THE RELATIONSHIP BETWEEN CATTLE GRAZING

AND SMALL MAMMAL COMMUNITY STRUCTURE

ON SOUTH TEXAS RANGELANDS

A Thesis

by

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ABSTRACT

Cattle grazing is known to affect ecosystems and potentially alter wildlife abundances and distributions. Small mammals are one group that respond quickly to environmental change and can be used to monitor ecosystems. The goal of this project was to determine how cattle grazing affects small mammal community structure in southern Texas rangeland dominated by tamaulipan thornscrub and coastal sand plain vegetation. My study focused on the East Foundation's San Antonio Viejo Ranch located in Jim Hogg County, Texas where I conducted an observational study within five relatively large (~61 ha) cattle exclosures that were constructed in 2011. Following nearly ten years of cattle exclusion, this study consisted of sampling small mammals and vegetation in a gradient design to understand the extent of the impact of cattle grazing on the small mammal community.

I expected to find that the small mammal community makeup (i.e., species richness, minimum number alive, sex ratios, age ratios) to be unique in at least two locations along the gradient: in the center of the cattle exclosure, and at the farthest point sampled outside of the cattle exclosure, with a possibility of unique makeup along the boundary of the exclosure. I found that minimum number alive, and age ratios were influenced by the presence of cattle while sex ratios and species richness were not.

My research provides insight on how cattle influences small mammal communities. By sampling in a gradient manner, I was able to evaluate the impact of the edge effects on this target community which is vital since fragmentation and edge effects at various scales could be negatively impacting wildlife on private ranches. My results suggested that small mammal relative abundance is negatively correlated with cattle grazing. Also, my data supported the presence of an edge effect on age ratios with young individuals being caught most often along

the edge of the exclosure. By ensuring small mammal diversity and abundances are not severely

negatively impacted, ranch managers can help maintain environmental processes that small

mammals are involved in which could increase native forage for cattle.

CONTRIBUTORS AND FUNDING SOURCES

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1. INTRODUCTION

Ecosystems change over time in response to natural and human causes. These changes impact distribution and abundance of wildlife and the ways wildlife interact with the surrounding environment. Cattle grazing is one example of a human influence that is known to impact ecosystems by removing live and dead plant materials (Altesor et al. 2006), and by modifying soil nutrient content (Bakker et al. 2004; Steffens et al. 2008). Cattle grazing can also benefit savanna ecosystems by suppressing woody encroachment (Bueno et al. 2011).

Cattle grazing and other human activities can cause various scales of fragmentation to ecosystems and therefore influence the organisms associated with that scale. According to Hodges (2008), landscapes cannot be determined to be connected or fragmented without considering a specific organism or group of organisms. This is because landscape connectivity or lack thereof depends on scales of movement and land use, which can vary tremendously depending on the organism. This scale-specific fragmentation can lead to an increase in edge effects at a similar spatial scale. An edge effect is a change in species abundance and community structure in the ecotone between two contrasting ecosystems (Murcia,1995; Ewers and Didham, 2006). Studies have shown that edge effects influence population dynamics and species persistence in fragmented areas (Zurita et al. 2012). The concept of edge has been argued to be an artifact of spatial scale. This is because at a small scale, edges can be infinite while at a larger scale, ecosystems that once seemed different are now similar (Guthery, 2008). Ting and Shaolin (2008) described three spatial scales at which edges and their subsequent effects can be identified (1) large-scale type: biome ecotone, (2) meso-scale type: ecological ecotone and (3) small-scale type: community ecotone (Ting and Shaolin, 2008). In this case, I researched landscape

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fragmentation and the subsequent edge effects associated with the small mammal community (small-scale type) caused by cattle grazing.

Small mammals, particularly rats, mice, squirrels, moles and rabbits, are known to respond quickly to environmental changes due to their rapid reproductive cycles (Bueno et al. 2011; Baumgardt et al., 2019). Since they respond quickly, this means that shortly after a disturbance or while a disturbance is occurring, the small mammal community will begin to shift. This makes small mammals an ideal focal group for understanding disturbances and changes to ecosystems that are currently being impacted. While small mammals are important indicators of changing environments, they are also of interest because they are a valuable food source for many predators (Baumgardt et al. 2019), disperse seeds which increases plant species diversity, are engaged in nitrogen cycling (Bakker et al., 2004) and carbon exchange (Liu et al., 2013), and can be used to assess grassland health (Bueno et al. 2011). Small mammals are also seed predators which may influence seedling establishment (Schnurr et al., 2004).

Studies have found varying differences in small mammal abundances, sex ratios and age ratios between grazed and ungrazed locations, but they have not quantified the extent of these impacts. Most research on small mammals have used paired points of grazed and ungrazed locations. Data from paired plots were then compared to look for differences (Jones, 2000). While range types and grazing levels can be vastly different across these studies, as a general review I will discuss some of their findings. A few examples of studies that used paired points include a study by Bueno et al. (2011) in Canada who found that, for both meadow voles (*Microtus pennsylvanicus*) and deer mice (*Peromyscus maniculatus*), the age ratio was significantly different between ungrazed and grazed plots. They found that adults were found more often in ungrazed sites (adult/juvenile ratio of 3.48) while juveniles were found more often

in grazed sites (adult/juvenile ratio of 0.84). Their reasoning for this was that adults were outcompeting juveniles for the areas with more resources (Bueno et al. 2011). Another study that used paired points (Pearson et al., 2001) conducted in Montana found a significant difference in sex ratios of deer mice between areas that had dense vegetation and areas that did not. Bowers and Smith (1979) also found a significant difference in sex ratios of deer mice in Tasmania. They claimed that female deer mice selected areas with more vegetation cover or areas with higher plant water potential, which resulted in a tradeoff between resource abundance and range size. In this study females had smaller ranges, while males were occupying larger ranges (Bowers and Smith, 1979). Others in China found negative correlations between small mammal species diversity and grazing intensity (Cao et al., 2016). Cao et al. (2016) explained that small mammal species diversity decreased with an increase in grazing intensity (Cao et al., 2016). They claim this is because grazing decreases structural complexity of vegetation which is critical for many small mammal species (Cao et al. 2016). A review of the research that has been conducted on this topic indicates that many studies have used data that were only collected during one year (Schieltz et al. 2016).

Cattle ranching has been a major Texas industry for nearly three centuries (Richardson and Hinton, 2010) however, no studies addressing the impact of cattle grazing on small mammals has been conducted in the south Texas region. I conducted my research to understand the relationship between cattle grazed areas and ungrazed exclosures with small mammal communities in the south Texas region. After nearly ten years of cattle exclusion, I sampled small mammals in and around several relatively large cattle exclosures of about 60.7 hectares (~150 acres) in a gradient method. My objectives and predictions for this project were:

1. To determine the relationship between cattle grazing and small mammal community structure:

    a. Prediction: Small mammal community structure (species richness, abundance, sex ratios, age ratios) will be different in at least two locations along the gradient; in the center of the cattle exclosure, and at the farthest point from the cattle exclosure, with a possibility of distinct difference along the boundary of the exclosure. The prediction was that the center of the cattle exclosure will be far enough from grazed areas to allow the small mammals in that area to be least impacted by the edge effect of the surrounding cattle grazing. Additionally, I hypothesized that the farthest point away from the exclosures would have individuals that were not occupying the ungrazed areas, therefore they are least impacted by the ungrazed exclosures. The boundary of the exclosure may have a unique make up of individuals using both grazed and ungrazed areas.

    b. Prediction: The zones in between these locations will be transitional or a combination of the two distinct structures found around them.

    c. Prediction: Adult females will be caught within the exclosure most frequently and juvenile males will be caught outside the exclosure most frequently, i.e. female to male sex ratio will be negatively correlated with distance from the center of the exclosure and adult to juvenile ratio will be negatively correlated with distance from the center of the exclosure.

d. Prediction: Minimum number alive (MNA) (described below) and species richness will be negatively correlated with distance from the center of the exclosure.

2. To determine if cattle altering the vegetation structure was causing the changes in the small mammal community structure:

    a. Prediction: The alteration on the vegetation structure will be a driving force that is changing the small mammal community structure because small mammals have known preferences for vegetation traits for food, cover, and predator evasion. Vegetation parameters (vegetation height, live cover, litter depth) will present similar linear trends as the small mammal community parameters.

3. To determine if a small-scale (community level) edge effect is influencing small mammal distribution:

    a. Prediction: The boundary of the exclosure will be a transition zone between the grazed and the ungrazed areas, resulting in a distinct community makeup for all small mammal community parameters: MNA, spences richness, sex ratios, and age ratios.

    b. Prediction: Sex ratio will be close to 1:1, age ratio will be close to 1:1 along the edge.

2. STUDY AREA

My study was conducted on East Foundation's San Antonio Viejo Ranch, which is located 25 km south of Hebbronville, Texas within Jim Hogg and Starr counties. The ranch's 61,000 hectares, as with its other landholdings, are used as a living laboratory to promote the advancement of land stewardship through ranching, science, and education. Mean annual temperature for this region is 22 ℃, ranging from 7℃ to 35 ℃ and the mean annual rainfall for this region is 50.3 cm. This area is comprised of two main vegetation types, tamaulipan thornscrub and coastal sandplain. The surface soil texture varies across the property. The large cattle exclosures fall mostly within the loamy fine sand category, but fine sand, fine sandy loam and loam are also present within the exclosures (Figure 1). The vegetation in and around these exclosures varies in make-up. I ranked the inside and outside of each exclosure on a scale of 1 to 5. A 5 represents an extremely dense, woody thornscrub and a 1 represents an open savanna. For all exclosures, the vegetation inside and outside was very similar and earned the same ranking. Beginning with the southmost exclosure, the inside and outside earned a rank 5. Continuing north, the second exclosure earned a 4, the third exclosure earned a 3, the fourth exclosure earned a 3, then the northmost exclosure, exclosure 5, earned a 1. The standard stocking rate ranges from 21 to 27 hectares per animal unit depending on the time of year and environmental conditions.
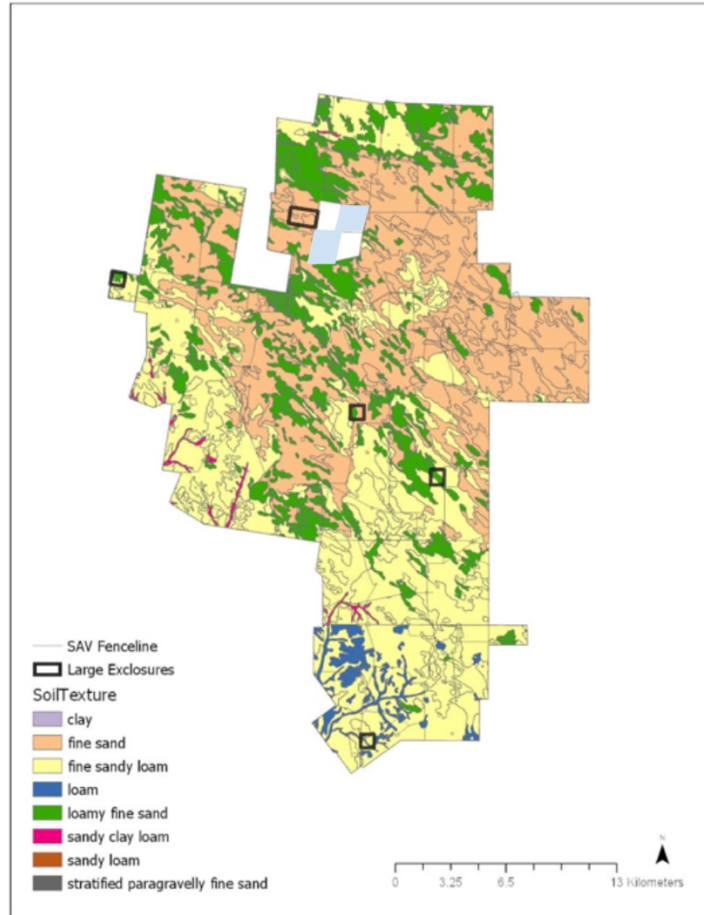
Figure 1. Surface Soil Texture Map. Surface soil texture across the San Antonio Viejo Ranch. The 61-hectare cattle exclosures used in this study are outlined in black.

