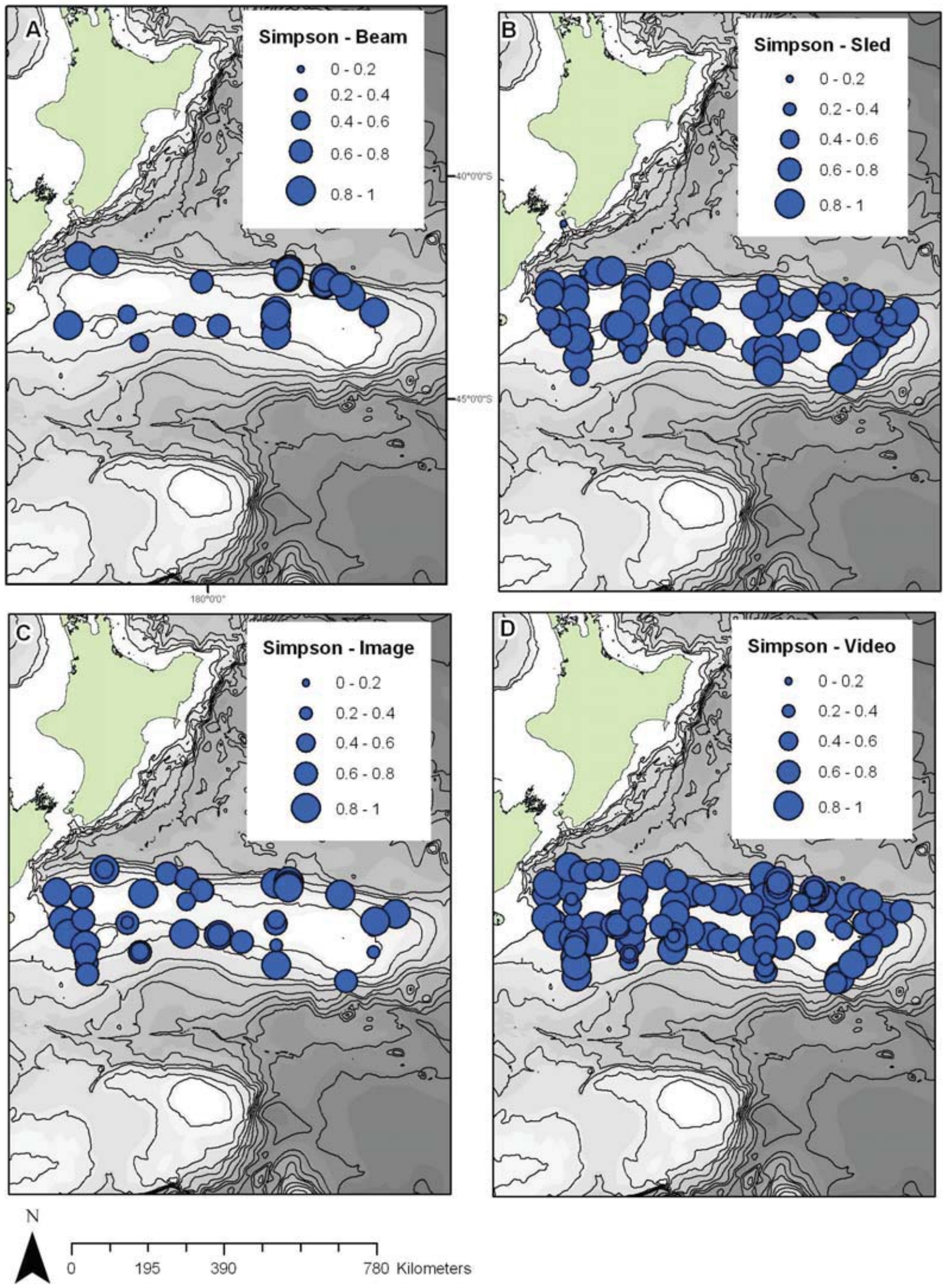


**Figure 21: Simpson's Diversity over the Chatham Rise found by (a) Beam trawl; (b) Seamount sled; (c) Still images (based on summed total of 10 replicates per station); and (d) Video.**

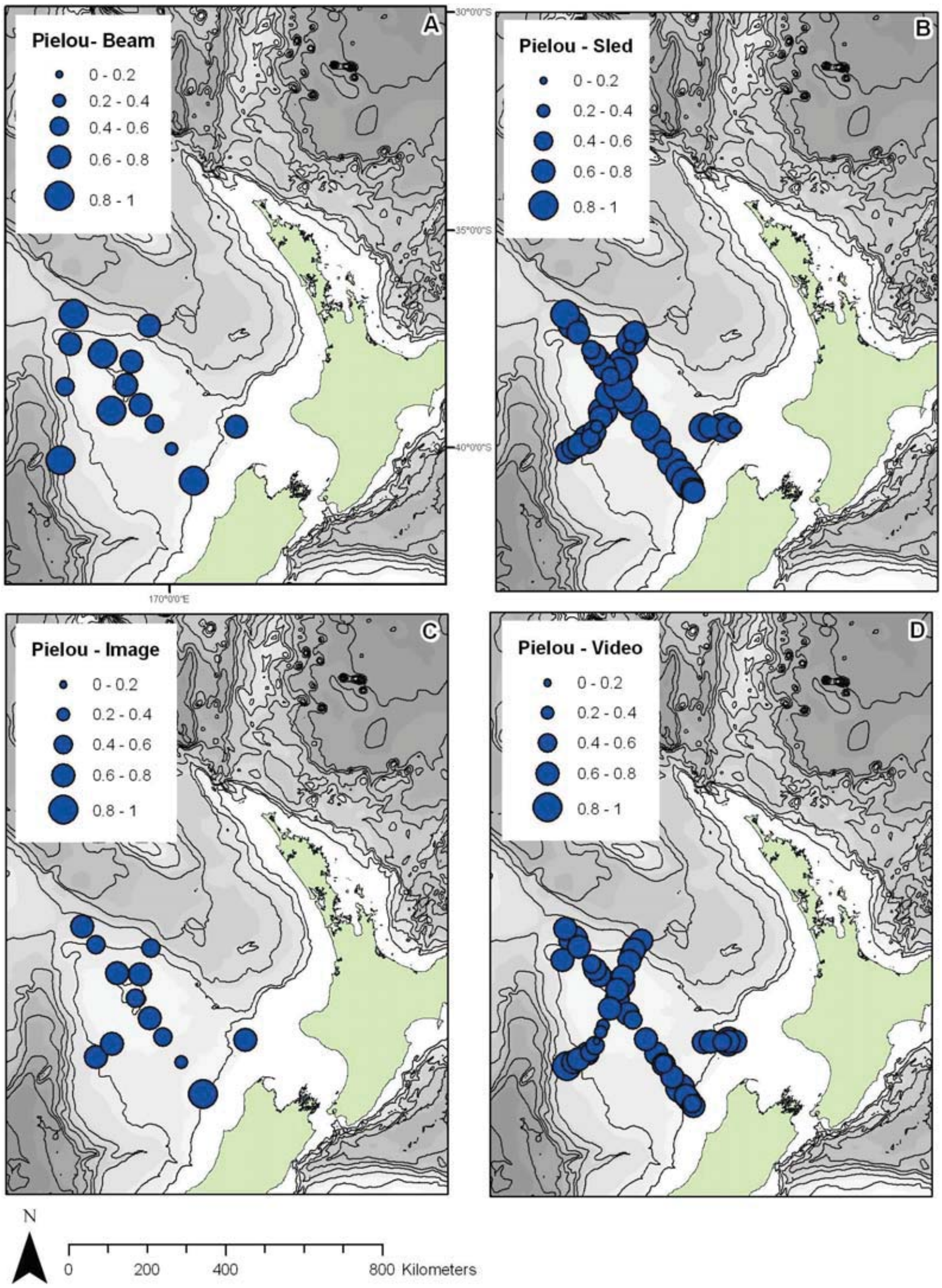


**Figure 22: Pielou's Evenness over the Challenger Plateau found by (a) Beam trawl; (b) Seamount sled; (c) Still images (based on summed total of 10 replicates per station); and (d) Video.**

