Appendix of GLM outputs

2024-05-23

This is the code used to produce the results in Cahill & Chenuil, and knits to produce the full outputs of the analyses conducted.

# Analyses with full dataset (starting n = 978)

1. Are there more CSss or pseudo-CS overall, considering only cases where morphology was measured? (n = 492)

Pearson's Chi-squared test with Yates' continuity correction  
   
 data: cbind(expected, observed)  
 X-squared = 24.723, df = 1, p-value = 6.619e-07

1. Are there differences across phyla or classes? (n = 492)

Single term deletions  
   
 Model:  
 CSss ~ phylum\_wormsV1  
 Df Deviance AIC LRT Pr(>Chi)  
 <none> 612.48 642.48   
 phylum\_wormsV1 14 631.73 633.73 19.249 0.1557

Single term deletions  
   
 Model:  
 CSss ~ phylum\_class  
 Df Deviance AIC LRT Pr(>Chi)   
 <none> 549.38 635.38   
 phylum\_class 42 631.73 633.73 82.354 0.0001979 \*\*\*  
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Since phylum\_class is significant, we will now use this as a random factor in subsequent models.

1. Is the probability of CSss associated with year of description? (n = 492)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ yearb + (1 | phylum\_class)  
 Data: surveymorpho  
   
 AIC BIC logLik deviance df.resid   
 538.1 550.2 -266.1 532.1 412   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.9167 -1.0852 0.5701 0.7388 1.1237   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.4049 0.6363   
 Number of obs: 415, groups: phylum\_class, 41  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)  
 (Intercept) -1.0217218 2.1249649 -0.481 0.631  
 yearb 0.0008689 0.0011261 0.772 0.440  
   
 Correlation of Fixed Effects:  
 (Intr)  
 yearb -0.996

1. Is there a relationship between the number of CS in easily-accessible or inaccessible habitats and time? (n = 972)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: Difficult ~ yearb + (1 | phylum\_class)  
 Data: surveyaccess  
   
 AIC BIC logLik deviance df.resid   
 544.5 558.7 -269.3 538.5 830   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -0.8243 -0.3683 -0.2557 -0.1867 6.8326   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 1.379 1.175   
 Number of obs: 833, groups: phylum\_class, 45  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) -1.544e+01 1.540e+00 -10.027 <2e-16 \*\*\*  
 yearb 6.727e-03 7.947e-04 8.465 <2e-16 \*\*\*  
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 yearb -0.969

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: Easy ~ yearb + (1 | phylum\_class)  
 Data: surveyaccess  
   
 AIC BIC logLik deviance df.resid   
 764.2 778.4 -379.1 758.2 830   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -0.9769 -0.5137 -0.3571 -0.2603 3.9045   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 1.013 1.007   
 Number of obs: 833, groups: phylum\_class, 45  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 3.470069 2.076215 1.671 0.0947 .  
 yearb -0.002680 0.001117 -2.400 0.0164 \*  
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 yearb -0.994

1. Is habitat connectivity (variable HKK) associated with CSss? (n = 492)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ HKKv3 + (1 | phylum\_class)  
 Data: surveymorpho  
   
 AIC BIC logLik deviance df.resid   
 581.5 593.8 -287.7 575.5 449   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -2.3029 -1.1119 0.6233 0.7640 1.1755   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.3137 0.5601   
 Number of obs: 452, groups: phylum\_class, 42  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 0.5222582 0.1731721 3.016 0.00256 \*\*  
 HKKv3 0.0008152 0.0004124 1.977 0.04806 \*   
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 HKKv3 -0.320

1. Are CSss more common in rocky or soft sediment habitats? (n = 227) What about when only considering shallow-water species? (n = 192)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Hsubstrate + (1 | phylum\_class)  
 Data: surveysed  
   
 AIC BIC logLik deviance df.resid   
 281.5 291.8 -137.7 275.5 224   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.8099 -1.1580 0.5525 0.8636 0.8636   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0 0   
 Number of obs: 227, groups: phylum\_class, 31  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 0.2933 0.1992 1.473 0.14083   
 HsubstrateSediment 0.8932 0.2910 3.069 0.00214 \*\*  
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 HsbstrtSdmn -0.684

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Hsubstrate + (1 | phylum\_class)  
 Data: shallow  
   
 AIC BIC logLik deviance df.resid   
 237.8 247.6 -115.9 231.8 189   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -2.1515 -1.0379 0.5159 0.7907 1.0332   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.1182 0.3438   
 Number of obs: 192, groups: phylum\_class, 31  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 0.2197 0.2431 0.904 0.36621   
 HsubstrateSediment 1.0627 0.3403 3.123 0.00179 \*\*  
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 HsbstrtSdmn -0.632

1. Are CSss more common in sympatry or no? (n = 486)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Sympatric + (1 | phylum\_class)  
 Data: surveymorpho  
   
 AIC BIC logLik deviance df.resid   
 611.9 624.5 -303.0 605.9 483   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -2.1845 -1.1038 0.5460 0.7155 1.0469   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.2389 0.4888   
 Number of obs: 486, groups: phylum\_class, 43  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 1.1725 0.2125 5.517 3.46e-08 \*\*\*  
 SympatricTRUE -0.6869 0.2137 -3.214 0.00131 \*\*   
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 SymptrcTRUE -0.703

1. Are species in sympatry more likely to have ecological differentiation? (n=147)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: Eco\_diff ~ Sympatric + (1 | phylum\_class)  
 Data: survey  
   
 AIC BIC logLik deviance df.resid   
 157.4 166.4 -75.7 151.4 145   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -2.0354 0.4913 0.4913 0.4913 0.5774   
   
 Random effects:  
 Groups Name Variance Std.Dev.   
 phylum\_class (Intercept) 8.275e-16 2.877e-08  
 Number of obs: 148, groups: phylum\_class, 27  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 1.0986 0.3651 3.009 0.00262 \*\*  
 SympatricTRUE 0.3228 0.4387 0.736 0.46187   
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 SymptrcTRUE -0.832

1. Are CSss more common in species with ecological differentiation? (n = 107)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Eco\_diff + (1 | phylum\_class)  
 Data: surveymorpho  
   
 AIC BIC logLik deviance df.resid   
 128.8 136.9 -61.4 122.8 104   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -2.1714 -1.0158 0.4605 0.6387 0.9874   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.503 0.7092   
 Number of obs: 107, groups: phylum\_class, 24  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 2.0688 0.6704 3.086 0.00203 \*\*  
 Eco\_diffYes -1.5193 0.6840 -2.221 0.02634 \*   
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 Eco\_diffYes -0.895

