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A data driven bioregionalisation to underpin shellfish fisheries restoration, Nelson Bays, New Zealand

New Zealand Aquatic Environment and Biodiversity Report No. 205

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ISSN 1179-6480 (online)
ISBN 978-1-98-857145-4 (online)

December 2018

New Zealand Government

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EXECUTIVE SUMMARY

Handley, S.J.; Dunn, A.; Hadfield, M. (2018). A data driven bioregionalisation to underpin shellfish fisheries restoration, Nelson Bays, New Zealand.

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The first step to developing an ecosystem model for Nelson Bays is to partition the study area into geographical regions based on representative ecosystem properties by carrying out a bioregionalisation. A data-driven bioregionalisation was constructed using historic shellfish biomass estimates and the multivariate BVSTEP method to best match with the spatial variability of a range of environmental variables. Surprisingly, only two of nineteen variables; maximum salinity and DON, were chosen by BVSTEP as best matching historic shellfish density distributions, excluding estimates of pelagic primary production. Despite the low correlation of the two environmental variables resulting from BVSTEP, the clustering in our analysis delineated fifteen regions that satisfied the aim of creating broad spatial areas that formed distinct spatial regions of the bioregionalisation. The potential for an ecosystem model to test hypotheses regarding importance of understanding historic habitat change and optimum habitat requirements of target shellfish is discussed.

1. INTRODUCTION

Nelson Bays, comprising Tasman Bay and Golden Bay are economically significant inshore waters utilised commercially and by local communities for recreational activities, aquaculture, and wild finfish and shellfish fisheries (Figure 1). At their peak, wild fisheries for green lipped mussels (*Perna canaliculus*), oysters (*Tiostrea chilensis*) and scallops (*Pecten novaezelandiae*) had combined revenues of about $90M per annum, and provided significant socio-economic benefits to commercial and non-commercial stakeholders including recreational fishers and Maori customary take (Michael et al. 2015). These fisheries have declined to low levels over the last decade and commercial fishing has ceased except for scallop dredging in beds in the outer Marlborough Sounds (Figure 1). Stakeholders desire the restoration of the sustainable production of these shellfish fisheries. Outcomes from two stakeholder workshops led to consensus that NIWA should develop an Ecosystem Model for Nelson Bays as a tool to investigate the relative importance of factors implicated in the decline of shellfish stocks in the bays (Michael et al. 2015). The cause of the observed shellfisheries declines in Nelson Bays are unknown, but are likely to be a combination of anthropogenic and environmental effects that may be synergistic and non-linear (e.g. Kemp et al. 2005). It is anticipated that development of an ecosystem model will have wider societal utility to inform management of all fishery resources in the region and demonstrate the utility of this approach.

To develop some types of ecosystem models it is necessary to first partition the study area into geographical regions based on predictable ecosystem properties, known as a bioregionalisation (Butler et al. 2001). Bioregionalisation has been described as a process that aims to partition a broad spatial area into distinct spatial regions, using a range of biological and physical information (Grant et al. 2006). Geographical partitioning can be undertaken using physical, environmental and biological characteristics endeavouring to separate regions that are relatively homogenous with representative ecosystem properties, such that the properties of each bioregion differ in the species composition, or their physical and ecological attributes (Grant et al. 2006).

Bioregionalisation in the marine environment is considered more complex than terrestrial equivalents, as apart from the distinct edges of rocky reefs, regional boundaries in the oceans are likely to be less sharp (or more 'fuzzy'), and may be more variable due to the three dimensional and fluid nature of the marine environment (Grant et al. 2006). Biogeographic classifications provide a foundation or assessment of representativeness, and have been used to develop ecologically representative networks of protected areas (Spalding et al. 2007; Shears et al. 2008). Various approaches have been used to classify large ocean areas into meaningful management units at different scales, recognising that to be useful to marine planning and for management the different classifications should depict scale-dependent complexity in a succinct form at the appropriate scales (e.g. Sharp et al. 2007; Lyne 2009). Large-scale global classification schemes have been developed, recognizing the need for hierarchical approaches, where large realms encompass provinces which contain nested ecoregions (Spalding et al. 2007). For example, Nelson Bays is in the Temperate Australasian realm, in the Southern New Zealand ecoregion, and nested in the province of Central New Zealand (Spalding et al. 2007). Subsequent biogeographic classifications by Shears et al. (2008) place Nelson Bays in the bioregion of Abel.

It is important to a-priori determine the purpose of a bioregionalisation, because describing the marine environment can be done in a variety of ways each subject to inherent limitations, so there is no single best bioregionalisation, rather they must be tailored for their end use (Grant et al. 2006; Sharp et al. 2007). Examples of limitations of bioregionalisations include: maps produced from classifications are inherently static representations of dynamic systems; that spatial classifications are not equipped to deal with spatial connectivity or temporal variations; and that they are insensitive to dispersal barriers and stochastic colonisation or historic events (Sharp et al. 2007). The process of developing bioregionalisations can involve some subjectivity, for example, using expert knowledge, available literature or ecological first principles to decide which data sets to include (Grant et al. 2006; Spalding et al. 2007; Sharp et al. 2010).

The purpose of the bioregionalisation described herein was to use a data-driven approach to partition Nelson Bays into regions of importance to historic shellfish populations. The aim, when faced with an abundance of environmental data, was to use multivariate statistical methods to determine which environmental and biological parameters available for Nelson Bays best matched the historic spatial distribution and density of these shellfish species, and use univariate statistical methods to guide the clustering of data to construct the bioregions. This approach acknowledges that biological species data should be utilised whenever available to manage biological resources (Sharp et al. 2007) and applies statistical methods to minimise subjectivity when constructing a bioregionalisation.

