Investigation of Arthropod Diversity across Invaded and Restored Saltmarsh Communities

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Abstract

Ecosystem restoration has been a critical strategy for alleviating ecological damages. Jiang et al. (2022) investigated restoration of saltmarshes in the Yangtze estuary of China as saltmarshes provide an important role in nutrient cycling and are highly vulnerable to invasions. Our study finds differences in Shannon diversity index (SDI) across invaded and restored communities where an increase in soil and leaf traits associated with principal component axis one (PC1) increases SDI. This change in PC1 is associated with increased leaf nitrogen and soil pH and decreased soil nitrogen and carbon, plant biomass and density . PC1 is consistent in its ability to predict differences in diversity between the five communities.

Introduction

Ecosystem restoration is a critical strategy for mitigating the ecological damage caused by invasive species. While saltmarshes are particularly vulnerable to plant invasions [1], they are important for nutrient cycling [2]. Restoration efforts often involve the removal of invasive species and the reintroduction of native plants, a process that can partially restore ecosystem functions. However, the extent to which such interventions fully recover pre-invasion dynamics remains an area of active investigation [3].

Recent work by Jian et al. (2022) explored how arthropod assemblages and their trophic interactions change between communities at varying degrees of invasion (Figure 1), in addition to the abiotic and biotic variables that may explain these differences. The authors were correct in their prediction that invasion of the exotic plant *Spartina alterniflora* in Chinese saltmarshes will result in changes in arthropod diversity and trophic interactions, as well as that, those said changes can be *reversed* with the *removal* of the invasive plant and *restoration* of the native plant *Phragmites australis*. The authors also found that aboveground biomass, plant density, leaf nitrogen, and soil salinity could jointly explain the variation in arthropod community structure among plant communities.

In our current study, we leverage the dataset [4] to determine which environmental variables are the best predictors of arthropod *diversity*. We set out to investigate: if different saltmarsh communities significantly differ in their SDI? Within a community, which soil or plant traits, represented by principal component axes, are the strongest predictor of SDI? Do the predictor traits (PC1 and/or PC2) differ based on different community types?

Methods

Data Description

Using Jiang et al.'s (2022) *Rawdata.xlsx*, we separated and simplified each sheet as their own .csv Then, we rearranged the *Arthrpod_List.csv* data frame columns and rows We used this transformed data frame to calculate SDI and then added their values on the rest of the data frames (*Plant_Traits.csv* and *Soil Traits.csv*) for future analysis of predictors of SDI[1].

Data Analysis

We calculated SDI using the `diversity(index = "shannon")` function from the `vegan` package (and manually to ensure accuracy). The SDI index was chosen as it measures diversity by considering both species richness and evenness and was used by Jiang et al. (2022) allowing

1. *Refer to the appendix for a detailed description of the columns in plant_trais.csv and soil_traits.csv*

comparability (Figure 3). However with SDI alone, we cannot decipher which species have a major influence on controlling community dynamics. For that, we must compare each species' population size, density, biomass, productivity, etc.

After we calculated the SDI for each site, we conducted maximum log-likelihood estimations for a normal, gamma, and inverse gaussian probability density distribution to determine what type of linear regression model to use for future analysis (Table 1, Figure 4). We then conducted a pairwise correlation analysis, ran a principal component analysis with the 11 plant and soil traits (Figure 5), and loaded the PC axes onto a linear mixed model. We used Akaike Information Criterion to determine the best model.

Results

The average SDI for each of the five communities was calculated (Figure 2) and was found to be equivalent to Jiang et al. (2022). Using the MLE, the normal distribution had the highest log likelihood (Table 1, Figure 4).

Pairwise correlations revealed significant relationships among soil traits with soil moisture, soil C and N showing strong positive correlation ($r > 0.85$) while plant traits such as plant density and leaf N had weak correlations with other variables (Figure 5??). PC1 (55.64%) and PC2 (10.5%) explained most of the variance in SDt (Figure 6). PC1 was not dominated by any specific trait (excluding leaf and soil P, and leaf C) contributing ~9.6% of the total variance whilst PC2 was primarily influenced by soil C (20.1%) and plant density (16.3%) (Table 2). Using regressions of SDI on PC1 and PC2 for each community compared to the regression on all sites with differing intercepts determined that 'Community' should be used as a random effect in our models.

