

TRhizo-localAdaptation

Microbiome x Nitrogen Global Analyses (Alternate)

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Load Packages & Data

```
## Load the tidyverse
library(tidyverse)

## Packages for analysis
library(broom)
library(easystats)
library(emmeans)
library(lme4)
library(lmerTest)

## Read in data
biomass.data <- read_rds(file = "data/cleaned_biomass_data.rds")
nodule.data <- read_rds(file = "data/cleaned_nodule_data.rds")

## Recode to Microbiome Global to test for global effects
# Biomass data
biomass.data$Microbiome_Global<- if_else(
  biomass.data$Microbiome == "Local", "Local", "Nonlocal_Global"
)
# Nodule data
nodule.data$Microbiome_Global<- if_else(
  nodule.data$Microbiome == "Local", "Local", "Nonlocal_Global"
)

## Read in workspace
# load("data_analysis/2-microbiome_x_nitrogen-analyses/M_x_N-alternate_global_analyses-workspace.RData")
```

Aboveground Biomass $M \times N$ Model

```
aboveground.biomass.MN.global.LMM <- lmer(  
  sqrt(Aboveground_Biomass) ~ Microbiome_Global* Nitrogen  
  + (1 | Microbiome_Global:Population)  
  + (1 | Nitrogen:Population)  
  + (1 | Microbiome_Global:Nitrogen:Population)  
  + (1 | Population)  
  + (1 | Block),  
  data = biomass.data,  
  REML = TRUE  
)
```

Check Model Assumptions

```
## Check model convergence  
check_convergence(aboveground.biomass.MN.global.LMM)  
# Model converged  
  
## Check for boundary singularity  
check_singularity(aboveground.biomass.MN.global.LMM)  
# No singularity  
  
## Visual assessment of model diagnostics  
check_model(aboveground.biomass.MN.global.LMM)  
# Visual check = assumptions met  
  
## Check normality of fixed effects (Shapiro-Wilk test)  
check_normality(aboveground.biomass.MN.global.LMM, effects = "fixed")  
# Suggests statistical non-normality of residuals (P < 0.001)  
# Mixed-effects models are robust to this assumption  
  
## Check normality of random effects  
check_normality(aboveground.biomass.MN.global.LMM, effects = "random")  
# M:P = Good  
# N:P = Non-normality detected (P = 0.006)  
# M:N:P = Non-normality detected (P = 0.002)  
# P = Good  
# B = Good  
  
## Check for non-constant variance of residuals (Breusch-Pagan test)  
check_heteroscedasticity(aboveground.biomass.MN.global.LMM)  
# Statistical evidence for heteroscedasticity (P < 0.001)  
  
## Check for homogeneity of variance (Bartlett test)  
check_homogeneity(aboveground.biomass.MN.global.LMM)  
# Variances differ between groups (P < 0.001)  
  
## Check for outliers  
check_outliers(aboveground.biomass.MN.global.LMM)  
# 2 outliers detected
```

Marginal & Conditional R²

```
## Calculate the marginal and conditional R-squared
MuMIn::r.squaredGLMM(aboveground.biomass.MN.global.LMM)
# Marginal = 0.230
# Conditional = 0.394
```

ANOVA

```
## Fit an ANOVA with Type III sums-of-squares
aboveground.biomass.MN.global.LMM.anova <- anova(
  object = aboveground.biomass.MN.global.LMM,
  type = "III",
  ddf = "Kenward-Roger"
)
```

Table 1: ANOVA table for the Aboveground Biomass M x N Model.

	Sums-of-Squares	Mean-Square	Num_df	Den_df	F	P-value
Microbiome_Global	0.090	0.090	1	28.468	4.054	0.054
Nitrogen	3.855	3.855	1	32.443	173.774	0.000
Microbiome_Global:Nitrogen	0.012	0.012	1	31.409	0.542	0.467

Partial η^2 for Fixed Effects

Table 2: Table of the effect sizes for the fixed effects in the Aboveground Biomass M x N Model.

