Statistical Tables for Vascular Plant Association with Moss

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12/18/2018

### Table 1. Summary of linear model for moss cover across the gradient

##   
## Call:  
## lm(formula = `Moss patch` ~ poly(distance, 2), data = coverWide)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -0.18346 -0.05748 0.01005 0.05832 0.16382   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 0.21043 0.01838 11.450 3.10e-10 \*\*\*  
## poly(distance, 2)1 0.58389 0.08814 6.624 1.89e-06 \*\*\*  
## poly(distance, 2)2 -0.27200 0.08814 -3.086 0.00583 \*\*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 0.08814 on 20 degrees of freedom  
## Multiple R-squared: 0.7275, Adjusted R-squared: 0.7003   
## F-statistic: 26.7 on 2 and 20 DF, p-value: 2.255e-06

### Table 2. Model summary for all vascular plant species association with moss across the gradient

##   
## Call:  
## glm(formula = hit ~ transect \* cover\_category, family = "quasibinomial",   
## data = no\_shrub)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -2.0070 -0.9398 -0.6358 0.9921 1.8429   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) -1.582074 0.256476 -6.169 1.71e-09 \*\*\*  
## transect 0.009554 0.001883 5.073 6.04e-07 \*\*\*  
## cover\_categorymoss 0.397831 0.791233 0.503 0.615   
## transect:cover\_categorymoss 0.004460 0.005403 0.825 0.410   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for quasibinomial family taken to be 1.000952)  
##   
## Null deviance: 550.74 on 397 degrees of freedom  
## Residual deviance: 477.88 on 394 degrees of freedom  
## AIC: NA  
##   
## Number of Fisher Scoring iterations: 4

### Table 3. F-tests all vascular plant species association with moss

## Analysis of Deviance Table  
##   
## Model: quasibinomial, link: logit  
##   
## Response: hit  
##   
## Terms added sequentially (first to last)  
##   
##   
## Df Deviance Resid. Df Resid. Dev F Pr(>F)  
## NULL 397 550.74   
## transect 1 54.321 396 496.42 54.2698 1.033e-12  
## cover\_category 1 17.837 395 478.58 17.8201 3.017e-05  
## transect:cover\_category 1 0.698 394 477.88 0.6973 0.4042  
##   
## NULL   
## transect \*\*\*  
## cover\_category \*\*\*  
## transect:cover\_category   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

### Table 4. Model summary for exotic species association with moss across the gradient

##   
## Call:  
## glm(formula = hit ~ transect \* cover\_category, family = "quasibinomial",   
## data = edata)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.7874 -0.5235 -0.4406 -0.3869 2.3190   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) -2.6487039 0.4074276 -6.501 2.42e-10 \*\*\*  
## transect 0.0033512 0.0029068 1.153 0.250   
## cover\_categorymoss 1.0190557 0.9327303 1.093 0.275   
## transect:cover\_categorymoss -0.0005181 0.0060485 -0.086 0.932   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for quasibinomial family taken to be 1.007397)  
##   
## Null deviance: 316.04 on 397 degrees of freedom  
## Residual deviance: 301.79 on 394 degrees of freedom  
## AIC: NA  
##   
## Number of Fisher Scoring iterations: 5

### Table 5. F-tests for fixed effects of exotic species association with moss

## Analysis of Deviance Table  
##   
## Model: quasibinomial, link: logit  
##   
## Response: hit  
##   
## Terms added sequentially (first to last)  
##   
##   
## Df Deviance Resid. Df Resid. Dev F Pr(>F)  
## NULL 397 316.04   
## transect 1 5.0021 396 311.04 4.9654 0.026423  
## cover\_category 1 9.2459 395 301.80 9.1780 0.002611  
## transect:cover\_category 1 0.0074 394 301.79 0.0073 0.931838  
##   
## NULL   
## transect \*   
## cover\_category \*\*  
## transect:cover\_category   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

### Table 6. Model summary for native species association with moss across the gradient

##   
## Call:  
## glm(formula = hit ~ transect \* cover\_category, family = "quasibinomial",   
## data = ndata)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -1.4191 -0.9418 -0.6062 1.1673 2.0462   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) -2.047545 0.291565 -7.023 9.60e-12 \*\*\*  
## transect 0.009502 0.002022 4.700 3.61e-06 \*\*\*  
## cover\_categorymoss 0.428501 0.789715 0.543 0.588   
## transect:cover\_categorymoss 0.000458 0.005093 0.090 0.928   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for quasibinomial family taken to be 1.008294)  
##   
## Null deviance: 509.84 on 397 degrees of freedom  
## Residual deviance: 467.80 on 394 degrees of freedom  
## AIC: NA  
##   
## Number of Fisher Scoring iterations: 4

