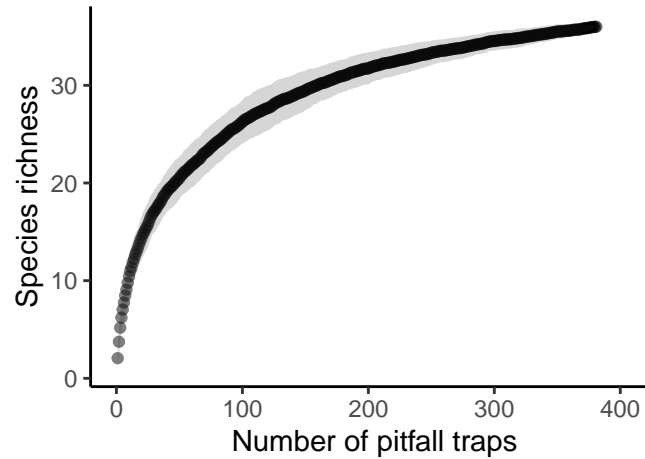# Big Thicket Ant Analysis

Marion Donald

10/3/2020

Species accumulation curve richness estimates

	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

We observed 36 species across the two years of the study, with an estimated total number of species present in this area to be approximately 42 +/- 6 species based on a Chao1 estimate (vegan R-package).

Rank abundance curves
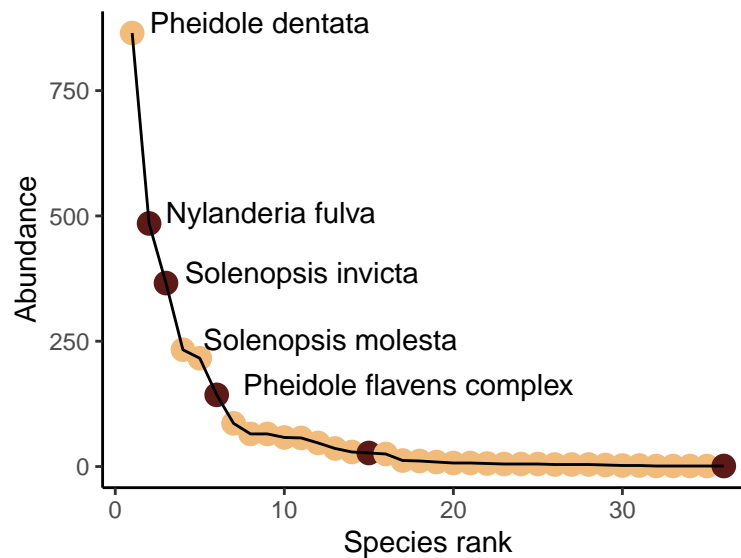
We used a rank abundance curve to visualize the evenness and relative abundance of native (tan) and invasive (maroon) species. *Need to get the name next to S. molesta.*

1

Alpha and Beta diversity from Gabriela's pitfall data – grouped by Site, Year, and Month

```
##    Year Month Site Nylanderia fulva_sum Solenopsis invicta_sum
## 1 2014     5  101                     41                       3
##    shannon_div_alpha
## 1          0.8304663
```

