

Figures produced in the following Practical exercises document –

Legendre, P. & O. Gauthier. 2021. Spatial, temporal, and space-time analysis of community and other oceanographic data for iAtlantic researchers. 30 pages.

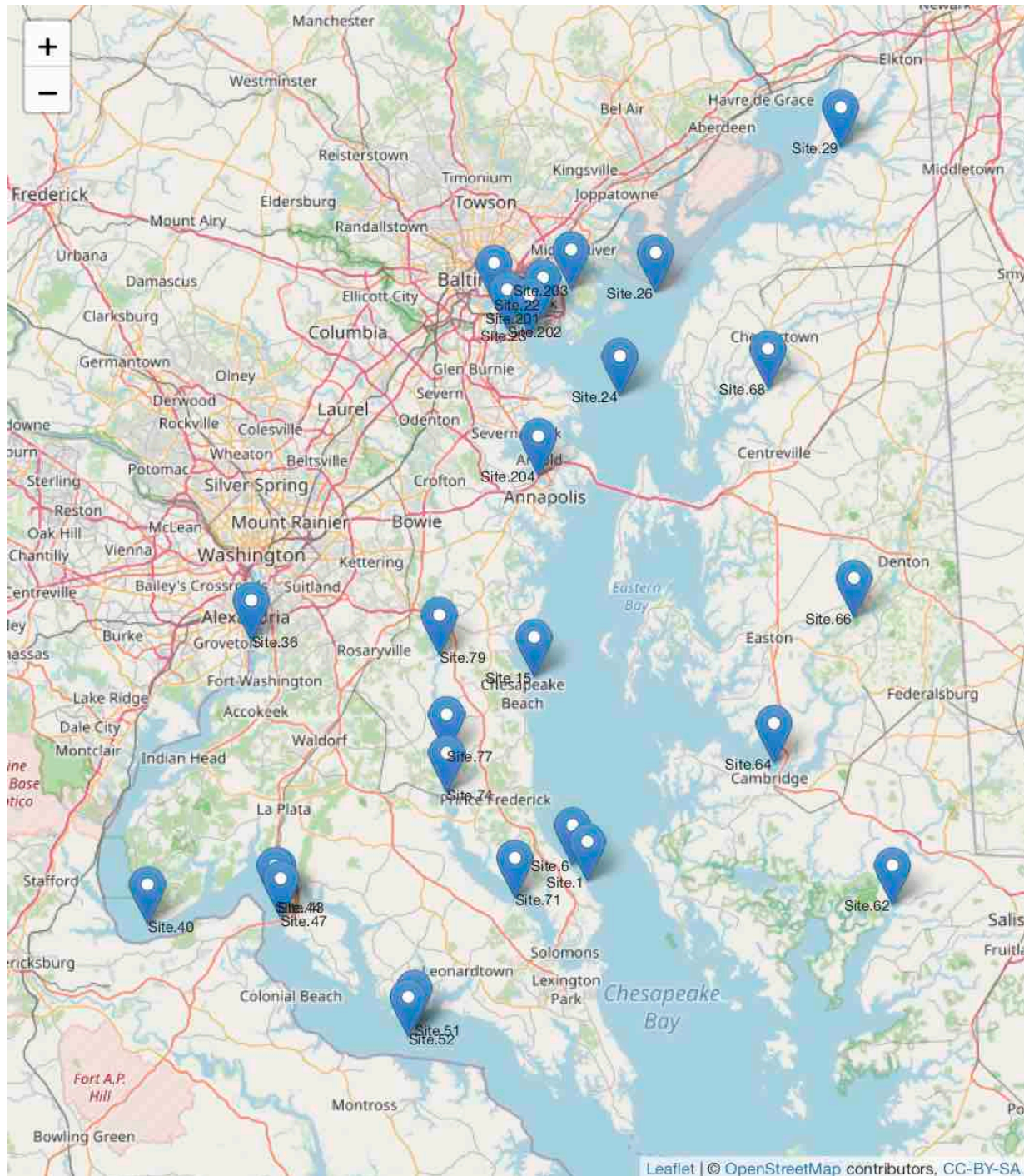


Figure 1 – Map of the 27 sampling sites of the Chesapeake Bay ecological survey. Sites #36 and 79 are freshwater, the other 25 are brackish. Site labels written in small type underneath the pointers.

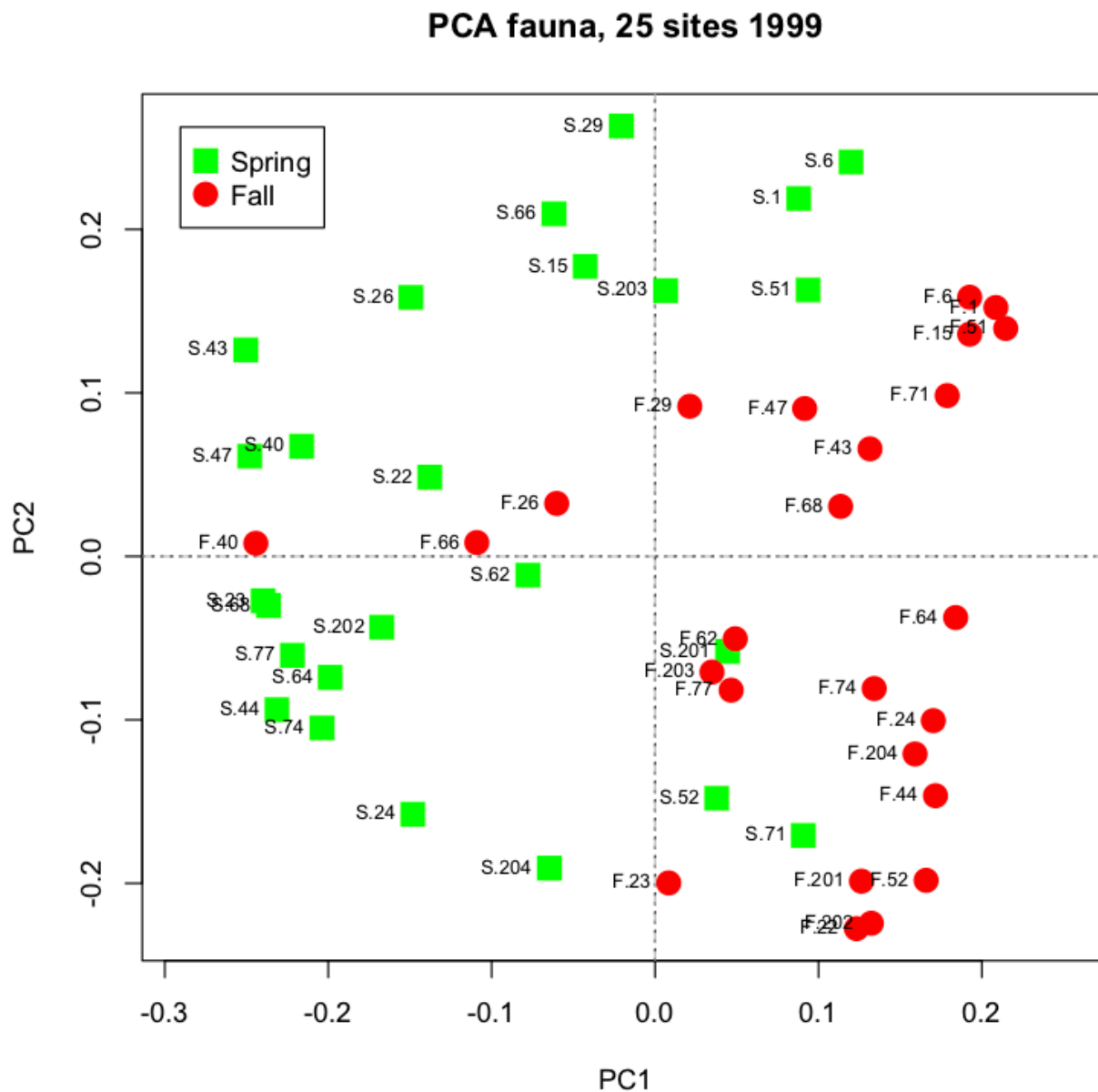


Figure 2 – Principal component analysis (PCA) ordination plot of the Hellinger-transformed faunal data, 25 brackish sites, year 1999. Only the sites are shown in this plot.

