Appendix of GLMM Outputs

2024-04-15

## Full list of GLMM outputs for Cahill & Chenuil

These results are the full outputs of the analyses conducted in Cahill & Chenuil to understand cryptic species.

# 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, I 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  
## optimizer (Nelder\_Mead) convergence code: 0 (OK)  
## Model failed to converge with max|grad| = 0.0635708 (tol = 0.002, component 1)  
## Model is nearly unidentifiable: very large eigenvalue  
## - Rescale variables?  
## Model is nearly unidentifiable: large eigenvalue ratio  
## - Rescale variables?

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  
## optimizer (Nelder\_Mead) convergence code: 0 (OK)  
## Model failed to converge with max|grad| = 0.046852 (tol = 0.002, component 1)  
## Model is nearly unidentifiable: very large eigenvalue  
## - Rescale variables?  
## Model is nearly unidentifiable: large eigenvalue ratio  
## - Rescale variables?

## 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  
## optimizer (Nelder\_Mead) convergence code: 0 (OK)  
## Model failed to converge with max|grad| = 0.154402 (tol = 0.002, component 1)  
## Model is nearly unidentifiable: very large eigenvalue  
## - Rescale variables?  
## Model is nearly unidentifiable: large eigenvalue ratio  
## - Rescale variables?

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  
## optimizer (Nelder\_Mead) convergence code: 0 (OK)  
## Model failed to converge with max|grad| = 0.00249359 (tol = 0.002, component 1)  
## Model is nearly unidentifiable: very large eigenvalue  
## - Rescale variables?

1. Is habitat stability associated with CSss? What about a model that includes both stability and connectivity (n = 492)

## Generalized linear mixed model fit by maximum likelihood (Laplace  
## Approximation) [glmerMod]  
## Family: binomial ( logit )  
## Formula: CSss ~ Hstable + (1 | phylum\_class)  
## Data: surveymorpho  
##   
## AIC BIC logLik deviance df.resid   
## 623.2 635.8 -308.6 617.2 489   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -2.3187 -1.1324 0.6098 0.7218 1.0001   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## phylum\_class (Intercept) 0.2208 0.4699   
## Number of obs: 492, groups: phylum\_class, 43  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 0.5515 0.1555 3.548 0.000389 \*\*\*  
## HstableTRUE 0.7342 0.2771 2.649 0.008069 \*\*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr)  
## HstableTRUE -0.321

## Generalized linear mixed model fit by maximum likelihood (Laplace  
## Approximation) [glmerMod]  
## Family: binomial ( logit )  
## Formula: CSss ~ Hstable + HKKv3 + (1 | phylum\_class)  
## Data: surveymorpho  
##   
## AIC BIC logLik deviance df.resid   
## 580.0 596.5 -286.0 572.0 448   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -2.2479 -1.1363 0.5843 0.7174 1.2197   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## phylum\_class (Intercept) 0.3332 0.5773   
## Number of obs: 452, groups: phylum\_class, 42  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 4.731e-01 1.776e-01 2.664 0.00772 \*\*  
## HstableTRUE 7.306e-01 4.066e-01 1.797 0.07238 .   
## HKKv3 6.723e-05 5.850e-04 0.115 0.90850   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr) HsTRUE  
## HstableTRUE -0.136   
## HKKv3 -0.124 -0.714  
## optimizer (Nelder\_Mead) convergence code: 0 (OK)  
## Model failed to converge with max|grad| = 0.00341633 (tol = 0.002, component 1)  
## Model is nearly unidentifiable: very large eigenvalue  
## - Rescale variables?  
## Model is nearly unidentifiable: large eigenvalue ratio  
## - Rescale variables?