1. Are biological traits (hard skeleton, fertilization type, presence of external genitalia, image-forming vision) associated with CSss? (n = 464)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ hard\_skeleton + (1 | phylum\_class)  
 Data: surveymorpho  
   
 AIC BIC logLik deviance df.resid   
 597.3 609.7 -295.6 591.3 461   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.9032 -1.1096 0.5773 0.7634 0.9510   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.2719 0.5215   
 Number of obs: 464, groups: phylum\_class, 39  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 0.9118 0.2812 3.243 0.00118 \*\*  
 hard\_skeletonY -0.3557 0.3428 -1.038 0.29946   
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 hard\_skltnY -0.822

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ ferti + (1 | phylum\_class)  
 Data: surveymorpho  
   
 AIC BIC logLik deviance df.resid   
 598.4 614.9 -295.2 590.4 460   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.7939 -1.2097 0.5646 0.7251 1.0472   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.1889 0.4346   
 Number of obs: 464, groups: phylum\_class, 39  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)  
 (Intercept) 0.3321 0.3391 0.979 0.327  
 fertiE 0.5330 0.3890 1.370 0.171  
 fertiI 0.1985 0.4729 0.420 0.675  
   
 Correlation of Fixed Effects:  
 (Intr) fertiE  
 fertiE -0.851   
 fertiI -0.771 0.642

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ genitals + (1 | phylum\_class)  
 Data: surveymorpho  
   
 AIC BIC logLik deviance df.resid   
 599.3 615.8 -295.6 591.3 460   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.7480 -1.1816 0.5749 0.7428 0.9035   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.1864 0.4317   
 Number of obs: 464, groups: phylum\_class, 39  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)  
 (Intercept) 0.39876 0.49083 0.812 0.417  
 genitalsN 0.38638 0.52283 0.739 0.460  
 genitalsY 0.02626 0.58537 0.045 0.964  
   
 Correlation of Fixed Effects:  
 (Intr) gntlsN  
 genitalsN -0.939   
 genitalsY -0.838 0.779

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ image + (1 | phylum\_class)  
 Data: surveymorpho  
   
 AIC BIC logLik deviance df.resid   
 598.2 610.6 -296.1 592.2 461   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.7974 -1.1105 0.5738 0.7416 0.9985   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.2847 0.5336   
 Number of obs: 464, groups: phylum\_class, 39  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 0.7171 0.1958 3.663 0.000249 \*\*\*  
 imageY -0.1342 0.3467 -0.387 0.698703   
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 imageY -0.565

1. Is larval type associated with CSss? (n = 305)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Larv\_type + (1 | phylum\_class)  
 Data: surveylarvmorpho  
   
 AIC BIC logLik deviance df.resid   
 400.1 415.0 -196.1 392.1 301   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.7841 -1.1164 0.5660 0.7549 1.1493   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.3637 0.6031   
 Number of obs: 305, groups: phylum\_class, 42  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 0.64617 0.28208 2.291 0.022 \*  
 Larv\_typeLT -0.29186 0.40209 -0.726 0.468   
 Larv\_typePT -0.01534 0.32303 -0.047 0.962   
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr) Lrv\_LT  
 Larv\_typeLT -0.603   
 Larv\_typePT -0.677 0.457

1. Are CSss more common in particular geographic zones? (n = 368)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Trop + (1 | phylum\_class)  
 Data: tropmorpho  
   
 AIC BIC logLik deviance df.resid   
 480.2 491.9 -237.1 474.2 365   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.8238 -1.1178 0.5790 0.7781 1.1275   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.3473 0.5893   
 Number of obs: 368, groups: phylum\_class, 40  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 0.5126 0.2602 1.970 0.0488 \*  
 TropTRUE 0.1181 0.2640 0.447 0.6545   
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 TropTRUE -0.729

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Npol + (1 | phylum\_class)  
 Data: npolmorpho  
   
 AIC BIC logLik deviance df.resid   
 479.0 490.8 -236.5 473.0 365   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.8281 -1.0439 0.5597 0.7781 1.1771   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.3477 0.5897   
 Number of obs: 368, groups: phylum\_class, 40  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 0.6500 0.1842 3.529 0.000418 \*\*\*  
 NpolTRUE -0.4120 0.3517 -1.171 0.241426   
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 NpolTRUE -0.251

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Ntemp + (1 | phylum\_class)  
 Data: ntempmorpho  
   
 AIC BIC logLik deviance df.resid   
 479.6 491.3 -236.8 473.6 365   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.9980 -1.1366 0.5695 0.7576 1.1032   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.3485 0.5904   
 Number of obs: 368, groups: phylum\_class, 40  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 0.8022 0.2871 2.794 0.0052 \*\*  
 NtempTRUE -0.2583 0.2820 -0.916 0.3597   
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 NtempTRUE -0.784

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Spol + (1 | phylum\_class)  
 Data: spolmorpho  
   
 AIC BIC logLik deviance df.resid   
 476.8 488.5 -235.4 470.8 365   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.9065 -1.1244 0.5552 0.7604 1.1682   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.3985 0.6312   
 Number of obs: 368, groups: phylum\_class, 40  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 0.5134 0.1895 2.710 0.00673 \*\*  
 SpolTRUE 1.0896 0.6187 1.761 0.07823 .   
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 SpolTRUE -0.217

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Stemp + (1 | phylum\_class)  
 Data: stempmorpho  
   
 AIC BIC logLik deviance df.resid   
 480.4 492.1 -237.2 474.4 365   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.8126 -1.1524 0.5623 0.7540 1.0884   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.3444 0.5869   
 Number of obs: 368, groups: phylum\_class, 40  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 0.58026 0.21676 2.677 0.00743 \*\*  
 StempTRUE 0.03252 0.23005 0.141 0.88757   
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 StempTRUE -0.572

1. What about the bestglm to determine which factors are most important?

First with all data

HKKv3 phylum\_class Sympatric Criterion  
 1 TRUE FALSE TRUE 589.6304  
 2 TRUE FALSE FALSE 599.6097  
 3 FALSE FALSE TRUE 618.2374  
 4 FALSE FALSE FALSE 631.7294  
 5 TRUE TRUE TRUE 810.5695  
 6 TRUE TRUE FALSE 818.5512  
 7 FALSE TRUE TRUE 837.3658

