TRhizo-localAdaptation
Local Adaptation Indices

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Contents

Load Packages & Data

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

## Packages for analysis
library(broom)
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")
```

Linear Mixed Effects Models

```r
## Aboveground biomass
aboveground.biomass.LA.LMM <- lmer(
  sqrt(Aboveground_Biomass) ~ Microbiome * Nitrogen
    + (1 | Microbiome:Population)
    + (1 | Nitrogen:Population)
    + (1 | Microbiome:Nitrogen:Population)
    + (1 | Population)
    + (1 | Block),
  data = biomass.data,
  REML = TRUE
)


## Belowground biomass
belowground.biomass.LA.LMM <- lmer(
  sqrt(Belowground_Biomass) ~ Microbiome * Nitrogen
    + (1 | Microbiome:Population)
    + (1 | Nitrogen:Population)
    + (1 | Microbiome:Nitrogen:Population)
    + (1 | Population)
    + (1 | Block),
  data = biomass.data,
  REML = TRUE
)


## Nodule density
nodule.density.LA.LMM <- lmer(
  log(Nodule_Density + 1) ~ Microbiome * Nitrogen
    + (1 | Microbiome:Population)
    + (1 | Nitrogen:Population)
    + (1 | Microbiome:Nitrogen:Population)
    + (1 | Population)
    + (1 | Block),
  data = nodule.data,
  REML = TRUE
)


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

Best Linear Unbiased Predictors (BLUPs)

```r
## Set the calculate_MxNxP_BLUPs function
calculate_MxNxP_BLUPs <- function(lme4_model) {
  ranef(lme4_model)$`Microbiome:Nitrogen:Population` %>%
    tibble::rownames_to_column("Microbiome_Nitrogen_Population") %>%
    dplyr::rename(Estimate = 2)
}


## Aboveground biomass
aboveground.biomass.uncleaned.BLUPs <- calculate_MxNxP_BLUPs(
  aboveground.biomass.LA.LMM
) %>%
  separate(
    col = Microbiome_Nitrogen_Population,
    c("Microbiome", "Nitrogen", "Population"),
    sep = ":"
  )


## Belowground biomass
belowground.biomass.uncleaned.BLUPs <- calculate_MxNxP_BLUPs(
  belowground.biomass.LA.LMM
) %>%
  separate(
    col = Microbiome_Nitrogen_Population,
    c("Microbiome", "Nitrogen", "Population"),
    sep = ":"
  )


## Nodule density
nodule.density.uncleaned.BLUPs <- calculate_MxNxP_BLUPs(
  nodule.density.LA.LMM
) %>%
  separate(
    col = Microbiome_Nitrogen_Population,
    c("Microbiome", "Nitrogen", "Population"),
    sep = ":"
  )


## Fixing nodule density
fixing.nodule.density.uncleaned.BLUPs <- calculate_MxNxP_BLUPs(
  fixing.nodule.density.LA.LMM
) %>%
  separate(
    col = Microbiome_Nitrogen_Population,
    c("Microbiome", "Nitrogen", "Population"),
    sep = ":"
  )
```

Measures of Local Adaptation

Data Management

```r
## Add re-coded Microbiome_Global to calculate global nonlocal effects
# Aboveground biomass
aboveground.biomass.uncleaned.BLUPs$Microbiome_Global <- (
  if_else(aboveground.biomass.uncleaned.BLUPs$Microbiome == "Local", "Local", "Nonlocal_Global")
)

# Belowground biomass
belowground.biomass.uncleaned.BLUPs$Microbiome_Global <- (
  if_else(belowground.biomass.uncleaned.BLUPs$Microbiome == "Local", "Local", "Nonlocal_Global")
)

# Nodule density
nodule.density.uncleaned.BLUPs$Microbiome_Global <- (
  if_else(nodule.density.uncleaned.BLUPs$Microbiome == "Local", "Local", "Nonlocal_Global")
)

# Fixing nodule density
fixing.nodule.density.uncleaned.BLUPs$Microbiome_Global <- (
  if_else(fixing.nodule.density.uncleaned.BLUPs$Microbiome == "Local", "Local", "Nonlocal_Global")
)
```