1. Are CSss more common in rocky or soft sediment habitats? (n = 227) What about when only considering shallow-water species? (n = 193)

## 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  
## 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   
## 240.8 250.6 -117.4 234.8 190   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -2.1054 -1.0391 0.5245 0.7905 1.0307   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## phylum\_class (Intercept) 0.1174 0.3426   
## Number of obs: 193, groups: phylum\_class, 31  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 0.2159 0.2416 0.894 0.3715   
## HsubstrateSediment 1.0190 0.3371 3.023 0.0025 \*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr)  
## HsbstrtSdmn -0.638

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=978)

## 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  
## optimizer (Nelder\_Mead) convergence code: 0 (OK)  
## boundary (singular) fit: see help('isSingular')

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 = 292)

## 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   
## 372.7 387.4 -182.4 364.7 288   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -1.9163 -1.2082 0.5684 0.6936 1.0485   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## phylum\_class (Intercept) 0.2241 0.4734   
## Number of obs: 292, groups: phylum\_class, 42  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 0.9430 0.2875 3.280 0.00104 \*\*  
## Larv\_typeLT -0.5358 0.3977 -1.347 0.17793   
## Larv\_typePT -0.1634 0.3347 -0.488 0.62527   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr) Lrv\_LT  
## Larv\_typeLT -0.658   
## Larv\_typePT -0.733 0.525

1. Are CSss more common in particular geographic zones? (n = 367)

## 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   
## 478.3 490.0 -236.1 472.3 364   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -1.8211 -1.1342 0.5703 0.7685 1.1084   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## phylum\_class (Intercept) 0.3455 0.5878   
## Number of obs: 367, groups: phylum\_class, 39  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 0.55190 0.26280 2.100 0.0357 \*  
## TropTRUE 0.08883 0.26556 0.334 0.7380   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr)  
## TropTRUE -0.731

## 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   
## 477.4 489.1 -235.7 471.4 364   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -1.8272 -1.0541 0.5591 0.7565 1.1449   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## phylum\_class (Intercept) 0.347 0.589   
## Number of obs: 367, groups: phylum\_class, 39  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 0.6593 0.1850 3.565 0.000364 \*\*\*  
## NpolTRUE -0.3550 0.3561 -0.997 0.318822   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr)  
## NpolTRUE -0.242

## 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   
## 477.6 489.3 -235.8 471.6 364   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -1.9937 -1.1428 0.5680 0.7538 1.0957   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## phylum\_class (Intercept) 0.3471 0.5891   
## Number of obs: 367, groups: phylum\_class, 39  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 0.8130 0.2877 2.826 0.00472 \*\*  
## NtempTRUE -0.2488 0.2821 -0.882 0.37787   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr)  
## NtempTRUE -0.781

## 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   
## 474.9 486.6 -234.4 468.9 364   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -1.9138 -1.1305 0.5545 0.7587 1.1584   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## phylum\_class (Intercept) 0.394 0.6277   
## Number of obs: 367, groups: phylum\_class, 39  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 0.5338 0.1897 2.814 0.00489 \*\*  
## SpolTRUE 1.0738 0.6180 1.738 0.08228 .   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr)  
## SpolTRUE -0.212

## 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   
## 478.4 490.1 -236.2 472.4 364   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -1.8093 -1.1615 0.5570 0.7484 1.0759   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## phylum\_class (Intercept) 0.3431 0.5857   
## Number of obs: 367, groups: phylum\_class, 39  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 0.60792 0.21850 2.782 0.0054 \*\*  
## StempTRUE 0.01556 0.23064 0.067 0.9462   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr)  
## StempTRUE -0.574

# 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, I 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  
## optimizer (Nelder\_Mead) convergence code: 0 (OK)  
## Model failed to converge with max|grad| = 0.0301761 (tol = 0.002, component 1)  
## Model is nearly unidentifiable: very large eigenvalue  
## - Rescale variables?  
## Model is nearly unidentifiable: large eigenvalue ratio  
## - Rescale variables?

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  
## optimizer (Nelder\_Mead) convergence code: 0 (OK)  
## Model failed to converge with max|grad| = 0.0450756 (tol = 0.002, component 1)  
## Model is nearly unidentifiable: very large eigenvalue  
## - Rescale variables?  
## Model is nearly unidentifiable: large eigenvalue ratio  
## - Rescale variables?

