# fit\_re

#### FG multivariate regression with random intercept for site

# final FG model thank you

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: 280)

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

total post-warmup draws = 6000

Multilevel Hyperparameters:

~Site (Number of levels: 14)

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

sd(Herbivore\_Intercept) 0.59 0.14 0.38 0.92 1.00 2138 3531

sd(Invertivore\_Intercept) 0.50 0.13 0.31 0.79 1.00 3102 3536

sd(Mesopredator\_Intercept) 0.71 0.17 0.46 1.11 1.00 2950 3240

sd(HTLP\_Intercept) 0.78 0.20 0.49 1.24 1.00 3371 3853

cor(Herbivore\_Intercept,Invertivore\_Intercept) 0.68 0.21 0.16 0.95 1.00 2840 3884

cor(Herbivore\_Intercept,Mesopredator\_Intercept) 0.68 0.21 0.14 0.95 1.00 2736 3503

cor(Invertivore\_Intercept,Mesopredator\_Intercept) 0.72 0.20 0.22 0.96 1.00 3218 3728

cor(Herbivore\_Intercept,HTLP\_Intercept) 0.54 0.24 -0.03 0.89 1.00 2541 3503

cor(Invertivore\_Intercept,HTLP\_Intercept) 0.54 0.24 -0.01 0.88 1.00 2712 3794

cor(Mesopredator\_Intercept,HTLP\_Intercept) 0.61 0.22 0.07 0.91 1.00 3494 4286

Regression Coefficients:

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

Herbivore\_Intercept 4.77 0.37 4.02 5.50 1.00 1918 2504

Invertivore\_Intercept 4.37 0.32 3.73 4.99 1.00 2075 2889

Mesopredator\_Intercept 5.20 0.45 4.29 6.09 1.00 2058 2899

HTLP\_Intercept 3.90 0.49 2.93 4.84 1.00 2275 3198

Herbivore\_ClassificationFringing 0.44 0.48 -0.52 1.38 1.00 1695 2448

Herbivore\_ClassificationPinnacle 0.63 0.45 -0.28 1.55 1.00 1739 2264

Invertivore\_ClassificationFringing -0.02 0.40 -0.81 0.79 1.00 1976 2916

Invertivore\_ClassificationPinnacle 0.51 0.40 -0.27 1.32 1.00 2067 2816

Mesopredator\_ClassificationFringing -0.54 0.57 -1.66 0.62 1.00 1968 2874

Mesopredator\_ClassificationPinnacle 0.40 0.55 -0.67 1.52 1.00 2065 3072

HTLP\_ClassificationFringing -0.99 0.62 -2.22 0.22 1.00 2173 3511

HTLP\_ClassificationPinnacle 0.18 0.60 -1.01 1.40 1.00 2189 3066

Further Distributional Parameters:

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

shape\_Herbivore 2.07 0.17 1.75 2.41 1.00 10457 4736

shape\_Invertivore 1.80 0.15 1.52 2.10 1.00 10003 3825

shape\_Mesopredator 1.17 0.09 1.00 1.35 1.00 10207 4464

shape\_HTLP 1.30 0.11 1.10 1.52 1.00 9596 4113

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 Classification Intercept Effect Predicted\_Log Predicted

1 Herbivore Shipwreck 4.771859 0.00000000 4.771859 118.13863

2 Herbivore Fringing 4.771859 0.43881101 5.210670 183.21673

3 Herbivore Pinnacle 4.771859 0.62998700 5.401846 221.81546

4 Invertivore Shipwreck 4.370558 0.00000000 4.370558 79.08775

5 Invertivore Fringing 4.370558 -0.01611308 4.354445 77.82361

6 Invertivore Pinnacle 4.370558 0.51067558 4.881234 131.79314

7 Mesopredator Shipwreck 5.203107 0.00000000 5.203107 181.83641

8 Mesopredator Fringing 5.203107 -0.53638230 4.666725 106.34889

9 Mesopredator Pinnacle 5.203107 0.40125978 5.604367 271.61000

10 HTLP Shipwreck 3.903513 0.00000000 3.903513 49.57628

11 HTLP Fringing 3.903513 -0.98937727 2.914135 18.43287

12 HTLP Pinnacle 3.903513 0.17542616 4.078939 59.08273

# try with “zones” instead of pinnacle and fringing

> summary(fit\_zone)

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 ~ Zone + (1 | p | Site)

Invertivore ~ Zone + (1 | p | Site)

Mesopredator ~ Zone + (1 | p | Site)

HTLP ~ Zone + (1 | p | Site)