And now with the shallow-water rocky vs soft sed dataset

Hsubstrate HKKv3 phylum\_class Sympatric Criterion  
 1 FALSE TRUE FALSE FALSE 230.2928  
 2 FALSE TRUE FALSE TRUE 232.1653  
 3 TRUE TRUE FALSE FALSE 232.3110  
 4 TRUE TRUE FALSE TRUE 234.8614  
 5 TRUE FALSE FALSE FALSE 242.7391  
 6 FALSE FALSE FALSE FALSE 244.4214  
 7 TRUE FALSE FALSE TRUE 245.1846  
 8 FALSE FALSE FALSE TRUE 246.5525  
 9 FALSE TRUE TRUE TRUE 437.4595  
 10 FALSE FALSE TRUE FALSE 448.1791

# Analyses with species where reproductive isolation is clear based on multiple datatypes (see main text) (starting n = 535)

1. Are there more CSss or pseudo-CS overall, considering only cases where morphology was measured? (n = 411)

Pearson's Chi-squared test with Yates' continuity correction  
   
 data: cbind(expected, observed)  
 X-squared = 6.5374, df = 1, p-value = 0.01056

1. Are there differences across phyla or classes? (n = 411)

Single term deletions  
   
 Model:  
 CSss ~ phylum\_wormsV1  
 Df Deviance AIC LRT Pr(>Chi)  
 <none> 544.78 572.78   
 phylum\_wormsV1 13 556.00 558.00 11.227 0.5918

Single term deletions  
   
 Model:  
 CSss ~ phylum\_class  
 Df Deviance AIC LRT Pr(>Chi)   
 <none> 480.14 562.14   
 phylum\_class 40 556.00 558.00 75.866 0.0005308 \*\*\*  
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Since phylum\_class is significant, we will now use this as a random factor in subsequent models.

1. Is the probability of CSss associated with year of description? (n = 347)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ yearb + (1 | phylum\_class)  
 Data: surveymorpho  
   
 AIC BIC logLik deviance df.resid   
 470.2 481.7 -232.1 464.2 344   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.6013 -1.0523 0.6258 0.8677 1.2616   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.4022 0.6342   
 Number of obs: 347, groups: phylum\_class, 38  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)  
 (Intercept) 2.363e-01 2.356e+00 0.10 0.920  
 yearb 2.486e-05 1.249e-03 0.02 0.984  
   
 Correlation of Fixed Effects:  
 (Intr)  
 yearb -0.997

1. Is there a relationship between the number of CS in easily-accessible or inaccessible habitats and time? (n = 450)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: Difficult ~ yearb + (1 | phylum\_class)  
 Data: surveyaccess  
   
 AIC BIC logLik deviance df.resid   
 281.3 293.6 -137.6 275.3 447   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -0.7469 -0.3353 -0.2496 -0.1607 5.7341   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 2.013 1.419   
 Number of obs: 450, groups: phylum\_class, 40  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) -15.643204 4.304056 -3.635 0.000278 \*\*\*  
 yearb 0.006718 0.002194 3.061 0.002203 \*\*   
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 yearb -0.992

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: Easy ~ yearb + (1 | phylum\_class)  
 Data: surveyaccess  
   
 AIC BIC logLik deviance df.resid   
 469.6 481.9 -231.8 463.6 447   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -0.8804 -0.5395 -0.4297 -0.3171 2.8111   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.6441 0.8026   
 Number of obs: 450, groups: phylum\_class, 40  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 3.335200 2.317550 1.439 0.1501   
 yearb -0.002517 0.001247 -2.017 0.0437 \*  
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 yearb -0.995

1. Is habitat connectivity (variable HKK) associated with CSss? (n = 378)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ HKKv3 + (1 | phylum\_class)  
 Data: surveymorpho  
   
 AIC BIC logLik deviance df.resid   
 506.2 518.0 -250.1 500.2 375   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -2.2457 -1.0083 0.4956 0.8503 1.1579   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.363 0.6025   
 Number of obs: 378, groups: phylum\_class, 40  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 0.1446182 0.1921296 0.753 0.4516   
 HKKv3 0.0010014 0.0004296 2.331 0.0198 \*  
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 HKKv3 -0.303

1. Are CSss more common in rocky or soft sediment habitats? (n = 190) What about when only considering shallow-water species? (n = 157)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Hsubstrate + (1 | phylum\_class)  
 Data: surveysed  
   
 AIC BIC logLik deviance df.resid   
 252.9 262.7 -123.5 246.9 187   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.6649 -1.0554 0.6449 0.8796 1.0140   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.05896 0.2428   
 Number of obs: 190, groups: phylum\_class, 30  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 0.1108 0.2215 0.500 0.617   
 HsubstrateSediment 0.7629 0.3195 2.388 0.017 \*  
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 HsbstrtSdmn -0.631

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Hsubstrate + (1 | phylum\_class)  
 Data: shallow  
   
 AIC BIC logLik deviance df.resid   
 209.8 219.0 -101.9 203.8 154   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.9713 -0.9053 0.6046 0.8025 1.1785   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.2454 0.4954   
 Number of obs: 157, groups: phylum\_class, 30  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 0.002481 0.267123 0.009 0.9926   
 HsubstrateSediment 0.917421 0.376245 2.438 0.0148 \*  
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 HsbstrtSdmn -0.605

1. Are CSss more common in sympatry or no? (n = 407)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Sympatric + (1 | phylum\_class)  
 Data: surveymorpho  
   
 AIC BIC logLik deviance df.resid   
 545.8 557.8 -269.9 539.8 404   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.8355 -1.0922 0.6342 0.8309 1.1967   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.2933 0.5416   
 Number of obs: 407, groups: phylum\_class, 41  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 0.6533 0.2298 2.842 0.00448 \*\*  
 SympatricTRUE -0.3665 0.2277 -1.610 0.10748   
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 SymptrcTRUE -0.701

1. Are species in sympatry more likely to have ecological differentiation? (n=140)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: Eco\_diff ~ Sympatric + (1 | phylum\_class)  
 Data: survey  
   
 AIC BIC logLik deviance df.resid   
 134.2 143.0 -64.1 128.2 137   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -2.2492 0.4446 0.4446 0.4446 0.4830   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0 0   
 Number of obs: 140, groups: phylum\_class, 25  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 1.4553 0.4198 3.467 0.000526 \*\*\*  
 SympatricTRUE 0.1658 0.4966 0.334 0.738423   
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 SymptrcTRUE -0.845