2. Materials and Methods

2.1 Study location

The seabed of Nelson Bays comprises soft sediment sloping gradually to about 130 m depth. The bays are intensively fished, by trawling and seining for finfishes including flatfish species (*Rhombosolea plebius*, *R. leporina*, *R. tapirina*), barracouta (*Thyrsites atun*), snapper (*Pagrus auratus*), tarakihi (*Nemadactylus macropterus*) and red cod (*Pseudophycis bachus*), and historically by dredging for scallops (*Pecten novaezelandiae*), oysters (*Ostrea chilensis*) and green lipped mussels (*Perna canaliculus*). Recreational and customary fishing for finfish and shellfish is also important for local communities. Oceanographic currents influence the Nelson Bays. Subtropical waters of the central Tasman Sea, manifested locally as an extension of the D'Urville Current flowing north up the west coast of South Island, are reflected into the western Cook Strait and then into the bays (Harris 1990; Zeldis 2008). Nutrient enriched upwelled water from the Kahurangi region (Figure 1) advected into the western Strait can provide a strong source of nutrients to the bays. Terrigenous nutrient sources are derived via rivers from lower catchments supporting horticulture and livestock farming, and from their hinterlands containing exotic forestry (*Pinus radiata*), native forest or regenerating scrub (Zeldis 2008). Major rivers in Golden Bay include the Aorere and Takaka rivers, with the Moteuka and Waimea Rivers dominating drainage into Tasman Bay (Figure 1), but with many smaller rivers and streams. As the shellfish species are managed by legally defined fisheries Statistical Areas, the boundary of the ecosystem of Nelson Bays was set to comprise Statistical Area 038, but excluded estuaries, harbours and Croisilles Harbour due to lack of commercial fishing and other data limitations at those locations.

2.2 Statistical and spatial approach adopted for bioregionalisation

To evaluate which of the twenty available environmental data layers (Table 1) best matched the distribution of historic shellfish densities, the stepwise BVSTEP procedure in PRIMER v7 (Clarke & Warwick 1998; Clarke & Gorley 2015) was used to select the best possible rank-order match between a matrix generated from historic shellfish densities and the inter-point distances derived from sets of environmental variables. BVSTEP allows for faster exploration of the subset combinations of the former BIOENV analysis (Clarke & Ainsworth 1993). To provide estimates of historic densities for scallops, dredge oysters and green lipped mussels, data collected from historic inshore scallop fishery biomass surveys between 1994 and 2012 (Williams et al. 2014) were krig interpolated using ArcMap v10.0 (ESRI Inc. 1999–2010) (Figure 2). The distribution and densities were expressed as volumes converted from fish-bins of shellfish: 240 scallops = 45 litres (1 bin); 475.2 oysters = 45 litres; 28.125 kg of green lipped mussels = 45 litres after Williams et al. (2014). Nineteen environmental data layers were similarly interpolated to GIS raster layers or used in the format as supplied (see Table 1 for data set descriptions and sources). A dataset was generated by extracting values for each shellfish density and environmental raster layer using a 1 km point-grid and the Spatial Analyst tool 'extract multiple values to points' in ArcMap. In PRIMER, the shellfish data were converted to a Bray-Curtis similarity matrix (Bray & Curtis 1957) and that matrix was compared to sets of environmental variables that had been first normalised and the sediment grain-size data had been $\log_{10}$ transformed to achieve even distribution

in Draftsman's plots. The BVSTEP analysis used 99 permutations for the Spearman's rank-order comparisons, and the Global BEST test was used to test for statistical significance of the null hypothesis of no agreement in multivariate pattern between the biological and environmental datasets. Once the results of the BVSTEP and BEST analysis were known, the sub-set of best environmental layers was analysed by a dissimilarity-based hierarchical classification after the methods of Grant et al. (2006).

As a guide to deciding on the optimum number of bioregions to generate by hierarchical classification, the sum of squared error (SSE) estimates for 25 cluster solutions were plotted using the 'kmeans.R' script after Peeples (2011) in the R statistical package v3.2.2 (http://cran.r-project.org/). The hierarchical clustering to define the bioregions was then carried out using BiodiversityR GUI (Kindt & Coe 2005) setting the number of cluster solutions to 15. Clusters were joined based on the average distance between all the members or unweighted pair-groups method with arithmetic mean (UPGMA), using a Gower distance metric (Grant et al. 2006). The non-hierarchical algorithm used was the CLARA clustering routine (Kaufman & Rousseeuw 1990). The Gower distance was implemented by first range-standardising each variable (0–1) and then applying a Manhattan (city-block) distance metric (Grant et al. 2006).

2.3 Data representation

To visualize the relationship between the historic scallop biomass and the data layers generating each cluster region, a Bray–Curtis similarity matrix (Bray & Curtis 1957) was created followed by an unconstrained ordination by non-metric multidimensional scaling (n-MDS; Kruskal & Wish 1978). To investigate the most salient relationships between the clusters of data points and the variables used in the classification procedure, Pearson correlations of a selection of environmental variables with individual n-MDS axes were plotted as vector biplots, where the lengths of the biplot vectors represent the correlation scores. Statistical analyses were performed using the PERMANOVA+ for PRIMER package (Anderson et al. 2008).

