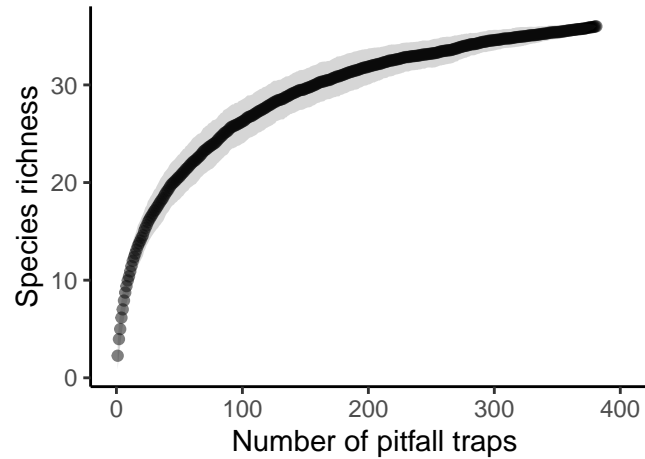


Big Thicket Ant Analysis

Marion Donald

12/3/2020

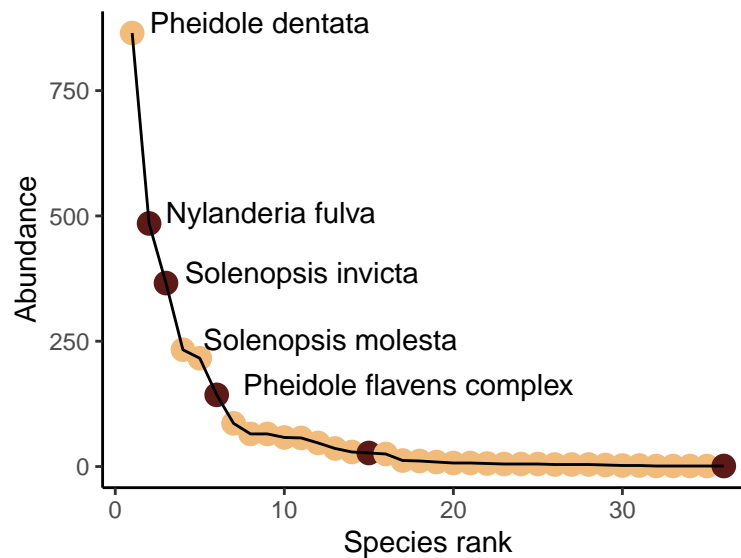
Species accumulation curve richness estimates



| | 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

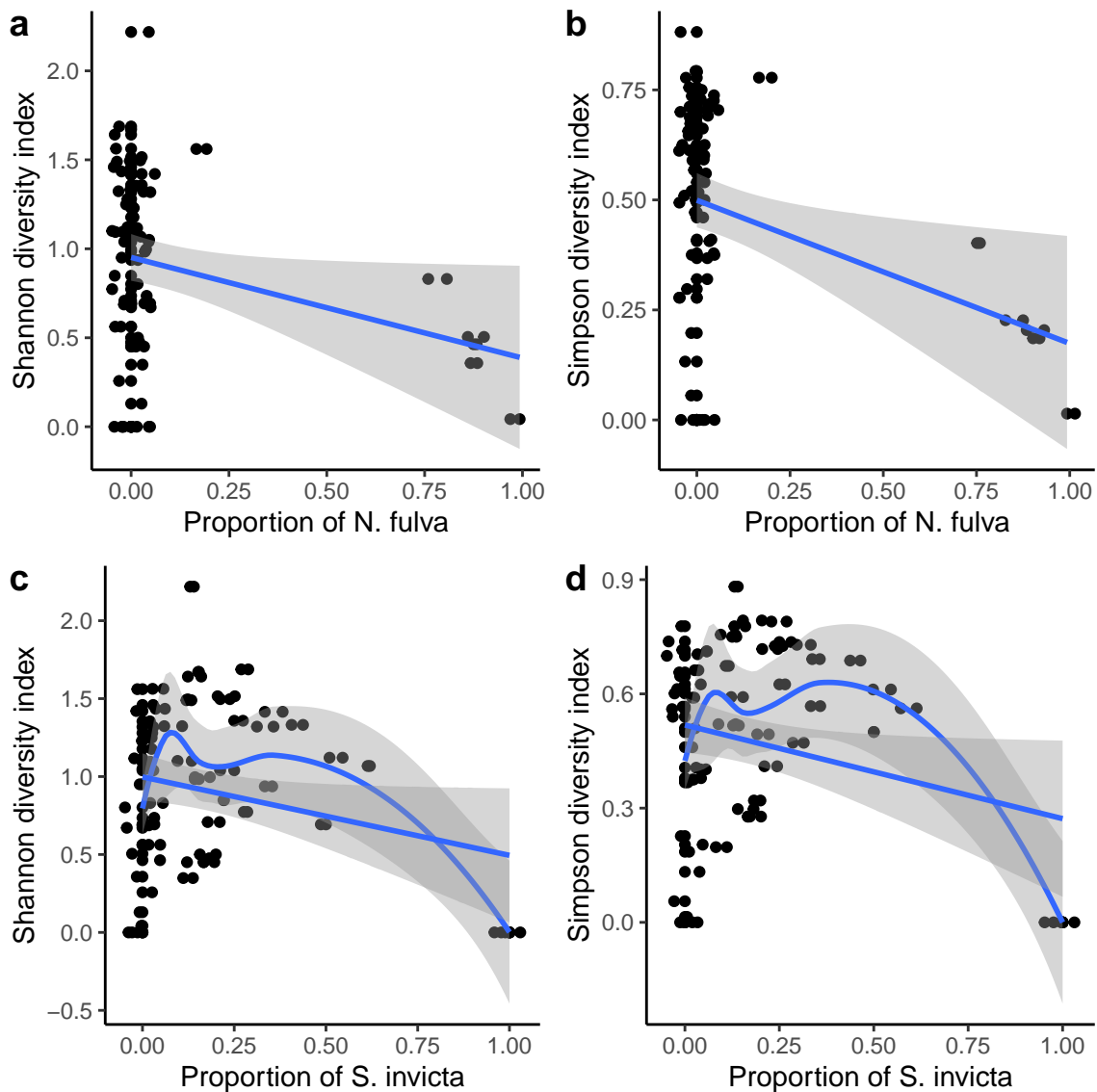


We used a rank abundance curve to visualize the evenness and relative abundance of native (tan) and invasive (maroon) species. *Need to get the name next to S. molesta.* (These are data from both Gabriela and Meghan.)