Aboveground Biomass LA Indices

```r
## Local - Nonlocal_Global
aboveground.biomass.LA.global.data <- aboveground.biomass.uncleaned.BLUPs %>%
  select(Population, Microbiome_Global, Nitrogen, Estimate) %>%
  group_by(Population, Microbiome_Global, Nitrogen) %>%
  summarise(AG_Biomass = mean(Estimate), .groups = "keep") %>%
  pivot_wider(names_from = Microbiome_Global, values_from = AG_Biomass) %>%
  mutate(AG_Biomass_LA_Global = Local - Nonlocal_Global) %>%
  ungroup()

## Local - Nonlocal_Rural
aboveground.biomass.LA.rural.data <- aboveground.biomass.uncleaned.BLUPs %>%
  select(Population, Microbiome, Nitrogen, Estimate) %>%
  filter(Microbiome != "Nonlocal_U") %>%
  group_by(Population, Microbiome, Nitrogen) %>%
  summarise(AG_Biomass = mean(Estimate), .groups = "keep") %>%
  pivot_wider(names_from = Microbiome, values_from = AG_Biomass) %>%
  mutate(AG_Biomass_LA_Rural = Local - Nonlocal_R) %>%
  ungroup()

## Local - Nonlocal_Urban
aboveground.biomass.LA.urban.data <- aboveground.biomass.uncleaned.BLUPs %>%
  select(Population, Microbiome, Nitrogen, Estimate) %>%
  filter(Microbiome != "Nonlocal_R") %>%
  group_by(Population, Microbiome, Nitrogen) %>%
  summarise(AG_Biomass = mean(Estimate), .groups = "keep") %>%
  pivot_wider(names_from = Microbiome, values_from = AG_Biomass) %>%
  mutate(AG_Biomass_LA_Urban = Local - Nonlocal_U) %>%
  ungroup()
```

Belowground Biomass LA Indices

```r
## Local - Nonlocal_Global
belowground.biomass.LA.global.data <- belowground.biomass.uncleaned.BLUPs %>%
  select(Population, Microbiome_Global, Nitrogen, Estimate) %>%
  group_by(Population, Microbiome_Global, Nitrogen) %>%
  summarise(BG_Biomass = mean(Estimate), .groups = "keep") %>%
  pivot_wider(names_from = Microbiome_Global, values_from = BG_Biomass) %>%
  mutate(BG_Biomass_LA_Global = Local - Nonlocal_Global) %>%
  ungroup()

## Local - Nonlocal_Rural
belowground.biomass.LA.rural.data <- belowground.biomass.uncleaned.BLUPs %>%
  select(Population, Microbiome, Nitrogen, Estimate) %>%
  filter(Microbiome != "Nonlocal_U") %>%
  group_by(Population, Microbiome, Nitrogen) %>%
  summarise(BG_Biomass = mean(Estimate), .groups = "keep") %>%
  pivot_wider(names_from = Microbiome, values_from = BG_Biomass) %>%
  mutate(BG_Biomass_LA_Rural = Local - Nonlocal_R) %>%
  ungroup()

## Local - Nonlocal_Urban
belowground.biomass.LA.urban.data <- belowground.biomass.uncleaned.BLUPs %>%
  select(Population, Microbiome, Nitrogen, Estimate) %>%
  filter(Microbiome != "Nonlocal_R") %>%
  group_by(Population, Microbiome, Nitrogen) %>%
  summarise(BG_Biomass = mean(Estimate), .groups = "keep") %>%
  pivot_wider(names_from = Microbiome, values_from = BG_Biomass) %>%
  mutate(BG_Biomass_LA_Urban = Local - Nonlocal_U) %>%
  ungroup()
```

