

Model summaries

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2025-02-04

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Introduction

This document summarizes statistical models developed to analyze plant community observations. Six generalized linear mixed models (GLMMs) were fit to examine two aspects of plant communities: species richness (count data) and percent cover abundance (continuous proportions from 0-1). For each response variable, three plant groups were analyzed: all native species, native forbs (a subset of native species), and non-native species. For each combination of response variable and plant group, the best-performing model from a candidate set of models was selected.

The formulation, model summary, marginal means, and contrasts are provided in this document for each of the six models.

Abundance

Native species

```
mod_abun_nat <- lme4::lmer(  
  value_log ~ treatment + f_year + plot_type + (1 + treatment | plot_name),  
  data = abun_nat, REML = FALSE)
```

Model summary table

Linear mixed model fit by maximum likelihood ['lmerMod']
Formula: value_log ~ treatment + f_year + plot_type + (1 + treatment |
plot_name)
Data: abun_nat

AIC	BIC	logLik	deviance	df.resid
1276.4	1315.0	-628.2	1256.4	340

Scaled residuals:

Min	1Q	Median	3Q	Max
-9.0807	-0.3177	0.0545	0.3909	2.6511

Random effects:

Groups	Name	Variance	Std.Dev.	Corr
plot_name	(Intercept)	1.9620	1.401	
	treatmentGrazed	0.9545	0.977	-0.82
Residual		1.4807	1.217	

Number of obs: 350, groups: plot_name, 57

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	1.85441	0.25436	7.290
treatmentGrazed	0.69151	0.18377	3.763
f_year5	-0.01986	0.24891	-0.080
f_year6	0.14507	0.18350	0.791
f_year7	0.37800	0.18449	2.049
plot_typew	0.47645	0.33782	1.410

Correlation of Fixed Effects:

	(Intr)	trtmnG	f_yry5	f_yry6	f_yry7
tretmntGrzd	-0.598				
f_year5	-0.362	-0.002			
f_year6	-0.444	-0.001	0.504		
f_year7	-0.444	-0.001	0.499	0.602	
plot_typew	-0.299	-0.015	0.007	0.033	0.039

Marginal means

treatment	estimate	conf_low	conf_high	p_value	statistic
Ungrazed	9.19	5.86	14.43	0	9.64
Grazed	18.36	13.09	25.75	0	16.85

Contrasts

term	contrast	estimate	conf_low	conf_high	p_value	statistic
Grazing treatment	Grazed - Ungrazed	1.99	1.39	2.85	0.0001893	3.73
Year	2020 - 2019	0.98	0.60	1.60	0.9363998	-0.08
Year	2021 - 2019	1.16	0.81	1.66	0.4292022	0.79
Year	2022 - 2019	1.46	1.02	2.10	0.0404693	2.05
Year	2021 - 2020	1.18	0.76	1.82	0.4590555	0.74
Year	2022 - 2020	1.49	0.96	2.31	0.0755708	1.78
Year	2022 - 2021	1.26	0.92	1.74	0.1556813	1.42
Plot type	WAN - PER	1.61	0.83	3.12	0.1584235	1.41

Native forb species

```
mod_abun_frb <- lme4::lmer(  
  value_log ~ treatment + f_year + plot_type + (1 + treatment | plot_name),  
  data = abun_frb, REML = FALSE)
```

Model summary table

Linear mixed model fit by maximum likelihood ['lmerMod']
Formula: value_log ~ treatment + f_year + plot_type + (1 + treatment |
plot_name)
Data: abun_frb

AIC	BIC	logLik	deviance	df.resid
1359.7	1398.3	-669.8	1339.7	340

Scaled residuals:

Min	1Q	Median	3Q	Max
-9.1420	-0.2796	0.0281	0.3446	2.7247

Random effects:

Groups	Name	Variance	Std.Dev.	Corr
plot_name	(Intercept)	6.0834	2.4665	
	treatmentGrazed	0.9378	0.9684	-0.37
Residual		1.4346	1.1978	

Number of obs: 350, groups: plot_name, 57

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	1.264933	0.397223	3.184
treatmentGrazed	0.802116	0.181555	4.418
f_year5	-0.007815	0.252554	-0.031
f_year6	0.214688	0.182093	1.179
f_year7	0.509775	0.183085	2.784
plot_typew	0.893098	0.766800	1.165

Correlation of Fixed Effects:

	(Intr)	trtmnG	f_yry5	f_yry6	f_yry7
tretmntGrzd	-0.325				
f_year5	-0.235	0.000			
f_year6	-0.285	0.000	0.514		
f_year7	-0.285	0.000	0.509	0.608	
plot_typew	-0.412	-0.004	0.004	0.014	0.017

