TRhizo-localAdaptation
Cockerham's Test (Alternate)

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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")
```

Quantify Genetic Variation

Data Management

```r
## Aboveground biomass data
# Local | Ambient N
aboveground.biomass.local.ambient.N.data <- biomass.data %>%
  filter(Nitrogen == "Ambient_N") %>%
  select(Population, Microbiome, Block, Aboveground_Biomass) %>%
  filter(Microbiome == "Local")
# Rural | Ambient N
aboveground.biomass.rural.ambient.N.data <- biomass.data %>%
  filter(Nitrogen == "Ambient_N") %>%
  select(Population, Microbiome, Block, Aboveground_Biomass) %>%
  filter(Microbiome == "Nonlocal_R")
# Urban | Ambient N
aboveground.biomass.urban.ambient.N.data <- biomass.data %>%
  filter(Nitrogen == "Ambient_N") %>%
  select(Population, Microbiome, Block, Aboveground_Biomass) %>%
  filter(Microbiome == "Nonlocal_U")


# Local | N Addition
aboveground.biomass.local.N.addition.data <- biomass.data %>%
  filter(Nitrogen == "N_Addition") %>%
  select(Population, Microbiome, Block, Aboveground_Biomass) %>%
  filter(Microbiome == "Local")
# Rural | N Addition
aboveground.biomass.rural.N.addition.data <- biomass.data %>%
  filter(Nitrogen == "N_Addition") %>%
  select(Population, Microbiome, Block, Aboveground_Biomass) %>%
  filter(Microbiome == "Nonlocal_R")
# Urban | N Addition
aboveground.biomass.urban.N.addition.data <- biomass.data %>%
  filter(Nitrogen == "N_Addition") %>%
  select(Population, Microbiome, Block, Aboveground_Biomass) %>%
  filter(Microbiome == "Nonlocal_U")



## Nodule density
# Local | Ambient N
nodule.density.local.ambient.N.data <- nodule.data %>%
  filter(Nitrogen == "Ambient_N") %>%
  select(Population, Microbiome, Block, Nodule_Density) %>%
  filter(Microbiome == "Local")
# Rural | Ambient N
nodule.density.rural.ambient.N.data <- nodule.data %>%
  filter(Nitrogen == "Ambient_N") %>%
  select(Population, Microbiome, Block, Nodule_Density) %>%
  filter(Microbiome == "Nonlocal_R")
# Urban | Ambient N
nodule.density.urban.ambient.N.data <- nodule.data %>%
  filter(Nitrogen == "Ambient_N") %>%
  select(Population, Microbiome, Block, Nodule_Density) %>%
  filter(Microbiome == "Nonlocal_U")
```

```r
# Local | N Addition
nodule.density.local.N.addition.data <- nodule.data %>%
  filter(Nitrogen == "N_Addition") %>%
  select(Population, Microbiome, Block, Nodule_Density) %>%
  filter(Microbiome == "Local")
# Rural | N Addition
nodule.density.rural.N.addition.data <- nodule.data %>%
  filter(Nitrogen == "N_Addition") %>%
  select(Population, Microbiome, Block, Nodule_Density) %>%
  filter(Microbiome == "Nonlocal_R")
# Urban | N Addition
nodule.density.urban.N.addition.data <- nodule.data %>%
  filter(Nitrogen == "N_Addition") %>%
  select(Population, Microbiome, Block, Nodule_Density) %>%
  filter(Microbiome == "Nonlocal_U")


## Fixing nodule density data
# Local
fixing.nodule.density.local.data <- nodule.data %>%
  select(Population, Microbiome, Block, Fixing_Nodule_Density) %>%
  filter(Microbiome == "Local")
# Rural
fixing.nodule.density.rural.data <- nodule.data %>%
  select(Population, Microbiome, Block, Fixing_Nodule_Density) %>%
  filter(Microbiome == "Nonlocal_R")
# Urban
fixing.nodule.density.urban.data <- nodule.data %>%
  select(Population, Microbiome, Block, Fixing_Nodule_Density) %>%
  filter(Microbiome == "Nonlocal_U")
```

Aboveground Biomass

```r
## Aboveground biomass
# Ambient N | Local
aboveground.biomass.local.ambient.N.Vg.LMM <- lmer(
  sqrt(Aboveground_Biomass) ~ Block + (1 | Population),
  data = aboveground.biomass.local.ambient.N.data,
  REML = TRUE
)

aboveground.biomass.local.ambient.N.Vg.df <- data.frame(
  VarCorr(aboveground.biomass.local.ambient.N.Vg.LMM)
) %>%
  filter(grp == "Population") %>%
  add_column(Microbiome = "Local") %>%
  add_column(Nitrogen = "Ambient_N")

