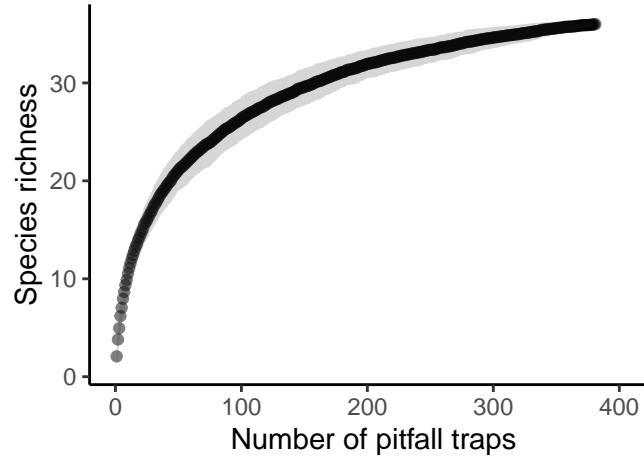


Big Thicket Ant Analysis

Marion Donald

8/20/2019

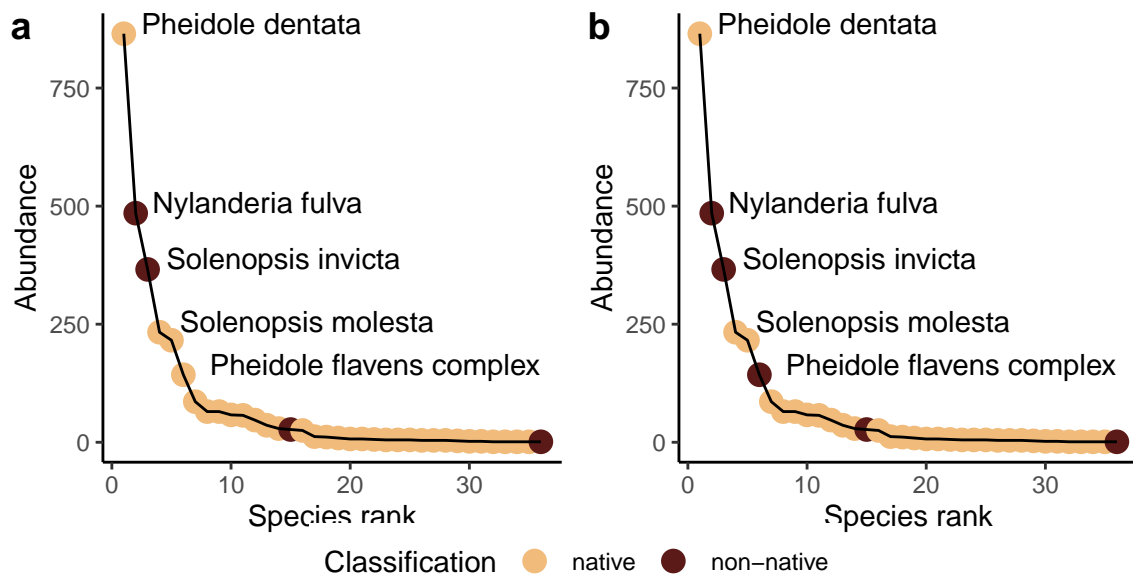
Species accumulation curve richness estimates



Species accumulation curve from 381 pitfall traps, collected by Gabriela and Meghan. Here, we used the function ‘specaccum’ from the vegan package in R, which estimates the number of species for a given number of sampled sites. Richness estimates are shown as points with +/- the standard deviation as the shaded ribbon. We then extrapolated the number of unobserved species, using the function ‘specpool’ from the vegan package in R. We compared this estimate of unobserved species with the number of observed species to determine the efficacy of our sampling.