### Table 7. F-tests for fixed effects of native species association with moss

## Analysis of Deviance Table  
##   
## Model: quasibinomial, link: logit  
##   
## Response: hit  
##   
## Terms added sequentially (first to last)  
##   
##   
## Df Deviance Resid. Df Resid. Dev F Pr(>F)  
## NULL 397 509.84   
## transect 1 37.667 396 472.17 37.3572 2.367e-09  
## cover\_category 1 4.359 395 467.81 4.3229 0.03825  
## transect:cover\_category 1 0.008 394 467.80 0.0081 0.92833  
##   
## NULL   
## transect \*\*\*  
## cover\_category \*   
## transect:cover\_category   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

### Table 8. Model summary for annual exotic grass association with moss across the gradient

##   
## Call:  
## glm(formula = hit ~ transect \* cover\_category, family = "quasibinomial",   
## data = agdata)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.5508 -0.3234 -0.3075 -0.2792 2.5844   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) -2.908440 0.516880 -5.627 3.49e-08 \*\*\*  
## transect -0.001812 0.004282 -0.423 0.672   
## cover\_categorymoss -1.033222 1.571595 -0.657 0.511   
## transect:cover\_categorymoss 0.011595 0.009843 1.178 0.240   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for quasibinomial family taken to be 1.012459)  
##   
## Null deviance: 170.16 on 397 degrees of freedom  
## Residual deviance: 166.31 on 394 degrees of freedom  
## AIC: NA  
##   
## Number of Fisher Scoring iterations: 6

### Table 9. F-tests for fixed effects of annual exotic grass association with moss

## Analysis of Deviance Table  
##   
## Model: quasibinomial, link: logit  
##   
## Response: hit  
##   
## Terms added sequentially (first to last)  
##   
##   
## Df Deviance Resid. Df Resid. Dev F Pr(>F)  
## NULL 397 170.16   
## transect 1 0.36435 396 169.79 0.3599 0.5489  
## cover\_category 1 1.98997 395 167.81 1.9655 0.1617  
## transect:cover\_category 1 1.49582 394 166.31 1.4774 0.2249

### Table 10. Model summary for Vulpia association with moss across the gradient

##   
## Call:  
## glm(formula = hit ~ transect \* cover\_category, family = "quasibinomial",   
## data = vdata)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.6208 -0.2696 -0.2570 -0.2483 2.6465   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) -3.4921597 0.6211251 -5.622 3.57e-08 \*\*\*  
## transect 0.0009023 0.0047055 0.192 0.848   
## cover\_categorymoss -2.4506051 2.0761305 -1.180 0.239   
## transect:cover\_categorymoss 0.0192531 0.0120927 1.592 0.112   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for quasibinomial family taken to be 0.9758196)  
##   
## Null deviance: 140.47 on 397 degrees of freedom  
## Residual deviance: 134.40 on 394 degrees of freedom  
## AIC: NA  
##   
## Number of Fisher Scoring iterations: 6

### Table 11. F-tests for fixed effects of Vulpia association with moss

## Analysis of Deviance Table  
##   
## Model: quasibinomial, link: logit  
##   
## Response: hit  
##   
## Terms added sequentially (first to last)  
##   
##   
## Df Deviance Resid. Df Resid. Dev F Pr(>F)   
## NULL 397 140.47   
## transect 1 1.9751 396 138.50 2.0241 0.15562   
## cover\_category 1 1.2851 395 137.21 1.3169 0.25184   
## transect:cover\_category 1 2.8148 394 134.40 2.8845 0.09022 .  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

### Table 12. Model summary for Bromus association with moss across the gradient

##   
## Call:  
## glm(formula = hit ~ transect \* cover\_category, family = "quasibinomial",   
## data = bdata)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.46285 -0.19687 -0.14342 -0.09031 3.07873   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) -3.535492 0.841380 -4.202 3.28e-05 \*\*\*  
## transect -0.012071 0.010593 -1.140 0.255   
## cover\_categorymoss 1.859290 2.062584 0.901 0.368   
## transect:cover\_categorymoss -0.005915 0.018359 -0.322 0.747   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for quasibinomial family taken to be 0.8968185)  
##   
## Null deviance: 53.707 on 397 degrees of freedom  
## Residual deviance: 50.697 on 394 degrees of freedom  
## AIC: NA  
##   
## Number of Fisher Scoring iterations: 8

### Table 13. F-tests for fixed effects of Bromus association with moss

## Analysis of Deviance Table  
##   
## Model: quasibinomial, link: logit  
##   
## Response: hit  
##   
## Terms added sequentially (first to last)  
##   
##   
## Df Deviance Resid. Df Resid. Dev F Pr(>F)  
## NULL 397 53.707   
## transect 1 1.67701 396 52.030 1.8700 0.1723  
## cover\_category 1 1.24136 395 50.789 1.3842 0.2401  
## transect:cover\_category 1 0.09157 394 50.697 0.1021 0.7495