# multivariate with timed fish swims added in

| **Functional Group** | **Baseline (Shipwreck)** | **Fringing vs. Shipwreck** | **Pinnacle vs. Shipwreck** | **Significance** |
| --- | --- | --- | --- | --- |
| **Herbivores** | 4.70 (4.44, 4.97) | +0.96 (0.65, 1.25) | +0.93 (0.61, 1.23) | Both Fringing and Pinnacle are significantly higher than Shipwrecks. |
| **Invertivores** | 4.23 (3.97, 4.49) | +0.54 (0.23, 0.84) | +1.00 (0.68, 1.31) | Both increases are statistically significant (Pinnacle shows a larger effect). |
| **Mesopredators** | 4.99 (4.67, 5.34) | +0.06 (-0.33, 0.44) | +0.84 (0.43, 1.23) | Only Pinnacle is significantly higher; Fringing does not differ from Shipwrecks. |
| **HTLP** | 3.54 (3.24, 3.86) | -0.32 (-0.67, 0.02) | +0.62 (0.25, 0.98) | Pinnacle is significantly higher; Fringing is not significantly different (trend toward lower counts). |

*Numbers in parentheses represent the 95% credible intervals.*

**Plain-Language Interpretation**

* **Herbivores:**  
  The baseline (Shipwreck) log count is about 4.70. Both Fringing and Pinnacle sites show a statistically significant increase in Herbivore counts (by approximately 0.96 and 0.93, respectively), meaning that Herbivores are more abundant at both Fringing and Pinnacle sites compared to Shipwrecks.
* **Invertivores:**  
  With a baseline of about 4.23 on Shipwrecks, Invertivores are significantly more abundant in Fringing sites (increase of about 0.54) and even more so in Pinnacle sites (increase of about 1.00). This indicates that Invertivores are much higher at Pinnacles relative to Shipwrecks.
* **Mesopredators:**  
  Mesopredators have a baseline log count of about 4.99. Here, only the Pinnacle sites show a statistically significant increase (an increase of about 0.84), while Fringing sites do not differ significantly from Shipwrecks.
* **HTLP Fish:**  
  For HTLP fish, the baseline is 3.54. Pinnacle sites show a significant increase (about 0.62 higher) compared to Shipwrecks. Fringing sites, on the other hand, show a slight decrease (–0.32), but this difference is not statistically significant.

**Overall Summary:**  
These results indicate that for several functional groups—especially Invertivores and HTLP fish—the assemblages on Pinnacle sites are significantly different (higher) compared to Shipwrecks. In contrast, Fringing reefs tend to be more similar to Shipwrecks, with only some groups (Herbivores) showing an increase. This suggests that, in terms of functional group composition, the fish assemblage on shipwrecks may be more similar to fringing reefs than to pelagic pinnacles.

> summary(results\_fg\_mv$fit\_fg\_mv)

Family: MV(negbinomial, negbinomial, negbinomial, negbinomial)

Links: mu = log; shape = identity

mu = log; shape = identity

mu = log; shape = identity

mu = log; shape = identity

Formula: Herbivore ~ Classification

Invertivore ~ Classification

Mesopredator ~ Classification

HTLP ~ Classification

Data: survey\_level (Number of observations: 243)

Draws: 4 chains, each with iter = 2000; warmup = 500; thin = 1;

total post-warmup draws = 6000

Regression Coefficients:

Estimate Est.Error l-95% CI u-95% CI Rhat Bulk\_ESS Tail\_ESS

Herbivore\_Intercept 4.70 0.13 4.44 4.97 1.00 6946 4005

Invertivore\_Intercept 4.23 0.13 3.97 4.49 1.00 7754 4285

Mesopredator\_Intercept 4.99 0.17 4.67 5.34 1.00 6349 4141

HTLP\_Intercept 3.54 0.16 3.24 3.86 1.00 7170 3988

Herbivore\_ClassificationFringing 0.96 0.15 0.65 1.25 1.00 6663 4565

Herbivore\_ClassificationPinnacle 0.93 0.16 0.61 1.23 1.00 6263 4553

Invertivore\_ClassificationFringing 0.54 0.15 0.23 0.84 1.00 7151 4762

Invertivore\_ClassificationPinnacle 1.00 0.16 0.68 1.31 1.00 7263 4981

Mesopredator\_ClassificationFringing 0.06 0.20 -0.33 0.44 1.00 5899 4410

Mesopredator\_ClassificationPinnacle 0.84 0.20 0.43 1.23 1.00 6034 4073

HTLP\_ClassificationFringing -0.32 0.18 -0.67 0.02 1.00 6557 5153

HTLP\_ClassificationPinnacle 0.62 0.18 0.25 0.98 1.00 6546 4662

Further Distributional Parameters:

