

TRhizo-localAdaptation

Microbiome x Nitrogen Global Model Fitting

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Load Packages & Data

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

## Packages for analysis
library(AICcmodavg)
library(broom)
library(easystats)
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_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/M_x_N-global_model_fitting-workspace.RData")
```

Aboveground Biomass

Aboveground Biomass M x N Model 1

```
aboveground.biomass.MN.LMM.1 <- 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 Aboveground Biomass M x N Model 1 Assumptions

```
## Check model convergence  
check_convergence(aboveground.biomass.MN.LMM.1)  
# Model converged  
  
## Check for boundary singularity  
check_singularity(aboveground.biomass.MN.LMM.1)  
# No singularity  
  
## Visual assessment of model diagnostics  
check_model(aboveground.biomass.MN.LMM.1)  
# Visual check = assumptions met  
  
## Check normality of fixed effects (Shapiro-Wilk test)  
check_normality(aboveground.biomass.MN.LMM.1, 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.LMM.1, 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.LMM.1)  
# Heteroscedasticity (non-constant error variance) detected (P < 0.001)  
  
## Check for homogeneity of variance (Bartlett test)  
check_homogeneity(aboveground.biomass.MN.LMM.1)  
# Variances differ between groups (P < 0.001)  
  
## Check for outliers
```

```
check_outliers(aboveground.biomass.MN.LMM.1)  
# 2 outliers detected
```

Aboveground Biomass M x N Model 2

```
aboveground.biomass.MN.LMM.2 <- lmer(  
  sqrt(Aboveground_Biomass) ~ Microbiome_Global * Nitrogen  
  + (Microbiome_Global | Population)  
  + (Nitrogen | Population)  
  + (Microbiome_Global:Nitrogen | Population)  
  + (1 | Population)  
  + (1 | Block),  
  data = biomass.data,  
  REML = TRUE  
)
```

Check Aboveground Biomass M x N Model 2 Assumptions

```
## Check model convergence  
check_convergence(aboveground.biomass.MN.LMM.2)  
# Model failed to converge  
  
## Check for boundary singularity  
check_singularity(aboveground.biomass.MN.LMM.2)  
# Singularity  
  
## Visual assessment of model diagnostics  
check_model(aboveground.biomass.MN.LMM.2)  
# Visual check = assumptions met  
  
## Check normality of fixed effects (Shapiro-Wilk test)  
check_normality(aboveground.biomass.MN.LMM.2, 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.LMM.2, effects = "random")  
# M:P = Bad  
# N:P = Baf  
# M:N:P = Bad  
# P = Bad  
# B = Good  
  
## Check for non-constant variance of residuals (Breusch-Pagan test)  
check_heteroscedasticity(aboveground.biomass.MN.LMM.2)  
# Heteroscedasticity (non-constant error variance) detected (P < 0.001)  
  
## Check for homogeneity of variance (Bartlett test)  
check_homogeneity(aboveground.biomass.MN.LMM.2)  
# Variances differ between groups (P < 0.001)  
  
## Check for outliers  
check_outliers(aboveground.biomass.MN.LMM.2)  
# 3 outliers detected
```

Aboveground Biomass M x N Model 3

```
aboveground.biomass.MN.LMM.3 <- lmer(  
  sqrt(Aboveground_Biomass) ~ Microbiome_Global * Nitrogen  
  + (1 | Population)  
  + (1 | Block),  
  data = biomass.data,  
  REML = TRUE  
)
```

Check Aboveground Biomass M x N Model 3 Assumptions

```
## Check model convergence  
check_convergence(aboveground.biomass.MN.LMM.3)  
# Model converged  
  
## Check for boundary singularity  
check_singularity(aboveground.biomass.MN.LMM.3)  
# No singularity  
  
## Visual assessment of model diagnostics  
check_model(aboveground.biomass.MN.LMM.3)  
# Visual check = assumptions met  
  
## Check normality of fixed effects (Shapiro-Wilk test)  
check_normality(aboveground.biomass.MN.LMM.3, 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.LMM.3, effects = "random")  
# P = Good  
# B = Good  
  
## Check for non-constant variance of residuals (Breusch-Pagan test)  
check_heteroscedasticity(aboveground.biomass.MN.LMM.3)  
# Heteroscedasticity (non-constant error variance) detected (P < 0.001)  
  
## Check for homogeneity of variance (Bartlett test)  
check_homogeneity(aboveground.biomass.MN.LMM.3)  
# Variances differ between groups (P < 0.001)  
  
## Check for outliers  
check_outliers(aboveground.biomass.MN.LMM.3)  
# No outliers detected
```

Aboveground Biomass M x N Model Comparisons

Table 1: AIC table comparing candidate Aboveground Biomass M x N Models 1-3.