	Species	chao	chao.se	jack1	jack1.se	jack2	boot	boot.se	n
All	36	41.98425	6.464946	41.98425	2.443061	44.97636	38.93038	1.436444	381

Rank abundance curves

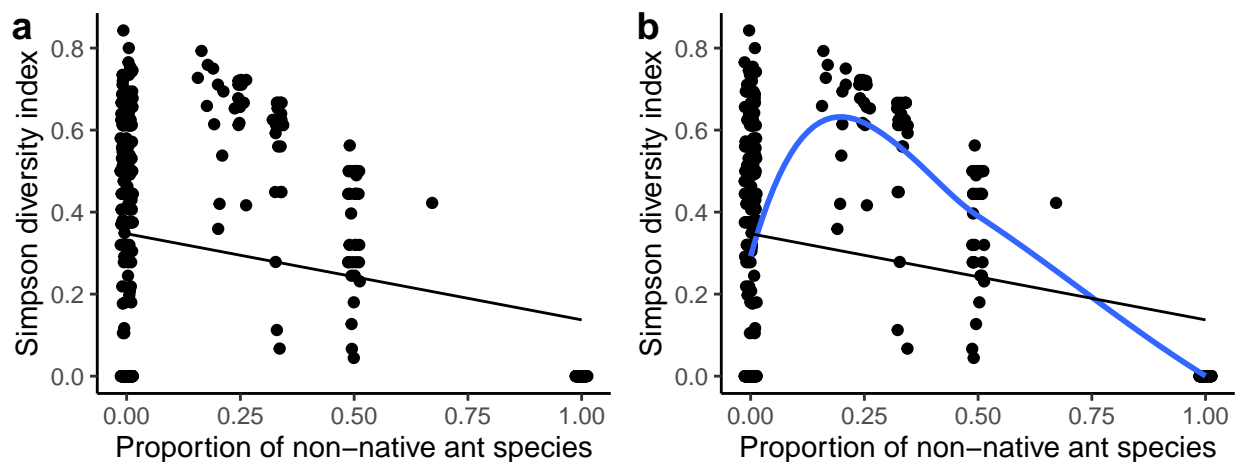


To visualize the evenness and relative abundance of the species, we created rank abundance curves. In these two figures, *Pheidole flavens* complex is classified as (a) a native species and (b) a non-native species. (Scott, I think it makes sense to only show one of these. So depending on how *P. flavens* is classified, we can use the corresponding figure.)