1. Are CSss more common in species with ecological differentiation? (n = 104)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Eco\_diff + (1 | phylum\_class)  
 Data: surveymorpho  
   
 AIC BIC logLik deviance df.resid   
 128 136 -61 122 101   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -2.0624 -1.0201 0.4849 0.6472 0.9814   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.499 0.7064   
 Number of obs: 104, groups: phylum\_class, 23  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 1.9101 0.6818 2.802 0.00508 \*\*  
 Eco\_diffYes -1.3675 0.6929 -1.974 0.04844 \*   
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 Eco\_diffYes -0.898

1. Are biological traits (hard skeleton, fertilization type, presence of external genitalia, image-forming vision) associated with CSss? (n = 386)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ hard\_skeleton + (1 | phylum\_class)  
 Data: surveymorpho  
   
 AIC BIC logLik deviance df.resid   
 523.1 535.0 -258.6 517.1 383   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.6046 -1.0560 0.6360 0.8315 1.1749   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.308 0.555   
 Number of obs: 386, groups: phylum\_class, 37  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)  
 (Intercept) 0.35549 0.31460 1.130 0.258  
 hard\_skeletonY -0.01755 0.37518 -0.047 0.963  
   
 Correlation of Fixed Effects:  
 (Intr)  
 hard\_skltnY -0.837

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ ferti + (1 | phylum\_class)  
 Data: surveymorpho  
   
 AIC BIC logLik deviance df.resid   
 523.5 539.3 -257.7 515.5 382   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.5893 -1.0214 0.6365 0.8406 1.2339   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.2026 0.4501   
 Number of obs: 386, groups: phylum\_class, 37  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)  
 (Intercept) -0.02255 0.35430 -0.064 0.949  
 fertiE 0.54989 0.40527 1.357 0.175  
 fertiI 0.30645 0.49189 0.623 0.533  
   
 Correlation of Fixed Effects:  
 (Intr) fertiE  
 fertiE -0.828   
 fertiI -0.769 0.603

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ genitals + (1 | phylum\_class)  
 Data: surveymorpho  
   
 AIC BIC logLik deviance df.resid   
 524.7 540.5 -258.3 516.7 382   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.5733 -1.0318 0.6398 0.8295 1.0938   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.237 0.4868   
 Number of obs: 386, groups: phylum\_class, 37  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)  
 (Intercept) 0.06329 0.54803 0.115 0.908  
 genitalsN 0.36233 0.58570 0.619 0.536  
 genitalsY 0.16316 0.64636 0.252 0.801  
   
 Correlation of Fixed Effects:  
 (Intr) gntlsN  
 genitalsN -0.936   
 genitalsY -0.848 0.777

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ image + (1 | phylum\_class)  
 Data: surveymorpho  
   
 AIC BIC logLik deviance df.resid   
 523.1 535.0 -258.6 517.1 383   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.6009 -1.0558 0.6362 0.8341 1.1777   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.3079 0.5549   
 Number of obs: 386, groups: phylum\_class, 37  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)  
 (Intercept) 0.34700 0.21225 1.635 0.102  
 imageY -0.01129 0.36710 -0.031 0.975  
   
 Correlation of Fixed Effects:  
 (Intr)  
 imageY -0.586

1. Is larval type associated with CSss? (n = 259)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Larv\_type + (1 | phylum\_class)  
 Data: surveylarvmorpho  
   
 AIC BIC logLik deviance df.resid   
 352.4 366.6 -172.2 344.4 255   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.6733 -0.9902 0.6193 0.8429 1.3615   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.4748 0.689   
 Number of obs: 259, groups: phylum\_class, 41  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)  
 (Intercept) 0.39951 0.30421 1.313 0.189  
 Larv\_typeLT -0.30259 0.43875 -0.690 0.490  
 Larv\_typePT -0.08442 0.34559 -0.244 0.807  
   
 Correlation of Fixed Effects:  
 (Intr) Lrv\_LT  
 Larv\_typeLT -0.599   
 Larv\_typePT -0.655 0.448

1. Are CSss more common in particular geographic zones? (n = 313)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Trop + (1 | phylum\_class)  
 Data: tropmorpho  
   
 AIC BIC logLik deviance df.resid   
 422.8 434.1 -208.4 416.8 310   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.7273 -0.9890 0.5981 0.8841 1.4770   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.4823 0.6945   
 Number of obs: 313, groups: phylum\_class, 37  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)  
 (Intercept) 0.1137 0.2919 0.389 0.697  
 TropTRUE 0.2511 0.2882 0.871 0.384  
   
 Correlation of Fixed Effects:  
 (Intr)  
 TropTRUE -0.725

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Npol + (1 | phylum\_class)  
 Data: npolmorpho  
   
 AIC BIC logLik deviance df.resid   
 423.1 434.3 -208.6 417.1 310   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.7124 -1.0446 0.6089 0.8818 1.3137   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.467 0.6834   
 Number of obs: 313, groups: phylum\_class, 37  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)  
 (Intercept) 0.3310 0.2051 1.614 0.106  
 NpolTRUE -0.2582 0.3734 -0.692 0.489  
   
 Correlation of Fixed Effects:  
 (Intr)  
 NpolTRUE -0.231

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Ntemp + (1 | phylum\_class)  
 Data: ntempmorpho  
   
 AIC BIC logLik deviance df.resid   
 423.1 434.3 -208.6 417.1 310   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.7772 -1.0206 0.6247 0.8592 1.3670   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.4791 0.6921   
 Number of obs: 313, groups: phylum\_class, 37  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)  
 (Intercept) 0.4641 0.3152 1.473 0.141  
 NtempTRUE -0.2090 0.3056 -0.684 0.494  
   
 Correlation of Fixed Effects:  
 (Intr)  
 NtempTRUE -0.771

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Spol + (1 | phylum\_class)  
 Data: spolmorpho  
   
 AIC BIC logLik deviance df.resid   
 420.5 431.8 -207.3 414.5 310   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.7217 -1.0325 0.6117 0.8652 1.4923   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.5767 0.7594   
 Number of obs: 313, groups: phylum\_class, 37  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 0.2086 0.2200 0.948 0.343   
 SpolTRUE 1.1255 0.6822 1.650 0.099 .  
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 SpolTRUE -0.242

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Stemp + (1 | phylum\_class)  
 Data: stempmorpho  
   
