

PREDICTING FRESHWATER AND OLIGOHALINE TIDAL MARSH VEGETATION COMMUNITIES IN THE VICINITY OF THE SAVANNAH NATIONAL WILDLIFE REFUGE

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Abstract. A large portion of the remaining tidal freshwater marshes left in the southeastern U.S. lies within the braided channels of the lower Savannah River deltaic marsh complex (Georgia, USA). These marshes occur upstream from the large shipping port of Savannah and have been subjected to a variety of hydrologic changes as a result of shipping channel modifications in recent decades. The Georgia Ports Authority and the U.S. Army Corps of Engineers funded the development of hydrodynamic and vegetation community models in order to predict impacts of future channel modifications on the sensitive freshwater/oligohaline marshes. The goal of this study was to document vegetation communities throughout the tidal freshwater and brackish range (roughly 0-7 parts per thousand (ppt)) of the lower Savannah River, identify the environmental conditions influencing their distribution, and predict community distributions based on the underlying gradients. Using a combination of classification trees, cluster, and indicator species analyses to identify community types and their environmental thresholds, our final model used average interstitial salinity of the prior growing season and soil percent organic content as the best predictor variables. The primary indicator species for each community were identified as *Eleocharis spp.*, which dominated the interior marshes in areas with <1.0ppt salinity, while *Zizaniopsis miliacea* dominated areas with lower soil organic content at <1.0ppt. *Scirpus validus* was dominant between 1.0-3.5ppt, while *Scirpus robustus* and *Spartina spp.* occurred at >3.5ppt average growing season salinity. Using these results with hydrodynamic model predictions of river salinity and marsh interstitial salinities, changes in total acreage of freshwater/oligohaline and brackish marshes can be estimated for a variety of shipping channel modifications.

INTRODUCTION

The productivity and value of tidal freshwater-oligohaline marsh communities to fish and wildlife have been well documented (Odum *et al.* 1984, Gough and Grace 1998, Mitsch and Gosselink 1993). Despite their

importance to downstream fisheries and estuaries, however, their distribution is much reduced from historical levels. A significant portion of the remaining tidal freshwater marshes left in the southeastern U.S. lies within the braided channels of the lower Savannah River deltaic marsh complex. Many studies have focused on the freshwater and brackish marshes of this area since the 1980's (Latham 1990, Kitchens *et al.* 2003, Pearlstine *et al.* 1990), specifically their distribution in response to downstream modifications for shipping industries. Previous studies have focused on documenting community shifts in response to a disturbance, which usually takes several years to accomplish and puts managers in a reactive position, rather than being proactive or adaptive. In the late 1990's, efforts began to provide managers with a predictive tool, capable of assessing impacts to sensitive freshwater and brackish marsh communities in the proposal phase, rather than several years after its inception. This predictive model would eliminate the time lag associated with determining the impacts of a given activity and would help to identify those proposals with potentially serious impacts before being implemented.

The goal of this study was to develop a predictive model by documenting vegetation communities throughout the tidal freshwater and brackish range (roughly 0-7ppt) of the lower Savannah River, identifying the environmental conditions influencing their distribution, and then predict community distributions based on the underlying gradients. Specifically, the goal was to build a predictive engine based on quantitative, ecologically meaningful measures that would be readily adaptable to GIS applications, and when coupled with predictive hydrologic models could characterize current and future conditions based on climatic or management changes (Kitchens *et al.* 2003).

METHODS

Model Development

The overall predictive ability of our model depended on the cohesion between the ecological, data, and statisti-

cal aspects of the model. Ecologically, we assumed the primary gradients determining species compositions and distributions in the tidal marshes were salinity and soils characteristics (Odum *et al.* 1984, Gough and Grace 1998). We also assumed that the soil salinity (interstitial) would be a more direct stressor than river water salinity (Howard and Mendelssohn 1999) and that the salinity gradient of interest was in the freshwater (<0.5 ppt) to brackish (7.0ppt) range (Kitchens *et al.* 2003). Our study was designed to sample along the entire gradient of interest, and was stratified within site to account for differences in soils, salinities, flushing rates, elevations, nutrient exchange, etc. between the interior and berm (edge) marsh communities. This design focused our sample efforts on the diverse interior communities (>10m from canals) and avoided the more terrestrial berm communities. Our data collection techniques consisted of robust estimates of plant abundance (stem densities and above-ground biomasses), and focused on the peak (June) growing season communities to eliminate seasonal variations. The statistical procedures we selected were all compatible with non-normal data, and the models we chose were favored over other commonly used models (Generalized Linear Models, Generalized Additive Models, Multiple Regressions, etc.) in the ecological literature (Franklin 1995, Vayssières *et al.* 2000, De'ath 2002, McCune and Grace 2002).