We used SDI as the response variable and combinations of the PC1 and PC2 and fixed effects in our linear mixed models. AIC indicated that the best model had PC1 as the predictor and community as a random effect (Figure 8). PC1 significantly positively predicted SDI ($\beta=0.05765$) , indicating higher values of PC1 are associated with greater SDI. 'Community' accounted for 4.11% of the variation in SDI a higher PC1 and by extension, SDI, is associated with higher leaf N, soil pH, and, to a lesser degree, leaf C and leaf P. While a lower PC1 and SDI is associated with a higher soil N, soil C, plant biomass, and density (Figure 7).

Discussion

We found restored wetlands to have the highest SDI and non-invaded wetlands to have the lowest. This perhaps unexpected finding has repeatedly been found across studies. Invasion of *Spartina* increases plant species richness, which increases arthropod diversity by creating more niches. Our model predicts this pattern with our baseline intercept of SDI differing but predictors remaining constant (Figure 9).

We found SDI to be most strongly predicted by increased leaf N and soil pH, and decreased soil N, soil C, plant biomass and density, consistent with Jiang et al. (2022), who identified overlapping predictors (leaf N, plant biomass, and density) but did not specify directional effects. Similar to other literature findings, our results suggest that leaf pH and leaf N are similarly correlated [5]. Increased leaf nutrients, in this case nitrogen, increases arthropod

diversity [6]. Additionally, the native *Phragmites* has higher leaf nitrogen levels than the exotic *Spartina* [7]. However, our results found that the monoculture phragmites communities had the lowest arthropod diversity. These patterns of diversity may differ when considering trophic levels, notably herbivores . Our findings indicate the importance of considering a wide breadth of variables, and their interactactions in invasive species management.

References

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Appendix

Figure #1: Description of the five different saltmarsh communities.

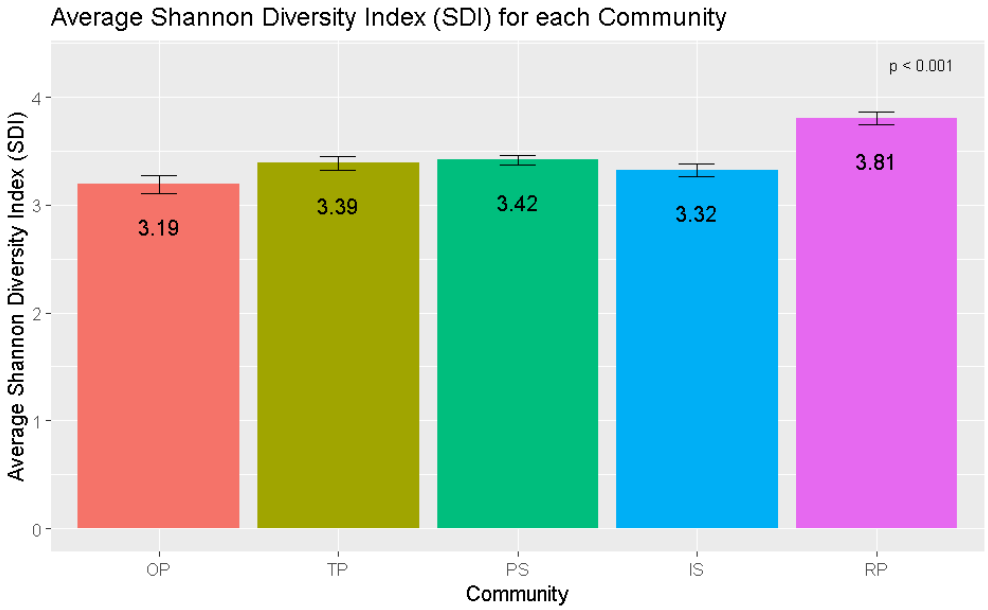

Figure #2: The average Shannon diversity index (SDI) of arthropod assemblages in the five plant communities (OP: original *Phragmites* monoculture, TP: threatened *Phragmites* monoculture, PS: *Phragmites–Spartina* mixture, IS: invasive *Spartina* monoculture, and RP: restored *Phragmites* monoculture). Standard Error = 0.036, $p < 0.001$ indicates a significant difference across communities.