 AIC BIC logLik deviance df.resid   
 423.6 434.8 -208.8 417.6 310   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.6898 -1.0390 0.6128 0.9021 1.3455   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.4767 0.6905   
 Number of obs: 313, groups: phylum\_class, 37  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)  
 (Intercept) 0.293102 0.240569 1.218 0.223  
 StempTRUE 0.009752 0.246670 0.040 0.968  
   
 Correlation of Fixed Effects:  
 (Intr)  
 StempTRUE -0.553

# Analyses with species where the number of CS per article = 1 (see main text) (starting n = 610)

1. Are there more CSss or pseudo-CS overall, considering only cases where morphology was measured? (n = 395)

Pearson's Chi-squared test with Yates' continuity correction  
   
 data: cbind(expected, observed)  
 X-squared = 12.612, df = 1, p-value = 0.0003832

1. Are there differences across phyla or classes? (n = 395)

Single term deletions  
   
 Model:  
 CSss ~ phylum\_wormsV1  
 Df Deviance AIC LRT Pr(>Chi)  
 <none> 508.00 538.00   
 phylum\_wormsV1 14 521.47 523.47 13.468 0.49

Single term deletions  
   
 Model:  
 CSss ~ phylum\_class  
 Df Deviance AIC LRT Pr(>Chi)   
 <none> 441.51 523.51   
 phylum\_class 40 521.47 523.47 79.959 0.0001783 \*\*\*  
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Since phylum\_class is significant, we will now use this as a random factor in subsequent models.

1. Is the probability of CSss associated with year of description? (n = 324)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ yearb + (1 | phylum\_class)  
 Data: surveymorpho  
   
 AIC BIC logLik deviance df.resid   
 427.1 438.4 -210.6 421.1 321   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -2.0220 -1.0370 0.5378 0.7912 1.4026   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.4763 0.6902   
 Number of obs: 324, groups: phylum\_class, 38  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)  
 (Intercept) -1.0590398 2.4903792 -0.425 0.671  
 yearb 0.0007534 0.0013246 0.569 0.569  
   
 Correlation of Fixed Effects:  
 (Intr)  
 yearb -0.997

1. Is there a relationship between the number of CS in easily-accessible or inaccessible habitats and time? (n = 493)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: Difficult ~ yearb + (1 | phylum\_class)  
 Data: surveyaccess  
   
 AIC BIC logLik deviance df.resid   
 281.7 294.3 -137.9 275.7 490   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -0.4852 -0.3162 -0.2666 -0.2248 5.1142   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0 0   
 Number of obs: 493, groups: phylum\_class, 43  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) -15.507783 3.917983 -3.958 7.55e-05 \*\*\*  
 yearb 0.006965 0.002057 3.386 0.00071 \*\*\*  
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 yearb -0.999

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: Easy ~ yearb + (1 | phylum\_class)  
 Data: surveyaccess  
   
 AIC BIC logLik deviance df.resid   
 533.2 545.8 -263.6 527.2 490   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -0.8715 -0.5756 -0.4697 -0.2807 3.2312   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.5226 0.7229   
 Number of obs: 493, groups: phylum\_class, 43  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)  
 (Intercept) 1.202283 2.145676 0.560 0.575  
 yearb -0.001292 0.001150 -1.123 0.261  
   
 Correlation of Fixed Effects:  
 (Intr)  
 yearb -0.996  
 optimizer (Nelder\_Mead) convergence code: 0 (OK)

1. Is habitat connectivity (variable HKK) associated with CSss? (n = 360)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ HKKv3 + (1 | phylum\_class)  
 Data: surveymorpho  
   
 AIC BIC logLik deviance df.resid   
 475.3 486.9 -234.6 469.3 357   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -2.2329 -1.0830 0.6319 0.8223 1.2029   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.2703 0.5199   
 Number of obs: 360, groups: phylum\_class, 40  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 0.3327135 0.1816082 1.832 0.0669 .  
 HKKv3 0.0007000 0.0004075 1.718 0.0858 .  
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 HKKv3 -0.329

1. Are CSss more common in rocky or soft sediment habitats? (n = 171) What about when only considering shallow-water species? (n = 153)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Hsubstrate + (1 | phylum\_class)  
 Data: surveysed  
   
 AIC BIC logLik deviance df.resid   
 225.2 234.6 -109.6 219.2 168   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.9704 -1.0191 0.5504 0.7656 1.1562   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.2409 0.4908   
 Number of obs: 171, groups: phylum\_class, 30  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 0.1906 0.2616 0.728 0.4664   
 HsubstrateSediment 0.7191 0.3481 2.066 0.0389 \*  
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 HsbstrtSdmn -0.597

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Hsubstrate + (1 | phylum\_class)  
 Data: shallow  
   
 AIC BIC logLik deviance df.resid   
 201.7 210.8 -97.9 195.7 150   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.9676 -1.0002 0.5665 0.7732 1.1357   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.187 0.4324   
 Number of obs: 153, groups: phylum\_class, 30  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 0.1300 0.2631 0.494 0.6213   
 HsubstrateSediment 0.8393 0.3702 2.267 0.0234 \*  
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 HsbstrtSdmn -0.606

1. Are CSss more common in sympatry or no? (n = 390)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Sympatric + (1 | phylum\_class)  
 Data: surveymorpho  
   
 AIC BIC logLik deviance df.resid   
 499.6 511.5 -246.8 493.6 387   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -2.3264 -1.0001 0.5396 0.7374 1.2725   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.2983 0.5462   
 Number of obs: 390, groups: phylum\_class, 40  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 1.0321 0.2419 4.266 1.99e-05 \*\*\*  
 SympatricTRUE -0.7335 0.2413 -3.040 0.00236 \*\*   
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 SymptrcTRUE -0.712

1. Are species in sympatry more likely to have ecological differentiation? (n=125)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: Eco\_diff ~ Sympatric + (1 | phylum\_class)  
 Data: survey  
   
 AIC BIC logLik deviance df.resid   
 116.6 125.1 -55.3 110.6 122   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -2.5115 0.3982 0.3982 0.3982 0.6030   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0 0   
 Number of obs: 125, groups: phylum\_class, 25  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 1.0116 0.4129 2.450 0.0143 \*  
 SympatricTRUE 0.8302 0.5095 1.629 0.1032   
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 SymptrcTRUE -0.810

1. Are CSss more common in species with ecological differentiation? (n = 91)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Eco\_diff + (1 | phylum\_class)  
 Data: surveymorpho  
   