3. Results

3.1 BVSTEP analysis

The BVSTEP analysis returned two environmental variables; maximum DON and maximum salinity as best matching the distribution of the shellfish in Nelson Bays, with a correlation coefficient of 0.335 (Figure 3). The Global BEST test observed value of p=0.335 far exceeded the mean of 99 permutations at 0.03, thus this test failed to reject the null hypothesis that there is no relationship between the shellfish density distributions and the environmental variables. The results of the k.means scree plot did not show a distinct 'elbow' or a dramatic reduction in sum of squared error (SSE), but there was a slight drop at 15 clusters (Fig 4) and as the slope after that point was close to the y-asymptote, 15 was chosen as the optimum hierarchical clustering solution.

3.2 Bioregionalisation

The hierarchical classification created seven cluster regions in Golden Bay and eight regions in Tasman Bay, divided by the Separation Point power fishing exclusion zone (Figure 5). Due to its size and exclusion of contact fishing (Handley et al. 2014) the Separation Point power fishing exclusion zone was arbitrarily set as the sixteenth bioregion (Region 9, Figure 5). The cluster regions from Golden Bay ranged from the distinctly shallow areas inside Farewell Spit (cluster 10), with an area of high current flow and increasing depth on the edge of the spit bank (14), and an area extending across the outer Golden Bay across to D'Urville Island (Figure 5). The inner areas of Tasman Bay were delineated into

five cluster regions. The deeper parts of Tasman Bay (1 and 2) clustered out as distinct from the inner Tasman Bay, with cluster 1 appearing to be influenced by water entering the bays from the west coast north of Farewell Spit.

3.3 Environmental relationship with scallop biomass

For the n-MDS plots, the stress of the 2D (0.04) and 3D plots (0.05) were very similar so for clarity the 3D plot was presented (Figure 6). When data points were expressed as bubbles representing the most valuable fisheries species (scallop biomass) decreasing biomass was correlated with maximum DON and to a lesser extent with maximum salinity (Figure 3) with greatest historic densities of scallops overlapping with bioregions 11, 12, and 16 in Golden Bay, and 7, and 5 in Tasman Bay (Figure 5). To illustrate how these environmental variables differed with depth and tidal current speed, these two environmental variables were included as vector bi-plots in Figure 6. Historic biomass of scallops was correlated with shallow sites characterized by low DON levels and to a lesser extent, maximum salinity values.

4. Discussion

This study is the first data-driven bioregionalisation of Nelson Bays using historic shellfish biomass estimates and the multivariate BVSTEP method to best match with the spatial variability of a range of environmental variables. BVSTEP has been used extensively to identify key species driving macrofaunal assemblages and to determine which environmental variables are likely to be driving fish assemblages (e.g. Przeslawski et al. 2013; Rowden et al. 2013) but this is the first time it has been used to evaluate which environmental variables should be included in a bioregionalisation. BVSTEP was developed from the BIOENV procedure and as it uses the rank similarities between the biotic and abiotic data sets by using forward selection of the ranks it reduces the computing burden, allowing for more environmental variables to be analysed. This method proved necessary in this study, as attempts to use stepwise multiple regression or the full BIOENV on the full datasets proved too computationally expensive to complete (Handley, unpub. results). As many of the environmental variables were represented by maximum, mean and minimum values, and these variables were correlated with bathymetry due to the gently sloping nature of the seabed of Nelson Bays, there is a high risk of multicollinearity. Collinearity makes it difficult to determine which variable is 'driving' the biotic assemblage, with conventional remedies including the deletion of co-correlated variables and retaining one as a proxy for that set, or grouping variables into blocks (Lee & Normark 2009). BVSTEP has been used to reduce the number of variables to test in such circumstances (e.g. Lee & Normark 2009; Zhang et al. 2012).

In data rich regions, researchers may have to use expert knowledge to reduce the choice between large ranges of data sets when developing a bioregionalisation, potentially introducing subjectivity. The use of BVSTEP in this study demonstrated its objectivity and utility, resulting surprisingly in only two of the original nineteen data layers calculated as best matching the shellfish biomass matrix. To validate the BVSTEP procedure results, the accompanying BEST test was found to be statistically significant, validating linkages between the shellfish biomass estimates and maximum salinity and DON. However, as the overall BVSTEP correlation was low, other unmeasured environmental factors may be more important to Nelson Bay's shellfish. Supported by the warning that 'correlation does not imply causation' (Simon 1954), maximum salinity and maximum DON in this case appear to provide best available proxies for unmeasured parameters. Maximum scallop biomass surveyed between 1994 and 2012 was present around the coastal fringes of Nelson Bays at moderate depths and current speeds where DON levels were low in summer months. These low DON levels likely indicate nutrient assimilation by phytoplankton entrained within the bays as food for scallops (Zeldis 2008). It is not known what the optimum habitat requirements for scallop growth are in New Zealand, and it was

surprising that estimates of pelagic primary production were excluded by BVSTEP. Perhaps this indicates that benthic microalgae as compared with pelagic primary producers may be more important as an unmeasured food source for scallops (Gillespie et al. 2000; Handley, unpub. data) or that there was a spatial mismatch in the distribution of primary producers and scallop populations. Not presented here, a BIOENV exploration of a sub-set of the data (sampled on an approximately 3 km grid), that took five days to compute, gave the same two environmental variables as solutions, with further addition of the remaining seventeen environmental layers reducing Spearman's correlations (Handley, unpub. results).