Data: survey\_level (Number of observations: 280)

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

total post-warmup draws = 6000

Multilevel Hyperparameters:

~Site (Number of levels: 14)

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

sd(Herbivore\_Intercept) 0.62 0.16 0.38 0.99 1.00 2452 3770

sd(Invertivore\_Intercept) 0.53 0.12 0.34 0.81 1.00 3158 3422

sd(Mesopredator\_Intercept) 0.79 0.17 0.52 1.18 1.00 2930 3717

sd(HTLP\_Intercept) 0.83 0.19 0.54 1.28 1.00 3039 3376

cor(Herbivore\_Intercept,Invertivore\_Intercept) 0.62 0.21 0.10 0.91 1.00 3356 4136

cor(Herbivore\_Intercept,Mesopredator\_Intercept) 0.56 0.22 0.04 0.88 1.00 3411 4261

cor(Invertivore\_Intercept,Mesopredator\_Intercept) 0.79 0.16 0.37 0.97 1.00 3257 4445

cor(Herbivore\_Intercept,HTLP\_Intercept) 0.41 0.26 -0.17 0.81 1.00 2867 3184

cor(Invertivore\_Intercept,HTLP\_Intercept) 0.71 0.20 0.21 0.96 1.00 2712 3810

cor(Mesopredator\_Intercept,HTLP\_Intercept) 0.68 0.20 0.19 0.94 1.00 3850 4478

Regression Coefficients:

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

Herbivore\_Intercept 5.19 0.23 4.73 5.66 1.00 1779 3109

Invertivore\_Intercept 4.59 0.20 4.19 4.99 1.00 1978 3092

Mesopredator\_Intercept 5.01 0.29 4.43 5.59 1.00 2057 3276

HTLP\_Intercept 3.26 0.30 2.66 3.84 1.00 2444 3644

Herbivore\_Zonepelagic 0.40 0.46 -0.51 1.33 1.00 2198 3020

Herbivore\_Zonewreck -0.42 0.44 -1.31 0.46 1.00 2408 3884

Invertivore\_Zonepelagic 0.16 0.40 -0.62 0.96 1.00 2297 3327

Invertivore\_Zonewreck -0.21 0.39 -0.98 0.56 1.00 2488 3545

Mesopredator\_Zonepelagic 0.60 0.58 -0.54 1.77 1.00 2264 3197

Mesopredator\_Zonewreck 0.21 0.56 -0.93 1.31 1.00 2678 3821

HTLP\_Zonepelagic 1.03 0.60 -0.12 2.20 1.00 2471 3970

HTLP\_Zonewreck 0.65 0.59 -0.52 1.81 1.00 2688 4017

Further Distributional Parameters:

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

shape\_Herbivore 2.08 0.17 1.75 2.43 1.00 10051 4057

shape\_Invertivore 1.80 0.15 1.52 2.10 1.00 10335 4547

shape\_Mesopredator 1.17 0.09 1.00 1.36 1.00 10621 4348

shape\_HTLP 1.30 0.11 1.09 1.52 1.00 10535 4053

Draws were sampled using sample(hmc). 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).

> loo\_compare(loo(fit\_re), loo(fit\_zone))

elpd\_diff se\_diff

fit\_re 0.0 0.0

fit\_zone -0.1 2.9

# species subset analysis

> summary(results\_species$fit\_brms)

Family: MV(negbinomial, negbinomial, negbinomial)

Links: mu = log; shape = identity

mu = log; shape = identity

mu = log; shape = identity

Formula: Parrotfish ~ Classification

Rabbitfish ~ Classification

Butterflyfish ~ Classification

Data: fish\_wide (Number of observations: 280)

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

Parrotfish\_Intercept 4.17 0.07 4.03 4.31 1.00 9042 5057

Rabbitfish\_Intercept 4.05 0.09 3.86 4.24 1.00 8395 4961

Butterflyfish\_Intercept 4.09 0.07 3.95 4.22 1.00 10174 5075

Parrotfish\_ClassificationPinnacle -0.56 0.11 -0.77 -0.35 1.00 9013 5495

Parrotfish\_ClassificationShipwreck -1.30 0.14 -1.57 -1.02 1.00 8246 5087

Rabbitfish\_ClassificationPinnacle 0.71 0.14 0.43 0.99 1.00 7797 5458

Rabbitfish\_ClassificationShipwreck 0.14 0.18 -0.19 0.50 1.00 8876 5039

Butterflyfish\_ClassificationPinnacle 0.01 0.10 -0.20 0.22 1.00 10224 5101

Butterflyfish\_ClassificationShipwreck -0.86 0.14 -1.12 -0.59 1.00 11073 5190

Further Distributional Parameters:

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

shape\_Parrotfish 1.49 0.13 1.25 1.74 1.00 10859 4927

shape\_Rabbitfish 0.89 0.07 0.77 1.04 1.00 9898 4861

shape\_Butterflyfish 1.64 0.14 1.39 1.92 1.00 10007 4840

Draws were sampled using sample(hmc). 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).