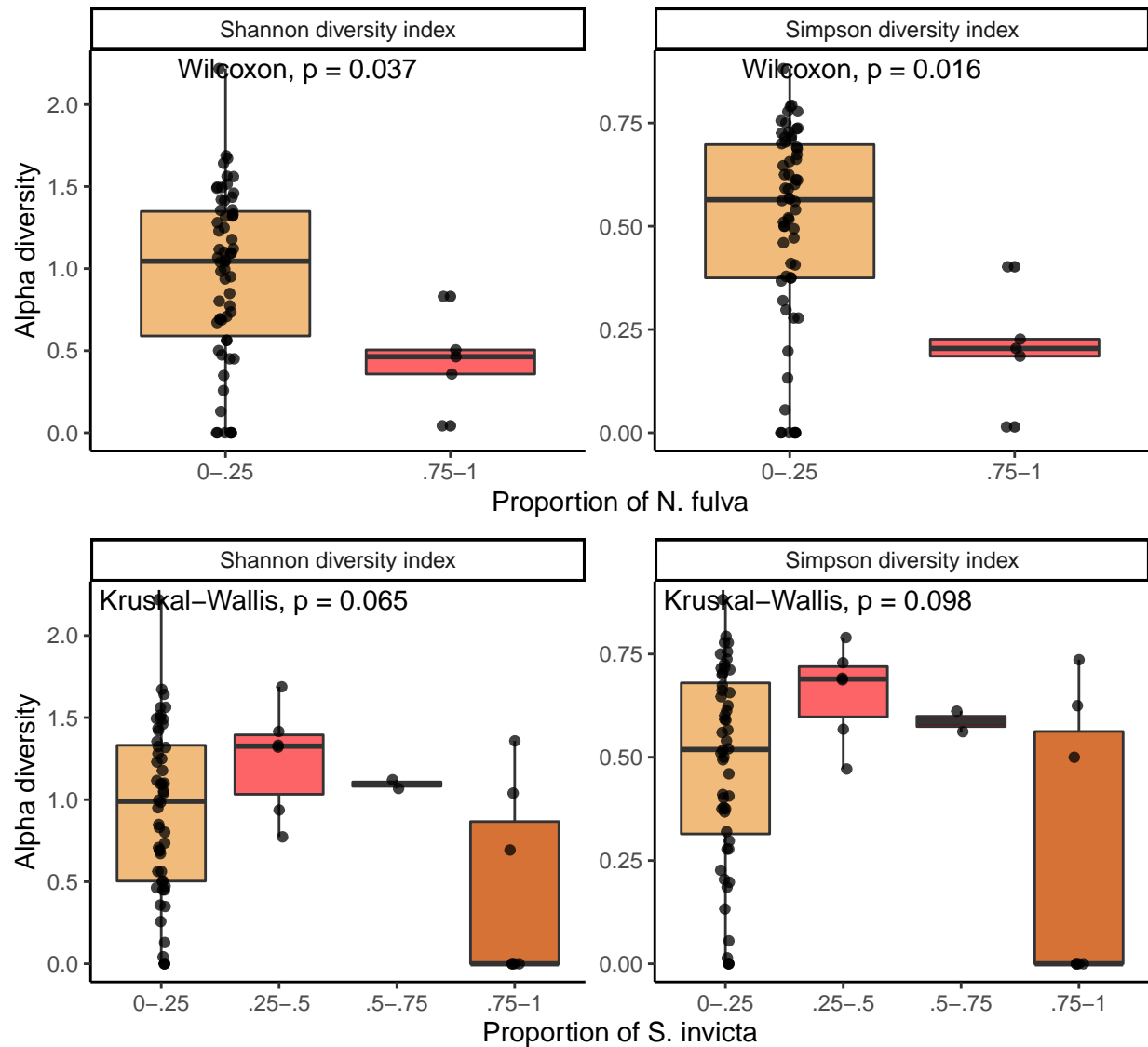
Alpha and Beta diversity from Gabriela's pitfall data – grouped by Site, Year, and Month

```
##   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'
```

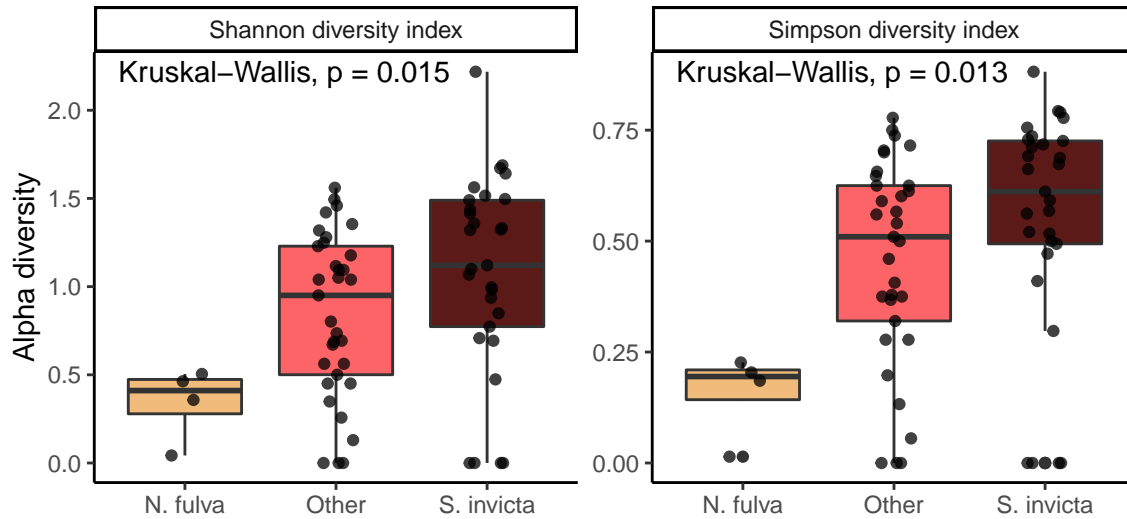


Shannon and Simpson alpha diversity indices in response to the proportion of *N. fulva* (a and b) and *S. invicta* (c and d). Linear and loess trend lines were fit to the data. *N. fulva* proportions bin pretty clearly between low and high. Alpha diversity has a more humped shaped relationship with the proportion of *S. invicta*. (Just Gabriela's data)



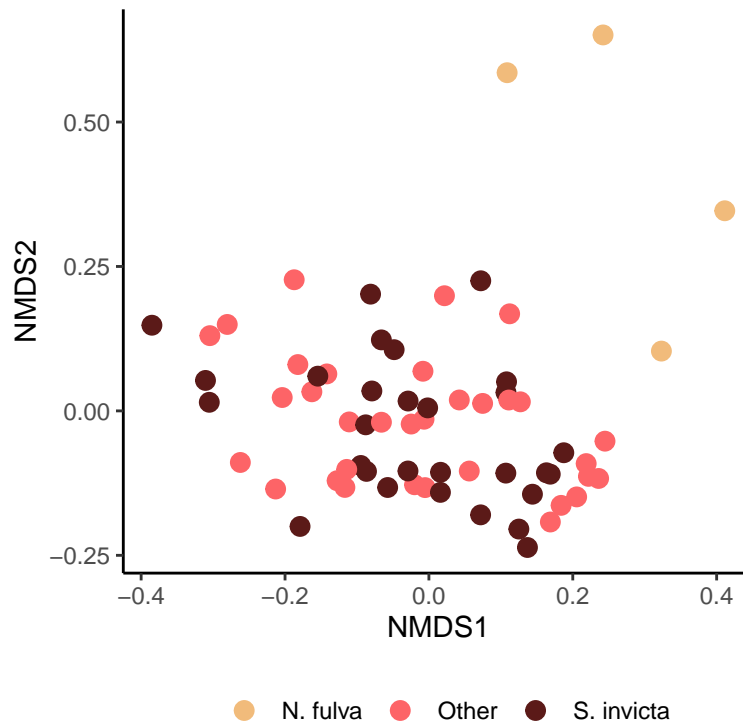
I think it's easier to see the pattern of reduced alpha diversity with the proportion of *N. fulva* and the peak of alpha diversity at intermediate proportion of *S. fulva* when the proportions are binned. (*Need to switch the colors, because their meaning ends up getting mixed up later on.)

```
## # 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 indices (Shannon and Simpson) binned by whether or not *N. fulva* or *S. invicta* is present. Makes it easy to see that *N. fulva* sites have the lowest alpha diversity, while sites with *S. invicta* or neither of these ant species have similar alpha diversity. 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.