Average Shannon diversity index for each of the five communities (OP)

Distribution	Max Log-Likelihood	Parameters
Normal	-19.28	Mean: 3.43, SD: 0.31
Gamma	-20.56	Shape: 116.1, Scale: 0.0295
Inverse Gaussian	-21.73	Mu: 3.4, Lambda: 379.6

Table #1: Results of maximum log-likelihood estimations for normal, gamma, and inverse gaussian probability density distributions. The normal distribution has the highest maximum log-likelihood and therefore is the most suitable distribution for SDI.

Variable (soil or plant trait)	PC1	PC2
Soil Carbon (soil_C)	-0.3270867	0.44789885
Soil Nitrogen (soil_N)	-0.3547747	0.37618972
Soil Phosphorus (soil_P)	-0.2202713	0.02402190
Soil pH (soil_pH)	0.3376054	-0.22697065
Soil Salinity (soil_sal)	-0.2806422	-0.39256180
Soil Water (soil_wat)	-0.3539508	0.23179513
Biomass Above Ground (biomass_above)	-0.3274486	-0.30076393
Plant Density (plant_dens)	-0.3154603	-0.40412756
Leaf Nitrogen (leaf_N)	0.3142092	0.06465172
Leaf Carbon (leaf_C)	0.2491950	0.08525667
Leaf Phosphorus (leaf_P)	0.1817902	0.36430053

Table #2: Results of `prcomp()` function for PC1 and PC2 with their respective trait associations where positive and negative values indicate clustered variables for their respective PC axis.

$$H' = -\sum_{i=1}^{R} p_i \ln p_i$$

p_i = the proportion of individuals of one species with respect to the total number of individuals of all species
R = number of unique species

Figure #3: Formula for calculating the Shannon diversity index (SDI) for each plot.

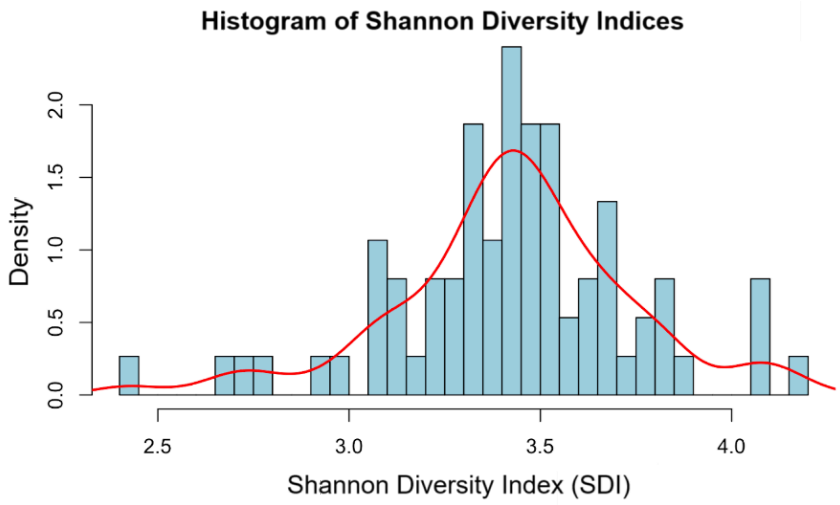

Figure #4: Histogram showing the distribution of the Shannon diversity indices (SDI), visually indicating a ‘near-normal’ distribution.