The small mammals that are found in this south Texas region include the southern plains woodrat (*Neotoma micropus*), Ord's kangaroo rat (*Dipodomys ordii*), Merriam's pocket mouse (*Perognathus merriami*), hispid pocket mouse (*Chaetodipus hispidus*), northern pygmy mouse (*Baiomys taylori*), white footed mouse (*Peromyscus leucopus*), Fulvous harvest mouse (*Reithrodontomys fulvescens*), hispid cotton rat (*Sigmodon hispidus*), Mexican ground squirrel (*Spermophilus mexicanus*), northern grasshopper mouse (*Onychomys leucogaster*), and the Mexican spiny pocket mouse (*Liomys irroratus*)(Baumgardt et al., 2019). These species vary in the vegetation they use and how they use it. Some rely on tall and short grasses (*Sigmodon*

hispidus, Perognathus merriami, Reithrodontomys fulvescens) (Davis and Schmidly, 1994),

while others rely on dense woody, cactus and litter cover (*Neotoma micropus*, *Peromyscus*

leucopus, Liomys irroratus) (Davis and Schmidly, 1994). The Ord's kangaroo rat (*Dipodomys*

ordii), like most kangaroo rats, prefer sparsely vegetated areas (Davis and Schmidly, 1994). The

vegetation requirements of these species dictate their responses to and distribution around the

grazed and ungrazed areas. Some species that are associated with open vegetation types are

known to increase with the presence of grazing (*Dipodomys merriami*) (Bueno et al., 2011), and

others, that are associated with ample ground cover, are known to decrease with the presence of

grazing (*Chaetodipus hispidus*, *Reithrodontomys megalotis*, *Peromyscus leucopus*, *Sigmodon*

hispidus) (Bock et al., 1984).

3. METHODS

Five cattle exclosures were constructed in 2011 on the East Foundation's San Antonio
Viejo Ranch (Figure 2). Exclosures 1-4 were ¼ of a section (60.7 ha [150 acres]) while
Exclosure 5 was ½ of a section (~150 ha [~375 acres]).
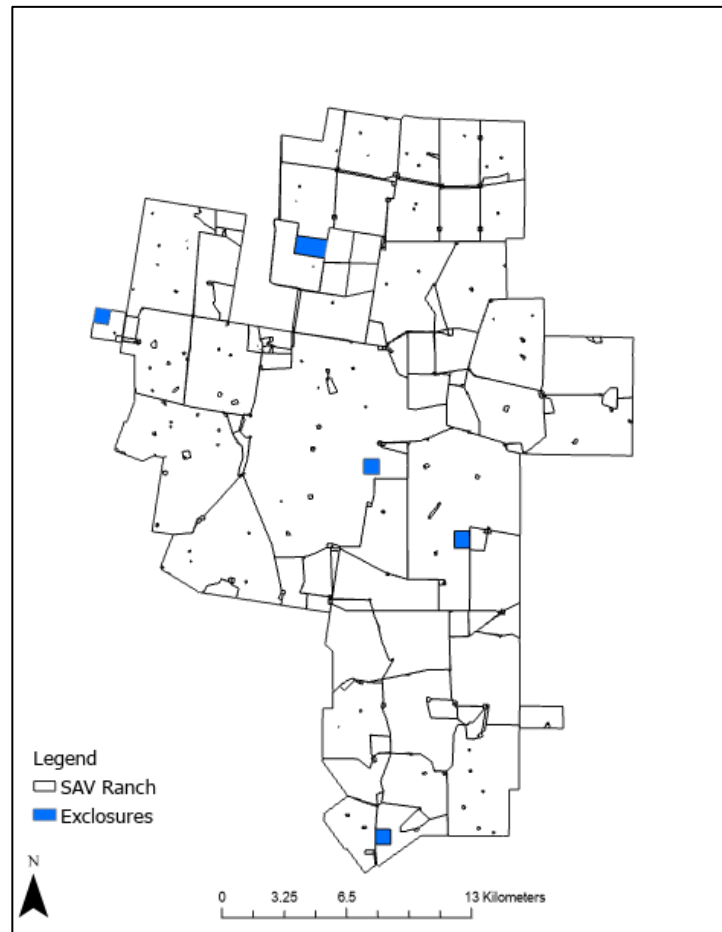

Figure 2. Exclosure Map. Map of the San Antonio Viejo Ranch with exclosures highlighted in blue. The southmost
exclosure was considered exclosure 1 and the northmost was considered exclosure 5.

These exclosures were not placed randomly, but rather were designed to capture the
dominant range sites on the San Antonio Viejo Ranch. The range sites that are represented by

these exclosures include: (1) gray sandy loam, (2) loamy sand/ red sandy loam, (3) loamy sand/ sandy (4) sandy loam/red sandy loam and (5) sandy/sandy hills.

I trapped small mammals using extra-large (10.2 x 11.4 x 38 cm, model XLF15) and large (7.6 x 9.5 x 30.5 cm, model XLK) Sherman-live traps (H. B. Sherman Traps, Inc., Tallahassee, FL) during the months of May – July for two consecutive years (2019 and 2020) (Texas A&M University IACUC permit 2016-0296). Small mammals were trapped at each of the five exclosures in a gradient manner in two directions. The impact of "no cattle grazing" was localized to the exclosure, therefore sampling this way allowed me to understand the extent of the impact outside of the exclosure (Morrison, 2008). Traps were placed in a 38 x 3 configuration with a 19 x 3 proportion of the grid being within the exclosure and the other 19 x 3 proportion being outside of the exclosure (Figure 3) with an inter-spacing of 25 meters, equating to a 925 meter long transect. These grids began in the center of the exclosure. My target community included all small mammals in and around these exclosures.

The distance of the gradient was greater than or equal to the maximum distance traveled by the small mammal species present at the San Antonio Viejo Ranch in a given day. For example, the Ord's Kangaroo Rat, one of the largest species on SAVR, typically travels <500 meters (COSEWIC, 2006). The southern plains Woodrat, another large species on SAVR, has been shown to travel a maximum distance of 55 meters in a day, with a home range of up to 3,840 square meters (Henke and Smith, 2000). This is important because I assumed that the population was closed during the trapping period.

The sampling design was meant to be an assessment line along a gradient rather than a grid since I was evaluating how individuals used the areas in and around exclosures and not estimating overall density. Rather than overall density, I used minimum number alive (MNA)

which was the total number of unique individuals trapped at a given area (Ferreira and van Aarde, 2000; Yarnell et al., 2007). I used this measure to compare relative density along the sampling gradient. Additionally, this method allowed me to use all of the capture data regardless of the number of captures, unlike calculating density where there are minimum capture/ recapture requirements (Dickman et al., 1989).
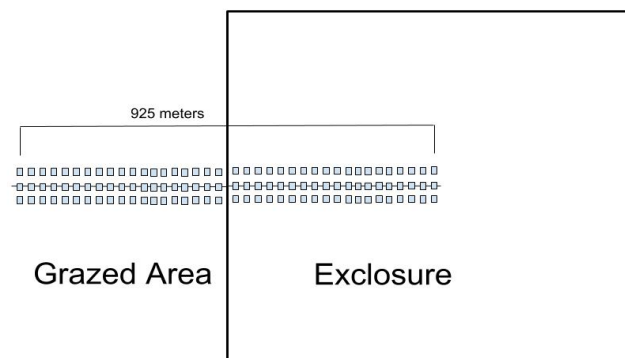
Figure 3. Trapping Diagram. Visualization of trapping configuration in relation to the exclosure. Blue squares represent Sherman-live traps. This was be conducted in two random directions on the San Antonio Viejo Ranch in 2019 and 2020.

Since cattle exclosures were not constructed randomly, to eliminate sampling bias, I sampled the exclosures in random directions. The traps followed a gradient from the center of the exclosure toward either (1) north, (2) south, (3) east, or (4) west. This was completed one time per year in two directions that were randomly selected without replacement. In the case of Exclosure 4, only two directions (south and east) are owned by the East Foundation and so I sampled in these directions. Also, for Exclosure 5, cattle were deferred from the pastures directly

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north and therefore I did not sample in that direction. Each year, all exclosures were sampled on two occasions, from May to mid-June and from mid-June to the end of July.