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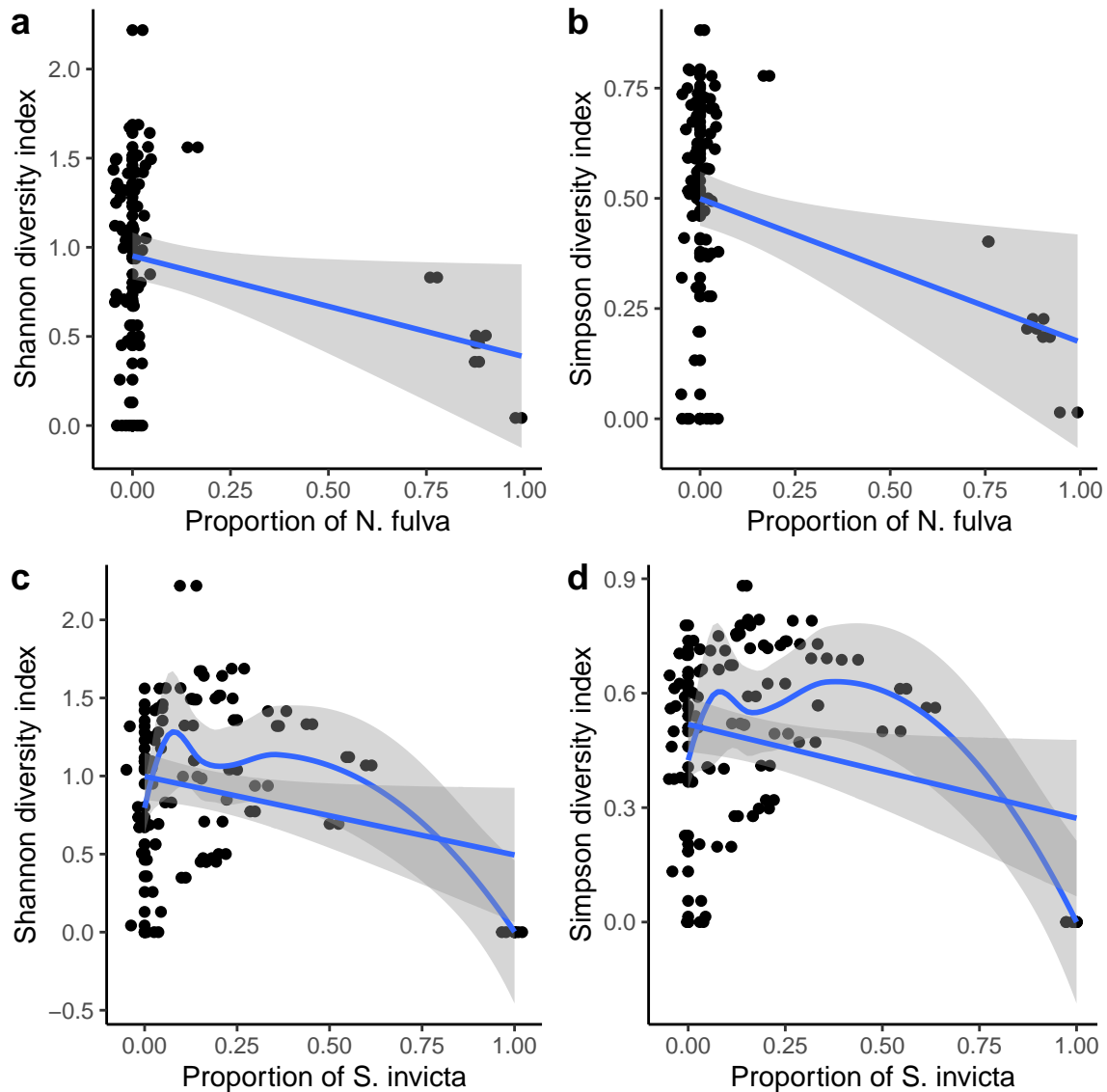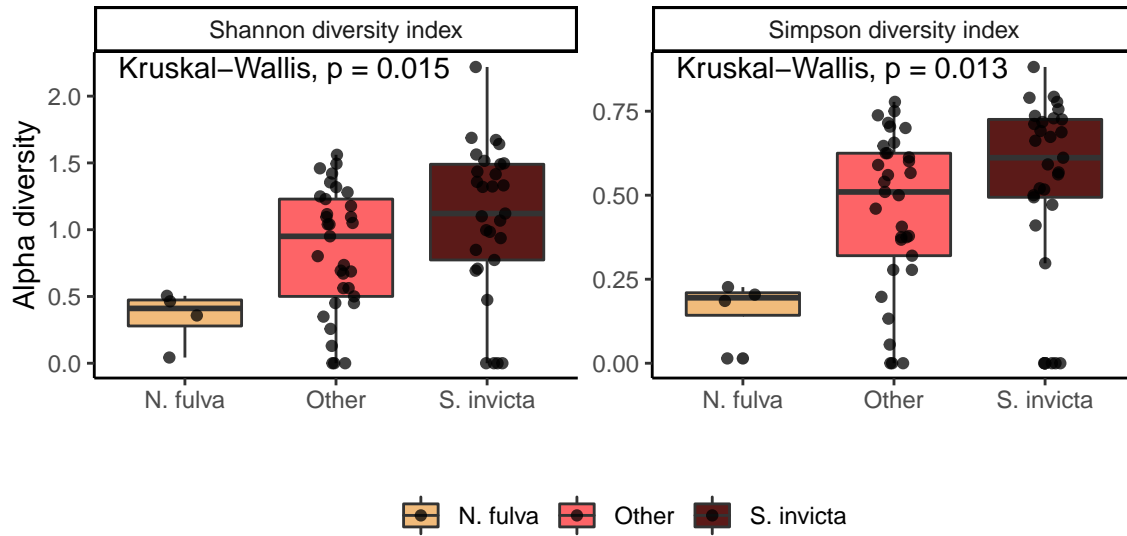