Term	Partial eta-squared	CI	CI_low	CI_high
Microbiome_Global	0.125	0.95	0.000	1
Nitrogen	0.843	0.95	0.754	1
Microbiome_Global:Nitrogen	0.017	0.95	0.000	1

ranova

```
## Fit a ranova
aboveground.biomass.MN.global.LMM.ranova <- ranova(
  aboveground.biomass.MN.global.LMM,
  reduce.terms = FALSE
)
```

Table 3: Summary of the ranova for the Aboveground Biomass M x N Model.

	n_parameters	log_likelihood	AIC	LRT	df	P-value
<none>	10	349.677	-679.353	NA	NA	NA
(1 Microbiome_Global:Population)	9	347.906	-677.811	3.542	1	0.060
(1 Nitrogen:Population)	9	348.333	-678.665	2.688	1	0.101
(1 Microbiome_Global:Nitrogen:Population)	9	349.677	-681.353	0.000	1	1.000
(1 Population)	9	345.743	-673.486	7.867	1	0.005
(1 Block)	9	347.586	-677.171	4.182	1	0.041

ICC for Random Effects

Table 4: Table of the effect sizes for the random effects in the Aboveground Biomass M x N Model.

Term	ICC
Microbiome_Global:Nitrogen:Population	0.000
Nitrogen:Population	0.037
Microbiome_Global:Population	0.044
Population	0.120
Block	0.012

Contrasts

```

aboveground.biomass.M.emmeans <- emmeans(
  aboveground.biomass.MN.global.LMM,
  specs = pairwise ~ Microbiome_Global,
  weights = "cells",
  adjust = "none"
)

aboveground.biomass.N.emmeans <- emmeans(
  aboveground.biomass.MN.global.LMM,
  specs = pairwise ~ Nitrogen,
  weights = "cells",
  adjust = "none"
)

aboveground.biomass.MxN.emmeans <- emmeans(
  aboveground.biomass.MN.global.LMM,
  specs = pairwise ~ Microbiome_Global | Nitrogen,
  weights = "cells",
  adjust = "none"
)

```

Table 5: Post-hoc comparisons of the main effect of Microbiome Global in the Aboveground Biomass ANOVA.

Term	Contrast	Null Value	Estimate	SE	df	t	P
Microbiome_Global	Local - Nonlocal_Global	0	0.029	0.014	28.467	2.027	0.052

Table 6: Post-hoc comparisons of the main effect of Nitrogen in the Aboveground Biomass ANOVA.

Term	Contrast	Null Value	Estimate	SE	df	t	P
Nitrogen	Ambient_N - N_Addition	0	-0.181	0.013	27.838	-13.515	0

Table 7: Post-hoc comparisons of the interaction between Microbiome Global and Nitrogen in the Aboveground Biomass ANOVA.

Factor_1	Factor_2	Contrast	Null Value	Estimate	SE	df	t	P
Ambient_N	Microbiome_Global	Local - Nonlocal_Global	0	0.021	0.018	54.694	1.149	0.255
N_Addition	Microbiome_Global	Local - Nonlocal_Global	0	0.037	0.018	53.866	2.045	0.046

Contrasts (Effect Sizes)

Table 8: Effect sizes for the constrasts by Microbiome Global in the Aboveground Biomass ANOVA.

Contrast	Cohen's d	SE	df	CI Lower	CI Upper
(Local - Nonlocal_Global)	0.197	0.097	28.467	-0.002	0.396

Table 9: Effect sizes for the constrasts by Nitrogen in the Aboveground Biomass ANOVA.

Contrast	Cohen's d	SE	df	CI Lower	CI Upper
(Ambient_N - N_Addition)	-1.215	0.095	27.838	-1.409	-1.021

Table 10: Effect sizes for the constrasts by Microbiome Global and Nitrogen in the Aboveground Biomass ANOVA.

Contrast	Nitrogen	Cohen's d	SE	df	CI Lower	CI Upper
(Local - Nonlocal_Global)	Ambient_N	0.141	0.122	54.694	-0.105	0.386
(Local - Nonlocal_Global)	N_Addition	0.250	0.123	53.866	0.005	0.496

Belowground Biomass $M \times N$ Model

```
belowground.biomass.MN.global.LMM <- lmer(  
  sqrt(Belowground_Biomass) ~ Microbiome_Global* Nitrogen  
  + (1 | Population)  
  + (1 | Block),  
  data = biomass.data,  
  REML = TRUE  
)
```

