

Environmental factors linked to tree regeneration within the Long Island Pine Barrens

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Abstract

The study of tree regeneration and the life cycles of the species of trees within the Long Island Pine Barrens was conducted to prevent the destruction of the biodiversity of the Long Island Pine Barrens. Because oak trees dominate pine trees in the regeneration cycle, the community of pitch pine trees has already begun to shrink, which could lead to their extinction in the Long Island Pine Barrens. Data and findings have been recorded using 93 designated plots of different forest communities and tree types on Brookhaven National Laboratory (BNL) property as a sample. The data collected consists of recordings from 2005, 2006, and 2011. These three years of data are the only recordings of the forest communities furthering the need to collect data from future years to create more statistically significant and rigorous results. Using descriptive statistics, non-parametric tests, and Nonmetric Multidimensional Scaling (NMS), we have been able to find correlations and create hypotheses about the nature of the tree regeneration cycle and forest community growth. For example, after an analysis of the data collected, we have concluded that the oak community has been dominating the pine community of the barrens left untouched by prescribed fires. In addition, different tree species dominate in the plots studied due to environmental factors one of which being an excessive overpopulation of white-tailed deer consuming upper level vegetation. The overall amount of pitch pine trees in the Long Island Pine Barrens has been diminishing over the time of this study. Throughout this study, both non-metric multi-dimensional theory and R® the statistical analysis program were necessary to understand as well as the learning of key factors that contribute to forest health and their effect on the forest. This study is being conducted to create a baseline for a continuing study of the Long Island Pine Barrens.

Introduction

A study of the Long Island Pine Barrens (LIPB) forest is currently being conducted at Brookhaven National Laboratory (BNL). The LIPB consists of mainly four species of trees: pitch pine, white oak, scarlet oak and black oak. Each of the species can be found in any of the four major community types found in the LIPB: Pitch Pine, Pine-Oak, Oak Pine, and Coastal Oak forests. These tree species in the communities follow a regeneration cycle of natural succession necessary for the conservation of biodiversity within the LIPB. However, there are a multitude of environmental factors which cause the regeneration cycle to be highly variable, predominantly the diet of herbivores within the area such as white-tailed deer, seed availability, the characteristics of forest gaps, and naturally caused forest fires (Millington, 103). If natural succession occurs, oak trees will invade the pitch pine forest and the barrens will eventually become a closed canopy forest (Jordan 152). However, the trees within Long Island Pine Barrens are failing to follow the order of natural succession due to many different environmental factors. A greater quantitative understanding of the ecological succession of the LIPB forest and the functional variation of each tree species is needed to make hypotheses about the succession of the forest (Sarr 1241). Using the data that has been collected in both 2005 and 2011, models of the distributions of species within the LIPB were made and analyzed in order to determine whether the forest is considered to be healthy. An analysis of the seedling and sapling counts

compared to the number of trees was conducted using regression and correlation models to determine if the forest is regenerating in accordance to the regeneration model. A visual model of the invasion of tree species into different forest communities was also analyzed to give inferences about the interactions of tree species given external environmental factors. After looking at the models created taken from the given years, the conclusion drawn was that the forest is not regenerating as it should compared to natural succession, and further analysis is needed understand the reasoning behind why the forest is not regenerating as expected.

2. Materials and Methods

2.1 Study Area

The data collected for the analysis was taken from the 91 plots located on site within BNL. That data set for 2005 consisted of the forest community of each plot, the species of trees within each plot and the count of each tree species, and the Diameter at Breast Height (DBH) of each tree. The DBH is the diameter of a given standing tree and is collected to determine a number of characteristics, two of which used for this study are age and growth rate. The DBH is also summed in order to give a basal area estimate of each species within each of the plots (Sarr 1244). This is done in order to compare the age and height of one species of tree within a plot to another. Doing this allows the growth of a tree species within a given plot to be analyzed in relation to the other trees in that same community. In 2011 as well as 2005, the number of seedlings and saplings found within each plot of each tree species was recorded for analysis. The DBH of each tree of each species within each plot was split into four quartiles based on height and summed in order to look at the plot as a whole and the biodiversity of each plot. The separation of the DBH of each tree species into quartiles creates a more specific data set when determining the growth of a tree species and whether that species is regenerating within that area.