Ecosystem model development elsewhere has benefited from past experience, and lessons have been learned to guide model development (Fulton et al. 2011). Ecosystem management approaches are gathering pace driven by the perception that single-species management by itself cannot deal effectively with complex biological systems faced with increasing demands on marine resources (Sharp et al. 2007; Fulton et al. 2011). We must however acknowledge that their development is often driven by necessity at locations faced with difficult management decisions or where former management approaches have failed to protect sustainable resource use (Zhou et al. 2010; Katsanevakis et al. 2011) - the present case being the failure of Nelson Bay's commercial shellfish beds. Despite the low correlation of the two environmental variables used in the classification, the clustering in our analysis delineated bioregions into broad spatial areas that created distinct spatial regions for ecosystem model development satisfying the aim of the study. However, the blindness of the process of bioregionalisation to stochastic shellfish colonisation and historical events (Sharp et al. 2007) is potentially relevant for Nelson Bays. Regarding historical events, the bay's soft sediment habitats are likely to have changed significantly over decades with increased sediment deposition (e.g. Goff & Chagué-Goff 1999) and homogenisation by contact fishing gear (Handley 2006; Handley et al. 2014). Although the aim of this study was to carry out the bioregionalisation using subjective methods, in the absence of bay-wide infaunal datasets, we deemed it necessary to acknowledge historic events and habitat change resulting from bottom-contact fishing methods. Handley et al. (2014) measured significant difference in sediment and infaunal composition between fished and unfished habitats inside and outside the Separation Point power fishing exclusion zone, therefore we chose to set this exclusion zone as a distinct bioregion. Significant reductions in shellfish populations outside New Zealand have been shown to have flow-on effects to nutrient regeneration and trophic pathways involving non-linear feedback mechanisms between the benthos, autotrophs and shellfish (e.g. Valiela et al. 2004; Kemp et al. 2005). It is anticipated that the use of an ecosystem model could be used to test if this historic habitat change can be implicated in the decline and lack of innate recovery of Nelson Bay's shellfish populations.

5. Acknowledgements

We thank: John Zeldis for providing nutrient and salinity data collected as part of the Foundation for Research Science and Technology-funded 'Coasts and Oceans' Outcome-Based Investment contract CO1X0501; Richard Gorman for providing modelled wave data; Tracey Osborne for providing ocean colour data, and Ben Knight, Cawthron Institute for benthic light estimates, NIWA Core Funding FIFI15401 and FIFI16401, and Matt Pinkerton and Peter Horn, and MPI reviewers for constructive comments on earlier versions of this manuscript.

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7. Tables and figures

Table 1: Description of the 19 environmental variables used in the BEST analysis and their data sources.

Environmental variable	Description and data source	Source
Depth	Nelson Bays bathymetry digitised from the original source.	Mitchell (1986)
Minimum DON, Mean DON, Maximum DON, Primary Production December, Primary Production July, Minimum Salinity, Mean Salinity, Maximum Salinity	Dissolved organic nitrogen (DON); Nutrient and salinity data were collected on four seasonal voyages aboard NIWA's vessel *Kaharoa* (8–12 Dec. 2001 (KAH0110), 25–29 Mar. 2002 (KAH0202), 8–13 Jul. 2002 (KAH0207), and 30 Aug.–3 Sep. 2002 (KAH02011)). These data were then krig interpolated using ArcMap.	Zeldis (2008)
Benthic Light	Percentage light reaching the benthos was derived from MODIS1 derived 1km diffuse attenuation coefficient at 490 nm (Kd490; updated from Mueller (2000)	B. Knight (unpub. data, Cawthron Institute).
Minimum 555 Maximum 555	Freshwater extent carrying calcite and chlorophyll particulates was estimated from NASA SeaWiFS satellite data at 555 nm (Richardson et al. 2004). The calcite product was chosen as a potential means of distinguishing recently arrived riverine sediments from re-suspended coastal sediments (Schwarz et al. 2009)	Osborne (2011).
Mean tidal current speed Maximum tidal current speed	Current speed in Tasman and Golden Bays was modelled using the ROMS model, which is a widely used ocean/coastal model (Haidvogel et al. 2008; Warner et al. 2008; MacCready et al. 2009). The model was set up on a rectangular 130 × 128 grid of 1 km^2 cells.	Zeldis et al. (2011)
Orbital current velocity	Orbital velocity at the seabed based on wave climatology derived from a 20 yr hindcast (1979–1988) of mean significant wave height.	Hadfield et al. (2002)

Environmental variable	Description and data source	Source
		Gorman et al. (2003)
Maximum wave height Mean wave height	Wave modelling was carried out using NIWA's operational forecasting system called NZWAVE_12 which incorporates wave and wind inputs from the weather forecasting model NZLAM_12 on a horizontal grid spacing of 12 km, nested in coarser-scale global models (Lane et al. 2009; Handley et al. 2014)	Lane et al. (2009)
January sea surface temperature July sea surface temperature	Calculated from the SST climatology at 4 km and 9 km resolution from 1993–1997 as summer (12 March) and winter (8 September) (M. Hadfield, pers. comm.).	Uddstrom & Oien (1999)
Sediment mean grain size	Mean grain size of sediment digitised from original source for the Ministry for Primary Industries (S. Nodder, NIWA, pers. comm.).	Mitchell (1987)