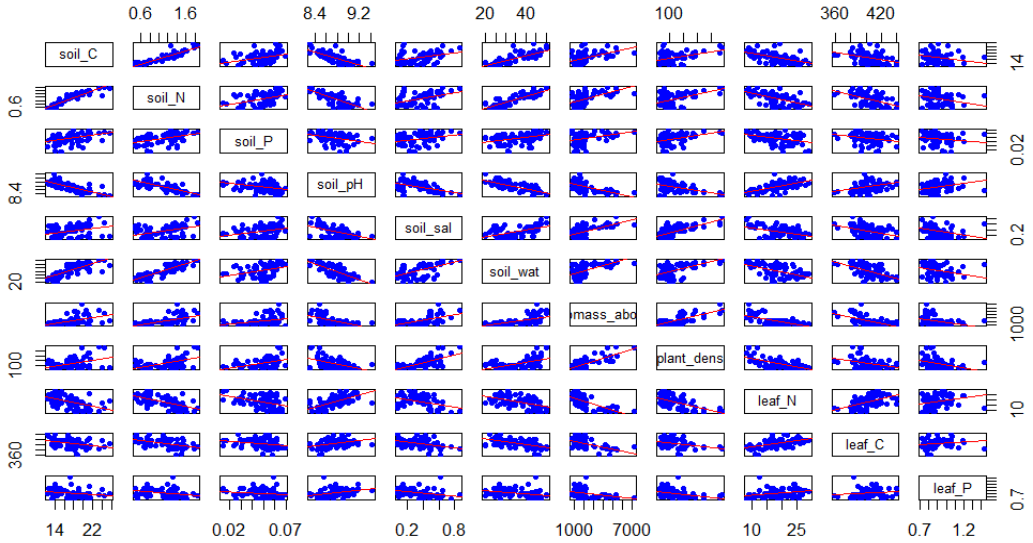

Figure #5: Paired correlations between all soil and plant traits with many traits being highly positive and negatively correlated with one another.

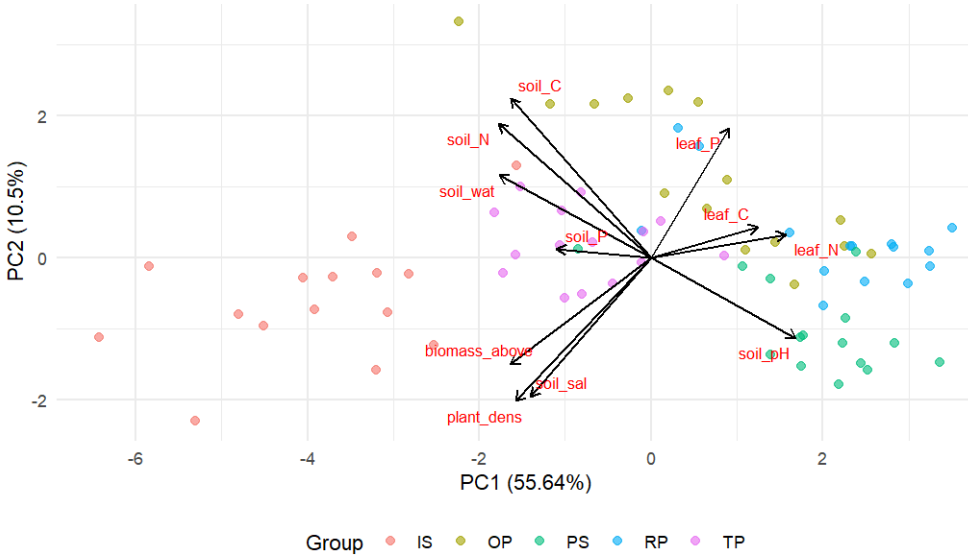

Figure #6: PCA biplot where all plant and soil traits contributed highly to the variance seen in our sites.