 AIC BIC logLik deviance df.resid   
 122.3 129.8 -58.1 116.3 88   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.8761 -1.0879 0.6616 0.7352 0.9326   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.2328 0.4825   
 Number of obs: 91, groups: phylum\_class, 22  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 1.5185 0.6941 2.188 0.0287 \*  
 Eco\_diffYes -1.0977 0.7205 -1.523 0.1277   
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 Eco\_diffYes -0.924

1. Are biological traits (hard skeleton, fertilization type, presence of external genitalia, image-forming vision) associated with CSss? (n = 368)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ hard\_skeleton + (1 | phylum\_class)  
 Data: surveymorpho  
   
 AIC BIC logLik deviance df.resid   
 484.0 495.7 -239.0 478.0 365   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.8656 -1.0668 0.5538 0.8029 1.2816   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.3586 0.5988   
 Number of obs: 368, groups: phylum\_class, 37  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)  
 (Intercept) 0.3664 0.3334 1.099 0.272  
 hard\_skeletonY 0.1447 0.3994 0.362 0.717  
   
 Correlation of Fixed Effects:  
 (Intr)  
 hard\_skltnY -0.834

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ ferti + (1 | phylum\_class)  
 Data: surveymorpho  
   
 AIC BIC logLik deviance df.resid   
 483.9 499.6 -238.0 475.9 364   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.8723 -1.0801 0.5483 0.7709 1.2833   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.2721 0.5216   
 Number of obs: 368, groups: phylum\_class, 37  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)  
 (Intercept) 0.15416 0.39884 0.387 0.699  
 fertiE 0.55987 0.45765 1.223 0.221  
 fertiI 0.06089 0.52567 0.116 0.908  
   
 Correlation of Fixed Effects:  
 (Intr) fertiE  
 fertiE -0.855   
 fertiI -0.769 0.655

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ genitals + (1 | phylum\_class)  
 Data: surveymorpho  
   
 AIC BIC logLik deviance df.resid   
 484.3 499.9 -238.1 476.3 364   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.8377 -1.0521 0.5631 0.7794 1.0782   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.2487 0.4987   
 Number of obs: 368, groups: phylum\_class, 37  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)  
 (Intercept) 0.15646 0.57206 0.273 0.784  
 genitalsN 0.47936 0.60851 0.788 0.431  
 genitalsY -0.06254 0.67360 -0.093 0.926  
   
 Correlation of Fixed Effects:  
 (Intr) gntlsN  
 genitalsN -0.940   
 genitalsY -0.849 0.799

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ image + (1 | phylum\_class)  
 Data: surveymorpho  
   
 AIC BIC logLik deviance df.resid   
 484.1 495.8 -239.1 478.1 365   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.8544 -1.0489 0.5586 0.8005 1.2434   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.3572 0.5976   
 Number of obs: 368, groups: phylum\_class, 37  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 0.469755 0.225590 2.082 0.0373 \*  
 imageY -0.007943 0.388424 -0.020 0.9837   
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 imageY -0.579

1. Is larval type associated with CSss? (n = 274)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Larv\_type + (1 | phylum\_class)  
 Data: surveylarvmorpho  
   
 AIC BIC logLik deviance df.resid   
 358.1 372.5 -175.0 350.1 270   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.9781 -1.0862 0.5240 0.7602 1.4404   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.5748 0.7582   
 Number of obs: 274, groups: phylum\_class, 39  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 0.58603 0.30772 1.904 0.0569 .  
 Larv\_typeLT -0.20821 0.43807 -0.475 0.6346   
 Larv\_typePT -0.03502 0.34273 -0.102 0.9186   
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr) Lrv\_LT  
 Larv\_typeLT -0.570   
 Larv\_typePT -0.621 0.413

1. Are CSss more common in particular geographic zones? (n = 295)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Trop + (1 | phylum\_class)  
 Data: tropmorpho  
   
 AIC BIC logLik deviance df.resid   
 389.3 400.3 -191.6 383.3 292   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.9964 -0.9744 0.5009 0.8051 1.3049   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.4028 0.6347   
 Number of obs: 295, groups: phylum\_class, 37  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)  
 (Intercept) 0.1290 0.3015 0.428 0.669  
 TropTRUE 0.3489 0.2990 1.167 0.243  
   
 Correlation of Fixed Effects:  
 (Intr)  
 TropTRUE -0.755

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Npol + (1 | phylum\_class)  
 Data: npolmorpho  
   
 AIC BIC logLik deviance df.resid   
 389.2 400.3 -191.6 383.2 292   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.9488 -1.0274 0.5131 0.8260 1.2955   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.4033 0.635   
 Number of obs: 295, groups: phylum\_class, 37  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 0.4586 0.2051 2.236 0.0253 \*  
 NpolTRUE -0.4505 0.3831 -1.176 0.2396   
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 NpolTRUE -0.263

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Ntemp + (1 | phylum\_class)  
 Data: ntempmorpho  
   
 AIC BIC logLik deviance df.resid   
 389.4 400.5 -191.7 383.4 292   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -2.2203 -1.0271 0.5361 0.7602 1.2919   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.4035 0.6352   
 Number of obs: 295, groups: phylum\_class, 37  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 0.6761 0.3268 2.069 0.0385 \*  
 NtempTRUE -0.3483 0.3212 -1.084 0.2782   
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 NtempTRUE -0.796

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Spol + (1 | phylum\_class)  
 Data: spolmorpho  
   
 AIC BIC logLik deviance df.resid   
 388.5 399.5 -191.2 382.5 292   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.9216 -1.0511 0.5204 0.7825 1.3442   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.4412 0.6642   
 Number of obs: 295, groups: phylum\_class, 37  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)  
 (Intercept) 0.3229 0.2096 1.540 0.123  
 SpolTRUE 0.9108 0.6510 1.399 0.162  
   
 Correlation of Fixed Effects:  
 (Intr)  
 SpolTRUE -0.233

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Stemp + (1 | phylum\_class)  
 Data: stempmorpho  
   
 AIC BIC logLik deviance df.resid   
 390.6 401.7 -192.3 384.6 292   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.9198 -1.0614 0.5251 0.7792 1.2443   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.3933 0.6271   
 Number of obs: 295, groups: phylum\_class, 37  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)  
 (Intercept) 0.38680 0.24410 1.585 0.113  
 StempTRUE 0.01593 0.25981 0.061 0.951  
   
