

# Heterogeneity of Cursorial Arthropod Species Composition and the Importance of Scale



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## Abstract

California coastal sage has experienced a significant reduction of 85 to 90 percent since European settlement. As a result, restoration efforts using native plant species were initiated, using arthropods as bioindicators of restoration success. In this study the restoration process of the Alta Vicente Ecological Reserve in Rancho Palos Verde was followed throughout the duration of a single restoration cycle. A series of nine pitfall arrays were placed for a two weeks along three transects, with one transect in a native habitat and two in the restoration area. Restoration effort was measured by comparing the arthropod community in the native habitat to that of the newly restored habitat.

## Introduction

For more than 130 years, the human population of California has grown faster on an annual basis than any other state in the nation (Grumbine 1994). From 1980 to 1990 California's population increased by approximately 670,000 people per year, with more than half the growth in Southern California (Armstrong 1993, California Department of Finance 1991). The effects of this dramatic growth have been observed in the coastal sage scrub natural community, which has been severely degraded and depleted, with published estimates indicating that 85 to 90 percent of the ecosystem has been destroyed (Murphy et al. 1992). The drastic reduction of coastal sage habitat, has initiated restoration projects focusing on restoring the native plant species. One promising avenue to develop more comprehensive assessments of ecological restoration projects has been the use of arthropod community structure as an indicator of the restoration in recreating a functioning natural community (Longcore 1999). Due to their large numbers, short generation times, and many trophic levels and niches they fill, insects should make good bioindicators for investigating the effects of human disturbances on natural habitats (Kremen et al. 1993).

There have been several studies based on the restoration of arthropod communities in areas that have been restored and disrupted. These studies were based over a specific period of time quantifying variation of arthropod diversity as a measure of restoration success. In contrast, this study will document changes in both native and "restored habitat" as restoration efforts are deployed. We report here the first step in this process, describing the distinctness of native and non-native cursorial arthropod communities between habitats.

Traditional coastal sage scrub habitat within Southern California includes the lands managed within the Palos Verdes Peninsula Land Conservancy (PVPLC). The PVPLC comprises both native and altered habitat. The mission of the PVPLC is to restore disturbed habitat to its natural biological state. They have implemented a strategy of removing non-native vegetation and planting native shrubs. The restoration process of the non-native habitat will be studied by using the arthropod community as bioindicators. The focus will be on the species abundance and diversity of the arthropod community throughout the length of the restoration process. The results reported here are the first step in this quantification. We document the uniqueness and distinction between native and non-native cursorial arthropod communities.

## Methods

- The Alta Vicente portion of the PVPLC reserve underwent a series of "grow and kill" regiments over a period of four months (July 2007 to November 2007).
- The deployment of pitfall traps took place three weeks prior to the beginning of the kill cycle and were collected after a two week period.
- A series of nine pitfall arrays were evenly spaced 25 meters apart and placed along three transects within the restoration area (Fig 1). One transect was within native habitat ("Native"), another was 50 m from the native transect ("Close"), and another was 75 meters from the native transect ("Far"). Each pitfall trap array consisted of three traps five meters apart in the shape of an equilateral triangle.
- The pitfall traps were made of a plastic plant pot container approximately 24 cm in diameter and 15 cm deep, which were placed into the ground with their tops leveled with the ground and filled with biodegradable antifreeze solution
- Data were analyzed using Primer E, nonparametric multivariate statistic software. We analyzed community species composition within transects (trapping arrays) and across transects.