Shannon and Simpson alpha diversity indices in response to the proportion of *N. fulva* (a and b) and *S. invicta* (c and d). Linear and loess trend lines were fit to the data. *N. fulva* proportions bin pretty clearly between low and high. Alpha diversity has a more humped shaped relationship with the proportion of *S. invicta*.
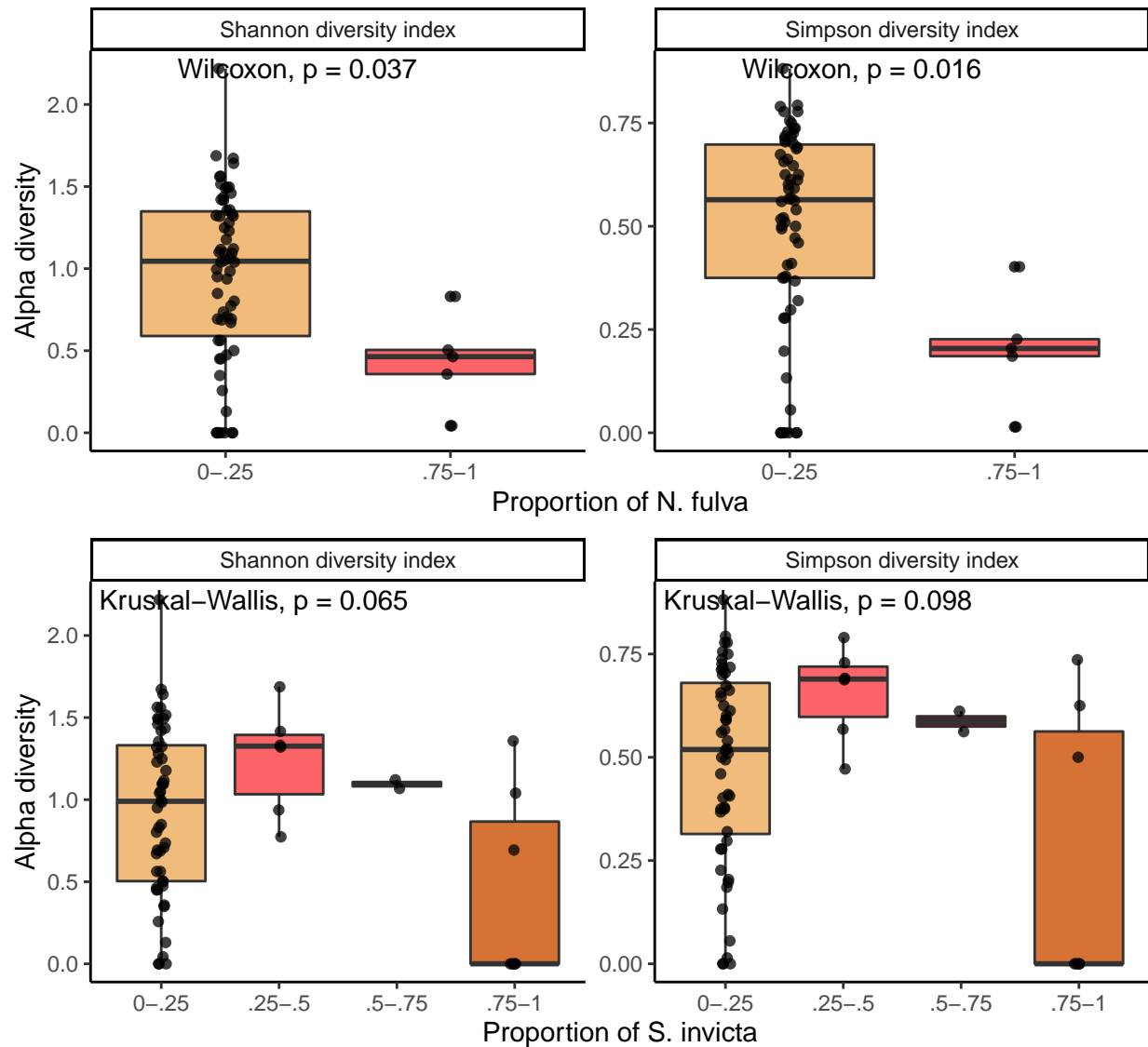
I think it's easier to see the pattern of reduced alpha diversity with the proportion of *N. fulva* and the peak of alpha diversity at intermediate proportion of *S. fulva* when the proportions are binned. (*Need to switch the colors, because their meaning ends up getting mixed up later on.)

```
## # A tibble: 1 x 5
##    Year Month  Site `Nylanderia fulva_sum` `Solenopsis invicta_sum`
##   <dbl> <dbl> <dbl>                  <dbl>                    <dbl>
## 1  2014     5   101                     41                        3
```

Alpha diversity indicies (Shannon and Simpson) binned by whether or not *N. fulva* or *S. invicta* is present. There was one station that had both of these species (Site 101 in May 2014 - 41 *N. fulva* and 3 *S. invicta*). This site was dropped from this analysis and the following beta diversity analyses.

NMDS visualization and beta diversity
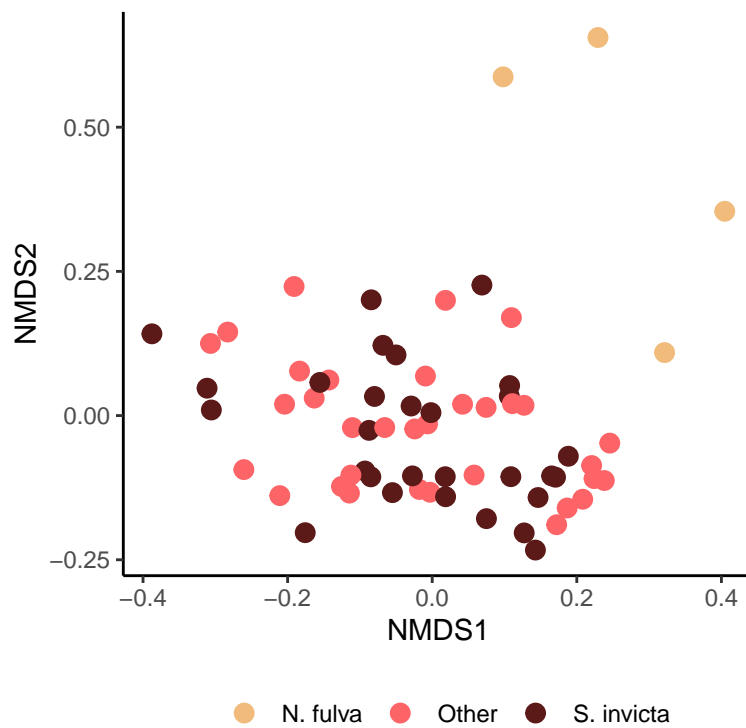
Visualization of the ant communities (using a Bray-Curtis dissimilarity matrix and k = 2). Each point represents the pooled community across pitfall traps within each site for each sampling period (Spring and Fall) within each year (2014 and 2015). *N. fulva* communities (tan) pull apart from the communities with *S. invicta* and neither *N. fulva* or *S. invicta*. While *S. invicta* communities appear to be similar in composition to communities with neither *N. fulva* or *S. invicta*.