I baited traps in the late afternoon (about 1800 hours) prior to the first trap night. Then, I checked and closed the traps each morning following baiting. The traps were baited with about a teaspoon (4.9 mm^2) of a peanut butter and rolled oats mixture prepared in approximately a 4:1 ratio by weight. Each trap was also provided with a Nestlet square (Ancare) for bedding material. All trap nights were conducted consecutively unless overnight temperatures were forecasted below 4 °C or a high probability of precipitation was forecasted. I implanted a passive integrated transponder (PIT) tag (HPT8 MiniChip; 8.4mm X 1.4 mm, 0.036 g; Biomark, Boise, Idaho) under the skin between the shoulder blades of each animal captured. I weighed and determined the sex of each individual, then I released the animals at the location of capture. After day 1, individuals were scanned for PIT-tags prior to processing and their unique code was recorded if they had been previously caught. I conducted sampling for five consecutive nights since this was when species accumulation reached a clear asymptote (Figure 4). This is important because you then have a good estimate of the community makeup for that sampling interval when the accumulation curve plateaus (McCain, 2004; Colwell and Coddington, 1994).
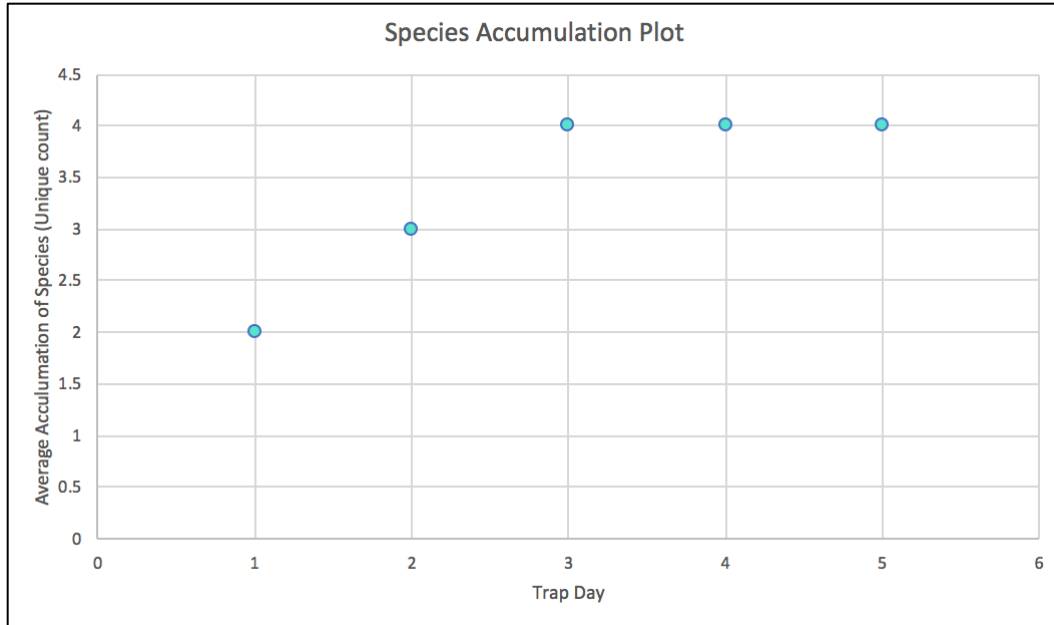
Figure 4. Species Accumulation Plot. The species accumulation curve calculated using data collected in 2019 and 2020 on the San Antonio Viejo Ranch in Jim Hogg county, Texas. A clear asymptote is reached by trap day 5.

Vegetation Sampling

Using a square meter quadrat, I sampled the vegetation for each grid during the week that particular grid was being sampled. I sampled the vegetation 25 meters off of the grid, running parallel to the trapping gradient to avoid the impact of trampling the vegetation prior to sampling. This allowed me to link the vegetation cover with the small mammals sampled during that same time period. Sampling was conducted along each gradient every 40 meters, for a total of 24 sample points per transect in a similar method to many studies that quantify the impact of cattle grazing on vegetation (Rosenstock,1996; Amiri et al. 2008; Hayes, 2003). From the meter square, I estimated percent litter cover, percent live herbaceous cover. I also measured the depth of the litter and the height of the live plant material. These measurements target the aspects of the vegetation that the small mammals are using and/or are reliant on (these vegetation preferences

are explained within the introduction). Additionally, I included an estimation of percent cover of cattle activity. Cattle activity was determined by cattle fecal matter or clear hoof action.

This information was used to identify zones in which the vegetation was distinct and where cattle activity was most prevalent along the gradient. I hypothesize that I would be able to distinguish three different vegetation zones (1) ungrazed areas, (2) grazed areas, and (3) transition zone approximately 50 m around the fence line.

4. ANALYSIS

Following the completion of each year, I organized the data by unique individual using the PIT- tag number. For each individual that I caught, I averaged the trap numbers they were caught at. Once averaged, the trap number was rounded so that every individual could be assigned a whole number for trap occurrence between 1 (center of the exclosure) and 38 (farthest point from exclosure). I then calculated the community elements per trap number for each year. Based on my hypotheses, I had four small mammal community parameters that I examined: (1) sex ratio, (2) age ratio, (3) minimum number alive and (4) species richness.

1. For sex ratio, I summed the total number of females and males captured per trap number. Then I divided the total number of females by the total number of males and vice versa. A sex ratio is undefined if the count of the second element is zero therefore, I used female to male ratio because it had more defined ratios than male to female since there were several traps where female individuals were not captured.

2. For age ratio, I summed the total number of adults and young captured per trap number. Then I divided the total number of adults by the total number of young. An age ratio is undefined if the count of the second element is zero therefore, I used young to adult ratio because it had a greater number of defined ratios than adult to young since there were several traps where young individuals were not captured.

3. For MNA, I summed the total number of individuals caught at each trap number.

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4. For species richness, I counted each unique species that was caught at each trap number. For example, if I caught 3 different species at trap number 4 throughout 2019 I would record species richness as 3 for trap number 4.

I completed each of these steps for 2019 and for 2020.

For cattle activity, there was obviously no recorded cattle activity inside of the cattle exclosure. Therefore, I analyzed these data without the data from the inside of the cattle exclosure to explore where cattle were most active relative to the location of the exclosure.

For small mammal population parameters, I first compared the data from inside of the exclosures to the data from outside of the exclosures. Then using the residual plots, I determined if the data presented a linear or a nonlinear trend (Larsen and McCleary, 1972). If the community parameter presented a linear trend, a mixed linear model was performed. For each mixed linear model year was included as a random effect. To accurately run a mixed linear model, I ensured that the assumptions of the model were met. The data must be normally distributed, have a homogeneous variance, and no autocorrelation is present (Muller and Stewart, 2006). To test normality in R, I used the Shapiro-Wilks test of normality. A significant p-value indicates that the data were not normally distributed. If the raw data were not normally distributed, I log transformed the data and retested the data with the Shapiro-Wilks test of normality. To ensure that the data had a homogeneous variance, I looked at the regression plots. If variance increases as the independent variable increases, the data do not have a homogeneous variance. If these assumptions could not be met, I performed a Kendall–Theil regression which is a nonparametric approach to linear regression when there is one independent and one dependent variable (De Toffol et al., 2009).

If a linear trend was not present, the data were grouped into two categories, (1) located inside of the cattle exclosure or (2) located outside of the cattle exclosure and then compared using a factorial ANOVA which included year as an independent variable. If the data were not normally distributed then I conducted a Kruskal-Wallis test, a non-parametric ANOVA equivalent using R (McKight and Najab, 2010).

I conducted threshold regressions which delineated one state from another, if such a numerical structure was present in the data. A breakpoint-based threshold model looks at the relationship between the response (here the small mammal community structure variables) and explanatory (here the distance from the center of the exclosure) variables, which changes at some point, termed the threshold (Muradian, 2001). This change is usually assumed to be a change in slope, however, this change does not need to be continuous, i.e., it can be a step function. The threshold does not need to change at a single point but can occur over a transition zone (Toms and Villard, 2015). Thresholds can occur as a breakpoint with no transition, a breakpoint with a smooth transition, a breakpoint as a step function or as a breakpoint with a step tranision (Toms and Villard, 2015).

I used Stata 16 (StataCorp. 2017. Stata Statistical Software: Release 15. College Station, TX: StataCorp LLC), which determined an optimal number of thresholds that delineate the states (Hansen, 1999; Stata, n.d.). Stata creates models with varying numbers of thresholds then using BIC, the models are ranked. The model that best represents the data had the optimal number of thresholds. The states between these thresholds are different.

BIC selects a model by finding a model that is most probable from a Bayesian perspective. BIC considers fit, complexity and sample size when ranking models (Johnson and Omland, 2004). I used BIC for model selection because in general, BIC is better for hypothesis

testing when there is a limited number of predictor variables while AIC would be better for complex forecasting models (Aho et al., 2014).

I tested models with 0,1 and 2 thresholds: (0) was no distinct change points along the gradient and thus potentially no difference in community structure along the gradient, (1) were two distinct states, most likely representing inside and outside of the exclosures, and (2) were three distinct states, most likely representing inside, outside and the boundary of the exclosure.

5. RESULTS

In 2019, I had a total of 853 captures which represented 439 unique individuals and 10 different species. The southern plains woodrat (*Neotoma micropus*), Merriam's pocket mouse (*Perognathus merriami*), and the hispid pocket mouse (*Chaetodipus hispidus*) made up a majority of the captures (Figure 5). In 2020, I had a total of 475 captures which represented 288 unique individuals and 7 different species (Figure 5). The southern plains woodrat (*Neotoma micropus*) dominated most of the captures. Additionally, we had a single surprising capture of a desert cottontail (*Sylvilagus audubonii*).
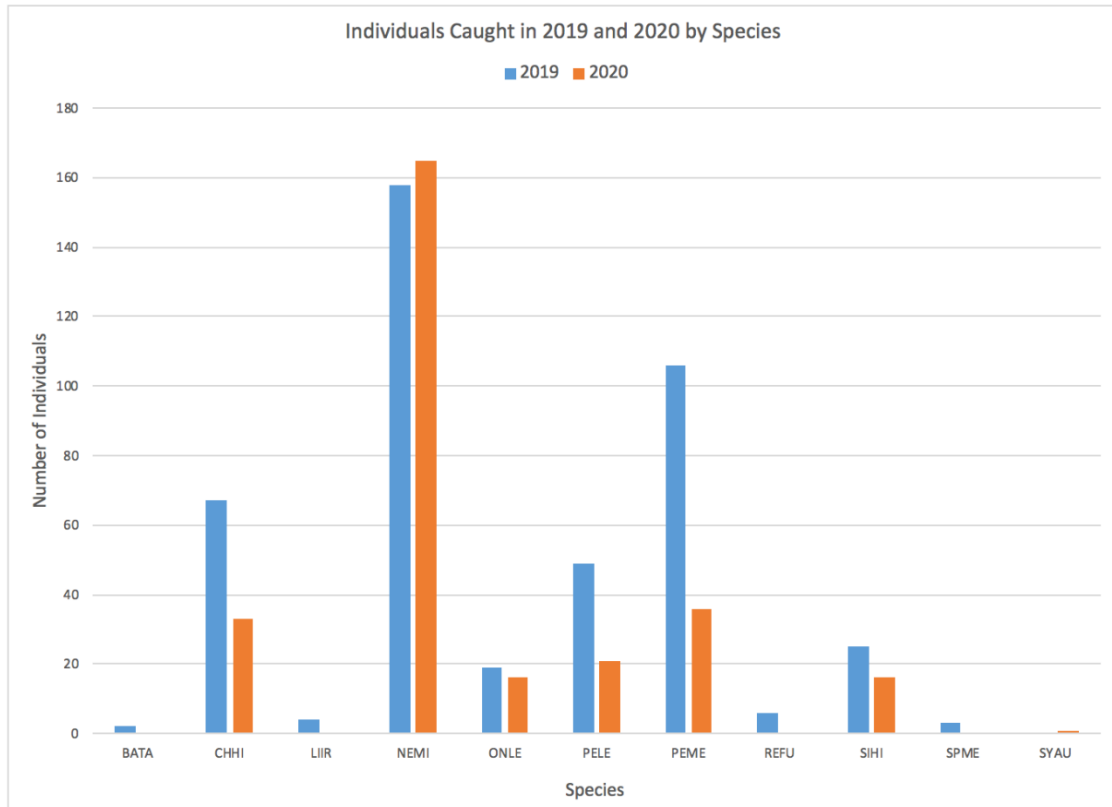
Figure 5. Species Specific Captures. 2019 and 2020 captures by species at the San Antonio Veijo Ranch in Jim Hogg county, Texas. Each species code is the first two letters of the genius and first two letters of the species name. Throughout this project, I caught *Baiomys taylori* (BATA), *Chaetodipus hispidus* (CHHI), *Liomys irroratus* (LIIR), *Neotoma micropus* (NEMI), *Onychomys leucogaster* (ONLE), *Peromyscus leucopus* (PELE)*, Perognathus merriami* (PEME), *Reithrodontomys fulvescens* (REFU), *Sigmodon hispidus* (SIHI), *Spermophilus mexicanus* (SPME), *Sylvilagus audubonii* (SYAU).