Nodule Density LA Indices

```r
## Local - Nonlocal_Global
nodule.density.LA.global.data <- nodule.density.uncleaned.BLUPs %>%
  select(Population, Microbiome_Global, Nitrogen, Estimate) %>%
  group_by(Population, Microbiome_Global, Nitrogen) %>%
  summarise(Nod_Density = mean(Estimate), .groups = "keep") %>%
  pivot_wider(names_from = Microbiome_Global, values_from = Nod_Density) %>%
  mutate(Nod_Density_LA_Global = Local - Nonlocal_Global) %>%
  ungroup()

## Local - Nonlocal_Rural
nodule.density.LA.rural.data <- nodule.density.uncleaned.BLUPs %>%
  select(Population, Microbiome, Nitrogen, Estimate) %>%
  filter(Microbiome != "Nonlocal_U") %>%
  group_by(Population, Microbiome, Nitrogen) %>%
  summarise(Nod_Density = mean(Estimate), .groups = "keep") %>%
  pivot_wider(names_from = Microbiome, values_from = Nod_Density) %>%
  mutate(Nod_Density_LA_Rural = Local - Nonlocal_R) %>%
  ungroup()

## Local - Nonlocal_Urban
nodule.density.LA.urban.data <- nodule.density.uncleaned.BLUPs %>%
  select(Population, Microbiome, Nitrogen, Estimate) %>%
  filter(Microbiome != "Nonlocal_R") %>%
  group_by(Population, Microbiome, Nitrogen) %>%
  summarise(Nod_Density = mean(Estimate), .groups = "keep") %>%
  pivot_wider(names_from = Microbiome, values_from = Nod_Density) %>%
  mutate(Nod_Density_LA_Urban = Local - Nonlocal_U) %>%
  ungroup()
```

Fixing Nodule Density LA Indices

```
## Local - Nonlocal_Global
fixing.nodule.density.LA.global.data <- fixing.nodule.density.uncleaned.BLUPs %>%
  select(Population, Microbiome_Global, Nitrogen, Estimate) %>%
  group_by(Population, Microbiome_Global, Nitrogen) %>%
  summarise(Fix_Nod_Density = mean(Estimate), .groups = "keep") %>%
  pivot_wider(names_from = Microbiome_Global, values_from = Fix_Nod_Density) %>%
  mutate(Fix_Nod_Density_LA_Global = Local - Nonlocal_Global) %>%
  ungroup()

## Local - Nonlocal_Rural
fixing.nodule.density.LA.rural.data <- fixing.nodule.density.uncleaned.BLUPs %>%
  select(Population, Microbiome, Nitrogen, Estimate) %>%
  filter(Microbiome != "Nonlocal_U") %>%
  group_by(Population, Microbiome, Nitrogen) %>%
  summarise(Fix_Nod_Density = mean(Estimate), .groups = "keep") %>%
  pivot_wider(names_from = Microbiome, values_from = Fix_Nod_Density) %>%
  mutate(Fix_Nod_Density_LA_Rural = Local - Nonlocal_R) %>%
  ungroup()

## Local - Nonlocal_Urban
fixing.nodule.density.LA.urban.data <- fixing.nodule.density.uncleaned.BLUPs %>%
  select(Population, Microbiome, Nitrogen, Estimate) %>%
  filter(Microbiome != "Nonlocal_R") %>%
  group_by(Population, Microbiome, Nitrogen) %>%
  summarise(Fix_Nod_Density = mean(Estimate), .groups = "keep") %>%
  pivot_wider(names_from = Microbiome, values_from = Fix_Nod_Density) %>%
  mutate(Fix_Nod_Density_LA_Urban = Local - Nonlocal_U) %>%
  ungroup()
```