Estimate Est.Error l-95% CI u-95% CI Rhat Bulk\_ESS Tail\_ESS

shape\_Herbivore 1.55 0.13 1.31 1.81 1.00 11248 3799

shape\_Invertivore 1.51 0.13 1.27 1.78 1.00 10243 4156

shape\_Mesopredator 1.00 0.08 0.85 1.16 1.00 11335 4618

shape\_HTLP 1.13 0.10 0.94 1.32 1.00 10470 4395

Draws were sampled using sampling(NUTS). For each parameter, Bulk\_ESS

and Tail\_ESS are effective sample size measures, and Rhat is the potential

scale reduction factor on split chains (at convergence, Rhat = 1).

# multivariate, with random effect for site

> print(summary(fit\_re))

Family: MV(negbinomial, negbinomial, negbinomial, negbinomial)

Links: mu = log; shape = identity

mu = log; shape = identity

mu = log; shape = identity

mu = log; shape = identity

Formula: Herbivore ~ Classification + (1 | p | Site)

Invertivore ~ Classification + (1 | p | Site)

Mesopredator ~ Classification + (1 | p | Site)

HTLP ~ Classification + (1 | p | Site)

Data: survey\_level (Number of observations: 108)

Draws: 4 chains, each with iter = 2000; warmup = 500; thin = 1;

total post-warmup draws = 6000

Multilevel Hyperparameters:

~Site (Number of levels: 12)

Estimate Est.Error l-95% CI u-95% CI Rhat Bulk\_ESS Tail\_ESS

sd(Herbivore\_Intercept) 0.82 0.23 0.49 1.37 1.00 2998 3865

sd(Invertivore\_Intercept) 0.76 0.23 0.43 1.32 1.00 3391 3884

sd(Mesopredator\_Intercept) 0.86 0.26 0.49 1.48 1.00 3584 4137

sd(HTLP\_Intercept) 0.91 0.26 0.53 1.56 1.00 3561 3727

cor(Herbivore\_Intercept,Invertivore\_Intercept) 0.67 0.23 0.08 0.97 1.00 3631 3988

cor(Herbivore\_Intercept,Mesopredator\_Intercept) 0.66 0.24 0.05 0.96 1.00 3712 4129

cor(Invertivore\_Intercept,Mesopredator\_Intercept) 0.72 0.22 0.16 0.97 1.00 4866 4961

cor(Herbivore\_Intercept,HTLP\_Intercept) 0.64 0.25 0.00 0.96 1.00 3936 4370

cor(Invertivore\_Intercept,HTLP\_Intercept) 0.58 0.27 -0.06 0.94 1.00 3854 4656

cor(Mesopredator\_Intercept,HTLP\_Intercept) 0.64 0.25 0.01 0.96 1.00 3868 4550

Regression Coefficients:

Estimate Est.Error l-95% CI u-95% CI Rhat Bulk\_ESS Tail\_ESS

Herbivore\_Intercept 4.82 0.52 3.78 5.85 1.00 2296 3056

Invertivore\_Intercept 4.36 0.48 3.43 5.32 1.00 2450 3298

Mesopredator\_Intercept 5.12 0.55 4.02 6.24 1.00 2619 3186

HTLP\_Intercept 3.67 0.58 2.55 4.81 1.00 2545 3243

Herbivore\_ClassificationFringing 0.51 0.74 -0.91 2.00 1.00 2672 3189

Herbivore\_ClassificationPinnacle 0.67 0.63 -0.59 1.95 1.00 2389 3416

Invertivore\_ClassificationFringing 0.25 0.69 -1.12 1.70 1.00 2944 3642

Invertivore\_ClassificationPinnacle 0.48 0.60 -0.76 1.66 1.00 2665 3275

Mesopredator\_ClassificationFringing 0.17 0.80 -1.38 1.76 1.00 3094 3986

Mesopredator\_ClassificationPinnacle 0.50 0.69 -0.92 1.89 1.00 2931 3520

HTLP\_ClassificationFringing -0.18 0.82 -1.77 1.41 1.00 2947 3252

HTLP\_ClassificationPinnacle 0.31 0.72 -1.11 1.74 1.00 2768 3301

Further Distributional Parameters:

Estimate Est.Error l-95% CI u-95% CI Rhat Bulk\_ESS Tail\_ESS

shape\_Herbivore 1.36 0.18 1.04 1.73 1.00 10869 3984

shape\_Invertivore 1.22 0.15 0.94 1.54 1.00 10109 4346

shape\_Mesopredator 0.76 0.10 0.59 0.96 1.00 12062 3325

shape\_HTLP 1.06 0.14 0.80 1.35 1.00 9735 4159

Draws were sampled using sampling(NUTS). For each parameter, Bulk\_ESS

and Tail\_ESS are effective sample size measures, and Rhat is the potential

scale reduction factor on split chains (at convergence, Rhat = 1).

