### 6. Predicting from final model

We will predict from the final model for the following six communities

1. p1 monoculture at low N
2. p1 monoculture at regular N
3. 50-50 p2-p3 mixture at low N
4. 50-50 p2-p3 mixture at regular N
5. Centroid mixture with 25% of each species at low N
6. Centroid mixture with 25% of each species at regular N

The model coefficients we’ll use are as follows

coef(mod\_final)

##### i. p1 monoculture at low N

The values for variables would be as follows

$$P\_{1}=1;P\_{2}=0;P\_{3}=0;P\_{4}=0;reg=0$$

The predicted response would be

$$\hat{y} = 9.779 \* 1 + 11.12 \* 0 + 6.237 \* 0 + 9.477 \* 0 + 26.70 \* (1 + 0) \* (0 + 0) + 17.621 \* (1\*0) + 9.05 \* (0\*0) + 2.204\*1\*0 + 1.765\*0\*0 + (-11.774) \* (1 + 0) \* (0 + 0) \* 0$$

All other terms would be zero and

$$\hat{y}=9.779\*1$$

$$\hat{y}=9.779$$

##### ii. p1 monoculture at regular N

The values for variables would be as follows

$$P\_{1}=1;P\_{2}=0;P\_{3}=0;P\_{4}=0;regN=1$$

The predicted response would be

$$\hat{y} = 9.779 \* 1 + 11.12 \* 0 + 6.237 \* 0 + 9.477 \* 0 + 26.70 \* (1 + 0) \* (0 + 0) + 17.621 \* (1\*0) + 9.05 \* (0\*0) + \\ 2.204\*1\*1 + 1.765\*0\*1 + (-11.774) \* (1 + 0) \* (0 + 0) \* 1$$

All other terms would be zero and

$$\hat{y}=9.779\*1+2.204\*1\*1$$

$$\hat{y}=11.983$$

##### iii. 50-50 p2-p3 mixture at low N

The values for variables would be as follows

$$P\_{1}=0;P\_{2}=0.5;P\_{3}=0.5;P\_{4}=0;regN=0$$

The predicted response would be

$$\hat{y} = 9.779 \* 0 + 11.12 \* 0.5 + 6.237 \* 0.5 + 9.477 \* 0 + 26.70 \* (0 + 0.5) \* (0.5 + 0) + 17.621 \* (0\*0.5) + 9.05 \* (0.5\*0) + 2.204\*0\*0 + 1.765\*0.5\*0 + (-11.774) \* (0 + 0.5) \* (0.5 + 0) \* 0$$

All other terms would be zero and

$$\hat{y}=11.12\*0.5+6.237\*0.5+26.70\*\left(0+0.5\right)\*\left(0.5+0\right)$$

$$\hat{y}=15.352$$

##### iv. 50-50 p2-p3 mixture at regular N

$$\hat{y}= 9.779 \* 0 + 11.12 \* 0.5 + 6.237 \* 0.5 + 9.477 \* 0 + 26.70 \* (0 + 0.5) \* (0.5 + 0) + 17.621 \* (0\*0.5) + 9.05 \* (0.5\*0) + 2.204\*0\*0 + 1.765\*0.5\*1 + (-11.774) \* (0 + 0.5) \* (0.5 + 0) \* 1$$

The values for variables would be as follows

$$P\_{1}=0;P\_{2}=0.5;P\_{3}=0.5;P\_{4}=0;regN=1$$

All other terms would be zero and

$$\hat{y}=11.12\*0.5+6.237\*0.5+26.70\*\left(0+0.5\right)\*\left(0.5+0\right)+1.765\*0.5\*1+\left(-11.774\right)\*\left(0+0.5\right)\*\left(0.5+0\right)\*1$$

$$\hat{y}=13.291$$

##### v. Centroid mixture with 25% of each species at low N

The values for variables would be as follows

$$P\_{1}=0.25;P\_{2}=0.25;P\_{3}=0.25;P\_{4}=0.25;regN=0$$

The predicted response would be

$$\hat{y} = 9.779 \* 0.25 + 11.119 \* 0.25 + 6.237 \* 0.25 + 9.477 \* 0.25 + 26.70 \* (0.25 + 0.25) \* (0.25 + 0.25) + 17.621 \* (0.25\*0.25) + 9.05 \* (0.25\*0.25) + 2.20\*0.25\*0 + 1.765\*0.25\*0 + (-11.774) \* (0.25 + 0.25) \* (0.25 + 0.25) \* 0$$

All other terms would be zero and

$$\hat{y} = 9.779 \* 0.25 + 11.119 \* 0.25 + 6.237 \* 0.25 + 9.477 \* 0.25 + 26.70 \* (0.25 + 0.25) \* (0.25 + 0.25) + 17.621 \* (0.25\*0.25) + 9.05 \* (0.25\*0.25)$$

$$\hat{y}=17.494$$

##### vi. Centroid mixture with 25% of each species at regular N

The values for variables would be as follows

$$P\_{1}=0.25;P\_{2}=0.25;P\_{3}=0.25;P\_{4}=0.25;regN=1$$

The predicted response would be

$$\hat{y} = 9.779 \* 0.25 + 11.119 \* 0.25 + 6.237 \* 0.25 + 9.477 \* 0.25 + \ 26.70 \* (0.25 + 0.25) \* (0.25 + 0.25) + 17.621 \* (0.25\*0.25) + 9.05 \* (0.25\*0.25) + \ 2.20\*0.25\*1 + 1.765\*0.25\*1 + (-11.774) \* (0.25 + 0.25) \* (0.25 + 0.25) \* 1$$

$$\hat{y}=15.543$$

##### Predictions using code

These predictions can be verified by using the predict() function

communities <- data.frame("p1" = c(1, 1, 0, 0, 0.25, 0.25),
 "p2" = c(0, 0, 0.5, 0.5, 0.25, 0.25),
 "p3" = c(0, 0, 0.5, 0.5, 0.25, 0.25),
 "p4" = c(0, 0, 0, 0, 0.25, 0.25),
 "regN" = c(0, 1,
 0, 1,
 0, 1))

# Add interaction terms
# Usually this won't be needed and the function automatically calculates
# these. However, since we include a specific interaction of the between
# FG term with the treatment variable, we need to supply the interactions
FG\_ints <- DI\_data(prop = c("p1", "p2", "p3", "p4"),
 FG = c("G", "G", "L", "L"),
 data = communities, what = "FG")
communities <- bind\_cols(communities, FG\_ints)

communities

predict(mod\_final, communities)