	Model	K	AICc	Delta_AICc	Model_Likelihood	AICc_Weight	Residual_LL	Summed_Weight
1	MN_Model_1	10	-679.088	0.000	1.000	0.807	349.677	0.807
3	MN_Model_3	7	-676.227	2.861	0.239	0.193	345.181	1.000
2	MN_Model_2	28	-653.067	26.021	0.000	0.000	355.535	1.000

Aboveground Biomass M x N Model 1 Subsets

Aboveground Biomass M x N Model 1.1

```
## Remove (1 | Microbiome_Global:Nitrogen:Population)
aboveground.biomass.MN.LMM.1.1 <- lmer(
  sqrt(Aboveground_Biomass) ~ Microbiome_Global * Nitrogen
  + (1 | Microbiome_Global:Population)
  + (1 | Nitrogen:Population)
  + (1 | Population)
  + (1 | Block),
  data = biomass.data,
  REML = TRUE
)
```

Check Aboveground Biomass M x N Model 1.1 Assumptions

```
## Check model convergence
check_convergence(aboveground.biomass.MN.LMM.1.1)
# Model converged

## Check for boundary singularity
check_singularity(aboveground.biomass.MN.LMM.1.1)
# No singularity

## Visual assessment of model diagnostics
check_model(aboveground.biomass.MN.LMM.1.1)
# Visual check = assumptions met

## Check normality of fixed effects (Shapiro-Wilk test)
check_normality(aboveground.biomass.MN.LMM.1.1, 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.LMM.1.1, effects = "random")
# M:P = Good
# N:P = Non-normality detected (P = 0.006)
# P = Good
# B = Good

## Check for non-constant variance of residuals (Breusch-Pagan test)
check_heteroscedasticity(aboveground.biomass.MN.LMM.1.1)
# Heteroscedasticity (non-constant error variance) detected (P < 0.001)

## Check for homogeneity of variance (Bartlett test)
check_homogeneity(aboveground.biomass.MN.LMM.1.1)
# Variances differ between groups (P < 0.001)

## Check for outliers
check_outliers(aboveground.biomass.MN.LMM.1.1)
# 2 outliers detected
```

Aboveground Biomass M x N Model 1.2

```
## Remove (1 | Microbiome_Global:Population) and (1 | Microbiome_Global:Nitrogen:Population)
aboveground.biomass.MN.LMM.1.2 <- lmer(
  sqrt(Aboveground_Biomass) ~ Microbiome_Global * Nitrogen
  + (1 | Nitrogen:Population)
  + (1 | Population)
  + (1 | Block),
  data = biomass.data,
  REML = TRUE
)
```

Check Aboveground Biomass M x N Model 1.2 Assumptions

```
## Check model convergence
check_convergence(aboveground.biomass.MN.LMM.1.2)
# Model converged

## Check for boundary singularity
check_singularity(aboveground.biomass.MN.LMM.1.2)
# No singularity

## Visual assessment of model diagnostics
check_model(aboveground.biomass.MN.LMM.1.2)
# Visual check = assumptions met

## Check normality of fixed effects (Shapiro-Wilk test)
check_normality(aboveground.biomass.MN.LMM.1.2, 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.LMM.1.2, effects = "random")
# N:P = Non-normality detected (P = 0.008)
# P = Good
# B = Good

## Check for non-constant variance of residuals (Breusch-Pagan test)
check_heteroscedasticity(aboveground.biomass.MN.LMM.1.2)
# Heteroscedasticity (non-constant error variance) detected (P < 0.001)

## Check for homogeneity of variance (Bartlett test)
check_homogeneity(aboveground.biomass.MN.LMM.1.2)
# Variances differ between groups (P < 0.001)

## Check for outliers
check_outliers(aboveground.biomass.MN.LMM.1.2)
# No outliers detected
```

Aboveground Biomass M x N Model 1.3

```
## Remove (1 | Nitrogen:Population) and (1 | Microbiome_Global:Nitrogen:Population)
aboveground.biomass.MN.LMM.1.3 <- lmer(
  sqrt(Aboveground_Biomass) ~ Microbiome_Global * Nitrogen
  + (1 | Microbiome_Global:Population)
  + (1 | Population)
  + (1 | Block),
  data = biomass.data,
  REML = TRUE
)
```