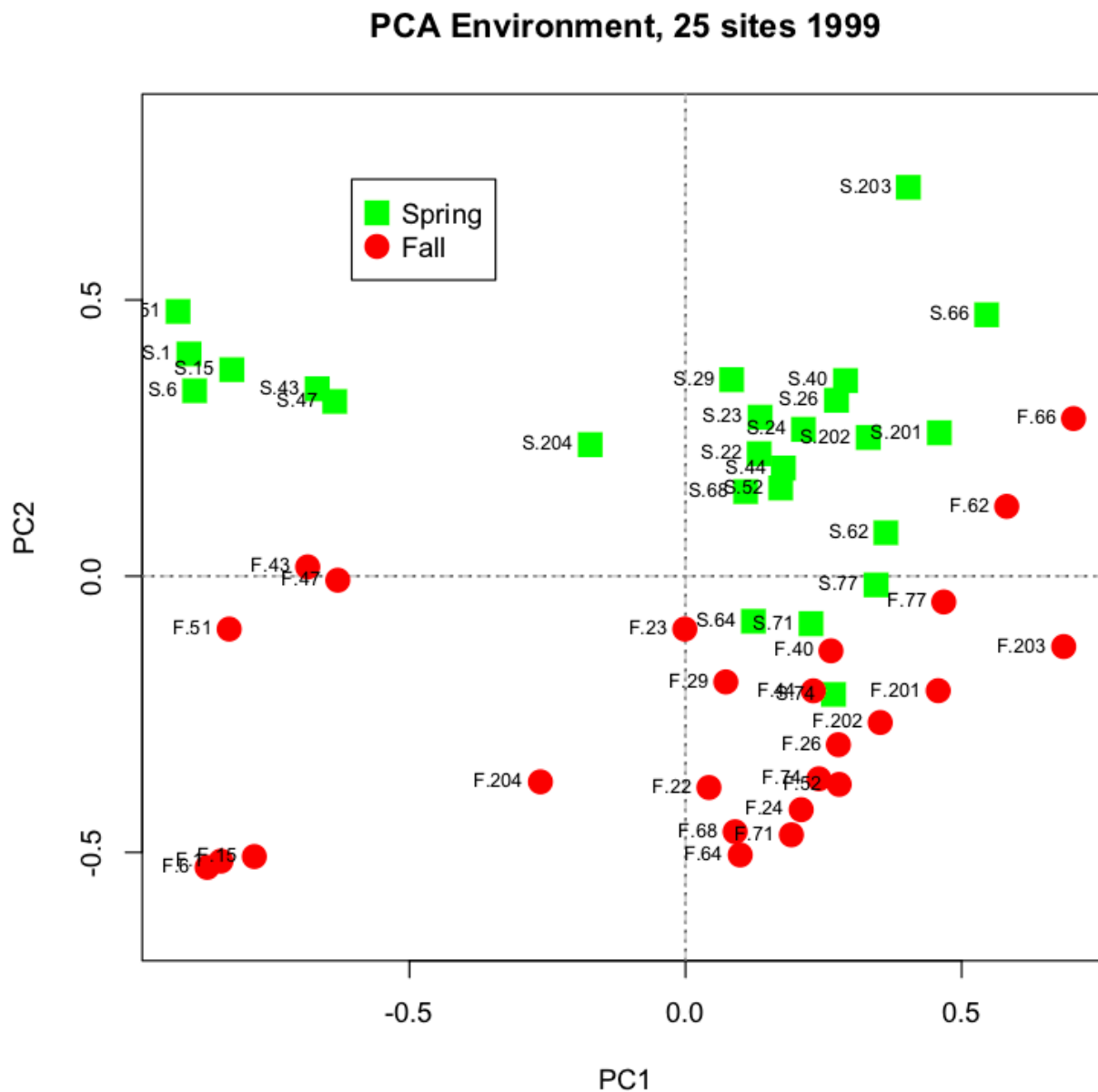


Figure 3 – Principal component analysis (PCA) ordination plot of the standardized environmental data, 25 brackish sites, year 1999. Only the sites are shown in this plot.

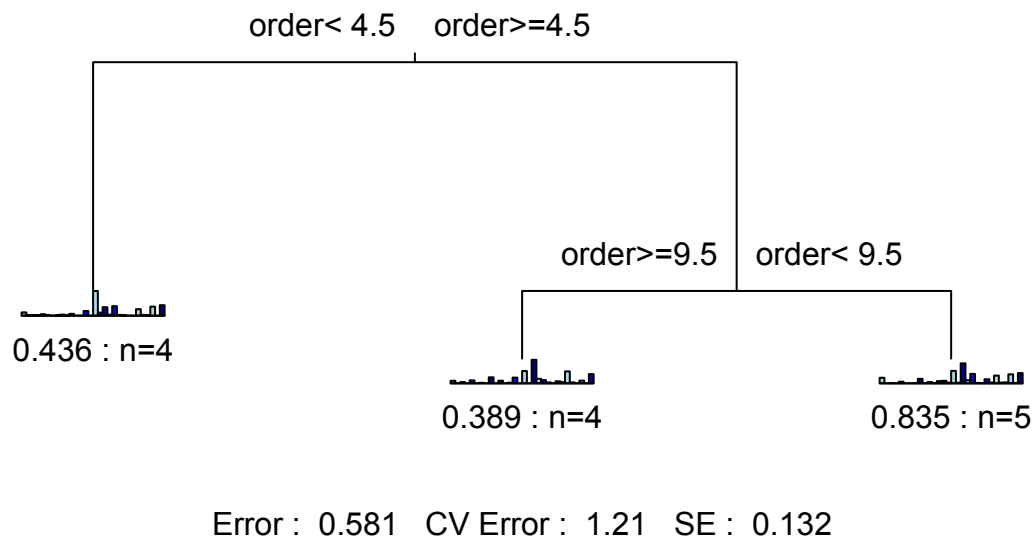


Figure 4 – Time-constrained clustering of the 13 years of faunal surveys (Hellinger-transformed data) at site 24, spring surveys, by multivariate regression tree (MRT) analysis of the faunal time series. The explanatory variable *Order* indicates the temporal positions, 1 to 13, of the years in the time series. The splitting points between years are shown for each split. The histograms underneath the end branches (*leaves*) of the tree represent the relative abundances of the 30 species captured in the surveys forming each group.