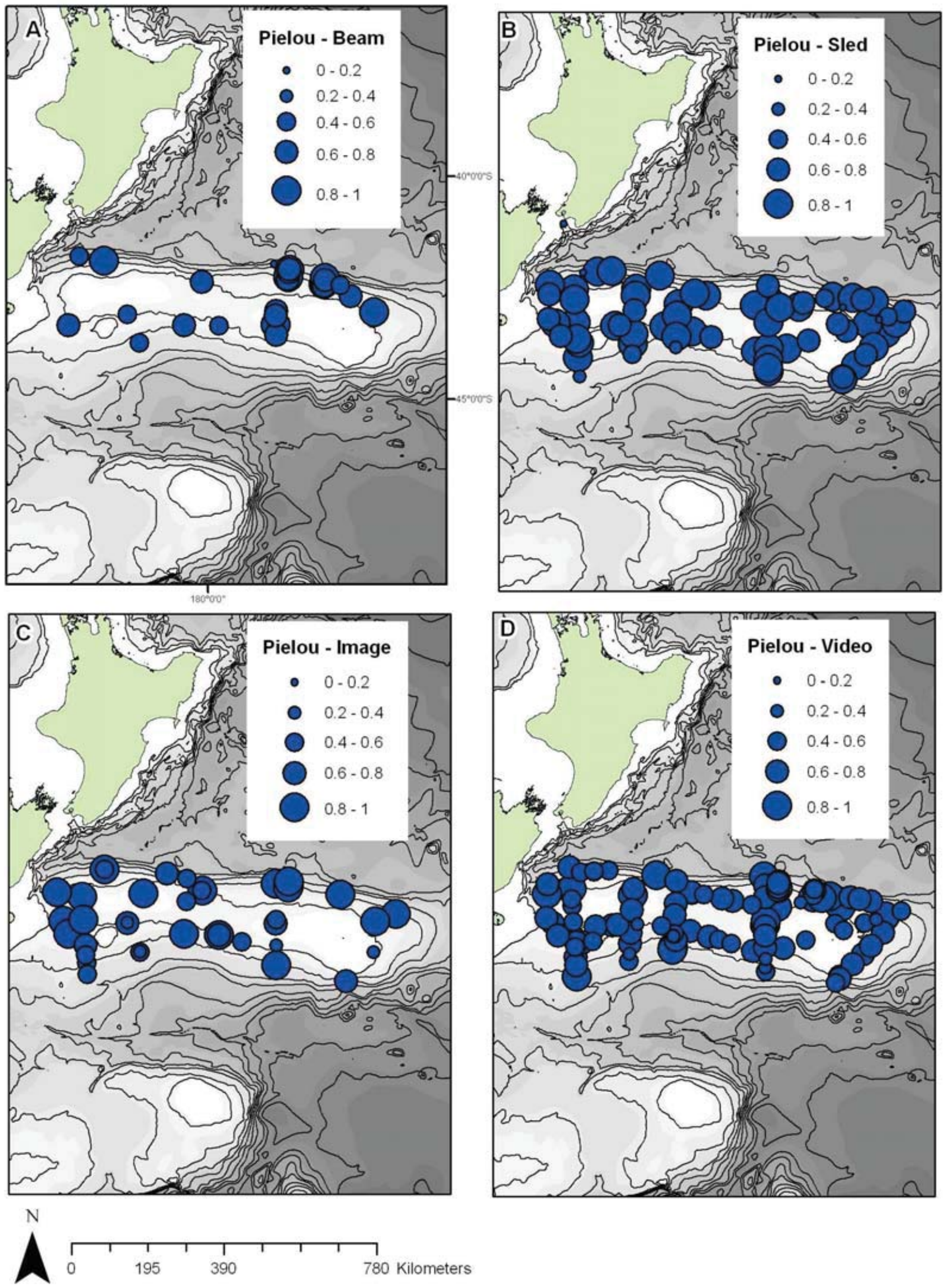


**Figure 23: Pielou's Evenness over the Chatham Rise found by (a) Beam trawl; (b) Seamount sled; (c) Still images (based on summed total of 10 replicates per station); and (d) Video.**

### 3.2.3 Diversity patterns for sampling strata, depth bands and sediment type

#### Initial sampling strata

Although sampling strata were designed to allocate sampling effort based on known environmental information (see NIWA Client report: WLG2008-27) and their potential effects on diversity, few consistent differences were observed between sampling strata at either location (Figure 24 & 25), Appendix 4). This pattern was consistent for all sampling methods (video data only presented here). Differences between diversity indices are to be expected because the different indices represent different aspects of diversity.

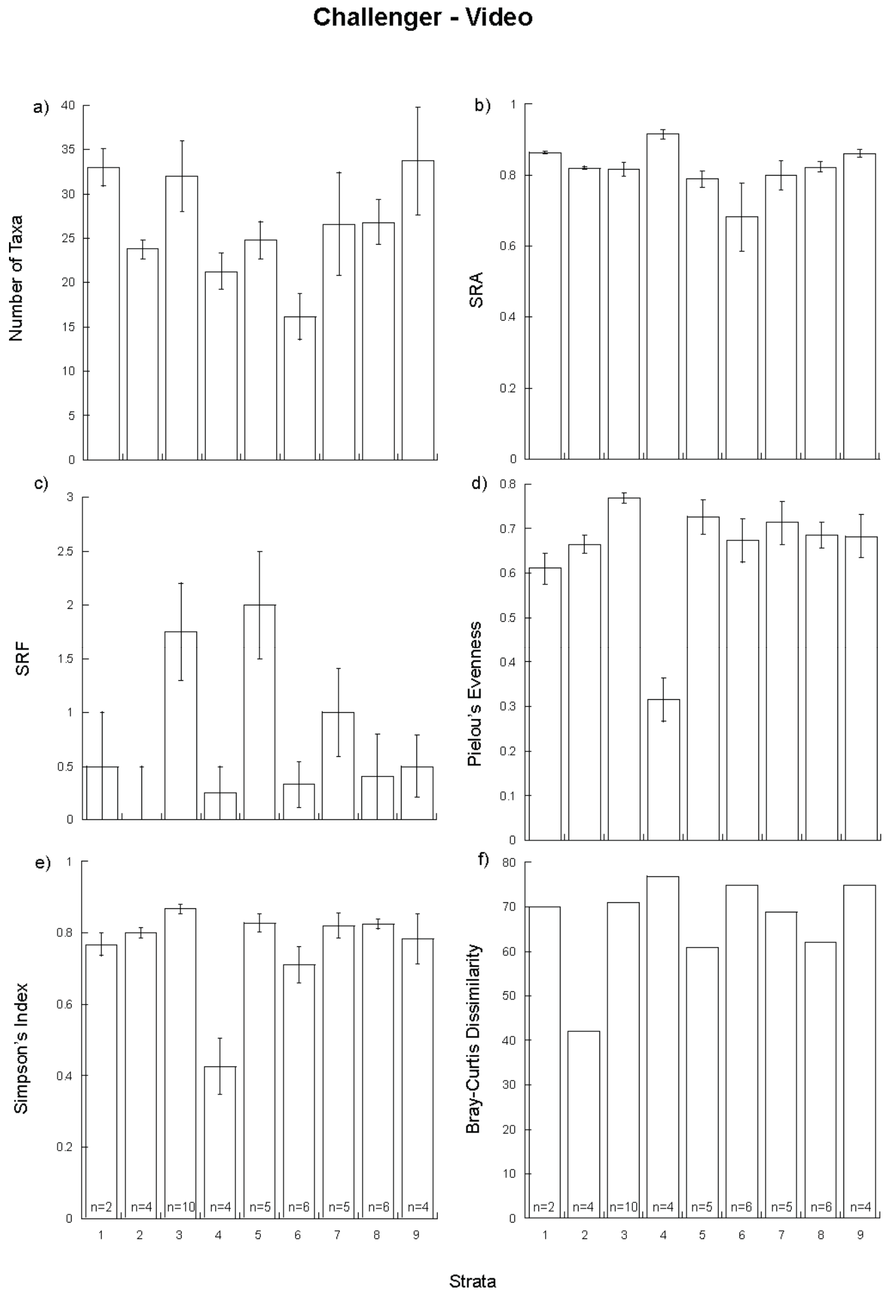


**Figure 24: Challenger Plateau diversity from video data in relation to initial sampling strata. Average (and standard errors) of (a) number of taxa (S), (b) % of low abundance taxa ($S_{RA}$), (c) number of infrequently occurring taxa ($S_{RF}$), (d) Pielou's Evenness, (e) Simpson's Diversity, and (f) Bray-Curtis dissimilarity (βdiss) The sample size (n) within each stratum is indicated.**