 Correlation of Fixed Effects:  
 (Intr)  
 StempTRUE -0.594

# Analyses with species where the number of individuals studied for genetics is greater than 20 (see main text) (starting n = 735)

1. Are there more CSss or pseudo-CS overall, considering only cases where morphology was measured? (n = 383)

Pearson's Chi-squared test with Yates' continuity correction  
   
 data: cbind(expected, observed)  
 X-squared = 17.054, df = 1, p-value = 3.633e-05

1. Are there differences across phyla or classes? (n = 383)

Single term deletions  
   
 Model:  
 CSss ~ phylum\_wormsV1  
 Df Deviance AIC LRT Pr(>Chi)  
 <none> 484.25 512.25   
 phylum\_wormsV1 13 495.88 497.88 11.631 0.5581

Single term deletions  
   
 Model:  
 CSss ~ phylum\_class  
 Df Deviance AIC LRT Pr(>Chi)   
 <none> 429.56 507.56   
 phylum\_class 38 495.88 497.88 66.326 0.002993 \*\*  
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Since phylum\_class is significant, we will now use this as a random factor in subsequent models.

1. Is the probability of CSss associated with year of description? (n = 319)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ yearb + (1 | phylum\_class)  
 Data: surveymorpho  
   
 AIC BIC logLik deviance df.resid   
 427.5 438.8 -210.8 421.5 316   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.5869 -1.1195 0.6330 0.7749 0.9653   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.1881 0.4337   
 Number of obs: 319, groups: phylum\_class, 37  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)  
 (Intercept) 4.014e-01 2.321e+00 0.173 0.863  
 yearb 3.457e-05 1.235e-03 0.028 0.978  
   
 Correlation of Fixed Effects:  
 (Intr)  
 yearb -0.998

1. Is there a relationship between the number of CS in easily-accessible or inaccessible habitats and time? (n = 616)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: Difficult ~ yearb + (1 | phylum\_class)  
 Data: surveyaccess  
   
 AIC BIC logLik deviance df.resid   
 384.8 398.1 -189.4 378.8 613   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -0.5092 -0.3377 -0.2924 -0.2632 4.4482   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.1192 0.3452   
 Number of obs: 616, groups: phylum\_class, 42  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) -10.481275 2.381952 -4.400 1.08e-05 \*\*\*  
 yearb 0.004322 0.001238 3.492 0.000479 \*\*\*  
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 yearb -0.996

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: Easy ~ yearb + (1 | phylum\_class)  
 Data: surveyaccess  
   
 AIC BIC logLik deviance df.resid   
 544.4 557.7 -269.2 538.4 613   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.0519 -0.4987 -0.2993 -0.1987 4.8431   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 2.096 1.448   
 Number of obs: 616, groups: phylum\_class, 42  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 6.295678 2.784139 2.261 0.0237 \*   
 yearb -0.004198 0.001485 -2.827 0.0047 \*\*  
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 yearb -0.994

1. Is habitat connectivity (variable HKK) associated with CSss? (n = 351)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ HKKv3 + (1 | phylum\_class)  
 Data: surveymorpho  
   
 AIC BIC logLik deviance df.resid   
 459.0 470.6 -226.5 453.0 348   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -2.0730 -1.1948 0.7208 0.7703 0.8725   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.081 0.2846   
 Number of obs: 351, groups: phylum\_class, 39  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 0.4538390 0.1459549 3.109 0.00187 \*\*  
 HKKv3 0.0008131 0.0004118 1.974 0.04835 \*   
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 HKKv3 -0.356

1. Are CSss more common in rocky or soft sediment habitats? (n = 160) What about when only considering shallow-water species? (n = 138)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Hsubstrate + (1 | phylum\_class)  
 Data: surveysed  
   
 AIC BIC logLik deviance df.resid   
 211.0 220.2 -102.5 205.0 157   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.5679 -1.1547 0.6378 0.8660 0.8660   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0 0   
 Number of obs: 160, groups: phylum\_class, 27  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 0.2877 0.2303 1.249 0.2116   
 HsubstrateSediment 0.6118 0.3341 1.831 0.0671 .  
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 HsbstrtSdmn -0.689  
 optimizer (Nelder\_Mead) convergence code: 0 (OK)  
 boundary (singular) fit: see help('isSingular')

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Hsubstrate + (1 | phylum\_class)  
 Data: shallow  
   
 AIC BIC logLik deviance df.resid   
 178.3 187.1 -86.2 172.3 135   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.7490 -1.0753 0.5718 0.9300 0.9300   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0 0   
 Number of obs: 138, groups: phylum\_class, 27  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 0.1452 0.2414 0.601 0.54757   
 HsubstrateSediment 0.9728 0.3692 2.635 0.00842 \*\*  
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 HsbstrtSdmn -0.654

1. Are CSss more common in sympatry or no? (n = 379)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Sympatric + (1 | phylum\_class)  
 Data: surveymorpho  
   
 AIC BIC logLik deviance df.resid   
 484.4 496.2 -239.2 478.4 376   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -2.0789 -1.0782 0.5517 0.7376 0.9771   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.1558 0.3947   
 Number of obs: 379, groups: phylum\_class, 39  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 1.1526 0.2290 5.033 4.84e-07 \*\*\*  
 SympatricTRUE -0.7716 0.2436 -3.168 0.00154 \*\*   
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 SymptrcTRUE -0.762

1. Are species in sympatry more likely to have ecological differentiation? (n=114)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: Eco\_diff ~ Sympatric + (1 | phylum\_class)  
 Data: survey  
   
 AIC BIC logLik deviance df.resid   
 104.9 113.1 -49.4 98.9 111   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -2.4175 0.3842 0.3984 0.4237 0.5247   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.08908 0.2985   
 Number of obs: 114, groups: phylum\_class, 27  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 1.4009 0.4768 2.938 0.0033 \*\*  
 SympatricTRUE 0.4276 0.5686 0.752 0.4520   
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 SymptrcTRUE -0.760

1. Are CSss more common in species with ecological differentiation? (n = 81)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Eco\_diff + (1 | phylum\_class)  
 Data: surveymorpho  
   
 AIC BIC logLik deviance df.resid   
 109.8 117.0 -51.9 103.8 78   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.7524 -1.1003 0.6308 0.7404 0.9367   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.2655 0.5152   
 Number of obs: 81, groups: phylum\_class, 23  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 1.3157 0.7133 1.844 0.0651 .  
 Eco\_diffYes -0.8085 0.7366 -1.098 0.2724   
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 Eco\_diffYes -0.915

