Spatial Boundaries of the Impact of Harvest on Beetle Ecology

Undergraduate Thesis Project - Purdue University Department of Entomology

George Ogilvie-Russell

2022-2023

Abstract

In our current era of climate change and urban development, understanding and improving forestry management practices is as important as ever. While methods vary widely, both shelterwood and partial clear-cutting offer the potential for more sustainable management practices. Much has been studied on the impact of these measures on both within clearing and greater forest ecology. However, there has been little research into the specific spatial and temporal parameters of the impact of these cuts. In this study, I looked into the extent to which these clear-cut and shelterwood harvests impact beetle ecology through space-time. Specifically, I looked at beetles from the family Cerambycidae through 12 years of data from the hardwood ecosystem experiment (HEE). We hypothesized that post-harvest there would be a radiating wave of increased diversity moving through space-time. Instead, we found the opposite effect, where diversity was pulled towards the treatment areas from the surrounding forest. This suggests that these sorts of management practices may have an intense impact on the distribution of the surrounding forests' cerambycid population.

Introduction

Cerambycidae, referred to by the common name of long-horned beetles, is a family of beetles characterized by elongated cylindrical bodies and black sweeping antennae, often three times longer than the body (Milne 1980). It is one of the largest and most ecologically diverse families, with many members of major economic importance. (Rossa 2020) Larvae primarily feed internally on a wide range of trees, anywhere from live to dead, dependent on the species of beetle. Adults have a more diverse palette, feeding on a variety of different biomass, everything from rotting trees to pollen from flowers. Due to their larvae's niche as wood borers, cerambycids are a family full of economically and ecologically important members. Species that feed on living trees can be especially problematic, a role often filled by invasive members of the family such as *Anoplophora glabripennis* and *Anoplophora chinenses*. However, the larvae of the majority of the family feed on weakened, dead, and decaying wood, making them an important part of the decomposition process. Additionally, adults play an important role in pollinating any number of flowering plants as well as acting as prey for a variety of different species, such as woodpeckers (Wang 2017).

The Hardwood Ecosystem Experiment (HEE) is a 100-year-long study of forests and forestry management practices. Starting in 2006, HEE's goal was to understand the "ecological and social impact of forest management through a replicated series of study areas established across 730 hectares into Indiana state forests" (Kalb 2013). The primary exploratory variable of the experiment was a collection of different management treatments applied to randomly selected landscapes. For this experiment in particular we looked at nine landscape areas consisting of three treatments; control, even-aged, and uneven-aged.

No Harvest

The three no-harvest units control for the study. They exist to be compared to the harvest groups acting as a baseline for the forest. They still receive the same monitoring and trapping that the harvesting units received.

Even-Age

The three even-aged landscapes were comprised of a combination of clear-cut and shelterwood harvesting practices.

Clear Cut

In the clear cuts, all woody stems greater than 30.48 cm in diameter at breast height were harvested. After that, all harvested woody stems were removed all non-standing oak, hickory, ash, tulip poplar, and black walnut species were felled or chemically treated, and the remaining trees were cut to within 15 cm of the ground. All vines were also removed and chemically treated on both ends.

Shelterwood

The shelterwood treatment is made up of a three-stage system (Smith 1997). A preparatory cut in 2008/2009 was done to remove bead story and understory layers with a timber stand improvement treatment. Several small overstory Kohl's were also removed with the specific intent not to create canopy gaps. 5 to 10 years after an additional establishment cut, focused on removing poorly formed canopy and sub-canopy trees will occur. Trees will be retained if they possess the following qualities; vigorous crowns with ample seed source or are of the species oak or hickory. A final overstory removal cut will occur 5 to 10 years after this not to exceed 20 years after the initial cut.

Uneven-Aged

The uneven-aged landscapes had patch-cutting with a selection of single trees. These patches ranged from .4-2 hectares within the greater landscape unit as seen in Figure 1. This management type is based on the current silver culture practices of the Indiana Department of Forestry. Single Tree selection occurs in order to maintain a properly balanced stand structure, with the goal of trees with a variety of ages and sizes across the unit (USDA 2003).

Buffers

Around each of the nine research areas existence surrounding buffer area is managed by the Indiana Department of Forestry. These areas do not receive treatment but are monitored and in our case trapped. These areas allow us to understand the permeating impact of the different management practices on the surrounding forest.