On Challenger Plateau, stratum 4 (on the southwest flank in depths 500-750 m, Figure 1) had the lowest Simpson's diversity and Pielou's evenness: this stratum also had low numbers of infrequently occurring taxa ($S_{RF}$) relative to strata 3 and 5, and low number of total taxa relative to strata 1, 9 and 3 (northern flanks in depths 750-1250 m). High variability in the number of total taxa was observed in strata 3, 7 (northern flanks in depths 500-750 m), and 9.

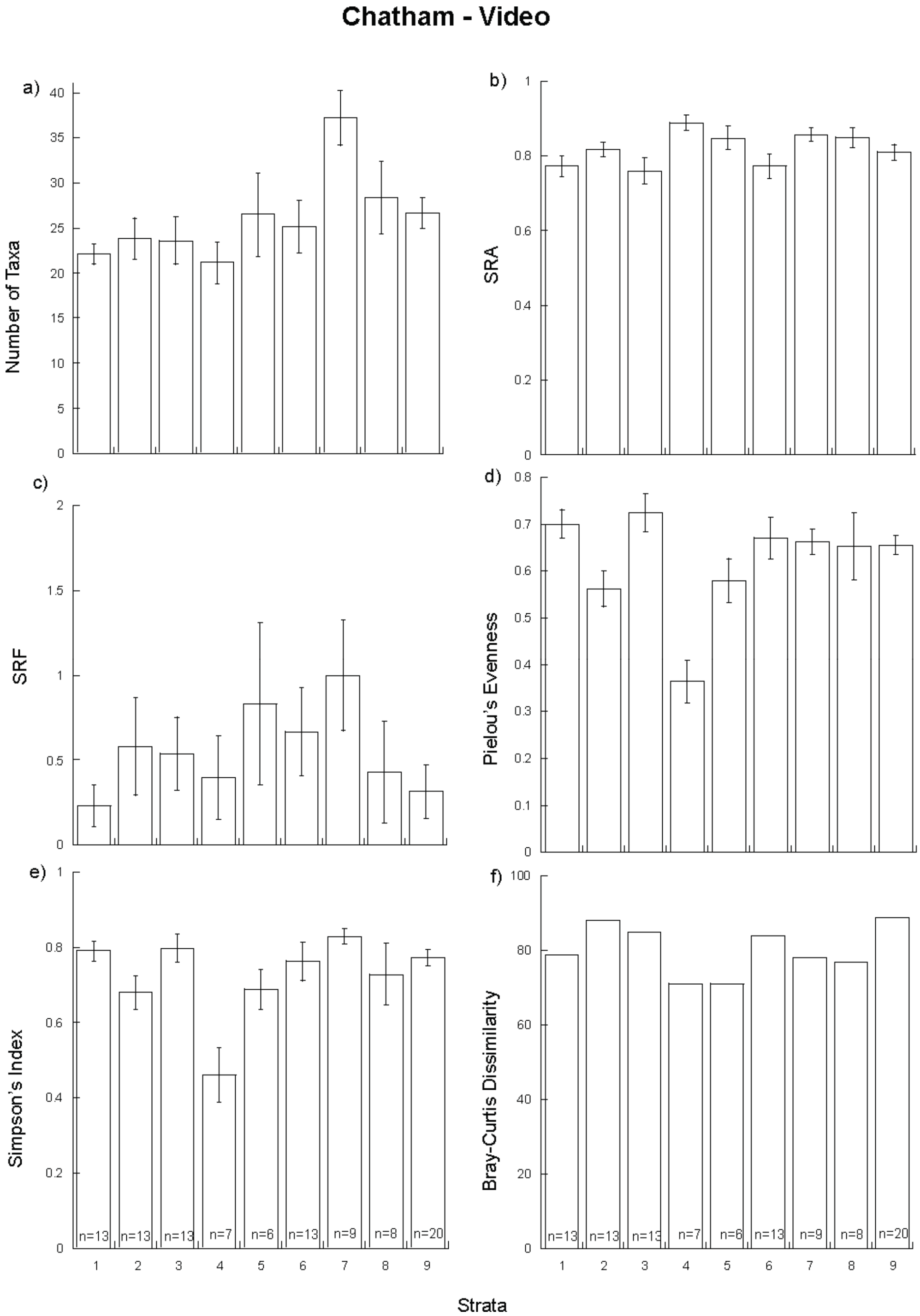


**Figure 25: Chatham Rise diversity from video data in relation to initial sampling strata. Average (and standard errors) of (a) number of total taxa (S), (b) % of low abundance taxa ($S_{RA}$), (c) number of infrequently occurring taxa ($S_{RF}$), (d) Pielou's Evenness, (e) Simpson's Diversity, and (f) Bray-Curtis dissimilarity (βdiss). The sample size (n) within each stratum is indicated.**

On the Chatham Rise stratum 7 (southeast and east flanks in depths 500-750 m, Figure 1) had the highest number of total taxa. Stratum 4 (southern central flank in depths 750-1250 m) had lowest Simpson's diversity and Pielou's evenness.

### 3.2.3.1 Patterns in variability across depth

No consistent patterns were observed across depth for any of the diversity measures at either location (Appendix 5). This lack of pattern with depth was consistent for all sampling methods (video data only presented here). Diversity values were lowest on Challenger Plateau in the shallowest depth category sampled (200-400 m), and highest at deepest depths (1800-2000 m) in four of the six diversity indices presented (Figure 26). Three of the indices showed a general increasing trend across all depths, while the other three were bimodal with peaks at mid depths and at the deepest depth sampled.