Marginal means

treatment	estimate	conf_low	conf_high	p_value	statistic
Ungrazed	6.62	2.99	14.67	3.2e-06	4.66
Grazed	14.77	6.91	31.56	0.0e+00	6.95

Contrasts

term	contrast	estimate	conf_low	conf_high	p_value	statistic
Grazing treatment	Grazed - Ungrazed	2.24	1.57	3.20	0.0000091	4.44
Year	2020 - 2019	0.99	0.60	1.63	0.9753140	-0.03
Year	2021 - 2019	1.24	0.87	1.77	0.2383996	1.18
Year	2022 - 2019	1.66	1.16	2.38	0.0053632	2.78
Year	2021 - 2020	1.25	0.81	1.93	0.3180508	1.00
Year	2022 - 2020	1.68	1.08	2.60	0.0208983	2.31
Year	2022 - 2021	1.34	0.98	1.84	0.0680230	1.82
Plot type	WAN - PER	2.44	0.54	10.98	0.2441375	1.16

Non-native species

```
mod_abun_non <- lme4::lmer(  
  value_sqrt ~ treatment + f_year + f_two_yr + (1 | plot_name),  
  data = abun_non, REML = FALSE)
```

Model summary table

Linear mixed model fit by maximum likelihood ['lmerMod']
Formula: value_sqrt ~ treatment + f_year + f_two_yr + (1 | plot_name)
Data: abun_non

AIC	BIC	logLik	deviance	df.resid
1363.4	1394.3	-673.7	1347.4	342

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.7324	-0.6178	0.0013	0.6209	3.1720

Random effects:

Groups	Name	Variance	Std.Dev.
plot_name	(Intercept)	1.690	1.300
Residual		2.053	1.433

Number of obs: 350, groups: plot_name, 57

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	8.759152	0.253033	34.617
treatmentGrazed	-0.005792	0.153194	-0.038
f_year5	-1.647313	0.298509	-5.518
f_year6	-3.286309	0.260348	-12.623
f_year7	-2.579846	0.217911	-11.839
f_two_yrt1	0.498907	0.277126	1.800

Correlation of Fixed Effects:

	(Intr)	trtmnG	f_yry5	f_yry6	f_yry7
tretmntGrzd	-0.303				
f_year5	-0.418	0.000			
f_year6	-0.396	0.000	0.493		
f_year7	-0.518	0.000	0.490	0.473	
f_two_yrt1	-0.061	0.000	-0.137	-0.555	0.050

Marginal means

treatment	estimate	conf_low	conf_high	p_value	statistic
Ungrazed	50.84	44.86	57.19	0	32.33
Grazed	50.76	44.79	57.10	0	32.31

Contrasts

term	contrast	estimate	conf_low	conf_high	p_value	statistic
Grazing treatment	Grazed - Ungrazed	0.00	0.09	0.09	0.9698410	-0.04
Year	2020 - 2019	2.71	4.98	1.13	0.0000000	-5.52
Year	2021 - 2019	10.80	14.41	7.71	0.0000000	-12.62
Year	2022 - 2019	6.66	9.04	4.63	0.0000000	-11.84
Year	2021 - 2020	2.69	4.81	1.17	0.0000000	-5.79
Year	2022 - 2020	0.87	2.14	0.16	0.0005503	-3.45
Year	2022 - 2021	0.50	0.05	1.42	0.0044046	2.85
2y Break	2y Break	0.25	0.00	1.09	0.0718153	1.80

Richness

Native species

```
mod_rich_nat <- glmmTMB::glmmTMB(  
  value ~  
    treatment +  
    f_year +  
    (1 | plot_type) +  
    (1 + treatment | plot_name),  
  data = rich_nat,  
  family = nbinom2,  
  control = glmmTMBControl(optimizer=optim,  
                             optArgs=list(method="BFGS")))
```

Model summary table

Family: nbinom2 (log)
Formula:
value ~ treatment + f_year + (1 | plot_type) + (1 + treatment | plot_name)
Data: rich_nat

AIC	BIC	logLik	deviance	df.resid
1651.3	1689.9	-815.7	1631.3	340

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.	Corr
plot_type	(Intercept)	6.484e-09	8.053e-05	
plot_name	(Intercept)	2.750e-01	5.244e-01	
	treatmentGrazed	6.847e-02	2.617e-01	-0.53

Number of obs: 350, groups: plot_type, 2; plot_name, 57

Dispersion parameter for nbinom2 family (): 2.12e+07

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.51511	0.09052	16.737	< 2e-16 ***
treatmentGrazed	0.29782	0.06151	4.842	1.29e-06 ***
f_year5	0.03782	0.08264	0.458	0.647
f_year6	-0.09177	0.06426	-1.428	0.153
f_year7	0.07803	0.06210	1.257	0.209