	Df	SumsOfSqs	MeanSqs	F.Model	R2	Pr(>F)

	Df	SumsOfSqs	MeanSqs	F.Model	R2	Pr(>F)
invader	2	2.7189368	1.3594684	8.318291	0.2083649	0.001
Year	1	0.1972493	0.1972493	1.206925	0.0151161	0.239
Residuals	62	10.1327353	0.1634312	NA	0.7765190	NA
Total	65	13.0489214	NA	NA	1.0000000	NA

Invasive species identity and absence significantly affects ant community composition (p = 0.001, $R^2 = 0.208$), while collection year was not a significant predictor of ant community composition (p = 0.263, $R^2 = 0.0151$).
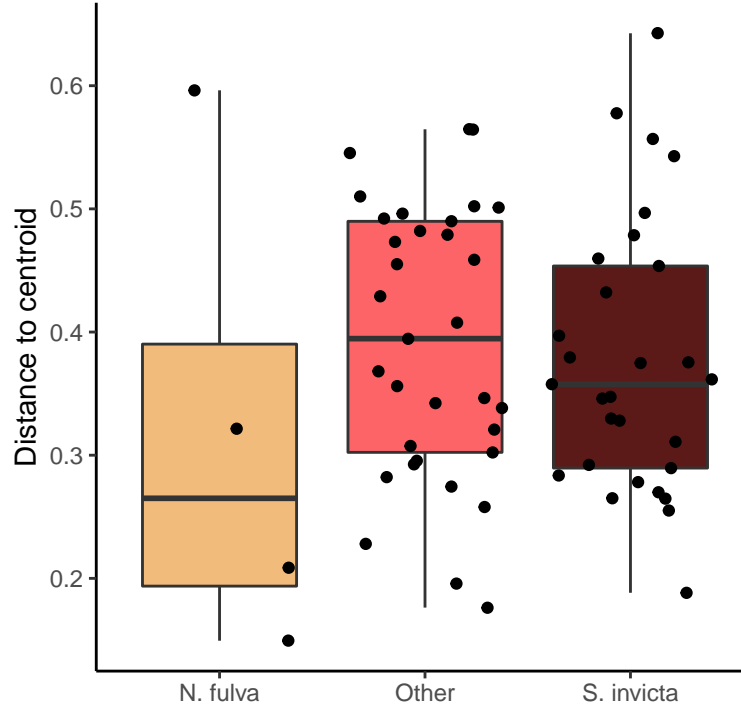

	diff	lwr	upr	p adj
S. invicta-N. fulva	0.0581420	-0.0905367	0.2068207	0.6180592
Other-N. fulva	0.0728987	-0.0746837	0.2204811	0.4660636
Other-S. invicta	0.0147567	-0.0561946	0.0857081	0.8719398

Beta diversity (distance to centroid) tends to be lower for ant communities with *N. fulva* compared to communities with either *S. invicta* or neither of these ant species. However, these results were not statistically significant based on a post-hoc Tukey HSD test (see table above).
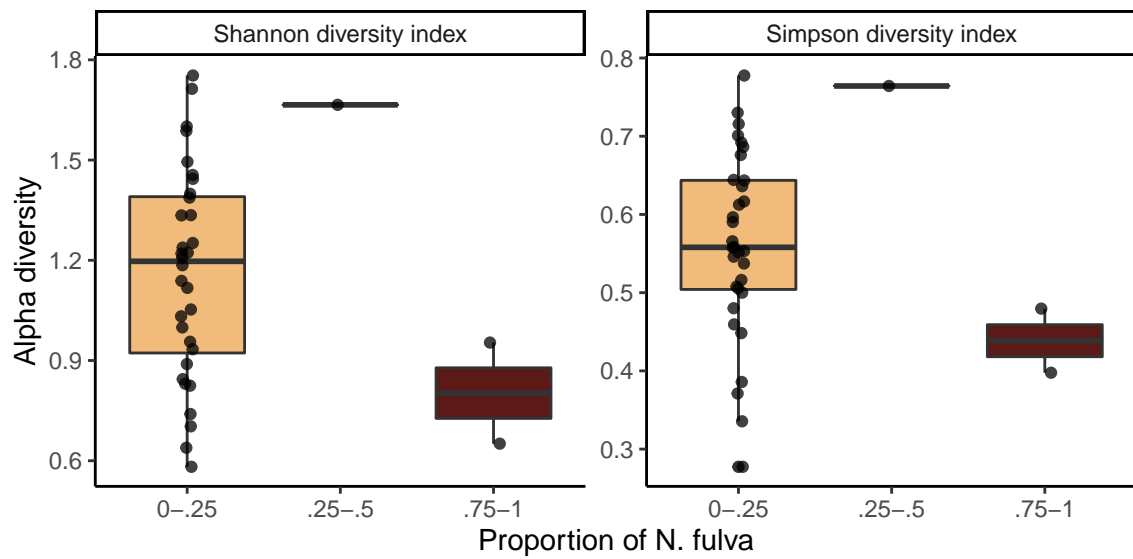
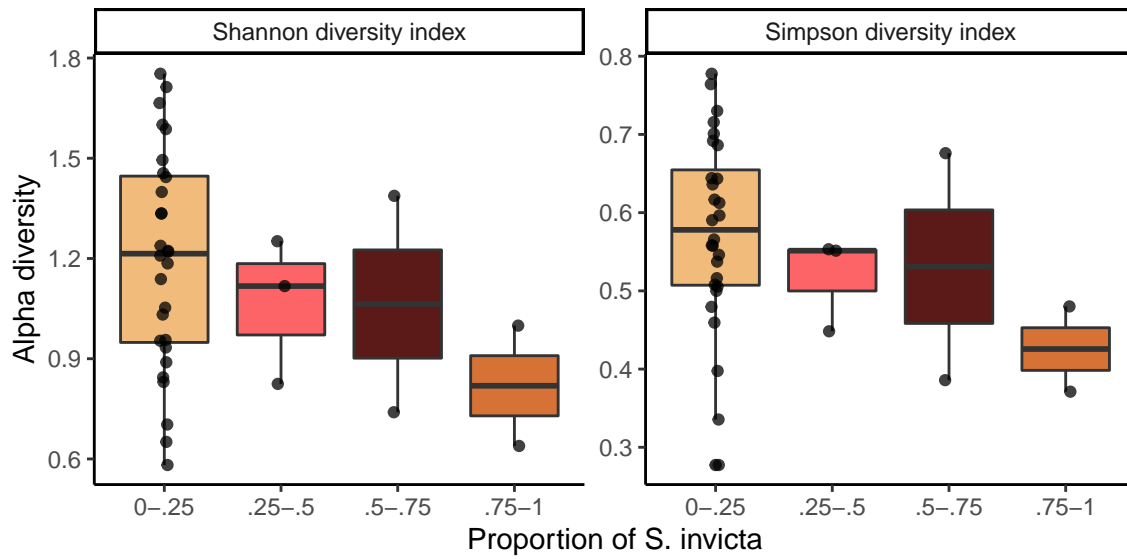## Alpha and Beta diversity from Gabriela's pitfall data – grouped by Site and Year