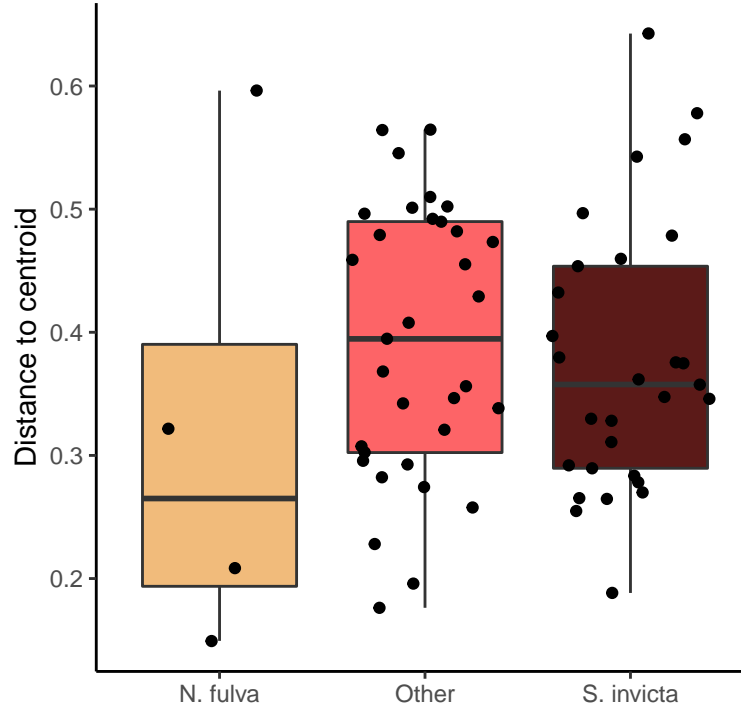
NMDS visualization and beta diversity



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) |
|-----------|----|------------|-----------|----------|-----------|--------|
| invader | 2 | 2.7189368 | 1.3594684 | 8.318291 | 0.2083649 | 0.001 |
| Year | 1 | 0.1972493 | 0.1972493 | 1.206925 | 0.0151161 | 0.259 |
| 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 ($p = 0.263$, $R^2 = 0.0151$).



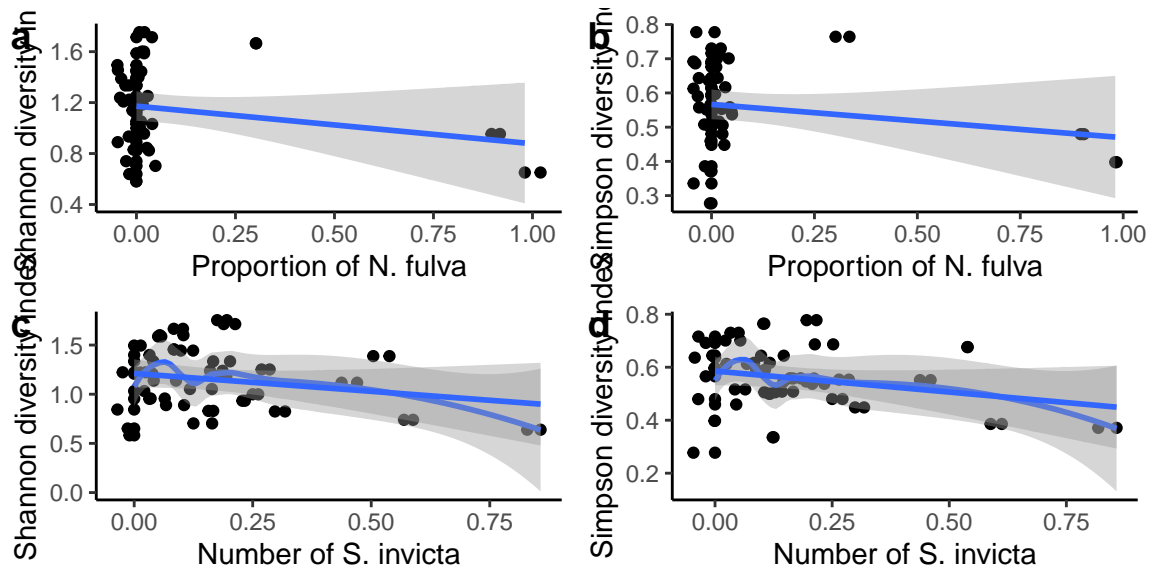
| | diff | lwr | upr | p adj |
|---------------------|-----------|------------|-----------|-----------|
| S. invicta-N. fulva | 0.0581420 | -0.0905367 | 0.2068207 | 0.6180592 |
