Statistical Tables for Moss Removal Experiment

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### Table 1. Fixed effects on Bromus survival

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| term | df | AIC | logLik | deviance |  | Df | P(>) |
| NULL | 2 | 176.77 | -86.39 | 172.77 | NA | NA | NA |
| stress | 3 | 175.04 | -84.52 | 169.04 | 3.73 | 1 | 0.05 |
| treatment | 5 | 168.36 | -79.18 | 158.36 | 10.68 | 2 | 0.00 |
| stress:treatment | 7 | 147.54 | -66.77 | 133.54 | 24.82 | 2 | 0.00 |

### Table 2. Multiple comparison test Bromus survival. P-values are adjusted by Sidak method for three tests.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| level1 | level2 | stress | estimate | std.error | df | z-val | p-val |
| Moss patch | Bare sand | Low | -2.68 | 0.66 | Inf | -4.07 | 0.00 |
| Moss patch | Moss removed | Low | -0.45 | 0.48 | Inf | -0.95 | 0.72 |
| Bare sand | Moss removed | Low | 2.23 | 0.65 | Inf | 3.41 | 0.00 |
| Moss patch | Bare sand | High | 2.35 | 0.99 | Inf | 2.37 | 0.05 |
| Moss patch | Moss removed | High | 2.75 | 1.00 | Inf | 2.75 | 0.02 |
| Bare sand | Moss removed | High | 0.39 | 0.63 | Inf | 0.62 | 0.90 |

### Table 3. Fixed effects on Bromus aboveground biomass

## refitting model(s) with ML (instead of REML)

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| term | df | AIC | logLik | deviance |  | Df | P(>) |
| NULL | 3 | 135.90 | -64.95 | 129.90 | NA | NA | NA |
| stress | 4 | 136.28 | -64.14 | 128.28 | 1.63 | 1 | 0.20 |
| treatment | 6 | 132.84 | -60.42 | 120.84 | 7.44 | 2 | 0.02 |
| stress:treatment | 8 | 132.57 | -58.28 | 116.57 | 4.27 | 2 | 0.12 |

### Table 4. Multiple comparison test Bromus biomass. P-values are adjusted by Sidak method for three tests.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| level1 | level2 | stress | estimate | std.error | df | t-val | p-val |
| Moss patch | Bare sand | Low | -0.45 | 0.36 | 31.13 | -1.24 | 0.53 |
| Moss patch | Moss removed | Low | 0.73 | 0.36 | 31.13 | 2.02 | 0.15 |
| Bare sand | Moss removed | Low | 1.17 | 0.35 | 30.11 | 3.39 | 0.01 |
| Moss patch | Bare sand | High | 0.09 | 0.36 | 31.13 | 0.26 | 0.99 |
| Moss patch | Moss removed | High | 0.27 | 0.35 | 30.11 | 0.77 | 0.83 |
| Bare sand | Moss removed | High | 0.17 | 0.36 | 31.13 | 0.49 | 0.95 |

### Table 5. Fixed effects on Bromus inflorescence production

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| term | df | Deviance | Dfdenom | Res. Dev. | F-val | P(>F) |
| NULL | NA | NA | 51 | 71.56 | NA | NA |
| stress | 1 | 14.74 | 50 | 56.82 | 19.26 | 0.00 |
| treatment | 2 | 5.99 | 48 | 50.83 | 3.91 | 0.03 |
| stress:treatment | 2 | 8.19 | 46 | 42.63 | 5.35 | 0.01 |

### Table 6. Multiple comparison Bromus inflorescence numbers. P-values are adjusted by Sidak method for three tests.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| level1 | level2 | stress | estimate | std.error | df | z-val | p-val |
| Moss patch | Bare sand | Low | -1.28 | 0.42 | Inf | -3.04 | 0.01 |
| Moss patch | Moss removed | Low | -0.18 | 0.51 | Inf | -0.34 | 0.98 |
| Bare sand | Moss removed | Low | 1.10 | 0.37 | Inf | 3.02 | 0.01 |
| Moss patch | Bare sand | High | -0.07 | 0.20 | Inf | -0.36 | 0.98 |
| Moss patch | Moss removed | High | 0.05 | 0.21 | Inf | 0.25 | 0.99 |
| Bare sand | Moss removed | High | 0.13 | 0.22 | Inf | 0.58 | 0.92 |