## 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  
## optimizer (Nelder\_Mead) convergence code: 0 (OK)  
## Model failed to converge with max|grad| = 0.134466 (tol = 0.002, component 1)  
## Model is nearly unidentifiable: very large eigenvalue  
## - Rescale variables?  
## Model is nearly unidentifiable: large eigenvalue ratio  
## - Rescale variables?

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  
## optimizer (Nelder\_Mead) convergence code: 0 (OK)  
## Model failed to converge with max|grad| = 0.00209297 (tol = 0.002, component 1)  
## Model is nearly unidentifiable: very large eigenvalue  
## - Rescale variables?

1. Is habitat stability associated with CSss? What about a model that includes both stability and connectivity (n = 411)

## Generalized linear mixed model fit by maximum likelihood (Laplace  
## Approximation) [glmerMod]  
## Family: binomial ( logit )  
## Formula: CSss ~ Hstable + (1 | phylum\_class)  
## Data: surveymorpho  
##   
## AIC BIC logLik deviance df.resid   
## 545.4 557.4 -269.7 539.4 408   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -2.1272 -0.9810 0.5524 0.8350 1.1551   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## phylum\_class (Intercept) 0.2197 0.4688   
## Number of obs: 411, groups: phylum\_class, 41  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 0.2135 0.1634 1.307 0.19122   
## HstableTRUE 0.8264 0.2901 2.849 0.00439 \*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr)  
## HstableTRUE -0.332

## Generalized linear mixed model fit by maximum likelihood (Laplace  
## Approximation) [glmerMod]  
## Family: binomial ( logit )  
## Formula: CSss ~ Hstable + HKKv3 + (1 | phylum\_class)  
## Data: surveymorpho  
##   
## AIC BIC logLik deviance df.resid   
## 504.0 519.7 -248.0 496.0 374   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -2.1883 -0.9376 0.4993 0.8684 1.0971   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## phylum\_class (Intercept) 0.4046 0.6361   
## Number of obs: 378, groups: phylum\_class, 40  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 0.0791345 0.2000884 0.395 0.6925   
## HstableTRUE 0.8536605 0.4315044 1.978 0.0479 \*  
## HKKv3 0.0001351 0.0006145 0.220 0.8260   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr) HsTRUE  
## HstableTRUE -0.162   
## HKKv3 -0.090 -0.716  
## optimizer (Nelder\_Mead) convergence code: 0 (OK)  
## Model failed to converge with max|grad| = 0.00283379 (tol = 0.002, component 1)  
## Model is nearly unidentifiable: very large eigenvalue  
## - Rescale variables?  
## Model is nearly unidentifiable: large eigenvalue ratio  
## - Rescale variables?

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

## 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   
## 240.8 250.6 -117.4 234.8 190   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -2.1054 -1.0391 0.5245 0.7905 1.0307   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## phylum\_class (Intercept) 0.1174 0.3426   
## Number of obs: 193, groups: phylum\_class, 31  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 0.2159 0.2416 0.894 0.3715   
## HsubstrateSediment 1.0190 0.3371 3.023 0.0025 \*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr)  
## HsbstrtSdmn -0.638

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  
## optimizer (Nelder\_Mead) convergence code: 0 (OK)  
## boundary (singular) fit: see help('isSingular')

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 = 246)

## 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   
## 329.8 343.8 -160.9 321.8 242   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -1.7911 -1.0502 0.6285 0.7611 1.2697   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## phylum\_class (Intercept) 0.331 0.5753   
## Number of obs: 246, groups: phylum\_class, 41  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 0.7222 0.3070 2.352 0.0187 \*  
## Larv\_typeLT -0.5946 0.4332 -1.373 0.1698   
## Larv\_typePT -0.2367 0.3560 -0.665 0.5061   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr) Lrv\_LT  
## Larv\_typeLT -0.641   
## Larv\_typePT -0.705 0.504

