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# Preliminary analysis towards the delineation of marine ecoregions in the Flemish Cap, Northwest Atlantic

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## Abstract

The delineation of ecologically coherent spatial units (ecoregions) constitutes the first step towards the identification of ecosystem-level spatial units that can serve as basis for the implementation of ecosystem approaches to fisheries. This study aimed to the delineation of ecoregions in the Flemish Cap (NAFO Div. 3M), Northwest Atlantic. Both physical (bathymetry, sea surface temperature, bottom temperature) and biological (chlorophyll a, primary production, demersal biomass, diversity, richness) variables were considered. Bathymetry data were derived from the GEBCO dataset, sea surface temperature data were acquired from satellite derived imagery, while bottom temperature, demersal biomass, diversity (Shannon's index), and richness were estimated from data collected on European Union surveys conducted in July on the Flemish Cap between 1988 and 2008. Datasets were analyzed and classified using principal components analysis and k-means clustering following Pepin et al (2010). The clustering results were mapped in order to examine spatial distributions of the clusters. The results from this analysis showed that optimal clustering occurred when the data were grouped into two clusters, separating the central-south, shallower areas from the northern deeper parts of the Flemish Cap. On this basis, it can be concluded that there are two identifiable ecoregions in the Flemish Cap.

## Introduction

The specification of regional ecosystem subunits (i.e. ecoregions) is the starting point in the process of identifying spatial management units for the purposes of an ecosystem approach to management of human activities in the marine environment (Fogarty and Keith, 2009; Zwanenburg et al., 2010). From an ecological point of view, the scale at which these ecosystem units are delineated should try to encompass the processes regulating the productivity and the dynamics of populations at many different trophic levels, from phytoplankton to fish species as well as community transitions.

Previous studies on the Flemish Cap (NAFO Div. 3M) have indicated that this region is a relatively isolated from the Newfoundland shelf from a population dynamics perspective. The Flemish Pass, characterized by depths in excess of 1400m, hinder the migration of demersal fish species to and from the Grand Banks; for example, an important demersal species like Atlantic cod (*Gadus morhua)* do not usually inhabit deeper areas (Templeman 1963, Konstantinov 1970; de Cardenas-Gonzalez 1996). From an oceanographic and hydrographic perspective, the shallow waters of the Flemish Cap present some distinct characteristics owed to the effects of large-scale oceanic circulation features like the Labrador (LC) and North Atlantic (NAC) currents (Maillet et al, 2005).

Although there are many studies on the Flemish Cap system, there has been no prior study dealing with the delineation of ecoregions in the Flemish Cap. The NAFO SC WGEAFM's "Roadmap for the developing of an Ecosystem Approach to Fisheries for NAFO" (NAFO 2010) indicated that one of the starting points for developing an ecosystem approach to fisheries for NAFO was the identification of ecosystem-level units which are suitable for management applications. The delineation of ecoregions is the first step towards the identification of such ecosystem-level units. In the present work we undertake this task by examining a set of variables similar to those used by Fogarty and Keith (2009) to identify ecoregions in the Flemish Cap area, Northwest Atlantic.

## Material and Methods

The same methodology used in the Northeast US Continental shelf (Fogarty and Keith, 2009), the Scotian shelf (Zwaneburg et al, 2010) and the Newfoundland and Labrador shelves (Pepin et al, 2010) was applied to the Flemish Cap. Both physical and biological variables were used to define areas with high biophysical similarity.

Bathymetry was obtained from the GEBCO (General Bathymetric Chart of the Ocean) dataset (www.gebco.net). Sea surface temperature, chlorophyll-*a*, and primary production were derived by satellite derived imagery. Sea surface temperature data were measured daily using NOAA (National Oceanographic and Atmospheric Administration) AVHRR (Advanced Very High Resolution Radiometer) satellite imagery starting in 1985 (for more information see www.nodc.noaa.gov/SatelliteData/pathfinder4km/). The Bedford Institute of Oceanography (BIO – Fisheries and Oceans Canada) provided the chlorophyll *a* (Chl-*a*) and primary production (PP) datasets (Platt et al. 2008). The original Chl-*a* datasets were acquired from the SeaWiFS (Sea Viewing Wide Field of View Sensor) satellite sensor mounted on the Orbview-2 satellite (for more information see www.geoeye.com). The Chl-*a* estimates were derived using the OC4.v4 algorithm (O'Reilly et al., 2000). PP estimates were derived from the Chl-*a* datasets as described in Platt et al. (2008). The PP image is the average over all years (98- 04) and the four Chl-*a* datasets are seasonal averages (spring, summer, fall, winter) over all years (97-07). To maintain consistency, the four Chl-*a* seasonal averages were averaged to produce a single Chl-*a* dataset, matching the PP dataset. The grid size of these datasets differ (even though PP was derived from Chl-*a*) because until 2004 the Chl-*a* dataset was provided in a 1.5 km grid size and this was the data used to create the PP dataset. However, after 2004 the Chl-*a* the grid size was increased to 4 km, hence the reason why the Chl-*a* grid size is at 4 km.

Demersal fish biomass, richness, and diversity (Shannon's index) were estimated from the data collected on the Flemish Cap during the European Union surveys conducted in July from 1988 – 2008. Bottom temperature data were obtained from CTD casts done in this survey. No data on surficial geology of the bottom was available.

These data were processed using ArcGIS software to make them spatially comparable. The demersal biological indices and bottom temperature were interpolated using the inverse distance weighted algorithm to create continuous surfaces that matched the continuous coverage of the remotely sensed imagery. All surfaces were spatially re-sampled to a common 20 km grid. The 20 km cell size was selected to maintain consistency with previous ecoregions analysis from the northeast US continental shelf (Fogarty and Keith, 2009), Scotian shelf (Zwanenburg et al., 2010), and the NL shelves (Pepin et al. 2010). Finally, the data were normalized [(x – mean (x)) / sd] to make them numerically comparable.