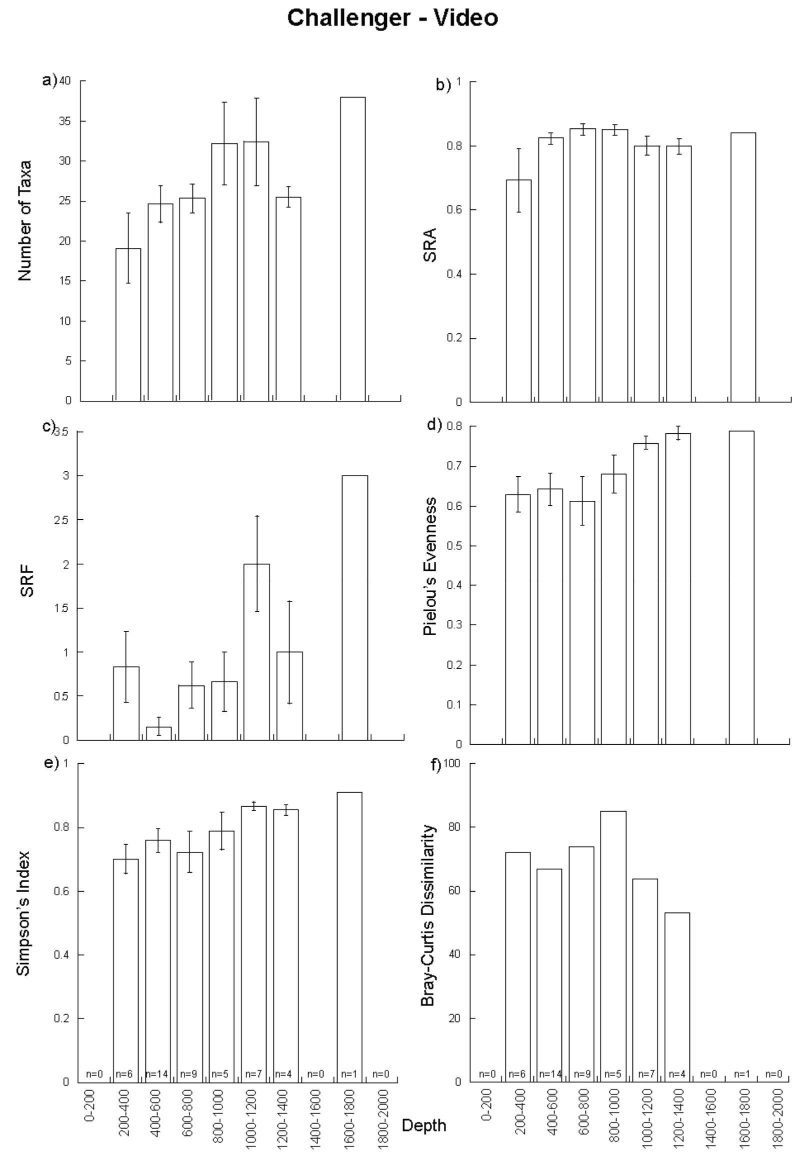


**Figure 26: Challenger Plateau DTIS video data by depth strata. Average (and standard errors) of (a) number of total taxa (S), (b) % of low abundance taxa ($S_{RA}$), (c) number of infrequently occurring taxa ($S_{RF}$), (d) Pielou's Evenness, (e) Simpson's Diversity, and (f) Bray-Curtis dissimilarity (βdiss) The sample size (n) within each stratum is indicated.**

Trends with depth at the Chatham Rise were even less apparent, with the similarity between indices limited to the shallowest depth (0-200 m) having lowest or second lowest values in 5 of 6 indices (though the shallowest depth had the largest value for the remaining diversity index, Bray-Curtis Dissimilarity) (Figure 27).

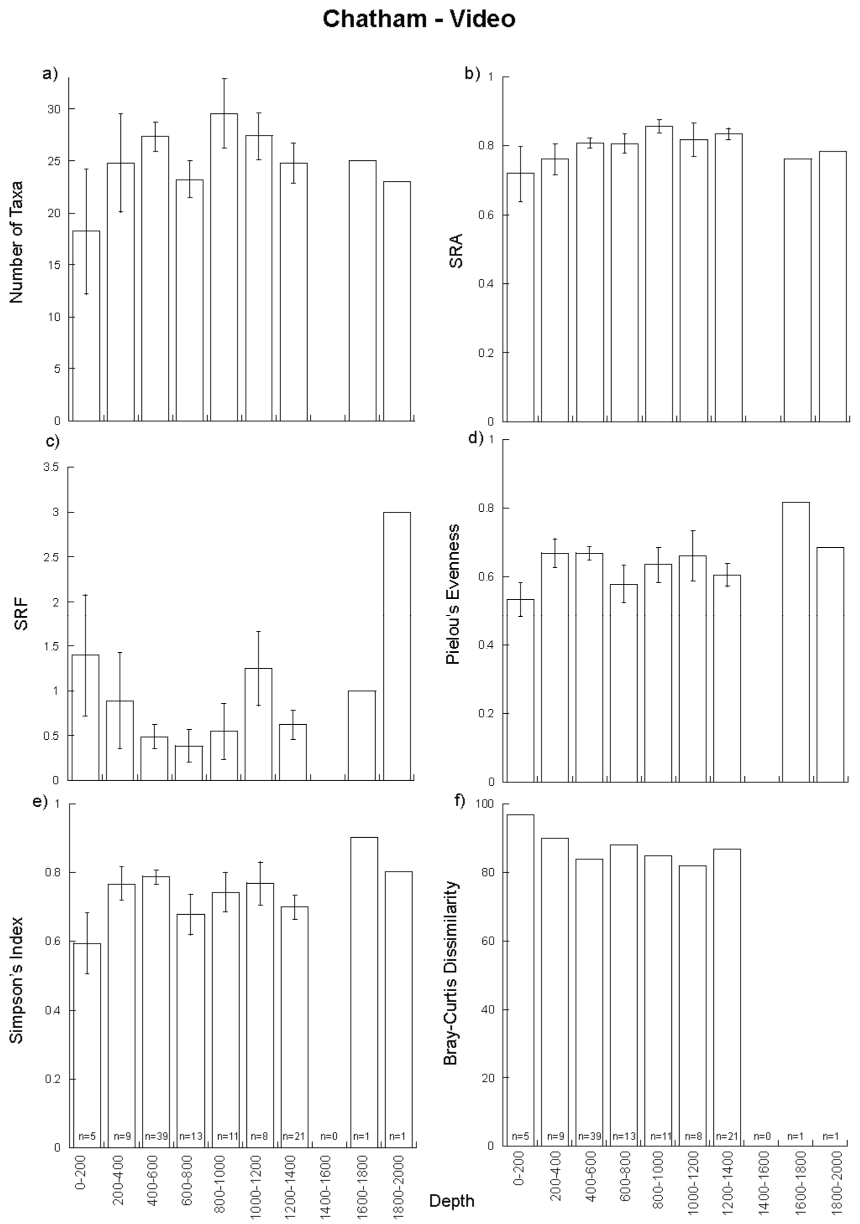


**Figure 27: Chatham Rise DTIS video data by depth strata. Average (and standard errors) of (a) number of total taxa (S), (b) % of low abundance taxa ($S_{RA}$), (c) number of infrequently occurring taxa ($S_{RF}$), (d) Pielou's Evenness, (e) Simpson's Diversity, and % dissimilarity as (f) Bray-Curtis dissimilarity (βdiss) The sample size (n) within each stratum is indicated.**

### 3.2.3 Patterns in variability across sediment class

The full range of sediment classes was only sampled using seamount sled and video data at Chatham Rise. However, the great majority of the sites sampled on both the Chatham Rise and Challenger Plateau were of mud substrate and therefore most samples were taken on this substrate class, limiting our ability to determine between sediment differences. For the video data from the Chatham Rise, the shell sediment class had the lowest value for all of the diversity indices presented, but only one video sample was analysed in this class (Figure 28). There were no significant differences between the other sediment classes (Appendix 6).