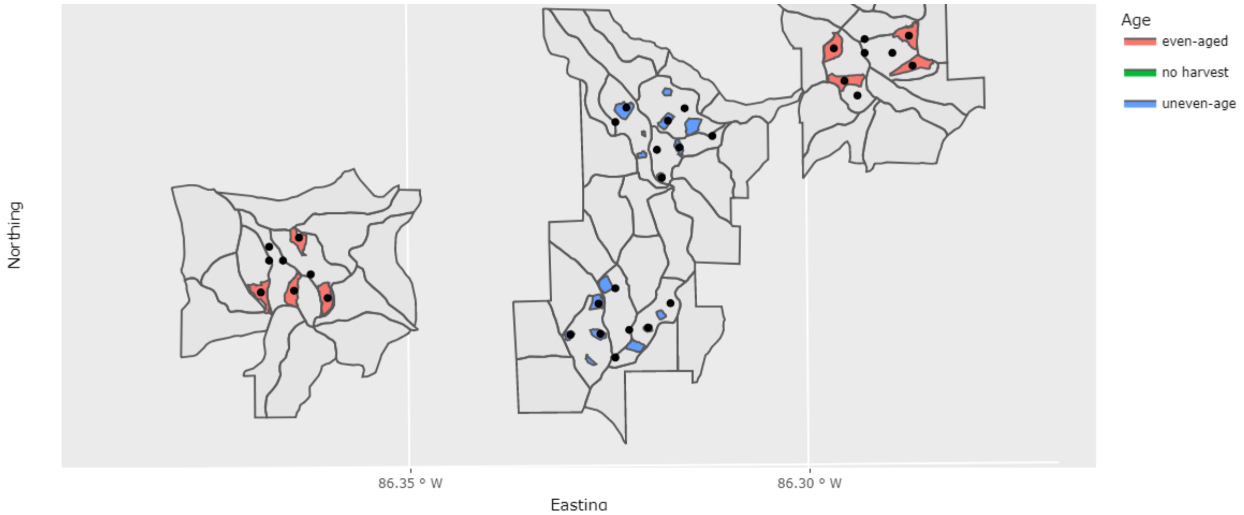

Figure 1: Rendered plot of the bottom four management units and their surrounding buffer areas. Two are even-aged and two are uneven-aged.

Methods

To collect our data we used a variety of different traps, panel traps, crossed-pane window traps, purple sticky traps, and Lindgren multiple-funnel traps across a 12-year. Data was collected every summer using student labor. The traps were dispersed throughout both the treatment areas and surrounding untreated buffer zones. The traps were sampled on a three-year cycle with the first two years spent sampling traps within the treatment unit, and the third year spent sampling traps in the buffer zone. This means that across the 12 years, we have four replicants of the three-year cycle. Across these 12 years, we covered 144 different traps for 3 months a year totaling 5,184 trap months.

Once the traps were collected and emptied the resulting catch was stored in alcohol and at the end of the summer the trapped insects were brought back to the lab for sorting and counting. All non-cerambycids were removed and the remaining cerambycids were sorted into species. This data was recorded along with their trap type, trap number, and year of collection. This set makes up the bulk of my data, with the other sets being the spatial data of the traps, the spatial data of the management units and buffers, and functional grouping data from Ashley Kissick's 2016 paper, Functional diversity enhances detection of ecosystem stability and resolution of predator-prey interactions within a multitrophic community.

To collect our data we used a variety of different traps, panel traps, crossed-pane window traps, purple sticky traps, and Lindgren multiple-funnel traps across a 12-year. Data was collected every summer using student labor. The traps were dispersed throughout both the treatment areas and surrounding untreated buffer zones. The traps were sampled on a three-year cycle with the first two years spent sampling traps within the treatment unit, and the third year spent sampling traps in the buffer zone. This means that across the 12 years, we have four replicants of the three-year cycle. Across these 12 years, we covered 144 different traps for 3 months a year totaling 5,184 trap months.

Once the traps were collected and emptied the resulting catch was stored in alcohol and at the end of the summer the trapped insects were brought back to the lab for sorting and counting. All non-cerambycids were removed and the remaining cerambycids were sorted into species. This data was recorded along with their trap type, trap number, and year of collection. This set makes up the bulk of my data, with the other sets being the spatial data of the traps, the spatial data of the management units and buffers, and functional grouping data from Ashley Kissick's 2016 paper, Functional diversity enhances detection of ecosystem stability and resolution of predator-prey interactions within a multitrophic community.