# multivariate, no random effects added in yet

> summary(results\_fg\_mv$fit\_fg\_mv)

Family: MV(negbinomial, negbinomial, negbinomial, negbinomial)

Links: mu = log; shape = identity

mu = log; shape = identity

mu = log; shape = identity

mu = log; shape = identity

Formula: Herbivore ~ Classification

Invertivore ~ Classification

Mesopredator ~ Classification

HTLP ~ Classification

Data: survey\_level (Number of observations: 108)

Draws: 4 chains, each with iter = 2000; warmup = 500; thin = 1;

total post-warmup draws = 6000

Regression Coefficients:

Estimate Est.Error l-95% CI u-95% CI Rhat Bulk\_ESS Tail\_ESS

Herbivore\_Intercept 4.70 0.18 4.37 5.07 1.00 7490 3827

Invertivore\_Intercept 4.23 0.17 3.90 4.58 1.00 7147 4129

Mesopredator\_Intercept 5.00 0.22 4.58 5.46 1.00 7259 4468

HTLP\_Intercept 3.55 0.21 3.16 3.96 1.00 8040 4415

Herbivore\_ClassificationFringing 0.52 0.30 -0.05 1.12 1.00 7644 4561

Herbivore\_ClassificationPinnacle 0.84 0.24 0.38 1.30 1.00 7147 4756

Invertivore\_ClassificationFringing 0.33 0.30 -0.24 0.92 1.00 7038 4948

Invertivore\_ClassificationPinnacle 0.60 0.23 0.13 1.05 1.00 7581 4918

Mesopredator\_ClassificationFringing 0.27 0.37 -0.44 1.01 1.00 7104 4465

Mesopredator\_ClassificationPinnacle 0.78 0.29 0.20 1.35 1.00 6986 3959

HTLP\_ClassificationFringing -0.16 0.35 -0.83 0.53 1.00 7301 4691

HTLP\_ClassificationPinnacle 0.79 0.27 0.27 1.32 1.00 7973 4751

Further Distributional Parameters:

Estimate Est.Error l-95% CI u-95% CI Rhat Bulk\_ESS Tail\_ESS

shape\_Herbivore 0.88 0.11 0.68 1.10 1.00 8322 4575

shape\_Invertivore 0.87 0.10 0.68 1.09 1.00 7674 4260

shape\_Mesopredator 0.57 0.07 0.44 0.71 1.00 8075 3970 overdisperson here

shape\_HTLP 0.67 0.08 0.53 0.84 1.00 7879 4646

Draws were sampled using sampling(NUTS). For each parameter, Bulk\_ESS

and Tail\_ESS are effective sample size measures, and Rhat is the potential

scale reduction factor on split chains (at convergence, Rhat = 1).

Mesopredators have alower shape value, meaning counts are less variable compared to other groups. The shape parameters indicate overdispersion.

Note: averaging vs summing replicate survey s

For a multivariate model using count data like this, it usually makes sense to aggregate replicates by summing them. Here’s why:

* **Preserving Total Abundance:**  
  Since your model uses counts (via a negative binomial likelihood) as the response, summing replicates preserves the overall number of individuals observed at a site. This is especially important when calculating proportions later or comparing absolute abundances.
* **Consistent Survey Effort:**  
  If the survey effort across replicates is similar, then the total count is a meaningful representation of the site’s assemblage. In this case, summing provides a comprehensive picture of the fish community at that site.
* **Model Requirements:**  
  Multivariate models in brms that use count data expect integer counts. Averaging might yield fractional counts, which would then need to be rounded—and rounding can sometimes obscure real differences in abundance.
* **Proportional Comparisons:**  
  If your goal is to compare the relative abundances (proportions) of functional groups or species among site types, summing replicates first and then calculating proportions retains the full information about the total observed fish at each site.

Thus, if your replicates (e.g., different surveys by different researchers on the same site) are conducted with similar effort, summing them is generally the preferred approach for this type of multivariate regression analysis. Just remember to exclude the surveys by "Keisha" (or any unwanted replicates) before aggregating.