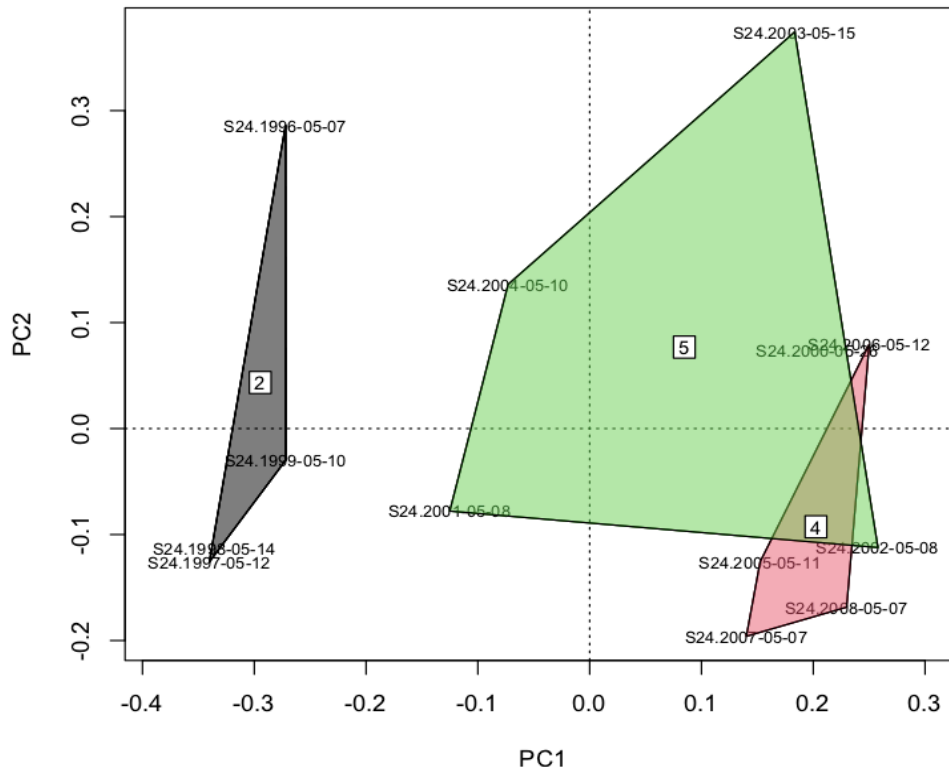


Figure 5 – PCA ordination of the 13 survey years at site 24, Hellinger-transformed data. Convex hulls show the 3-group (noted #2, #4, #5) MRT classification of years revealed by MRT in Figure 4.

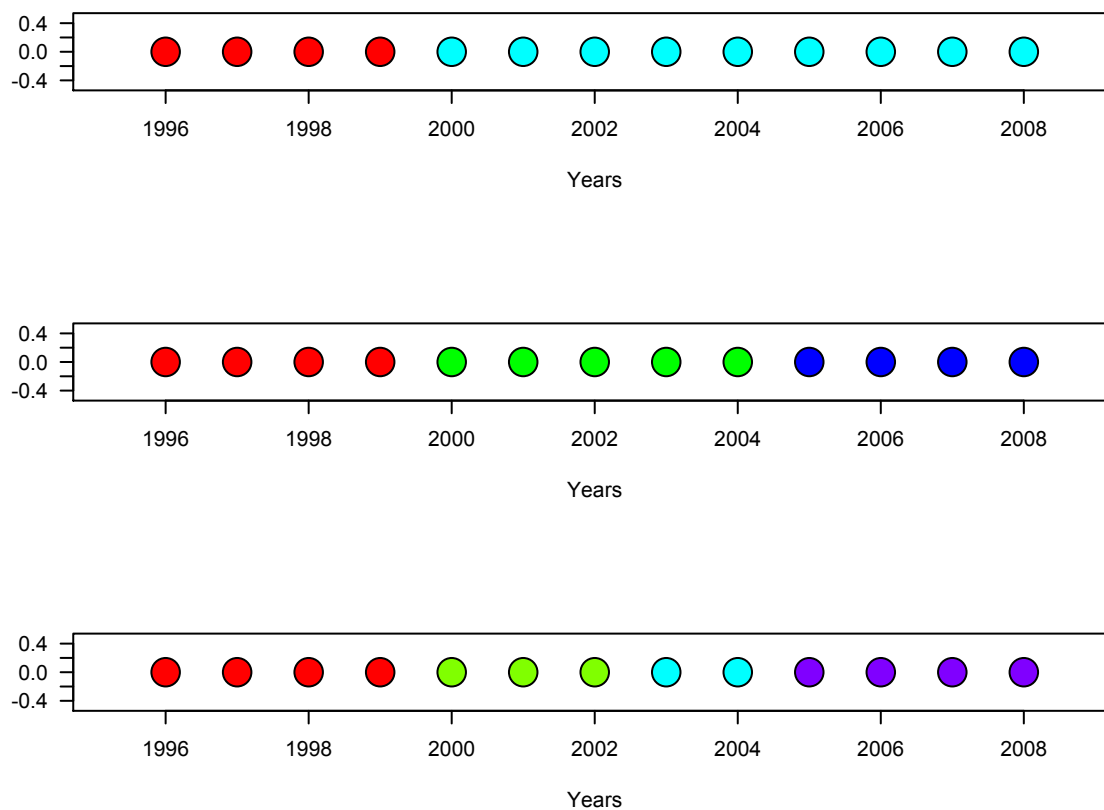
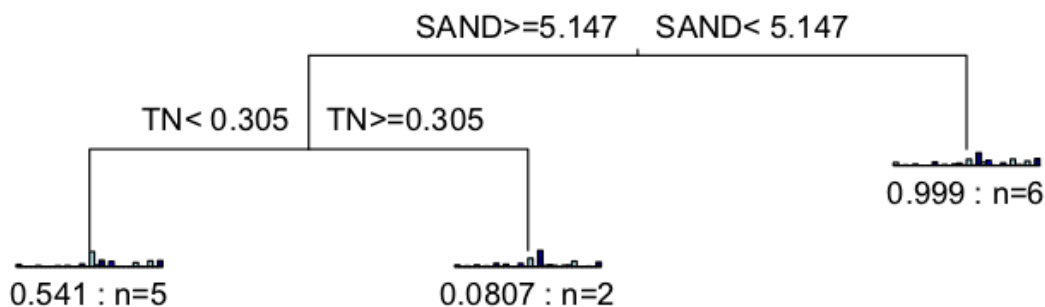


Figure 6 – Constrained hierarchical clustering results for the time series at site 24, 13 survey years, Hellinger distances. From top to bottom: time map clustering solutions into $k = 2, 3$ and 4 groups; the groups are differentiated by colours.



Error : 0.567 CV Error : 1.56 SE : 0.174

Figure 7a – Faunal variation among survey years (spring only) at site 24 explained by environmental variables through a MRT tree model. The first explanatory variable selected was Sand; the cutting point shown, 5.147, is the mean of two observed percentage values of sand, 4.7702 in the right-hand group and 5.5243 in the left-hand group. The second explanatory variable used in the tree construction was Total nitrogen (TN); the cutting point shown is 0.305, which is the mean between two observed percentage values, 0.30 and 0.31.