| Other-N. fulva | 0.0728987 | -0.0746837 | 0.2204811 | 0.4660636 |
| Other-S. invicta | 0.0147567 | -0.0561946 | 0.0857081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

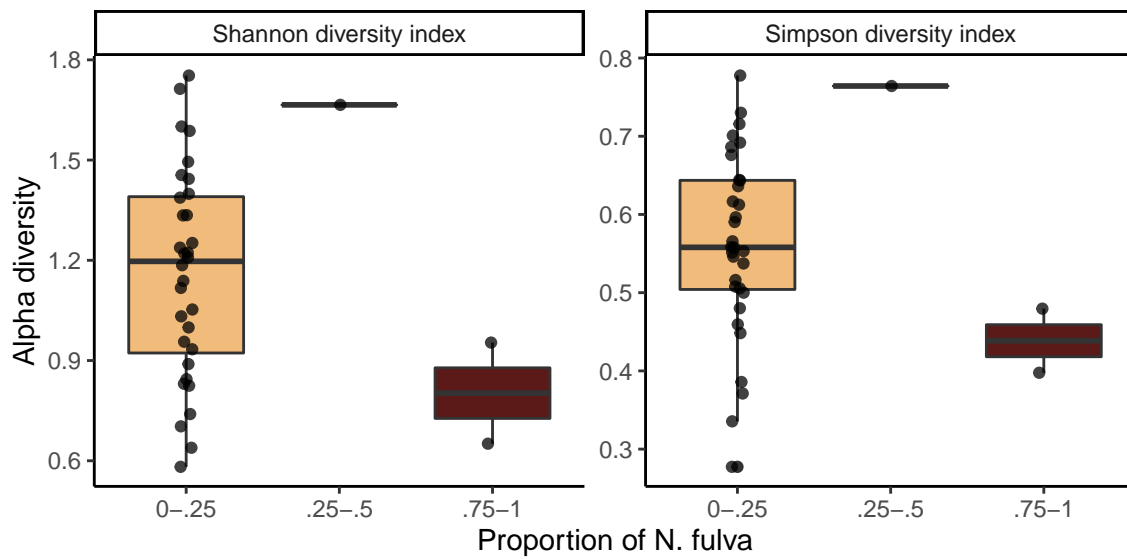
Alpha and Beta diversity from Gabriela's pitfall data – grouped by Site and Year

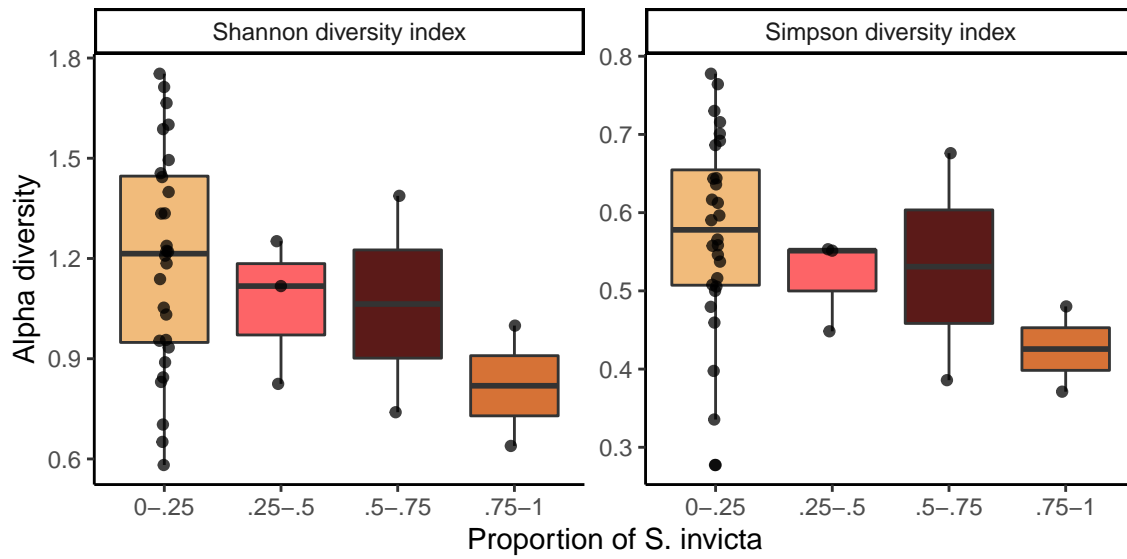
Combining months in this next version

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

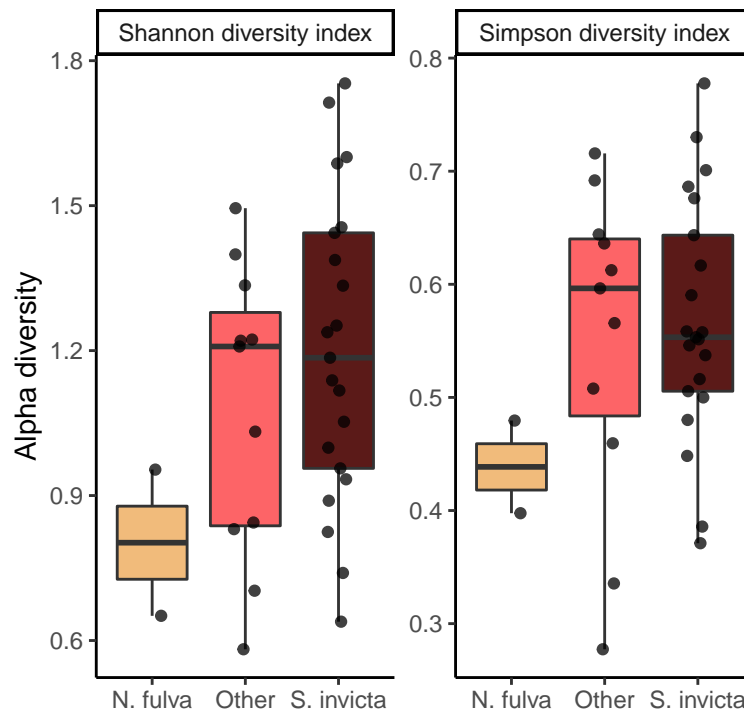


Similar to what we saw before, but now the hump shaped response for alpha diversity and *S. invicta* isn't as pronounced.