Alpha diversity – local species richness

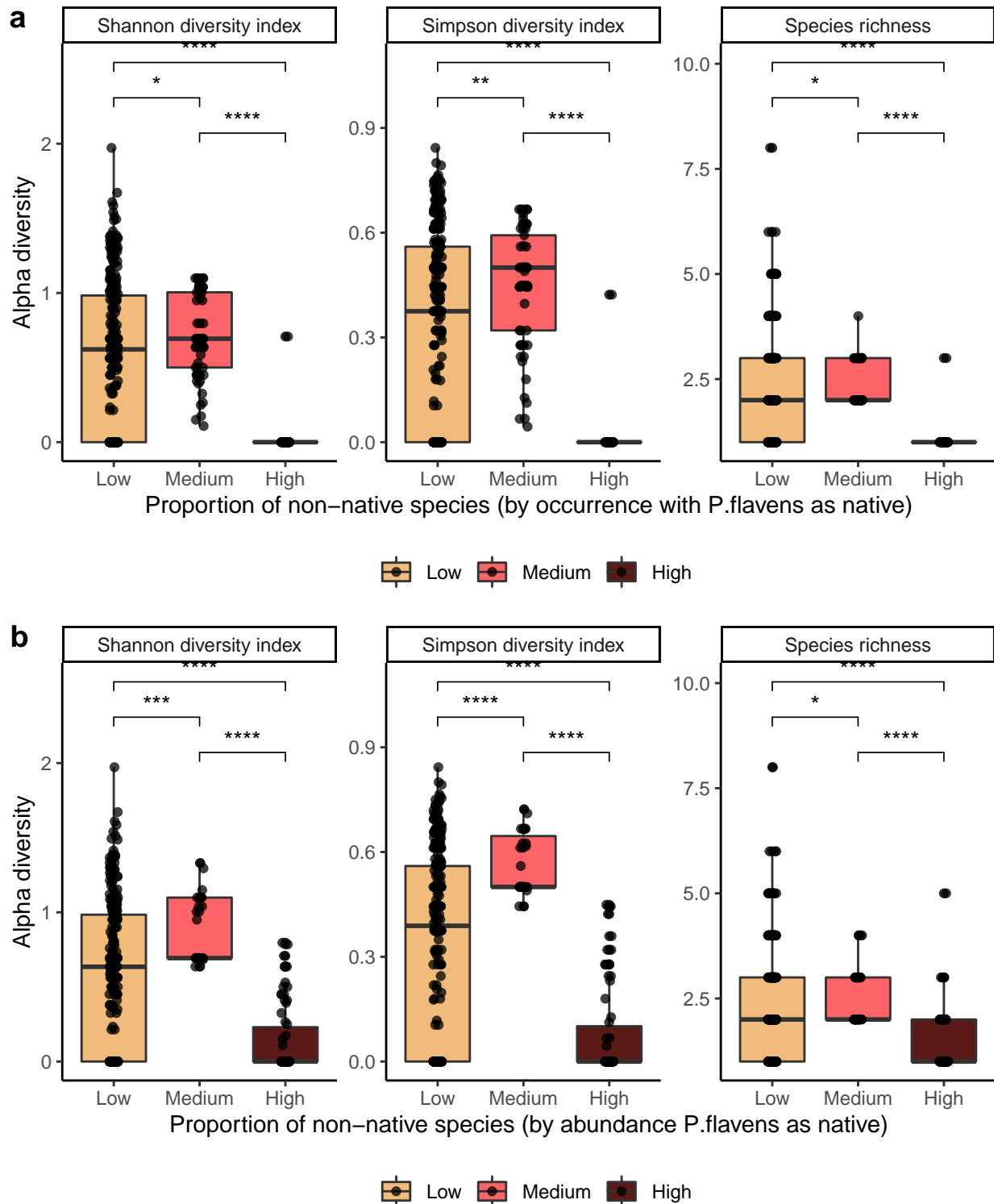
The original figure compared the proportion of non-native ant species out of total species with Shannon and Simpson diversity indices, and used a linear model to test for a correlation between the two. I think this might not be the best way to visualize these data or to test for a trend between alpha diversity and proportion of non-native ants, due to the non-linear spread of the data. Looking at this figure (a), richness appears to peak at an intermediate level of non-native proportion of total ant species. Alternatively, we could use the default loess model (b), which shows the peak at an intermediate proportion of non-native to total ant species.

```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```



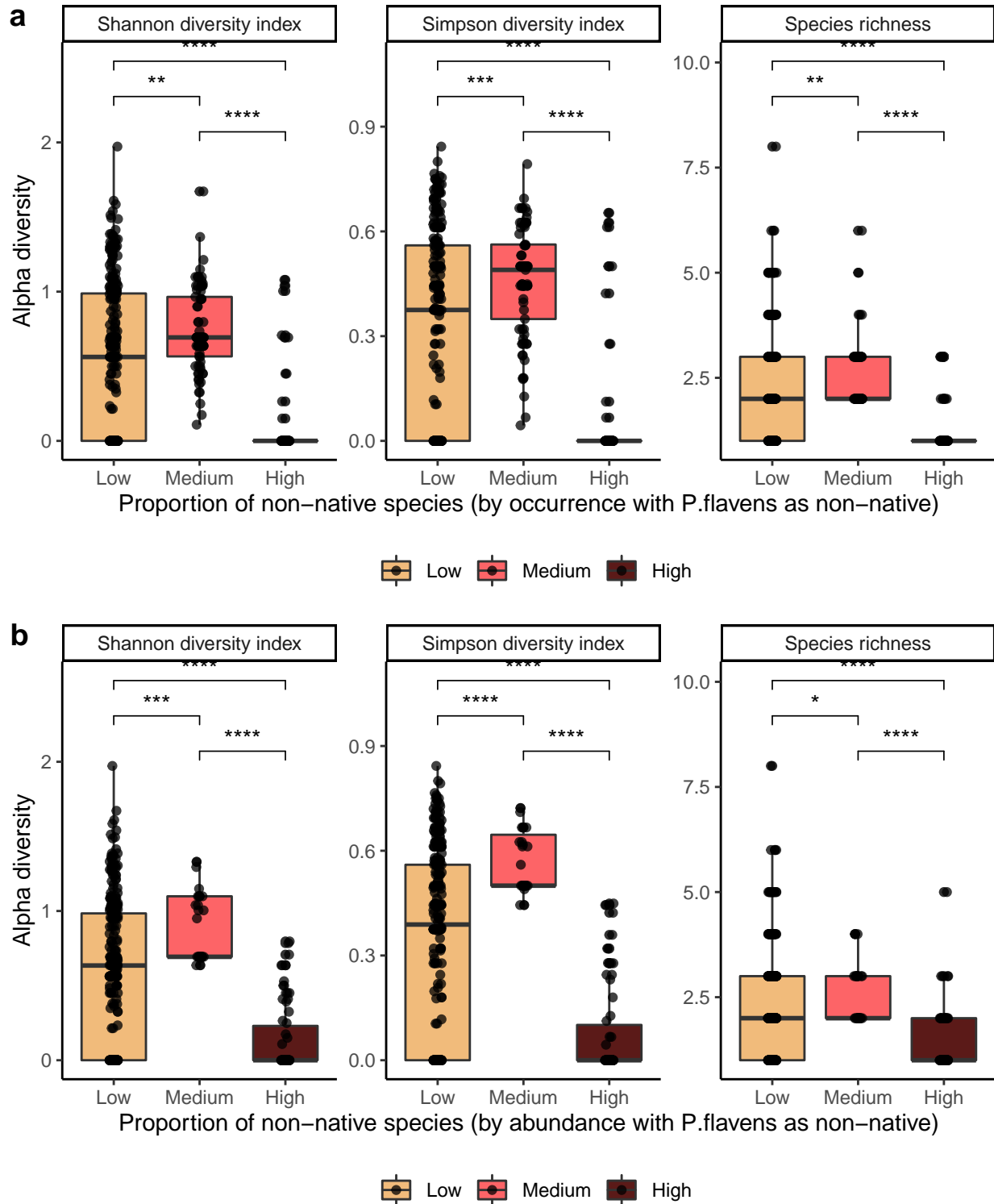
However, I think a better way to visualize these data is to bin the proportion of non-native ant species (or abundances) out of total species (or abundance) and compare alpha diversity across these categories using Wilcoxon tests.

Basing the proportion of non-native to total species by occurrence and abundance gives qualitatively the same result – alpha diversity peaks at an intermediate level of non-native species, and is lowest when the proportion of non-native species is high. This remains true whether or not *P. flavens* complex is classified as native or non-native.