First, the buffer geometries and harvest geometries were attached together to create a single shape file. Then this was overlaid with the spatial location of the traps. Then the distances from the traps to the treatment unit were calculated and stored. The traps that were within the treatment units had distances of zero. For the control, it was assumed that there was no clear area within either the buffer or the treatment area, so distances were calculated to the edge of the buffer zone. This distance was far greater than any of the distances calculated in the even and uneven-aged units.

Then the beetle data was loaded. Multiple statistics for calculated to determine beetle diversity such as Simpson's and Shannon's, but in the end we decided to go with species richness, a measure of the total number of unique species. This was calculated and associated with their respective traps which each had their own set of coordinate data in space. Once that was established a basic function was set up to analyze diversity in space. For this study, we needed to identify a greater functional grouping in order for us to break down greater ecological trends in the data set. We use this rudimentary function to test a variety of these functional groupings. The functional groupings originated from the previously mentioned paper by Ashley Kissick. The paper contained over 200 different functional groups and categorized every longhorn beetle species in the state of Indiana into them. Using this data we were able to test different functional groups to see which ones experienced the greatest impact from the treatment areas on a category-to-category basis.

After testing a variety of different functional groups such as plant part feeding behavior and adult feeding behavior, we ended up finding host condition to be the strongest grouping variable. Host condition is made up of five different categories, all stages in the life of a tree, and tells you if a specific species of beetle feeds on trees during that stage of their life. The stages are; living, weak, dying, dead, and decaying. We were able to test this by looking for patterns in the spatial distribution of the different groups. This section alone took four months due to the number of functional groups and the laundry list of testing mechanisms. Once we decided upon a functional group and host condition, we compared linear and nonlinear regression to see which one had a stronger match with the data. We ended up deciding to go with linear due to its comparably high P value and r squared across the different categories. Additionally, it would be far easier to analyze once we moved into three-dimensional space-time. After this, we decided to condense the three functional groups of feeding on weak, dying and dead hosts into one, as the majority of species that fall into one of these categories fall into all three. Finally, to account for the large amount of noise and variation in the forest on a year-to-year basis, we temporally adjusted the data by the control. To do this we found the mean diversity score of the control in each year and subtracted it from all the non-control trap diversity scores. We compared this to the unadjusted data and found that it did a great job of eliminating most of the year-to-year variation of the greater forest from the data (Figure 2 & 3).