1. Are CSss more common in particular geographic zones? (n = 312)

## 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   
## 421.3 432.5 -207.7 415.3 309   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -1.7304 -1.0041 0.5992 0.8827 1.4510   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## phylum\_class (Intercept) 0.4791 0.6922   
## Number of obs: 312, groups: phylum\_class, 36  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)  
## (Intercept) 0.1548 0.2940 0.527 0.598  
## TropTRUE 0.2216 0.2896 0.765 0.444  
##   
## 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   
## 421.6 432.8 -207.8 415.6 309   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -1.7147 -1.0503 0.6093 0.8881 1.3112   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## phylum\_class (Intercept) 0.4664 0.6829   
## Number of obs: 312, groups: phylum\_class, 36  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 0.3428 0.2050 1.672 0.0945 .  
## NpolTRUE -0.1994 0.3777 -0.528 0.5976   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr)  
## NpolTRUE -0.219

## 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   
## 421.5 432.7 -207.7 415.5 309   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -1.7723 -1.0233 0.6233 0.8564 1.3558   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## phylum\_class (Intercept) 0.4753 0.6894   
## Number of obs: 312, groups: phylum\_class, 36  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)  
## (Intercept) 0.4769 0.3150 1.514 0.130  
## NtempTRUE -0.1992 0.3056 -0.652 0.515  
##   
## Correlation of Fixed Effects:  
## (Intr)  
## NtempTRUE -0.770

## 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   
## 418.9 430.2 -206.5 412.9 309   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -1.7264 -1.0342 0.6111 0.8730 1.4772   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## phylum\_class (Intercept) 0.5686 0.7541   
## Number of obs: 312, groups: phylum\_class, 36  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)  
## (Intercept) 0.2322 0.2191 1.060 0.289  
## SpolTRUE 1.1075 0.6809 1.627 0.104  
##   
## Correlation of Fixed Effects:  
## (Intr)  
## SpolTRUE -0.236

## 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   
## 421.9 433.1 -207.9 415.9 309   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -1.7028 -1.0414 0.6121 0.8954 1.3279   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## phylum\_class (Intercept) 0.4723 0.6872   
## Number of obs: 312, groups: phylum\_class, 36  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)  
## (Intercept) 0.323109 0.241396 1.339 0.181  
## StempTRUE -0.007301 0.247177 -0.030 0.976  
##   
## Correlation of Fixed Effects:  
## (Intr)  
## StempTRUE -0.556

# Analyses with species where the number of CS per article = 1 (see main text) (starting n = 535)

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, I 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  
## optimizer (Nelder\_Mead) convergence code: 0 (OK)  
## Model failed to converge with max|grad| = 0.0318323 (tol = 0.002, component 1)  
## Model is nearly unidentifiable: very large eigenvalue  
## - Rescale variables?  
## Model is nearly unidentifiable: large eigenvalue ratio  
## - Rescale variables?

1. Is there a relationship between the number of CS in easily-accessible or inaccessible habitats and time? (n = 395)

## 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  
## 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: 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)  
## Model failed to converge with max|grad| = 0.111872 (tol = 0.002, component 1)  
## Model is nearly unidentifiable: very large eigenvalue  
## - Rescale variables?  
## Model is nearly unidentifiable: large eigenvalue ratio  
## - Rescale variables?

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  
## optimizer (Nelder\_Mead) convergence code: 0 (OK)  
## Model failed to converge with max|grad| = 0.00230785 (tol = 0.002, component 1)  
## Model is nearly unidentifiable: very large eigenvalue  
## - Rescale variables?

