Ocean Man; Marsh Population Regression

Jared Lourie

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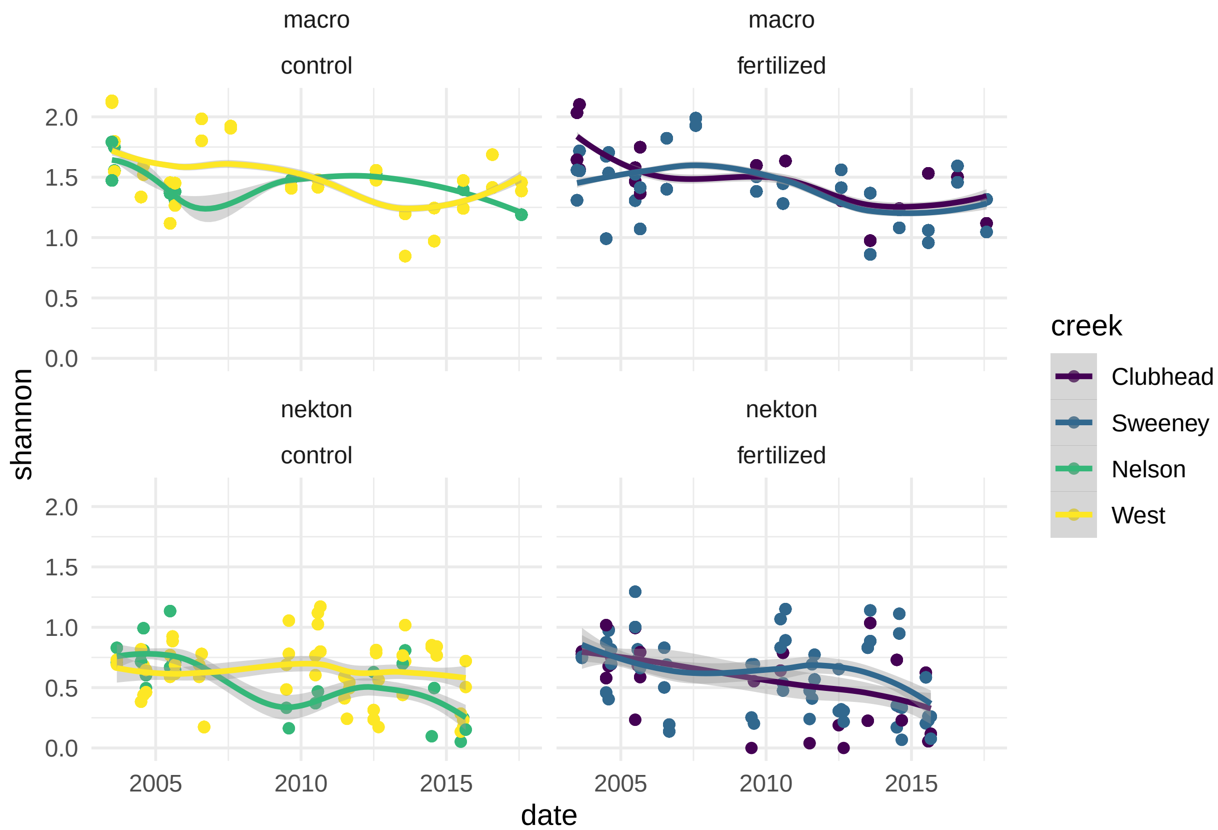
In order to understand the PIE LTER, you have to think like the Marsh Man or think like the green guy in the swamp, in tune with the environment and knees deep in the action as an ecologist should be. My first thoughts when approaching the ideas surrounding the TIDE project and understanding the impact of agricultural runoff were about ecological recovery from within the Plum Island ecosystem. If there were effects on the population or the geomorphology that would be adverse to those populations, would competitions and top-down or bottom-up effects end up reaching some sort of new stability, or would the ecosystem ultimately crash? Presumably a Pavlovian carrot thrown into the mix of a delicate ecosystem won't end over very well (EPA facts on poor fertilizer control). With this consideration in mind I joined data detailing information concerning Nekton and Macroinfaunal populations. For more context, the PIE LTER is the Plum Island Estuary long term ecology research group, a collaboration involving many professors and universities. The summary of the following merged dataset is created from these datasets created and uploaded by PI Linda Deegan et. al; Macroinfaunal & Nekton.