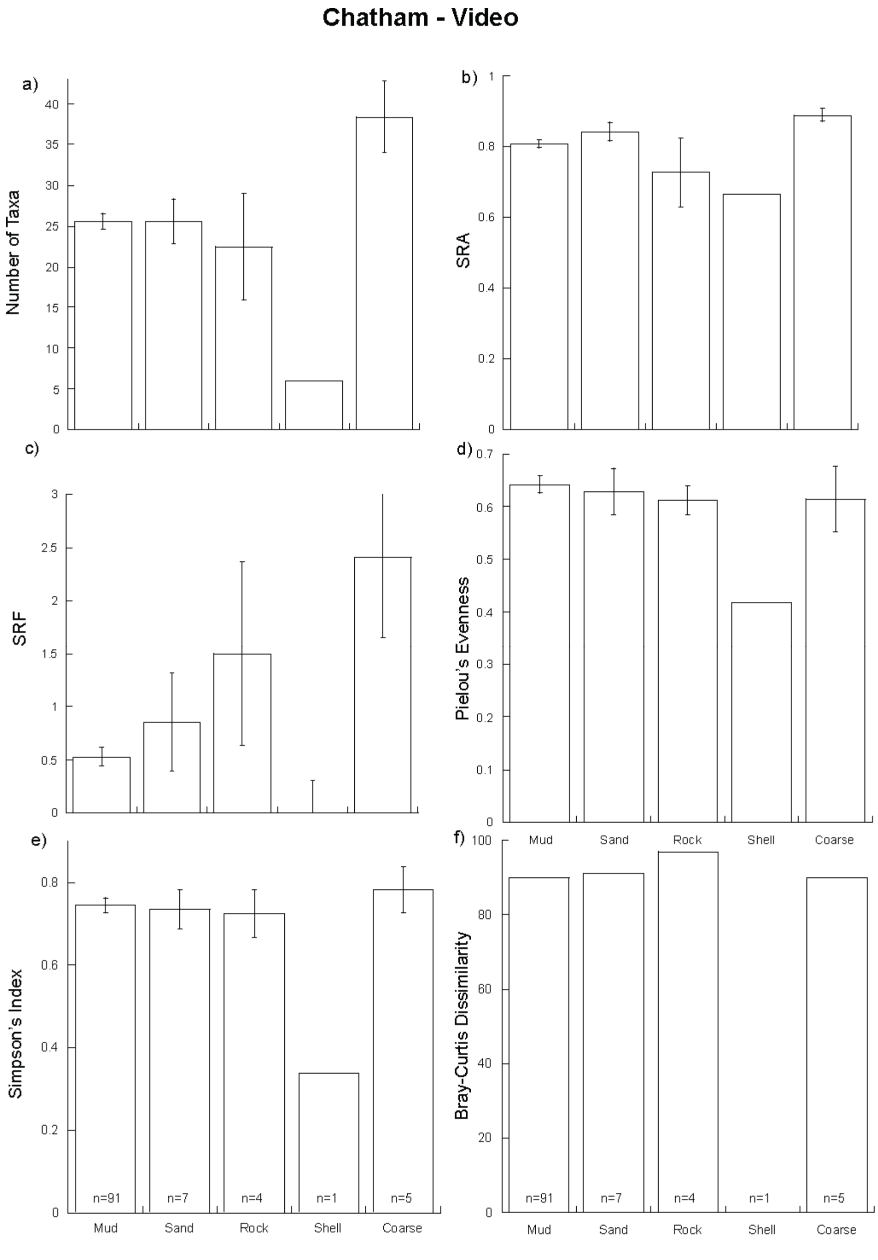


**Figure 28: Chatham Rise DTIS video data by sediment class. Average (and standard errors) of (a) number of total taxa (S), (b) % of low abundance taxa ($S_{RA}$), (c) number of infrequently occurring taxa ($S_{RF}$), (d) Pielou's Evenness, (e) Simpson's Diversity, and % dissimilarity as (f) Bray-Curtis dissimilarity (βdiss). The sample size (n) within each class is indicated.**

### 3.3 Summary of patterns in biodiversity across the Challenger Plateau and Chatham Rise

None of the sampling methods showed saturated taxon accumulation curves for either Chatham Rise or Challenger Plateau at the finest taxonomic resolution. These non-asymptotic taxon accumulation curves highlight the heterogeneity of benthic assemblages and habitats across the locations. This heterogeneity is also evident in the high β-diversity estimates (88-95% for both locations and across all sampling methods) and is maintained at all levels of taxonomic resolution tested (taxon, family, and order). Accumulation rates are slightly higher for Chatham Rise than Challenger Plateau, but not significantly so (Figure 29). Importantly, it appears that many of the taxa observed in the video data are common between the locations, i.e., the accumulation curve constructed using data for both locations together is not elevated relative to the curves for each location individually.

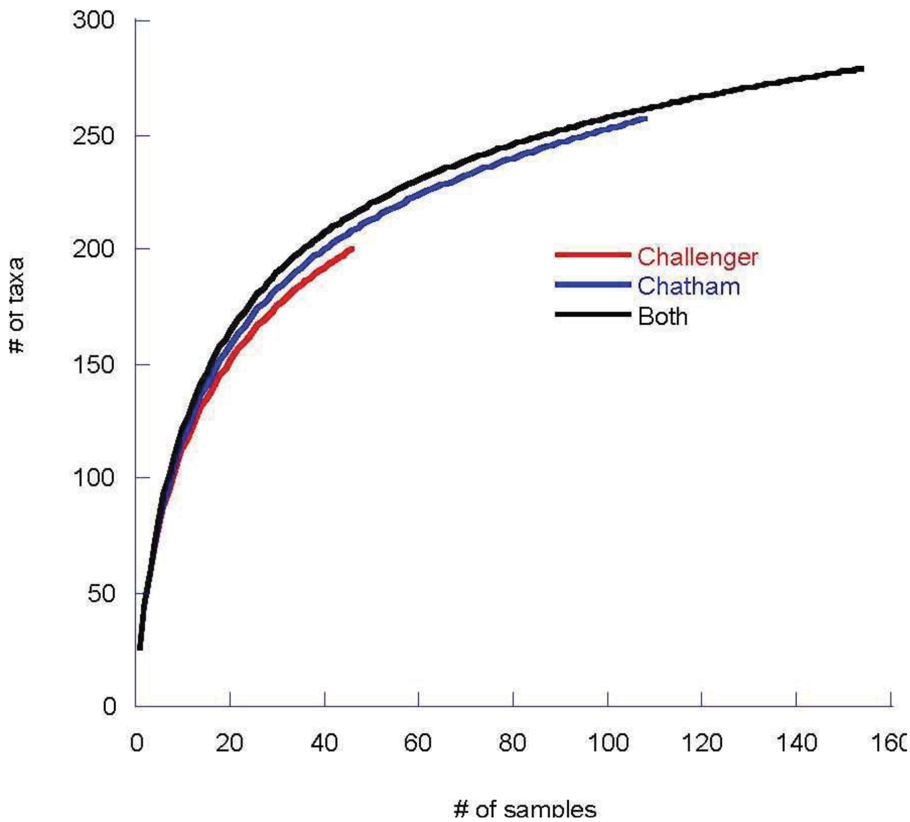


**Figure 29: Taxa accumulation curves for video data from Challenger Plateau, Chatham Rise and both locations together.**

Analysis of the DTIS data (both as video and still images) suggests that while all measures show increasing variability with increasing scale of sampling, for numbers of total taxa and for infrequently occurring taxa, much of the variability in biodiversity occurs at small-scales; within sites and within transects. For Simpson's diversity and Pielou's evenness, however, variability at the largest scale (that of the location) is also very high. These results will be analysed further under Objective 16 and incorporated into the suggested design of future sampling strategies.

Unsurprisingly, spatial patterns of diversity differed between the two locations. On the Challenger Plateau, generally higher numbers of taxa were observed in the north-eastern and north-western areas. A similar pattern was observed for the number of infrequently occurring taxa in the video data. On the Chatham Rise, highest numbers of taxa were observed on the southern slope, and lowest values on the top of the Rise and on the north-eastern slope. High numbers of infrequently occurring taxa were observed on the southern slope, and lowest values on the northern region of the plateau. Neither Simpson's diversity nor Pielou's evenness showed any strong spatial patterns across either location. Related to these findings, differences in diversity between initial sampling strata were few, and there were no consistent trends with depth. Interestingly, there were also no significant differences between biodiversity associated with mud, sand and rock substrates.

## 4. IMPLICATIONS AND RECOMMENDATIONS

### 4.1 Which diversity indices are the most informative?

Of the initial fourteen measures investigated, two exhibited similar values regardless of sampling method: McIntyre's dominance, and β–diversity as measured by average Bray Curtis dissimilarity of species abundances (βdiss). Another 6 measures appeared unaffected by sample unit size: Pielou's evenness; Smith-Wilson evenness; Simpson's Index; number of taxa rare in abundance ($S_{RA}$); number of taxa infrequent in occurrence ($S_{RF}$), and β-diversity as a ratio of γ to α diversity (βw). From the initial measures considered we have selected 6 indices that represent different aspects of biodiversity:

1. Number of taxa (species richness). This is a fundamental measure of biodiversity and as such we recommend its use despite its dependence on sample unit size. It is also useful in clarifying what other indices mean because it is more directly related to the raw sample data and has immediate intuitive meaning. Predictions of number of taxa at larger scales (γ-diversity per location) are also generally useful despite the uncertainty associated with extrapolation from limited numbers of samples.