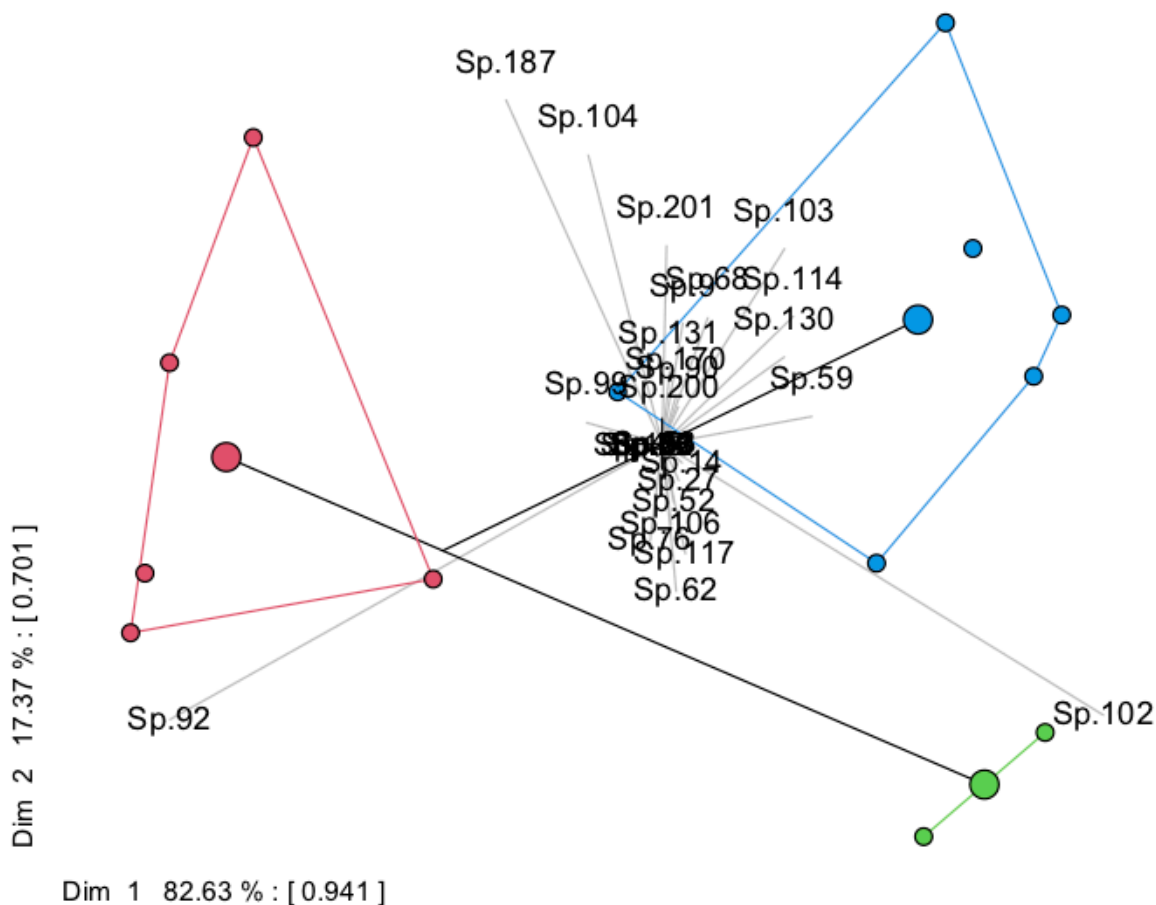


Figure 7b – PCA plot of the Hellinger-transformed data showing the 3 groups of the MRT tree in Figure 7a. The group centroids (larger circles) are connected following the MRT tree structure.

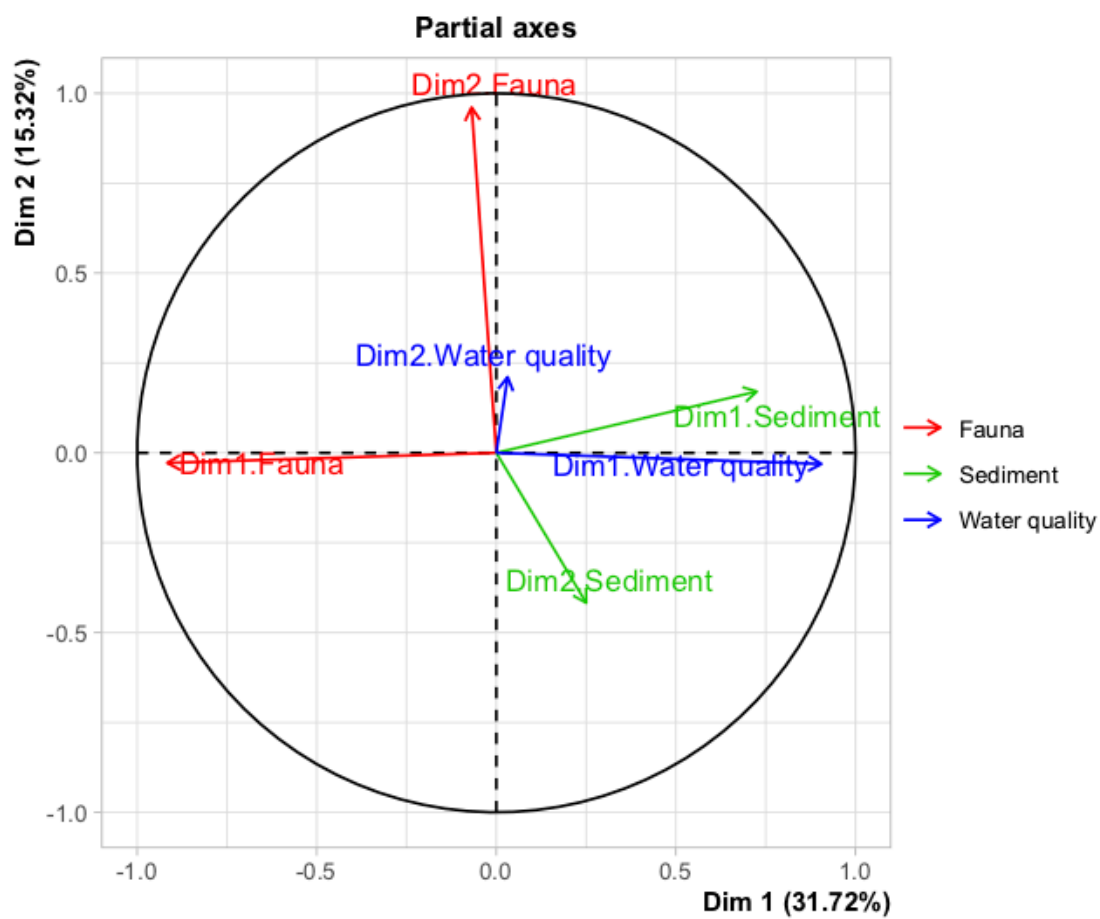


Figure 8a – Projection of the PCA axes of the three data sets — Fauna (red), Sediment (green), Water quality (blue) — on the MFA plane with axes 1 and 2. The black circle, with radius = 1, indicates the maximum possible length of the separate variable groups standardized axes.