2.2 Analytical tools

Throughout the study, Minitab 16® was the statistical program used to perform the statistical tests needed to draw conclusions about the LIPB. Boxplots, Anderson-Darling tests for normality, and regression models of two separate measurements were created using Minitab 16. In addition, using PC-ORD® to further understand the invasion of tree species into different communities gave us inferences as to the changes related to the regeneration cycles of the species in the LIPB.

Results

The number of pitch pine, black oak, white oak, or scarlet oak trees within all the 91 plots were recorded and analyzed. It was found that all pitch pine trees within all 91 plots make up 58% of all the trees in all the plots (see figure 1). This is expected as the Long Island Pine Barrens is composed of roughly 60% pitch pine trees. The percentages of black oak, white oak and scarlet oak are 13%, 15%, and 13% respectively. If the forest were to regenerate as naturally

expected, the percentages of all oak trees should increase and the amount of pitch pine trees should decrease due to the oak trees dominance in regeneration over pitch pine.

The first analytical test done was a test for normality of all DBH's for each species (see figure 2). Each DBH of each tree of one of the four major species (white oak, black oak, scarlet oak, and pitch pine) was tested for normality using the Anderson-Darling test. The purpose of these tests is to determine whether the tree species within all 91 plots is growing and reproducing normally in the forest community. After the analysis was run, all distributions were skewed to the left (skewness > 2 for all species). The distributions for white, scarlet and black oak revealed the first quartile was zero and that the median for both white and black oak was also zero. The distribution of pitch pine had all four quartiles present. When looking at each distribution, because the distributions of all the oak trees have zero for the first quartile, it makes the inference that there are very minimal seedlings and saplings, given the first quartile is the smallest size of a given tree. With the median of the black and white oak trees also being zero, it revealed there are also very minimal larger standing trees. This infers that there must be an external reason as to why the oak trees are not germinating in areas where they should be reproducing and invading the pitch pine trees.

In addition to the distribution of each major tree species, boxplots were created using Minitab 16 (see figure 3). Each boxplot uses the summation of all DBH's of each of the four major tree species within each of the 91 plots. Doing this allows a visual look at what the range of the sum of DBH's should be for each species and all existing plots that are outliers. As expected, the majority of the pitch pine trees exist within the range of the minimum and the maximum. Looking at the boxplots of each oak tree and knowing the quartiles from the distributions of each species, there are many major outliers indicating there are more taller standing oak trees then expected within the range. White and black oak both have a median at zero, thus reassuring there are a very minimal amount of small standing oak trees, and concluding the oak trees within the plots are not regenerating for an external reason.

The data set given included the count of each number of seedlings and saplings for each of the four major species black oak, white oak, scarlet oak and pitch pine within each of the 91 plots. A regression model was created using Minitab 16 to display the relationship between the number of seedling found in each plot and the sum of each DBH of all trees of the same species in each plot. The number of white oak seedlings in comparison to the summed DBH of all white oak trees in the coastal oak communities showed a positive correlation with the model equation $Y = 5.159 + .000320X$ at an R-squared value of 69.5% to fit the model (see figure 4). This regression is expected as oak trees in oak dominated plots should replace themselves in the community. However, looking at the black oak and scarlet oak trees, there is a negative correlation but at insignificant R-squared levels and therefore cannot be statistically significant. When looking at the correlation between each of the pitch pine seedlings and pitch pine trees within the pitch pine community, there was a negative correlation with the equation $Y = 7.830 - .000029X$ with an R-squared value of 20.4% (see figure 5). This concludes that the pitch pine

trees that should be regenerating within the pitch pine communities are not. This regression model backs the claim made by looking at the distributions of each species that the larger pitch pine trees are not producing seedlings and saplings that grow into the smaller standing trees for an external reason.