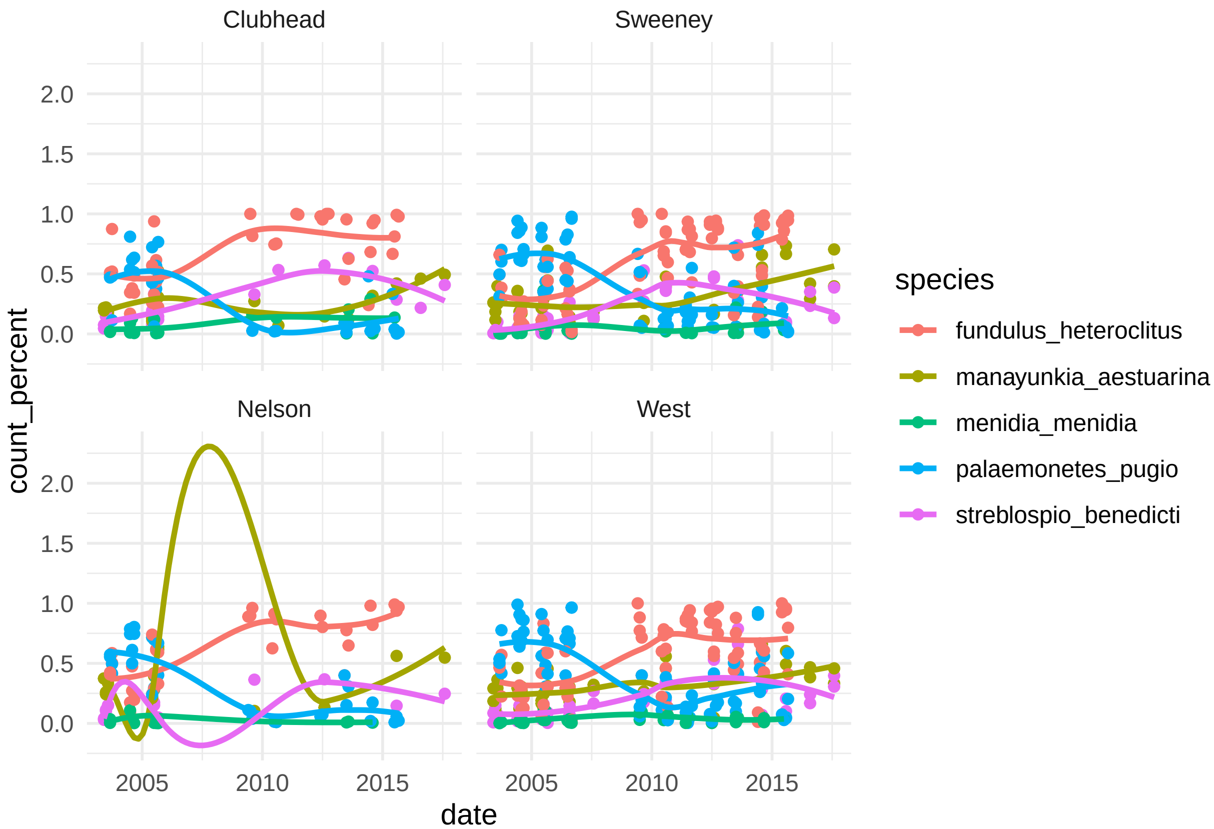
```
##       year          month             creek        branch
##  Min.   :2003   Min.   : 6.000   Clubhead: 684   Left :1935
##  1st Qu.:2004   1st Qu.: 7.000   Sweeney :1345   Right:2024
##  Median :2006   Median : 8.000   Nelson  : 566
##  Mean   :2008   Mean   : 7.611   West    :1364
##  3rd Qu.:2012   3rd Qu.: 8.000
##  Max.   :2017   Max.   :10.000
##    species              count              type      count_percent
##  Length:3959        Min.   :   0.00   macro :3136   Min.   :0.00000
##  Class :character   1st Qu.:   0.00   nekton: 823   1st Qu.:0.00000
##  Mode  :character   Median :   1.00                 Median :0.00165
##                     Mean   :  55.12                 Mean   :0.08765
##                     3rd Qu.:  19.00                 3rd Qu.:0.03913
##                     Max.   :1832.00                 Max.   :1.00000
##     shannon       total_count        treatment          date
##  Min.   :0.000   Min.   :   1   control    :1930   Min.   :2003-06-01
##  1st Qu.:1.046   1st Qu.: 493   fertilized:2029   1st Qu.:2004-07-01
##  Median :1.415   Median : 894                     Median :2006-06-01
##  Mean   :1.309   Mean   :1173                     Mean   :2008-08-05
##  3rd Qu.:1.597   3rd Qu.:1758                     3rd Qu.:2012-09-16
##  Max.   :2.133   Max.   :4126                     Max.   :2017-08-01
```