Combining months in this next version

```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```
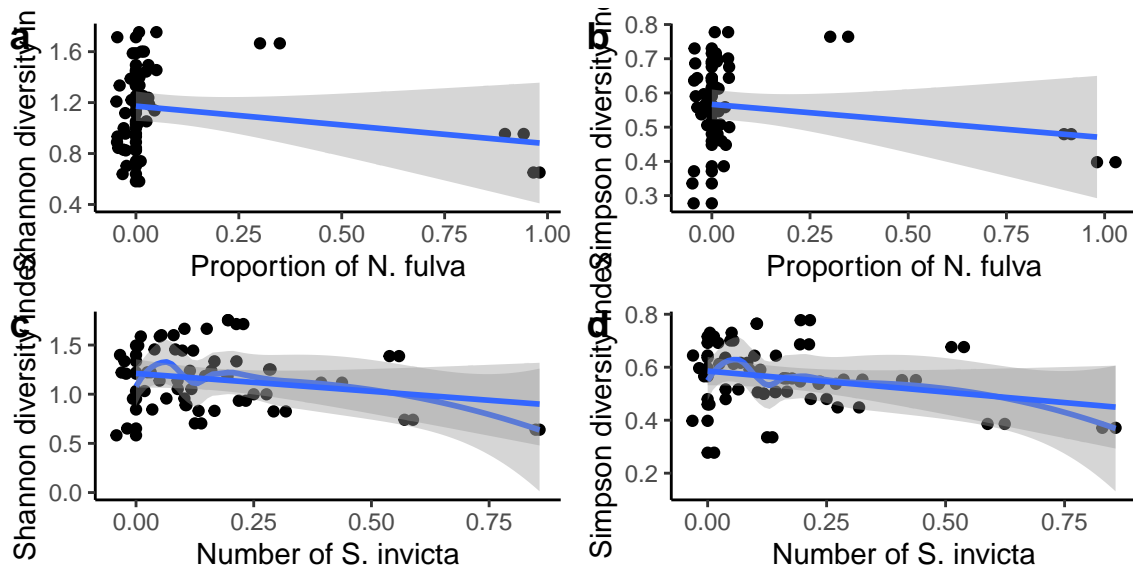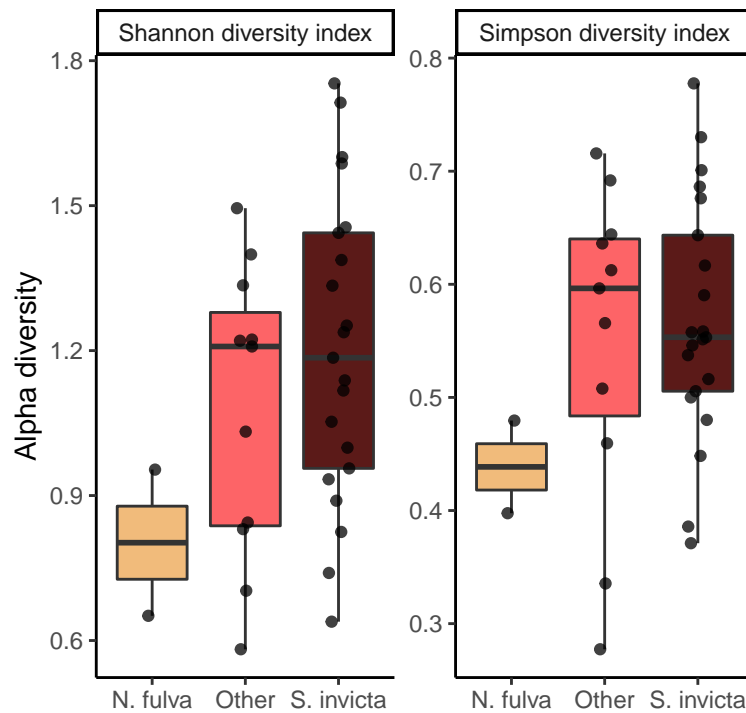
Similar to what we saw before, but now the hump shaped response for alpha diversity and *S. invicta* isn't as pronounced.

Alpha diversity tends to decrease with increasing proportions of *N. fulva* and *S. invicta* (but now we have very few points for medium to high proportions of these ants).

Think this figure is nice as it's clear that *N. fulva* communities have the lowest alpha diversity, while *S. invita* communities are similar to those that don't have either of these two species. Think this figure works better to be qualitative - since with only two points for *N. fulva* communities we don't have much power to say a lot.

NMDS visualization and beta diversity
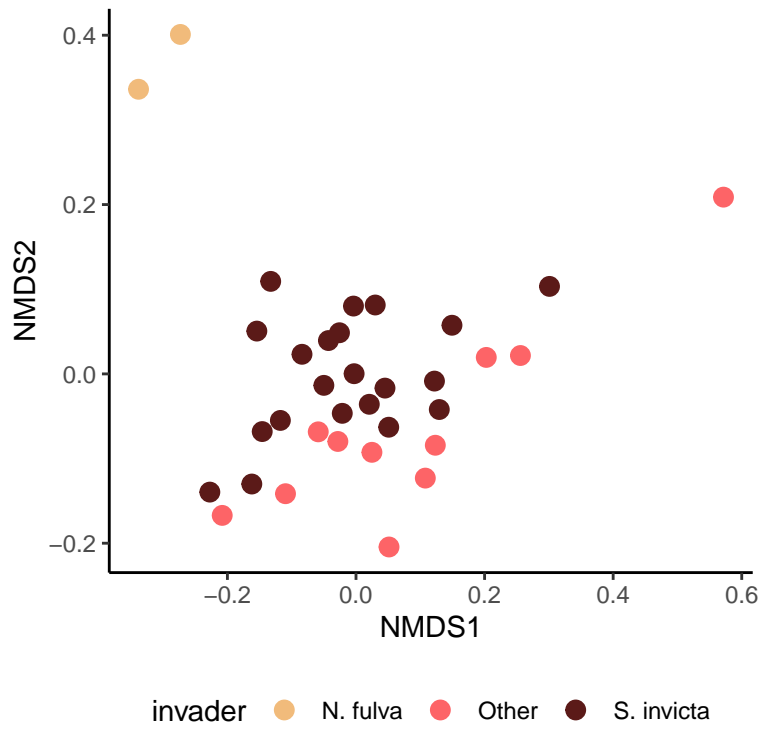
	Df	SumsOfSqs	MeanSqs	F.Model	R2	Pr(>F)
invader	2	0.985775	0.4928875	6.267027	0.2698858	0.043
Year	1	0.307356	0.3073560	3.908008	0.0841480	0.008
Residuals	30	2.359432	0.0786477	NA	0.6459661	NA