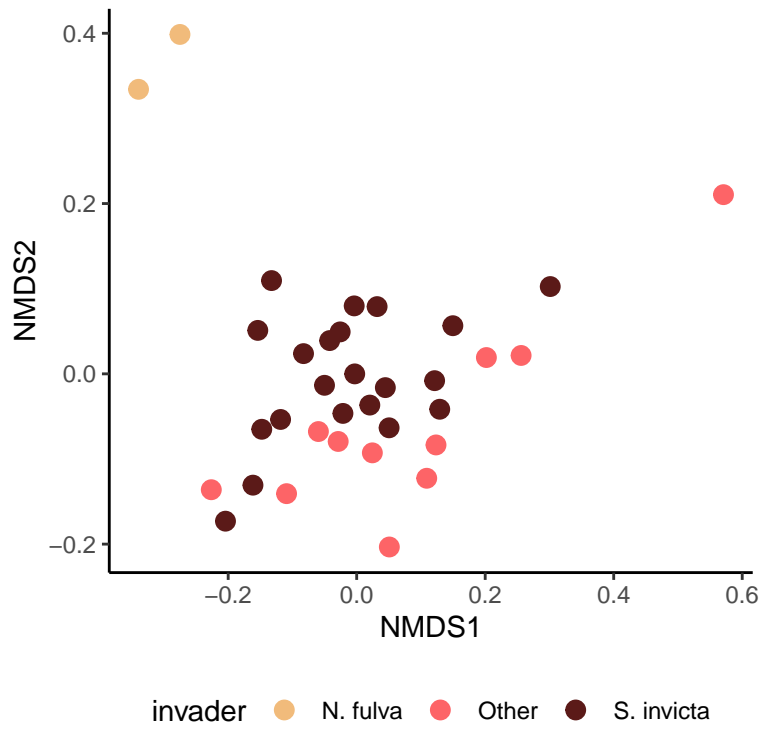


Alpha diversity tends to decrease with increasing proportions of *N. fulva* and *S. invicta* (but now we have very few points for medium to high proportions of these ants).



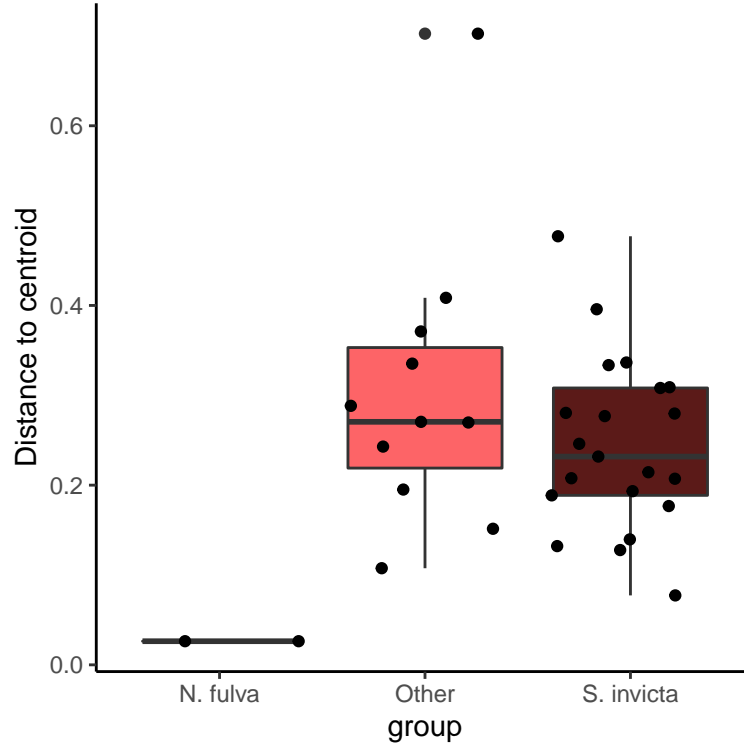
Think this figure is nice as it's clear that *N. fulva* communities have the lowest alpha diversity, while *S. invicta* communities are similar to those that don't have either of these two species. Think this figure works better to be qualitative - since with only two points for *N. fulva* communities 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 | 0.032 |
| Year | 1 | 0.307356 | 0.3073560 | 3.908008 | 0.0841480 | 0.009 |
| Residuals | 30 | 2.359432 | 0.0786477 | NA | 0.6459661 | NA |
| Total | 33 | 3.652563 | NA | NA | 1.0000000 | NA |

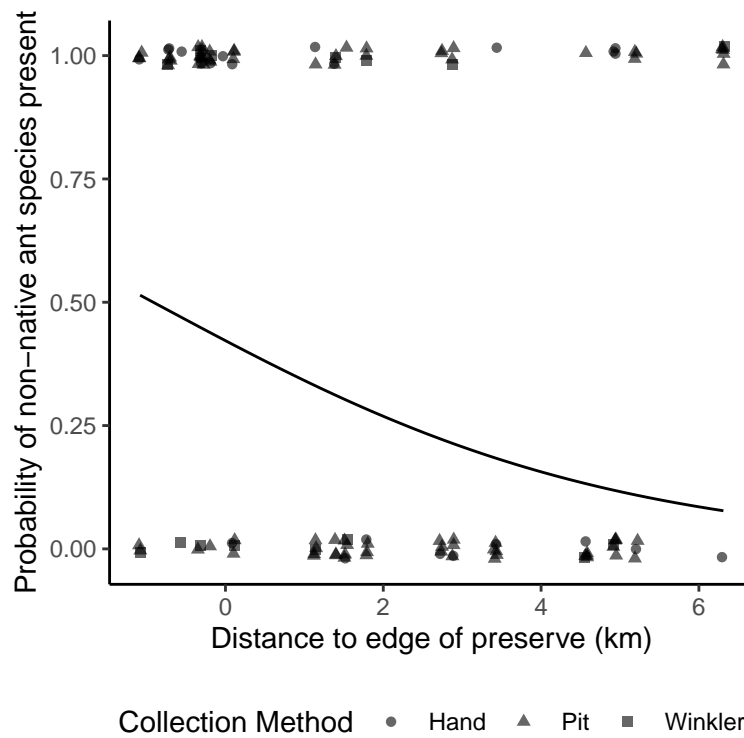
Invasive species identity and absence significantly affects ant community composition ($p = 0.044$, $R^2 = 0.269$), as does collection year ($p = 0.008$, $R^2 = 0.089$), but to a lesser extent as it only explains approximately 9% of the variance while invader identity explains nearly 27%.