Looking into the data a bit and using the package vegan to assign Shannon Diversity Index values, an understanding of ecosystem eveness and abundance can be visualized.



Macro Control appears to have normal oscillations of Shannon Diversity eveness, indicative of a pattern of population equilibrium and likely a Lotka-Volterra zero growth predator/prey & competition interaction. Interestingly enough nekton control seems to lose it's normal oscillation of diversity eveness, with both creeks tapering off and losing eveness and likely their nekton equilibria. Fertilized macro and nekton diversity curves appear to be tapering off with normal oscillation, indicative of a linear diversity or equilibria loss. A prelminary look at change in percent representation of species of interest by creek is not very revealing especially with some macro and nekton species being in the same model. As it appears above it seems as though nekton and macro overall are not linked. I would hypothesize that with the increased ability of aquatic species to travel throughout the PIE system, that nekton effects on population may spread, but without data or confirmation of individuals moving from treated to control creeks, it is only a thought. It is also entirely possible that the effects on nekton biodiversity are cause by an anthropogenic factor or other effect since the effect is prevalent in the control and treatment creeks.

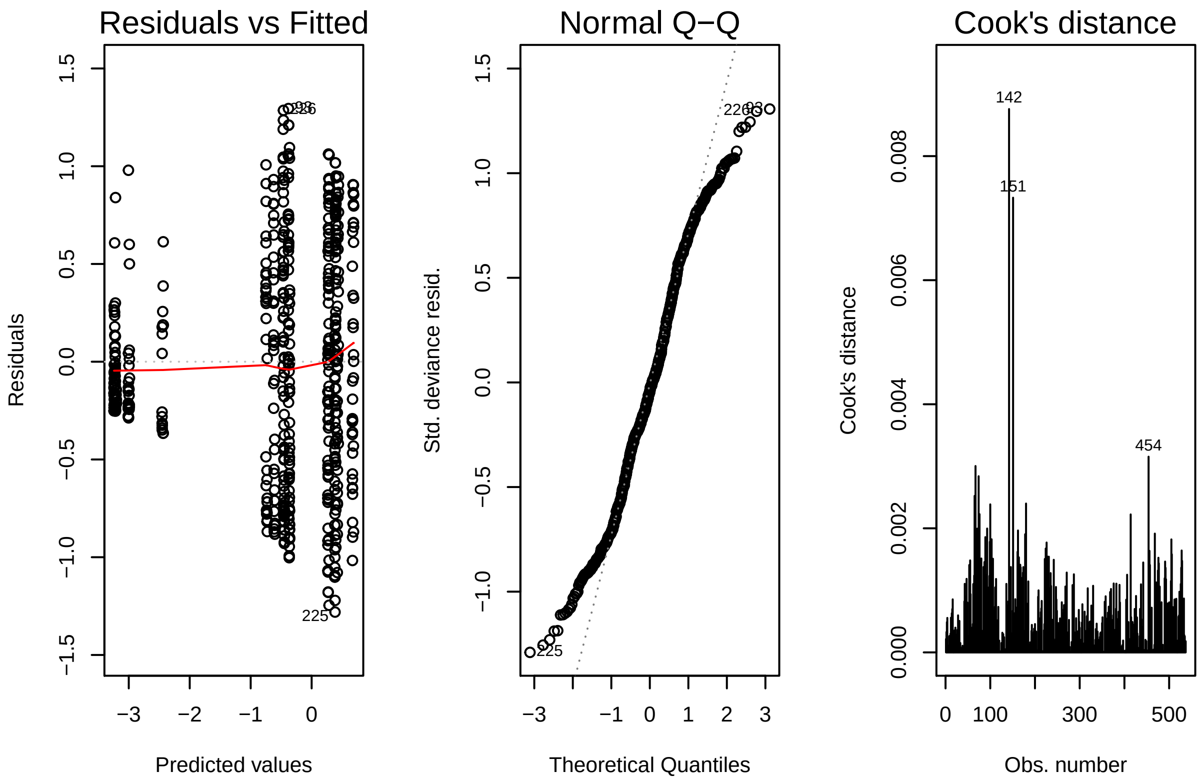
According to Sinéad M. Crotty et al, salt marsh biodiveristy is affected mostly by foundation or keystone species which allow for biodiversity to grow and accumulate within a marsh patchwork. I hypothesize that coastal eutrophication of the PIE network (Linda A. Deegan et. al) from nutrient enrichment affects a foundational species of nekton biodiversity that is interconnected to all of the creeks regardless of direct proximity to enrichment.



* There appears to be an unusual loss of equilibrium with observed creek sediment edge habitating worms in Nelson, the cause unclear in literature.

```