1. Is habitat stability associated with CSss? What about a model that includes both stability and connectivity (n = 395)

## Generalized linear mixed model fit by maximum likelihood (Laplace  
## Approximation) [glmerMod]  
## Family: binomial ( logit )  
## Formula: CSss ~ Hstable + (1 | phylum\_class)  
## Data: surveymorpho  
##   
## AIC BIC logLik deviance df.resid   
## 514.4 526.3 -254.2 508.4 392   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -2.1264 -1.0929 0.5683 0.7870 1.2344   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## phylum\_class (Intercept) 0.3318 0.576   
## Number of obs: 395, groups: phylum\_class, 41  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 0.4301 0.1830 2.351 0.0187 \*  
## HstableTRUE 0.3785 0.2978 1.271 0.2038   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr)  
## HstableTRUE -0.320

## Generalized linear mixed model fit by maximum likelihood (Laplace  
## Approximation) [glmerMod]  
## Family: binomial ( logit )  
## Formula: CSss ~ Hstable + HKKv3 + (1 | phylum\_class)  
## Data: surveymorpho  
##   
## AIC BIC logLik deviance df.resid   
## 477.3 492.8 -234.6 469.3 356   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -2.2308 -1.0820 0.6321 0.8229 1.2037   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## phylum\_class (Intercept) 0.2701 0.5197   
## Number of obs: 360, groups: phylum\_class, 40  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 0.3311217 0.1834888 1.805 0.0711 .  
## HstableTRUE 0.0270131 0.4484796 0.060 0.9520   
## HKKv3 0.0006729 0.0006064 1.110 0.2672   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr) HsTRUE  
## HstableTRUE -0.144   
## HKKv3 -0.112 -0.741  
## optimizer (Nelder\_Mead) convergence code: 0 (OK)  
## Model failed to converge with max|grad| = 0.00345689 (tol = 0.002, component 1)  
## Model is nearly unidentifiable: very large eigenvalue  
## - Rescale variables?  
## Model is nearly unidentifiable: large eigenvalue ratio  
## - Rescale variables?

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

## 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   
## 240.8 250.6 -117.4 234.8 190   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -2.1054 -1.0391 0.5245 0.7905 1.0307   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## phylum\_class (Intercept) 0.1174 0.3426   
## Number of obs: 193, groups: phylum\_class, 31  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 0.2159 0.2416 0.894 0.3715   
## HsubstrateSediment 1.0190 0.3371 3.023 0.0025 \*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr)  
## HsbstrtSdmn -0.638

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  
## optimizer (Nelder\_Mead) convergence code: 0 (OK)  
## boundary (singular) fit: see help('isSingular')

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 = 261)

## 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   
## 331.4 345.7 -161.7 323.4 257   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -2.1161 -1.1713 0.5422 0.6979 1.2789   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## phylum\_class (Intercept) 0.3602 0.6002   
## Number of obs: 261, groups: phylum\_class, 39  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 0.9226 0.3080 2.995 0.00274 \*\*  
## Larv\_typeLT -0.5449 0.4293 -1.269 0.20433   
## Larv\_typePT -0.1586 0.3559 -0.446 0.65582   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr) Lrv\_LT  
## Larv\_typeLT -0.625   
## Larv\_typePT -0.687 0.482

1. Are CSss more common in particular geographic zones? (n = 294)

## 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   
## 387.7 398.8 -190.9 381.7 291   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -1.9913 -0.9737 0.5451 0.7937 1.2778   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## phylum\_class (Intercept) 0.3998 0.6323   
## Number of obs: 294, groups: phylum\_class, 36  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)  
## (Intercept) 0.1740 0.3041 0.572 0.567  
## TropTRUE 0.3152 0.3009 1.047 0.295  
##   
## Correlation of Fixed Effects:  
## (Intr)  
## TropTRUE -0.759

## 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   
## 387.8 398.9 -190.9 381.8 291   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -1.9472 -1.0575 0.5136 0.8119 1.2582   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## phylum\_class (Intercept) 0.3999 0.6323   
## Number of obs: 294, groups: phylum\_class, 36  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 0.4687 0.2048 2.288 0.0221 \*  
## NpolTRUE -0.3906 0.3875 -1.008 0.3134   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr)  
## NpolTRUE -0.254

