# results after removal of outliers

# with “shipwreck” as baseline for hypothesis testing

> print(summary(results$fit))

Family: multinomial

Links: muInvertivore = logit; muMesopredator = logit; muHTLP = logit

Formula: cbind(Herbivore, Invertivore, Mesopredator, HTLP) | trials(total\_fish) ~ Classification

Data: survey\_level (Number of observations: 186)

Draws: 4 chains, each with iter = 2000; warmup = 400; thin = 1;

total post-warmup draws = 6400

Regression Coefficients:

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

muInvertivore\_Intercept -0.51 0.03 -0.56 -0.46 1.00 3224 4674

muMesopredator\_Intercept 0.28 0.02 0.24 0.32 1.00 3287 4332

muHTLP\_Intercept -1.17 0.03 -1.23 -1.10 1.00 3491 4264

muInvertivore\_ClassificationFringing -0.18 0.04 -0.25 -0.10 1.00 3913 4334

muInvertivore\_ClassificationPinnacle -0.25 0.03 -0.31 -0.19 1.00 3590 4735

muMesopredator\_ClassificationFringing -0.25 0.03 -0.31 -0.19 1.00 3644 4924

muMesopredator\_ClassificationPinnacle -0.08 0.02 -0.13 -0.03 1.00 3513 4294

muHTLP\_ClassificationFringing -0.72 0.05 -0.83 -0.62 1.00 4255 4749

muHTLP\_ClassificationPinnacle -0.03 0.04 -0.11 0.04 1.00 3811 4057

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).

> print(summary(results$fit\_re))

Family: multinomial

Links: muInvertivore = logit; muMesopredator = logit; muHTLP = logit

Formula: cbind(Herbivore, Invertivore, Mesopredator, HTLP) | trials(total\_fish) ~ Classification + (1 | Site)

Data: survey\_level (Number of observations: 186)

Draws: 4 chains, each with iter = 2000; warmup = 400; thin = 1;

total post-warmup draws = 6400

Multilevel Hyperparameters:

~Site (Number of levels: 12)

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

sd(muInvertivore\_Intercept) 0.51 0.15 0.31 0.87 1.00 4588 4657

sd(muMesopredator\_Intercept) 0.54 0.16 0.33 0.94 1.00 3761 3834

sd(muHTLP\_Intercept) 0.60 0.17 0.36 1.04 1.00 3814 4043

Regression Coefficients:

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

muInvertivore\_Intercept -0.53 0.31 -1.18 0.07 1.00 5275 3872

muMesopredator\_Intercept 0.28 0.33 -0.38 0.93 1.00 4580 3820

muHTLP\_Intercept -1.23 0.36 -1.95 -0.52 1.00 4941 4277

muInvertivore\_ClassificationFringing -0.23 0.44 -1.08 0.69 1.00 4872 4317

muInvertivore\_ClassificationPinnacle -0.10 0.39 -0.86 0.70 1.00 4518 3838

muMesopredator\_ClassificationFringing -0.49 0.47 -1.43 0.44 1.00 4861 3878

muMesopredator\_ClassificationPinnacle -0.15 0.40 -0.94 0.65 1.00 4004 3199

muHTLP\_ClassificationFringing -0.75 0.51 -1.73 0.27 1.00 5431 4168

muHTLP\_ClassificationPinnacle -0.44 0.45 -1.31 0.47 1.00 4553 4106

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).

| **Functional Group** | **Comparison** | **Difference** | **Uncertainty** | **95% CI** | **Significance** |
| --- | --- | --- | --- | --- | --- |
| **Invertivore** | Fringing vs. Shipwreck | -0.18 | ±0.04 | -0.25 to -0.10 | Statistically significant |
|  | Pinnacle vs. Shipwreck | -0.25 | ±0.03 | -0.31 to -0.19 | Statistically significant |
|  | Pinnacle vs. Fringing | -0.07 | ±0.03 | -0.13 to -0.009 | Statistically significant |
| **Mesopredator** | Fringing vs. Shipwreck | -0.25 | ±0.03 | -0.31 to -0.19 | Statistically significant |
|  | Pinnacle vs. Shipwreck | -0.08 | ±0.02 | -0.13 to -0.03 | Statistically significant |
|  | Pinnacle vs. Fringing | 0.17 | ±0.03 | 0.12 to 0.22 | Statistically significant |
| **HTLP** | Fringing vs. Shipwreck | -0.72 | ±0.05 | -0.83 to -0.62 | Statistically significant |
|  | Pinnacle vs. Shipwreck | -0.03 | ±0.04 | -0.11 to 0.04 | *Not statistically significant* |
|  | Pinnacle vs. Fringing | 0.69 | ±0.05 | 0.60 to 0.78 | Statistically significant |

*Note: The differences are measured relative to Shipwreck sites (the baseline). A negative difference indicates a lower contribution compared to Shipwreck, and a positive difference indicates a higher contribution.*

**Plain-Language Summary**

**Invertivore Group:**

* **Fringing vs. Shipwreck:** Fringing sites have a statistically significantly lower contribution of invertivores than Shipwreck sites (a difference of about 0.18 units).
* **Pinnacle vs. Shipwreck:** Pinnacle sites also show a statistically significant lower invertivore count compared to Shipwreck sites (about 0.25 units lower).
* **Pinnacle vs. Fringing:** The difference between Pinnacle and Fringing sites is statistically significant, with Pinnacle sites being about 0.07 units lower than Fringing sites.