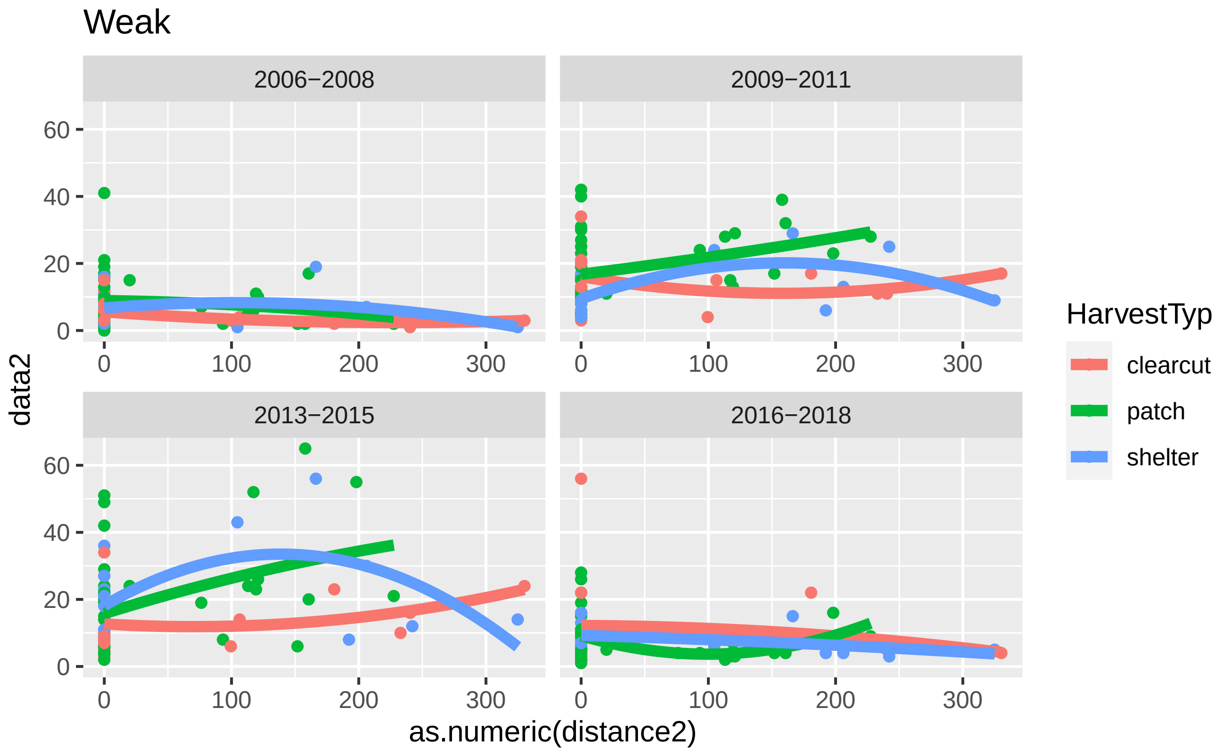

Figure 2: Plot of species richness of cerambycids that feed on weakened trees as seen in traps over space, not adjusted for control

Figure 3: Plot of species richness of cerambycids that feed on weakened-dying-dead trees as seen in traps over space, adjusted for control

Results

To analyze our processed data through spacetime we ran a multi-linear regression model (Figure 4). This showed us a significant relationship between our adjusted species richness and space-time, with p-values of .008, 6x10^-11, and 3x10^-7. Now that we know a relationship exists, the last step is to visualize it.

One of the goals coming into this experiment was to try and look for a permeating wave through space-time in relation to species diversity, in order to check for this we need to develop a plot that shows change in three dimensions. We decided to go with the wire mesh plot as it would allow for visualization of space-time as a topography. One issue however is that due to the 3-year cycle of sampling the axis of time did not fully act as a continuous variable. To solve this visualization, we first started out with an empty plot where X was time, Y was distance, and Z was adjusted species richness (ASR). We then generated the regression line of the adjusted species richness for each of the four three-year cycles. We suspended these regression lines in the center of each of their three-year increments in the wire mesh. This gave us a 3D plot with four sloped lines in space, all limited to the Y and Z axes. Then, in the way a rain fly is pulled across the tent, poles we laid a continuous 3D mesh across these four lines, where the specific spatial coordinates were determined as linear regression points between parallel points on the four 2D regression lines. This gave us three plots that could show radiating effects through space-time, one for each of the functional group categories (Figure 5,6,7).

All three plots showed a strong wave signal that was opposite to the one we hypothesized. Instead of a radiating wave of diversity pushing out across space-time, starting from year zero inside the treatment area, instead, we had waves of diversity pulled towards the treatment area across space-time. These waves differ from group to group, with more similar patterns between the weakened-dying-dead and the decay groups. In all three of the plots, we see that diversity increases over space-time as you get closer to the treatment areas and decreases as you get farther away. The wave then dissipates as you approach the final year replicant group, returning to the mean. While the timings and extent differ from group to group the same clear pattern exists in all of them.

```
## [1] "Residual standard error: 9.293 on 282 degrees of freedom"
## [2] "Multiple R-squared:  0.04735,\tAdjusted R-squared:  0.03384 "
## [3] "F-statistic: 3.504 on 4 and 282 DF,  p-value: 0.008214"

## [1] "Residual standard error: 18.51 on 282 degrees of freedom"
## [2] "Multiple R-squared:  0.1727,\tAdjusted R-squared:  0.1609 "
## [3] "F-statistic: 14.71 on 4 and 282 DF,  p-value: 6.259e-11"

## [1] "Residual standard error: 13.4 on 282 degrees of freedom"
## [2] "Multiple R-squared:  0.118,\tAdjusted R-squared:  0.1055 "
## [3] "F-statistic: 9.431 on 4 and 282 DF,  p-value: 3.614e-07"
```

Figure 4: summary of all 3 host conditions multi-linear regression statistical values of the adjusted species richness across space and time, with time grouped discretely into 4, 3 year replicates. Top is living host group, middle is weak-dying-dead host group and bottom is decay host group.