PC ORD is the multivariate data analysis program that was used to give a visual representation of the summed DBH of each tree type in each plot. With this program, a visual of the summed DBH of each tree type in each plot was created to determine if certain tree species are invading each of the different forest community types. Two major species were found to have a non-normal ordination in each of the four forest community types. Looking at the quartiles of the pitch pine trees, smaller pitch pine trees remain mainly in pitch pine communities. However, looking at the larger quartile trees, pitch pine trees become more abundant in other communities as well as other forest type plots. One hypothesis is that the larger pitch pine trees survive in other communities, but when trying to reproduce, the new seedlings and saplings are dominated by oak. Because of the lack of fire and oak dominance without it, the smaller trees do not reproduce in oak dominated communities.

Conclusions and Discussion

The majority of the LIPB is nutrient-impooverished fire-prone sandy soils. Because the majority is droughty soil, it is the perfect environment for pitch pine to thrive which explains why the percentage of coverage created by pitch pine trees was found to be roughly 58% in 2005 (Kurczewski 95). Because pitch pine is an indigenous plant community resulting from natural disturbances, without the upkeep of these natural occurrences, the pitch pines will move to only oak dominated communities and if continued, be dominated and wiped out by different species of oak trees. Oak trees are less fire-tolerant than pitch pine and therefore if a fire occurs in a given area, the pitch pine will survive and the burned oak will create the duff layer that is mineral rich and create the soil needed to pitch pine seedlings and saplings to germinate. This is the reasoning behind why there is a need to create prescribed fires and maintain the biodiversity of the pitch pine trees within the LIPB (Kurczewski 96-97).

Another reason as to why pitch pines trees are decreasing is the lack of mineral seed bedding and/or increasing shade. Pitch pine is shade intolerant, meaning without the amount of sunlight required, smaller pitch pine trees will not be able to grow and survive. Oak trees are shade tolerant and do not require as much sunlight as pitch pine trees and therefore will grow over the taller pitch pine trees and eventually move to close the canopy creating an environment not suitable for pitch pine to survive. Oak trees grow both faster and taller than pine trees. In an area where there are both pine and oak trees, the oak trees will grow and dominate the pitch pine trees and cause them to die out. This is why the pitch pine trees are dependent on natural fires to burn the oak and create the right environment for germination (Jordan 162). Maintaining the pine barrens with all the species and wildlife it contains requires frequent disturbance in order to maintain an open canopy for sunlight to reach the mid-level trees, create mineral soil needed for

pitch pine seedling establishment, and to prevent oak trees from dominating pine communities and creating the succession of hardwood floor (Jordan 165).

After analyzing the distributions of each of the total species of trees, the conclusion was drawn that oak seedlings and saplings are not being able to reach the minimum of the next quartile, stating that minimal oak trees are being able to grow to a height above the median of oak trees. The reasoning for this finding but be external from that of natural fires because of a lack there of. A possible hypothesis as to the limited number of small standing oak trees could be due to the high density of the deer population located in the LIPB. The heavy browsing of a high deer population can significantly affect the environment by inhibiting the growth of natural regeneration and even cause the extinction of different plant species (Casabon 112). Deer will eat the species of vegetation with the highest nutritional value. Oak seedlings and saplings are higher in nutritional value than pine and therefore will exhaust all oak seedlings and saplings before pine. The deer density on BNL property is roughly 10-15 deer per square mile when the optimal density of deer is 8 per square mile. With the overpopulation on-site, it is possible that the overpopulation of deer is exhausting the oak seedlings and saplings causing the lack of oak regeneration. However, this requires further data collection and study due to the lack of data containing only estimates of deer densities each season and is difficult to obtain significance from correlating the number of seedlings/saplings and deer densities.

Given the oak dominance over pitch pine in the model of natural succession, pitch pine forest should be converting into oak with the lack of natural occurrences that preserve pitch pine forests. However, as shown in the PC ORD model and analyzed in the regression models between pitch pine seedlings and saplings, older pitch pine trees still exist within oak communities, and both oak and pitch pine trees are failing to regenerate. From the models given, the visual representation shows the invasion of pitch pine trees in oak communities where through normal succession the oak trees should be moving into the pitch pine communities and regenerating into oak dominated communities.

