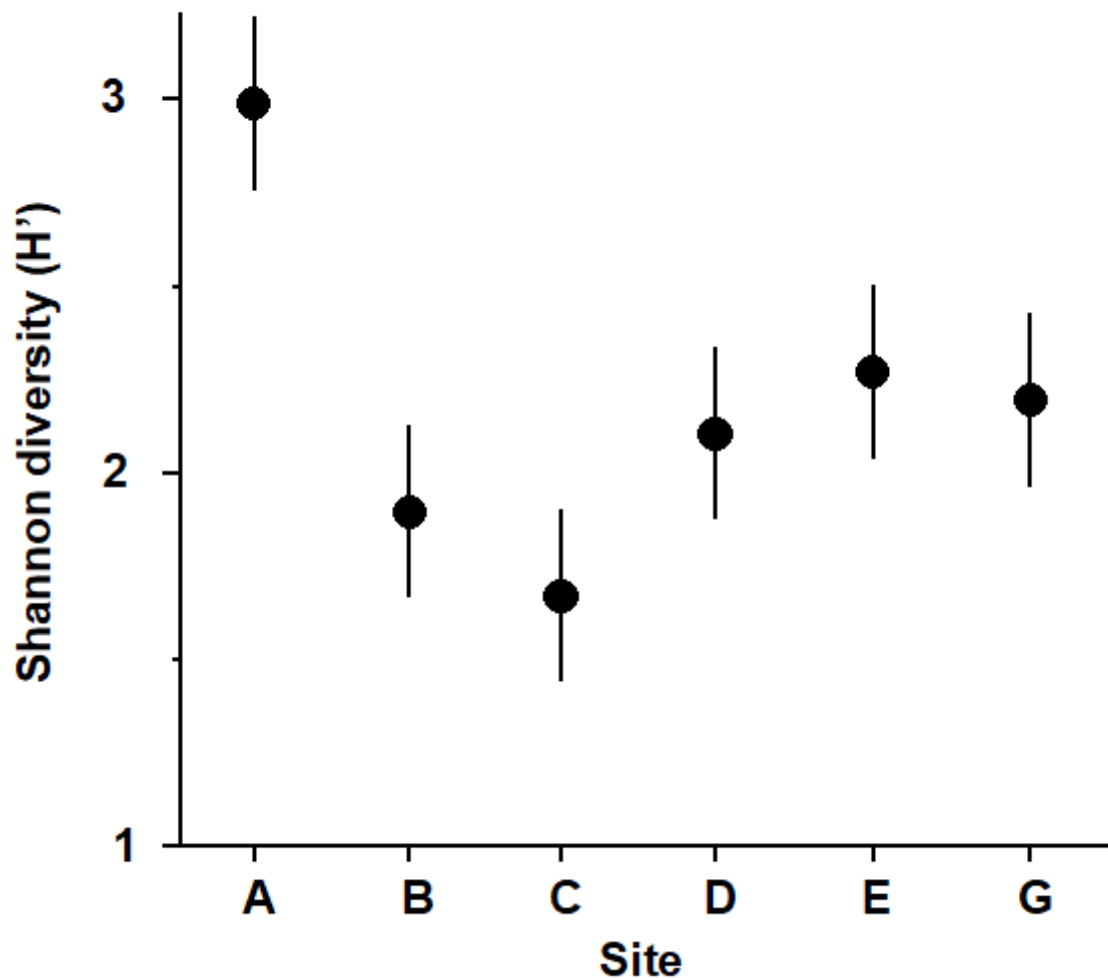


Fig. 1.2. Frierfjord macrofauna {F}. Means and 95% confidence intervals for Shannon diversity (H'), from four replicates at each of six sites (A-E, G).

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 0.1m^2 , biomass in mg per 0.1m^2 .

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

| | A1 | A2 | A3 | A4 | B1 | B2 | B3 | B4 |
|----------------------------|----|----|----|----|----|----|----|----|
| Abundance | | | | | | | | |
| <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 |
| | | | | | | | | |
| Biomass | | | | | | | | |
| <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> , <i>indet.</i> | 1 | 41 | 391 | 1 | 5 | 1 | 2 | 1 |
| <i>Polychaeta</i> , <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[¶], 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.

¶ Using the *PRIMER DIVERSE* routine.