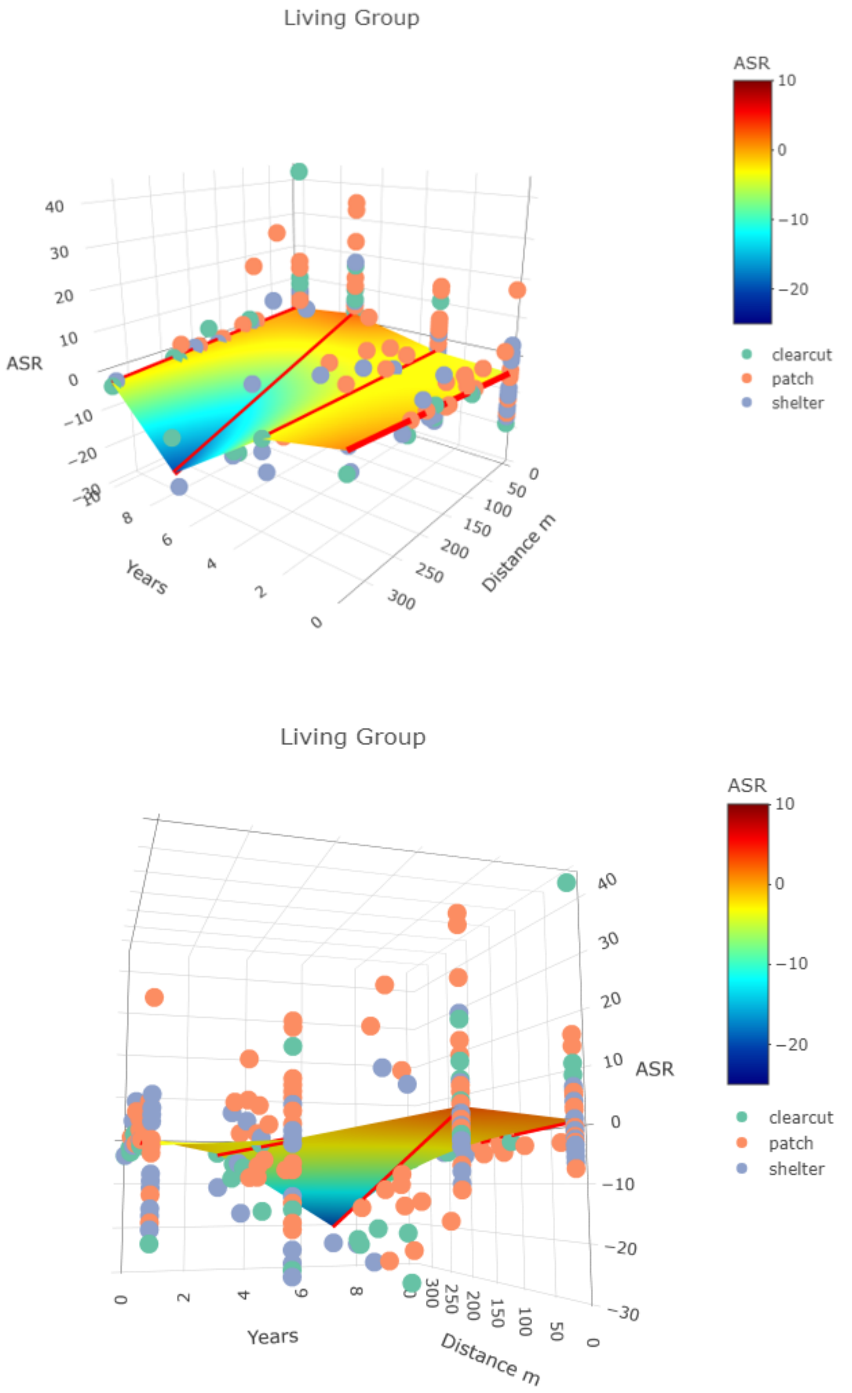

Figure 5: 3D wire mesh cerambycids that feed on living trees showing adjusted species richness (ASR) across space (meters) - time (years since treatment). A shift occurs after the second replicate group, around the 6-10 year range, where there is a wave of diversity moving out from the buffer to closer to the treatment areas. This effect levels off at the fourth replicate and returns to the mean