2. Pielou's evenness represents how abundance is spread across the taxa present and ranges from a possible 0 (dominated by one species) to 1 (all species have same abundances). Pielou's evennesswas selected rather than Smith-Wilson evenness because we did not find it to be affected by sample size and has a high ability to assign evenness correctly within a range of conditions. It is also the most commonly used measure of evenness. McIntyre's dominance (another way of considering the spread of abundances) is not recommended as a measure of diversity because number of taxa is not included in its calculation. However, this measure will be used in other objectives as it is a potential indicator of stress.

3. Simpson's diversity combines both the number of taxa and how abundance is distributed across them and, in contrast to the Shannon-Weiner index, was robust to differences in sample size.

4 & 5. Number of taxa rare in abundance ($S_{RA}$) calculated as the taxa representing 5% or less of the abundance, and number of infrequently occurring taxa ($S_{RF}$) calculated as the number of taxa only found once or twice across either location). These measures are of interest because rare species generally comprise a large proportion of overall species richness and there are indications that the proportion of rare taxa is of importance to ecosystem functioning and resilience (McCann et al. 1998). Both measures are recommended as they represent different aspects of rarity with the number of infrequently occurring taxa representing the degree of habitat specificity (Ellingsen et al. 2007). Taxa that are rare in abundance are often medium to large in size and thus may exert an undue influence on function (Thrush & Dayton 2002). For marine systems, only weak relationships are usually found between taxa that are low in abundance and the number of sites at which they occur (Ellingsen et al. 2007).

6. Abundance β–diversity, as measured by average Bray Curtis dissimilarity (βdiss). This measure is calculated on abundance data and represents the degree of dissimilarity between community compositions. It represents the heterogeneity aspect of biodiversity. Whittaker's β-diversity (βw), which also represents heterogeneity, is not recommended with these data as its calculation was problematic because of our inability to get a good prediction of γ-diversity, as reflected in the lack of asymptote in taxon accumulation curves for each location.

### 4.2 Influence of taxonomic resolution on diversity estimates

For four of the biodiversity indices (S, γ-diversity, Pielou's evenness, β-diversity as βdiss), the effect of decreasing the level of taxonomic resolution was investigated by making calculations at the scale of families and orders. Rarity indices were not included in this analysis because it does not make sense to calculate these at such taxonomic resolutions. Generally the same patterns were observed at coarser taxonomic resolutions as at the finest level (species, genera), although differences between sampling methods and locations became less pronounced, especially for Simpson's diversity and β-diversity (βdiss). Accumulation curves showed a progressive flattening of the curves with decreasing taxonomic resolution with differences between sampling methods still apparent. These results suggest that coarser taxonomic resolutions can be used for relative comparisons between sampling methods and locations. However, using the highest taxonomic resolution practical still remains the best option for biodiversity estimation. While the possibility of using coarser taxonomic levels for biodiversity surveys has the potential to reduce survey costs, it is also clear from these results that the coarser levels of taxonomic resolution achieved in the hyperbenthic macrofauna and benthic meiofauna data sets provide less detailed estimates of diversity than do the mega- and macro-epifauna datasets. This serves to highlight that there are practical problems associated with assessing biodiversity patterns using taxonomic groups or faunal size fractions which are either difficult to identify or for which accepted taxonomies and keys are not available. We have less taxonomic knowledge about the hyperbenthic macrofauna and benthic meiofauna, and consequently less ability to recognise taxa at the species level and define their diversity.

### 4.3 Influence of sampling method on biodiversity estimates

The four epifaunal sampling methods varied in the seabed area covered and the size range of fauna they collected. The effect of these differences could be seen on most of the biodiversity indices and manifested themselves in different ways for different indices. However, the selected indices (except for number of taxa) were not strongly influenced by the area covered. Importantly, for these four epifaunal methods, generalities derived from each sampling method for differences between initial sample strata, depth class, and sediment type were similar for all methods, such that we were able to represent them using the video data alone. General spatial patterns across the two locations did, however, differ between the sampling methods for the number of taxa and number of infrequently occurring taxa. Mostly these differences were observed between the seamount sled and the beam trawl data, and again between the still image data and the video data. This suggests that the non-destructive photographic surveying, by video in particular, is a viable alternative to physical sampling for routine measurement of benthic megafaunal biodiversity.

The differences between video and still image results, notably the low accumulation rate of taxa observed in the still image data, suggests that the still image data, while useful for assessing within-transect variability of the video data, is less useful than the video data for overall estimates and relative comparisons of biodiversity. In the present study, this is a consequence of the much smaller seabed area represented by the still image data, which in turn is a consequence of the time required to fully analyse each image.

Similarly, the higher values of $S_{RA}$ and $S_{RF}$ calculated from beam trawl data when compared with estimates from other methods is probably a function of an interaction between the size spectrum of the taxa sampled by the different methods and the number of stations sampled. Thus, the beam trawl samples the broadest size spectrum of organisms, and therefore potentially captures more of the infrequently occurring taxa, and was also deployed at relatively few stations which will tend to exaggerate the apparent rarity of those taxa that are caught.

The time required to process samples from each gear type largely dictates either the number of samples that can be processed or the level of taxonomic resolution that can be achieved for a given budget. As noted above with regard to taxonomic resolutions, an important point to emerge from the comparison of diversity estimates from the different gear types is that the two data sets derived from the smallest body size components of the benthos; the meiofauna (multicorer samples) and hyperbenthic fauna (Brenke sled samples), provided the least discrimination between sites and locations. This is almost certainly a consequence of the coarser level of taxonomic resolution achieved for these samples. This highlights an important consideration in the planning of biodiversity surveys and suggests that unless the necessary post-processing facilities are available, it is likely to be more effective to take many samples with a few gear types than to use many gear types and take fewer samples with each.

## 5. ACKNOWLEDGMENTS

The OS 20/20 Chatham-Challenger Post-Voyage Analysis Project is supported by a collaboration between the Ministry of Fisheries, Land Information New Zealand, and the Department of Conservation under cross-departmental research pool funding.
This report was reviewed, within NIWA, by Dr Ashley Rowden and Dr Don Robertson, and, within MFish, by Dr Mary Livingston.
Many thanks also go to Sarah Hailes, Kathryn Julian, and Lucie Caine for assistance with data compilation, statistical analyses, and production of figures.

# 6. APPENDICIES

## 6.1 Appendix 1

Results of statistical analyses on the differences between the station average of the biodiversity indices in relation to sampling methods and location. Sampling methods: B-Beam trawl; S- Seamount sled; V-Video; I- Still image summed over 10 replicates. Locations: T- Chatham; L- Challenger. In the difference column, codes with highest values come first and codes connected by lines are not significantly different to one another.

**Normal models**

| Index | Source | DF | MS | F-value | P-value | Difference |
|---|---|---|---|---|---|---|
| *Number of taxa* | Model | 7 | 3079.38 | 19.85 | <.0001 | |
| | Error | 351 | 155.14 | | | |
| | type | 3 | 6014.28 | 38.77 | <.0001 | B>V>S>I |
| | location | 1 | 166.87 | 1.08 | 0.3004 | |
| | type*location | 3 | 138.30 | 0.89 | 0.4457 | |
| *Margalef's richness* | Model | 7 | 44.85 | 12.17 | <.0001 | |
| | Error | 348 | 3.68 | | | |
| | type | 3 | 81.17 | 22.03 | <.0001 | |
| | location | 1 | 10.24 | 2.78 | 0.0965 | |
| | type*location | 3 | 10.47 | 2.84 | 0.0379 | |
| | Challenger | 3 | 41.72 | 10.42 | <.0001 | B>V S  S I |
| | Chatham | 3 | 59.99 | 16.88 | <.0001 | B > S V I |
| | B | 1 | 0.03 | 0 | 0.9575 | |
| | S | 1 | 19.95 | 4.55 | 0.0353 | T>L |
| | V | 1 | 3.41 | 1.46 | 0.2287 | |
| | I | 1 | 15.31 | 13.83 | 0.0005 | T>L |
| *Pielou's evenness* | Model | 7 | 0.238 | 9.02 | <.0001 | |
| | Error | 347 | 0.026 | | | |
| | type | 3 | 0.370 | 13.99 | <.0001 | S > B I V |
| | location | 1 | 0.056 | 2.11 | 0.1470 | |
| | type*location | 3 | 0.054 | 2.04 | 0.1081 | |
| *Shannon-Weiner Diversity* | Model | 7 | 2.86 | 7.22 | <.0001 | |
| | Error | 351 | 0.40 | | | |
| | type | 3 | 5.00 | 12.61 | <.0001 | |