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Marginal means

treatment	estimate	conf_low	conf_high	p_value	statistic
Ungrazed	5.21	4.98	5.43	0	44.92
Grazed	6.78	6.51	7.04	0	49.27

Contrasts

term	contrast	estimate	conf_low	conf_high	p_value	statistic
Grazing treatment	Grazed - Ungrazed	1.56	1.08	2.05	0.0000000	6.32
Year	2020 - 2019	0.23	-0.76	1.23	0.6489112	0.46
Year	2021 - 2019	-0.53	-1.25	0.20	0.1549246	-1.42
Year	2022 - 2019	0.49	-0.27	1.24	0.2068778	1.26
Year	2021 - 2020	-0.76	-1.62	0.10	0.0837824	-1.73
Year	2022 - 2020	0.26	-0.63	1.14	0.5692044	0.57
Year	2022 - 2021	1.01	0.37	1.66	0.0020601	3.08

Native forb species

```
mod_rich_frb <- glmmTMB::glmmTMB(
  value ~
    treatment +
    f_year +
    (1 | plot_type) +
    (1 + treatment | plot_name),
  data = rich_frb,
  family = nbinom2,
  control = glmmTMBControl(optimizer=optim,
                           optArgs=list(method="BFGS")))
```

Model summary table

Family: nbinom2 (log)

Formula:

value ~ treatment + f_year + (1 | plot_type) + (1 + treatment | plot_name)

Data: rich_frb

AIC	BIC	logLik	deviance	df.resid
NA	NA	NA	NA	340

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.	Corr
plot_type	(Intercept)	8.808e-06	0.002968	
plot_name	(Intercept)	3.241e-01	0.569313	
	treatmentGrazed	7.582e-02	0.275354	-0.57

Number of obs: 350, groups: plot_type, 2; plot_name, 57

Dispersion parameter for nbinom2 family (): 3.23e+07

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.36656	0.09741	14.029	< 2e-16 ***
treatmentGrazed	0.36180	0.06499	5.567	2.59e-08 ***
f_year5	0.03735	0.08670	0.431	0.6666
f_year6	-0.05981	0.06672	-0.896	0.3700
f_year7	0.13218	0.06424	2.058	0.0396 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Marginal means

treatment	estimate	conf_low	conf_high	p_value	statistic
Ungrazed	4.67	4.46	4.89	0	42.49
Grazed	6.41	6.14	6.67	0	47.50

Contrasts

term	contrast	estimate	conf_low	conf_high	p_value	statistic
Grazing treatment	Grazed - Ungrazed	1.75	1.26	2.23	0.0000000	7.05
Year	2020 - 2019	0.21	-0.74	1.15	0.6682591	0.43
Year	2021 - 2019	-0.32	-1.01	0.38	0.3712730	-0.89
Year	2022 - 2019	0.77	0.04	1.49	0.0380857	2.07
Year	2021 - 2020	-0.52	-1.35	0.30	0.2147835	-1.24
Year	2022 - 2020	0.56	-0.29	1.41	0.1954216	1.29
Year	2022 - 2021	1.08	0.46	1.71	0.0007096	3.39

Non-native species

```
mod_rich_non <- lme4::lmer(  
  value_sqrt ~  
    treatment +  
    f_year +  
    (1 + treatment | plot_name),  
  data = rich_non,  
  REML = FALSE)
```

Model summary table

Linear mixed model fit by maximum likelihood ['lmerMod']
Formula: value_sqrt ~ treatment + f_year + (1 + treatment | plot_name)
Data: rich_non

AIC	BIC	logLik	deviance	df.resid
327.5	362.2	-154.7	309.5	341

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.92735	-0.62279	0.01816	0.65747	2.56325

Random effects:

Groups	Name	Variance	Std.Dev.	Corr
plot_name	(Intercept)	0.07034	0.2652	
	treatmentGrazed	0.03699	0.1923	-0.10
Residual		0.10004	0.3163	

Number of obs: 350, groups: plot_name, 57

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	2.87898	0.05381	53.505
treatmentGrazed	0.13060	0.04240	3.080
f_year5	-0.10760	0.06506	-1.654
f_year6	-0.38581	0.04775	-8.081
f_year7	-0.36634	0.04799	-7.633

Correlation of Fixed Effects:

	(Intr)	trtmnG	f_yry5	f_yry6
tretmntGrzd	-0.293			
f_year5	-0.446	0.001		
f_year6	-0.536	0.000	0.506	
f_year7	-0.534	0.000	0.501	0.603

Marginal means

treatment	estimate	conf_low	conf_high	p_value	statistic
Ungrazed	7.10	6.65	7.55	0	61.90
Grazed	7.81	7.29	8.35	0	58.09