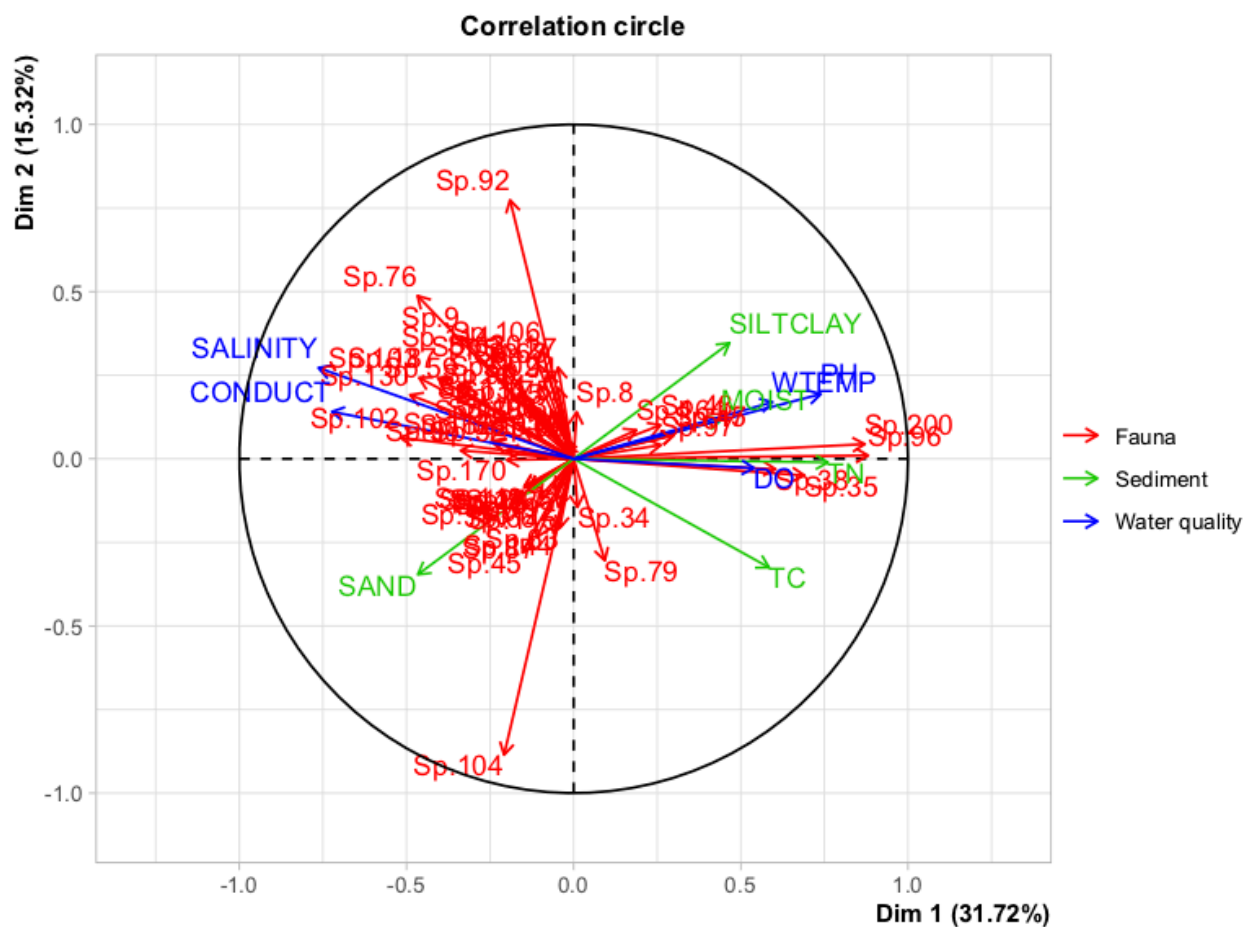


Figure 8b – Correlations between the variables of the three subsets and MFA axes 1 and 2. The black circle, with radius = 1, is a visual reference indicating the largest possible correlation.

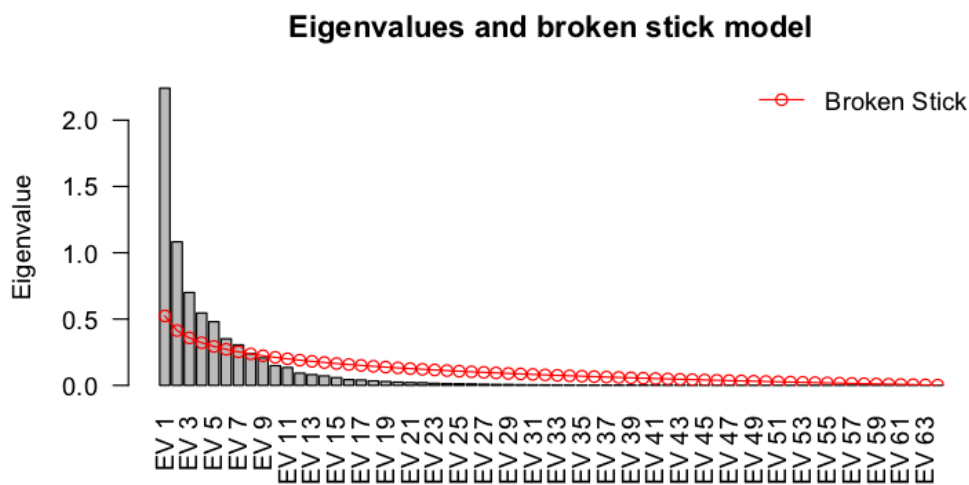


Figure 8c – Scree plot of the MFA eigenvalues (black rectangles) and the corresponding values of the broken stick model (red circles).