Seven sites were sampled in June of 2005 along the three main channels of the lower Savannah River. Each site consisted of six transects oriented roughly parallel to the main river channels and perpendicular to nearest drainage canals. This design produced 126 individual samples stratified across the salinity gradient (inter-site), soils gradient (inter- and intra-site), and from front to back marsh community (inter- and intra-transect). Above-ground, standing vegetation was collected from a randomly placed, 0.25 square meter (m²) quadrat within three meters of each sampling station (126 total), and the stem densities and dry biomasses of each species were recorded. Importance values were calculated for each species in each quadrat by averaging their relative biomass and relative density and expressing it as a percentage. That produced a value from 0 – 100 that gave a good estimate of species importance within a given quadrat and was not biased towards large, few-stemmed species (*Typha spp.*) or small, numerous-stemmed species (*Eleocharis spp.*) (McCune and Grace 2002). This calculation also relativized the dataset, eliminating the need for transformations typically applied to density or biomass data that can vary by orders of magnitude between species and samples.

Soil cores were collected from each sampling location in June of 2000 and June of 2001, using cylindrical aluminum corers. The corers measured seven centimeters (cm) in diameter and were used to extract the top 10cm of substrate for bulk densities (Blake and Hartge 1986) and per-

cent organic content (Chapman and Pratt 1961). We used the average bulk densities and percent organic contents from the 2000 and 2001 samples as soils variables in our model.

Interstitial marsh salinities were recorded every 15 minutes using YSI data sondes placed in double-nested PVC wells that were designed to keep surface water out and allow soil water in (Kitchens *et al.* 2003). One sonde was located at a middle sample station of one transect at each site. Salinities from March 1st to October 1st of the year prior to sample event were used to calculate the mean salinities of the previous growing season for each site. For example, the June 2005 sample used the salinity data from March 1st – October 1st of 2004. Non-growing season salinities were used in preliminary analyses but were less correlated with community shifts, presumably due to a lower plant response to stresses in the dormant season.

Analyses

Rare species were removed from the dataset by eliminating those that occurred in less than five percent of the samples. Two transects at a site were also eliminated from our analyses as salinities were poorly correlated with the salinity meter located on a slightly different watershed. The resulting matrix was 120 samples by 30 species.

A hierarchical, agglomerative cluster analysis was performed to find groups (or communities) of similar species compositions using the software PCORD 4.20 (McCune and Mefford 1999). Flexible beta (-0.25) linkage and Sorenson distance measures were chosen for their space conserving properties, compatibilities with each other, and their advantages with non-normal data (McCune and Grace 2002). This analysis grouped similar sample units based on species importance values using multiple species as a basis for deciding on the fusion of additional groups.

An indicator species analysis was performed to determine the optimum number of clusters for further analysis and to define those clusters in terms of representative species. This analysis uses the proportional abundance and frequency of a particular species in a particular cluster relative to its abundance and frequency in all other clusters (Dufrene and Legendre 1997). The level of clustering that produced the highest number of significant indicator species was chosen to define the number of community types, and those communities were defined by the corresponding species with high indicators values (McCune and Grace 2002).

A CART model (S-Plus Tree Library, De'ath 2002) was used to predict the communities identified by the cluster analysis using only the measured environmental variables. These models have been applied most often to classify habitats or vegetation communities based on environmental characteristics, resulting in an overall description of how different the groups are, which vari-

ables distinguish the groups and a predictive model that can classify new samples into those groups (Urban 2002). This procedure works by recursively partitioning the multidimensional dataset into subsets that are more homogeneous in terms of the response variable, in this case, cluster or community membership (Vayssières *et al.* 2000). The heterogeneity of each subset is measured as an impurity, calculated in our model using the Gini index (Breiman *et al.* 1984). The goal of each split is to maximize the reduction in impurity. The model identifies a single variable (and its threshold value) as the indicator for each branch of the tree, as opposed to groups being distinguished along multivariate axes as in discriminant analysis or logistic regression. This approach allows the inclusion of non-linear species responses and is unaffected by interactions among variables (Vayssières *et al.* 2000, McCune and Grace 2002).

Once the largest possible tree has been grown, a process of eliminating superfluous branches begins, called “pruning back to an honest tree” (Breiman *et al.* 1984). This is done by testing each subtree for its error rate based on data that were not used to grow the largest tree. Using cross validation, which acts as a test sample while extracting information for all the cases of a data set, the final tree is constructed from all of the data, using the best tree size (Vayssières *et al.* 2000). The performance of the model is measured by a misclassification rate, while the amount of variation explained by the tree is reported as 1-Relative Error, or more strictly, 1-Cross Validated Error.