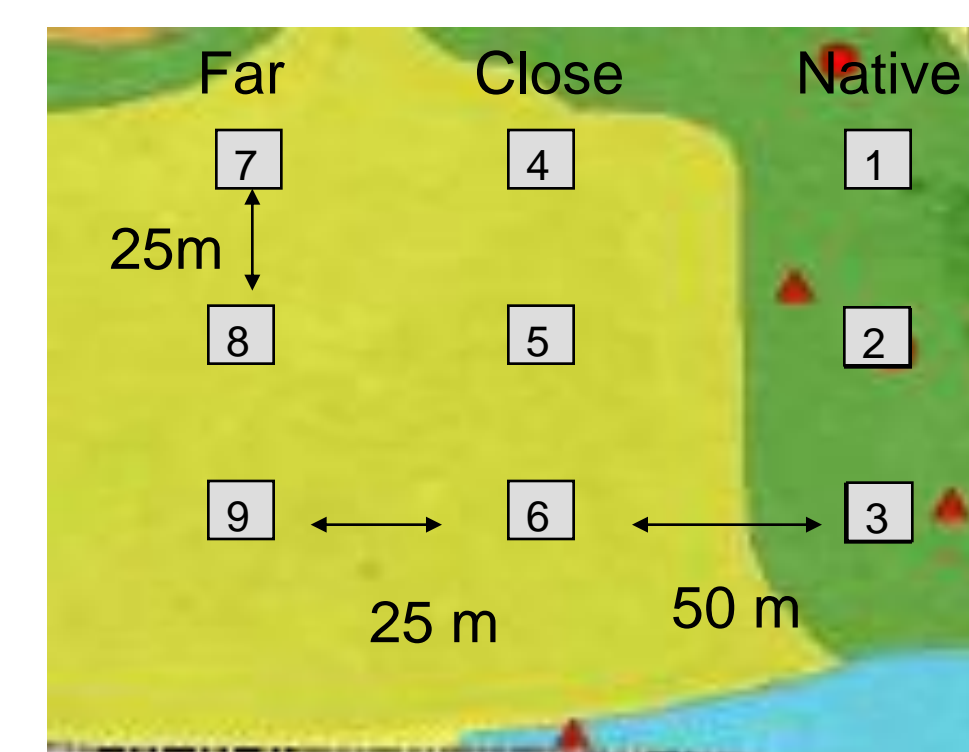


Figure 1. The trapping configuration within the studied area. Arrays are designated with unique numbers 1 – 9.

## Results

Summary statistics are provided in Table 1. We collected a total of 4396 individuals in 45 families within 23 orders. The native transect had approximately half the number of individuals as the transects in the restoration habitat, but had a similar number of families.

The MDS based on Bray Curtis similarities found unique structure within the arrays of all three transects (Figure 2). The arrays within each transect display similarity, except for the native habitat which displayed more species composition variation. Within arrays, the native transect there is similarity within array one and array two, but array three displays more variation than either of the two arrays. The transect closest to the native habitat had array four, five and six. Within both arrays four and six little variation was observed, but array five contained a more diverse group of taxa as seen in Figure 3. The transect furthest from the native habitat contained arrays seven, eight, and nine. Within array eight and nine similarities can be observed (Figure 3). But array seven displayed the most variation among the arrays of the transect furthest from the native habitat.

Table 1. Summary of the numbers of individuals, families and orders within each transect.

Transects	Number of Individuals	Families	Orders
Native	904	45	15
Close to Native	1747	44	19
Furthest From Native	1745	42	20