| | | | | | | |
|---|---|---|---|---|---|---|
| | location | 1 | 1.81 | 4.56 | 0.0334 | |
| | type*location | 3 | 1.37 | 3.45 | 0.0168 | |
| | Challenger | 3 | 3.20 | 9.14 | <.0001 | B V S > I |
| | Chatham | 3 | 3.16 | 7.6 | <.0001 | B S S V V I |
| | B | 1 | 0.03 | 0.09 | 0.7718 | |
| | S | 1 | 2.25 | 4.12 | 0.0449 | T>L |
| | V | 1 | 0.47 | 1.37 | 0.2437 | |
| | I | 1 | 2.43 | 8.89 | 0.0044 | T>L |
| *Simpson's Diversity* | Model | 7 | 0.107 | 3.5 | 0.0012 | |
| | Error | 348 | 0.031 | | | |
| | type | 3 | 0.138 | 4.49 | 0.0041 | |
| | location | 1 | 0.101 | 3.28 | 0.0711 | |
| | type*location | 3 | 0.093 | 3.02 | 0.0300 | |
| | Challenger | 3 | 0.094 | 2.9 | 0.0385 | B V S V S I |
| | Chatham | 3 | 0.146 | 4.84 | 0.0027 | S B I I V |
| | B | 1 | 0.001 | 0.06 | 0.8033 | |
| | S | 1 | 0.089 | 2.55 | 0.1130 | |
| | V | 1 | 0.041 | 1.5 | 0.2230 | |
| | I | 1 | 0.189 | 4.36 | 0.0418 | T>L |
| *Smith-Wilson evenness* | Model | 7 | 0.00569517 | 9.44 | <.0001 | |
| | Error | 345 | 0.0006032 | | | |
| | type | 3 | 0.01063258 | 17.63 | <.0001 | VBI>S |
| | location | 1 | 0.00051167 | 0.85 | 0.3577 | |
| | type*location | 3 | 0.00034503 | 0.57 | 0.6338 | |

**Poisson model**

| Index | Source | DF | Deviance | ChiSq | P-value | Difference |
|---|---|---|---|---|---|---|
| *Number of infrequently occurring taxa* | Model | 7 | 956.3072 | | | |
| | Error | 352 | 1355.3071 | | | |
| | type | 3 | | 132.0229 | <.0001 | B S >I V |
| | location | 1 | | 0.4729 | 0.4917 | |
| | type*location | 3 | | 4.8038 | 0.1867 | |

**Binomial models**

| Index | Source | DF | Deviance | P-value | ChiSq | P-value | Difference |
|---|---|---|---|---|---|---|---|
| *McIntyre's dominance* | Model | 7 | 4.8228 | 0.6816 | | | |
| | Error | 352 | 56.9042 | | | | |
| | type | 3 | | | 3.2302 | 0.3575 | |
| | location | 1 | | | 0.6168 | 0.4322 | |
| | type*location | 3 | | | 1.2094 | 0.7508 | |
| *Percentage of low abundance taxa* | Model | 7 | 30.4103 | <.0001 | | | |
| | Error | 352 | 109.8394 | | | | |
| | type | 3 | | | 24.9412 | <.0001 | V B > I S |
| | location | 1 | | | 0.0013 | 0.9713 | |
| | type*location | 3 | | | 0.4148 | 0.9372 | |

### 6.2 Appendix 2

Results of statistical analyses on the differences between the station average of the Taxonomic Distinctness calculated for Arthropoda, Cnidaria, Echinodermata and Mollusca related to sampling methods and location. Sampling methods: B-Beam trawl; S- Seamount sled; V- Video; I- Still image summed over 10 replicates. Locations: T- Chatham; L- Challenger. In the difference column, codes with highest values come first and codes connected by lines are not significantly different to one another.

**Location**

| | Source | DF | MS | F-value | P-value | Difference |
|---|---|---|---|---|---|---|
| **Challenger** | | | | | | |
| *Annelida* | Model | 1 | 30.40 | 0.05 | 0.8321 | |
| | Error | 54 | 669.63 | | | |
| *Arthropoda* | Model | 1 | 1259.85 | 7.67 | 0.0075 | B > V |
| | Error | 58 | 164.22 | | | |
| *Cnidaria* | Model | 1 | 0.91 | 0.00 | 0.9658 | |
| | Error | 58 | 490.69 | | | |
| *Echinodermata* | Model | 2 | 3974.97 | 5.38 | 0.0061 | B V V S |
| | Error | 99 | 739.07 | | | |
| **Chatham** | | | | | | |
| *Arthropoda* | Model | 3 | 1551.69 | 3.23 | 0.0231 | B I V I V S |
| | Error | 241 | 480.15 | | | |
| *Cnidaria* | Model | 2 | 436.29 | 1.12 | 0.3281 | |
| | Error | 174 | 388.98 | | | |
| *Echinodermata* | Model | 3 | 7548.77 | 11.87 | <.0001 | V B > S I |
| | Error | 241 | 636.22 | | | |
| *Mollusca* | Model | 3 | 6015.66 | 6.94 | 0.0002 | B V S > I |
| | Error | 241 | 867.07 | | | |

**Sampling method**

| | Source | DF | MS | F-value | P-value | Difference |
|---|---|---|---|---|---|---|
| **Beam Trawl** | | | | | | |
| *Arthropoda* | Model | 1 | 76.42 | 0.24 | 0.6258 | |
| | Error | 40 | 316.45 | | | |
| *Cnidaria* | Model | 1 | 421.34 | 0.66 | 0.4220 | |
| | Error | 40 | 640.27 | | | |
| **Video** | | | | | | |
| *Arthropoda* | Model | 1 | 454.85 | 2.00 | 0.1598 | |
| | Error | 152 | 227.94 | | | |
| *Cnidaria* | Model | 1 | 16.92 | 0.06 | 0.8102 | |
| | Error | 152 | 292.26 | | | |

## 6.3 Appendix 3

Results of statistical analyses on the differences between the station average of the biodiversity indices related to sampling methods and location at the family and order resolutions. Sampling methods: B- Beam trawl; S- Seamount sled; V- Video; I- Still image summed over 10 replicates. Locations: T- Chatham; L- Challenger. In the difference column, codes with highest values come first and codes connected by lines are not significantly different to one another.

**Normal models**

| Family level | Source | DF | MS | F-value | P-value | Difference |
|---|---|---|---|---|---|---|
| *Number of taxa* | Model | 7 | 1819.1 | 17.55 | <.0001 | |
| | Error | 345 | 103.7 | | | |
| | location | 1 | 56.8 | 0.55 | 0.4598 | |
| | type | 3 | 3909.3 | 37.72 | <.0001 | B>VS>I |
| | location*type | 3 | 145.1 | 1.40 | 0.2427 | |
| *Pielou's Evenness* | Model | 7 | 0.273 | 10.29 | <.0001 | |
| | Error | 344 | 0.027 | | | |
| | location | 1 | 0.091 | 3.43 | 0.0649 | |
| | type | 3 | 0.409 | 15.39 | <.0001 | |
| | location*type | 3 | 0.071 | 2.66 | 0.0484 | |
| | Challenger | 3 | 0.098 | 3.43 | 0.0199 | S B I B I V |
| | Chatham | 3 | 0.538 | 21.00 | <.0001 | S>BI>V |
| | Beam | 1 | 0.015 | 0.79 | 0.3794 | |
| | Image | 1 | 0.102 | 2.75 | 0.1034 | |
| | Sesled | 1 | 0.091 | 3.42 | 0.0670 | T>L |
| | Video | 1 | 0.046 | 1.85 | 0.1764 | |
| *Simpson's Index* | Model | 7 | 0.160 | 5.45 | <.0001 | |
| | Error | 344 | 0.029 | | | |
| | location | 1 | 0.153 | 5.23 | 0.0228 | |
| | type | 3 | 0.211 | 7.20 | 0.0001 | |
| | location*type | 3 | 0.117 | 4.01 | 0.0080 | |
| | Challenger | 3 | 0.115 | 3.79 | 0.0126 | B S V > I |
| | Chatham | 3 | 0.246 | 8.53 | <.0001 | S B I I V |
| | Beam | 1 | 0.003 | 0.22 | 0.6449 | |
| | Image | 1 | 0.236 | 5.68 | 0.0208 | T>L |
| | Sled | 1 | 0.148 | 5.39 | 0.0221 | T>L |
| | Video | 1 | 0.048 | 1.62 | 0.2057 | |