The final output is a pruned tree with barplots under each leaf showing the composition of the final groups, as well as the number of samples in that leaf. Threshold values of the variables determining the splits are shown at each node. The best fit tree incorporated average prior growing season salinity (interstitial), and soil percent organic content.

RESULTS AND DISCUSSION

The cluster and indicator species analyses identified four main communities (Figure 1). The most frequently occurring was dominated by *Scirpus validus* (SCIVA) with 35% of the samples belonging to that group, followed by a community of *Zizaniopsis miliacea* and *Polygonum spp.* (ZIZMI_POLSP) (32%) and an *Eleocharis spp.* (ELESP) community (20%). *Galium tinctorium* (GALTI) and *Sagittaria latifolia* (SAGLT) were secondary indicators for the ELESP community, while *Aster tenuifolius* (ASTTE) was a secondary indicator for the community dominated by *Spartina spp.* and *Scirpus robustus* (SPASP_SCIRO).

The CART model had good classification rates for most of the communities based on the salinity and soil organic content variables, but one leaf consisted of a

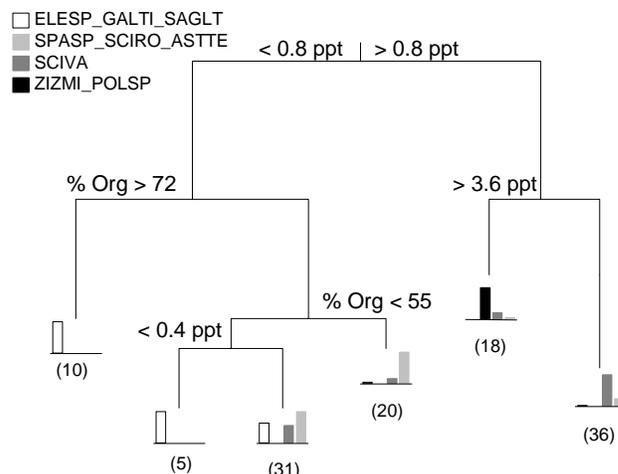


Figure 1. CART model showing the distribution of the four communities identified by the Cluster and Indicator Species analyses. Numbers in parentheses indicate the total number of samples in the leaf and barplots show community membership of those samples. Leaves with more than one dominant community have higher misclassification rates. CV Error = 0.50, CV Misclassification Rate = 0.33.

mixture of the ELESP, ZIZMI and SCIVA communities. These communities all occurred relatively equally at low salinity levels (0.4-0.8ppt) and in highly organic soils (>55%), and were unable to be further classified based only on those environmental characteristics. Obviously, at very low levels salinity will cease to be a major factor in determining community composition and elevation or inter-specific competition begin playing a larger role (Odum *et al.* 1984).

There were 100% classification rates for the ELESP community at <0.8ppt average prior growing season salinity in areas with >72% soil organic content, and again at <0.4ppt and >55% organic content. These areas were predominantly the interior marshes of our most freshwater sites, while the ZIZMI_POLSP community occurred at lower soil organic content and <0.8ppt, or closer to the drainage creeks in the freshwater areas.

The largest group (36/120) was classified as the SCIVA community, dominating those areas between 0.8-3.6ppt, while the SPASP_SCIRO_ASTTE became the dominant community at higher salinities. These results show the extreme effects small changes in average growing season salinities can have on vegetation communities. Essentially, there were three communities identified at <1.0ppt, while only two occurred between 1.0-7.0ppt. This highlights the importance of being able to predict even subtle changes in growing season salinities at the freshwater end of the gradient.

The intent of our model was to provide users of co-developed hydrodynamic models of the river salinity and marsh interstitial salinity with a predictive engine that would determine marsh communities based on salinity

outputs from user-specified hydrologic scenarios. It should be stated, however, that our model is based on a snapshot of an extremely dynamic system that does not respond linearly to disturbance or fluctuation. Grace and Guntenspergen (1999) showed that the distribution of salt marsh communities was largely affected by extreme historical disturbances, in addition to current salinities. Most statistical models are based on an assumption that vegetation is in equilibrium with the environment, or where change is at least slow relative to the lifespan of the biota. The overall success of these models depends on the degree to which history and disturbance are important to the system (Austin 2002). Certainly there are channel modifications or disturbances that would produce effects beyond the predictive range of our model. There must be thresholds that once passed would affect distributions for many years after returning to normal conditions. However, this model is an important tool for managers and stakeholders in helping to identify the best options regarding future changes to the lower Savannah River.

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