The high dimensionality of this database was reduced by means of a principal components analysis (PCA). The first four principal components (PCs) containing the bulk of the variance were used as input variables in a k-means clustering using the algorithm of Legendre (2001). Different runs were carried out considering a number of clusters ranging from 2 to 6. The optimal number of clusters was determined using the Calinski-Harabasz statistic (Legendre 2001).

## Results and Discussion

The Flemish Cap is dome-shaped, with the top around 120m depth and the steepest relief on the southeast side (Figure 1). The annual mean sea surface temperature showed an increasing gradient from the northwest to the southeast related with the front formed by the Labrador and the North Atlantic currents in the south and east of the Flemish Cap (Figure 2). The chlorophyll-*a* annual average and the cumulative primary production exhibited a patchy pattern throughout the Flemish Cap (Figures 3 and 4 respectively). The biological variables exhibit clear patterns as a function of depth (Figure 5). The biomass was highest between 200 and 500m, encircling the shallowest areas, although the highest concentration was found on the southwest side of the bank (Figure 6). Richness and Shannon's diversity index increased with depth, mainly on the northern parts of the bank (Figures 7 and 8 respectively). There were differences in neighbouring bottom temperature values as a result of the inter-annual variability. Despite this variability, the highest temperatures formed a ring surrounding the cap, and the cap itself had the lowest bottom temperatures (Figure 9).

The first four principal components of the PCA analysis explained 88% of the total variance (63% in the first two PCs) (Table 1). The first PC loadings (35% explained variance) were dominated by the biological variables (demersal biomass, diversity, and richness). The demersal biomass presented a positive influence, while the diversity and richness exhibited an important negative effect. The second PC (28% explained variance) was mainly influenced by the physical variables: bathymetry showed a positive loading, while the sea surface temperature,

bottom temperature, and primary production exhibited negative loadings. The third PC was determined mainly by the bottom temperature and demersal biomass, both with positive loadings. These similar positive loadings could be a reflection of the similarity in the distribution of higher temperatures and higher biomass concentrations around the cap. The fourth PC was mainly influenced by the demersal biomass (negative loading).

The first four PCs were employed in the k-means clustering process. The Calinski-Harabasz statistic results (Figure 10) indicated that optimal clustering occurred when the data were grouped into two clusters. The mapped result (Figure 11) illustrated that this division separated the central-south and generally shallower areas (hereafter referred to as the on-shelf and upper continental slope, shelf-UCS) from the northern deeper parts of the Flemish Cap (hereafter referred to as the lower continental slope, LCS). This subdivision is in agreement with the distribution of biological and physical variables (dominating the first and second PC respectively) in the two clusters. The mean values by 20 km x 20 km cells of each of these variables showed that there were important differences. The shelf-UCS presented a higher mean biomass value by cell than the LCS, while the opposite was found for the Shannon's diversity index and richness values (Figure 12). Except for bathymetry (much higher in the LCS than the shelf-UCS), all the physical and production related variables presented consistently higher values in the shelf-UCS.

This division indicates that the Flemish Cap is formed of two ecoregions, essentially different in the base of productivity and diversity. The shelf-UCS ecoregion presented a higher primary production on the surface as well as a higher biomass of demersal fish than the LCS ecoregion. On the other hand, diversity was much higher in the LCS ecoregion, not only because the species richness almost doubled the number of species in relation to the shelf-UCS, but the biomass distribution on these species was much more uniform.

These results support that Flemish Cap is conformed by two distinct ecoregions when physical and biological values are analyzed. These two ecoregions comprised the on-shelf and upper continental slope and the lower continental slope areas. However, an examination of the species composition in these ecoregions as well as considerations of the energy transfers between them would be necessary in order to determine if these ecoregions should be considered standing alone units or if they should be combined for the purpose of defining ecosystem-level units suitable for management applications.

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**Table 1**. Principal components analysis results. The first four PC are presented (88% of total variance explained). The most influential biophysical variables for each PC are highlighted in grey.

| | **PC1** | **PC2** | **PC3** | **PC4** |
|---|---|---|---|---|
| **Eigenvalues** | 1.7235 | 1.3937 | 0.7970 | 0.4442 |
| **% Variance** | 35% | 28% | 16% | 9% |
| **Cumulative Variance** | 35% | 63% | 79% | 88% |
| | **Eigenvectors** | | | |
| Bathymetry | 0.10454 | 0.57319 | 0.14507 | 0.30679 |
| Bottom Temperature | 0.04418 | -0.43016 | 0.80411 | 0.39465 |
| Sea Surface Temperature | 0.15248 | -0.46273 | -0.2705 | -0.115 |
| Chlorphyll-a | 0.14596 | 0.13426 | -0.03974 | 0.11308 |
| Primary Production | 0.18681 | -0.46518 | -0.12771 | -0.14191 |
| Demersal Biomass | 0.41868 | 0.19366 | 0.45014 | -0.75467 |
| Demersal Diversity | -0.60976 | -0.0171 | 0.14373 | -0.15482 |
| Demersal Richness | -0.60047 | -0.00905 | 0.13425 | -0.33239 |