The study of forest health is necessary in order to preserve both the biodiversity of the forest as well as the extinction of important resources species produce within the forest. Long term data collection is necessary in order to impact management control decisions and allow the examination of the importance of tree regeneration in upland-hardwood lowland-conifer forests (Millington 111). Multiple years of forestry data are required in order to start to fully understand the regeneration cycle of specific forests as well as stating discoveries with statistical significance. Given the data set only includes data from 2005 and 2011, finding correlations and statistical significance is not easily accomplished. This study, as we as all other forestry studies of regeneration cycles, requires the collection of as many years of data as possible in order to fully determine what defines a forest as healthy and the significance of why a healthy forest must be preserved.

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References

- Acevedo, M.f., D.l. Urban, and H.h. Shugart. "Models of Forest Dynamics Based on Roles of Tree Species." *Ecological Modelling* 87.1-3 (1996): 267-84. Web.
- Bataineh, Mohammad, Laura Kenefic, Aaron Weiskittel, Robert Wagner, and John Brissette. "Influence of Partial Harvesting and Site Factors on the Abundance and Composition of Natural Regeneration in the Acadian Forest of Maine, USA." *Forest Ecology and Management* 306 (2013): 96-106. Web.
- Casabon, Christine, and David Pothier. "Browsing of Tree Regeneration by White-tailed Deer in Large Clearcuts on Anticosti Island, Quebec." *Forest Ecology and Management* 253.1-3 (2007): 112-19. Web.
- Jordan, Marilyn J. "Conceptual Ecological Models for the Long Island Pitch Pine Barrens: Implications for Managing Rare Plant Communities." *Forest Ecology and Management* 185 (2003): 151-68. Elsevier. Web. July-Aug. 2014.
- Kurczewski, Frank E. "Historical Changes in the Pine Barrens of Central Suffolk County, New York." *Northeastern Naturalist* 7.2 (2000): 95-112. JSTOR. Web. 04 Aug. 2014. <<http://www.jstor.org/stable/10.2307/3858645?ref=no-x-route:a8c1b401437a4ef4509f4ef4c1316ea6>>.
- Millington, James D.a., Michael B. Walters, Megan S. Matonis, Edward J. Laurent, Kimberly R. Hall, and Jianguo Liu. "Combined Long-term Effects of Variable Tree Regeneration and Timber Management on Forest Songbirds and Timber Production." *Forest Ecology and Management* 262.5 (2011): 718-29. Web.
- Sarr, Daniel A., David E. Hibbs, Jeffrey P.a. Shatford, and Rick Momsen. "Influences of Life History, Environmental Gradients, and Disturbance on Riparian Tree Regeneration in Western Oregon." *Forest Ecology and Management* 261.7 (2011): 1241-253. Web.
- Waterman, Jayson R. "The Influence of Mountain Laurel on Regeneration in Pitch Pine Canopy Gaps of the Coweeta Basin, North Carolina, U.S.A." *Canadian Journal of Forest Research* 25.11 (1995): 1756-762. Web.