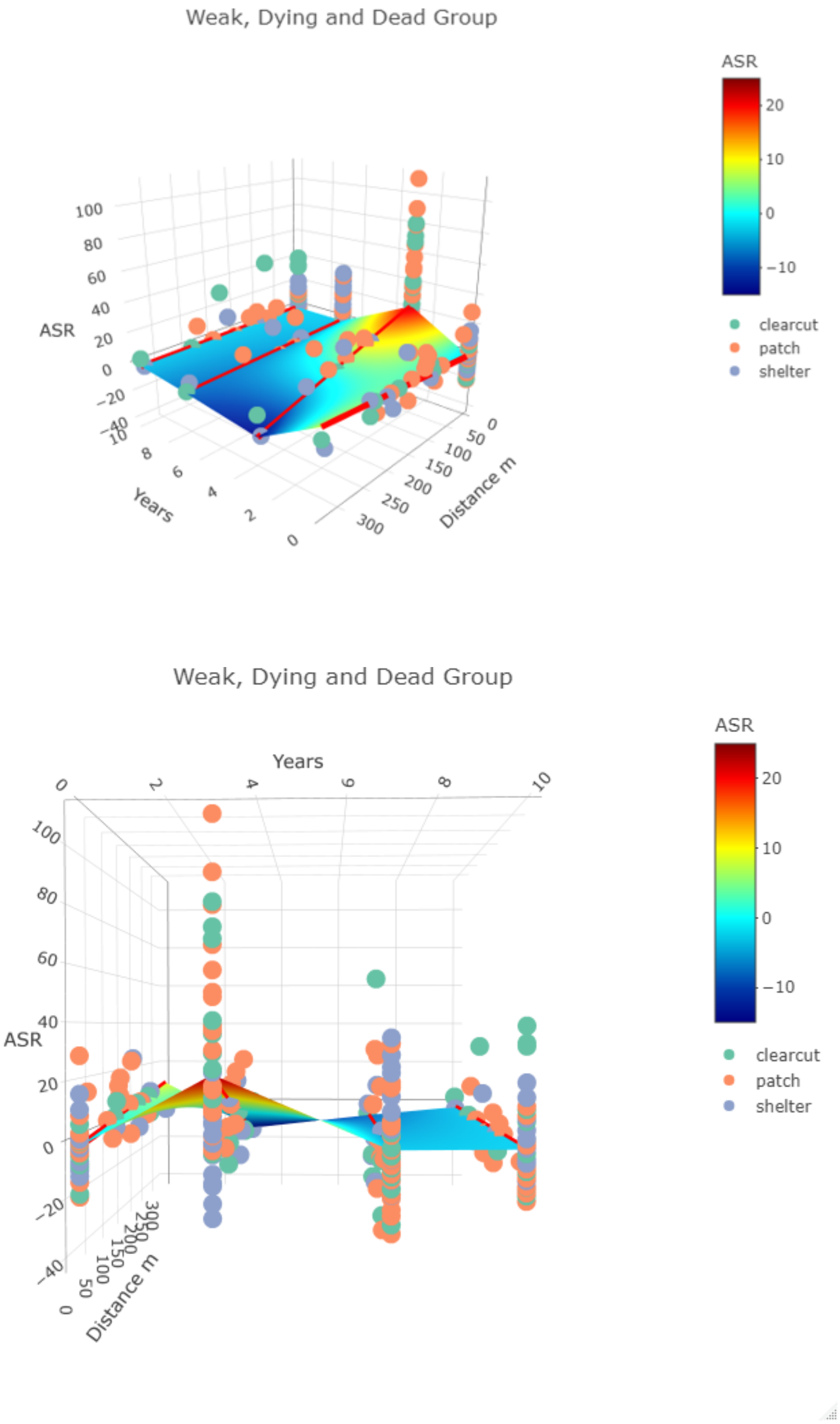

Figure 6: 3D wire mesh cerambycids that feed on weakened-dying-dead trees showing adjusted species richness (ASR) across space (meters) - time (years since treatment). A shift occurs after the first replicate group, from years 0-5, where the diversity shifts away from the outskirts of the buffer, towards the treatment areas. After this, it levels off and returns to the mean.