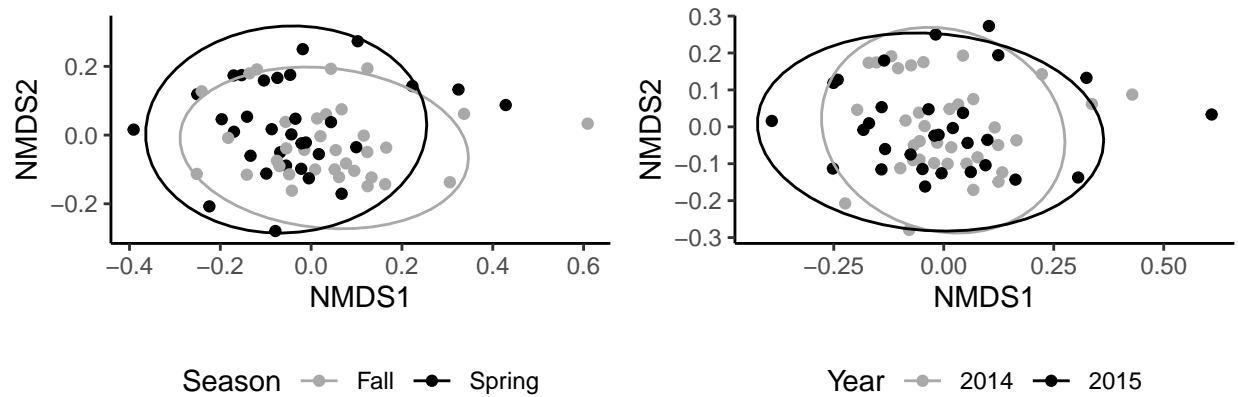
These are the proportion of non-native species (with *P. flavens* complex as native) by (a) occurrence and (b) abundance, binned them by low (0-.33) medium (.34-.66) and high (.67-1.0), and compared these categories

with three difference measures of local diversity (Shannon, Simpson, and species richness). Qualitatively, the trends are similar between the two sets of figures.



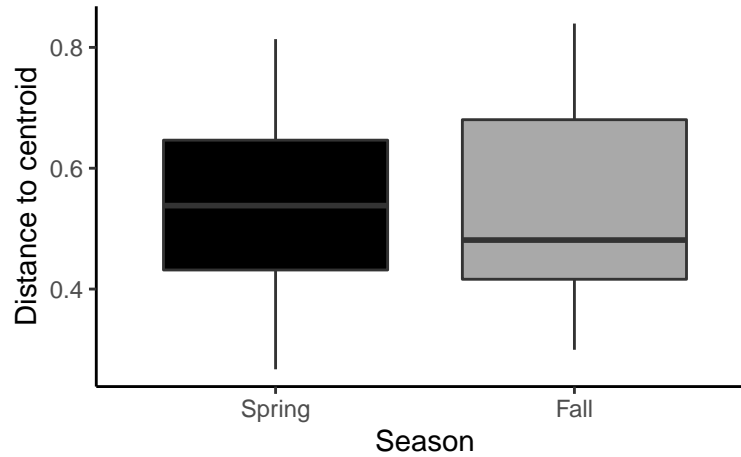
These are the proportion of non-native species (with *P. flavens* complex as non-native) by (a) occurrence and (b) abundance, binned them by low (0-.33) medium (.34-.66) and high (.67-1.0), and compared these categories with three difference measures of local diversity (Shannon, Simpson, and species richness). Qualitatively, the trends are similar between the two sets of figures.

NMDS



Visualization of the ant communities (using a bray-curtis dissimilarity matrix). Each point represents the pooled community across pitfall traps within each site. Colors represent (a) seasons and (b) years. We can use PERMANOVA analyses to test whether ant community composition varied between seasons and years. PERMANOVA tests for differences in the