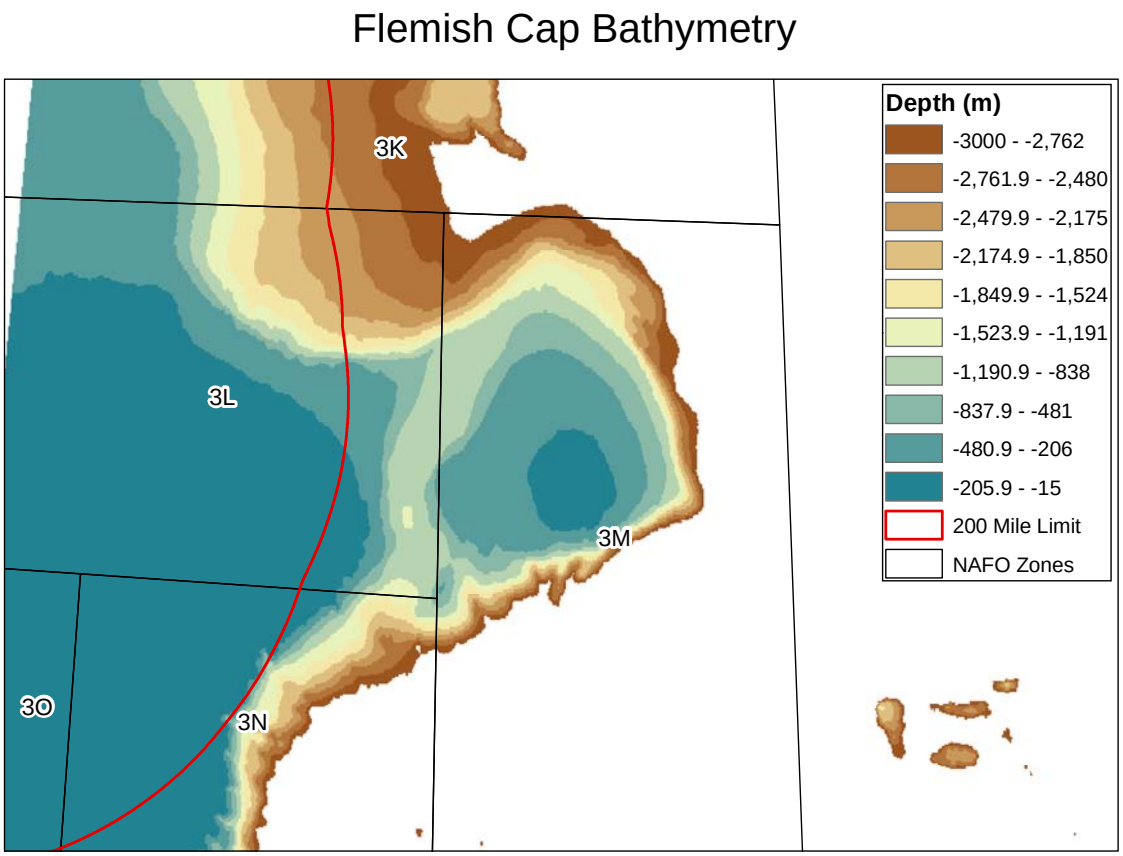


**Figure 1**. Bathymetry of the Flemish Cap and surrounding areas.

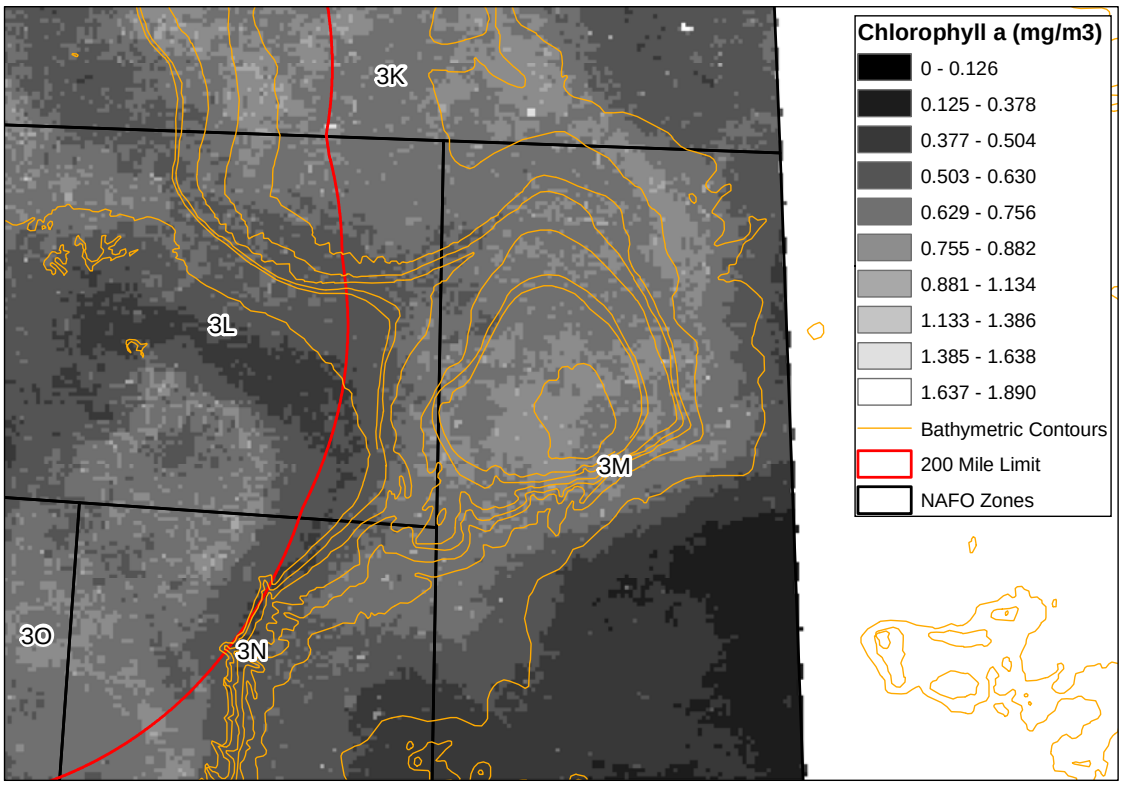


**Figure 2**. Mean chlorophyll-*a* values of the Flemish Cap and surrounding areas.

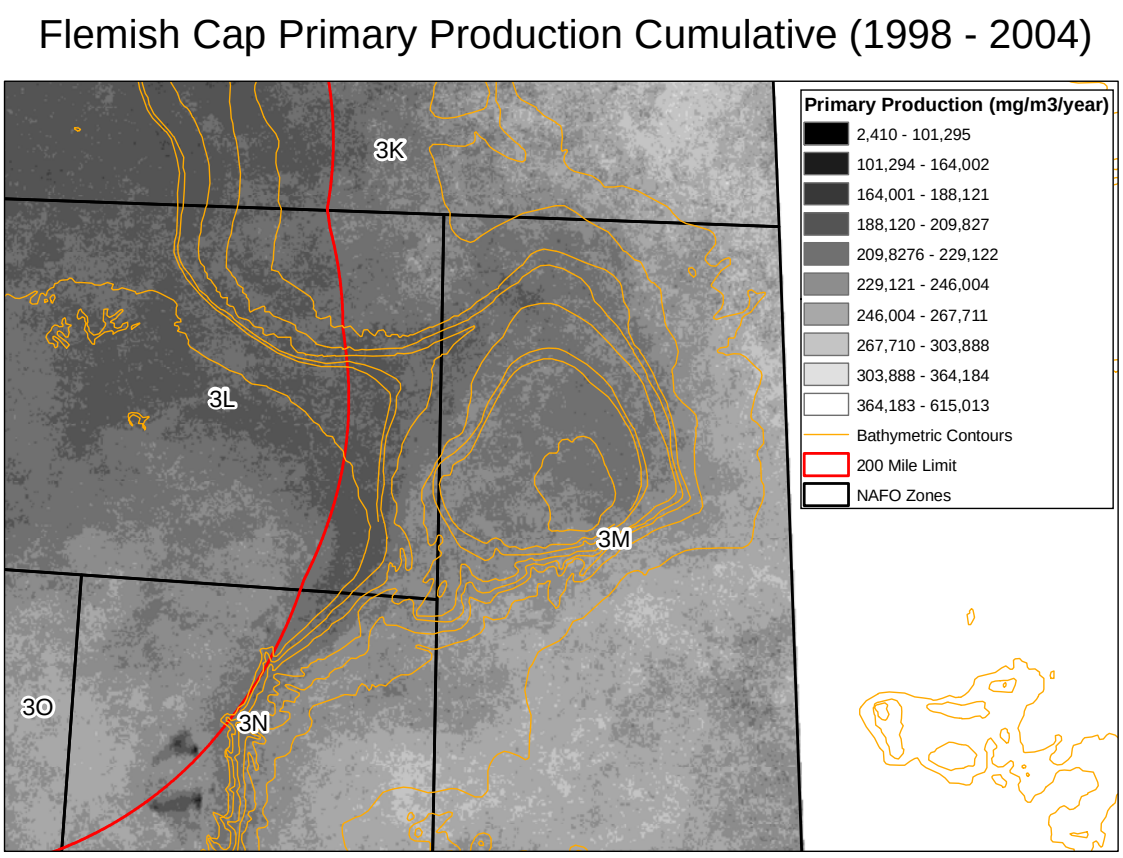