## 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 -190.8 381.7 291   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -2.2138 -1.0307 0.5348 0.7602 1.2806   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## phylum\_class (Intercept) 0.4001 0.6325   
## Number of obs: 294, groups: phylum\_class, 36  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 0.6883 0.3268 2.106 0.0352 \*  
## NtempTRUE -0.3377 0.3213 -1.051 0.2932   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr)  
## NtempTRUE -0.795

## 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   
## 386.8 397.8 -190.4 380.8 291   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -1.9238 -1.0577 0.5198 0.7751 1.3305   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## phylum\_class (Intercept) 0.4353 0.6598   
## Number of obs: 294, groups: phylum\_class, 36  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 0.3461 0.2092 1.654 0.0981 .  
## SpolTRUE 0.8935 0.6502 1.374 0.1694   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr)  
## SpolTRUE -0.230

## 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   
## 388.8 399.9 -191.4 382.8 291   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -1.9202 -1.0675 0.5220 0.7739 1.2390   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## phylum\_class (Intercept) 0.3911 0.6254   
## Number of obs: 294, groups: phylum\_class, 36  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 0.419399 0.245705 1.707 0.0878 .  
## StempTRUE -0.004594 0.260573 -0.018 0.9859   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr)  
## StempTRUE -0.599

# 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, I 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  
## optimizer (Nelder\_Mead) convergence code: 0 (OK)  
## Model failed to converge with max|grad| = 0.0731545 (tol = 0.002, component 1)  
## Model is nearly unidentifiable: very large eigenvalue  
## - Rescale variables?  
## Model is nearly unidentifiable: large eigenvalue ratio  
## - Rescale variables?

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  
## optimizer (Nelder\_Mead) convergence code: 0 (OK)  
## Model failed to converge with max|grad| = 0.305356 (tol = 0.002, component 1)  
## Model is nearly unidentifiable: very large eigenvalue  
## - Rescale variables?  
## Model is nearly unidentifiable: large eigenvalue ratio  
## - Rescale variables?

## 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  
## optimizer (Nelder\_Mead) convergence code: 0 (OK)  
## Model failed to converge with max|grad| = 0.0171075 (tol = 0.002, component 1)  
## Model is nearly unidentifiable: very large eigenvalue  
## - Rescale variables?  
## Model is nearly unidentifiable: large eigenvalue ratio  
## - Rescale variables?

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  
## optimizer (Nelder\_Mead) convergence code: 0 (OK)  
## Model failed to converge with max|grad| = 0.00334272 (tol = 0.002, component 1)  
## Model is nearly unidentifiable: very large eigenvalue  
## - Rescale variables?

1. Is habitat stability associated with CSss? What about a model that includes both stability and connectivity (n = 383)

## Generalized linear mixed model fit by maximum likelihood (Laplace  
## Approximation) [glmerMod]  
## Family: binomial ( logit )  
## Formula: CSss ~ Hstable + (1 | phylum\_class)  
## Data: surveymorpho  
##   
## AIC BIC logLik deviance df.resid   
## 496.2 508.0 -245.1 490.2 380   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -1.9411 -1.2149 0.6545 0.7565 0.8579   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## phylum\_class (Intercept) 0.08875 0.2979   
## Number of obs: 383, groups: phylum\_class, 39  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 0.5109 0.1449 3.527 0.00042 \*\*\*  
## HstableTRUE 0.5413 0.2967 1.825 0.06805 .   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr)  
## HstableTRUE -0.381

## Generalized linear mixed model fit by maximum likelihood (Laplace  
## Approximation) [glmerMod]  
## Family: binomial ( logit )  
## Formula: CSss ~ Hstable + HKKv3 + (1 | phylum\_class)  
## Data: surveymorpho  
##   
## AIC BIC logLik deviance df.resid   
## 460.7 476.1 -226.3 452.7 347   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -2.0608 -1.1794 0.6712 0.7754 0.8809   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## phylum\_class (Intercept) 0.08255 0.2873   
## Number of obs: 351, groups: phylum\_class, 39  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 0.4358736 0.1494378 2.917 0.00354 \*\*  
## HstableTRUE 0.2531323 0.4405288 0.575 0.56556   
## HKKv3 0.0005611 0.0006025 0.931 0.35171   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr) HsTRUE  
## HstableTRUE -0.201   
## HKKv3 -0.090 -0.731  
## optimizer (Nelder\_Mead) convergence code: 0 (OK)  
## Model failed to converge with max|grad| = 0.00488505 (tol = 0.002, component 1)  
## Model is nearly unidentifiable: very large eigenvalue  
## - Rescale variables?  
## Model is nearly unidentifiable: large eigenvalue ratio  
## - Rescale variables?