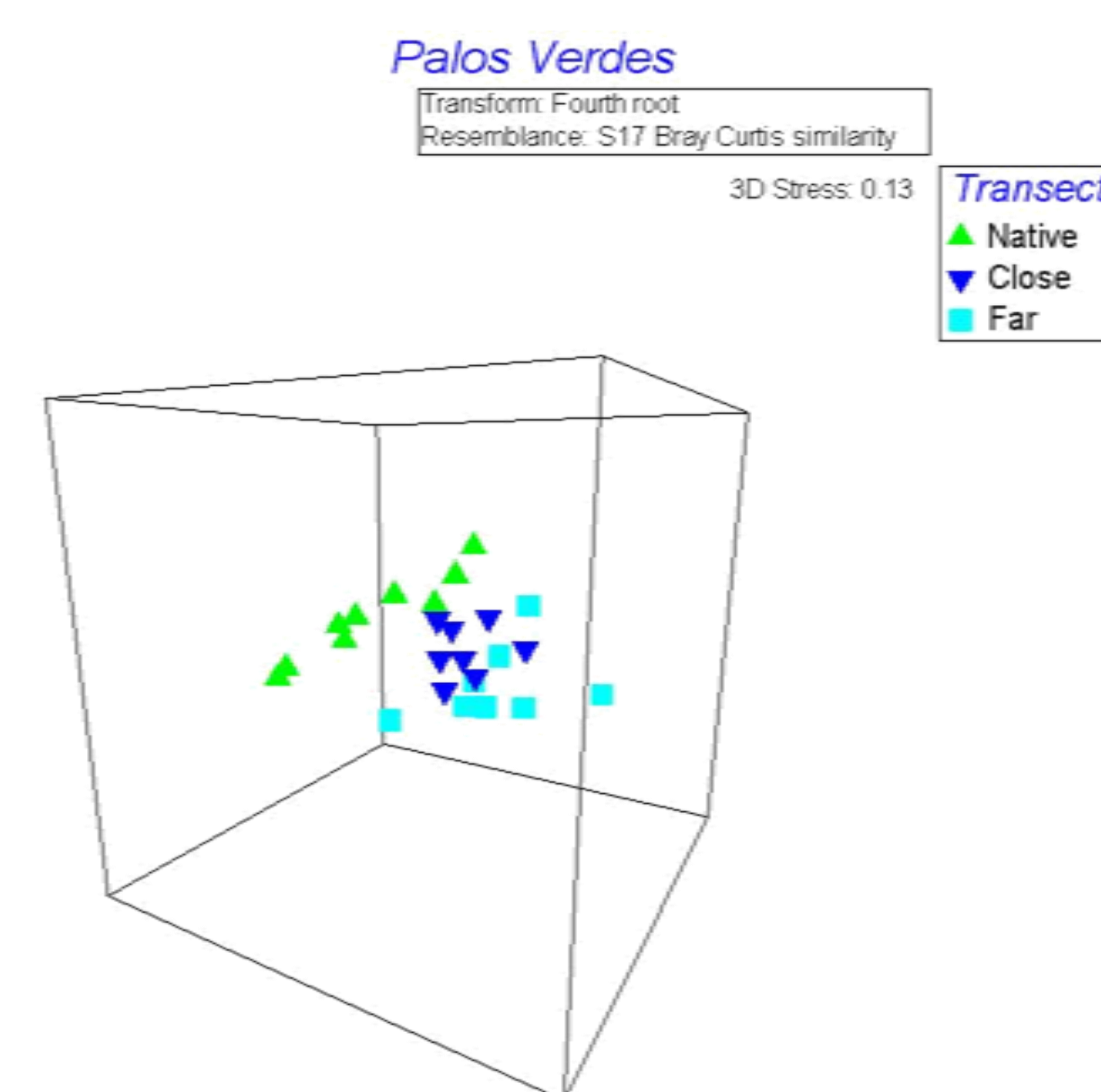


Figure 2. MDS plot of the three transects, native, close, and far.