| | 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.)

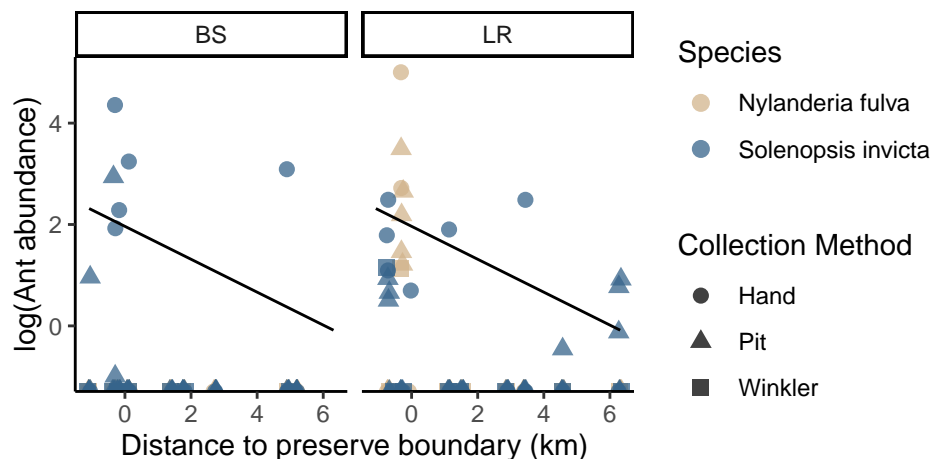
Probability of non-native ants decreases within the preserve



| | 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 |

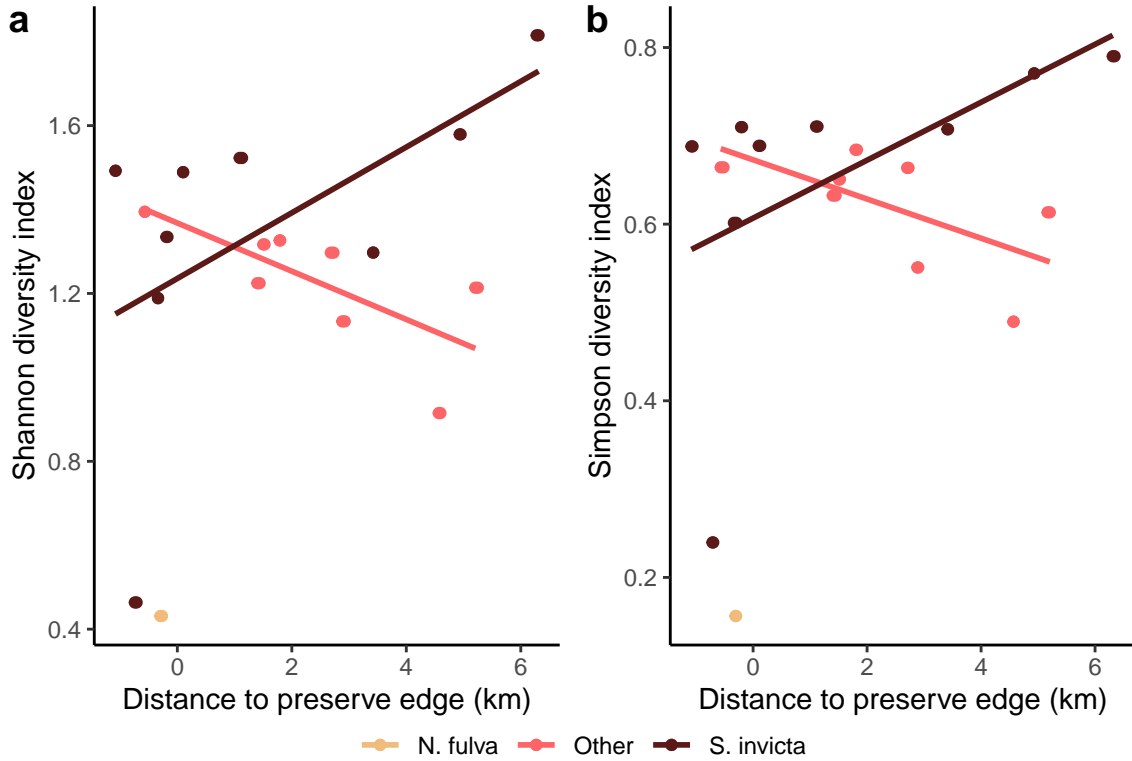
Each point represents whether or not a non-native ant species was detected in the sample, shapes represent the method of collection (Hand = circles, Pitfall traps = triangles, and Winkler = squares). The fitted line is the Binomial model estimates for the probability of the presence of a non-native ant 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

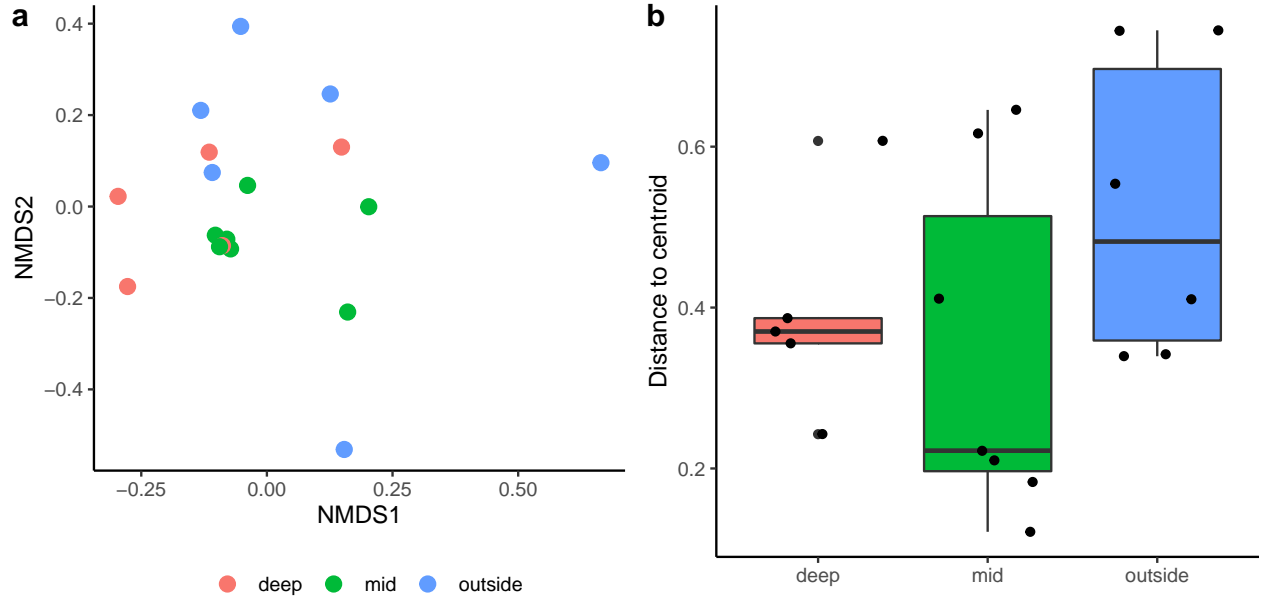


| | Df | AIC | BIC | logLik | deviance | Chisq | Chi Df | Pr(>Chisq) |
|--------------|----|----------|----------|-----------|----------|----------|--------|------------|
| lmer_inv_0 | 3 | 1645.781 | 1656.509 | -819.8907 | 1639.781 | NA | NA | NA |
| lmer_inv_fit | 4 | 1644.667 | 1658.971 | -818.3334 | 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 *S. invicta* is present and decreases when *S. invicta* and *N. fulva* are absent.