Minimum Number Alive

I predicted that minimum number alive (MNA) would be negatively correlated with the distance from the center of the exclosure.

The average MNA inside of the cattle exclosure was 10.6 while the outside was 8.6. Therefore, there was a ~19% decrease in MNA on average outside of the cattle exclosure from inside of the cattle exclosure.

The MNA data were not drawn from a normal distribution (Shapiro-Wilk normality test, p-value = 0.003) and could not be transformed in such a way that they would be normally distributed. It was determined that trap number significantly impacted the MNA (Figure 6). From the regression, with every 250-meter change in distance from the center of the exclosure, MNA decreased by 1 individual or by ~8.5%.
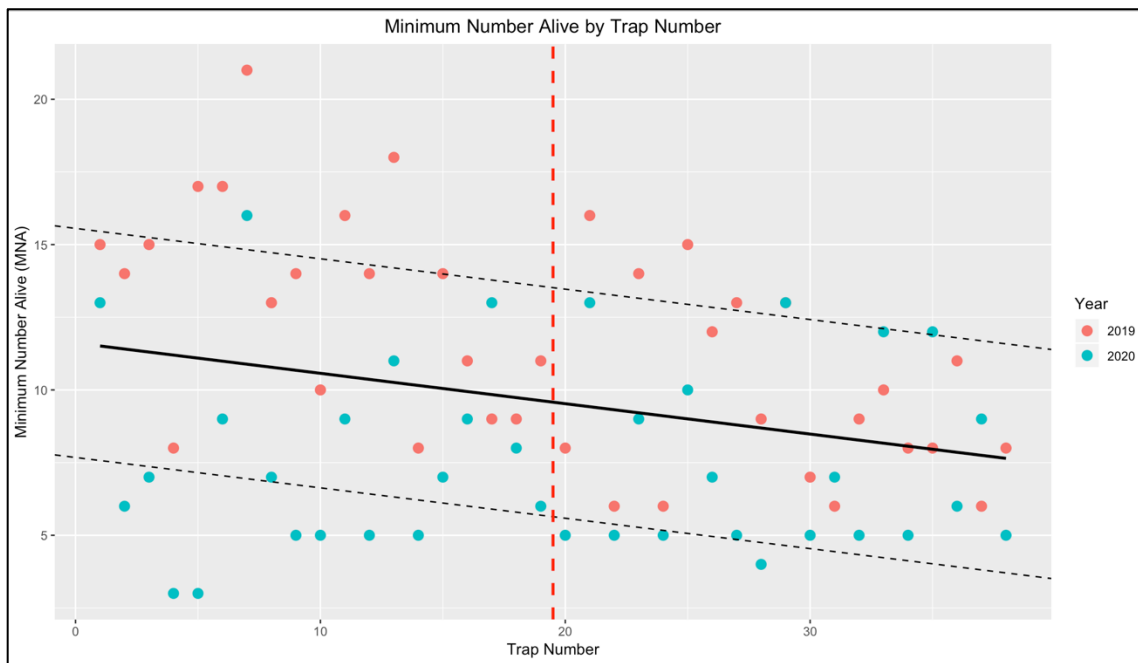

Figure 6. MNA Model. Scatterplot of the MNA data in relation to the trap number based on data collected in 2019 and 2020 on the San Antonio Viejo Ranch. The linear model is shown as the solid black line while the standard error of the model is shown as the dashed lines. The exclosure fence line is shown as the dashed red line. The points are color coated by year.

The threshold regression determined that, based on the BIC, the model that best fit these data had no thresholds.

For *Peromyscus leucopus, Perognathus merriami, Liomys irroratus* and *Spermophilus mexicanus* there were more individuals caught outside of the cattle exclosure than inside of the

cattle exclosure (Table 1). All of the *Spermophilus mexicanus* captures were outside of the cattle

exclosure. For *Baiomys taylori, Chaetodipus hispidus, Neotoma micropus, Onychomys*

leucogaster, Reithrodontomys fulvescens, Sigmodon hispidus, and *Sylvilagus audubonii* there

were more individuals caught inside of the cattle exclosure than outside of the cattle exclosure.

All of the *Baiomys taylori, Reithrodontomys fulvescens*, and *Sylvilagus audubonii* were caught

inside of the cattle exclosure (Table 1). Additionally, a large majority of *Sigmodon hispidus*

captures were inside of the cattle exclosure and they were not caught past trap number 30 outside

of the exclosure.

Species	Unique Individuals **Inside** Cattle Exclosure	Unique Individuals **Outside** Cattle Exclosure
BATA	2	0
CHHI	58	42
LIIR	0	4
NEMI	185	136
ONLE	20	15
PELE	29	41
PEME	66	76
REFU	6	0
SIHI	35	6
SPME	0	3
SYAU	1	0

Table 1. Species Captures. Species specific captures from data collected at the San Antonio Viejo Ranch in 2019

and 2020. Captures are noted to be from either inside or outside of the cattle exclosures.

Species Richness

I predicted that species richness would be negatively correlated with distance from the

center of the exclosure.

The average species richness inside of the cattle exclosure was 3.8 while the outside was 3.5. Therefore, there was a ~11% difference in species richness on average outside of the cattle exclosure from inside of the cattle exclosure however, these differences were not significant.

The raw data were not drawn from a normal distribution nor were the transformed data. There was not a significant difference of species richness inside of the cattle exclosures versus outside of the cattle exclosures (Kruskal-Wallis test, p-value = 0.382). These data do not present a linear trend and therefore violate the assumption of linearity for a linear regression model.
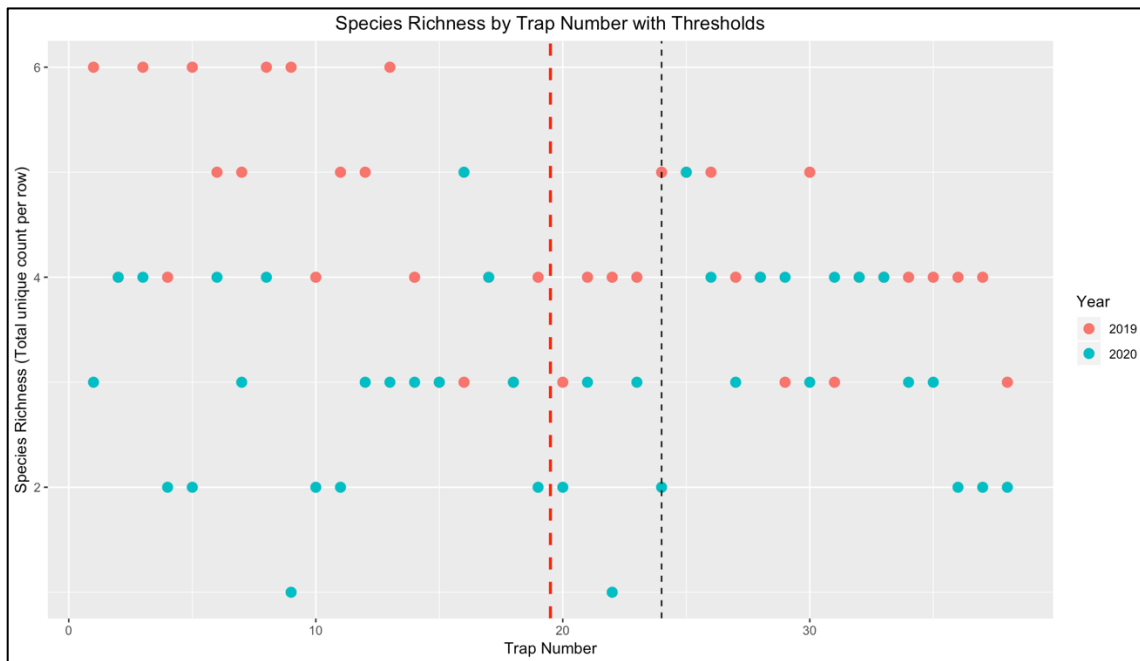

Figure 7. Species Richness Threshold. Scatterplot of the species richness in relation to the trap number based on data collected in 2019 and 2020 on the San Antonio Viejo Ranch. The exclosure fence line is shown as the dashed red line while threshold is shown as the black dashed line. Points are color coated by year.

I determined, based on the BIC, that the model that best fit these data had one threshold along the trapping gradient for species richness. The threshold was determined to be at trap number 24 (Figure 7).

While the means are not significantly different, on the inside of the cattle exclosure I caught a maximum of 6 unique species while on the outside of the cattle exclosure, I caught a maximum of 5 unique species. Additionally, ~29% of the traps inside of the cattle exclosure had 5 or more unique species present while only ~11% of traps located outside of the cattle exclosure had 5 or more unique species.

Sex Ratio

To address my prediction that females would be found most often within the boundaries of the exclosure and that males would be found more often outside of the boundaries of the exclosure, I looked at the female to male sex ratio. If the ratio was unable to be calculated (when male captures = 0), it was left out of the plot and analysis (Figure 8).