### Table 7. Fixed effects on Vulpia survival

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| term | df | AIC | logLik | deviance |  | Df | P(>) |
| NULL | 2 | 237.68 | -116.84 | 233.68 | NA | NA | NA |
| stress | 3 | 236.07 | -115.04 | 230.07 | 3.60 | 1 | 0.06 |
| treatment | 5 | 207.10 | -98.55 | 197.10 | 32.97 | 2 | 0.00 |
| stress:treatment | 7 | 210.53 | -98.26 | 196.53 | 0.58 | 2 | 0.75 |

### Table 8. Multiple comparison for Vulpia survival. P-values are adjusted by Sidak method for three tests.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| level1 | level2 | stress | estimate | std.error | df | z-val | p-val |
| Moss patch | Bare sand | Low | 1.36 | 0.46 | Inf | 2.96 | 0.01 |
| Moss patch | Moss removed | Low | 2.09 | 0.51 | Inf | 4.13 | 0.00 |
| Bare sand | Moss removed | Low | 0.72 | 0.50 | Inf | 1.45 | 0.38 |
| Moss patch | Bare sand | High | 1.10 | 0.46 | Inf | 2.39 | 0.05 |
| Moss patch | Moss removed | High | 1.57 | 0.47 | Inf | 3.36 | 0.00 |
| Bare sand | Moss removed | High | 0.47 | 0.44 | Inf | 1.08 | 0.63 |

### Table 9. Fixed effects on Vulpia aboveground biomass

## refitting model(s) with ML (instead of REML)

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| term | df | AIC | logLik | deviance |  | Df | P(>) |
| NULL | 3 | 137.16 | -65.58 | 131.16 | NA | NA | NA |
| stress | 4 | 138.95 | -65.48 | 130.95 | 0.21 | 1 | 0.65 |
| treatment | 6 | 137.98 | -62.99 | 125.98 | 4.97 | 2 | 0.08 |
| stress:treatment | 8 | 140.80 | -62.40 | 124.80 | 1.18 | 2 | 0.55 |

### Table 10. Fixed effects on Vulpia inflorescence production

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| term | df | Deviance | Dfdenom | Res. Dev. | F-val | P(>F) |
| NULL | NA | NA | 43 | 127.38 | NA | NA |
| stress | 1 | 1.60 | 42 | 125.78 | 0.53 | 0.47 |
| treatment | 2 | 2.59 | 40 | 123.19 | 0.43 | 0.65 |
| stress:treatment | 2 | 1.11 | 38 | 122.09 | 0.18 | 0.83 |

### Table 11. Model summary for Bromus survival

## Generalized linear mixed model fit by maximum likelihood (Laplace  
## Approximation) [glmerMod]  
## Family: binomial ( logit )  
## Formula: cbind(final\_count, trials - final\_count) ~ stress + treatment +   
## treatment:stress + (1 | block)  
## Data: b  
##   
## AIC BIC logLik deviance df.resid   
## 147.5 161.5 -66.8 133.5 47   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -3.2753 -0.4215 0.2578 0.5981 1.4084   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## block (Intercept) 1.927 1.388   
## Number of obs: 54, groups: block, 18  
##   
## Fixed effects:  
## Estimate Std. Error z value  
## (Intercept) 0.08258 0.57390 0.144  
## stressHigh stress 4.25120 1.20719 3.522  
## treatmentBare sand 2.68325 0.65901 4.072  
## treatmentMoss removed 0.45248 0.47794 0.947  
## stressHigh stress:treatmentBare sand -5.03806 1.20411 -4.184  
## stressHigh stress:treatmentMoss removed -3.19845 1.11174 -2.877  
## Pr(>|z|)   
## (Intercept) 0.885588   
## stressHigh stress 0.000429 \*\*\*  
## treatmentBare sand 4.67e-05 \*\*\*  
## treatmentMoss removed 0.343785   
## stressHigh stress:treatmentBare sand 2.86e-05 \*\*\*  
## stressHigh stress:treatmentMoss removed 0.004015 \*\*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr) strsHs trtmBs trtmMr sHs:Bs  
## strssHghstr -0.467   
## trtmntBrsnd -0.296 0.171   
## trtmntMssrm -0.407 0.203 0.372   
## strssHst:Bs 0.157 -0.658 -0.563 -0.209   
## strssHst:Mr 0.169 -0.719 -0.181 -0.437 0.697