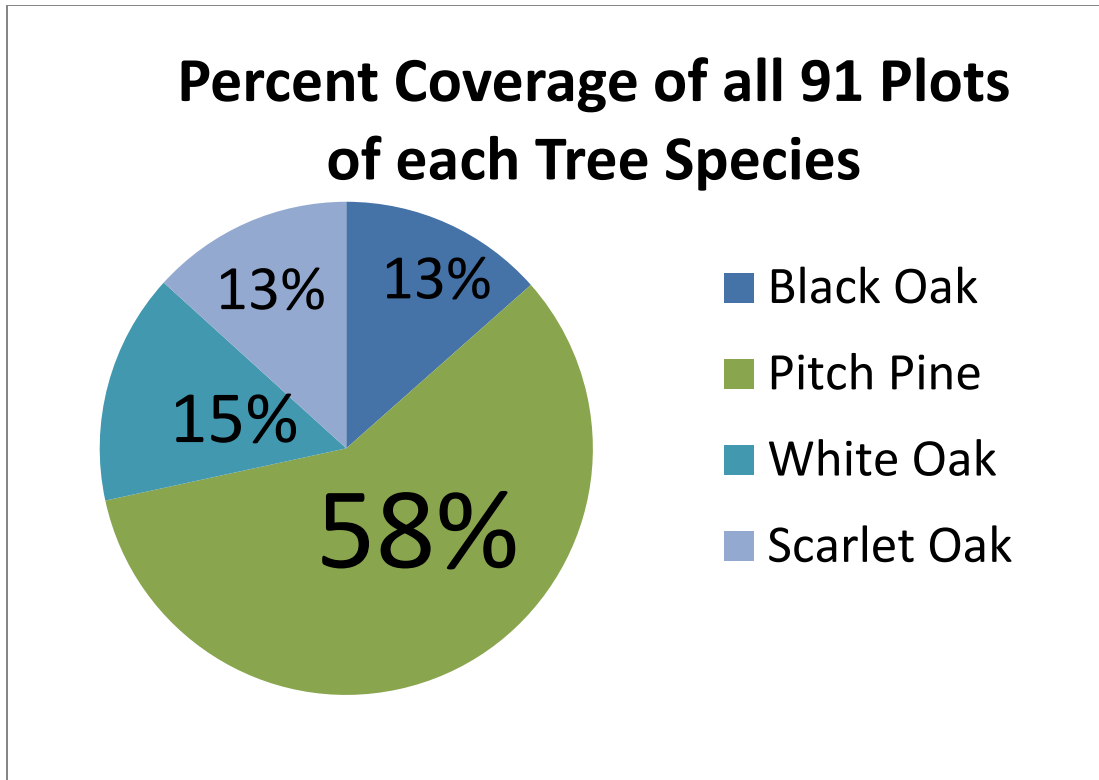


Figure 1: Pie chart of the percent coverage of each of the four major tree species found within the 91 plots.

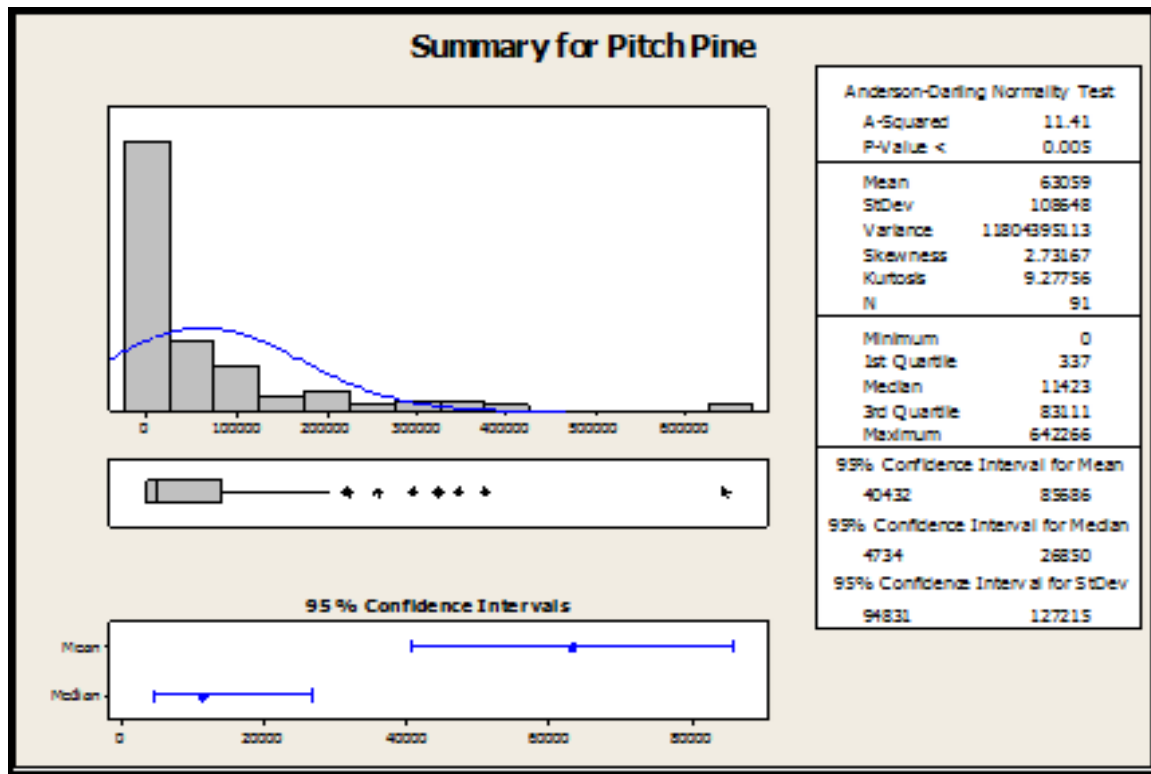


Figure 2: Distribution of Pitch pine trees found within the 91 plots.