The average sex ratio (F:M) inside of the cattle exclosure was 0.94 while the outside was 1.03. Therefore, there was a ~10% difference in female to male sex ratio on average outside of the cattle exclosure from inside of the cattle exclosure however, these differences were not significant (factorial ANOVA, p-value = 0.484).

The raw sex ratio data were drawn from a normal distribution (Shapiro-Wilk normality test, p-value = 0.160) The mixed linear model indicated that trap number did not significantly impact the sex ratio (Figure 8).
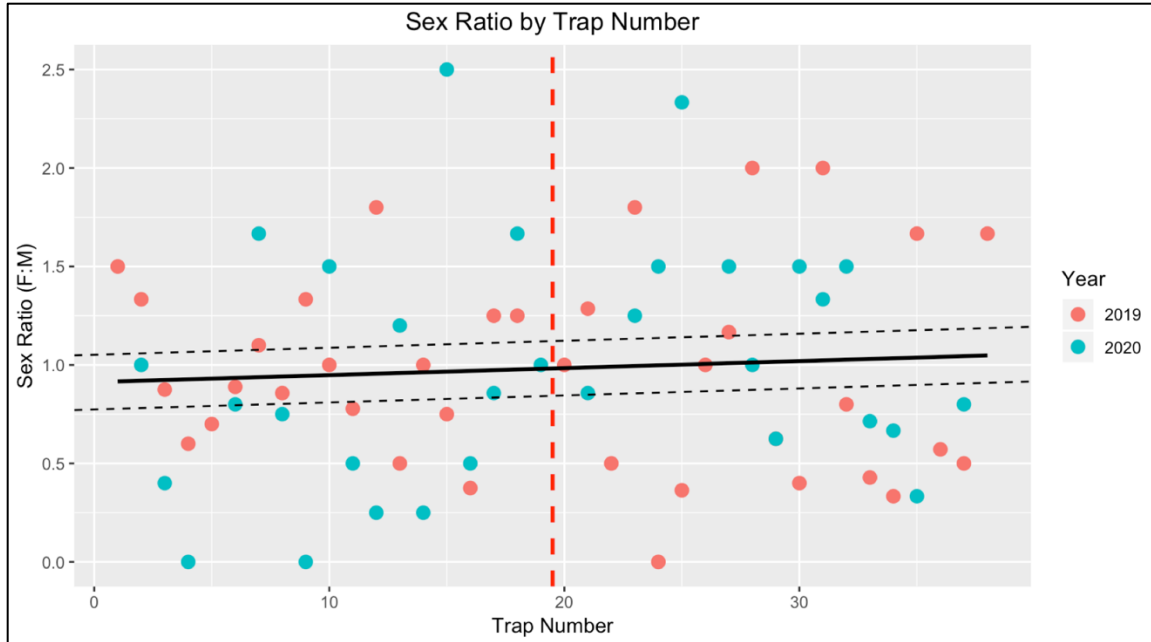
Figure 8. Sex Ratio Model. Scatterplot of the female to male sex ratio in relation to the trap number based on data collected in 2019 and 2020 on the San Antonio Viejo Ranch. The linear model is shown as the solid black line while the standard error of the model is shown as the dashed lines. The exclosure fence line is shown as the dashed red line. The points are color coated by year.

I conducted a threshold regression and using BIC, it was determined that there were 0 thresholds or changepoints along the trapping gradient for sex ratio.

Age Ratio

To address my prediction that adults would be found more often within the boundaries of the exclosure and young would be found more often outside of the exclosure, I analyzed the young to adult ratio.

The average young:adult age ratio inside of the cattle exclosure was 0.16 while the outside was 0.31. Therefore, there was a ~94% increase in the young to adult age ratio on average outside of the cattle exclosure from inside of the cattle exclosure.

The raw age ratio data were not drawn from a normal distribution and the data could not be transformed in a way to make it normal (Shapiro-Wilk normality test, p-value = 6.731e-08). These data do not present a linear trend and therefore violate the assumption of linearity for a linear regression model.
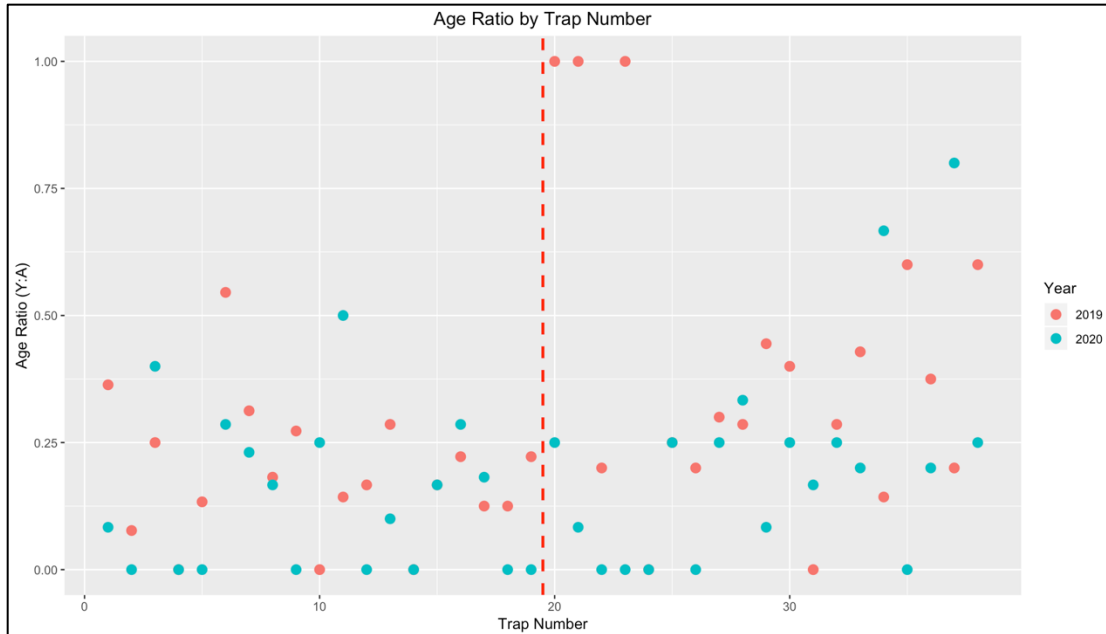

Figure 9. Age Ratio Plot. Scatterplot of the young to adult age ratio in relation to the trap number based on data collected in 2019 and 2020 on the San Antonio Viejo Ranch. The exclosure fence line is shown as the dashed red line. Points are color coated by year.

It was determined that age ratio (Y:A) inside and outside of the cattle exclosures were significantly different (Kruskal-Wallis test, p-value = 0.014). It was also determined that the model that best fit these data had 2 thresholds along the trapping gradient for sex ratio. The thresholds are located at trap number 19 and trap number 21 (Figure 10).
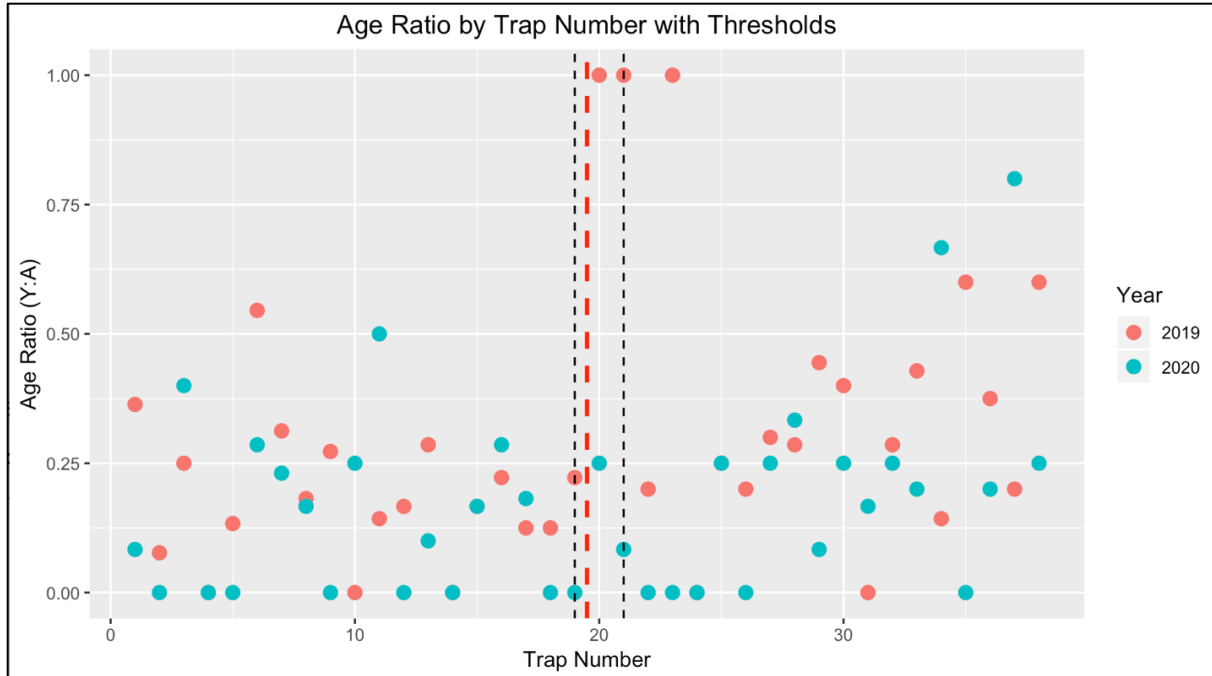
Figure 10. Age Ratio Thresholds. Scatterplot of the young to adult age ratio in relation to the trap number based on data collected in 2019 and 2020 on the San Antonio Viejo Ranch. Points are color coated by year. Thresholds are shown as black dashed lines while the exclosure boundary is shown as a dashed red line.

There were three regions of distinctness in age ratio along the trapping gradient. Inside of the cattle exclosure, age ratio averaged at about 0.17, the edge of the cattle exclosure averaged at about 0.43 and outside of the cattle exclosure averaged at about 0.28. The percent change of age ratio from the inside of the cattle exclosure to the edge of the exclosure was ~155% increase. The percent change of age ratio from the inside of the cattle exclosure to the outside of the cattle exclosure was ~68% increase. The percent change from the edge of the cattle exclosure to the outside of the cattle exclosure was ~34% decrease.