Check Aboveground Biomass M x N Model 1.3 Assumptions

```
## Check model convergence
check_convergence(aboveground.biomass.MN.LMM.1.3)
# Model converged

## Check for boundary singularity
check_singularity(aboveground.biomass.MN.LMM.1.3)
# No singularity

## Visual assessment of model diagnostics
check_model(aboveground.biomass.MN.LMM.1.3)
# Visual check = assumptions met

## Check normality of fixed effects (Shapiro-Wilk test)
check_normality(aboveground.biomass.MN.LMM.1.3, 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.LMM.1.3, effects = "random")
# M:P = Good
# P = Good
# B = Good

## Check for non-constant variance of residuals (Breusch-Pagan test)
check_heteroscedasticity(aboveground.biomass.MN.LMM.1.3)
# Heteroscedasticity (non-constant error variance) detected (P < 0.001)

## Check for homogeneity of variance (Bartlett test)
check_homogeneity(aboveground.biomass.MN.LMM.1.3)
# Variances differ between groups (P < 0.001)

## Check for outliers
check_outliers(aboveground.biomass.MN.LMM.1.3)
# No outliers detected
```

Aboveground Biomass M x N Comparisons-Focal Models & Subsets

Table 2: AIC table comparing candidate Aboveground Biomass M x N Model 3, Model 1, and Model 1 subsets (Aboveground Biomass M x N Models 1.1-1.3).

	Model	K	AICc	Delta_AICc	Model_Likelihood	AICc_Weight	Residual_LL	Summed_Weight
3	MN_Model_1.1	9	-681.136	0.000	1.000	0.504	349.677	0.504
2	MN_Model_1	10	-679.088	2.049	0.359	0.181	349.677	0.685
5	MN_Model_1.3	8	-679.062	2.075	0.354	0.179	347.617	0.863
4	MN_Model_1.2	8	-677.764	3.372	0.185	0.093	346.969	0.957
1	MN_Model_3	7	-676.227	4.909	0.086	0.043	345.181	1.000

Belowground Biomass

Belowground Biomass M x N Model 1

```
belowground.biomass.MN.LMM.1 <- lmer(  
  sqrt(Belowground_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 Belowground Biomass M x N Model 1 Assumptions

```
## Check model convergence  
check_convergence(belowground.biomass.MN.LMM.1)  
# Model converged  
  
## Check for boundary singularity  
check_singularity(belowground.biomass.MN.LMM.1)  
# No singularity  
  
## Visual assessment of model diagnostics  
check_model(belowground.biomass.MN.LMM.1)  
# Visual check = assumptions met  
  
## Check normality of fixed effects (Shapiro-Wilk test)  
check_normality(belowground.biomass.MN.LMM.1, 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.LMM.1, 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(belowground.biomass.MN.LMM.1)  
# Heteroscedasticity (non-constant error variance) detected (P < 0.001)  
  
## Check for homogeneity of variance (Bartlett test)  
check_homogeneity(belowground.biomass.MN.LMM.1)  
# Variances differ between groups (P < 0.001)  
  
## Check for outliers
```

```
check_outliers(belowground.biomass.MN.LMM.1)
# No outliers detected
```

Belowground Biomass M x N Model 2

```
belowground.biomass.MN.LMM.2 <- lmer(  
  sqrt(Belowground_Biomass) ~ Microbiome_Global * Nitrogen  
    + (Microbiome_Global | Population)  
    + (Nitrogen | Population)  
    + (Microbiome_Global:Nitrogen | Population)  
    + (1 | Population)  
    + (1 | Block),  
  data = biomass.data,  
  REML = TRUE  
)
```

Check Belowground Biomass M x N Model 2 Assumptions

```
## Check model convergence  
check_convergence(belowground.biomass.MN.LMM.2)  
# Model converged  
  
## Check for boundary singularity  
check_singularity(belowground.biomass.MN.LMM.2)  
# Singularity  
  
## Visual assessment of model diagnostics  
check_model(belowground.biomass.MN.LMM.2)  
# Visual check = assumptions met  
  
## Check normality of fixed effects (Shapiro-Wilk test)  
check_normality(belowground.biomass.MN.LMM.2, 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.LMM.2, 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(belowground.biomass.MN.LMM.2)  
# Heteroscedasticity (non-constant error variance) detected (P < 0.001)  
  