**Figure 3**. Mean annual cumulative primary production of the Flemish Cap and surrounding areas.

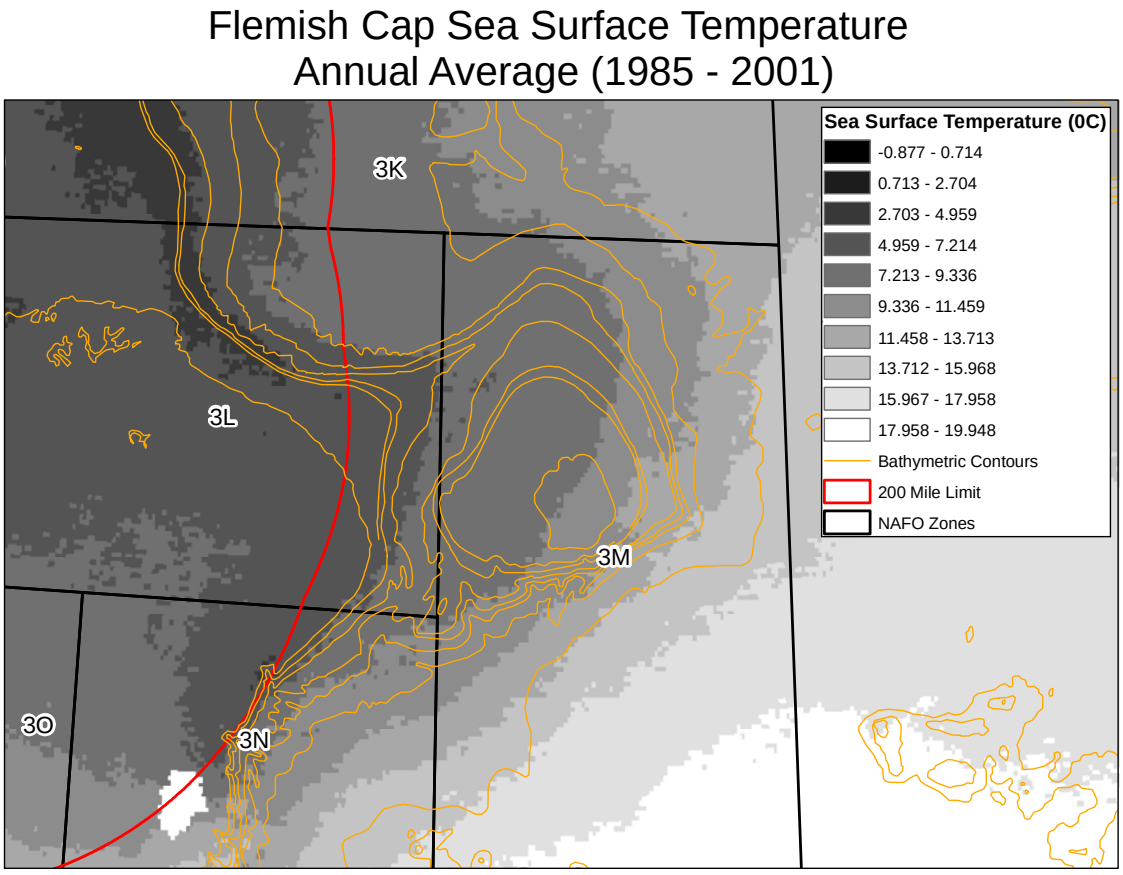


**Figure 4**. Mean annual sea surface temperature of the Flemish Cap and surrounding areas.

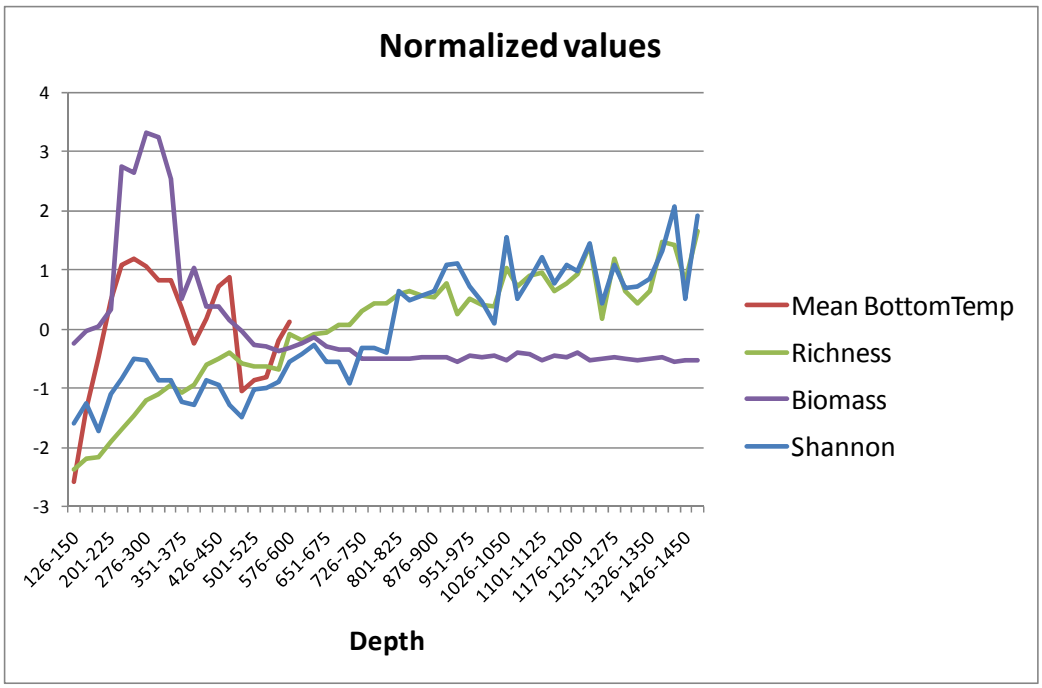