Vegetation Data

To address the prediction that the vegetation parameters will present a linear trend, I analyzed the vegetation height, litter depth and percent live cover data using linear models. In

general, the vegetation makeup in and around the cattle exclosures varied across the property however, the outside of the cattle exclosures tended to have a greater make up of desert Christmas cactus (*Cylindropuntia leptocaulis)* and prickly pear cactus (*Opuntia engelmanni)*. A majority of the inside of the exclosures were savanna type landscapes with honey mesquite trees (*Prosopis glandulosa)* scattered throughout. The two southmost exclosures, however, were made up of dense brush inside and outside of the exclosures.

Vegetation Height

The herbaceous vegetation height data were not drawn from a normal distribution (Shapiro-Wilk normality test, p-value = 0.007) and the data could not be transformed in a way to make it normal. The herbaceous vegetation height data had a linear trend. The results of the regression were significant therefore, herbaceous vegetation height is significantly predicted by the sample number (Figure 11). From the regression, with every 100-meter change in distance from the center of the exclosure, vegetation height decreased by 4 cm or by ~5%.
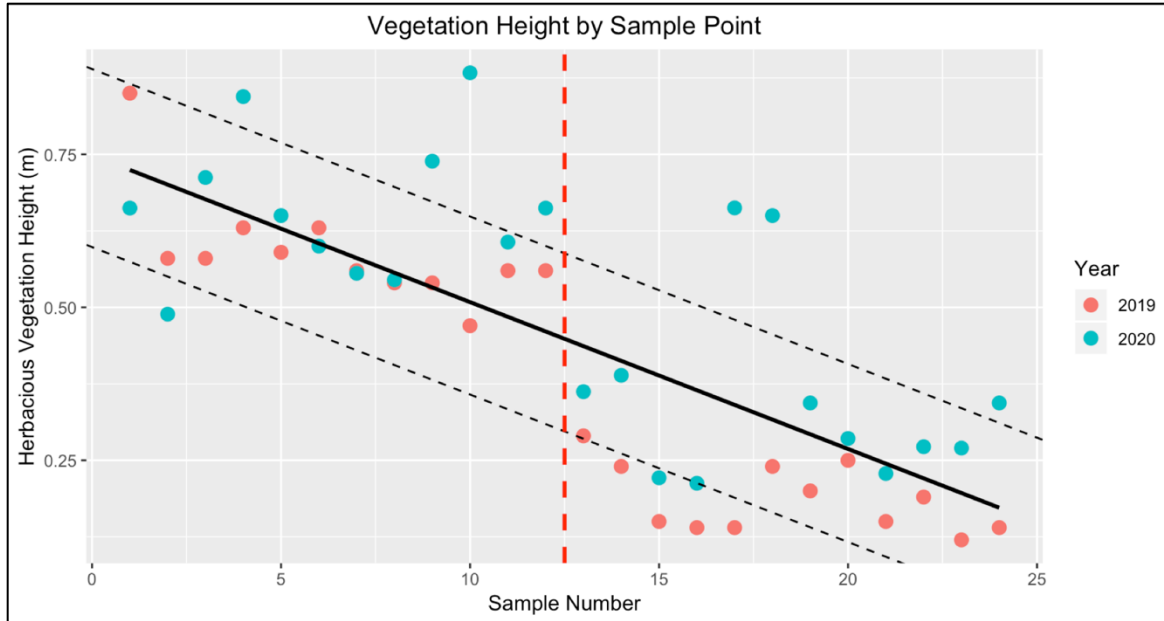
Figure 11. Vegetation Height Model. Scatterplot of the herbaceous vegetation height in relation to the sample number based on data collected in 2019 and 2020 on the San Antonio Viejo Ranch. The exclosure fence line is shown as the dashed red line. The linear model is shown as the solid black line while the standard error of the model is shown as the dashed lines. Points are color coated by year.

The threshold regression determined that the model that best fit these data had 1 threshold along the sampling gradient for vegetation height at sample number 12 (Figure 12).
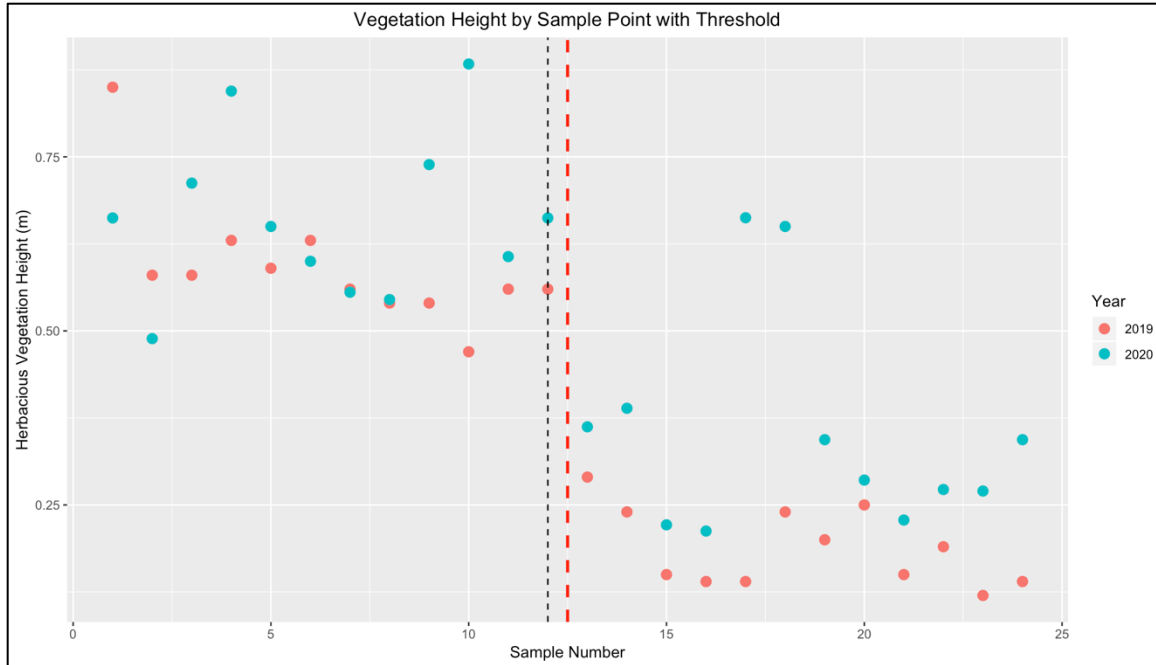
Figure 12. Vegetation Height Threshold. Scatterplot of the herbaceous vegetation height in relation to the sample number based on data collected in 2019 and 2020 on the San Antonio Viejo Ranch. The exclosure fence line is shown as the dashed red line and the threshold is shown as a dashed black line. Points are color coated by year.

Litter Depth

The litter depth data were not drawn from a normal distribution (Shapiro-Wilk normality test, p-value = 6.786e-05) and the data could not be transformed in a way to make them normal. The litter depth data presented a linear trend.

The regression determined litter depth was significantly predicted by the sample number (Figure 13). From the regression, for every 100-meter change in distance from the center of the exclosure, litter depth decreased by 0.37 cm or by ~8%.

Figure 13. Litter Depth Model. Scatterplot of the litter depth data in relation to the sample number based on data collected in 2019 and 2020 on the San Antonio Viejo Ranch. The exclosure fence line is shown as the dashed red line. The linear model is shown as the solid black line while the standard error of the model is shown as the dashed lines. Points are color coated by year.

It was determined that the model that best fit these data had two thresholds along the sampling gradient for litter depth. The thresholds were determined to be at sample point 6 and sample point 12 (Figure 14).
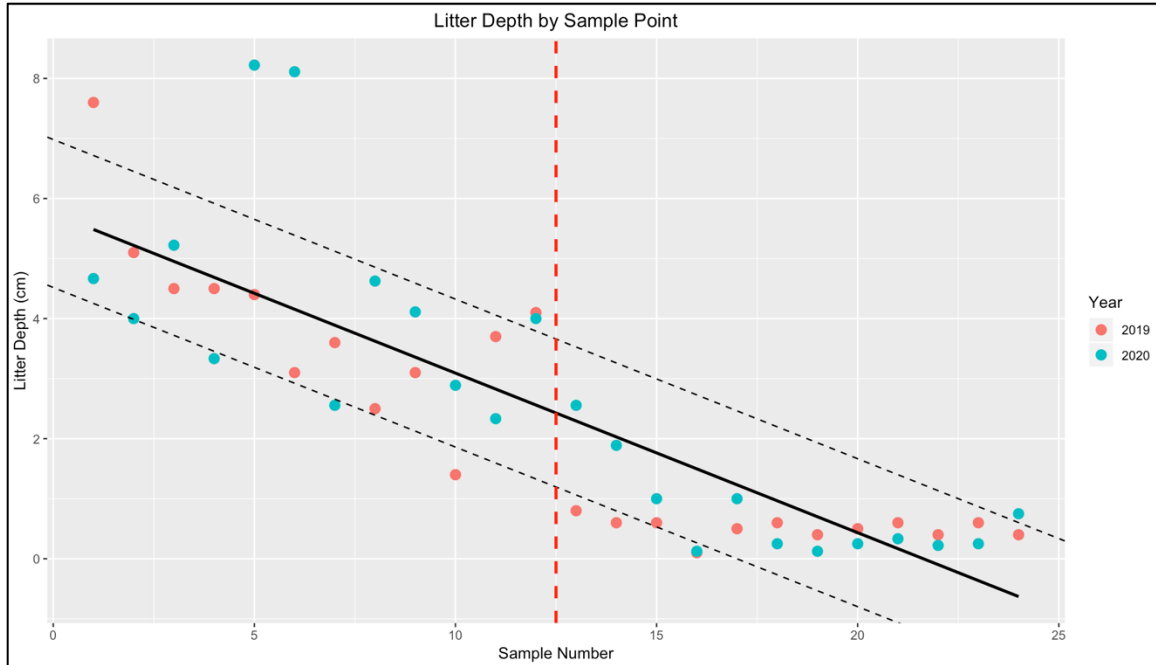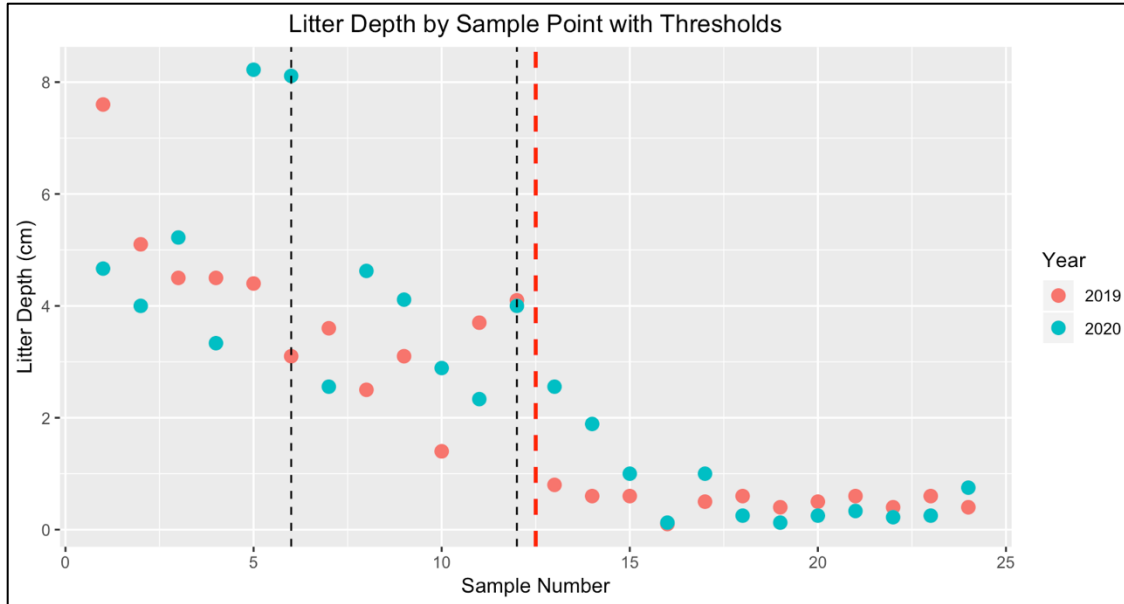
Figure 14. Litter Depth Thresholds. Scatterplot of the litter depth in relation to the sample number based on data collected in 2019 and 2020 on the San Antonio Viejo Ranch. The exclosure fence line is shown as the dashed red line and the threshold is shown as a dashed black line. Points are color coated by year.