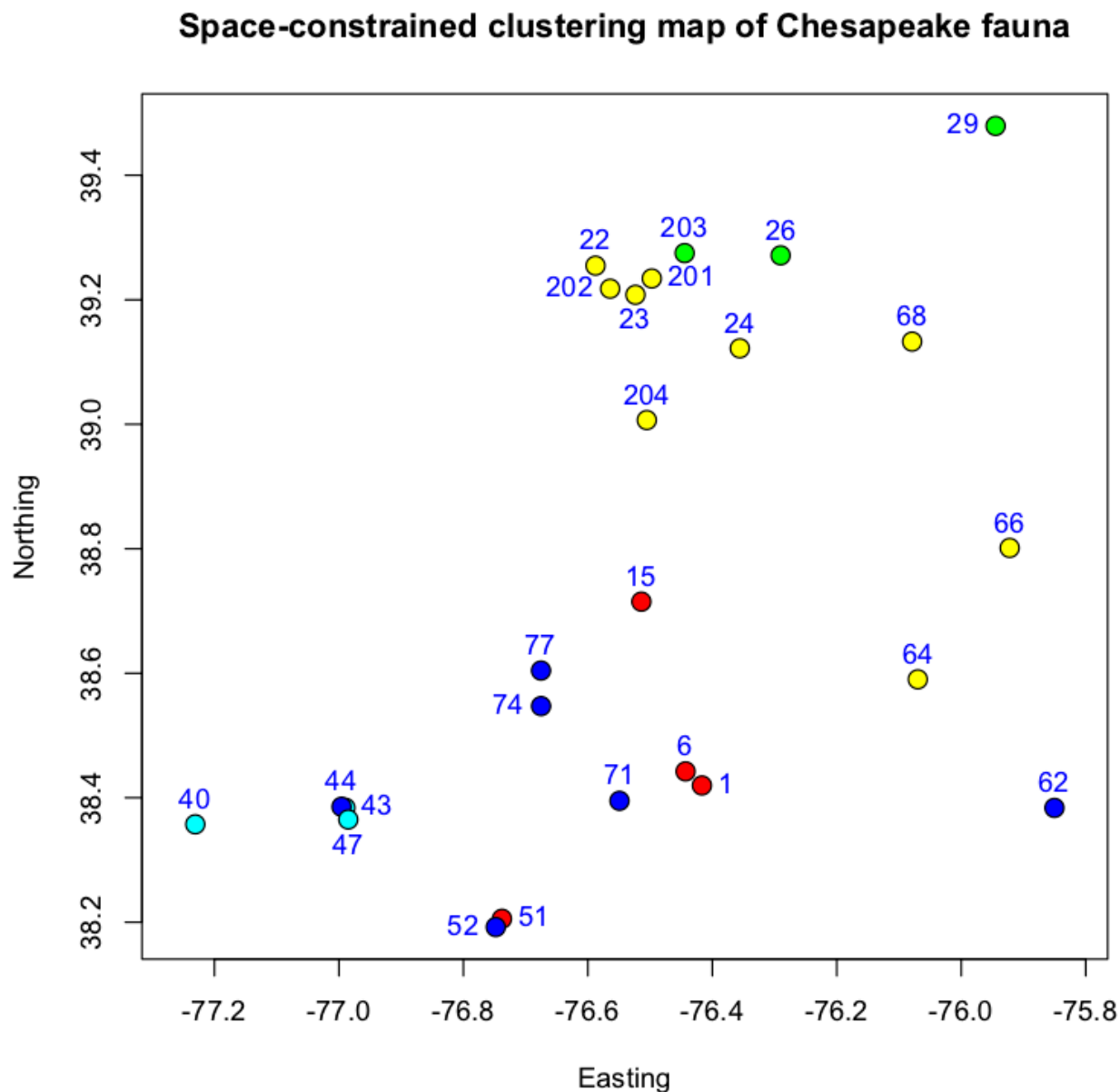


Figure 9a – Map of the 25 brackish sites in Chesapeake Bay (without landscape background) showing the space-constrained hierarchical clustering result with $k = 5$ groups (colours), based upon analysis of the Hellinger-transformed faunal data. A map of the Chesapeake survey sites with landscape background is shown in Figure 1.

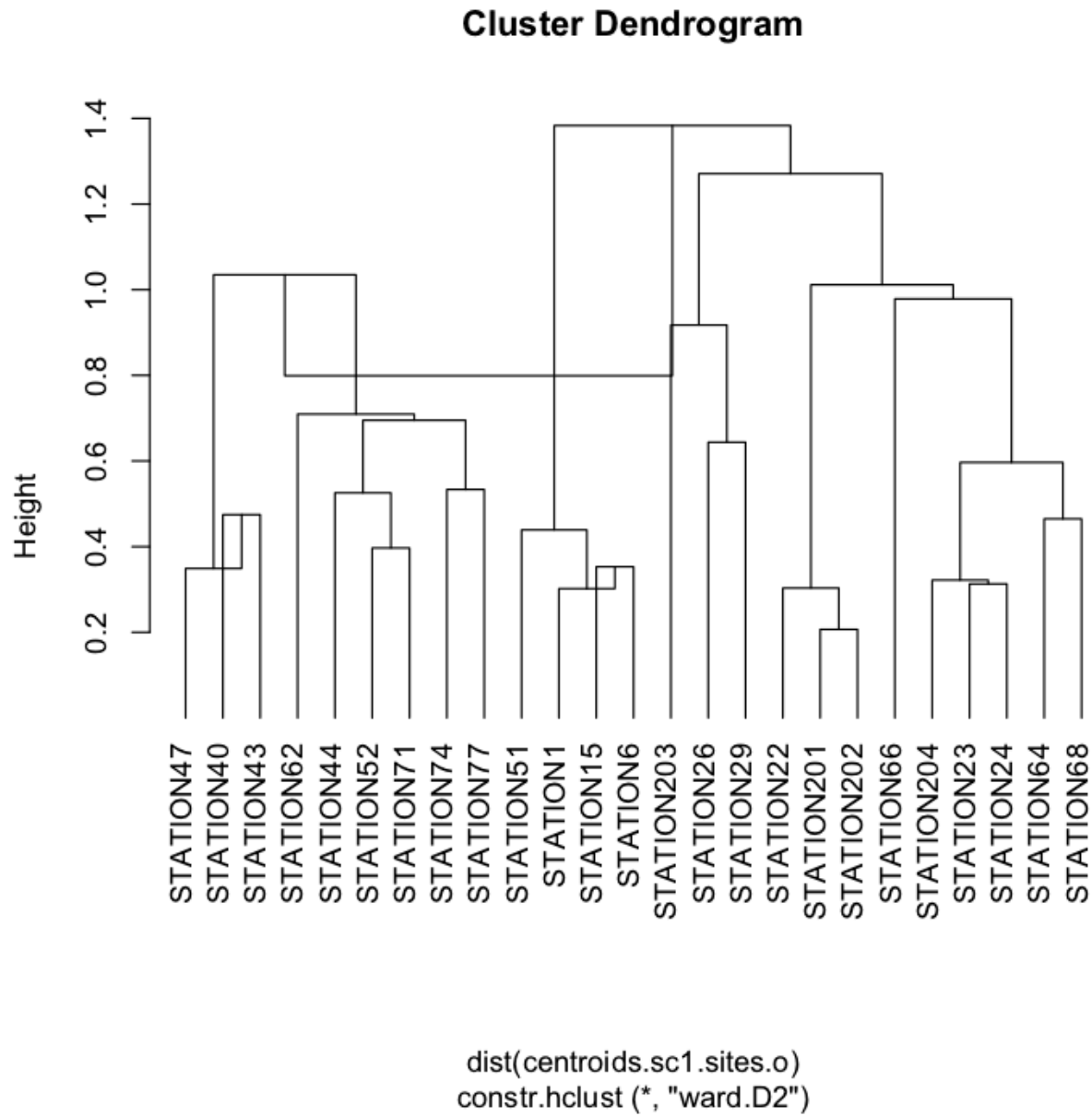


Figure 9b – Dendrogram of the space-constrained hierarchical clustering results of the faunal data. The dendrogram contains reversals; they are caused by imposition of the constraint during the hierarchical agglomeration procedure.

Exercise – In the dendrogram, identify the five groups mapped in Figure 9a after noting the site labels of the members of each group.