Total	33	3.652563	NA	NA	1.0000000	NA

Invasive species identity and absence significantly affects ant community composition (p = 0.044, $R^2 = 0.269$), as does collection year (p = 0.008, $R^2 = 0.089$), but to a lesser extent as it only explains approximately 9% of the variance while invader identity explains nearly 27%.
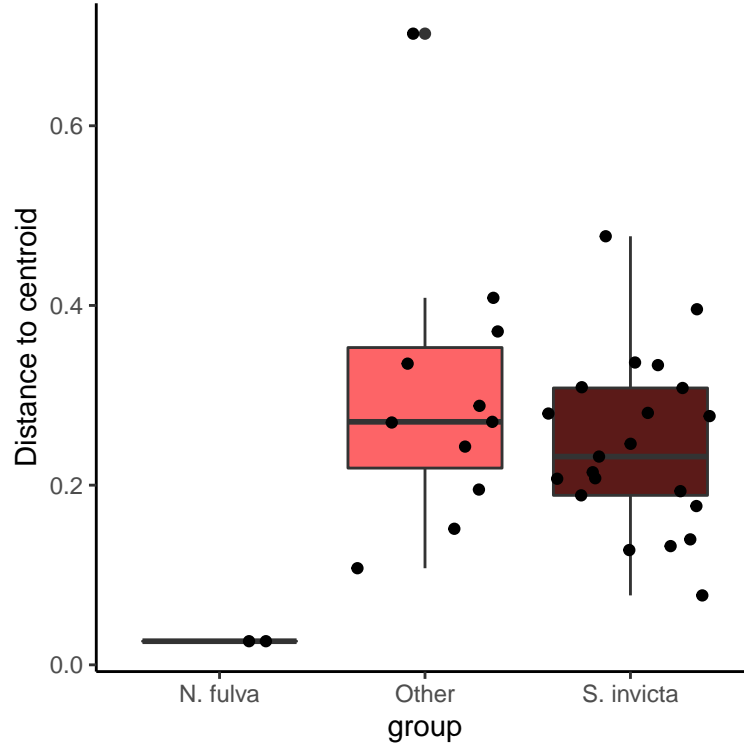
	diff	lwr	upr	p adj
S. invicta-N. fulva	0.2184299	0.0015248	0.4353351	0.0481321
Other-N. fulva	0.2775782	0.0522627	0.5028936	0.0131480
Other-S. invicta	0.0591483	-0.0499454	0.1682419	0.3873285

Beta diversity (distance to centroid) is significantly lower for ant communities with *N. fulva* compared to communities with either *S. invicta* (Tukey post-hoc HSD p = 0.048) or neither of these ant species (Tukey post-hoc HSD p = 0.013. While *S. invicta* communities and communities with neither of these ant species had similar beta diversities (Tukey post-hoc HSD p = 0.387). This indicates that ant communities with *N. fulva* are more similar in species composition than are