Percent Herbaceous Live Cover

The live herbaceous cover data were not drawn from a normal distribution (Shapiro-Wilk normality test, p-value = 0.020) and the data could not be transformed in a way to make them normal. The data presented a linear trend.

Percent live herbaceous cover was significantly predicted by the sample number (Figure 15). From the regression, for every 100-meter change in distance from the center of the exclosure, percent live cover decreased by ~5%.

Figure 15. Live Herbaceous Model. Scatterplot of the percent live herbaceous cover data in relation to the sample number based on data collected in 2019 and 2020 on the San Antonio Viejo Ranch. The exclosure fence line is shown as the dashed red line. The linear model is shown as the solid black line while the standard error of the model is shown as the dashed lines. Points are color coated by year.

It was determined that the mode that best fit these data had one threshold at sample point number 13 for live herbaceous cover (Figure 16).
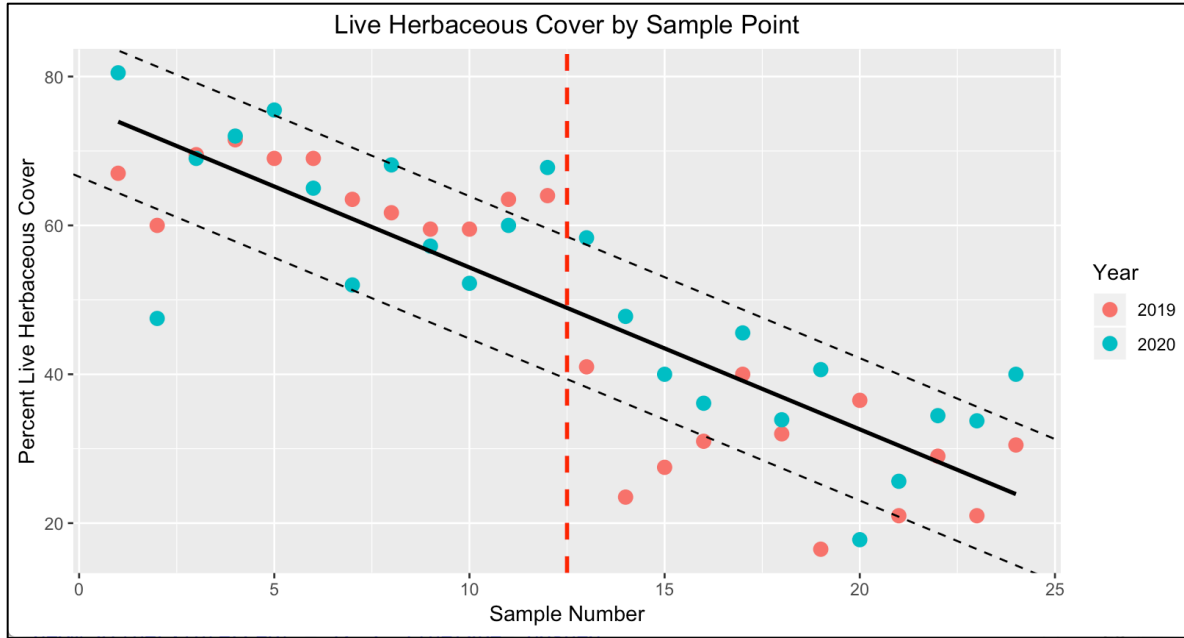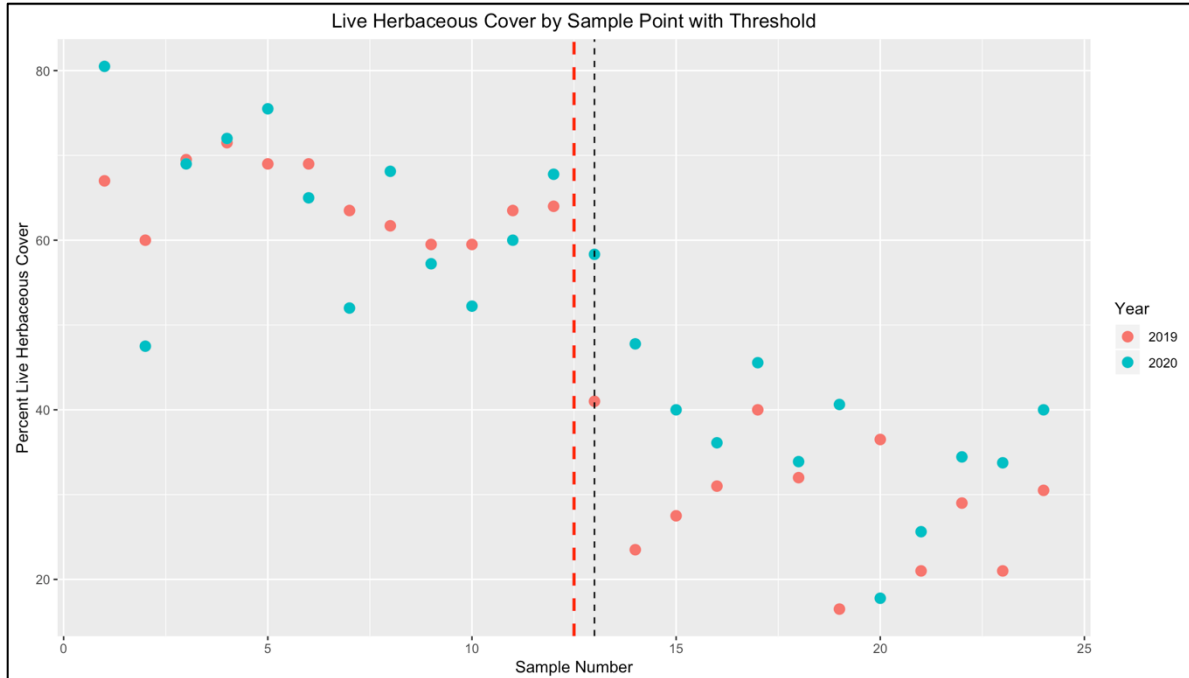
Figure 16. Live Herbaceous Threshold. Scatterplot of the percent live herbaceous cover data in relation to the sample number based on data collected in 2019 and 2020 on the San Antonio Viejo Ranch The exclosure fence line is shown as the dashed red line and the threshold is shown as a dashed black line. Points are color coated by year.

Cattle Activity

To determine where cattle were most active, I examined the percent cover of cattle activity data.

The data, however, was obviously heteroscedastic so I log transformed the data. The log transformation of the data was determined to be drawn from a normal distribution (Shapiro-Wilk normality test, p-value = 0.691).

The linear regression determined that sample number significantly predicted the cattle activity (Figure 17). From the regression, for every 100-meter change in distance from the center of the exclosure, cattle activity increased by ~15%.
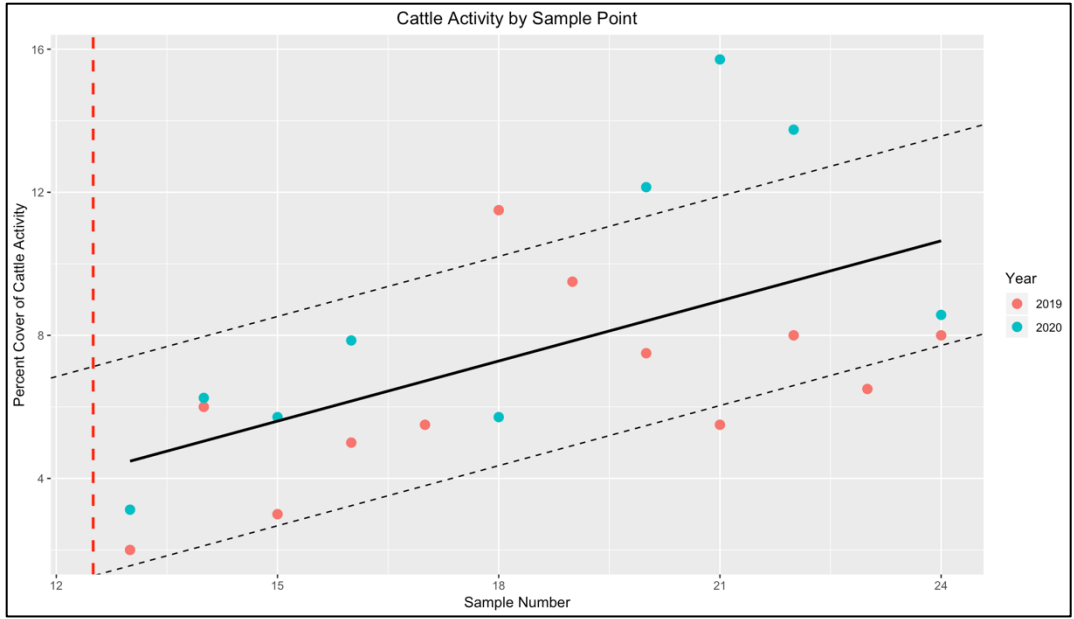
Figure 17. Cattle Activity Model. Scatterplot of the percent cover of the cattle activity data in relation to the sample number based on data collected in 2019 and 2020 on the San Antonio Viejo Ranch. The linear model is shown as the solid black line while the standard error of the model is shown as the dashed lines. Points are color coated by year. This plot excludes points inside of the cattle exclosure and 3 outliers.