(a) NMDS visualization of ant communities colored by distance to edge ($k = 2$) - distance to edge is not a significant predictor of ant community composition (PERMANOVA $p = 0.056$, $R^2 = 0.172$) and (b) beta diversity of these communities was similar across the different distances (Tukey post-hoc HSD $p > 0.05$). Each point represents the pooled community across all collection methods within a Site Code. Colors represent outside the preserve (< 0 km), mid distance within the preserve (0-3 km), and deep within the preserve (> 3 km).

Adonis PERMANOVA table

| | Df | SumsOfSqs | MeanSqs | F.Model | R2 | Pr(>F) |
|-----------|----|-----------|-----------|----------|-----------|--------|
| dist_bins | 2 | 0.7557619 | 0.3778809 | 1.567338 | 0.1728554 | 0.043 |
| Residuals | 15 | 3.6164594 | 0.2410973 | NA | 0.8271446 | NA |
| Total | 17 | 4.3722213 | NA | NA | 1.0000000 | NA |

Tukey post-hoc HSD table

| | diff | lwr | upr | p adj |
|--------------|-----------|------------|-----------|-----------|
| deep-mid | 0.0482238 | -0.2367225 | 0.3331702 | 0.8996570 |
| outside-mid | 0.1781641 | -0.0925766 | 0.4489048 | 0.2341406 |
| outside-deep | 0.1299402 | -0.1647341 | 0.4246145 | 0.5022522 |