communities with out *N. fulva*. (N.B. only have two data points here but they cluster together and are super separate from the other classifications, so I think this is a valid interpretation.)

Probability of non-native ants decreases within the preserve
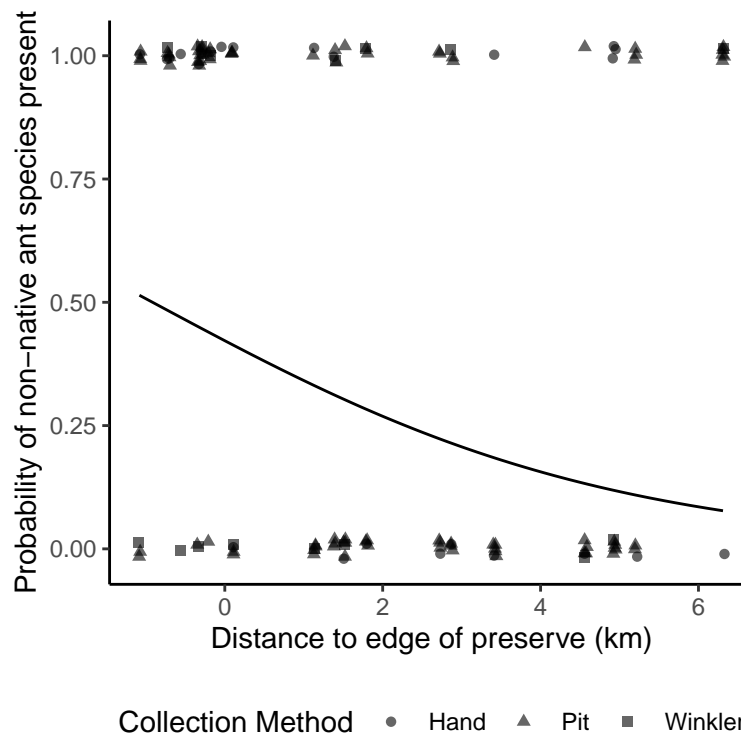
|	Df	AIC	BIC	logLik	deviance	Chisq	Chi Df	Pr(>Chisq)
glmer_all_0	2	223.8708	229.4788	-109.9354	219.8708	NA	NA	NA
glmer_all_fit	3	209.6907	218.1028	-101.8453	203.6907	16.18009	1	5.76e-05

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. This was an improved fit with site as a random effect and distance to preserve edge compared to that of the intercept with the random effect of site.

## Abundances of *S. invicta* and *N fulva* at each collection site
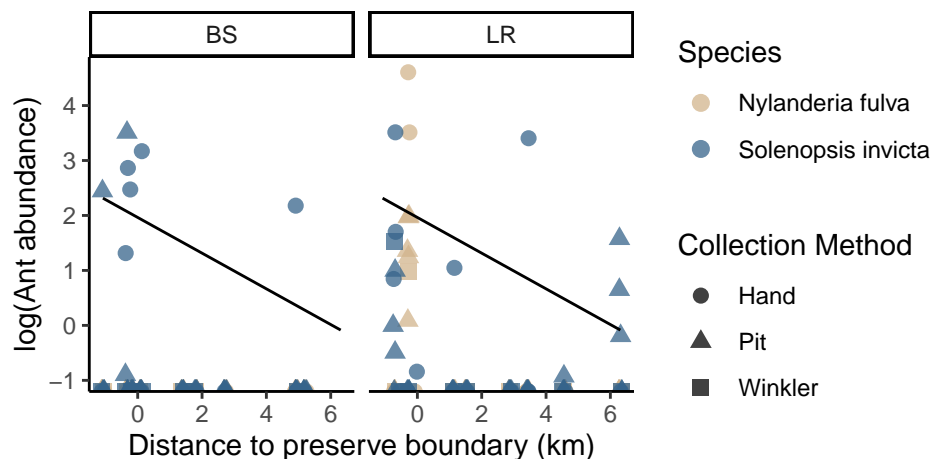
	Df	AIC	BIC	logLik	deviance	Chisq	Chi Df	Pr(>Chisq)
lmer_inv_0	3	1645.781	1656.509	-819.8907	1639.781	NA	NA	NA
lmer_inv_fit	4	1644.667	1658.971	-818.3334	1636.667	3.114593	1	0.0775939