## Check for homogeneity of variance (Bartlett test)  
check_homogeneity(belowground.biomass.MN.LMM.2)  
# Variances differ between groups (P < 0.001)  
  
## Check for outliers  
check_outliers(belowground.biomass.MN.LMM.2)  
# No outliers detected
```

Belowground Biomass M x N Model 3

```
belowground.biomass.MN.LMM.3 <- lmer(  
  sqrt(Belowground_Biomass) ~ Microbiome_Global * Nitrogen  
  + (1 | Population)  
  + (1 | Block),  
  data = biomass.data,  
  REML = TRUE  
)
```

Check Belowground Biomass M x N Model 3 Assumptions

```
## Check model convergence  
check_convergence(belowground.biomass.MN.LMM.3)  
# Model converged  
  
## Check for boundary singularity  
check_singularity(belowground.biomass.MN.LMM.3)  
# No singularity  
  
## Visual assessment of model diagnostics  
check_model(belowground.biomass.MN.LMM.3)  
# Visual check = assumptions met  
  
## Check normality of fixed effects (Shapiro-Wilk test)  
check_normality(belowground.biomass.MN.LMM.3, 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.LMM.3, effects = "random")  
# P = Good  
# B = Good  
  
## Check for non-constant variance of residuals (Breusch-Pagan test)  
check_heteroscedasticity(belowground.biomass.MN.LMM.3)  
# Heteroscedasticity (non-constant error variance) detected (P < 0.001)  
  
## Check for homogeneity of variance (Bartlett test)  
check_homogeneity(belowground.biomass.MN.LMM.3)  
# Variances differ between groups (P < 0.001)  
  
## Check for outliers  
check_outliers(belowground.biomass.MN.LMM.3)  
# No outliers detected
```


Belowground Biomass M x N Model Comparisons

Table 3: AIC table comparing candidate Belowground Biomass M x N Models 1-3.

	Model	K	AICc	Delta_AICc	Model_Likelihood	AICc_Weight	Residual_LL	Summed_Weight
3	MN_Model_3	7	-1259.362	0.000	1.000	0.944	636.749	0.944
1	MN_Model_1	10	-1253.715	5.648	0.059	0.056	636.990	1.000
2	MN_Model_2	28	-1221.754	37.608	0.000	0.000	639.878	1.000

Nodule Density

Nodule Density M x N Model 1

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

Check Nodule Density M x N Model 1 Assumptions

```
## Check model convergence  
check_convergence(nodule.density.MN.LMM.1)  
# Model converged  
  
## Check for boundary singularity  
check_singularity(nodule.density.MN.LMM.1)  
# No singularity  
  
## Visual assessment of model diagnostics  
check_model(nodule.density.MN.LMM.1)  
# Visual check = assumptions met  
  
## Check normality of fixed effects (Shapiro-Wilk test)  
check_normality(nodule.density.MN.LMM.1, 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.LMM.1, 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.LMM.1)  
# Heteroscedasticity (non-constant error variance) detected (P < 0.001)  
  
## Check for homogeneity of variance (Bartlett test)  
check_homogeneity(nodule.density.MN.LMM.1)  
# Variances differ between groups (P < 0.001)  
  
## Check for outliers
```

```
check_outliers(nodule.density.MN.LMM.1)
# 1 outlier detected
```

Nodule Density M x N Model 2

```
nodule.density.MN.LMM.2 <- lmer(  
  log(Nodule_Density + 1) ~ Microbiome_Global * Nitrogen  
  + (Microbiome_Global | Population)  
  + (Nitrogen | Population)  
  + (Microbiome_Global:Nitrogen | Population)  
  + (1 | Population)  
  + (1 | Block),  
  data = nodule.data,  
  REML = TRUE  
)
```

Check Nodule Density M x N Model 2 Assumptions

```
## Check model convergence  
check_convergence(nodule.density.MN.LMM.2)  
# Model failed to converge  
  
## Check for boundary singularity  
check_singularity(nodule.density.MN.LMM.2)  
# Singularity  
  
## Visual assessment of model diagnostics  
check_model(nodule.density.MN.LMM.2)  
# Visual check = assumptions met  
  
## Check normality of fixed effects (Shapiro-Wilk test)  
check_normality(nodule.density.MN.LMM.2, 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.LMM.2, 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.LMM.2)  
# Heteroscedasticity (non-constant error variance) detected (P < 0.001)  
  