Correlation Matrices for Local Adaptation Indices

Local - Nonlocal$_{\text{Global}}$ Local Adaptation Correlation Matrix

```r
## Local - Nonlocal_Global data
# Subset local adaptation indices
aboveground.biomass.global <- aboveground.biomass.LA.global.data %>%
  select(Population, Nitrogen, AG_Biomass_LA_Global)
belowground.biomass.global <- belowground.biomass.LA.global.data %>%
  select(Population, Nitrogen, BG_Biomass_LA_Global)
nodule.density.global <- nodule.density.LA.global.data %>%
  select(Population, Nitrogen, Nod_Density_LA_Global)
fixing.nodule.density.global <- fixing.nodule.density.LA.global.data %>%
  select(Population, Nitrogen, Fix_Nod_Density_LA_Global)

# Combine the data
global.local.adaptation.correlation.data <- aboveground.biomass.LA.global.data %>%
  select(Population, Nitrogen) %>%
  left_join(aboveground.biomass.global, by = c("Population", "Nitrogen")) %>%
  left_join(belowground.biomass.global, by = c("Population", "Nitrogen")) %>%
  left_join(nodule.density.global, by = c("Population", "Nitrogen")) %>%
  left_join(fixing.nodule.density.global, by = c("Population", "Nitrogen")) %>%
  drop_na()
```

Local - Nonlocal~Rural~ Local Adaptation Correlation Matrix

```
## Local - Nonlocal_Rural data
# Subset local adaptation indices
aboveground.biomass.rural <- aboveground.biomass.LA.rural.data %>%
  select(Population, Nitrogen, AG_Biomass_LA_Rural)
belowground.biomass.rural <- belowground.biomass.LA.rural.data %>%
  select(Population, Nitrogen, BG_Biomass_LA_Rural)
nodule.density.rural <- nodule.density.LA.rural.data %>%
  select(Population, Nitrogen, Nod_Density_LA_Rural)
fixing.nodule.density.rural <- fixing.nodule.density.LA.rural.data %>%
  select(Population, Nitrogen, Fix_Nod_Density_LA_Rural)

# Combine the data
rural.local.adaptation.correlation.data <- aboveground.biomass.LA.rural.data %>%
  select(Population, Nitrogen) %>%
  left_join(aboveground.biomass.rural, by = c("Population", "Nitrogen")) %>%
  left_join(belowground.biomass.rural, by = c("Population", "Nitrogen")) %>%
  left_join(nodule.density.rural, by = c("Population", "Nitrogen")) %>%
  left_join(fixing.nodule.density.rural, by = c("Population", "Nitrogen")) %>%
  drop_na()
```

Local - Nonlocal$_{\text{Urban}}$ Local Adaptation Correlation Matrix

```r
## Local - Nonlocal_Urban data
# Subset local adaptation indices
aboveground.biomass.urban <- aboveground.biomass.LA.urban.data %>%
  select(Population, Nitrogen, AG_Biomass_LA_Urban)
belowground.biomass.urban <- belowground.biomass.LA.urban.data %>%
  select(Population, Nitrogen, BG_Biomass_LA_Urban)
nodule.density.urban <- nodule.density.LA.urban.data %>%
  select(Population, Nitrogen, Nod_Density_LA_Urban)
fixing.nodule.density.urban <- fixing.nodule.density.LA.urban.data %>%
  select(Population, Nitrogen, Fix_Nod_Density_LA_Urban)

# Combine the data
urban.local.adaptation.correlation.data <- aboveground.biomass.LA.urban.data %>%
  select(Population, Nitrogen) %>%
  left_join(aboveground.biomass.urban, by = c("Population", "Nitrogen")) %>%
  left_join(belowground.biomass.urban, by = c("Population", "Nitrogen")) %>%
  left_join(nodule.density.urban, by = c("Population", "Nitrogen")) %>%
  left_join(fixing.nodule.density.urban, by = c("Population", "Nitrogen")) %>%
  drop_na()
```

Export Data

R Session Information

Table 1: Packages required for data management and analysis.

Package	Loaded Version	Date
broom	1.0.5	2023-06-09
dplyr	1.1.2	2023-04-20
forcats	1.0.0	2023-01-29
ggplot2	3.4.2	2023-04-03
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
purrr	1.0.1	2023-01-10
readr	2.1.4	2023-02-10
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