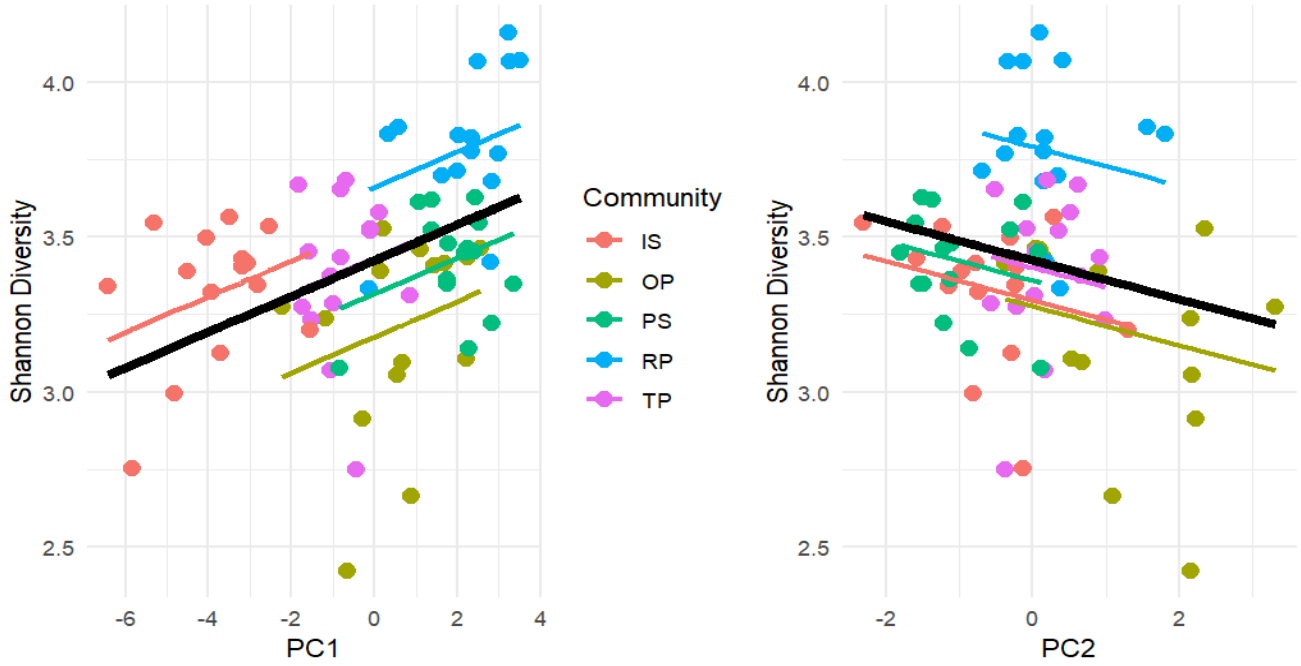

Figure #7: Showing the relationships between SDI and PC1 and PC2 across five communities where the thick black line represents the fixed effect component for all sites while the coloured lines show community-specific fitted values accounting for random effects

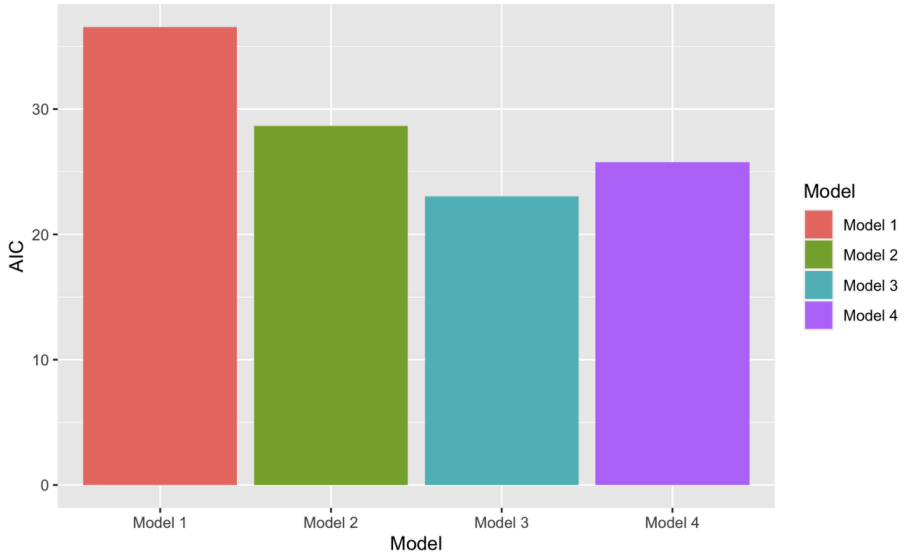

Figure #8: Showing the relative AIC values of the four models created and tested where 'Model 3' was the best, having significantly the lowest AIC (2 ≥ Difference)