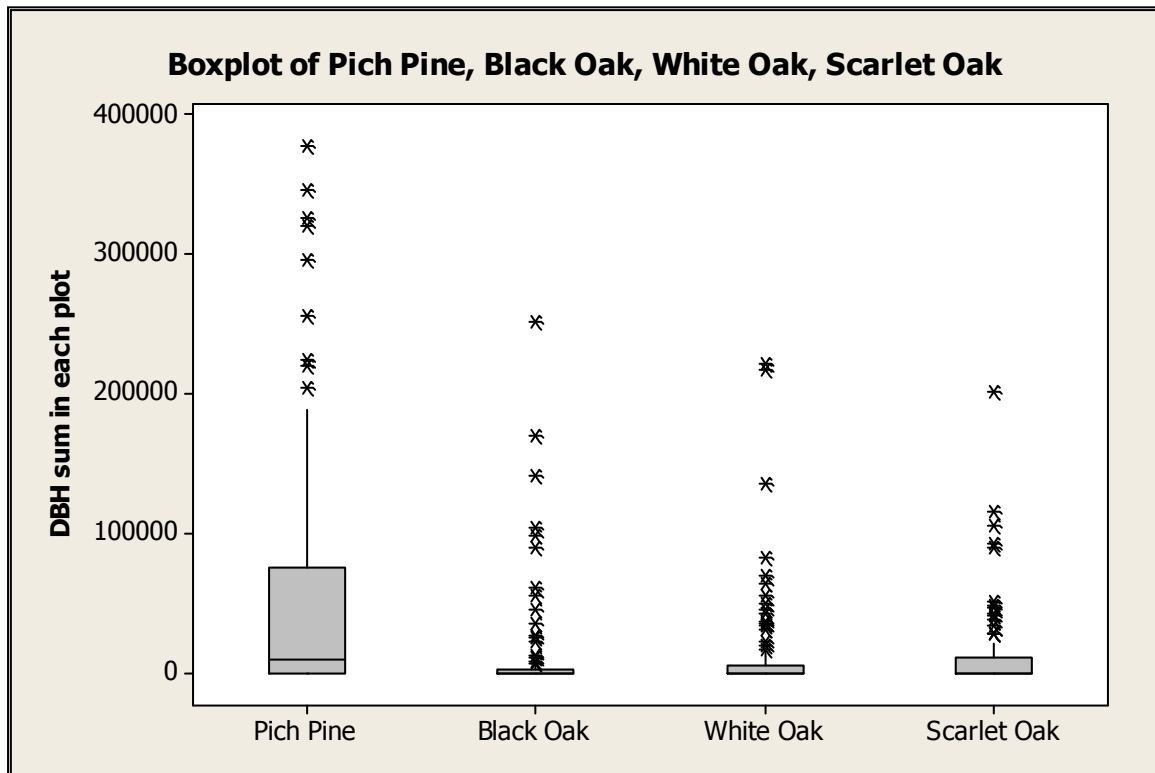


Figure 3: Boxplots of the four major species of trees with outliers.