| Order level | Source | DF | MS | F-value | P-value | Difference |
|---|---|---|---|---|---|---|
| *Number of taxa* | Model | 7 | 809.15 | 17.55 | <.0001 | |
| | Error | 345 | 46.10 | | | |

| | | | | | | |
|---|---|---|---|---|---|---|
| | location | 1 | 49.41 | 1.07 | 0.3013 | |
| | type | 3 | 1742.46 | 37.79 | <.0001 | B>V>S>I |
| | location*type | 3 | 67.08 | 1.45 | 0.2266 | |
| *Pielou's Evenness* | Model | 7 | 0.224 | 9.00 | <.0001 | |
| | Error | 340 | 0.025 | | | |
| | location | 1 | 0.147 | 5.91 | 0.0155 | T>L |
| | type | 3 | 0.367 | 14.70 | <.0001 | S>I B V |
| | location*type | 3 | 0.063 | 2.51 | 0.0588 | |
| *Simpson's Diversity* | Model | 7 | 0.081 | 2.68 | 0.0104 | |
| | Error | 341 | 0.030 | | | |
| | type | 3 | 0.079 | 2.61 | 0.0512 | |
| | location | 1 | 0.241 | 7.96 | 0.0051 | |
| | location*type | 3 | 0.086 | 2.83 | 0.0385 | |
| | Challenger | 3 | 0.072 | 2.16 | 0.0969 | |
| | Chatham | 3 | 0.094 | 3.27 | 0.0221 | S B I B I V |
| | Beam | 1 | 0.132 | 5.38 | 0.0257 | T > L |
| | Image | 1 | 0.143 | 3.99 | 0.0510 | |
| | Sled | 1 | 0.063 | 1.81 | 0.1810 | |
| | Video | 1 | 0.023 | 0.84 | 0.3597 | |

### 6.4 Appendix 4

Results of statistical analyses on the differences between initial sampling strata of the biodiversity indices calculated from video data from Challenger Plateau and Chatham Rise. Model types other than normal are given in brackets.

**Challenger Plateau**

| | Source | DF | deviance/df | ChiSq | P-value |
|---|---|---|---|---|---|
| *Number of taxa (poisson)* | Model | 8 | 6.91 | 55.30 | <.0001 |
| | Error | 37 | 3.35 | | . |
| *Number of infrequently occurring taxa (poisson)* | Model | 8 | 2.6 | 1.06 | <.0001 |
| | Error | 37 | 1.04 | | . |
| *% low abundance taxa (binomial)* | Model | 8 | 0.03 | 9.39 | 0.3108 |
| | Error | 37 | 0.02 | | |
| | Source | DF | MS | F-value | P-value |
| *Pielou's Evenness* | Model | 8 | 0.08 | 9.39 | <.0001 |
| | Error | 37 | 0.01 | | |
| *Simpson's Diversity* | Model | 8 | 0.08 | 8.46 | <.0001 |
| | Error | 37 | 0.01 | | |

**Chatham Rise**

| | Source | DF | MS | F-value | P-value |
|---|---|---|---|---|---|
| *Number of taxa* | Model | 8 | 212.23 | 2.50 | 0.0162 |
| | Error | 99 | 84.84 | | |
| *Pielou's Evenness* | Model | 8 | 0.10 | 5.39 | <.0001 |
| | Error | 99 | 0.02 | | |
| *Simpson's Diversity* | Model | 8 | 0.10 | 4.28 | 0.0002 |
| | Error | 99 | 0.02 | | |
| | Source | DF | deviance/df | ChiSq | P-value |
| *% low abundance taxa (bionomial)* | Model | 8 | 0.02 | 1.86 | 0.0741 |
| | Error | 99 | 0.01 | | |
| *Number of infrequently occurring taxa (poisson)* | Model | 8 | 8.97 | 1.11 | 0.3854 |
| | Error | 99 | 100 | | |

### 6.5 Appendix 5

Results of statistical analyses on differences between depth for the biodiversity indices calculated from video data from Challenger Plateau and Chatham Rise. Model types other than normal are given in brackets.

| | Source | DF | MS | F-value | P-value |
|---|---|---|---|---|---|
| *Number of taxa* | Model | 15 | 107.73 | 1.10 | 0.3654 |
| | Error | 138 | 98.27 | | |
| | Depth | 8 | 141.75 | 1.44 | 0.1842 |
| | location | 1 | 68.22 | 0.69 | 0.4062 |
| | Depth*location | 6 | 69.32 | 0.71 | 0.6458 |
| *Pielou's Evenness* | Model | 15 | 0.028 | 1.21 | 0.2727 |
| | Error | 138 | 0.023 | | |
| | Depth | 8 | 0.030 | 1.30 | 0.2493 |
| | location | 1 | 0.019 | 0.84 | 0.3599 |
| | Depth*location | 6 | 0.024 | 1.03 | 0.4060 |
| *Simpson's Diversity* | Model | 15 | 0.035 | 1.35 | 0.1820 |
| | Error | 138 | 0.026 | | |
| | Depth | 8 | 0.037 | 1.43 | 0.1893 |
| | location | 1 | 0.020 | 0.77 | 0.3811 |
| | Depth*location | 6 | 0.023 | 0.90 | 0.4968 |
| *% low abundance taxa (bionomial)* | Model | 15 | 0.014 | 1.24 | 0.2489 |
| | Error | 138 | 0.011 | | |
| | Depth | 8 | 0.021 | 1.89 | 0.0665 |
| | location | 1 | 0.000 | 0.01 | 0.9222 |
| | Depth*location | 6 | 0.007 | 0.57 | 0.7503 |
| *Number of infrequently occurring taxa (poisson)* | Model | 15 | 36.3 | 2.42 | 0.0014 |
| | Error | 138 | 167.1 | | |
| | Depth | 8 | 32.77 | | <0.0001 |
| | location | 1 | 0.59 | | 0.4416 |
| | Depth*location | 6 | 4.89 | | 0.5581 |

### 6.6 Appendix 6

Results of statistical analyses on differences between sediment types for the biodiversity indices calculated from video data from Chatham Rise. Model types other than normal are given in brackets.

| | Source | DF | MS | F-value | P-value |
|---|---|---|---|---|---|
| *Number of taxa* | Model | 4 | 308.65 | 3.59 | 0.0088 |
| | Error | 103 | 86.04 | | |
| *Pielou's Evenness* | Model | 4 | 0.014 | 0.56 | 0.6915 |
| | Error | 103 | 0.025 | | |
| *Simpson's Diversity* | Model | 4 | 0.044 | 1.55 | 0.1930 |
| | Error | 103 | 0.028 | | |

| | Source | DF | Deviance/DF | Chi sq | P-value |
|---|---|---|---|---|---|
| *% low abundance taxa (bionomial)* | Model | 4 | 0.14 | 8.85 | 0.0650 |
| | Error | 103 | 0.06 | | |
| *Number of infrequently occurring taxa (poisson)* | Model | 4 | 5.54 | 15.02 | 0.0047 |
| | Error | 103 | 2.06 | | . |

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