Check Model Assumptions

```
## Check model convergence  
check_convergence(belowground.biomass.MN.global.LMM)  
# Model converged  
  
## Check for boundary singularity  
check_singularity(belowground.biomass.MN.global.LMM)  
# No singularity  
  
## Visual assessment of model diagnostics  
check_model(belowground.biomass.MN.global.LMM)  
# Visual check = assumptions met  
  
## Check normality of fixed effects (Shapiro-Wilk test)  
check_normality(belowground.biomass.MN.global.LMM, effects = "fixed")  
# Suggests statistical non-normality of residuals (P < 0.001)  
# Mixed-effects models are robust to this assumption  
  
## Check normality of random effects  
check_normality(belowground.biomass.MN.global.LMM, effects = "random")  
# P = Good  
# B = Good  
  
## Check for non-constant variance of residuals (Breusch-Pagan test)  
check_heteroscedasticity(belowground.biomass.MN.global.LMM)  
# Statistical evidence for heteroscedasticity (P < 0.001)  
  
## Check for homogeneity of variance (Bartlett test)  
check_homogeneity(belowground.biomass.MN.global.LMM)  
# Variances differ between groups (P < 0.001)  
  
## Check for outliers  
check_outliers(belowground.biomass.MN.global.LMM)  
# No outliers detected
```

Marginal & Conditional R²

```
## Calculate the marginal and conditional R-squared
MuMIn::r.squaredGLMM(belowground.biomass.MN.global.LMM)
# Marginal = 0.288
# Conditional = 0.373
```

ANOVA

```
## Fit an ANOVA with Type III sums-of-squares
belowground.biomass.MN.global.LMM.anova <- anova(
  object = belowground.biomass.MN.global.LMM,
  type = "III",
  ddf = "Kenward-Roger"
)
```

Table 11: ANOVA table for the Belowground Biomass M x N Model.

	Sums-of-Squares	Mean-Square	Num_df	Den_df	F	P-value
Microbiome_Global	0.018	0.018	1	803.909	1.520	0.218
Nitrogen	3.860	3.860	1	805.166	329.021	0.000
Microbiome_Global:Nitrogen	0.003	0.003	1	806.873	0.255	0.614

Partial η^2 for Fixed Effects

Table 12: Table of the effect sizes for the fixed effects in the Belowground Biomass M x N Model.

Term	Partial eta-squared	CI	CI_low	CI_high
Microbiome_Global	0.002	0.95	0.000	1
Nitrogen	0.290	0.95	0.249	1
Microbiome_Global:Nitrogen	0.000	0.95	0.000	1

ranova

```
## Fit a ranova
belowground.biomass.MN.global.LMM.ranova <- ranova(
  belowground.biomass.MN.global.LMM,
  reduce.terms = FALSE
)
```

Table 13: Summary of the ranova for the Belowground Biomass M x N Model.

	n_parameters	log_likelihood	AIC	LRT	df	P-value
<none>	7	636.749	-1259.497	NA	NA	NA
(1 Population)	6	613.515	-1215.031	46.467	1	0.000
(1 Block)	6	634.422	-1256.843	4.654	1	0.031

ICC for Random Effects

Table 14: Table of the effect sizes for the random effects in the Belowground Biomass M x N Model.

Term	ICC
Population	0.105
Block	0.014

Contrasts

```
belowground.biomass.M.emmeans <- emmeans(
  belowground.biomass.MN.global.LMM,
  specs = pairwise ~ Microbiome_Global,
  weights = "cells",
  adjust = "none"
)

belowground.biomass.N.emmeans <- emmeans(
  belowground.biomass.MN.global.LMM,
  specs = pairwise ~ Nitrogen,
  weights = "cells",
  adjust = "none"
)

belowground.biomass.MxN.emmeans <- emmeans(
  belowground.biomass.MN.global.LMM,
  specs = pairwise ~ Microbiome_Global | Nitrogen,
  weights = "cells",
  adjust = "none"
)
```

Table 15: Post-hoc comparisons of the main effect of Microbiome Global in the Belowground Biomass ANOVA.

Term	Contrast	Null Value	Estimate	SE	df	t	P
Microbiome_Global	Local - Nonlocal_Global	0	0.01	0.008	803.923	1.249	0.212

Table 16: Post-hoc comparisons of the main effect of Nitrogen in the Belowground Biomass ANOVA.

Term	Contrast	Null Value	Estimate	SE	df	t	P
Nitrogen	Ambient_N - N_Addition	0	-0.147	0.008	803.673	-19.536	0

Table 17: Post-hoc comparisons of the interaction between Microbiome Global and Nitrogen in the Belowground Biomass ANOVA.