### Table 12. Model summary for Bromus biomass

## Linear mixed model fit by REML ['lmerMod']  
## Formula: l\_mass ~ stress \* treatment + (1 | block)  
## Data: b  
##   
## REML criterion at convergence: 121.7  
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -3.0544 -0.5063 0.1066 0.4900 2.0698   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## block (Intercept) 0.09445 0.3073   
## Residual 0.54079 0.7354   
## Number of obs: 52, groups: block, 18  
##   
## Fixed effects:  
## Estimate Std. Error t value  
## (Intercept) 3.6435 0.2812 12.958  
## stressHigh stress 0.3360 0.3868 0.869  
## treatmentBare sand 0.4466 0.3587 1.245  
## treatmentMoss removed -0.7275 0.3587 -2.028  
## stressHigh stress:treatmentBare sand -0.5383 0.5073 -1.061  
## stressHigh stress:treatmentMoss removed 0.4610 0.4988 0.924  
##   
## Correlation of Fixed Effects:  
## (Intr) strsHs trtmBs trtmMr sHs:Bs  
## strssHghstr -0.727   
## trtmntBrsnd -0.680 0.494   
## trtmntMssrm -0.680 0.494 0.533   
## strssHst:Bs 0.481 -0.656 -0.707 -0.377   
## strssHst:Mr 0.489 -0.667 -0.383 -0.719 0.508

### Table 13. Model summary for Bromus inflorescence production

##   
## Call:  
## glm(formula = infls ~ offset(log\_final\_count) + stress \* treatment,   
## family = "quasipoisson", data = bfdata)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -2.79372 -0.74489 0.02459 0.24521 2.20760   
##   
## Coefficients:  
## Estimate Std. Error t value  
## (Intercept) -1.5261 0.3913 -3.900  
## stressHigh stress 1.4537 0.4150 3.503  
## treatmentBare sand 1.2782 0.4207 3.038  
## treatmentMoss removed 0.1761 0.5123 0.344  
## stressHigh stress:treatmentBare sand -1.2059 0.4663 -2.586  
## stressHigh stress:treatmentMoss removed -0.2290 0.5542 -0.413  
## Pr(>|t|)   
## (Intercept) 0.000311 \*\*\*  
## stressHigh stress 0.001036 \*\*   
## treatmentBare sand 0.003915 \*\*   
## treatmentMoss removed 0.732555   
## stressHigh stress:treatmentBare sand 0.012933 \*   
## stressHigh stress:treatmentMoss removed 0.681390   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for quasipoisson family taken to be 0.7655792)  
##   
## Null deviance: 71.563 on 51 degrees of freedom  
## Residual deviance: 42.634 on 46 degrees of freedom  
## AIC: NA  
##   
## Number of Fisher Scoring iterations: 5