**Figure 5**. The normalized values by depth range of the bottom temperature and the biological variables employed in the analysis.

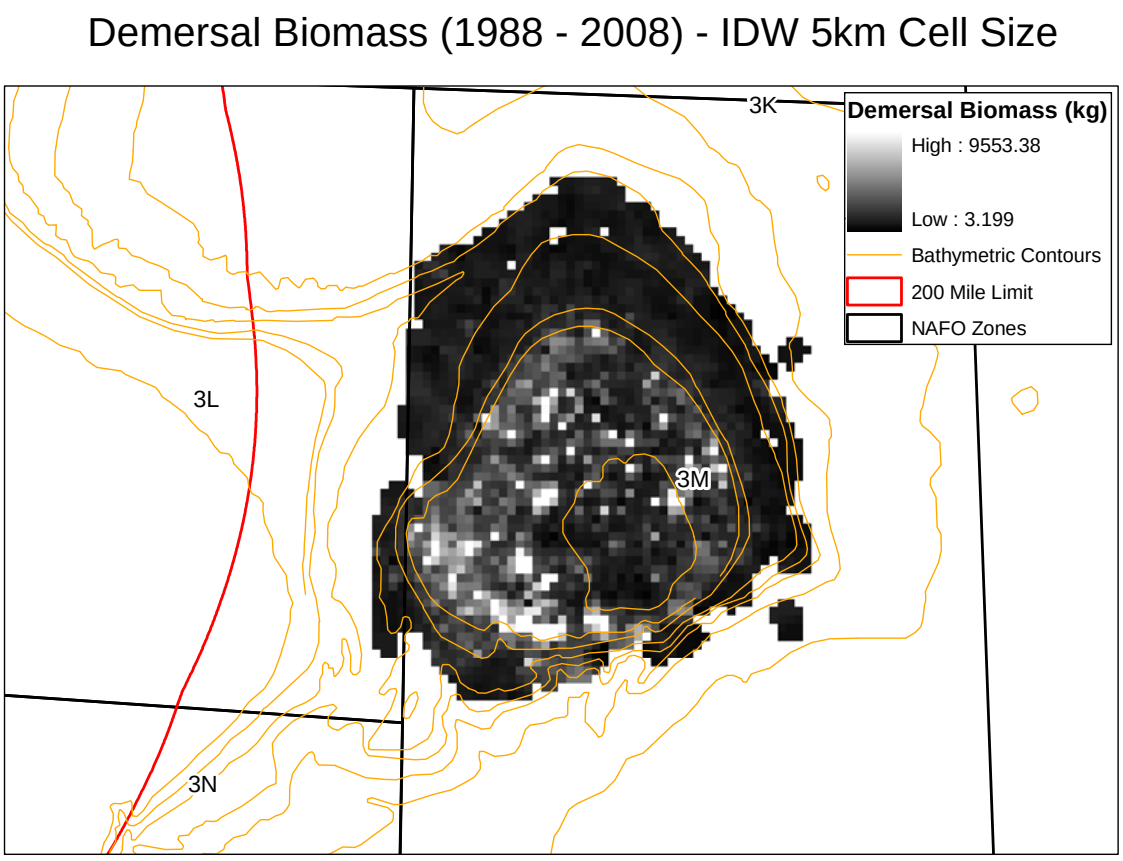


**Figure 6**. Interpolated demersal fish biomass based on catches from the European Union Flemish Cap surveys (1988-2008) at a 5 km cell size.