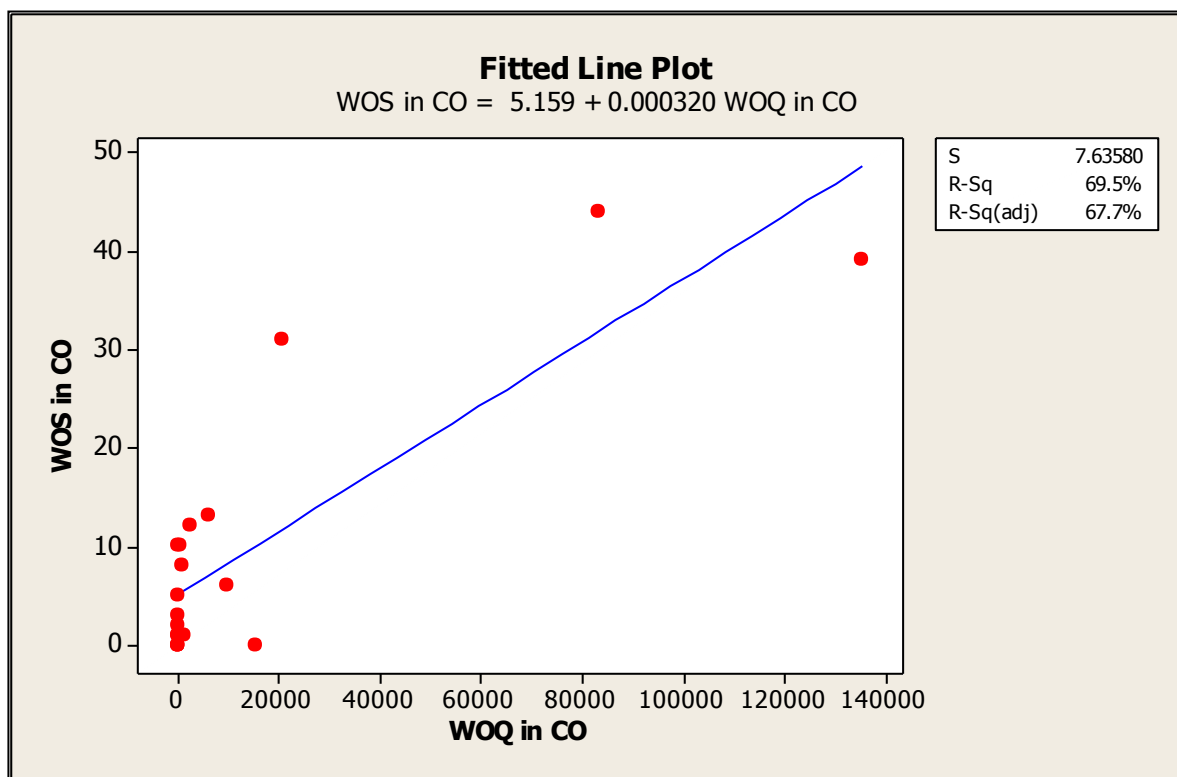


Figure 4: Regression model of white oak seedlings and white oak trees within the coastal oak community.