## Check for homogeneity of variance (Bartlett test)  
check_homogeneity(nodule.density.MN.LMM.2)  
# Variances differ between groups (P < 0.001)  
  
## Check for outliers  
check_outliers(nodule.density.MN.LMM.2)  
# 1 outlier detected
```

Nodule Density M x N Model 3

```
nodule.density.MN.LMM.3 <- lmer(  
  log(Nodule_Density + 1) ~ Microbiome_Global * Nitrogen  
  + (1 | Population)  
  + (1 | Block),  
  data = nodule.data,  
  REML = TRUE  
)
```

Check Nodule Density M x N Model 3 Assumptions

```
## Check model convergence  
check_convergence(nodule.density.MN.LMM.3)  
# Model converged  
  
## Check for boundary singularity  
check_singularity(nodule.density.MN.LMM.3)  
# No singularity  
  
## Visual assessment of model diagnostics  
check_model(nodule.density.MN.LMM.3)  
# Visual check = assumptions met  
  
## Check normality of fixed effects (Shapiro-Wilk test)  
check_normality(nodule.density.MN.LMM.3, 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.LMM.3, effects = "random")  
# P = Good  
# B = Good  
  
## Check for non-constant variance of residuals (Breusch-Pagan test)  
check_heteroscedasticity(nodule.density.MN.LMM.3)  
# Heteroscedasticity (non-constant error variance) detected (P < 0.001)  
  
## Check for homogeneity of variance (Bartlett test)  
check_homogeneity(nodule.density.MN.LMM.3)  
# Variances differ between groups (P < 0.001)  
  
## Check for outliers  
check_outliers(nodule.density.MN.LMM.3)  
# No outliers detected
```

Nodule Density M x N Model Comparisons

Table 4: AIC table comparing candidate Nodule Density M x N Models 1-3.

	Model	K	AICc	Delta_AICc	Model_Likelihood	AICc_Weight	Residual_LL	Summed_Weight
3	MN_Model_3	7	-151.427	0.000	1.000	0.754	82.781	0.754
1	MN_Model_1	10	-149.191	2.236	0.327	0.246	84.728	1.000
2	MN_Model_2	28	-118.612	32.815	0.000	0.000	88.306	1.000

Nodule Density M x N Model 1 Subsets

Nodule Density M x N Model 1.1

```
## Remove (1 | Microbiome_Global:Nitrogen:Population)
nodule.density.MN.LMM.1.1 <- lmer(
  log(Nodule_Density + 1) ~ Microbiome_Global * Nitrogen
  + (1 | Microbiome_Global:Population)
  + (1 | Nitrogen:Population)
  + (1 | Population)
  + (1 | Block),
  data = nodule.data,
  REML = TRUE
)
```

Check Nodule Density M x N Model 1.1 Assumptions

```
## Check model convergence
check_convergence(nodule.density.MN.LMM.1.1)
# Model converged

## Check for boundary singularity
check_singularity(nodule.density.MN.LMM.1.1)
# No singularity

## Visual assessment of model diagnostics
check_model(nodule.density.MN.LMM.1.1)
# Visual check = assumptions met

## Check normality of fixed effects (Shapiro-Wilk test)
check_normality(nodule.density.MN.LMM.1.1, 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.LMM.1.1, effects = "random")
# M:P = Good
# N:P = Good
# P = Good
# B = Good

## Check for non-constant variance of residuals (Breusch-Pagan test)
check_heteroscedasticity(nodule.density.MN.LMM.1.1)
# Heteroscedasticity (non-constant error variance) detected (P < 0.001)

## Check for homogeneity of variance (Bartlett test)
check_homogeneity(nodule.density.MN.LMM.1.1)
# Variances differ between groups (P < 0.001)

## Check for outliers
check_outliers(nodule.density.MN.LMM.1.1)
# 1 outlier detected
```

Nodule Density M x N Model 1.2

```
## Remove (1 | Microbiome_Global:Population) and (1 | Microbiome_Global:Nitrogen:Population)
nodule.density.MN.LMM.1.2 <- lmer(
  log(Nodule_Density + 1) ~ Microbiome_Global * Nitrogen
  + (1 | Nitrogen:Population)
  + (1 | Population)
  + (1 | Block),
  data = nodule.data,
  REML = TRUE
)
```

Check Nodule Density M x N Model 1.2 Assumptions

```
## Check model convergence
check_convergence(nodule.density.MN.LMM.1.2)
# Model converged

