### 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

The predicted response would be

All other terms would be zero and

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

The values for variables would be as follows

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

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

The values for variables would be as follows

The predicted response would be

All other terms would be zero and

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

The values for variables would be as follows

All other terms would be zero and

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

The values for variables would be as follows

The predicted response would be

All other terms would be zero and

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

The values for variables would be as follows

The predicted response would be

##### 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)