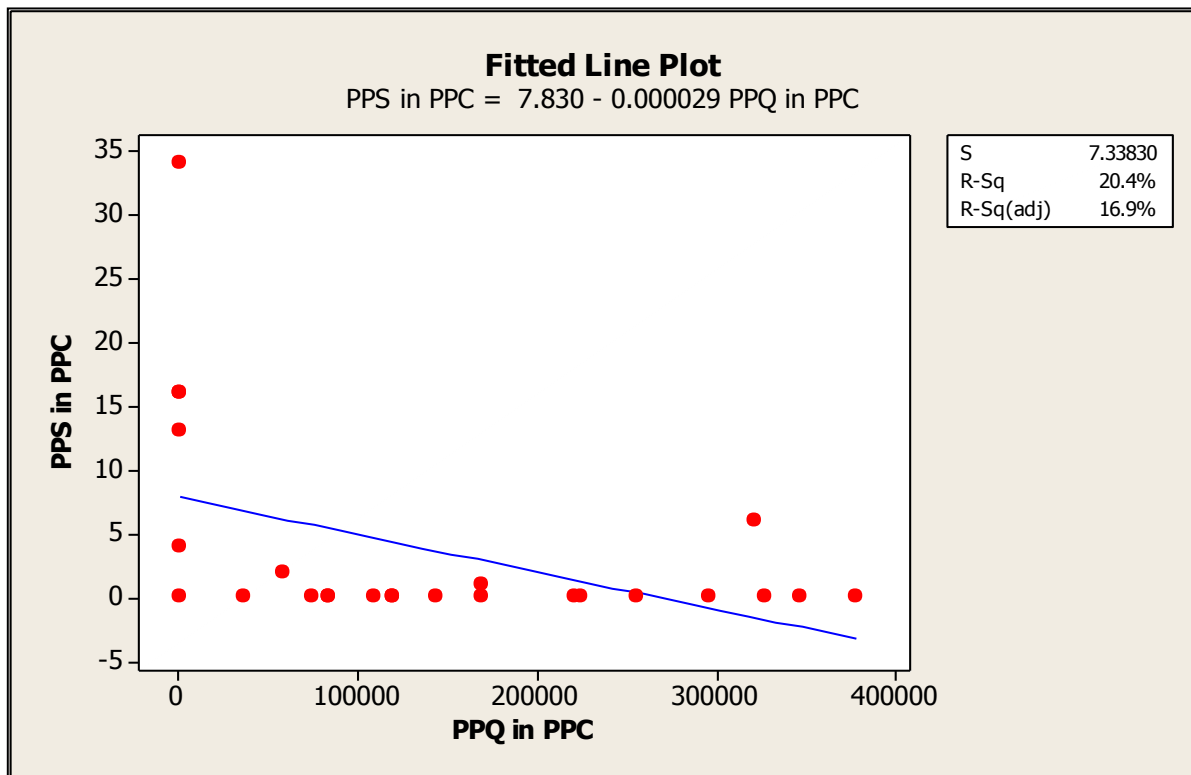


Figure 5: Regression model of pitch pine seedlings and pitch pine trees within the Pitch pine forest communities.

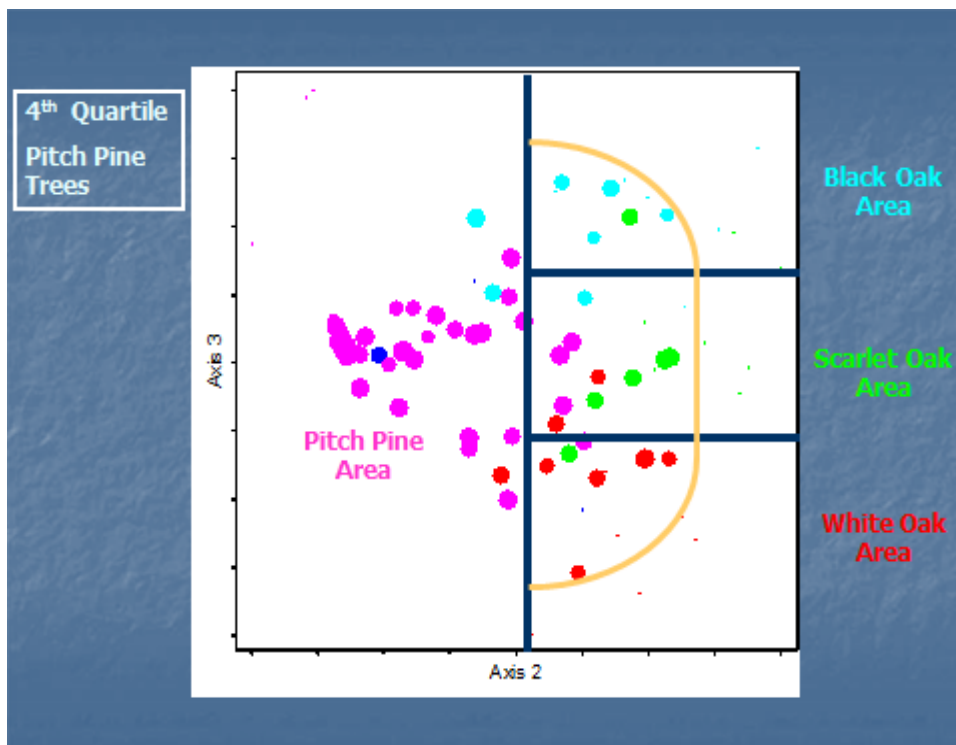


Figure 6: PC ORD output showing the invading 4th quartile trees into oak communities