##   contrast                                     estimate    SE  df z.ratio p.value
##   Clubhead fundulus_heteroclitus effect           1.703 0.359 Inf   4.741  <.0001
##   Sweeney fundulus_heteroclitus effect            1.413 0.280 Inf   5.044  <.0001
##   Nelson fundulus_heteroclitus effect             1.455 0.369 Inf   3.943  0.0002
##   West fundulus_heteroclitus effect               1.301 0.278 Inf   4.686  <.0001
##   Clubhead menidia_menidia effect                -1.419 0.838 Inf -1.694  0.1083
##   Sweeney menidia_menidia effect                 -1.974 0.878 Inf -2.248  0.0421
##   Nelson menidia_menidia effect                  -2.186 1.199 Inf -1.823  0.0911
##   West menidia_menidia effect                    -2.208 0.786 Inf -2.807  0.0120
##   Clubhead palaemonetes_pugio effect              0.285 0.391 Inf   0.730  0.4656
##   Sweeney palaemonetes_pugio effect               0.567 0.287 Inf   1.974  0.0726
##   Nelson palaemonetes_pugio effect                0.409 0.380 Inf   1.076  0.3075
##   West palaemonetes_pugio effect                  0.653 0.285 Inf   2.293  0.0421
##
## Results are given on the log odds ratio (not the response) scale.
## P value adjustment: fdr method for 12 tests
```

A likelihood binomial logit regression model reveals some differences between species across the creeks, but with poor significance and standard error values it is difficult to confirm the potency of the effect. The regression model in itself is questionable with a tight resids vs fitted plot, a qq plot that has a fit center but tapering ends, yet small cook's distance values generally under 0.005. Poor significance of contrast related to the shrimp and silverback species is likely due to their low abundance in observation, a sample size error combined with the not quite fit model. However when looking at count percent data for the three nekton species specifically, the data 'appears' uniform but not normal based on skew/kurtosis values.




```
## summary statistics
## ------
## min:  0.001589825   max:  1
## median:  0.3895131
## mean:  0.4137851
## estimated sd:  0.3332816
## estimated skewness:  0.2870194
## estimated kurtosis:  1.67811
```