Contrasts

term	contrast	estimate	conf_low	conf_high	p_value	statistic
Grazing treatment	Grazed - Ungrazed	0.02	0.00	0.05	0.0019249	3.10
Year	2020 - 2019	0.01	0.06	0.00	0.0981746	-1.65
Year	2021 - 2019	0.15	0.23	0.09	0.0000000	-8.08
Year	2022 - 2019	0.13	0.21	0.07	0.0000000	-7.63
Year	2021 - 2020	0.08	0.15	0.03	0.0000017	-4.79
Year	2022 - 2020	0.07	0.14	0.02	0.0000093	-4.43
Year	2022 - 2021	0.00	0.00	0.01	0.6481379	0.46

Environment

You must run the scripts in `fxn_summarize_models()` with `marginaleffects_0.5.0`. If you use a later version you could (and probably will) get different results.

Get `marginaleffects_0.5.0` from cran by running these 2 lines:

```
# Uncomment (remove the #) code to run

# packageurl <- "https://cran.r-project.org/src/contrib/Archive/marginaleffects/marginaleffects_0
# install.packages(packageurl, repos=NULL, type="source")
```

Then confirm the package version:

```
# Uncomment (remove the #) code to run

# sessionInfo()
```

Session info

R version 4.4.0 (2024-04-24)

Platform: aarch64-apple-darwin20

Running under: macOS 15.2

Matrix products: default

BLAS: /Library/Frameworks/R.framework/Versions/4.4-arm64/Resources/lib/libRblas.0.dylib

LAPACK: /Library/Frameworks/R.framework/Versions/4.4-arm64/Resources/lib/libRlapack.dylib; LAPACK

locale:

[1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8

time zone: America/Los_Angeles

tzcode source: internal

attached base packages:

[1] stats graphics grDevices utils datasets methods base

other attached packages:

[1] stringr_1.5.1	see_0.9.0	sessioninfo_1.2.2
[4] readxl_1.4.3	performance_0.13.0	MuMIn_1.48.4
[7] MASS_7.3-64	marginaleffects_0.5.0	lme4_1.1-36
[10] Matrix_1.7-0	knitr_1.48	kableExtra_1.4.0
[13] janitor_2.2.1	here_1.0.1	glue_1.8.0
[16] ggplot2_3.5.1	glmmTMB_1.1.10	forcats_1.0.0
[19] emmeans_1.10.6	dplyr_1.1.4	DHARMa_0.4.7
[22] broom.mixed_0.2.9.6	broom_1.0.7	car_3.1-3

[25] carData_3.0-5

loaded via a namespace (and not attached):

[1] tidyselect_1.2.1	viridisLite_0.4.2	fastmap_1.2.0
[4] digest_0.6.37	estimability_1.5.1	timechange_0.3.0
[7] lifecycle_1.0.4	magrittr_2.0.3	compiler_4.4.0
[10] rlang_1.1.4	tools_4.4.0	utf8_1.2.4
[13] yaml_2.3.10	data.table_1.16.4	bit_4.0.5
[16] xml2_1.3.6	abind_1.4-8	withr_3.0.2
[19] purrr_1.0.2	numDeriv_2016.8-1.1	stats4_4.4.0
[22] grid_4.4.0	fansi_1.0.6	xtable_1.8-4
[25] colorspace_2.1-1	future_1.34.0	globals_0.16.3
[28] scales_1.3.0	insight_1.0.1	cli_3.6.3
[31] mvtnorm_1.3-2	crayon_1.5.3	rmarkdown_2.28
[34] reformulas_0.4.0	generics_0.1.3	rstudioapi_0.16.0
[37] tzdb_0.4.0	minqa_1.2.8	splines_4.4.0
[40] parallel_4.4.0	cellranger_1.1.0	vctrs_0.6.5
[43] boot_1.3-31	jsonlite_1.8.8	hms_1.1.3
[46] bit64_4.0.5	Formula_1.2-5	listenv_0.9.1
[49] systemfonts_1.1.0	tidyr_1.3.1	parallelly_1.41.0
[52] nloptr_2.1.1	codetools_0.2-20	lubridate_1.9.4
[55] stringi_1.8.4	gtable_0.3.5	munsell_0.5.1
[58] tibble_3.2.1	furrr_0.3.1	pillar_1.9.0
[61] htmltools_0.5.8.1	R6_2.5.1	TMB_1.9.16
[64] Rdpack_2.6.2	rprojroot_2.0.4	vroom_1.6.5
[67] evaluate_1.0.3	lattice_0.22-6	readr_2.1.5
[70] rbibutils_2.3	backports_1.5.0	snakecase_0.11.1
[73] Rcpp_1.0.13	checkmate_2.3.2	svglite_2.1.3
[76] coda_0.19-4.1	nlme_3.1-166	mgcv_1.9-1
[79] xfun_0.48	pkgconfig_2.0.3	