# Ambient N | Rural
aboveground.biomass.rural.ambient.N.Vg.LMM <- lmer(
  sqrt(Aboveground_Biomass) ~ Block + (1 | Population),
  data = aboveground.biomass.rural.ambient.N.data,
  REML = TRUE
)

aboveground.biomass.rural.ambient.N.Vg.df <- data.frame(
  VarCorr(aboveground.biomass.rural.ambient.N.Vg.LMM)
) %>%
  filter(grp == "Population") %>%
  add_column(Microbiome = "Rural") %>%
  add_column(Nitrogen = "Ambient_N")

# Ambient N | Urban
aboveground.biomass.urban.ambient.N.Vg.LMM <- lmer(
  sqrt(Aboveground_Biomass) ~ Block + (1 | Population),
  data = aboveground.biomass.urban.ambient.N.data,
  REML = TRUE
)

aboveground.biomass.urban.ambient.N.Vg.df <- data.frame(
  VarCorr(aboveground.biomass.urban.ambient.N.Vg.LMM)
) %>%
  filter(grp == "Population") %>%
  add_column(Microbiome = "Urban") %>%
  add_column(Nitrogen = "Ambient_N")


# N Addition | Local
aboveground.biomass.local.N.addition.Vg.LMM <- lmer(
  sqrt(Aboveground_Biomass) ~ Block + (1 | Population),
  data = aboveground.biomass.local.N.addition.data,
  REML = TRUE
)

aboveground.biomass.local.N.addition.Vg.df <- data.frame(
```

```r
  VarCorr(aboveground.biomass.local.N.addition.Vg.LMM)
) %>%
  filter(grp == "Population") %>%
  add_column(Microbiome = "Local") %>%
  add_column(Nitrogen = "N_Addition")

# N Addition | Rural
aboveground.biomass.rural.N.addition.Vg.LMM <- lmer(
  sqrt(Aboveground_Biomass) ~ Block + (1 | Population),
  data = aboveground.biomass.rural.N.addition.data,
  REML = TRUE
)

aboveground.biomass.rural.N.addition.Vg.df <- data.frame(
  VarCorr(aboveground.biomass.rural.N.addition.Vg.LMM)
) %>%
  filter(grp == "Population") %>%
  add_column(Microbiome = "Rural") %>%
  add_column(Nitrogen = "N_Addition")

# N Addition | Urban
aboveground.biomass.urban.N.addition.Vg.LMM <- lmer(
  sqrt(Aboveground_Biomass) ~ Block + (1 | Population),
  data = aboveground.biomass.urban.N.addition.data,
  REML = TRUE
)

aboveground.biomass.urban.N.addition.Vg.df <- data.frame(
  VarCorr(aboveground.biomass.urban.N.addition.Vg.LMM)
) %>%
  filter(grp == "Population") %>%
  add_column(Microbiome = "Urban") %>%
  add_column(Nitrogen = "N_Addition")
```

Nodule Density

```r
## Nodule density
# Ambient N | Local
nodule.density.local.ambient.N.Vg.LMM <- lmer(
  log(Nodule_Density + 1) ~ Block + (1 | Population),
  data = nodule.density.local.ambient.N.data,
  REML = TRUE
)

nodule.density.local.ambient.N.Vg.df <- data.frame(
  VarCorr(nodule.density.local.ambient.N.Vg.LMM)
) %>%
  filter(grp == "Population") %>%
  add_column(Microbiome = "Local") %>%
  add_column(Nitrogen = "Ambient_N")

# Ambient N | Rural
nodule.density.rural.ambient.N.Vg.LMM <- lmer(
  log(Nodule_Density + 1) ~ Block + (1 | Population),
  data = nodule.density.rural.ambient.N.data,
  REML = TRUE
)

nodule.density.rural.ambient.N.Vg.df <- data.frame(
  VarCorr(nodule.density.rural.ambient.N.Vg.LMM)
) %>%
  filter(grp == "Population") %>%
  add_column(Microbiome = "Rural") %>%
  add_column(Nitrogen = "Ambient_N")