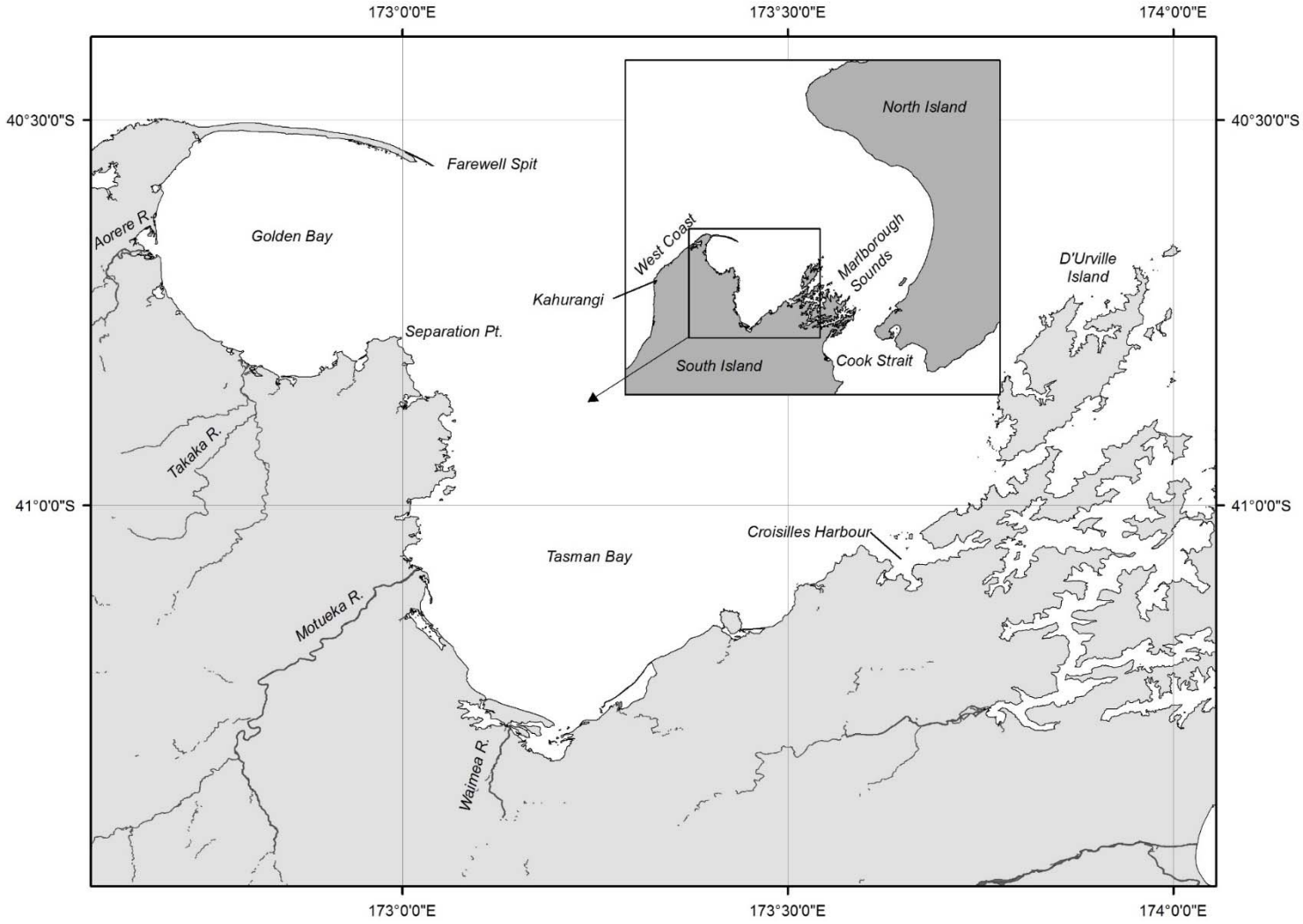

Figure 1: Location map of study area showing Nelson Bays and rivers feeding into them.