### all species

> summary(results\_all\_species$fit\_mv)

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

Links: mu = log; shape = identity

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mu = log; shape = identity

mu = log; shape = identity

Formula: Angelfish ~ Classification

Batfish ~ Classification

Butterflyfish ~ Classification

Cleaner\_Wrasse ~ Classification

Emperorfish ~ Classification

Parrotfish ~ Classification

Rabbitfish ~ Classification

Red\_Breast ~ Classification

Slingjaw ~ Classification

Squirrel.Soldier ~ Classification

Sweetlips ~ Classification

Thicklip ~ Classification

Trevally ~ Classification

Triggerfish ~ Classification

lrg\_Grouper ~ Classification

lrg\_Snapper ~ Classification

sml\_Grouper ~ Classification

sml\_snapper ~ Classification

Data: fish\_species\_wide (Number of observations: 280)

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

Angelfish\_Intercept 1.22 0.09 1.04 1.41 1.00 11081 4309

Batfish\_Intercept -0.98 0.28 -1.51 -0.43 1.00 8063 4972

Butterflyfish\_Intercept 4.09 0.07 3.95 4.22 1.00 9798 4841

CleanerWrasse\_Intercept 2.51 0.09 2.34 2.70 1.00 10437 4593

Emperorfish\_Intercept 2.17 0.11 1.95 2.39 1.00 8188 4277

Parrotfish\_Intercept 4.17 0.07 4.02 4.31 1.00 11793 4464

Rabbitfish\_Intercept 4.04 0.09 3.86 4.23 1.00 9967 3957

RedBreast\_Intercept 2.82 0.09 2.66 3.00 1.00 9683 3795

Slingjaw\_Intercept 2.08 0.09 1.91 2.26 1.00 11831 4125

SquirrelSoldier\_Intercept 2.50 0.16 2.19 2.83 1.00 8735 4079

Sweetlips\_Intercept 2.38 0.19 2.02 2.76 1.00 9281 4550

Thicklip\_Intercept 2.08 0.08 1.91 2.25 1.00 10494 4409

Trevally\_Intercept 1.90 0.12 1.66 2.14 1.00 8218 5137

Triggerfish\_Intercept 1.13 0.09 0.96 1.30 1.00 11440 4160

lrgGrouper\_Intercept 2.14 0.09 1.97 2.32 1.00 8107 4407

lrgSnapper\_Intercept 0.48 0.17 0.15 0.82 1.00 7753 4167

smlGrouper\_Intercept 3.86 0.08 3.70 4.02 1.00 9796 4709

smlsnapper\_Intercept 3.76 0.16 3.46 4.08 1.00 8520 4973

Angelfish\_ClassificationPinnacle 0.48 0.13 0.22 0.75 1.00 11220 4774

Angelfish\_ClassificationShipwreck -0.24 0.18 -0.60 0.11 1.00 11719 4301

Batfish\_ClassificationPinnacle 2.17 0.37 1.44 2.92 1.00 8727 4509

Batfish\_ClassificationShipwreck 0.92 0.49 -0.01 1.91 1.00 8659 4595

Butterflyfish\_ClassificationPinnacle 0.01 0.10 -0.19 0.21 1.00 10194 4985

Butterflyfish\_ClassificationShipwreck -0.86 0.13 -1.12 -0.59 1.00 9928 4346

CleanerWrasse\_ClassificationPinnacle 0.16 0.13 -0.10 0.43 1.00 9538 4220

CleanerWrasse\_ClassificationShipwreck -1.09 0.18 -1.45 -0.73 1.00 9659 4692

Emperorfish\_ClassificationPinnacle 0.86 0.17 0.53 1.19 1.00 9597 5045

Emperorfish\_ClassificationShipwreck 0.53 0.22 0.11 0.98 1.00 8696 4563

Parrotfish\_ClassificationPinnacle -0.56 0.11 -0.77 -0.34 1.00 11624 4845

Parrotfish\_ClassificationShipwreck -1.29 0.14 -1.57 -1.00 1.00 9711 4970