# Ambient N | Urban
nodule.density.urban.ambient.N.Vg.LMM <- lmer(
  log(Nodule_Density + 1) ~ Block + (1 | Population),
  data = nodule.density.urban.ambient.N.data,
  REML = TRUE
)

nodule.density.urban.ambient.N.Vg.df <- data.frame(
  VarCorr(nodule.density.urban.ambient.N.Vg.LMM)
) %>%
  filter(grp == "Population") %>%
  add_column(Microbiome = "Urban") %>%
  add_column(Nitrogen = "Ambient_N")


# N Addition | Local
nodule.density.local.N.addition.Vg.LMM <- lmer(
  log(Nodule_Density + 1) ~ Block + (1 | Population),
  data = nodule.density.local.N.addition.data,
  REML = TRUE
)

nodule.density.local.N.addition.Vg.df <- data.frame(
```

```r
  VarCorr(nodule.density.local.N.addition.Vg.LMM)
) %>%
  filter(grp == "Population") %>%
  add_column(Microbiome = "Local") %>%
  add_column(Nitrogen = "N_Addition")

# N Addition | Rural
nodule.density.rural.N.addition.Vg.LMM <- lmer(
  log(Nodule_Density + 1) ~ Block + (1 | Population),
  data = nodule.density.rural.N.addition.data,
  REML = TRUE
)

nodule.density.rural.N.addition.Vg.df <- data.frame(
  VarCorr(nodule.density.rural.N.addition.Vg.LMM)
) %>%
  filter(grp == "Population") %>%
  add_column(Microbiome = "Rural") %>%
  add_column(Nitrogen = "N_Addition")

# N Addition | Urban
nodule.density.urban.N.addition.Vg.LMM <- lmer(
  log(Nodule_Density + 1) ~ Block + (1 | Population),
  data = nodule.density.urban.N.addition.data,
  REML = TRUE
)

nodule.density.urban.N.addition.Vg.df <- data.frame(
  VarCorr(nodule.density.urban.N.addition.Vg.LMM)
) %>%
  filter(grp == "Population") %>%
  add_column(Microbiome = "Urban") %>%
  add_column(Nitrogen = "N_Addition")
```

Fixing Nodule Density

```r
## Fixing nodule density
# Local
fixing.nodule.density.local.Vg.LMM <- lmer(
  log(Fixing_Nodule_Density + 1) ~ Block + (1 | Population),
  data = fixing.nodule.density.local.data,
  REML = TRUE
)

fixing.nodule.density.local.Vg.df <- data.frame(VarCorr(fixing.nodule.density.local.Vg.LMM)) %>%
  filter(grp == "Population") %>%
  add_column(Microbiome = "Local") %>%
  add_column(Nitrogen = "Combined")

# Rural
fixing.nodule.density.rural.Vg.LMM <- lmer(
  log(Fixing_Nodule_Density + 1) ~ Block + (1 | Population),
  data = fixing.nodule.density.rural.data,
  REML = TRUE
)

fixing.nodule.density.rural.Vg.df <- data.frame(VarCorr(fixing.nodule.density.rural.Vg.LMM)) %>%
  filter(grp == "Population") %>%
  add_column(Microbiome = "Rural") %>%
  add_column(Nitrogen = "Combined")

# Urban
fixing.nodule.density.urban.Vg.LMM <- lmer(
  log(Fixing_Nodule_Density + 1) ~ Block + (1 | Population),
  data = fixing.nodule.density.urban.data,
  REML = TRUE
)

fixing.nodule.density.urban.Vg.df <- data.frame(VarCorr(fixing.nodule.density.urban.Vg.LMM)) %>%
  filter(grp == "Population") %>%
  add_column(Microbiome = "Urban") %>%
  add_column(Nitrogen = "Combined")
```

Export Genetic Variation Data

```r
## Combine and export data for management in Excel in prep for Cockerham's test
# Bind aboveground biomass data
aboveground.biomass.combined.Vg.data <- bind_rows(
  aboveground.biomass.local.ambient.N.Vg.df,
  aboveground.biomass.rural.ambient.N.Vg.df,
  aboveground.biomass.urban.ambient.N.Vg.df,
  aboveground.biomass.local.N.addition.Vg.df,
  aboveground.biomass.rural.N.addition.Vg.df,
  aboveground.biomass.urban.N.addition.Vg.df
)


# Bind nodule density data
nodule.density.combined.Vg.data <- bind_rows(
  nodule.density.local.ambient.N.Vg.df,
  nodule.density.rural.ambient.N.Vg.df,
  nodule.density.urban.ambient.N.Vg.df,
  nodule.density.local.N.addition.Vg.df,
  nodule.density.rural.N.addition.Vg.df,
  nodule.density.urban.N.addition.Vg.df
)