## Check for boundary singularity
check_singularity(nodule.density.MN.LMM.1.2)
# No singularity

## Visual assessment of model diagnostics
check_model(nodule.density.MN.LMM.1.2)
# Visual check = assumptions met

## Check normality of fixed effects (Shapiro-Wilk test)
check_normality(nodule.density.MN.LMM.1.2, 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.LMM.1.2, effects = "random")
# N:P = Good
# P = Good
# B = Good

## Check for non-constant variance of residuals (Breusch-Pagan test)
check_heteroscedasticity(nodule.density.MN.LMM.1.2)
# Heteroscedasticity (non-constant error variance) detected (P < 0.001)

## Check for homogeneity of variance (Bartlett test)
check_homogeneity(nodule.density.MN.LMM.1.2)
# Variances differ between groups (P < 0.001)

## Check for outliers
check_outliers(nodule.density.MN.LMM.1.2)
# No outliers detected
```


Nodule Density M x N Model 1.3

```
## Remove (1 | Nitrogen:Population) and (1 | Microbiome_Global:Nitrogen:Population)
nodule.density.MN.LMM.1.3 <- lmer(
  log(Nodule_Density + 1) ~ Microbiome_Global * Nitrogen
  + (1 | Microbiome_Global:Population)
  + (1 | Population)
  + (1 | Block),
  data = nodule.data,
  REML = TRUE
)
```

Check Nodule Density M x N Model 1.3 Assumptions

```
## Check model convergence
check_convergence(nodule.density.MN.LMM.1.3)
# Model converged

## Check for boundary singularity
check_singularity(nodule.density.MN.LMM.1.3)
# No singularity
```

```
## Visual assessment of model diagnostics
check_model(nodule.density.MN.LMM.1.3)
# Visual check = assumptions met

## Check normality of fixed effects (Shapiro-Wilk test)
check_normality(nodule.density.MN.LMM.1.3, 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.LMM.1.3, effects = "random")
# M:P = Good
# P = Good
# B = Good

## Check for non-constant variance of residuals (Breusch-Pagan test)
check_heteroscedasticity(nodule.density.MN.LMM.1.3)
# Heteroscedasticity (non-constant error variance) detected (P < 0.001)

## Check for homogeneity of variance (Bartlett test)
check_homogeneity(nodule.density.MN.LMM.1.3)
# Variances differ between groups (P < 0.001)

## Check for outliers
check_outliers(nodule.density.MN.LMM.1.3)
# No outliers detected
```

Nodule Density M x N Comparisons-Focal Models & Subsets

Table 5: AIC table comparing candidate Nodule Density M x N Model 3, Model 1, and Model 1 subsets (Nodule Density M x N Models 1.1-1.3).

	Model	K	AICc	Delta_AICc	Model_Likelihood	AICc_Weight	Residual_LL	Summed_Weight
4	MN_Model_1.2	8	-152.097	0.000	1.000	0.384	84.135	0.384
1	MN_Model_3	7	-151.427	0.670	0.715	0.274	82.781	0.658
3	MN_Model_1.1	9	-150.190	1.908	0.385	0.148	84.203	0.806
5	MN_Model_1.3	8	-149.495	2.602	0.272	0.104	82.834	0.910
2	MN_Model_1	10	-149.191	2.906	0.234	0.090	84.728	1.000

Fixing Nodule Density

Fixing Nodule Density M x N Model 1

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

Check Fixing Nodule Density M x N Model 1 Assumptions

```
## Check model convergence  
check_convergence(fixing.nodule.density.MN.LMM.1)  
# Model converged  
  
## Check for boundary singularity  
check_singularity(fixing.nodule.density.MN.LMM.1)  
# No singularity  
  
## Visual assessment of model diagnostics  
check_model(fixing.nodule.density.MN.LMM.1)  
# Visual check = assumptions met  
  
## Check normality of fixed effects (Shapiro-Wilk test)  
check_normality(fixing.nodule.density.MN.LMM.1, 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.LMM.1, effects = "random")  
# M:P = Good  
# N:P = Good  
# M: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.LMM.1)  
# Heteroscedasticity (non-constant error variance) detected (P < 0.001)  
  
## Check for homogeneity of variance (Bartlett test)  
check_homogeneity(fixing.nodule.density.MN.LMM.1)  
# Variances differ between groups (P < 0.001)  
  
## Check for outliers
```

```
check_outliers(fixing.nodule.density.MN.LMM.1)
# 1 outlier detected
```

Fixing Nodule Density M x N Model 2

