Predicting Community Assemblage in The Rocky Intertidal of Acadia National Park  
Data Preprocessing, Feature Engineering,

and Initial Modeling Report

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# Introduction

## Background

Intertidal communities in the Gulf of Maine are experiencing rapid change, including changes in vertical zonation (Trott 2022) and introduction of invasive and range expanding species (Cohen et al. 1995, Yamada 2001, Epifanio 2013, Johnson 2015, Cheng et al. 2025). These changes may compound over time into significant changes to community structure. Because of this and the importance of these ecosystems ecologically and as a source of ecosystem services, including as interpretive spaces in National Parks, it is important that we understand what the future holds for the rocky intertidal in the Gulf of Maine, and which factors contribute most to that future.

## Research Question

The primary research question posed by this analysis is: can we accurately predict how the percent cover of ecosystem engineers *Ascophyllum nodosum* and *Fucus vesiculosus* of the rocky intertidal in Acadia National Park will change in the near future, and what variables (including substrate composition and invertebrate abundance) are the strongest predictors of said percent cover? While long-term monitoring has been ongoing through the Northeast Temperate Network (NETN) in the Inventory and Monitoring Division of the National Park Service (NPS) since 2013, no significant analysis has been done on this subject since that protocol began.

I hypothesize that presence and abundance of motile invertebrates will significantly predict the substrate percent cover of *Fucus vesiculosus* (Linnaeus 1753) and *Ascophyllum nodosum* (Linnaeus 1753) in the Acadia rocky intertidal over time.

I predict that an increase in the abundance of motile invertebrates *Littorina obtusata* will be associated with a significant reduction in the algal cover of *F. vesiculosus* and *A. nodosum*, as these periwinkles have been shown to feed on both of these species (Hadlock 1979, Watson and Norton 1987). I predict that *Littorina littorea* abundance will not significantly predict the algal cover of *F. vesiculosus* and *A. nodosum*, as this species has been shown to avoid feeding on these species (Watson and Norton 1985).

# Methods

## Data Preprocessing

The target variables, *F. vesiculosus* and *A. nodosum* percent cover, and multiple predictor variables, as percentage data, are bounded on a scale from 0 to 100. While random forest does not assume unbounded data, the zero skewed, bounded data may cause issues, so a logit-transform with an epsilon value of 0.0001 was used.

## Feature Engineering

Previously, I explored unsupervised feature engineering processes with limited success in reducing dimensionality of the data. I performed a non-parametric multidimensional scaling analysis using Bray-Curtis dissimilarity, and a principal component analysis using untransformed and Hellinger-transformed data. NMDS produced no distinct clustering, though it is generally regarded as effective for clustering ecological community data CITATION. Principal components did not sufficiently capture the variability in the data. Additionally, PCA, even with Hellinger-transformed data, has been shown to be ineffective when working with ecological community data (Minchin and Rennie 2010). Because of this, and to maintain interpretability of the final model, unsupervised feature engineering is not explored any further.

An out-of-bag random forest model was used to examine the importance of each predictor in predicting *F. vesiculosus* and *A. nodosum* percent cover. The 10 lowest contributing features were removed.

## Training – Test Split

The equation is used to calculate the optimal training-test split for the dataset, as this is generally viewed as the ideal method for determining this split (Joseph 2022). The dataset in use has a sufficiently large sample size to parameter (*n*:*p*) ratio, so the theoretical optimal split is sufficient and there is no need to specifically tailor the split to accommodate the structure of the data.

## Initial Model

The initial model selected for this analysis is a random forest model as it is a non-parametric machine learning method that handles mixed data types, the skewed distribution, and non-linear relationships between predictors that has been examined in the NETN monitoring data and is oftentimes found in ecological data. Additionally, random forest handles multicollinearity well which has been observed in the NETN data to a small extent. Out-of-bag (OOB) error is used as a first estimate of test error. An OOB model is computationally cheap, fast, and helps protect against data leakage while still having comparable performance to a fully fleshed out, cross-validated model.

# Results

## Data Preprocessing

The progressive data transformation strategy that I employed yielded mixed to poor results. The square root and log(x + 1) transformations did not improve the distribution, meaning that models that require a normal distribution are not a good option moving forward. The presence-absence transformation did improve the distribution, though it reduces the value of the analysis substantially. Presence and abundance is a less granular metric than abundance, making it inherently less informative.

## Feature Engineering

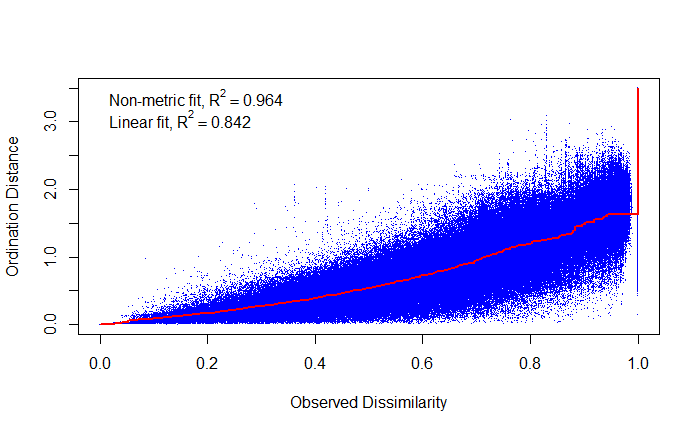


Figure 1 - Non-metric Multidimensional Scaling (NMDS) Plot. The NMDS plot shows little clustering and a high stress (>0.2) despite a relatively strong fit to the data (R^2 = 0.964).