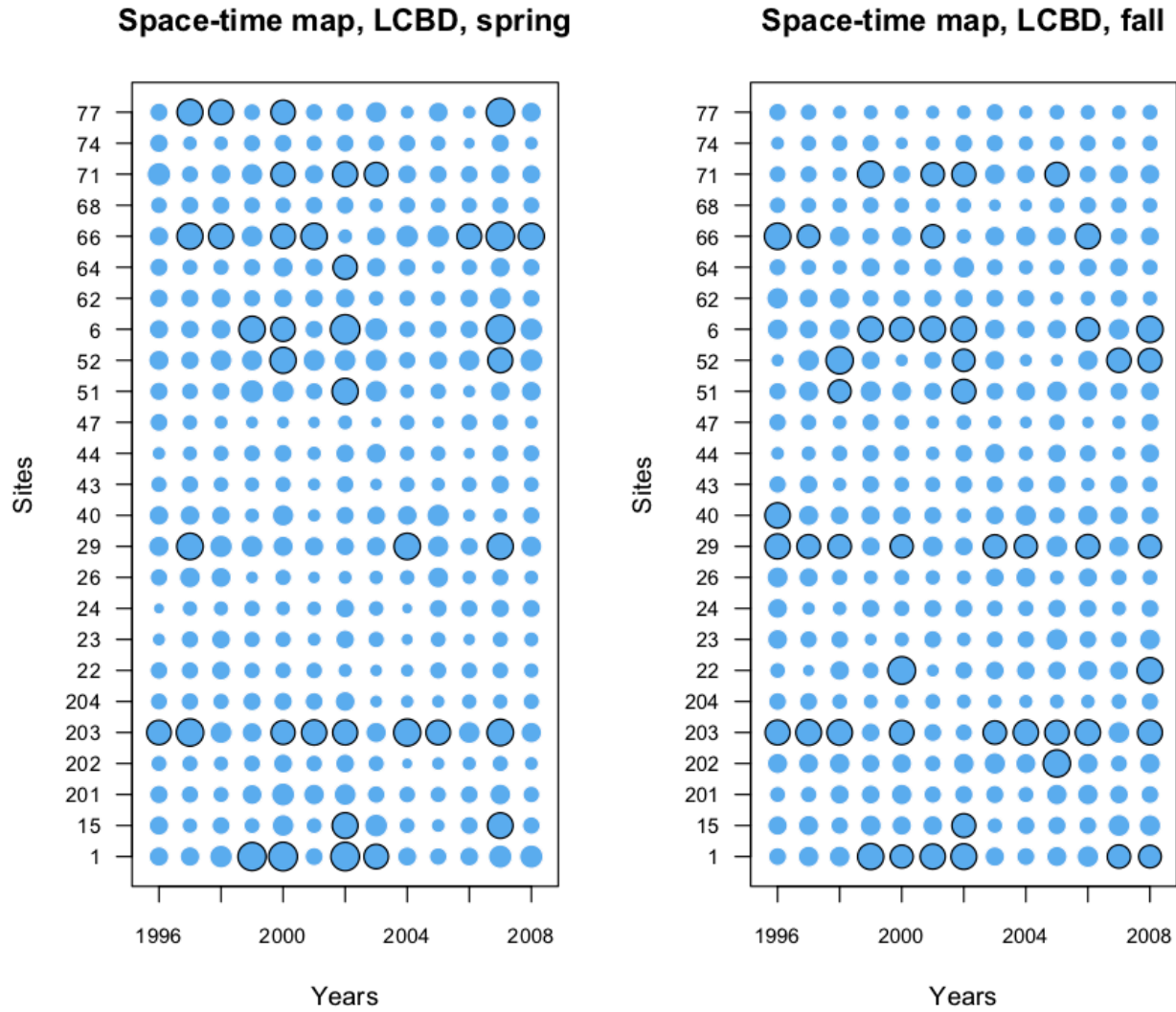


Figure 10a – Space-time maps (25 brackish sites, 13 years) of LCBD indices computed separately for the spring and fall surveys. Within each map, the surface areas of the circles are proportional to the LCBD values. Circles with a black rim indicate significant LCBD values at the 0.05 level.

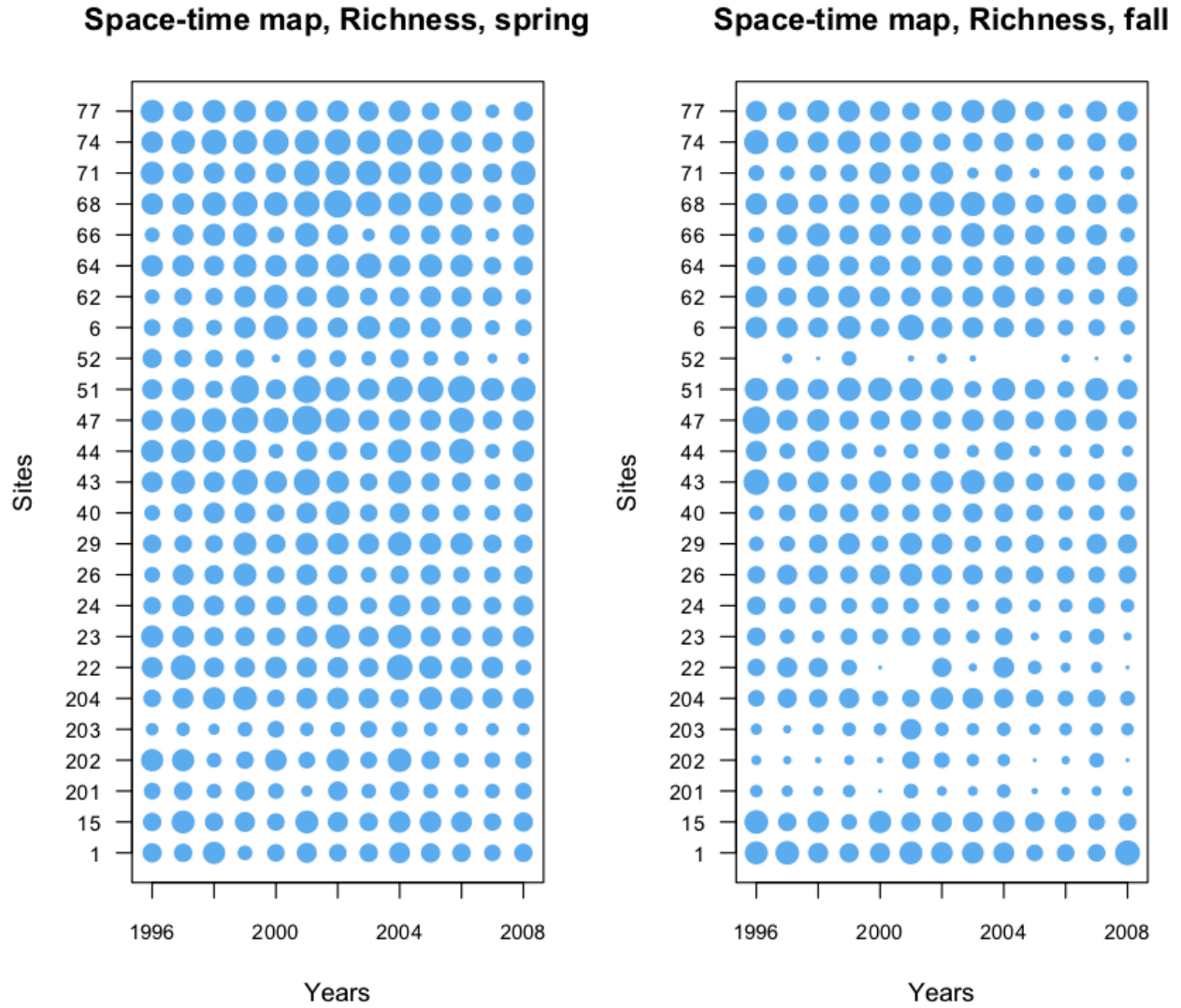


Figure 10b – Space-time maps (25 brackish sites, 13 years) of taxonomic richness computed separately for the spring and fall surveys.