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

## 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   
## 240.8 250.6 -117.4 234.8 190   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -2.1054 -1.0391 0.5245 0.7905 1.0307   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## phylum\_class (Intercept) 0.1174 0.3426   
## Number of obs: 193, groups: phylum\_class, 31  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 0.2159 0.2416 0.894 0.3715   
## HsubstrateSediment 1.0190 0.3371 3.023 0.0025 \*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr)  
## HsbstrtSdmn -0.638

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 = 236)

## 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   
## 300.8 314.7 -146.4 292.8 232   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -1.7270 -1.2233 0.6035 0.6807 0.8820   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## phylum\_class (Intercept) 0.09167 0.3028   
## Number of obs: 236, groups: phylum\_class, 39  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 0.93157 0.31608 2.947 0.00321 \*\*  
## Larv\_typeLT -0.48262 0.42472 -1.136 0.25582   
## Larv\_typePT -0.07187 0.37242 -0.193 0.84698   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr) Lrv\_LT  
## Larv\_typeLT -0.704   
## Larv\_typePT -0.806 0.586

1. Are CSss more common in particular geographic zones? (n = 289)

## 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   
## 384.8 395.8 -189.4 378.8 286   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -1.6913 -1.1155 0.5913 0.7744 1.1624   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## phylum\_class (Intercept) 0.2609 0.5108   
## Number of obs: 289, groups: phylum\_class, 35  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)  
## (Intercept) 0.2168 0.2925 0.741 0.459  
## TropTRUE 0.3487 0.2994 1.164 0.244  
##   
## Correlation of Fixed Effects:  
## (Intr)  
## TropTRUE -0.788

## 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   
## 383.9 394.9 -189.0 377.9 286   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -1.6935 -1.0930 0.5905 0.7783 1.1721   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## phylum\_class (Intercept) 0.3153 0.5615   
## Number of obs: 289, groups: phylum\_class, 35  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 0.5650 0.1957 2.887 0.00388 \*\*  
## NpolTRUE -0.5637 0.3800 -1.484 0.13794   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr)  
## NpolTRUE -0.278

## 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   
## 385.9 396.9 -189.9 379.9 286   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -1.7507 -1.0840 0.6191 0.7698 0.9937   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## phylum\_class (Intercept) 0.2884 0.537   
## Number of obs: 289, groups: phylum\_class, 35  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 0.6128 0.3035 2.019 0.0435 \*  
## NtempTRUE -0.1612 0.3080 -0.523 0.6008   
## ---  
## 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   
## 384.2 395.2 -189.1 378.2 286   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -1.6588 -1.0856 0.6050 0.7723 1.0581   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## phylum\_class (Intercept) 0.3526 0.5938   
## Number of obs: 289, groups: phylum\_class, 35  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 0.4185 0.1992 2.101 0.0357 \*  
## SpolTRUE 0.8523 0.6448 1.322 0.1863   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr)  
## SpolTRUE -0.241

## 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   
## 386.1 397.1 -190.1 380.1 286   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -1.6562 -1.0905 0.6150 0.7693 1.0239   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## phylum\_class (Intercept) 0.2876 0.5362   
## Number of obs: 289, groups: phylum\_class, 35  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 0.46541 0.23776 1.957 0.0503 .  
## StempTRUE 0.03679 0.25782 0.143 0.8865   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr)  
## StempTRUE -0.635