I determined that the model that best fit these data had two thresholds at sample point numbers 13 and 17 (Figure 18).
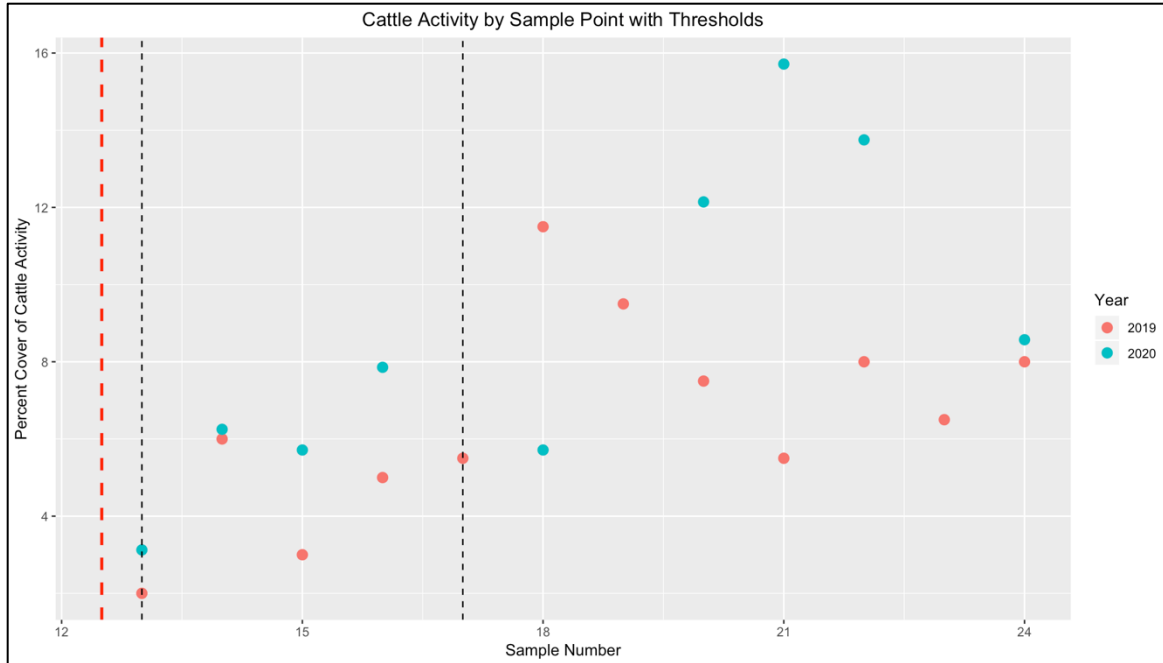
Figure 18. Cattle Activity Thresholds. Scatterplot of the percent cover of the cattle activity data in relation to the sample number based on data collected in 2019 and 2020 on the San Antonio Viejo Ranch. The exclosure fence line is shown as the dashed red line while the thresholds are shown as the dashed black lines. Points are color coated by year.

Below is a summary of all linear mixed effect model statistics (Table 2) and a summary of all of the threshold regression statistics (Table 3).

Model	Parameter	Coef	SE	df	p value
MNA	Intercept	2.330	0.237	1.250	**0.039**
	Trap number	-0.008	0.004	73.000	**0.037**
Sex ratio	Intercept	0.913	0.139	66.000	**<0.001**
	Trap number	0.004	0.006	66.000	0.572
Vegetation height	Intercept	0.749	0.042	46.000	**<0.001**
	Sample number	-0.024	0.003	46.000	**<0.001**
Litter depth	Intercept	5.750	0.367	46.000	**<0.001**
	Sample number	-0.267	0.026	46.000	**<0.001**
Live herbaceous	Intercept	76.107	2.850	46.000	**<0.001**
	Sample number	-2.175	0.200	46.000	**<0.001**
Cattle activity	Intercept	-2.798	3.370	19.000	0.417
	Sample number	0.560	0.181	19.000	**0.006**

Table 2. Model Summaries. Summary of all linear mixed effect model statistics from data collected in 2019 and 2020 on the San Antonio Viejo Ranch. Significant p-values (< 0.05) are in bold.

Model	Threshold Value (Trap or Sample Number)	SSR	BIC
MNA	–	–	218.312
Species richness	24	91.727	27.286
Age ratio	19	3.693	-220.325
	21	3.333	
Sex ratio	–	–	9.405
Vegetation height	12	0.705	-190.957
Litter depth	6	50.579	26.954
	12	60.955	
Live herbaceous	13	2979.085	209.766
Cattle activity	17	276.672	99.563

Table 3. Threshold Summaries. Summary of all threshold regression statistics from data collected in 2019 and 2020 on the San Antonio Viejo Ranch.

6. DISCUSSION

This study began 8 years after the construction of cattle exclosures on the East Foundation's San Antonio Viejo Ranch in southern Texas. In that time, the areas inside and outside of these exclosures were able adapt and change without much intervention. The areas inside of these exclosures showed no signs of the cattle grazing that once occurred there. Following all of this time without cattle grazing, I was able to conclude that relative abundance (MNA) was negatively correlated with distance from the center of the exclosure, which supports my hypothesis. Interestingly, the threshold regression indicated that there were no changepoint's suggesting that potentially the decrease in relative abundance was uniform. This finding is unique since similar studies did not find differences in abundance (Bueno et al., 2011, Cao et al., 2016, Pearson et al., 2001). Other studies could have failed to detect changes in relative abundance due to their sampling which used paired points rather than a gradient method.

Recall from the introduction the different vegetation requirements per species. *Chaetodipus hispidus*, *Reithrodontomys megalotis*, *Peromyscus leucopus*, and *Sigmodon hispidus* are associated with ample ground cover and have been shown to decrease with the presence of grazing (Bock et al., 1984). The results of my study align with these findings for all species except *Peromyscus leucopus*, since we saw an increase in these individuals outside of the cattle exclosure. This may be because *Peromyscus leucopus* relies on dense woody, and cactus cover which, in general, is what I saw more often on the outside of the cattle exclosures. There were no *Reithrodontomys megalotis* captures outside of the cattle exclosure and very few captures of *Sigmodon hispidus* outside of the cattle exclosure. There were less *Chaetodipus hispidus* individuals outside of the cattle exclosure, however not much less. Cao et al., 2016,

found that *Spermophilus dauricus* increased when grazing intensity increased which aligns with my *Spermophilus mexicanus* captures only occurring outside of the cattle exclosure.

I hypothesized that species richness would be negatively correlated with distance from the center of the exclosure, however, the results did not support this hypothesis. The threshold located ~125 m from the exclosure fence line could suggest that the impact of the exclosure continues in a 125 m buffer around the exclosure for species diversity. This finding was different than Cao et al., 2016, who found that species richness significantly declined as grazing activity increased. My results most likely do not align with theirs because they researched areas with much higher grazing intensity. The San Antonio Viejo Ranch averages at about 0.042 Au/ha while Cao's study looked at regions with as high as 0.92 Au/ha for 6 months of the year for several years.

I hypothesized that sex-ratio would be different along the sampling gradient and this was not supported by my results. These findings align with several others that also did not find cattle grazing to impact sex ratio (Bueno et al. 2011, Peles and Barrett 1996; Schmidt et al. 2005).

My hypothesis that age ratio would be different along the sampling gradient was supported by my results. My data indicated that the age ratio inside of the cattle exclosure and the age ratio outside of the cattle exclosure were significantly different. In addition to this finding, the threshold regression determined that there were two thresholds along the sampling gradient for age ratio. These changepoint's occurred along the exclosure boundary, and at trap ~ 50 m past the fence line suggesting there was a transitional zone for small mammal age ratio, indicting an edge effect. In general, we saw a higher proportion of young to adult individuals outside of the cattle exclosure compared to inside of the exclosure, which agrees with the findings of Bueno et al. (2011). They suggest that this was due to adult territoriality which does

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not allow young to establish territories in areas with more suitable habitat makeup (Bueno et al., 2011). The results of my study show that the highest proportion of young to adults were caught along the fence line of the exclosure therefore, by using the conclusion of Bueno et al., (2011), this area would be least suitable for small mammals. This area would likely be less desirable due to the two contrasting ecosystems which creates fragmentation at a small mammal scale.

I hypothesized that vegetation structure would present a linear trend and negatively correlate with distance from the center of the exclosure. The results of the vegetation analysis support my hypotheses.

I hypothesized that cattle activity would be the driving force of the small mammal community changes, and I expected opposite trends in cattle activity than the community parameters. I determined that cattle activity was significantly positively correlated with distance from the exclosure. Thus, in general, cattle activity increases as distance from the cattle exclosure increases. With these results, I conclude that an increase in cattle activity decreases herbaceous vegetation height, litter depth and percent live cover. This would align with the conclusions of Altesor et al., (2006). These changes are likely why I saw a decrease in MNA and changes in age-ratio across the gradient.

Some of the trends that I saw could have been due to changes in weather patterns. Being that this region is generally hot and dry, yearly precipitation and temperatures influence these ecosystems. My captures in 2019 were nearly double than my 2020 captures. According to NOAA, rainfall in May-July in 2019 was 14.4 cm and in 2020 the same period saw 23.7 cm of rainfall (NOAA, 2020). This wouldn't explain why I saw a decrease in captures in 2020 however, the impact of rainfall or lack thereof could have a delayed impact on the ecosystem. In 2018, this region saw 26.8 cm of rainfall and therefore a delay would explain why I had high

captures in 2019 and low captures in 2020. Additionally, these trends in small mammal and

vegetation make-up could have been due to other factors such as brush management which the

East Foundation has done outside of the cattle exclosures, soil type, or other unknown factors.

7. MANAGEMENT IMPLICATIONS AND CONCLUSIONS

While I found changes in small mammal distribution, they were not so extensive that I believe their persistence is at risk in any way. Edge effects on these groups were minor in this area as well. Since small mammals promote plant species diversity, help maintain nitrogen cycling and carbon exchange, they can be beneficial to native rangelands and therefore also to ranching operations. If managers desired to ensure higher abundances of this group, they could create areas that excluded cattle on their properties since I did see slightly higher abundances inside of the cattle exclosures. Cattle rotation, however, may provide the same impact if cattle were left off of pastures for extended periods of time between rotation. Additional research on this topic should be conducted. The results of my study indicate that no actions must be taken by ranch managers to have strong small mammal populations in the south Texas region since it is likely that weather is driving much of the changes in these communities.

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