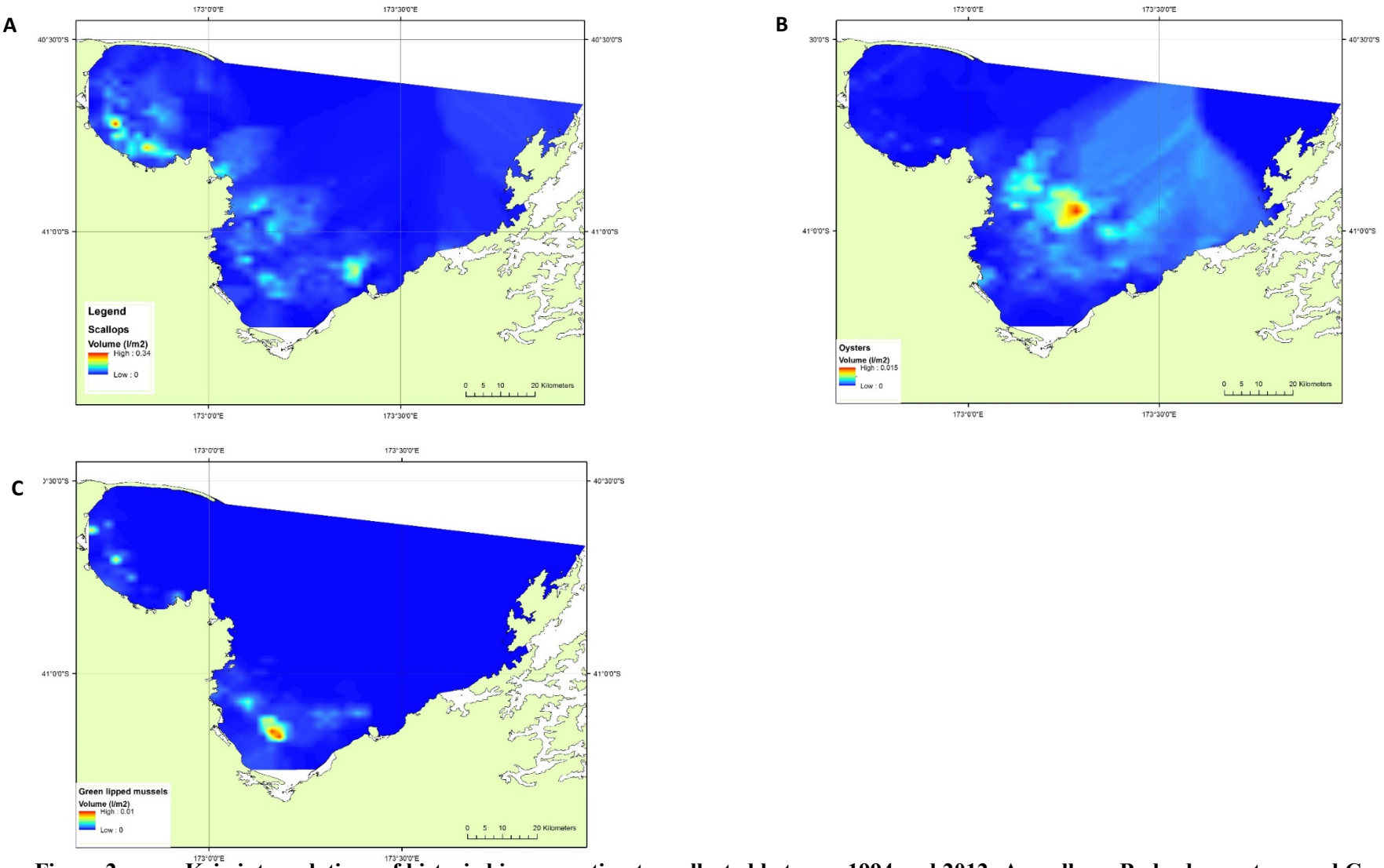

Figure 2: Krig interpolations of historic biomass estimates collected between 1994 and 2012: A, scallops, B, dredge oysters, and C, green lipped mussels.

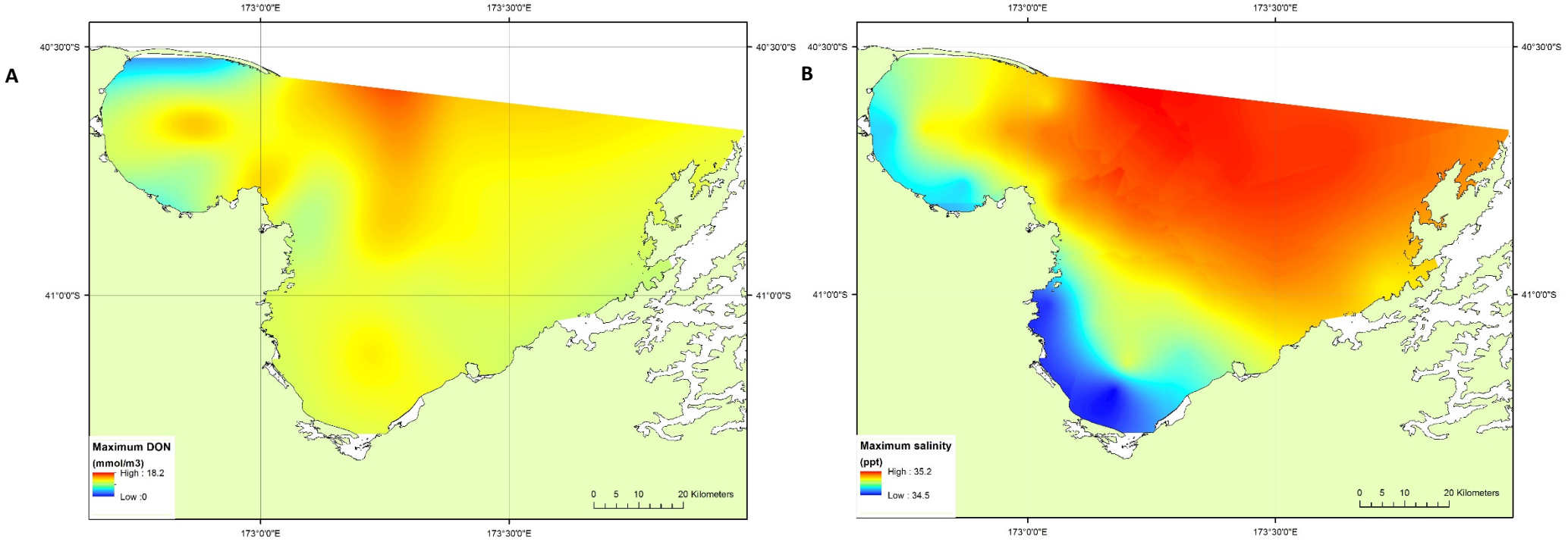

Figure 3: **Data layers chosen by BEST analysis to match historic shellfish biomass: A, maximum DON and B, maximum salinity levels.**