Factor_1	Factor_2	Contrast	Null Value	Estimate	SE	df	t	P
Ambient_N	Microbiome_Global	Local - Nonlocal_Global	0	0.014	0.011	803.928	1.228	0.220
N_Addition	Microbiome_Global	Local - Nonlocal_Global	0	0.006	0.011	807.074	0.514	0.608

Contrasts (Effect Sizes)

Table 18: Effect sizes for the constrasts by Microbiome Global in the Belowground Biomass ANOVA.

Contrast	Cohen's d	SE	df	CI Lower	CI Upper
(Local - Nonlocal_Global)	0.092	0.074	803.923	-0.053	0.237

Table 19: Effect sizes for the constrasts by Nitrogen in the Belowground Biomass ANOVA.

Contrast	Cohen's d	SE	df	CI Lower	CI Upper
(Ambient_N - N_Addition)	-1.353	0.077	803.673	-1.503	-1.202

Table 20: Effect sizes for the constrasts by Microbiome Global and Nitrogen in the Belowground Biomass ANOVA.

Contrast	Nitrogen	Cohen's d	SE	df	CI Lower	CI Upper
(Local - Nonlocal_Global)	Ambient_N	0.128	0.105	803.928	-0.077	0.334
(Local - Nonlocal_Global)	N_Addition	0.054	0.104	807.074	-0.151	0.259

Nodule Density $M \times N$ Model

```
nodule.density.MN.global.LMM <- lmer(  
  log(Nodule_Density + 1) ~ Microbiome_Global* Nitrogen  
  + (1 | Microbiome_Global:Population)  
  + (1 | Nitrogen:Population)  
  + (1 | Microbiome:Nitrogen:Population)  
  + (1 | Population)  
  + (1 | Block),  
  data = nodule.data,  
  REML = TRUE  
)
```

Check Model Assumptions

```
## Check model convergence  
check_convergence(nodule.density.MN.global.LMM)  
# Model converged
```

```
## Check for boundary singularity  
check_singularity(nodule.density.MN.global.LMM)  
# Singularity
```

```
## Visual assessment of model diagnostics  
check_model(nodule.density.MN.global.LMM)  
# Visual check = assumptions met
```

```
## Check normality of fixed effects (Shapiro-Wilk test)  
check_normality(nodule.density.MN.global.LMM, effects = "fixed")  
# Suggests statistical non-normality of residuals ( $P < 0.001$ )  
# Mixed-effects models are robust to this assumption
```

```
## Check normality of random effects  
check_normality(nodule.density.MN.global.LMM, effects = "random")  
# M:P = Good  
# N:P = Good  
# M:N:P = Good  
# P = Good  
# B = Good
```

```
## Check for non-constant variance of residuals (Breusch-Pagan test)  
check_heteroscedasticity(nodule.density.MN.global.LMM)  
# Statistical evidence for heteroscedasticity ( $P < 0.001$ )
```

```
## Check for homogeneity of variance (Bartlett test)  
check_homogeneity(nodule.density.MN.global.LMM)  
# Variances differ between groups ( $P < 0.001$ )
```

```
## Check for outliers  
check_outliers(nodule.density.MN.global.LMM)  
# 6 outliers detected
```

Marginal & Conditional R²

```
## Calculate the marginal and conditional R-squared
MuMIn::r.squaredGLMM(nodule.density.MN.global.LMM)
# Marginal = 0.055
# Conditional = 0.263
```

ANOVA

```
## Fit an ANOVA with Type III sums-of-squares
nodule.density.MN.global.LMM.anova <- anova(
  object = nodule.density.MN.global.LMM,
  type = "III",
  ddf = "Kenward-Roger"
)
```

Table 21: ANOVA table for the Nodule Density M x N Model.

	Sums-of-Squares	Mean-Square	Num_df	Den_df	F	P-value
Microbiome_Global	0.694	0.694	1	31.390	18.108	0.000
Nitrogen	0.322	0.322	1	35.652	8.400	0.006
Microbiome_Global:Nitrogen	0.043	0.043	1	89.952	1.111	0.295

Partial η^2 for Fixed Effects

Table 22: Table of the effect sizes for the fixed effects in the Nodule Density M x N Model.