Rabbitfish\_ClassificationPinnacle 0.71 0.14 0.44 0.99 1.00 9301 4782

Rabbitfish\_ClassificationShipwreck 0.14 0.18 -0.20 0.50 1.00 8926 4523

RedBreast\_ClassificationPinnacle -0.26 0.13 -0.51 -0.01 1.00 10570 4923

RedBreast\_ClassificationShipwreck -1.09 0.17 -1.42 -0.74 1.00 10023 4756

Slingjaw\_ClassificationPinnacle -1.33 0.14 -1.61 -1.05 1.00 7723 4120

Slingjaw\_ClassificationShipwreck -2.34 0.23 -2.78 -1.90 1.00 7830 3977

SquirrelSoldier\_ClassificationPinnacle 1.44 0.24 0.98 1.92 1.00 9926 4804

SquirrelSoldier\_ClassificationShipwreck 0.00 0.31 -0.57 0.62 1.00 7964 4427

Sweetlips\_ClassificationPinnacle 1.20 0.28 0.67 1.75 1.00 9437 4900

Sweetlips\_ClassificationShipwreck 1.44 0.35 0.77 2.15 1.00 9132 4534

Thicklip\_ClassificationPinnacle -0.62 0.13 -0.87 -0.38 1.00 10390 4781

Thicklip\_ClassificationShipwreck -1.84 0.19 -2.22 -1.47 1.00 9011 4983

Trevally\_ClassificationPinnacle 1.68 0.18 1.34 2.03 1.00 8289 4939

Trevally\_ClassificationShipwreck 0.89 0.24 0.44 1.37 1.00 8392 4472

Triggerfish\_ClassificationPinnacle -0.34 0.13 -0.60 -0.08 1.00 11314 4671

Triggerfish\_ClassificationShipwreck -0.62 0.18 -0.97 -0.25 1.00 9147 4625

lrgGrouper\_ClassificationPinnacle 0.74 0.13 0.48 0.99 1.00 9510 4986

lrgGrouper\_ClassificationShipwreck 0.11 0.17 -0.22 0.44 1.00 9470 4953

lrgSnapper\_ClassificationPinnacle 1.63 0.24 1.15 2.11 1.00 8769 4579

lrgSnapper\_ClassificationShipwreck 2.51 0.30 1.93 3.12 1.00 8373 4699

smlGrouper\_ClassificationPinnacle 0.26 0.12 0.03 0.50 1.00 9391 4479

smlGrouper\_ClassificationShipwreck -0.76 0.15 -1.06 -0.45 1.00 8928 4391

smlsnapper\_ClassificationPinnacle 1.50 0.24 1.03 1.97 1.00 8485 5100

smlsnapper\_ClassificationShipwreck 1.17 0.30 0.60 1.79 1.00 8256 4773

Further Distributional Parameters:

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

shape\_Angelfish 1.25 0.15 0.99 1.56 1.00 12165 4180

shape\_Batfish 0.15 0.02 0.11 0.20 1.00 10915 4482

shape\_Butterflyfish 1.64 0.13 1.39 1.92 1.00 14597 3920

shape\_CleanerWrasse 1.07 0.10 0.88 1.29 1.00 11965 4280

shape\_Emperorfish 0.64 0.05 0.54 0.75 1.00 11016 4018

shape\_Parrotfish 1.49 0.13 1.25 1.74 1.00 11382 4533

shape\_Rabbitfish 0.90 0.07 0.77 1.03 1.00 11880 4491

shape\_RedBreast 1.12 0.11 0.93 1.34 1.00 9583 4959

shape\_Slingjaw 1.18 0.15 0.91 1.50 1.00 10453 4764

shape\_SquirrelSoldier 0.31 0.03 0.26 0.37 1.00 9069 4547

shape\_Sweetlips 0.23 0.02 0.19 0.27 1.00 10990 4271

shape\_Thicklip 1.35 0.17 1.06 1.72 1.00 12462 4730

shape\_Trevally 0.57 0.04 0.49 0.66 1.00 12563 4577

shape\_Triggerfish 1.73 0.25 1.29 2.27 1.00 12403 4076

shape\_lrgGrouper 1.12 0.10 0.94 1.34 1.00 10525 4183

shape\_lrgSnapper 0.34 0.03 0.28 0.41 1.00 12600 4613

shape\_smlGrouper 1.28 0.11 1.08 1.50 1.00 10941 3969

shape\_smlsnapper 0.31 0.03 0.27 0.37 1.00 11068 4475

Draws were sampled using sample(hmc). 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).