**Mesopredator Group:**

* **Fringing vs. Shipwreck:** Fringing sites have statistically significantly lower mesopredator counts compared to Shipwreck sites (a difference of about 0.25 units).
* **Pinnacle vs. Shipwreck:** Pinnacle sites are statistically significantly closer to Shipwreck sites (only about 0.08 units lower).
* **Pinnacle vs. Fringing:** The difference is statistically significant, with Pinnacle sites having approximately 0.17 units higher mesopredator counts than Fringing sites.

**HTLP Group:**

* **Fringing vs. Shipwreck:** Fringing sites have a statistically significant lower HTLP contribution than Shipwreck sites (about 0.72 units lower).
* **Pinnacle vs. Shipwreck:** Pinnacle sites show almost no difference from Shipwreck sites (a difference of about -0.03 units, which is not statistically significant).
* **Pinnacle vs. Fringing:** The difference between Pinnacle and Fringing sites is statistically significant, with Pinnacle sites having about 0.69 units higher HTLP counts than Fringing sites.

**Overall Interpretation:**

* **Nearly all differences are significant – except for HTLPs between shipwrecks and pinnacles. Otherwise, all functional groups have significant differences between the three site types.**
* For the HTLP group—a key indicator of overall fish composition—Shipwreck sites are nearly identical to Pinnacle sites and differ markedly **(Significantly)** from Fringing sites.
* For invertivores and mesopredators, although both Fringing and Pinnacle sites have lower counts compared to Shipwreck sites, the differences suggest that Pinnacle sites are closer to Shipwreck sites than Fringing sites are.
* In summary, these results indicate that, in terms of fish community composition, Shipwreck sites are more similar to Pinnacle sites than to Fringing sites.

# with “fringing as baseline”

(no random intercept for site)

Family: multinomial

Links: muInvertivore = logit; muMesopredator = logit; muHTLP = logit

Formula: cbind(Herbivore, Invertivore, Mesopredator, HTLP) | trials(total\_fish) ~ Classification

Data: survey\_level (Number of observations: 186)

Draws: 4 chains, each with iter = 2000; warmup = 400; thin = 1;

total post-warmup draws = 6400

Regression Coefficients:

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

muInvertivore\_Intercept -0.68 0.03 -0.74 -0.63 1.00 4492 4838

muMesopredator\_Intercept 0.03 0.02 -0.02 0.08 1.00 4156 4248

muHTLP\_Intercept -1.89 0.05 -1.98 -1.80 1.00 4322 4204

muInvertivore\_ClassificationPinnacle -0.07 0.03 -0.13 -0.01 1.00 4308 4552

muInvertivore\_ClassificationShipwreck 0.18 0.04 0.10 0.26 1.00 4213 4290

muMesopredator\_ClassificationPinnacle 0.17 0.03 0.12 0.22 1.00 4237 4288

muMesopredator\_ClassificationShipwreck 0.25 0.03 0.19 0.31 1.00 4256 4420

muHTLP\_ClassificationPinnacle 0.69 0.05 0.59 0.79 1.00 4377 4497

muHTLP\_ClassificationShipwreck 0.72 0.06 0.61 0.83 1.00 4458 4011

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).

(with random intercept for site)

Family: multinomial

Links: muInvertivore = logit; muMesopredator = logit; muHTLP = logit

Formula: cbind(Herbivore, Invertivore, Mesopredator, HTLP) | trials(total\_fish) ~ Classification + (1 | Site)

Data: survey\_level (Number of observations: 186)

Draws: 4 chains, each with iter = 2000; warmup = 400; thin = 1;

total post-warmup draws = 6400

Multilevel Hyperparameters:

~Site (Number of levels: 12)

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

sd(muInvertivore\_Intercept) 0.51 0.15 0.31 0.87 1.00 4228 4622

sd(muMesopredator\_Intercept) 0.54 0.15 0.33 0.94 1.00 4357 3944

sd(muHTLP\_Intercept) 0.59 0.17 0.36 1.02 1.00 4117 4379

Regression Coefficients:

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

muInvertivore\_Intercept -0.76 0.31 -1.37 -0.14 1.00 4855 4476

muMesopredator\_Intercept -0.21 0.33 -0.87 0.45 1.00 5787 4095

muHTLP\_Intercept -1.96 0.36 -2.67 -1.24 1.00 4856 4419

muInvertivore\_ClassificationPinnacle 0.12 0.38 -0.64 0.88 1.00 4280 4223

muInvertivore\_ClassificationShipwreck 0.23 0.44 -0.63 1.11 1.00 4836 3955

muMesopredator\_ClassificationPinnacle 0.34 0.40 -0.48 1.14 1.00 4917 3926

muMesopredator\_ClassificationShipwreck 0.49 0.47 -0.44 1.43 1.00 5484 4026

muHTLP\_ClassificationPinnacle 0.29 0.43 -0.58 1.16 1.00 4493 4089

muHTLP\_ClassificationShipwreck 0.74 0.49 -0.22 1.71 1.00 4969 4410

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).