```
fixing.nodule.density.MN.LMM.2 <- lmer(  
  log(Fixing_Nodule_Density + 1) ~ Microbiome_Global * Nitrogen  
  + (Microbiome_Global | Population)  
  + (Nitrogen | Population)  
  + (Microbiome_Global:Nitrogen | Population)  
  + (1 | Population)  
  + (1 | Block),  
  data = nodule.data,  
  REML = TRUE  
)
```

Check Fixing Nodule Density M x N Model 2 Assumptions

```
## Check model convergence  
check_convergence(fixing.nodule.density.MN.LMM.2)  
# Model failed to converge  
  
## Check for boundary singularity  
check_singularity(fixing.nodule.density.MN.LMM.2)  
# No singularity  
  
## Visual assessment of model diagnostics  
check_model(fixing.nodule.density.MN.LMM.2)  
# Visual check = assumptions met  
  
## Check normality of fixed effects (Shapiro-Wilk test)  
check_normality(fixing.nodule.density.MN.LMM.2, 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.LMM.2, effects = "random")  
# M:P = Bad  
# N:P = Bad  
# M:N:P = Bad  
# P = Good  
# B = Good  
  
## Check for non-constant variance of residuals (Breusch-Pagan test)  
check_heteroscedasticity(fixing.nodule.density.MN.LMM.2)  
# Heteroscedasticity (non-constant error variance) detected (P < 0.001)  
  
## Check for homogeneity of variance (Bartlett test)  
check_homogeneity(fixing.nodule.density.MN.LMM.2)  
# Variances differ between groups (P < 0.001)  
  
## Check for outliers  
check_outliers(fixing.nodule.density.MN.LMM.2)  
# 2 outliers detected
```

Fixing Nodule Density M x N Model 3

```
fixing.nodule.density.MN.LMM.3 <- lmer(  
  log(Fixing_Nodule_Density + 1) ~ Microbiome_Global * Nitrogen  
    + (1 | Population)  
    + (1 | Block),  
  data = nodule.data,  
  REML = TRUE  
)
```

Check Fixing Nodule Density M x N Model 3 Assumptions

```
## Check model convergence  
check_convergence(fixing.nodule.density.MN.LMM.3)  
# Model converged  
  
## Check for boundary singularity  
check_singularity(fixing.nodule.density.MN.LMM.3)  
# No singularity  
  
## Visual assessment of model diagnostics  
check_model(fixing.nodule.density.MN.LMM.3)  
# Visual check = assumptions met  
  
## Check normality of fixed effects (Shapiro-Wilk test)  
check_normality(fixing.nodule.density.MN.LMM.3, 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.LMM.3, effects = "random")  
# 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.LMM.3)  
# Heteroscedasticity (non-constant error variance) detected (P < 0.001)  
  
## Check for homogeneity of variance (Bartlett test)  
check_homogeneity(fixing.nodule.density.MN.LMM.3)  
# Variances differ between groups (P < 0.001)  
  
## Check for outliers  
check_outliers(fixing.nodule.density.MN.LMM.3)  
# 1 outlier detected
```

Fixing Nodule Density M x N Model Comparisons

Table 6: AIC table comparing candidate Fixing Nodule Density M x N Models 1-3.

	Model	K	AICc	Delta_AICc	Model_Likelihood	AICc_Weight	Residual_LL	Summed_Weight
3	MN_Model_3	7	-920.035	0.000	1.000	0.657	467.085	0.657
1	MN_Model_1	10	-918.735	1.300	0.522	0.343	469.500	1.000
2	MN_Model_2	28	-885.064	34.971	0.000	0.000	471.532	1.000

Fixing Nodule Density M x N Model 1 Subsets

Fixing Nodule Density M x N Model 1.1

```
## Remove (1 | Microbiome_Global:Nitrogen:Population)
fixing.nodule.density.MN.LMM.1.1 <- 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 Fixing Nodule Density M x N Model 1.1 Assumptions

```
## Check model convergence
check_convergence(fixing.nodule.density.MN.LMM.1.1)
# Model converged

## Check for boundary singularity
check_singularity(fixing.nodule.density.MN.LMM.1.1)
# No singularity

## Visual assessment of model diagnostics
check_model(fixing.nodule.density.MN.LMM.1.1)
# Visual check = assumptions met

## Check normality of fixed effects (Shapiro-Wilk test)
check_normality(fixing.nodule.density.MN.LMM.1.1, 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.LMM.1.1, 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.LMM.1.1)
# Heteroscedasticity (non-constant error variance) detected (P < 0.001)

## Check for homogeneity of variance (Bartlett test)
check_homogeneity(fixing.nodule.density.MN.LMM.1.1)
# Variances differ between groups (P < 0.001)

## Check for outliers
check_outliers(fixing.nodule.density.MN.LMM.1.1)
# 1 outlier detected
```