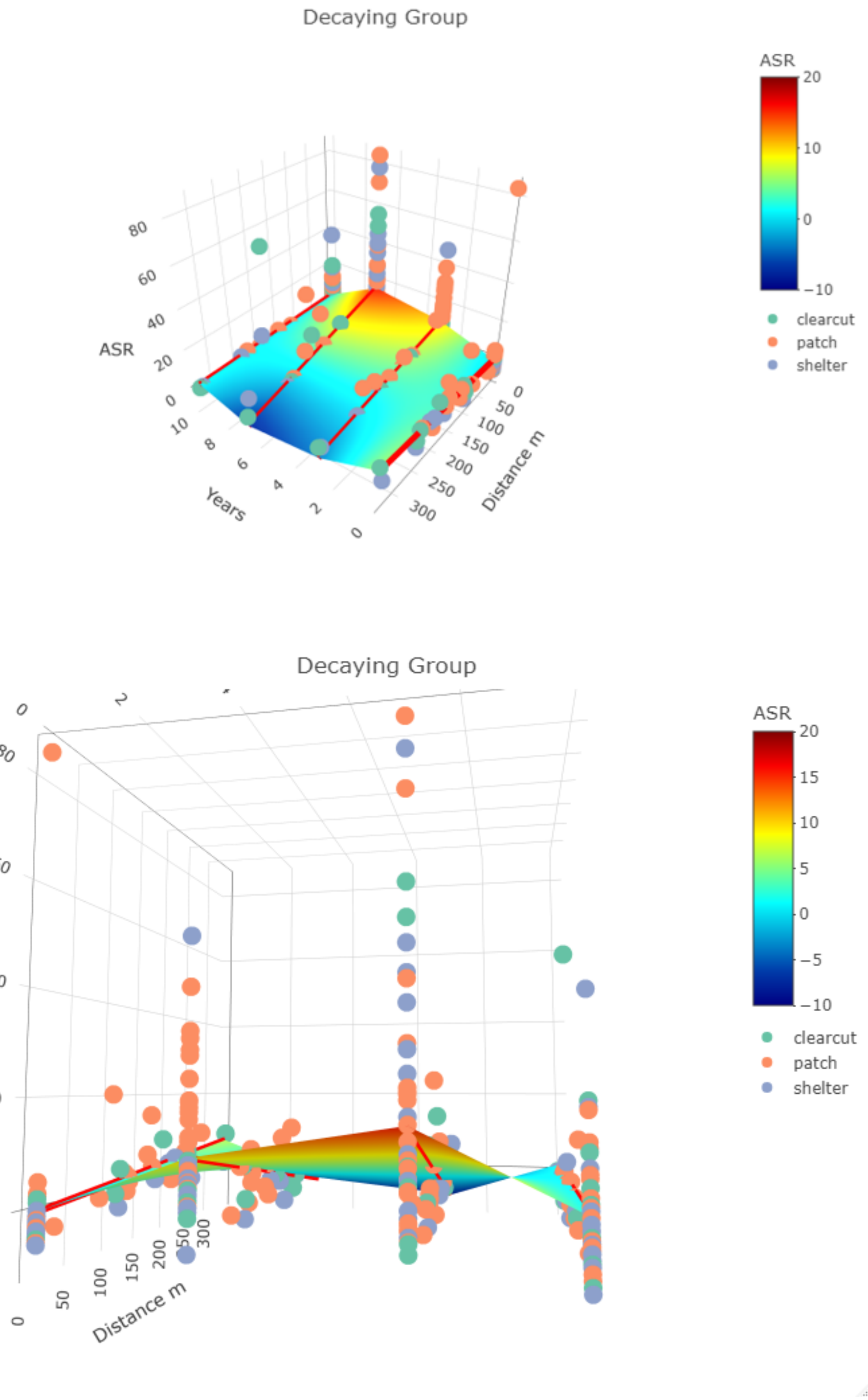

Figure 7: 3D wire mesh cerambycids that feed on decaying trees showing adjusted species richness (ASR) across space (meters) - time (years since treatment). Similarly to Figures 5 and 6, this plot shows a vacuum-like wave, where diversity is pulled towards the treatment areas around the time of the second and third replicant group, years 3-8, and then returning to the mean

Discussion

From the plots, we can conclude that our hypothesis was incorrect. However, they also do not support the null hypothesis, as there is a clear trend in the data. The plot suggests that the different treatments, even-aged and uneven-aged, both pulled in the surrounding diversity in the immediate years after their application. Additionally, this effect is not instantaneous and takes time to permeate outwardly. This effect also begins to dissipate 5 to 10 years after the initial treatment. While this is not the effect we were expecting, it is not an irrational outcome. Clear cuts allow for a variety of new species to quickly establish in areas previously dominated by dense overstory. Large numbers of shrubs, flowering ephemerals, and understory trees are able to thrive in the disrupted areas. As cerambycids are a diverse group of specialists this opening is likely to attract many of these species. As these species must come from somewhere, it is not irrational that they are pulled from the surrounding forest area. Additionally, the functional groups line up well with their specific timings. The weakened-dying-dead (WDD) group is the first to shift with effects visible in the second temporal replicant. The remnants of the cut trees left standing fall within the category of dying and dead, so we would expect to see an immediate migration for the WDD group. The decaying group sees its greatest impact during both the second and especially the third replicant. This lines up with the remaining dead trees beginning to decay. Finally, the living group sees its greatest effect in the third replicant and minor effects in the fourth. This lines up, as new trees would begin to grow in the treatment areas attracting beetles that feed on living trees. Unfortunately, there is no data from before the treatment as it would be helpful to see the living functional groups trapping data from before the treatments. We would expect to see a massive drop off after the treatments as the number of living trees in the treatment areas was massively reduced during the treatment. However, as the data is normalized to the control, we can see that in the first year, the living functional group has a regression line with a positive slope in an intercept below zero. This suggests that when compared to the rest of the forest, there initially was a drop off in the diversity of living host feeders in the treatment areas that dissipated as you get farther from the treatment areas. This aligns with what would expect to see.