The NMDS plot (Figure 1) revealed no strong clustering, and had an accompanying stress value above 0.2, which is a threshold at which the results are generally considered dubious (Clarke 1993, Dexter et al. 2018). This suggests that the NMDS is not doing an adequate job of capturing the true dimensionality in the data, and that any groupings (which are already not readily apparent from Figure 1) are not trustworthy.

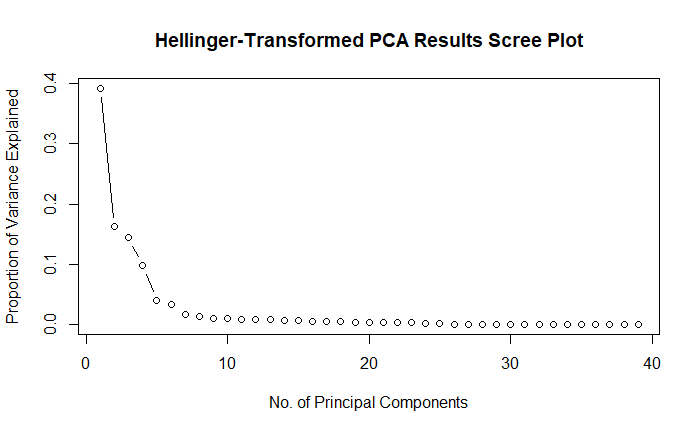


Figure 2 - Scree plot examining the proportion of variance captured by the Principal Component Analysis on Hellinger-transformed data. PC1 captures 39.5% of the data, followed by PC2 and PC3 with a much lower 16.25% and 14.4%, respectively. After PC3, each component contributes a negligible amount to explaining the variation in the data.

The Hellinger-transformed PCA, shown in the Scree plot in Figure 2, had slightly more promising results than the NMDS, and was an improvement over the exploratory PCA I conducted during the Exploratory Data Analysis portion of this project. The Hellinger-transformed PCA did a moderate job at capturing the variability in the data, with the first principal component accounting for 39.25%, the second component accounting for 16.25%, and the third accounting for 14.4%. After the first component the accounted for variability saw a precipitous drop, which continued after the third principal component as well. This is an improvement in performance to the earlier PCA, but still leaves much to be desired in explaining the variability in the data.

# Discussion

## Conclusions

The overarching conclusion from this preprocessing and feature engineering analysis is that the zero-inflated nature of the data is still dominant. It may not be feasible to resolve this issue with preprocessing, data transformation, or feature engineering. Instead, models specifically tailored to a non-normally distributed dataset, or a zero-inflated dataset, may be a more suitable option for this analysis. Dimensionality reducing techniques like NMDS and PCA showed some limited success, especially in tandem with data preprocessing tools like the Hellinger transformation, but these may alter the interpretability of the data too far to be worthwhile, even if they were highly successful in capturing the variation and dissimilarity in the data. The removal of features will all zeroes in their counts or percent cover data is worthwhile, though the removal of *Carcinas maenas*, the European Green Crab, is still an error caused by incorrect data, in my opinion. I have not yet heard back from the Data Manager regarding the repaired dataset, so for now it will stay removed. I hope to see it return as it is an ecologically significant invasive species, which has drawn a lot of attention from both academics and the public in recent years.

## Next Steps

I took a preliminary stab at the next step of this analysis, which is to explore non-parametric models and other suitable techniques for modeling with a zero-inflated dataset like this. I ran two out-of-box random forest models to get a sense of how that non-parametric model would do, without jeopardizing the testing set by inviting data leakage. This model was fit well to the training set, explaining ~95% of the variance in both *Fucus* and *Ascophyllum* percent cover, but it failed to predict accurately, with a mean error of squared residuals value of 46.6 and 70.7, respectively (on a scale out of 100). I experimented with a logit-transformation on only the percent cover values, as they are bounded (0 – 100), with an epsilon value of 0.0001. This resulted in improved performance compared to the unmodified out of bag random forest model, so I intend to explore this avenue further. I also intend to branch out to other models that may handle the data well, such as gradient boosting. I have also been looking into how I might use a feedforward neural network for this problem, but I am not confident that I have the sample size I need to do so. I am thinking if I reduce the number of features down, either by combining algal species into groups (i.e., red algae, brown algae, green algae), or by trimming down the less informative groups (i.e., other substrate, unidentified substrate, rock, etc.), or even limiting the scope to *just* investigating the impact of motile invertebrates on *Ascophyllum* and *Fucus*, rather than the other substrates and algae as well.

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