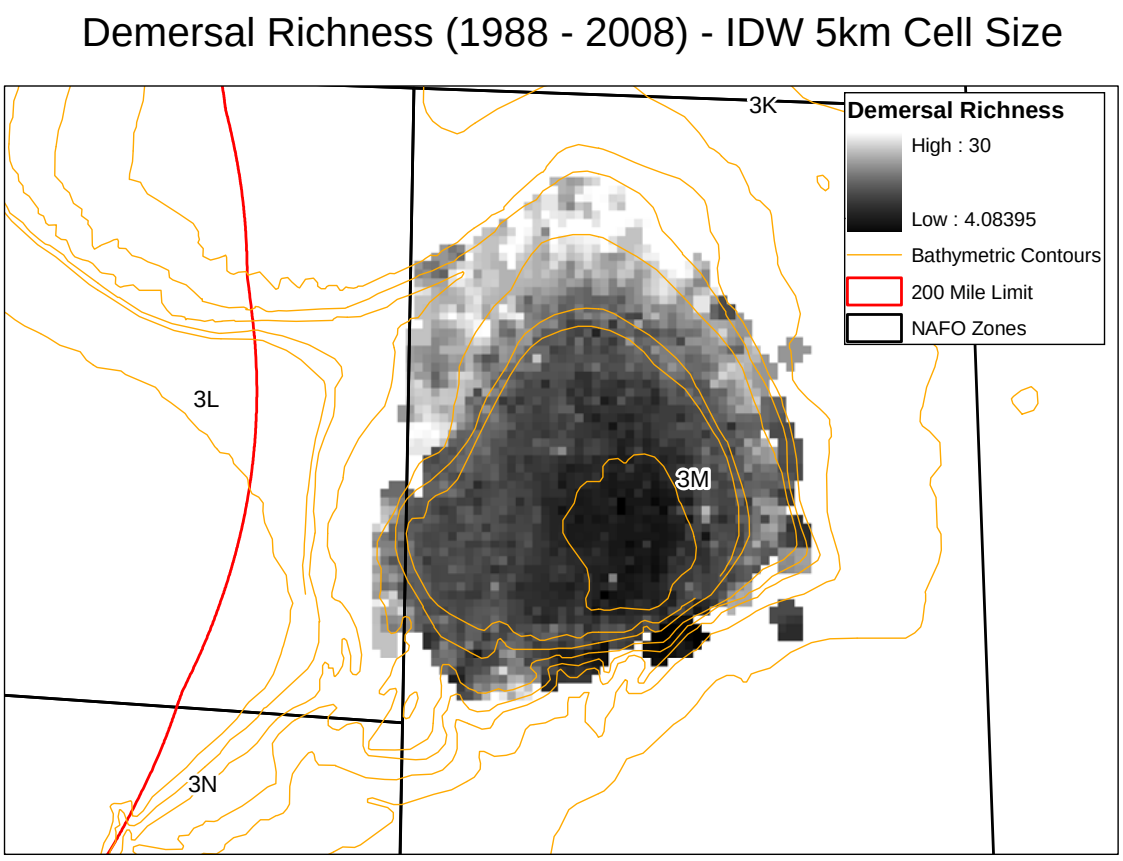


**Figure 7**. Interpolated demersal fish species richness based on catches from the European Union Flemish Cap surveys (1988-2008) at a 5 km cell size.

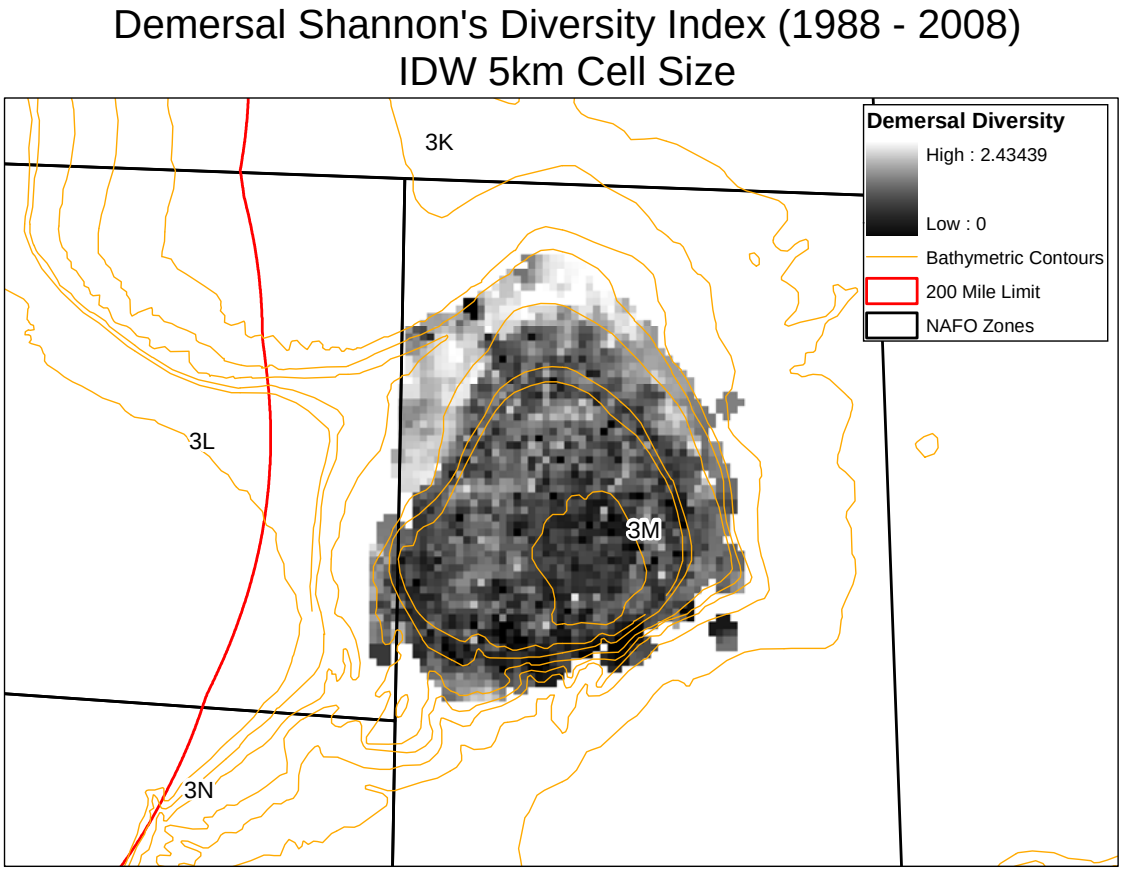


**Figure 8**. Interpolated demersal Shannon's diversity index values based on catches from the European Union Flemish Cap surveys (1988-2008) at a 5 km cell size.