One potential issue with the data in the study is sample size. Even though we have over 5,000 trap months, we are limited in replicants due to the sheer size of the study. Each replicant contains three years of trapping data across hundreds of traps. Thankfully, we should have access to two additional replicants of data, covering the recent six years of the Harwood Ecosystem Experiment, soon. Once we have these we can look to see if the patterns continue to regress to the mean, or if longer-term effects exist in the data. Another potential issue, is it the data is unevenly collected throughout the three replicants. In an ideal scenario, the traps would be sampled in a random order over the course of the three replicants, the due to the size of the experiment across tens of thousands of hectors this is untenable. We try to reduce this effect by grouping the years as replicants instead of using time as a strictly continuous variable, however, it still does not account for all variation that occurs in less than the three-year time frame. Additional errors in data such as misidentification and incorrect data entry may exist, but due to the size of the data and the number of individuals responsible for cataloging and entering the data this type of error should be distributed normally across the data set.

For future analysis, the addition of two replicants will greatly increase the statistical power of the study. Further investigation into the difference between the types of treatment, clear-cut, shelterwood, and uneven-age silviculture, would be more tenable with more data. Understanding the complex dynamics of forest management methods such as this can potentially provide new and exciting practices. For instance, the results of this study may inform improved species survey practices for beetles, as the use of clearcuts may help to concentrate beetle diversity into a small area for trapping. Other potential options such as clearcuts and pheromone traps could be used in combination to pull in specific invasive species from a greater forest area. Our results suggest the ability of these cuts to concentrate specific members of a cerambycid population based on their feeding habits at different times. Overall this shows promise to reduce the total analyzed or treated land area necessary to capture a specific amount of beetle diversity or specific cerambycid type. More research is necessary to understand these dynamics and the specifics of their application, but overall this study shows promise.

References

Milne, L., & Milne, M. (1980). *The Audubon Society Field Guide to North American Insects and Spiders* (8th ed., p. 590). Alfred A. Knopf, Inc.

Kissick, Ashley Lorraine, *"Functional diversity enhances detection of ecosystem stability and resolution of predator-prey interactions within a multitrophic community"* (2016). Open Access Dissertations. 960. https://docs.lib.purdue.edu/open_access_dissertations/960

"Study Design – Hardwood Ecosystem Experiment." Hardwood Ecosystem Experiment, Purdue University, heeforeststudy.org/study-design/. Accessed 1 Dec. 2023.

Kalb, Rebecca A.; Mycroft, Cortney J. 2013. *The hardwood ecosystem experiment: goals, design, and implementation.* In: Swihart, Robert K.; Saunders, Michael R.; Kalb, Rebecca A.; Haulton, G. Scott; Michler, Charles H., eds. 2013. *The Hardwood Ecosystem Experiment: a framework for studying responses to forest management.* Gen. Tech. Rep. NRS-P-108. Newtown Square, PA: U.S. Department of Agriculture, Forest Service, Northern Research Station: 41-51.

R. Rossa & J. Goczał (2021) *Global diversity and distribution of longhorn beetles* (Coleoptera: Cerambycidae), The European Zoological Journal, 88:1, 289-302, DOI: 10.1080/24750263.2021.1883129

Smith, D.M.; Larson, B.C.; Kelty, M.J.; Ashton, P.M.S. 1997. *The practice of silviculture.* 8th ed. New York: John Wiley and Sons, Inc. 537 p.

Shin, N.R., Shin, S., Okamura, Y., Kirsch, R., Lombard, V., Svacha, P., Denux, O., Augustin, S., Henrissat, B., McKenna, D.D. and Pauchet, Y. (2021), *Larvae of longhorned beetles (Coleoptera; Cerambycidae) have evolved a diverse and phylogenetically conserved array of plant cell wall degrading enzymes.* Syst Entomol, 46: 784-797. https://doi.org/10.1111/syen.12488

Lacey, E.S., Ginzel, M.D., Millar, J.G. et al. *Male-Produced Aggregation Pheromone of the Cerambycid Beetle Neoclytus acuminatus acuminatus.* J Chem Ecol 30, 1493–1507 (2004). https://doi.org/10.1023/B:JOEC.0000042064.25363.42