Term	Partial eta-squared	CI	CI_low	CI_high
Microbiome_Global	0.366	0.95	0.151	1
Nitrogen	0.191	0.95	0.035	1
Microbiome_Global:Nitrogen	0.012	0.95	0.000	1

ranova

```
## Fit a ranova
nodule.density.MN.global.LMM.ranova <- ranova(
  nodule.density.MN.global.LMM,
  reduce.terms = FALSE
)
```

Table 23: Summary of the ranova for the Nodule Density M x N Model.

	n_parameters	log_likelihood	AIC	LRT	df	P-value
<none>	10	97.331	-174.663	NA	NA	NA
(1 Microbiome_Global:Population)	9	97.331	-176.663	0.000	1	1.000
(1 Nitrogen:Population)	9	97.331	-176.663	0.000	1	1.000
(1 Microbiome:Nitrogen:Population)	9	84.203	-150.406	26.256	1	0.000
(1 Population)	9	94.936	-171.872	4.791	1	0.029
(1 Block)	9	96.955	-175.909	0.753	1	0.385

ICC for Random Effects

Table 24: Table of the effect sizes for the random effects in the Nodule Density M x N Model.

Term	ICC
Microbiome:Population	0.000
Nitrogen:Population	0.000
Microbiome:Nitrogen:Population	0.158
Population	0.058
Block	0.004

Contrasts

```

nodule.density.M.emmeans <- emmeans(
  nodule.density.MN.global.LMM,
  specs = pairwise ~ Microbiome_Global,
  weights = "cells",
  adjust = "none"
)

nodule.density.N.emmeans <- emmeans(
  nodule.density.MN.global.LMM,
  specs = pairwise ~ Nitrogen,
  weights = "cells",
  adjust = "none"
)

nodule.density.MxN.emmeans <- emmeans(
  nodule.density.MN.global.LMM,
  specs = pairwise ~ Microbiome_Global | Nitrogen,
  weights = "cells",
  adjust = "none"
)

```

Table 25: Post-hoc comparisons of the main effect of Microbiome Global in the Nodule Density ANOVA.

Term	Contrast	Null Value	Estimate	SE	df	t	P
Microbiome_Global	Local - Nonlocal_Global	0	0.087	0.02	31.39	4.252	0

Table 26: Post-hoc comparisons of the main effect of Nitrogen in the Nodule Density ANOVA.

Term	Contrast	Null Value	Estimate	SE	df	t	P
Nitrogen	Ambient_N - N_Addition	0	0.066	0.019	28.085	3.452	0.002

Table 27: Post-hoc comparisons of the interaction between Microbiome Global and Nitrogen in the Nodule Density ANOVA.

Factor_1	Factor_2	Contrast	Null Value	Estimate	SE	df	t	P
Ambient_N	Microbiome_Global	Local - Nonlocal_Global	0	0.065	0.029	88.672	2.263	0.026
N_Addition	Microbiome_Global	Local - Nonlocal_Global	0	0.108	0.029	87.121	3.754	0.000

Contrasts (Effect Sizes)

Table 28: Effect sizes for the constrasts by Microbiome Global in the Nodule Density ANOVA.

Contrast	Cohen's d	SE	df	CI Lower	CI Upper
(Local - Nonlocal_Global)	0.442	0.104	31.39	0.229	0.655

Table 29: Effect sizes for the constrasts by Nitrogen in the Nodule Density ANOVA.

Contrast	Cohen's d	SE	df	CI Lower	CI Upper
(Ambient_N - N_Addition)	0.338	0.098	28.085	0.137	0.539

Table 30: Effect sizes for the constrasts by Microbiome Global and Nitrogen in the Nodule Density ANOVA.

Contrast	Nitrogen	Cohen's d	SE	df	CI Lower	CI Upper
(Local - Nonlocal_Global)	Ambient_N	0.333	0.147	88.672	0.040	0.625
(Local - Nonlocal_Global)	N_Addition	0.552	0.148	87.121	0.258	0.845

Fixing Nodule Density $M \times N$ Model

```
fixing.nodule.density.MN.global.LMM <- lmer(  
  log(Fixing_Nodule_Density + 1) ~ Microbiome_Global* Nitrogen  
  + (1 | Microbiome_Global:Population)  
  + (1 | Nitrogen:Population)  
  + (1 | Population)  
  + (1 | Block),  
  data = nodule.data,  
  REML = TRUE  
)
```