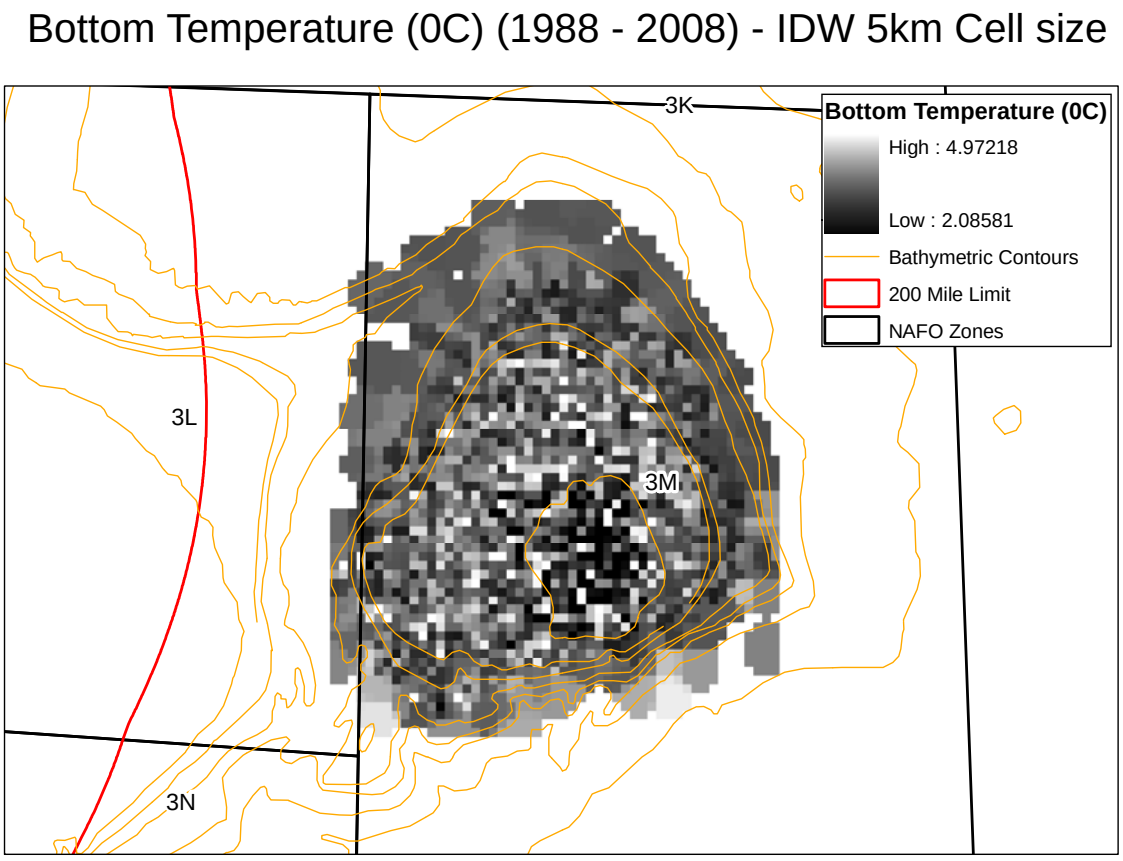


**Figure 9.** Interpolated average bottom temperature values based on data collected during the European Union Flemish Cap surveys (1988-2008) at a 5 km cell size

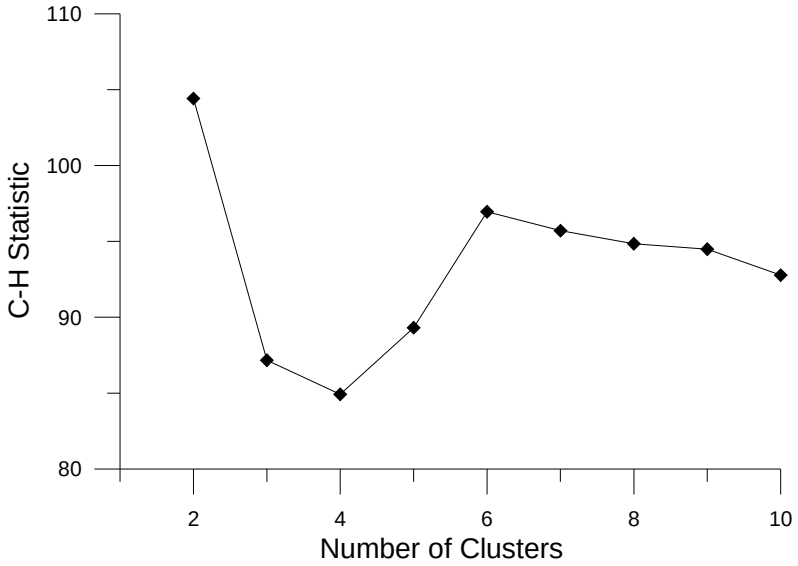


**Figure 10.** Plot of the Calinski-Harabasz statistic for the different number of clusters obtained with the k-means clustering technique. The maximum value indicates the optimal number of clusters, in this case the optimal number of clusters is two (2).