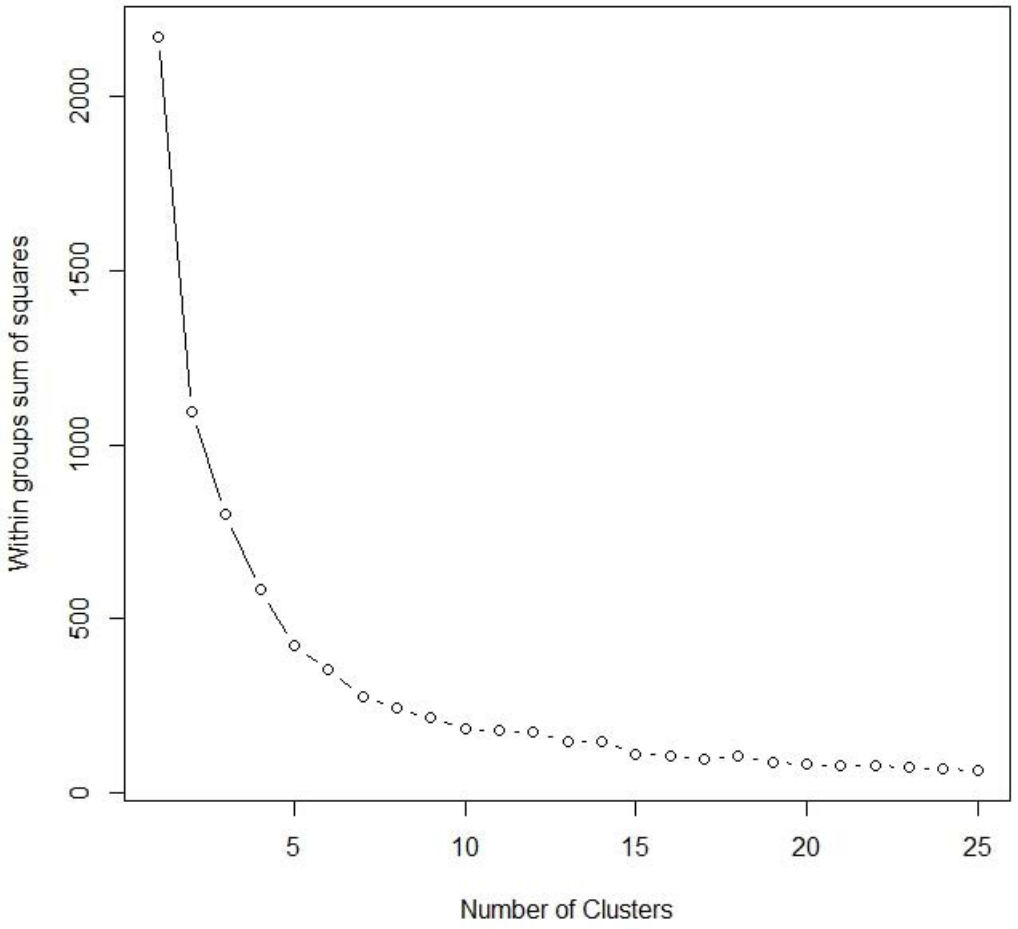

Figure 4: Sum of Squared Error (SSE) scree plot for clustering of environmental data to determine the number of clusters.