Fixing Nodule Density M x N Model 1.2

```
## Remove (1 | Microbiome_Global:Population) and (1 | Microbiome_Global:Nitrogen:Population)
fixing.nodule.density.MN.LMM.1.2 <- lmer(
  log(Fixing_Nodule_Density + 1) ~ Microbiome_Global * Nitrogen
  + (1 | Nitrogen:Population)
  + (1 | Population)
  + (1 | Block),
  data = nodule.data,
  REML = TRUE
)
```

Check Fixing Nodule Density M x N Model 1.2 Assumptions

```
## Check model convergence
check_convergence(fixing.nodule.density.MN.LMM.1.2)
# Model converged
```

```
## Check for boundary singularity
check_singularity(fixing.nodule.density.MN.LMM.1.2)
# No singularity
```

```
## Visual assessment of model diagnostics
check_model(fixing.nodule.density.MN.LMM.1.2)
# Visual check = assumptions met
```

```
## Check normality of fixed effects (Shapiro-Wilk test)
check_normality(fixing.nodule.density.MN.LMM.1.2, 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.LMM.1.2, effects = "random")
# 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.LMM.1.2)
# Heteroscedasticity (non-constant error variance) detected (P < 0.001)
```

```
## Check for homogeneity of variance (Bartlett test)
check_homogeneity(fixing.nodule.density.MN.LMM.1.2)
# Variances differ between groups (P < 0.001)
```

```
## Check for outliers
check_outliers(fixing.nodule.density.MN.LMM.1.2)
# 1 outlier detected
```

Fixing Nodule Density M x N Model 1.3

```
## Remove (1 | Nitrogen:Population) and (1 | Microbiome_Global:Nitrogen:Population)
fixing.nodule.density.MN.LMM.1.3 <- lmer(
  log(Fixing_Nodule_Density + 1) ~ Microbiome_Global * Nitrogen
  + (1 | Microbiome_Global:Population)
  + (1 | Population)
  + (1 | Block),
  data = nodule.data,
  REML = TRUE
)
```

Check Fixing Nodule Density M x N Model 1.3 Assumptions

```
## Check model convergence
check_convergence(fixing.nodule.density.MN.LMM.1.3)
# Model converged

## Check for boundary singularity
check_singularity(fixing.nodule.density.MN.LMM.1.3)
# No singularity
```

```
## Visual assessment of model diagnostics
check_model(fixing.nodule.density.MN.LMM.1.3)
# Visual check = assumptions met

## Check normality of fixed effects (Shapiro-Wilk test)
check_normality(fixing.nodule.density.MN.LMM.1.3, 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.LMM.1.3, effects = "random")
# M: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.LMM.1.3)
# Heteroscedasticity (non-constant error variance) detected (P < 0.001)

## Check for homogeneity of variance (Bartlett test)
check_homogeneity(fixing.nodule.density.MN.LMM.1.3)
# Variances differ between groups (P < 0.001)

## Check for outliers
check_outliers(fixing.nodule.density.MN.LMM.1.3)
# 1 outlier detected
```

Fixing Nodule Density M x N Comparisons-Focal Models & Subsets

Table 7: AIC table comparing candidate Fixing Nodule Density M x N Model 3, Model 1, and Model 1 subsets (Fixing Nodule Density M x N Models 1.1-1.3).

	Model	K	AICc	Delta_AICc	Model_Likelihood	AICc_Weight	Residual_LL	Summed_Weight
4	MN_Model_1.2	8	-922.423	0.000	1.000	0.492	469.298	0.492
3	MN_Model_1.1	9	-920.782	1.641	0.440	0.217	469.499	0.709
1	MN_Model_3	7	-920.035	2.388	0.303	0.149	467.085	0.858
2	MN_Model_1	10	-918.735	3.688	0.158	0.078	469.500	0.935
5	MN_Model_1.3	8	-918.362	4.061	0.131	0.065	467.268	1.000

R Session Information

Table 8: Packages required for data management and analysis.

Package	Loaded Version	Date
AICcmodavg	2.3-2	2023-03-20
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
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