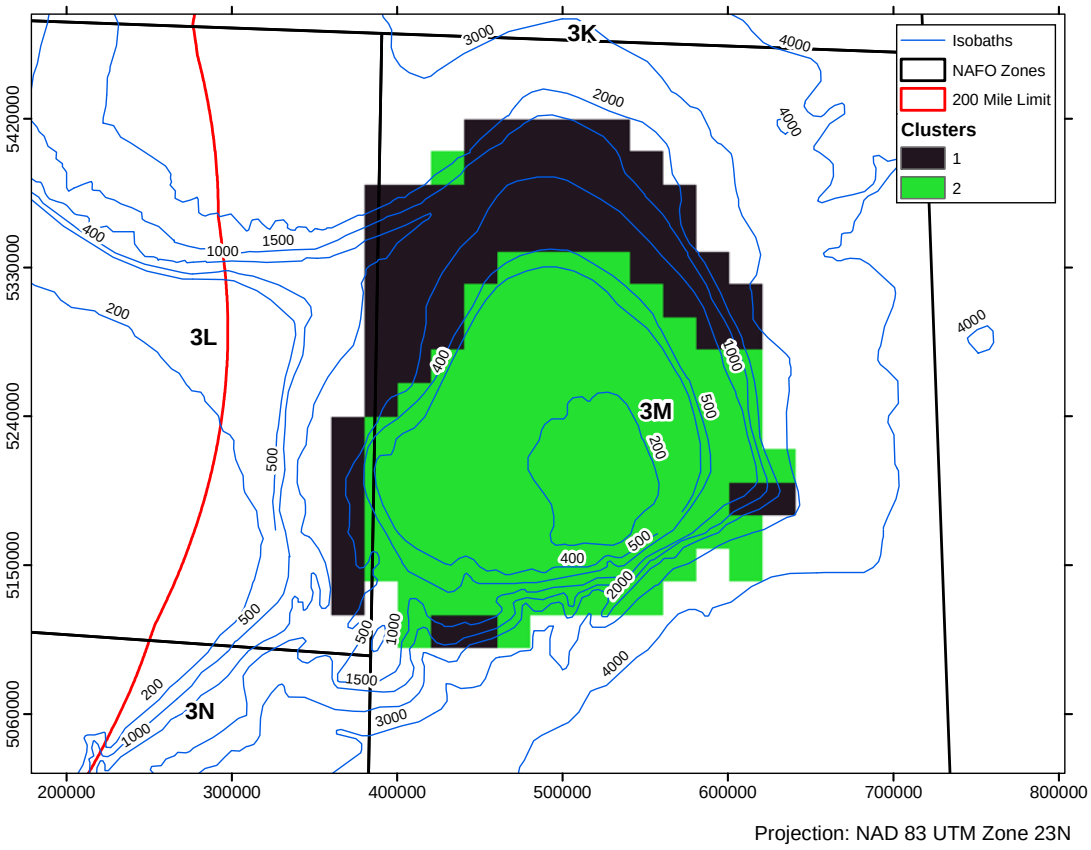


**Figure 11**. Map of the two clusters (shelf-UCS: green color; LCS: black color) obtained from the k-means clustering.

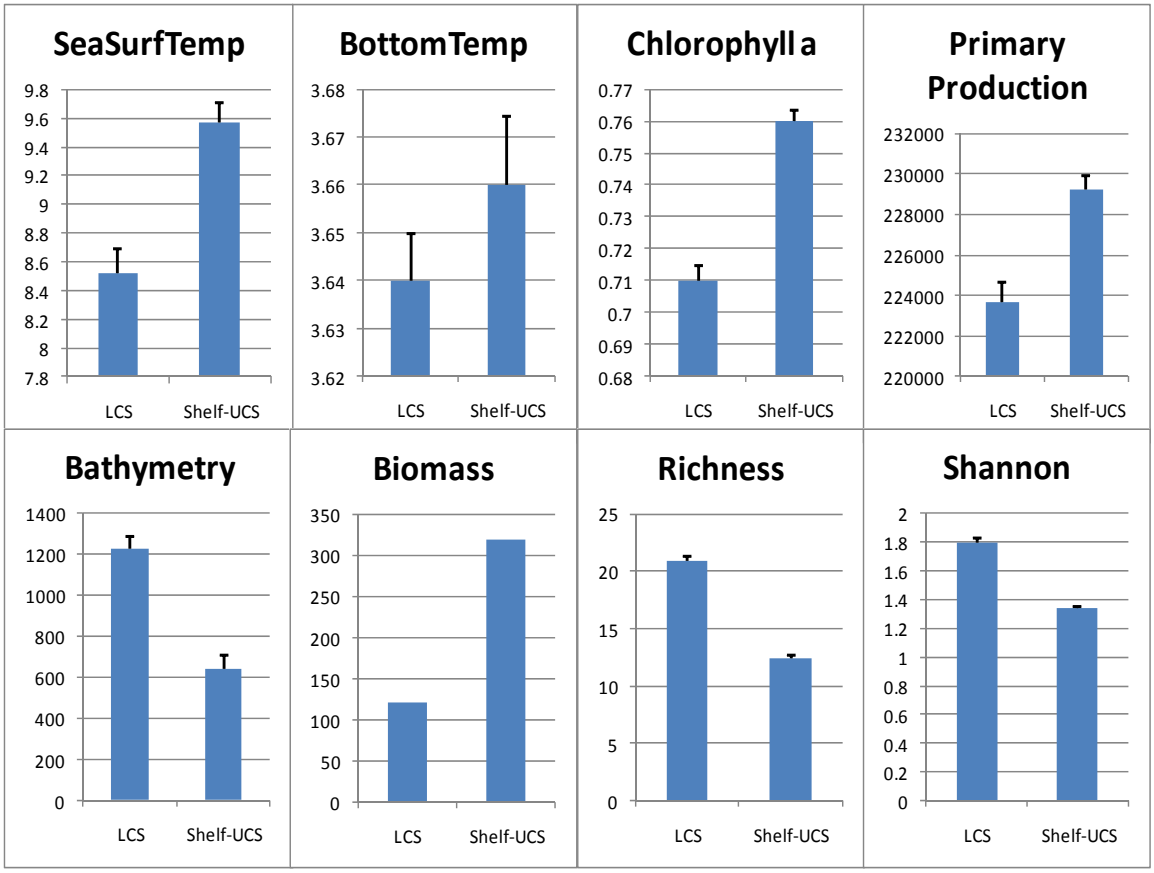


**Figure 12.** Mean and standard deviation values obtained from the 20km x 20km cells for each explanatory variable in the two obtained clusters.