Statistical Tables for Moss Removal Experiment

Andrew Kleinhesselink

12/18/2018

### Table 1. Fixed effects on Bromus survival

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| term | AIC | logLik | deviance |  | Df | P(>) |
| NULL | 176.77 | -86.39 | 172.77 | NA | NA | NA |
| position | 175.04 | -84.52 | 169.04 | 3.73 | 1 | 0.053 |
| treatment | 168.36 | -79.18 | 158.36 | 10.68 | 2 | 0.005 |
| position:treatment | 147.54 | -66.77 | 133.54 | 24.82 | 2 | 0.000 |

### Table 2a. Multiple comparison test Bromus survival. Results are given on the log odds ratio (not the response) scale. P-values are adjusted by Sidak method for three tests.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| treatment | position | emmean | SE | df | asymp.LCL | asymp.UCL | .group |
| Moss patch | SE | 0.08 | 0.57 | Inf | -1.43 | 1.59 | a |
| Moss removed | SE | 0.54 | 0.58 | Inf | -0.99 | 2.06 | a |
| Bare sand | SE | 2.77 | 0.73 | Inf | 0.83 | 4.70 | b |
| Moss removed | NW | 1.59 | 0.66 | Inf | -0.15 | 3.33 | ab |
| Bare sand | NW | 1.98 | 0.69 | Inf | 0.15 | 3.81 | ab |
| Moss patch | NW | 4.33 | 1.07 | Inf | 1.53 | 7.14 | b |

### Table 2b. Multiple comparison test Bromus survival between means within gradient position. Results are given on the log odds ratio (not the response) scale. P-values are adjusted by Sidak method for three tests.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| treatment | position | emmean | SE | df | asymp.LCL | asymp.UCL | .group |
| Moss patch | SE | 0.08 | 0.57 | Inf | -1.29 | 1.45 | a |
| Moss removed | SE | 0.54 | 0.58 | Inf | -0.85 | 1.92 | a |
| Bare sand | SE | 2.77 | 0.73 | Inf | 1.01 | 4.52 | b |
| Moss removed | NW | 1.59 | 0.66 | Inf | 0.01 | 3.17 | a |
| Bare sand | NW | 1.98 | 0.69 | Inf | 0.32 | 3.64 | ab |
| Moss patch | NW | 4.33 | 1.07 | Inf | 1.78 | 6.88 | b |

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

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

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| term | AIC | logLik | deviance |  | Df | P(>) |
| NULL | 135.90 | -64.95 | 129.90 | NA | NA | NA |
| position | 136.28 | -64.14 | 128.28 | 1.63 | 1 | 0.20 |
| treatment | 132.84 | -60.42 | 120.84 | 7.44 | 2 | 0.02 |
| position:treatment | 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.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| treatment | emmean | SE | df | lower.CL | upper.CL | .group |
| Moss patch | 3.81 | 0.20 | 46.41 | 3.33 | 4.30 | ab |
| Bare sand | 4.01 | 0.20 | 46.41 | 3.52 | 4.49 | b |
| Moss removed | 3.31 | 0.19 | 46.06 | 2.84 | 3.79 | a |

### 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 |
| position | 1 | 14.74 | 50 | 56.82 | 19.3 | 0.000 |
| treatment | 2 | 5.99 | 48 | 50.83 | 3.9 | 0.027 |
| position:treatment | 2 | 8.19 | 46 | 42.63 | 5.4 | 0.008 |

### Table 6. Multiple comparison Bromus inflorescence numbers. Results are given on the log (not the response) scale. P-values are adjusted by Sidak method for three tests.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| treatment | position | emmean | SE | df | asymp.LCL | asymp.UCL | .group |
| Moss patch | SE | -0.25 | 0.39 | Inf | -1.28 | 0.78 | a |
| Moss removed | SE | -0.08 | 0.33 | Inf | -0.95 | 0.79 | a |
| Bare sand | SE | 1.03 | 0.15 | Inf | 0.62 | 1.43 | b |
| Moss removed | NW | 1.15 | 0.16 | Inf | 0.73 | 1.57 | b |
| Moss patch | NW | 1.20 | 0.14 | Inf | 0.84 | 1.57 | b |
| Bare sand | NW | 1.27 | 0.15 | Inf | 0.89 | 1.66 | b |

### Table 7. Fixed effects on Vulpia survival

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| term | AIC | logLik | deviance |  | Df | P(>) |
| NULL | 237.68 | -116.84 | 233.68 | NA | NA | NA |
| position | 236.07 | -115.04 | 230.07 | 3.60 | 1 | 0.058 |
| treatment | 207.10 | -98.55 | 197.10 | 32.97 | 2 | 0.000 |
| position:treatment | 210.53 | -98.26 | 196.53 | 0.58 | 2 | 0.750 |

### Table 8. Multiple comparison for Vulpia survival. Results are given on the log odds ratio (not the response) scale. P-values are adjusted by Sidak method for three tests.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| treatment | emmean | SE | df | asymp.LCL | asymp.UCL | .group |
| Moss patch | 0.85 | 0.26 | Inf | 0.23 | 1.47 | b |
| Bare sand | -0.39 | 0.25 | Inf | -0.98 | 0.20 | a |
| Moss removed | -0.97 | 0.27 | Inf | -1.60 | -0.33 | a |

