> summary(fit\_total)

Loading required namespace: rstan

Family: negbinomial

Links: mu = log; shape = identity

Formula: total\_fish\_density ~ s(cots\_density\_ha) + (1 | Site)

Data: total\_fish\_df (Number of observations: 49)

Draws: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;

total post-warmup draws = 4000

Smoothing Spline Hyperparameters:

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

sds(scots\_density\_ha\_1) 0.29 0.33 0.01 1.34 1.01 366 71

Multilevel Hyperparameters:

~Site (Number of levels: 5)

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

sd(Intercept) 0.44 0.26 0.15 1.07 1.01 732 1894

Regression Coefficients:

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

Intercept 7.48 0.22 7.05 7.91 1.00 942 877

scots\_density\_ha\_1 0.59 0.82 -0.49 3.66 1.02 259 69

Further Distributional Parameters:

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

shape 14.94 3.37 9.19 22.10 1.01 1047 1162

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).

Warning message:

There were 51 divergent transitions after warmup. Increasing adapt\_delta above 0.99 may help. See http://mc-stan.org/misc/warnings.html#divergent-transitions-after-warmup

> summary(fit\_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: fish\_herb ~ s(cots\_density\_ha) + (1 | Site)

fish\_invert ~ s(cots\_density\_ha) + (1 | Site)

fish\_meso ~ s(cots\_density\_ha) + (1 | Site)

fish\_htlp ~ s(cots\_density\_ha) + (1 | Site)

Data: cotsxfish\_wide (Number of observations: 49)

Draws: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;

total post-warmup draws = 4000

Smoothing Spline Hyperparameters:

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

sds(fishherb\_scots\_density\_ha\_1) 0.44 0.31 0.06 1.21 1.00 1544 1344

sds(fishinvert\_scots\_density\_ha\_1) 0.30 0.36 0.01 1.31 1.00 1178 1593

sds(fishmeso\_scots\_density\_ha\_1) 0.39 0.37 0.02 1.38 1.00 1730 2153

sds(fishhtlp\_scots\_density\_ha\_1) 0.61 0.65 0.02 2.40 1.00 1496 1975

Multilevel Hyperparameters:

~Site (Number of levels: 5)

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

sd(fishherb\_Intercept) 0.15 0.13 0.01 0.47 1.00 1059 1302

sd(fishinvert\_Intercept) 0.19 0.16 0.01 0.60 1.00 1068 1568

sd(fishmeso\_Intercept) 0.98 0.48 0.40 2.20 1.00 1364 2094

sd(fishhtlp\_Intercept) 0.95 0.51 0.37 2.31 1.00 1473 2461

Regression Coefficients:

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

fishherb\_Intercept 6.31 0.09 6.11 6.50 1.00 2511 2231

fishinvert\_Intercept 6.37 0.12 6.15 6.62 1.00 2066 2019

fishmeso\_Intercept 6.17 0.46 5.27 7.08 1.00 960 1260

fishhtlp\_Intercept 4.29 0.46 3.34 5.23 1.00 1440 1573

fishherb\_scots\_density\_ha\_1 0.66 0.78 -0.79 2.34 1.00 2979 2579

fishinvert\_scots\_density\_ha\_1 0.27 0.69 -0.93 1.97 1.00 1883 1153

fishmeso\_scots\_density\_ha\_1 0.94 0.96 -0.72 3.19 1.00 1971 1830

fishhtlp\_scots\_density\_ha\_1 -0.38 1.66 -2.58 4.19 1.00 1838 1864

Further Distributional Parameters:

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

shape\_fishherb 11.91 2.70 7.39 17.87 1.00 3982 2714

shape\_fishinvert 13.05 2.89 8.16 19.25 1.00 5036 3223

shape\_fishmeso 4.84 1.06 3.04 7.14 1.00 4233 3038

shape\_fishhtlp 2.67 0.57 1.66 3.91 1.00 4829 2936

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).

Warning message:

There were 2 divergent transitions after warmup. Increasing adapt\_delta above 0.99 may help. See http://mc-stan.org/misc/warnings.html#divergent-transitions-after-warmup

> summary(fit\_spp)

Family: MV(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 ~ s(cots\_density\_ha) + (1 | Site)

Butterflyfish ~ s(cots\_density\_ha) + (1 | Site)

Cleaner\_Wrasse ~ s(cots\_density\_ha) + (1 | Site)

Emperorfish ~ s(cots\_density\_ha) + (1 | Site)

Parrotfish ~ s(cots\_density\_ha) + (1 | Site)

Rabbitfish ~ s(cots\_density\_ha) + (1 | Site)

Red\_Breast ~ s(cots\_density\_ha) + (1 | Site)

Slingjaw ~ s(cots\_density\_ha) + (1 | Site)

Squirrel.Soldier ~ s(cots\_density\_ha) + (1 | Site)

Sweetlips ~ s(cots\_density\_ha) + (1 | Site)

Thicklip ~ s(cots\_density\_ha) + (1 | Site)

Trevally ~ s(cots\_density\_ha) + (1 | Site)