locations of multivariate groups. We used the `adonis` function of `vegan`. As we had repeated community measures within site, we constrained permutations to within sites (using the “`strata`” argument). We included season and year as fixed effects in the models. These analyses confirmed that season had a significant effect on community composition and explained approximately 5% of the variation ($R^2 = 0.055$)

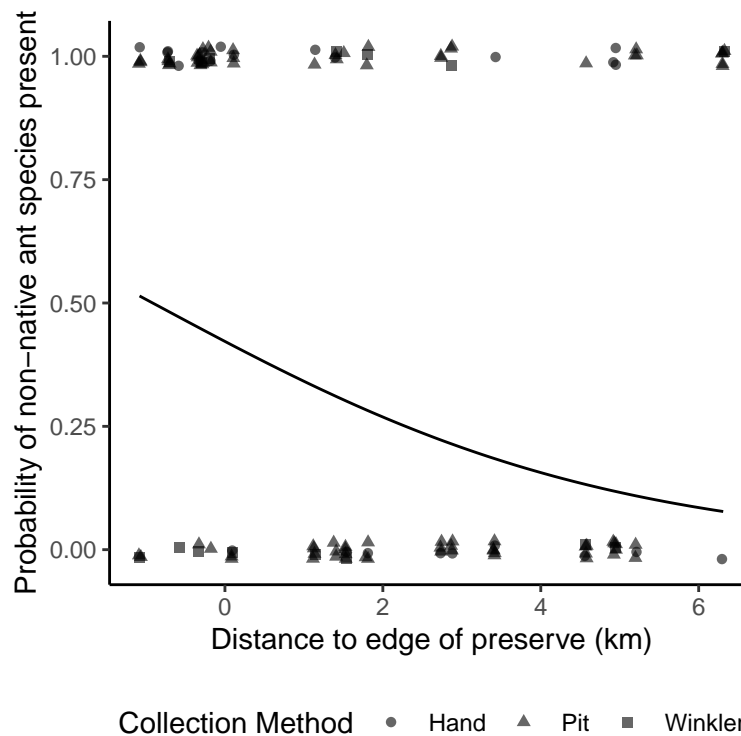
```
##
## Call:
## adonis(formula = dist_BC ~ Season * Year, data = data_GZ_clean_subset_2, strata = data_GZ_clean_subset_2$Site)
##
## Blocks: strata
## Permutation: free
## Number of permutations: 999
##
## Terms added sequentially (first to last)
##
##              Df SumsOfSqs MeanSqs F.Model    R2 Pr(>F)
## Season         1    1.1493  1.14926   3.7083 0.05481  0.001 ***
## Year           1    0.2428  0.24277   0.7833 0.01158  0.451
## Season:Year     1    0.3624  0.36243   1.1694 0.01728  0.162
## Residuals      62   19.2150  0.30992         0.91633
## Total          65   20.9694         1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



```
## Analysis of Variance Table
##
## Response: Distances
##           Df Sum Sq  Mean Sq F value Pr(>F)
## Groups      1  0.00352  0.0035168    0.1447  0.7049
## Residuals  64  1.55496  0.0242963
```