1. Are biological traits (hard skeleton, fertilization type, presence of external genitalia, image-forming vision) associated with CSss? (n = 361)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ hard\_skeleton + (1 | phylum\_class)  
 Data: surveymorpho  
   
 AIC BIC logLik deviance df.resid   
 474.0 485.7 -234.0 468.0 358   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.6649 -1.2024 0.6342 0.7480 0.8793   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.1304 0.3612   
 Number of obs: 361, groups: phylum\_class, 36  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 0.7349 0.2688 2.734 0.00626 \*\*  
 hard\_skeletonY -0.2237 0.3205 -0.698 0.48512   
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 hard\_skltnY -0.836

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ ferti + (1 | phylum\_class)  
 Data: surveymorpho  
   
 AIC BIC logLik deviance df.resid   
 475.0 490.6 -233.5 467.0 357   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.5784 -1.2378 0.6416 0.7821 0.8686   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.0466 0.2159   
 Number of obs: 361, groups: phylum\_class, 36  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)  
 (Intercept) 0.3544 0.2479 1.430 0.153  
 fertiE 0.4168 0.3099 1.345 0.179  
 fertiI 0.1122 0.3640 0.308 0.758  
   
 Correlation of Fixed Effects:  
 (Intr) fertiE  
 fertiE -0.750   
 fertiI -0.706 0.487

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ genitals + (1 | phylum\_class)  
 Data: surveymorpho  
   
 AIC BIC logLik deviance df.resid   
 474.6 490.1 -233.3 466.6 357   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.4577 -1.2374 0.6860 0.6860 0.9129   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 4e-14 2e-07   
 Number of obs: 361, groups: phylum\_class, 36  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 0.1823 0.2708 0.673 0.501   
 genitalsN 0.5715 0.3062 1.866 0.062 .  
 genitalsY 0.2438 0.3535 0.689 0.491   
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr) gntlsN  
 genitalsN -0.884   
 genitalsY -0.766 0.677  
 optimizer (Nelder\_Mead) convergence code: 0 (OK)  
 boundary (singular) fit: see help('isSingular')

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ image + (1 | phylum\_class)  
 Data: surveymorpho  
   
 AIC BIC logLik deviance df.resid   
 474.5 486.2 -234.3 468.5 358   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.6158 -1.1897 0.6274 0.7373 0.8704   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.1497 0.3869   
 Number of obs: 361, groups: phylum\_class, 36  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 0.574435 0.192020 2.992 0.00278 \*\*  
 imageY 0.009647 0.313183 0.031 0.97543   
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 imageY -0.620

1. Is larval type associated with CSss? (n = 249)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Larv\_type + (1 | phylum\_class)  
 Data: surveylarvmorpho  
   
 AIC BIC logLik deviance df.resid   
 330.4 344.5 -161.2 322.4 245   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.7428 -1.1760 0.5901 0.7567 0.9650   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.2984 0.5463   
 Number of obs: 249, groups: phylum\_class, 38  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 0.57550 0.30807 1.868 0.0617 .  
 Larv\_typeLT -0.16350 0.43133 -0.379 0.7046   
 Larv\_typePT 0.06981 0.36192 0.193 0.8470   
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr) Lrv\_LT  
 Larv\_typeLT -0.631   
 Larv\_typePT -0.724 0.489

1. Are CSss more common in particular geographic zones? (n = 290)

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Trop + (1 | phylum\_class)  
 Data: tropmorpho  
   
 AIC BIC logLik deviance df.resid   
 386.4 397.4 -190.2 380.4 287   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.6927 -1.1169 0.5908 0.7751 1.1839   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.2589 0.5088   
 Number of obs: 290, groups: phylum\_class, 36  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)  
 (Intercept) 0.1734 0.2888 0.60 0.548  
 TropTRUE 0.3837 0.2974 1.29 0.197  
   
 Correlation of Fixed Effects:  
 (Intr)  
 TropTRUE -0.785

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Npol + (1 | phylum\_class)  
 Data: npolmorpho  
   
 AIC BIC logLik deviance df.resid   
 385.3 396.3 -189.7 379.3 287   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.6954 -1.0925 0.5898 0.7791 1.2045   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.3183 0.5642   
 Number of obs: 290, groups: phylum\_class, 36  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 0.5570 0.1955 2.849 0.00438 \*\*  
 NpolTRUE -0.6197 0.3760 -1.648 0.09932 .   
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 NpolTRUE -0.284

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Ntemp + (1 | phylum\_class)  
 Data: ntempmorpho  
   
 AIC BIC logLik deviance df.resid   
 387.7 398.7 -190.9 381.7 287   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.7553 -1.0799 0.6211 0.7725 1.0020   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.2908 0.5393   
 Number of obs: 290, groups: phylum\_class, 36  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 0.6029 0.3035 1.986 0.047 \*  
 NtempTRUE -0.1727 0.3079 -0.561 0.575   
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 NtempTRUE -0.797

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Spol + (1 | phylum\_class)  
 Data: spolmorpho  
   
 AIC BIC logLik deviance df.resid   
 386 397 -190 380 287   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.6524 -1.0825 0.6056 0.7743 1.0694   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.3596 0.5997   
 Number of obs: 290, groups: phylum\_class, 36  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 0.3965 0.1999 1.983 0.0473 \*  
 SpolTRUE 0.8712 0.6461 1.348 0.1775   
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 SpolTRUE -0.248

Generalized linear mixed model fit by maximum likelihood (Laplace  
 Approximation) [glmerMod]  
 Family: binomial ( logit )  
 Formula: CSss ~ Stemp + (1 | phylum\_class)  
 Data: stempmorpho  
   
 AIC BIC logLik deviance df.resid   
 388 399 -191 382 287   
   
 Scaled residuals:   
 Min 1Q Median 3Q Max   
 -1.6593 -1.0859 0.6205 0.7763 1.0267   
   
 Random effects:  
 Groups Name Variance Std.Dev.  
 phylum\_class (Intercept) 0.288 0.5367   
 Number of obs: 290, groups: phylum\_class, 36  
   
 Fixed effects:  
 Estimate Std. Error z value Pr(>|z|)   
 (Intercept) 0.43392 0.23543 1.843 0.0653 .  
 StempTRUE 0.05835 0.25693 0.227 0.8203   
 ---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
   
 Correlation of Fixed Effects:  
 (Intr)  
 StempTRUE -0.631