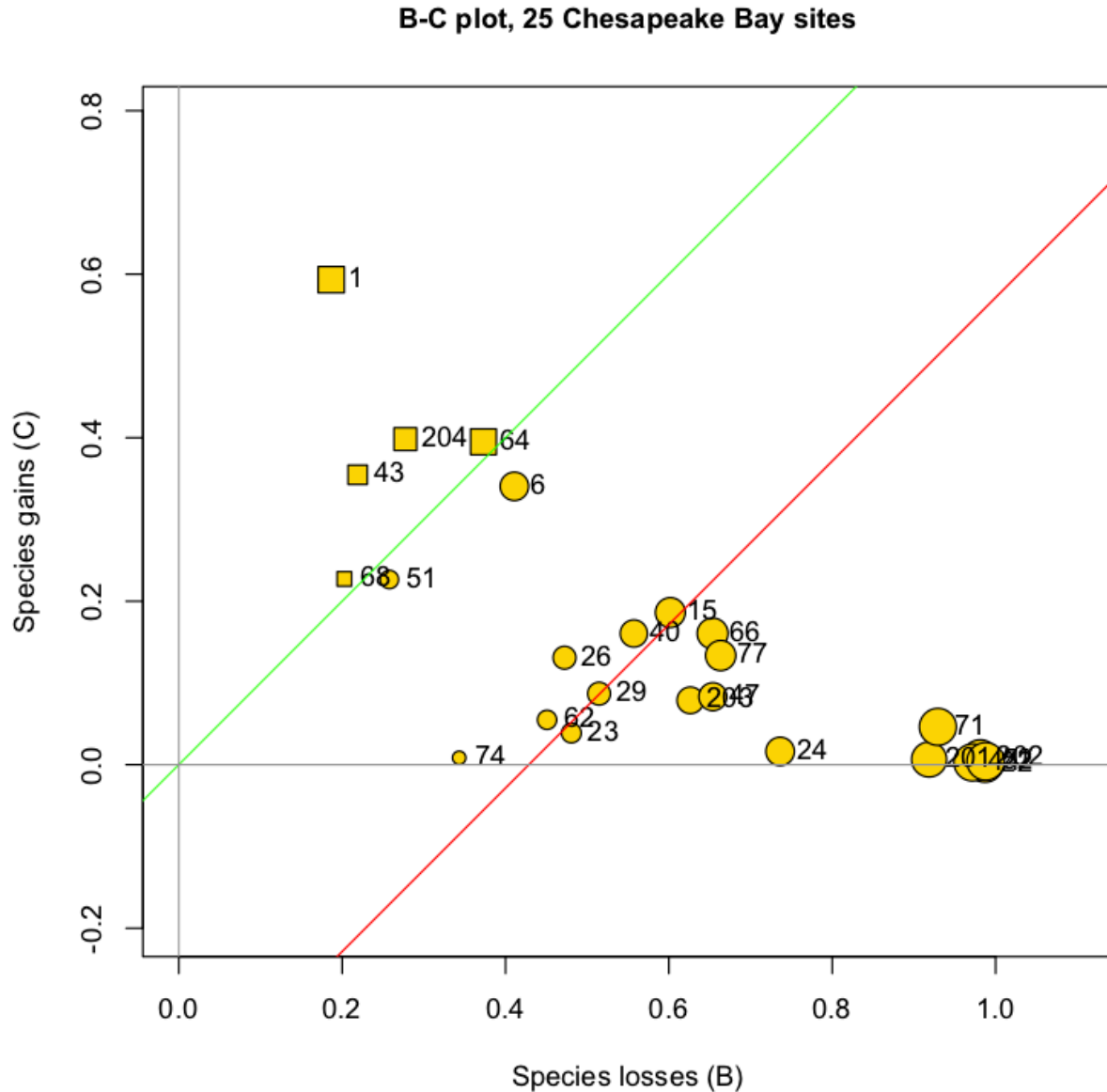


Figure 11a – Temporal beta diversity analysis: B-C plot comparing the community composition data of the spring and fall surveys of year 2003, 25 brackish sites. The *percentage difference* coefficient (aka Bray-Curtis) was used to compare the spring and fall surveys at each site.

Green line with slope of 1: line where gains equal losses ($C = B$). The **red line** is drawn parallel to the green line (i.e. with a slope of 1), passing through the centroid of the points. Its position below the green line indicates that, on average, species losses dominated gains between the spring and the fall surveys.

The dissimilarity $D = (B + C)$ increases from the lower-left to the upper-right corners of the plot. Symbol diameters are proportional to the values of dissimilarity D . Squares: sites where $C > B$ (gains dominate). Circles: sites where $B > C$ (losses dominate).

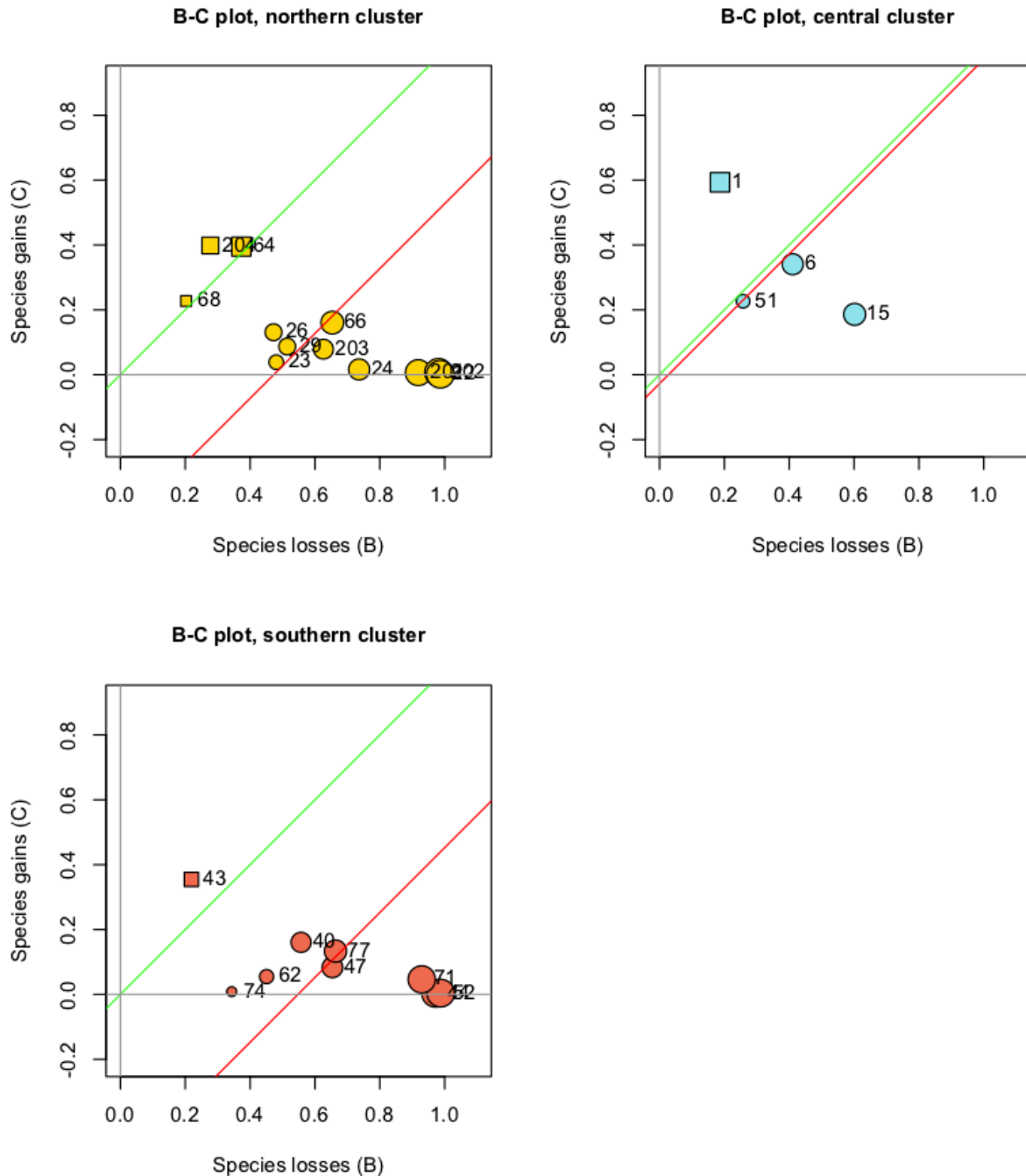


Figure 11b – Temporal beta diversity analysis: B-C plots comparing the community composition data of the spring and fall surveys of year 2003, computed separately for the three clusters of sites identified by space-constrained hierarchical clustering in section 6.1.3. Symbol diameters are proportional to the TBI statistics, which are $D = (B + C)$.

In the northern and southern clusters, the green line is above the red line, indicating that species losses dominated gains from spring to fall in the year 2003 in these two groups. In the central cluster, the red and green lines are in the same position, indicating that for this small group (4 sites only), gains and losses were equivalent. More sites would have led to a stronger conclusion about this small site cluster.