Returning to the literature there is an obvious effect on mummichog size because of geomorpological and bottom-up community change (James A. Nelson et al.) and change in its population abundance is clear in the model. Maybe then the lack of clarity or signifcance detected should be understood by exploring bottom-up effects specifically on the other species of interest in the model, silverbacks and the pugio shrimp rather then just trying to understand ecosystem diversity or population counts. Growing population size as shown in my model doesn't reflect the reality of poorer diets leading to smaller sized individuals. Looking at the literature and understanding the change in mummichog diet from not accessing the grasses I would deduce that silverbacks are more prevalent in their food search which would be a variable in the decreased silverback population; however, I wouldn't attribute silverback decline to that one relationship entirely. Without a firm understanding of new ecosystem relationships, risk effects, and predation due to a loss of a food source understanding treated areas is a game of analytics and not ecological fundamentals with my dataset. Abstracting it is clear that nekton and macroinfaunal species are declining more in treatment zones than control zones, but significance when parsing to that level is generally lost.

```
## type = macro:
##  contrast              estimate    SE  df z.ratio p.value
```

```
##  Left Clubhead effect      59.6  54.0 Inf   1.104 0.3082
##  Right Clubhead effect   -457.5  37.2 Inf -12.304 <.0001
##  Left Sweeney effect      -69.8  32.6 Inf  -2.142 0.0430
##  Right Sweeney effect     -77.9  32.6 Inf  -2.389 0.0271
##  Left Nelson effect       134.2  42.4 Inf   3.164 0.0031
##  Right Nelson effect      514.1  54.0 Inf   9.520 <.0001
##  Left West effect        -134.3  32.6 Inf  -4.119 0.0001
##  Right West effect         31.6  32.6 Inf   0.969 0.3323
##
## type = nekton:
##  contrast              estimate    SE  df z.ratio p.value
##  Left Clubhead effect      78.4 110.7 Inf   0.708 0.7137
##  Right Clubhead effect   -100.3  78.3 Inf  -1.281 0.5637
##  Left Sweeney effect      -10.5  62.2 Inf  -0.168 0.9889
##  Right Sweeney effect     -40.8  65.8 Inf  -0.620 0.7137
##  Left Nelson effect       -85.4  79.4 Inf  -1.076 0.5637
##  Right Nelson effect       -1.6 115.0 Inf  -0.014 0.9889
##  Left West effect          92.0  62.2 Inf   1.479 0.5637
##  Right West effect         68.2  62.5 Inf   1.091 0.5637
##
## P value adjustment: fdr method for 8 tests
```

```
## type = macro:
##  contrast        estimate   SE  df z.ratio p.value
##  Clubhead effect  -263.93 27.4 Inf -9.628  <.0001
##  Sweeney effect    -32.64 22.4 Inf -1.457  0.1936
##  Nelson effect     306.70 29.9 Inf 10.246  <.0001
##  West effect       -10.14 22.4 Inf -0.452  0.6510
##
## type = nekton:
##  contrast        estimate   SE  df z.ratio p.value
##  Clubhead effect   -33.39 57.2 Inf -0.583  0.7461
##  Sweeney effect     -8.56 44.0 Inf -0.195  0.8457
##  Nelson effect     -55.41 58.4 Inf -0.949  0.6851
##  West effect        97.36 43.2 Inf  2.251  0.0975
##
## P value adjustment: fdr method for 4 tests
```

I think if I wanted to have a better understanding of population counts and the effects of treatment on them, I would need a more in depth framework with more specific covariates to interpret, a method to account for general anthropogenic noise or effects on all creeks, and a better understanding of modified individual behaviour in response to treatment. Optimally my guess is to understand nekton population representation I will need bayesian beta regression with a larger dataset. Without even having more behavioural data, I think understanding at what probability under what conditions I may pull a mummichog out of a hat will help with trying to create auxillary hypotheses about new top-down and bottom-up effects.