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 and distance to edge as a fixed effect. However, this was only a slight improvement over the null model (intercept and site as a random effect). (*To me, this suggests that distance to edge of preserve is not a strong predictor of abundances of these two ant species and that this is most likely due to the high number of zeros and very low abundances in the data set. I think we could cut this figure and just include the stronger result (above) from the binomial model.*)
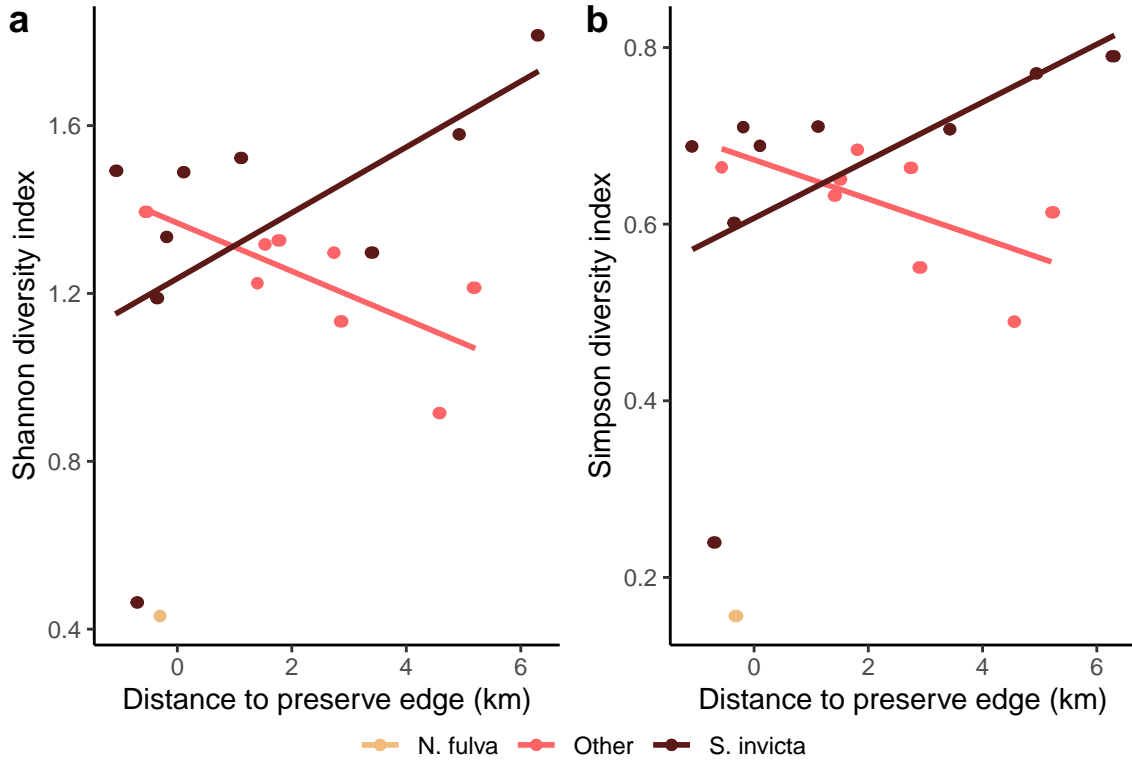
Alpha diversity increases in the interior of the preserve when when *S. invicta* is present and decreases when *S. invicta* and *N. fulva* are absent.
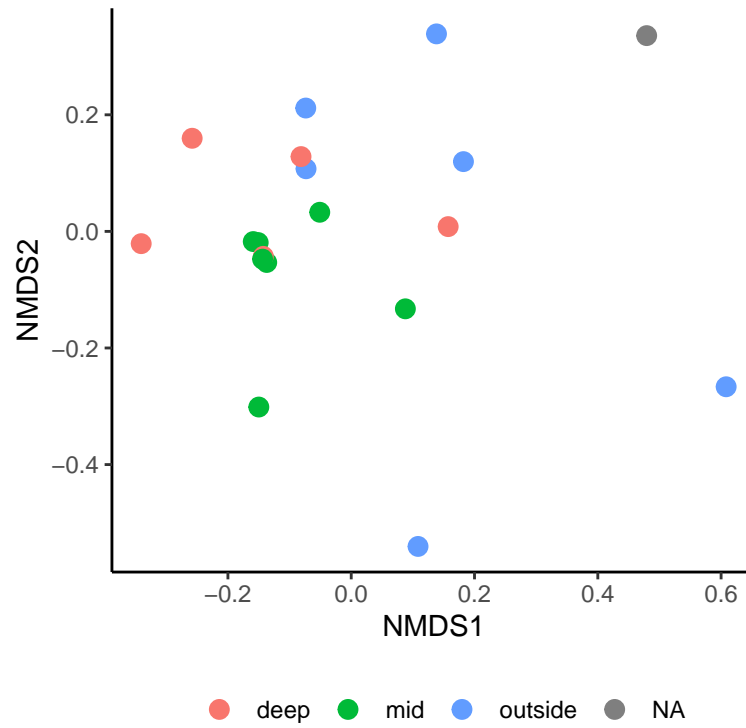
Visualization of the ant communities (using a Bray-Curtis dissimilarity matrix and k = 2). Each point represents the pooled community across pitfall traps. Colors represent outisde the preserve, mid distance within the preserve (0-3 km), and deep within the preserve (>3 km). *Running into an issue with the distance measures - since one of them is NA – need to figure out why this one is missing.*