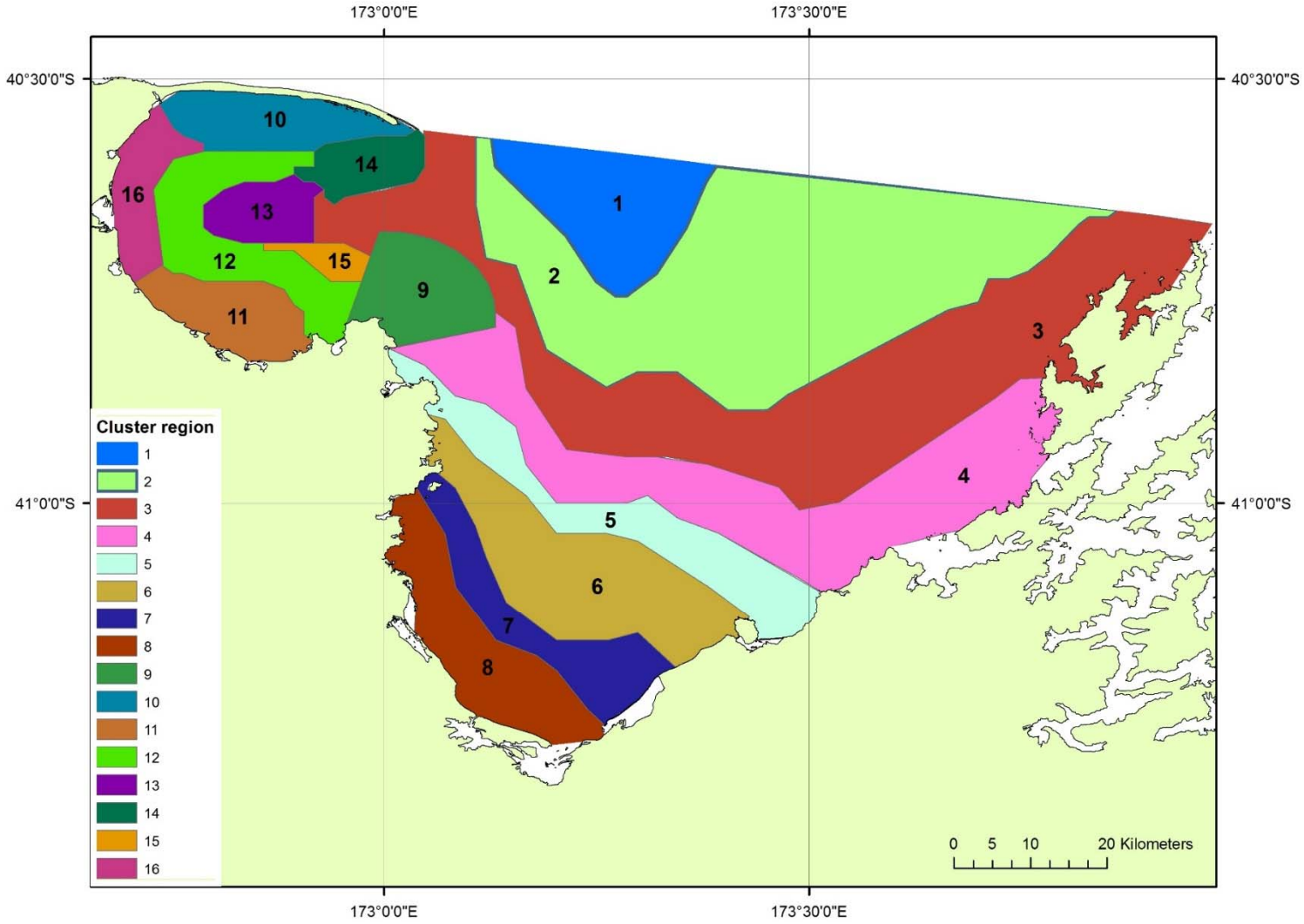

Figure 5: Nelson Bays bioregionalisation produced by data-driven hierarchical clustering into 15 regions with the addition of region 9 which was arbitrarily set due to its size and protection from contact fishing methods.

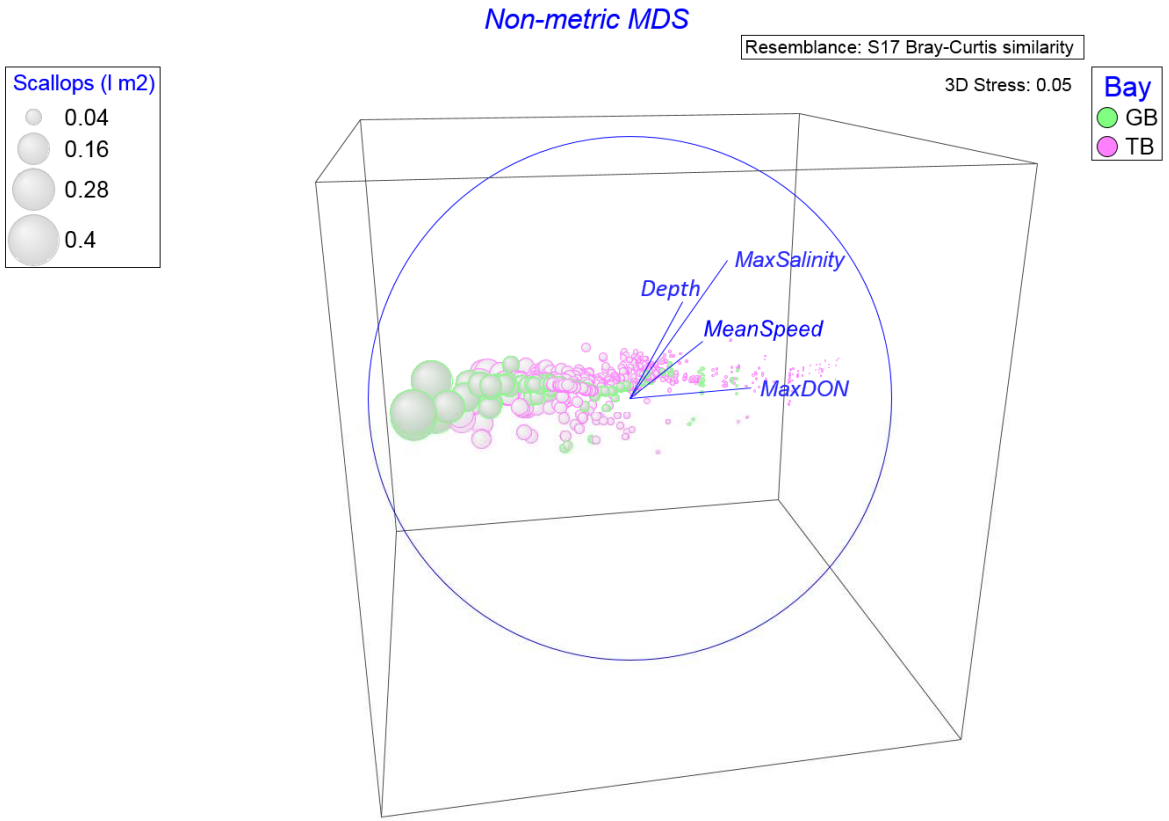

Figure 6: Non-metric multidimensional scaling (n-MDS) plot of historic shellfish populations from biomass estimates collected between 1994 and 2012. Bubbles represent the volume of scallops (litres m^{-2}) collected from survey tows. Vector plots show Pearson correlations with the axes for bathymetry, maximum salinity, mean tidal current speed and maximum dissolved organic nitrogen (DON).