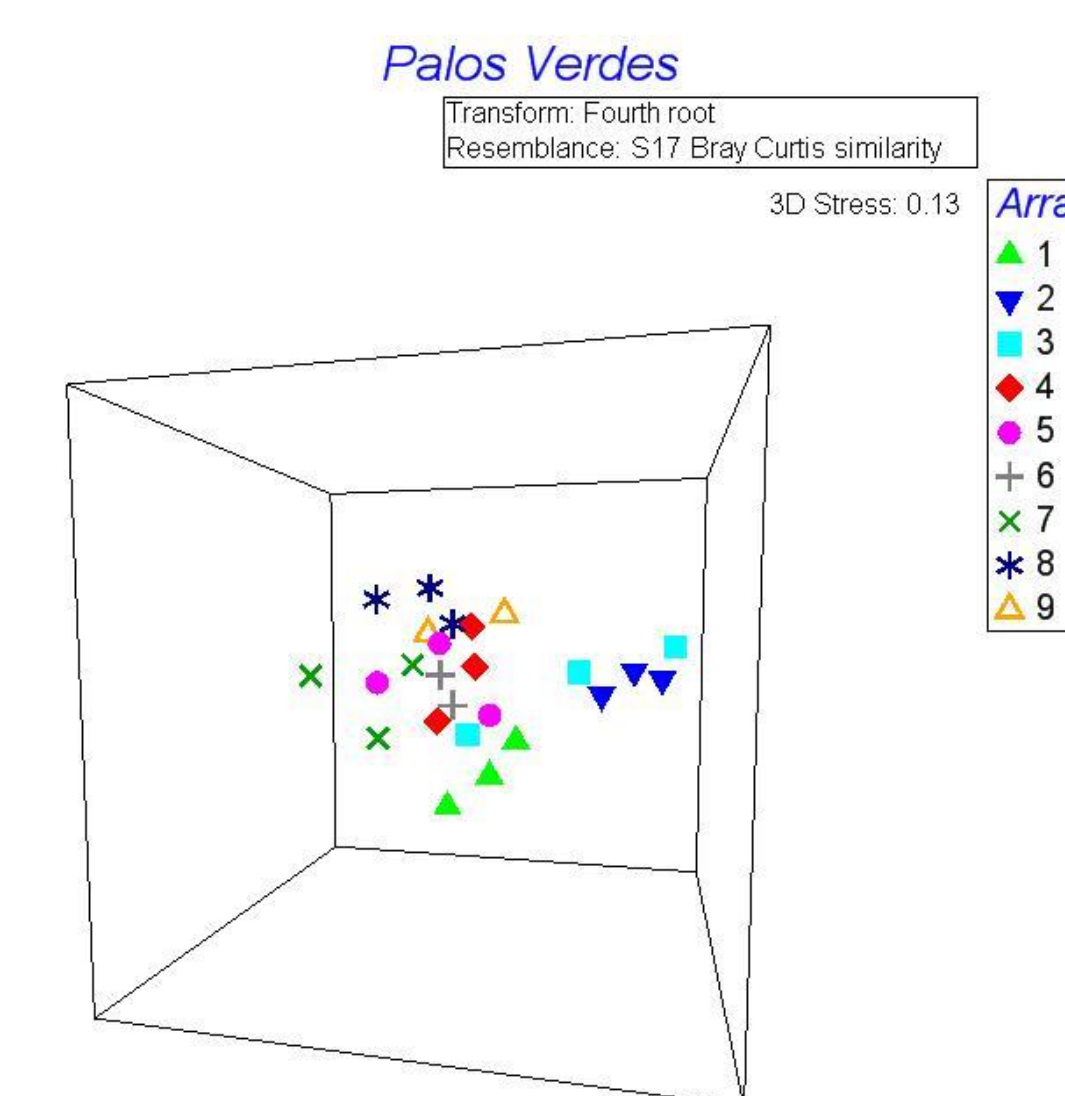


Figure 3. MDS: Similarity among arrays of all three transects. Native arrays: 1,2,3. Close arrays: 4,5,6. Far arrays: 7,8,9.

When comparing the transects for similarity using a one-way ANOSIM, we found that the native and close transects were significantly different, with an R value of 0.325 and a P value of 0.006 (Table 2). A greater difference was observed between the native and the far transects that had an R value of 0.392 and a P value of 0.002. The close and far transects had a smaller R value of 0.058 with a P value of 0.2, indicating that they are similar.

The SIMPER was used to determine which taxa are driving the differences among the transects (Table 3). We found that no single taxon contributed to more than six percent of the difference. In the native transect Formicidae were dominant, with a contribution of 0.366 percent. Also, the Ectopsicidae contributed 0.184 percent. Siphonoptera had a contribution of 0.0928 and the Fortificulidae contributed 0.0771 percent. In the close transect the Formicidae was also the dominant taxon as in the native transect. The Gnaphosidae with comprised 0.133 percent. The Ectopsicidae followed with 0.115 percent and Fortificulidae had a 0.107 percent contribution. The far transect had Gnaphosidae as its main contributor of 0.196 percent. The Formicidae followed with 0.195 percent contribution. Fortificulidae had a 0.133 percent contribution and Oecobiidae contributed 0.105 percent.

Table 2. ANOSIM One Way Analysis of the similarities among transects.

Transects	R Significance	P Value
Native, Close	0.325	0.006
Native, Far	0.392	0.002
Close, Far	0.058	0.200

Table 3. SIMPER - percent contribution of taxa among the transects.

Transect	Families	% Contribution
Native	Formicidae	0.366
	Ectopsicidae	0.184
	Siphonoptera	0.0928
	Fortificulidae	0.0771
Close	Formicidae	0.215
	Gnaphosidae	0.133
	Ectopsicidae	0.115
	Fortificulidae	0.107
Far	Gnaphosidae	0.196
	Formicidae	0.195
	Fortificulidae	0.133
	Oecobiidae	0.105

## Conclusions

Heterogeneity was found at multiple scales, within the transects and across transects. The native transect was distinct from the non-native transects. The two non-natives were more similar to each other than either was to the native transect indicating that the community species compositions of the non-native and the native communities were unique. The native transect had more variation across its arrays than the non-native transects and this was likely driven by a north-south gradient.

This represent baseline data to quantify the efficacy of restoration efforts as they unfold in this coastal sage habitat. Sampling will continue throughout the planned grow-and-kill cycle. Our efforts will continue to monitor the species composition as they change.

## References

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