

## EEB 5301 Homework 4

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### Problem 1

The students' suggestion of doubling plant densities will not allow the aphid population to grow amidst ladybug predation. The predator-prey relationship was unstable at a carrying capacity of 1,000 aphids and remains unstable at a carrying capacity of 1,200 aphids. The phase diagram below shows that the predator isocline remains to the left of the prey isocline hump for both scenarios, indicating an unstable predator-prey relationship. The black prey isocline is the original scenario and the blue isocline is the scenario where the plant density is doubled.

```
r = 0.001
a = 0.5
k1 = 1000
k2 = 1200
h = 0.02083
q = 1/3
f = 0.01
N1 = 1:k1
N2 = 1:k2
Prey1 = (r * N1 * (1 - (N1/k1)) * (a * N1))/(1 +
  a * h * N1)
Prey2 = (r * N2 * (1 - (N2/k2)) * (a * N2))/(1 +
  a * h * N2)
Predator = (q/(f * a - a * h * q))
plot(x = N1, y = Prey1, bty = "n", ylim = c(0,
  15), type = "l", xlab = "Number of Prey",
  ylab = "Number of Predators")
abline(v = Predator, col = "red", lty = 2)
lines(Prey2, col = "blue")
```

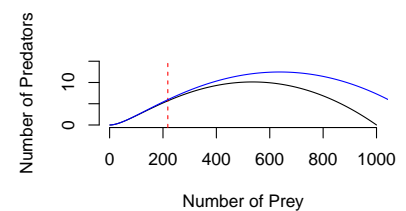


Figure 1: Phase Plane Diagram

### Problem 2

#### Part a

```
specnumber(dune.sum1)
```

```
## 1 2 4 5
## 20 19 13 21
```

As moisture increases, species richness decreases from moisture levels 1 to 4, but then increases at level 5. The most species rich level is 5 while level 4 is the least species rich.

*Part b*

```
sort( diversity(dune.sum1) )

##           4           1           2           5
## 2.486948 2.702316 2.765128 2.784814
```

According to Shannon's Index, the moisture level is ranked  $5 > 2 > 1 > 4$  in order of highest diversity to lowest.

*Part c*

```
sort( exp( diversity(dune.sum1) ) )

##           4           1           2           5
## 12.02452 14.91423 15.88107 16.19680

sort( 1/( diversity(dune.sum1, index = "invsimpson") ) )

##           2           5           1           4
## 0.07066360 0.07292591 0.07846400 0.08888514
```

The effective number of species between Simpson's and Shannon's index are almost flipped. Moisture level 4 has the lowest effective number of species according to Shannon's index while the level 4 is considered the having the highest effective number of species according to Simpson's.

*Part d*

```
diversity(dune.sum1[1, ], index = "invsimpson")

## [1] 12.7447
```

Taking the inverse of Simpson's index yields the probability of finding the same two species in a sample, in this case this is 7.8%.

*Part e*

```
radPlot(x = dune.sum1[1, ], cex.axis = 0.75, cex.lab = 0.75)

## NULL

radPlot(x = dune.sum1[2, ], add = TRUE, col = "blue")
```

```
## NULL

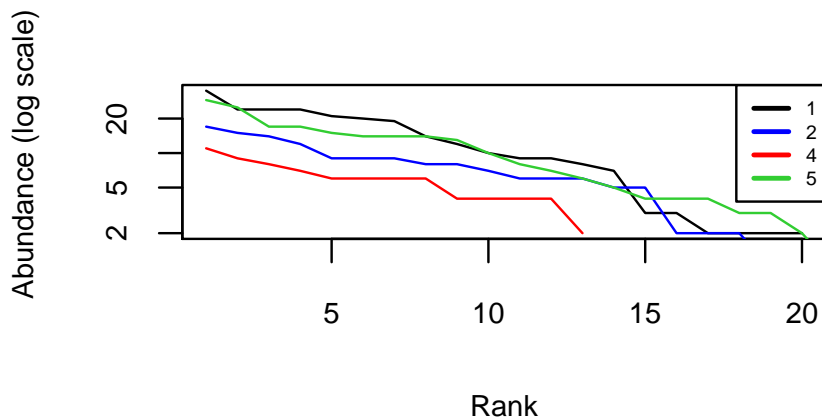
radPlot(x = dune.sum1[3, ], add = TRUE, col = "red")

## NULL

radPlot(x = dune.sum1[4, ], add = TRUE, col = "limegreen")

## NULL

legend("topright", legend = c("1", "2", "4", "5"),
      col = c("black", "blue", "red", "limegreen"),
      lty = 1, lwd = 2, cex = 0.5)
```



### Part f

Based on the plot above, moisture level 1, appears to be the most even since it has the flattest slope. However, this is not much flatter than level 5.

One way to better quantify evenness would be to calculate the Hill's ratio from either of the diversity indices above.

### Part g

Simpson's index tends to be less sensitive to rare species than Shannon's index. It is weighted towards the most abundant species. In part c, Simpson's index tended to favor level 4 as the most diverse, which makes sense from the graph in part e that shows level 4 as the most dominated by common abundant species (i.e. lack of sensitivity towards rare species).

### Part h

```
library(knitr)
rarefaction_data <- data.frame('Moisture Level 1' = c(rarefy(dune.sum1[1,
```

```

], sample = 2), rarefy(dune.sum1[1, ], sample = 10),
rarefy(dune.sum1[1, ], sample = 100)), 'Moisture Level 2' = c(rarefy(dune.sum1[2,
], sample = 2), rarefy(dune.sum1[2, ], sample = 10),
rarefy(dune.sum1[2, ], sample = 100)), 'Moisture Level 4' = c(rarefy(dune.sum1[3,
], sample = 2), rarefy(dune.sum1[3, ], sample = 10),
rarefy(dune.sum1[3, ], sample = 100)), 'Moisture Level 5' = c(rarefy(dune.sum1[4,
], sample = 2), rarefy(dune.sum1[4, ], sample = 10),
rarefy(dune.sum1[4, ], sample = 100)))

## Warning in rarefy(dune.sum1[3, ], sample
## = 100): Requested 'sample' was larger than
## smallest site maximum (77)

rownames(rarefaction_data) <- c("2", "10", "100")

kable(rarefaction_data)

```

	Moisture.Level.1	Moisture.Level.2	Moisture.Level.4	Moisture.Level.5
2	1.925237	1.935881	1.923103	1.931406
10	7.310870	7.600222	7.166188	7.503399
100	18.067247	18.426356	13.000000	19.554621

The expected number of species for each moisture level are listed in the table above. Different sampling efforts within different moisture levels may yield more rare species thus affecting the overall diversity metrics (especially depending which index is used).

#### Part i

```

vegdist(dune.sum1)

##           1           2           4
## 2 0.4045802
## 4 0.7125382 0.4727273
## 5 0.6258065 0.5363128 0.5753425

```

Based on the dissimilarity index table above, the larger the distance between moisture levels, the higher the difference in indices. For example, when moisture level 1 is compared to the other moisture levels, the distance index increases with the distance between moisture levels.