Triggerfish ~ s(cots\_density\_ha) + (1 | Site)

lrg\_Grouper ~ s(cots\_density\_ha) + (1 | Site)

lrg\_Snapper ~ s(cots\_density\_ha) + (1 | Site)

sml\_Grouper ~ s(cots\_density\_ha) + (1 | Site)

sml\_Snapper ~ s(cots\_density\_ha) + (1 | Site)

Data: spp\_wide (Number of observations: 49)

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

total post-warmup draws = 6000

Smoothing Spline Hyperparameters:

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

sds(Angelfish\_scots\_density\_ha\_1) 0.76 0.72 0.02 2.68 1.00 2763 3208

sds(Butterflyfish\_scots\_density\_ha\_1) 0.30 0.36 0.01 1.38 1.00 1729 2276

sds(CleanerWrasse\_scots\_density\_ha\_1) 0.42 0.45 0.01 1.76 1.00 2126 2855

sds(Emperorfish\_scots\_density\_ha\_1) 0.56 0.56 0.02 2.07 1.00 2854 3317

sds(Parrotfish\_scots\_density\_ha\_1) 0.56 0.39 0.06 1.57 1.00 2098 1813

sds(Rabbitfish\_scots\_density\_ha\_1) 0.30 0.30 0.01 1.12 1.00 2506 2984

sds(RedBreast\_scots\_density\_ha\_1) 0.30 0.34 0.01 1.21 1.00 2979 3318

sds(Slingjaw\_scots\_density\_ha\_1) 0.54 0.56 0.02 2.09 1.00 2107 3453

sds(SquirrelSoldier\_scots\_density\_ha\_1) 0.75 0.71 0.03 2.64 1.00 3154 3309

sds(Sweetlips\_scots\_density\_ha\_1) 1.23 1.08 0.05 4.04 1.00 2946 2911

sds(Thicklip\_scots\_density\_ha\_1) 0.39 0.40 0.01 1.51 1.00 1995 2618

sds(Trevally\_scots\_density\_ha\_1) 0.76 0.77 0.02 2.85 1.00 2358 3118

sds(Triggerfish\_scots\_density\_ha\_1) 1.51 0.93 0.30 3.84 1.00 1700 1494

sds(lrgGrouper\_scots\_density\_ha\_1) 0.49 0.52 0.01 1.98 1.00 2561 3218

sds(lrgSnapper\_scots\_density\_ha\_1) 1.01 0.97 0.03 3.57 1.00 3067 3154

sds(smlGrouper\_scots\_density\_ha\_1) 0.30 0.33 0.01 1.17 1.00 2748 3244

sds(smlSnapper\_scots\_density\_ha\_1) 0.77 0.71 0.03 2.67 1.00 2512 3712

Multilevel Hyperparameters:

~Site (Number of levels: 5)

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

sd(Angelfish\_Intercept) 0.73 0.52 0.06 2.00 1.00 1458 1652

sd(Butterflyfish\_Intercept) 0.23 0.19 0.02 0.71 1.00 1345 1919

sd(CleanerWrasse\_Intercept) 0.38 0.26 0.09 1.06 1.00 2321 2252

sd(Emperorfish\_Intercept) 1.05 0.57 0.33 2.50 1.00 1440 2004

sd(Parrotfish\_Intercept) 0.49 0.32 0.10 1.31 1.00 1543 1884

sd(Rabbitfish\_Intercept) 0.20 0.19 0.01 0.70 1.00 1523 2006

sd(RedBreast\_Intercept) 0.68 0.39 0.23 1.67 1.00 1919 3268

sd(Slingjaw\_Intercept) 0.46 0.33 0.06 1.31 1.00 1325 1545

sd(SquirrelSoldier\_Intercept) 1.26 0.65 0.36 2.90 1.00 1875 1636

sd(Sweetlips\_Intercept) 0.70 0.64 0.02 2.39 1.00 2071 2794

sd(Thicklip\_Intercept) 0.15 0.17 0.01 0.57 1.00 1916 2009

sd(Trevally\_Intercept) 1.35 0.67 0.55 3.11 1.00 2237 3462

sd(Triggerfish\_Intercept) 0.47 0.35 0.05 1.36 1.00 1466 1478

sd(lrgGrouper\_Intercept) 0.25 0.27 0.01 0.91 1.00 2037 2578

sd(lrgSnapper\_Intercept) 0.69 0.59 0.03 2.18 1.00 2263 3058

sd(smlGrouper\_Intercept) 0.30 0.23 0.06 0.90 1.00 1763 2498

sd(smlSnapper\_Intercept) 1.94 0.80 0.91 3.93 1.00 2443 3505

Regression Coefficients:

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

Angelfish\_Intercept 2.79 0.42 1.91 3.61 1.00 1991 2284

Butterflyfish\_Intercept 5.63 0.14 5.36 5.92 1.00 2456 1807

CleanerWrasse\_Intercept 4.16 0.21 3.72 4.57 1.00 2373 2308

Emperorfish\_Intercept 3.40 0.53 2.31 4.47 1.00 1942 2237

Parrotfish\_Intercept 5.63 0.26 5.09 6.13 1.00 2175 2417

Rabbitfish\_Intercept 5.49 0.14 5.24 5.79 1.00 2559 2661

RedBreast\_Intercept 3.99 0.33 3.30 4.68 1.00 2050 2661

Slingjaw\_Intercept 3.24 0.26 2.72 3.77 1.00 2018 2290

SquirrelSoldier\_Intercept 4.24 0.61 2.99 5.46 1.00 2338 2886

Sweetlips\_Intercept 1.31 0.50 0.19 2.31 1.00 3330 2227

Thicklip\_Intercept 3.73 0.12 3.52 3.98 1.00 3139 1845

Trevally\_Intercept 3.26 0.64 1.87 4.52 1.00 1885 2624

Triggerfish\_Intercept 2.47 0.28 1.89 2.98 1.00 2869 2849

lrgGrouper\_Intercept 3.51 0.19 3.16 3.88 1.00 3463 2336

lrgSnapper\_Intercept 1.51 0.48 0.53 2.49 1.00 3497 3000

smlGrouper\_Intercept 5.41 0.18 5.07 5.79 1.00 2457 2303

smlSnapper\_Intercept 4.92 0.85 3.22 6.60 1.00 2170 2445

Angelfish\_scots\_density\_ha\_1 1.20 1.96 -2.04 6.03 1.00 3195 3474

Butterflyfish\_scots\_density\_ha\_1 0.26 0.63 -1.06 1.69 1.00 2572 2252

CleanerWrasse\_scots\_density\_ha\_1 0.29 1.19 -1.42 3.57 1.00 2411 1936

Emperorfish\_scots\_density\_ha\_1 1.18 1.50 -1.57 4.73 1.00 3025 2700

Parrotfish\_scots\_density\_ha\_1 0.94 1.07 -0.99 3.26 1.00 3058 3716

Rabbitfish\_scots\_density\_ha\_1 -0.09 0.74 -1.58 1.55 1.00 4082 3398

RedBreast\_scots\_density\_ha\_1 0.17 0.73 -1.38 1.74 1.00 3771 3254

Slingjaw\_scots\_density\_ha\_1 0.31 1.12 -1.86 2.93 1.00 3607 2893

SquirrelSoldier\_scots\_density\_ha\_1 1.10 1.95 -2.95 5.36 1.00 3116 3023

Sweetlips\_scots\_density\_ha\_1 0.96 3.32 -4.55 9.05 1.00 2993 2671

Thicklip\_scots\_density\_ha\_1 0.66 0.94 -1.11 2.88 1.00 2925 2657

Trevally\_scots\_density\_ha\_1 -1.24 2.01 -4.37 3.92 1.00 2759 2152

Triggerfish\_scots\_density\_ha\_1 0.78 2.23 -3.66 5.29 1.00 3844 3671

lrgGrouper\_scots\_density\_ha\_1 -0.47 1.32 -2.56 2.95 1.00 2909 2662

lrgSnapper\_scots\_density\_ha\_1 0.36 2.86 -5.24 6.97 1.00 2895 2286

smlGrouper\_scots\_density\_ha\_1 -0.06 0.75 -1.90 1.19 1.00 3219 3041

smlSnapper\_scots\_density\_ha\_1 1.92 2.17 -1.43 7.53 1.00 2873 2213

Further Distributional Parameters:

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

shape\_Angelfish 1.28 0.34 0.74 2.07 1.00 4545 4056

shape\_Butterflyfish 12.35 2.91 7.33 18.64 1.00 6782 4175

shape\_CleanerWrasse 4.69 1.05 2.90 6.95 1.00 6716 4449

shape\_Emperorfish 1.75 0.42 1.05 2.70 1.00 6751 4096

shape\_Parrotfish 6.46 1.48 3.95 9.75 1.00 6007 4582

shape\_Rabbitfish 6.47 1.39 4.04 9.48 1.00 7849 4337

shape\_RedBreast 5.92 1.48 3.40 9.13 1.00 7708 4082

shape\_Slingjaw 4.62 1.29 2.61 7.68 1.00 5847 4004

shape\_SquirrelSoldier 0.84 0.17 0.54 1.21 1.00 6797 4614

shape\_Sweetlips 0.33 0.10 0.18 0.57 1.00 8602 4813

shape\_Thicklip 5.29 1.26 3.19 8.14 1.00 8093 4700

shape\_Trevally 1.34 0.29 0.84 1.97 1.00 8151 4373

shape\_Triggerfish 2.41 0.65 1.39 3.93 1.00 5301 4616

shape\_lrgGrouper 2.56 0.58 1.60 3.81 1.00 8104 4221

shape\_lrgSnapper 0.32 0.09 0.18 0.52 1.00 7190 3824

shape\_smlGrouper 8.33 1.86 5.15 12.35 1.00 6515 4031

shape\_smlSnapper 1.02 0.21 0.66 1.47 1.00 8556 4279

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).