Check Model Assumptions

```
## Check model convergence  
check_convergence(fixing.nodule.density.MN.global.LMM)  
# Model converged  
  
## Check for boundary singularity  
check_singularity(fixing.nodule.density.MN.global.LMM)  
# No singularity  
  
## Visual assessment of model diagnostics  
check_model(fixing.nodule.density.MN.global.LMM)  
# Visual check = assumptions met  
  
## Check normality of fixed effects (Shapiro-Wilk test)  
check_normality(fixing.nodule.density.MN.global.LMM, effects = "fixed")  
# Suggests statistical non-normality of residuals (P < 0.001)  
# Mixed-effects models are robust to this assumption  
  
## Check normality of random effects  
check_normality(fixing.nodule.density.MN.global.LMM, effects = "random")  
# M:P = Good  
# N:P = Good  
# P = Non-normality detected (P < 0.001)  
# B = Good  
  
## Check for non-constant variance of residuals (Breusch-Pagan test)  
check_heteroscedasticity(fixing.nodule.density.MN.global.LMM)  
# Statistical evidence for heteroscedasticity (P < 0.001)  
  
## Check for homogeneity of variance (Bartlett test)  
check_homogeneity(fixing.nodule.density.MN.global.LMM)  
# Variances differ between groups (P < 0.001)  
  
## Check for outliers  
check_outliers(fixing.nodule.density.MN.global.LMM)  
# 1 outlier detected
```

Marginal & Conditional R²

```
## Calculate the marginal and conditional R-squared
MuMIn::r.squaredGLMM(fixing.nodule.density.MN.global.LMM)
# Marginal = 0.041
# Conditional = 0.162
```

ANOVA

```
## Fit an ANOVA with Type III sums-of-squares
fixing.nodule.density.MN.global.LMM.anova <- anova(
  object = fixing.nodule.density.MN.global.LMM,
  type = "III",
  ddf = "Kenward-Roger"
)
```

Table 31: ANOVA table for the Fixing Nodule Density M x N Model.

	Sums-of-Squares	Mean-Square	Num_df	Den_df	F	P-value
Microbiome_Global	0.444	0.444	1	29.102	25.754	0.000
Nitrogen	0.112	0.112	1	32.602	6.524	0.016
Microbiome_Global:Nitrogen	0.012	0.012	1	769.770	0.672	0.413

Partial η^2 for Fixed Effects

Table 32: Table of the effect sizes for the fixed effects in the Fixing Nodule Density M x N Model.

Term	Partial eta-squared	CI	CI_low	CI_high
Microbiome_Global	0.469	0.95	0.244	1
Nitrogen	0.167	0.95	0.019	1
Microbiome_Global:Nitrogen	0.001	0.95	0.000	1

ranova

```
## Fit a ranova
fixing.nodule.density.MN.global.LMM.ranova <- ranova(
  fixing.nodule.density.MN.global.LMM,
  reduce.terms = FALSE
)
```

Table 33: Summary of the ranova for the Fixing Nodule Density M x N Model.

	n_parameters	log_likelihood	AIC	LRT	df	P-value
<none>	9	469.499	-920.999	NA	NA	NA
(1 Microbiome_Global:Population)	8	469.298	-922.596	0.403	1	0.526
(1 Nitrogen:Population)	8	467.268	-918.535	4.463	1	0.035
(1 Population)	8	468.582	-921.165	1.834	1	0.176
(1 Block)	8	461.985	-907.969	15.030	1	0.000

ICC for Random Effects

Table 34: Table of the effect sizes for the random effects in the Fixing Nodule Density M x N Model.

Term	ICC
Microbiome_Global:Population	0.012
Nitrogen:Population	0.042
Population	0.039
Block	0.032

Contrasts

```
fixing.nodule.density.M.emmeans <- emmeans(
  fixing.nodule.density.MN.global.LMM,
  specs = pairwise ~ Microbiome_Global,
  weights = "cells",
  adjust = "none"
)

fixing.nodule.density.N.emmeans <- emmeans(
  fixing.nodule.density.MN.global.LMM,
  specs = pairwise ~ Nitrogen,
  weights = "cells",
  adjust = "none"
)

fixing.nodule.density.MxN.emmeans <- emmeans(
  fixing.nodule.density.MN.global.LMM,
  specs = pairwise ~ Microbiome_Global | Nitrogen,
  weights = "cells",
  adjust = "none"
)
```

Table 35: Post-hoc comparisons of the main effect of Microbiome Global in the Fixing Nodule Density ANOVA.