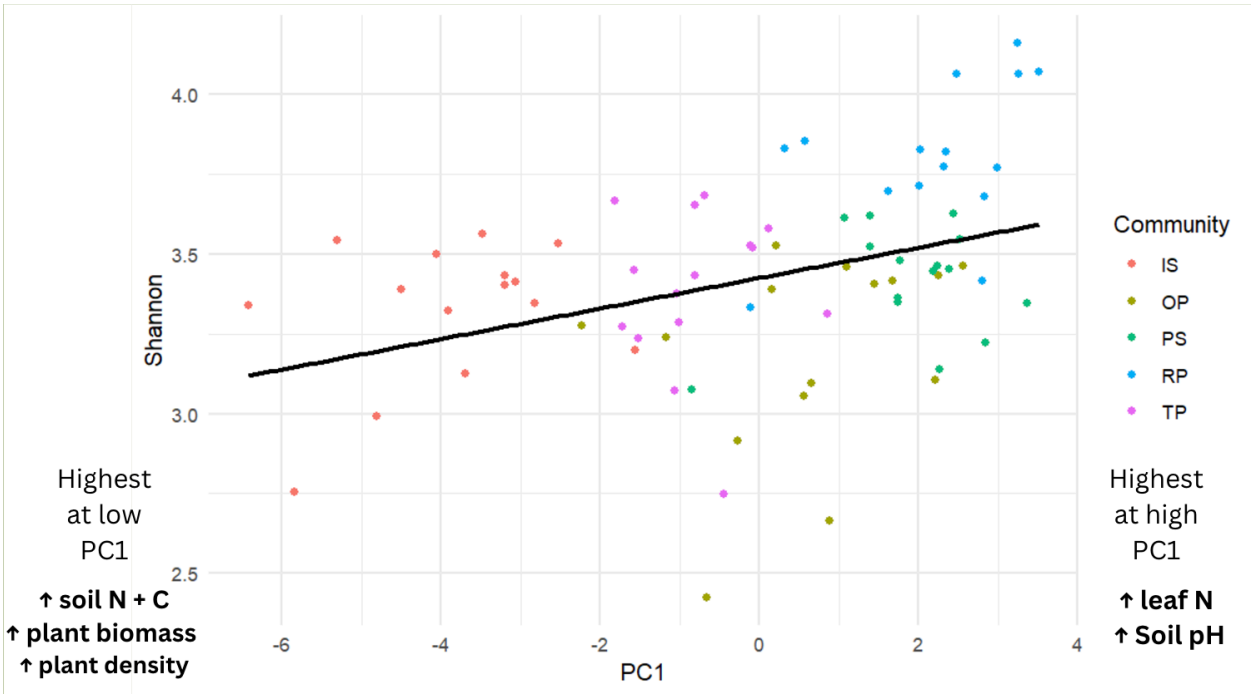

Figure #9: Showing regression of Shannon diversity index (SDI) on PC1 where sites are divided by colour into their communities and specific plant and soil traits are labelled on either side of the x-axis where they are directionally the highest (e.g. leaf N highest at high PC1)

Supplementary Material (R-file)
https://drive.google.com/file/d/1KUDP9uy7KgFAIZgYJ_RJomjeOoN8nGwW/view?usp=sharing

Table A1: Description of each soil and plant trait from plant_traits.csv and soil_traits.csv.

Trait Name (units)	**Column Name**	**Notes**
Soil Carbon (mg/g)	soil_C	Analyzed with an element analyzer (FlashEA1112 Series, Thermo, USA).
Soil Nitrogen (mg/g)	soil_N	Analyzed with an element analyzer (FlashEA1112 Series, Thermo, USA).
Soil Phosphorus (mg/g)	soil_P	Measured by molybdenum-antimony colorimetry using a microplate reader (Synergy 2, BioTek, USA)
Soil pH	soil_pH	Determined using a multi-function tester (S975-uMix Seven Excellence, Mettler-Toledo, Switzerland).
Soil Salinity (%)	soil_sal	Determined using a multi-function tester (S975-uMix Seven Excellence, Mettler-Toledo, Switzerland).
Soil Water (%)	soil_wat	Estimated from the weight of a soil core before and after drying.
Aboveground Biomass (g/m^2)	biomass_above	Plant tissues were dried at 60 °C for 48 h and weighed to obtain their aboveground biomass. Used the average value across the site's five quadrats.
Plant Density ($individuals/m^2$)	plant_dens	Counted plant (stem) density ($individuals/m^2$) in each of the five quadrants and found the average for that site.
Leaf Nitrogen (mg/g)	leaf_N	Indicates the nutritional status of different plant samples (same method as used for soil samples). Used the average value across the site's five quadrats.
Leaf Carbon (mg/g)	leaf_C	Indicates the nutritional status of different plant samples (same method as used for soil samples). Used the average value across the site's five quadrats.
Leaf Phosphorus (mg/g)	leaf_P	Indicates the nutritional status of different plant samples (same method as used for soil samples). Used the average value across the site's five quadrats.