The PERMANOVA results can be affected when the multivariate dispersions are different across groups. To check this, we calculated multivariate dispersions, which are the distances of observations to their centroids, using the `betadisper` function of `vegan`. We compared the mean dispersion between the season groups using the `permutest` function with 999 permutations. We did not detect significant difference in dispersion, which indicates the spread of the communities (or beta diversity) is similar between seasons.

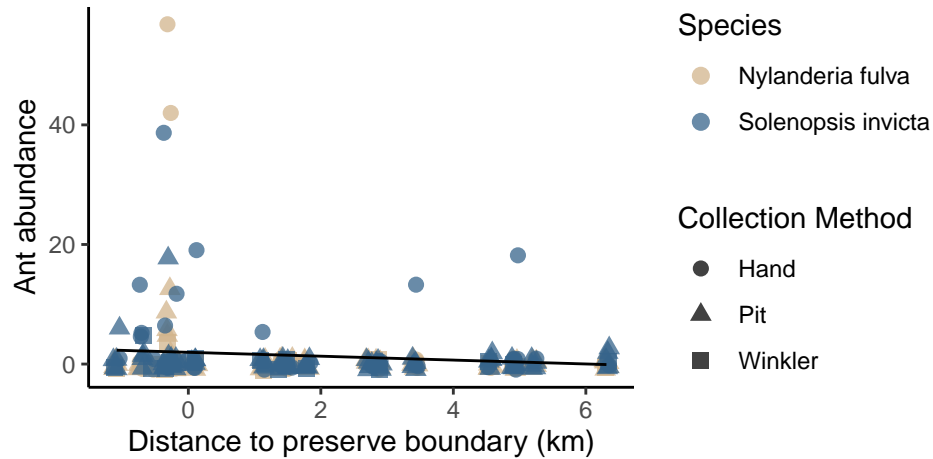
Probability of non-native ants decreases within the preserve



Each point represents whether or not a non-native ant species was detected in the sample, shapes represent

the method of collection (Hand = circles, Pitfall traps = triangles, and Winkler = squares). The fitted line is the Binomial model estimates for the probability of the presence of a non-native ant species within the trap, with site as a random effect.

Abundances of *S. invicta* and *N. fulva* at each collection site



Here, each point represents the abundance of *N. fulva* (tan) or *S. invicta* (blue) by collection method (Hand = circles, Pitfall traps = triangles, Winkler = squares) at a given sampling site that is some distance (km) to the nearest preserve boundary. The line is the best fit regression ($r^2 = .026$) with site as a random effect.

Next steps

- Decide whether to classify *P. fulvens* complex as native or non-native.
- Decide whether it makes more sense to present alpha diversity indices based on *occurrence* or *abundance*. (*I think abundance makes more sense, since the Shannon and Simpson indicies are abundance based*).