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

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

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| term | AIC | logLik | deviance |  | Df | P(>) |
| NULL | 137.16 | -65.58 | 131.16 | NA | NA | NA |
| position | 138.95 | -65.48 | 130.95 | 0.21 | 1 | 0.647 |
| treatment | 137.98 | -62.99 | 125.98 | 4.97 | 2 | 0.083 |
| position:treatment | 140.80 | -62.40 | 124.80 | 1.18 | 2 | 0.554 |

### 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 |
| position | 1 | 1.60 | 42 | 125.78 | 0.5 | 0.471 |
| treatment | 2 | 2.59 | 40 | 123.19 | 0.4 | 0.654 |
| position:treatment | 2 | 1.11 | 38 | 122.09 | 0.2 | 0.833 |

### 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) ~ position + treatment +   
## treatment:position + (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 Pr(>|z|)   
## (Intercept) 0.08258 0.57390 0.144 0.885588   
## positionNW 4.25120 1.20719 3.522 0.000429 \*\*\*  
## treatmentBare sand 2.68325 0.65901 4.072 4.67e-05 \*\*\*  
## treatmentMoss removed 0.45248 0.47794 0.947 0.343785   
## positionNW:treatmentBare sand -5.03806 1.20411 -4.184 2.86e-05 \*\*\*  
## positionNW:treatmentMoss removed -3.19845 1.11174 -2.877 0.004015 \*\*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr) pstnNW trtmBs trtmMr pNW:Bs  
## positionNW -0.467   
## trtmntBrsnd -0.296 0.171   
## trtmntMssrm -0.407 0.203 0.372   
## pstnNW:trBs 0.157 -0.658 -0.563 -0.209   
## pstnNW:trMr 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 ~ position \* 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  
## positionNW 0.3360 0.3868 0.869  
## treatmentBare sand 0.4466 0.3587 1.245  
## treatmentMoss removed -0.7275 0.3587 -2.028  
## positionNW:treatmentBare sand -0.5383 0.5073 -1.061  
## positionNW:treatmentMoss removed 0.4610 0.4988 0.924  
##   
## Correlation of Fixed Effects:  
## (Intr) pstnNW trtmBs trtmMr pNW:Bs  
## positionNW -0.727   
## trtmntBrsnd -0.680 0.494   
## trtmntMssrm -0.680 0.494 0.533   
## pstnNW:trBs 0.481 -0.656 -0.707 -0.377   
## pstnNW:trMr 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) + position \* 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 Pr(>|t|)   
## (Intercept) -1.5261 0.3913 -3.900 0.000311 \*\*\*  
## positionNW 1.4537 0.4150 3.503 0.001036 \*\*   
## treatmentBare sand 1.2782 0.4207 3.038 0.003915 \*\*   
## treatmentMoss removed 0.1761 0.5123 0.344 0.732555   
## positionNW:treatmentBare sand -1.2059 0.4663 -2.586 0.012933 \*   
## positionNW:treatmentMoss removed -0.2290 0.5542 -0.413 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) ~ position + treatment +   
## treatment:position + (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 Pr(>|z|)   
## (Intercept) 0.6292 0.3563 1.766 0.0774 .   
## positionNW 0.4220 0.5170 0.816 0.4144   
## treatmentBare sand -1.3638 0.4612 -2.957 0.0031 \*\*   
## treatmentMoss removed -2.0887 0.5062 -4.126 3.69e-05 \*\*\*  
## positionNW:treatmentBare sand 0.2655 0.6483 0.409 0.6822   
## positionNW:treatmentMoss removed 0.5168 0.6834 0.756 0.4495   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr) pstnNW trtmBs trtmMr pNW:Bs  
## positionNW -0.685   
## trtmntBrsnd -0.638 0.432   
## trtmntMssrm -0.586 0.395 0.469   
## pstnNW:trBs 0.450 -0.659 -0.705 -0.326   
## pstnNW:trMr 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 ~ position \* 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  
## positionNW -0.009068 0.524850 -0.017  
## treatmentBare sand -0.420551 0.503224 -0.836  
## treatmentMoss removed -1.195107 0.585297 -2.042  
## positionNW:treatmentBare sand 0.481850 0.692105 0.696  
## positionNW:treatmentMoss removed 0.701714 0.731126 0.960  
##   
## Correlation of Fixed Effects:  
## (Intr) pstnNW trtmBs trtmMr pNW:Bs  
## positionNW -0.707   
## trtmntBrsnd -0.514 0.363   
## trtmntMssrm -0.442 0.312 0.339   
## pstnNW:trBs 0.374 -0.528 -0.727 -0.246   
## pstnNW:trMr 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) + position \* 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 Pr(>|t|)   
## (Intercept) 0.48285 0.25325 1.907 0.0642 .  
## positionNW 0.08108 0.34076 0.238 0.8132   
## treatmentBare sand -0.24646 0.47202 -0.522 0.6046   
## treatmentMoss removed -0.60063 0.66404 -0.905 0.3714   
## positionNW:treatmentBare sand 0.22907 0.59507 0.385 0.7024   
## positionNW:treatmentMoss removed 0.42236 0.78327 0.539 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