Term	Contrast	Null Value	Estimate	SE	df	t	P
Microbiome_Global	Local - Nonlocal_Global	0	0.053	0.011	29.103	5.063	0

Table 36: Post-hoc comparisons of the main effect of Nitrogen in the Fixing Nodule Density ANOVA.

Term	Contrast	Null Value	Estimate	SE	df	t	P
Nitrogen	Ambient_N - N_Addition	0	0.029	0.012	27.912	2.413	0.023

Table 37: Post-hoc comparisons of the interaction between Microbiome Global and Nitrogen in the Fixing Nodule Density ANOVA.

Factor_1	Factor_2	Contrast	Null Value	Estimate	SE	df	t	P
Ambient_N	Microbiome_Global	Local - Nonlocal_Global	0	0.062	0.014	96.076	4.281	0.000
N_Addition	Microbiome_Global	Local - Nonlocal_Global	0	0.046	0.014	95.137	3.181	0.002

Contrasts (Effect Sizes)

Table 38: Effect sizes for the constrasts by Microbiome Global in the Fixing Nodule Density ANOVA.

Contrast	Cohen's d	SE	df	CI Lower	CI Upper
(Local - Nonlocal_Global)	0.407	0.081	29.103	0.242	0.573

Table 39: Effect sizes for the constrasts by Nitrogen in the Fixing Nodule Density ANOVA.

Contrast	Cohen's d	SE	df	CI Lower	CI Upper
(Ambient_N - N_Addition)	0.218	0.09	27.912	0.033	0.403

Table 40: Effect sizes for the constrasts by Microbiome Global and Nitrogen in theFixing Nodule Density ANOVA.

Contrast	Nitrogen	Cohen's d	SE	df	CI Lower	CI Upper
(Local - Nonlocal_Global)	Ambient_N	0.469	0.11	96.076	0.25	0.688
(Local - Nonlocal_Global)	N_Addition	0.347	0.11	95.137	0.13	0.565

Supplementary: Estimated Marginal Means

Aboveground Biomass $M \times N$ Model

Table 41: Estimated marginal means of the main effect of Microbiome Global in the Aboveground Biomass ANOVA.

Microbiome_Global	Estimate	SE	df	t	P
Local	0.335	0.017	49.138	19.443	0
Nonlocal_Global	0.306	0.016	36.111	19.208	0

Table 42: Estimated marginal means of the main effect of Nitrogen in the Aboveground Biomass ANOVA.

Nitrogen	Estimate	SE	df	t	P
Ambient_N	0.224	0.016	40.118	13.770	0
N_Addition	0.405	0.016	40.151	24.834	0

Table 43: Estimated marginal means of the interaction between Microbiome Global and Nitrogen in the Aboveground Biomass ANOVA.

Microbiome_Global	Nitrogen	Estimate	SE	df	t	P
Local	Ambient_N	0.239	0.020	83.457	11.967	0
Nonlocal_Global	Ambient_N	0.218	0.018	51.690	12.349	0
Local	N_Addition	0.430	0.020	82.762	21.582	0
Nonlocal_Global	N_Addition	0.393	0.018	51.756	22.278	0

Belowground Biomass $M \times N$ Model

Table 44: Estimated marginal means of the main effect of Microbiome Global in the Belowground Biomass ANOVA.

Microbiome_Global	Estimate	SE	df	t	P
Local	0.276	0.011	43.229	26.172	0
Nonlocal_Global	0.267	0.009	27.914	28.154	0

Table 45: Estimated marginal means of the main effect of Nitrogen in the Belowground Biomass ANOVA.

Nitrogen	Estimate	SE	df	t	P
Ambient_N	0.196	0.01	32.576	19.962	0
N_Addition	0.343	0.01	32.556	34.839	0

Table 46: Estimated marginal means of the interaction between Microbiome Global and Nitrogen in the Belowground Biomass ANOVA.

Microbiome_Global	Nitrogen	Estimate	SE	df	t	P
Local	Ambient_N	0.206	0.012	81.971	16.526	0
Nonlocal_Global	Ambient_N	0.192	0.011	42.377	18.251	0
Local	N_Addition	0.347	0.012	81.212	27.877	0
Nonlocal_Global	N_Addition	0.341	0.011	42.376	32.421	0

Nodule Density $M \times N$ Model

Table 47: Estimated marginal means of the main effect of Microbiome Global in the Nodule Density ANOVA.