### Table 14. Model summary for Vulpia survival

## Generalized linear mixed model fit by maximum likelihood (Laplace  
## Approximation) [glmerMod]  
## Family: binomial ( logit )  
## Formula: cbind(final\_count, trials - final\_count) ~ stress + treatment +   
## treatment:stress + (1 | block)  
## Data: v  
##   
## AIC BIC logLik deviance df.resid   
## 210.5 224.5 -98.3 196.5 47   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -2.18269 -1.02171 -0.07679 1.16905 2.47407   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## block (Intercept) 0.2107 0.459   
## Number of obs: 54, groups: block, 18  
##   
## Fixed effects:  
## Estimate Std. Error z value  
## (Intercept) 0.6292 0.3563 1.766  
## stressHigh stress 0.4220 0.5170 0.816  
## treatmentBare sand -1.3638 0.4612 -2.957  
## treatmentMoss removed -2.0887 0.5062 -4.126  
## stressHigh stress:treatmentBare sand 0.2655 0.6483 0.409  
## stressHigh stress:treatmentMoss removed 0.5168 0.6834 0.756  
## Pr(>|z|)   
## (Intercept) 0.0774 .   
## stressHigh stress 0.4144   
## treatmentBare sand 0.0031 \*\*   
## treatmentMoss removed 3.69e-05 \*\*\*  
## stressHigh stress:treatmentBare sand 0.6822   
## stressHigh stress:treatmentMoss removed 0.4495   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr) strsHs trtmBs trtmMr sHs:Bs  
## strssHghstr -0.685   
## trtmntBrsnd -0.638 0.432   
## trtmntMssrm -0.586 0.395 0.469   
## strssHst:Bs 0.450 -0.659 -0.705 -0.326   
## strssHst:Mr 0.429 -0.626 -0.339 -0.730 0.504

### Table 15. Model summary for Vulpia biomass

## Linear mixed model fit by REML ['lmerMod']  
## Formula: l\_mass ~ stress \* treatment + (1 | block)  
## Data: v  
##   
## REML criterion at convergence: 125.1  
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -1.71996 -0.59365 -0.03691 0.37380 1.88417   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## block (Intercept) 0.3757 0.6130   
## Residual 0.8639 0.9294   
## Number of obs: 44, groups: block, 18  
##   
## Fixed effects:  
## Estimate Std. Error t value  
## (Intercept) 2.706690 0.371125 7.293  
## stressHigh stress -0.009068 0.524850 -0.017  
## treatmentBare sand -0.420551 0.503224 -0.836  
## treatmentMoss removed -1.195107 0.585297 -2.042  
## stressHigh stress:treatmentBare sand 0.481850 0.692105 0.696  
## stressHigh stress:treatmentMoss removed 0.701714 0.731126 0.960  
##   
## Correlation of Fixed Effects:  
## (Intr) strsHs trtmBs trtmMr sHs:Bs  
## strssHghstr -0.707   
## trtmntBrsnd -0.514 0.363   
## trtmntMssrm -0.442 0.312 0.339   
## strssHst:Bs 0.374 -0.528 -0.727 -0.246   
## strssHst:Mr 0.354 -0.500 -0.271 -0.801 0.387

### Table 16. Model summary for Vulpia inflorescence production

##   
## Call:  
## glm(formula = infls ~ offset(log\_final\_count) + stress \* treatment,   
## family = "quasipoisson", data = vfdata)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -4.0258 -1.2668 -0.5920 0.0968 4.7472   
##   
## Coefficients:  
## Estimate Std. Error t value  
## (Intercept) 0.48285 0.25325 1.907  
## stressHigh stress 0.08108 0.34076 0.238  
## treatmentBare sand -0.24646 0.47202 -0.522  
## treatmentMoss removed -0.60063 0.66404 -0.905  
## stressHigh stress:treatmentBare sand 0.22907 0.59507 0.385  
## stressHigh stress:treatmentMoss removed 0.42236 0.78327 0.539  
## Pr(>|t|)   
## (Intercept) 0.0642 .  
## stressHigh stress 0.8132   
## treatmentBare sand 0.6046   
## treatmentMoss removed 0.3714   
## stressHigh stress:treatmentBare sand 0.7024   
## stressHigh stress:treatmentMoss removed 0.5929   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for quasipoisson family taken to be 3.01464)  
##   
## Null deviance: 127.38 on 43 degrees of freedom  
## Residual deviance: 122.09 on 38 degrees of freedom  
## AIC: NA  
##   
## Number of Fisher Scoring iterations: 5