Microbiome_Global	Estimate	SE	df	t	P
Local	0.389	0.020	68.286	19.532	0
Nonlocal_Global	0.303	0.016	30.201	18.818	0

Table 48: Estimated marginal means of the main effect of Nitrogen in the Nodule Density ANOVA.

Nitrogen	Estimate	SE	df	t	P
Ambient_N	0.364	0.017	41.516	20.900	0
N_Addition	0.298	0.017	41.579	17.059	0

Table 49: Estimated marginal means of the interaction between Microbiome Global and Nitrogen in the Nodule Density ANOVA.

Microbiome_Global	Nitrogen	Estimate	SE	df	t	P
Local	Ambient_N	0.408	0.026	134.888	15.696	0
Nonlocal_Global	Ambient_N	0.343	0.020	62.361	17.292	0
Local	N_Addition	0.371	0.026	132.079	14.303	0
Nonlocal_Global	N_Addition	0.263	0.020	62.752	13.158	0

Fixing Nodule Density $M \times N$ Model

Table 50: Estimated marginal means of the main effect of Microbiome Global in the Fixing Nodule Density ANOVA.

Microbiome_Global	Estimate	SE	df	t	P
Local	0.178	0.014	27.173	13.154	0
Nonlocal_Global	0.124	0.012	18.445	10.140	0

Table 51: Estimated marginal means of the main effect of Nitrogen in the Fixing Nodule Density ANOVA.

Nitrogen	Estimate	SE	df	t	P
Ambient_N	0.156	0.013	23.574	11.931	0
N_Addition	0.128	0.013	23.531	9.749	0

Table 52: Estimated marginal means of the interaction between Microbiome Global and Nitrogen in the Fixing Nodule Density ANOVA.

Microbiome_Global	Nitrogen	Estimate	SE	df	t	P
Local	Ambient_N	0.198	0.016	53.412	12.223	0
Nonlocal_Global	Ambient_N	0.136	0.014	30.084	9.738	0
Local	N_Addition	0.158	0.016	52.626	9.819	0
Nonlocal_Global	N_Addition	0.113	0.014	30.127	8.050	0

Export Data

```
## Export the aboveground biomass LMM
write_rds(
  aboveground.biomass.MN.global.LMM,
  file = "data/aboveground_biomass_MN_global_LMM.rds"
)

## Export the belowground biomass LMM
write_rds(
  belowground.biomass.MN.global.LMM,
  file = "data/belowground_biomass_MN_global_LMM.rds"
)

## Export the nodule density LMM
write_rds(
  nodule.density.MN.global.LMM,
  file = "data/nodule_density_MN_global_LMM.rds"
)

## Export the fixing nodule density LMM
write_rds(
  fixing.nodule.density.MN.global.LMM,
  file = "data/fixing_nodule_density_MN_global_LMM.rds"
)
```

R Session Information

Table 53: Packages required for data management and analysis.

Package	Loaded Version	Date
bayestestR	0.13.1	2023-04-07
broom	1.0.5	2023-06-09
correlation	0.8.4	2023-04-06
datawizard	0.8.0	2023-06-16
dplyr	1.1.2	2023-04-20
easystats	0.6.0	2022-11-29
effectsize	0.8.3	2023-01-28
emmeans	1.8.7	2023-06-23
forcats	1.0.0	2023-01-29
ggplot2	3.4.2	2023-04-03
insight	0.19.3	2023-06-29
kableExtra	1.3.4	2021-02-20
knitr	1.43	2023-05-25
lme4	1.1-34	2023-07-04
lmerTest	3.1-3	2020-10-23
lubridate	1.9.2	2023-02-10
Matrix	1.6-0	2023-07-08
modelbased	0.8.6	2023-01-13
parameters	0.21.1	2023-05-26
performance	0.10.4	2023-06-02
purrr	1.0.1	2023-01-10
readr	2.1.4	2023-02-10
report	0.5.7	2023-03-22
see	0.8.0	2023-06-05
stringr	1.5.0	2022-12-02
tibble	3.2.1	2023-03-20
tidyr	1.3.0	2023-01-24
tidyverse	2.0.0	2023-02-22