# Bind fixing nodule density data
fixing.nodule.density.combined.Vg.data <- bind_rows(
  fixing.nodule.density.local.Vg.df,
  fixing.nodule.density.rural.Vg.df,
  fixing.nodule.density.urban.Vg.df
)


## Bind all data together
combined.Vg.data <- bind_rows(
  aboveground.biomass.combined.Vg.data,
  nodule.density.combined.Vg.data,
  fixing.nodule.density.combined.Vg.data
) %>%
  add_column(Trait = c(
    rep("Aboveground_Biomass", 6),
    rep("Nodule_Density", 6),
    rep("Fixing_Nodule_Density", 3)
  )) %>%
  select(Trait, Microbiome:Nitrogen, vcov) %>%
  rename(Vg = vcov)

## Export data to prepare for Cockerham's test
write_csv(combined.Vg.data, file = "data/cockerham_data_uncleaned-alternate.csv")
```

Genetic Correlations

Data Management

```r
## Format data to calculate correlations
full.data <- nodule.data %>%
  full_join(
    biomass.data %>% select(UID, Aboveground_Biomass),
    by = c("UID")
  ) %>%
  select(
    Population:Nitrogen, Aboveground_Biomass, Nodule_Density:Fixing_Nodule_Density
  ) %>%
  drop_na()

## Local by Rural data
local.by.rural.data <- full.data %>%
  filter(Microbiome != "Nonlocal_U") %>%
  group_by(Population, Microbiome) %>%
  select(-c(Aboveground_Biomass, Nodule_Density)) %>%
  summarise(
    Fix_Nod_Density = mean(Fixing_Nodule_Density),
    .groups = "keep"
  ) %>%
  ungroup() %>%
  drop_na() %>%
  pivot_wider(names_from = Microbiome, values_from = Fix_Nod_Density)

## Local by Urban data
local.by.urban.data <- full.data %>%
  filter(Microbiome != "Nonlocal_R") %>%
  group_by(Population, Microbiome) %>%
  select(-c(Aboveground_Biomass, Nodule_Density)) %>%
  summarise(
    Fix_Nod_Density = mean(Fixing_Nodule_Density),
    .groups = "keep"
  ) %>%
  ungroup() %>%
  drop_na() %>%
  pivot_wider(names_from = Microbiome, values_from = Fix_Nod_Density)

## Rural by Urban data
rural.by.urban.data <- full.data %>%
  filter(Microbiome != "Local") %>%
  group_by(Population, Microbiome) %>%
  select(-c(Aboveground_Biomass, Nodule_Density)) %>%
  summarise(
    Fix_Nod_Density = mean(Fixing_Nodule_Density),
    .groups = "keep"
  ) %>%
  ungroup() %>%
  drop_na() %>%
  pivot_wider(names_from = Microbiome, values_from = Fix_Nod_Density)
```

```r
## Aboveground biomass and nodule density data (N-treatment specific)
# Local by Rural data
local.by.rural.nitrogen.data <- full.data %>%
  filter(Microbiome != "Nonlocal_U") %>%
  group_by(Population, Microbiome, Nitrogen) %>%
  summarise(
    AG_Biomass = mean(Aboveground_Biomass),
    Nod_Density = mean(Nodule_Density),
    .groups = "keep"
  ) %>%
  ungroup() %>%
  pivot_wider(names_from = Microbiome:Nitrogen, values_from = AG_Biomass:Nod_Density) %>%
  drop_na()

# Local by Urban data
local.by.urban.nitrogen.data <- full.data %>%
  filter(Microbiome != "Nonlocal_R") %>%
  group_by(Population, Microbiome, Nitrogen) %>%
  summarise(
    AG_Biomass = mean(Aboveground_Biomass),
    Nod_Density = mean(Nodule_Density),
    .groups = "keep"
  ) %>%
  ungroup() %>%
  pivot_wider(names_from = Microbiome:Nitrogen, values_from = AG_Biomass:Nod_Density) %>%
  drop_na()

# Rural by Urban data
rural.by.urban.nitrogen.data <- full.data %>%
  filter(Microbiome != "Local") %>%
  group_by(Population, Microbiome, Nitrogen) %>%
  summarise(
    AG_Biomass = mean(Aboveground_Biomass),
    Nod_Density = mean(Nodule_Density),
    .groups = "keep"
  ) %>%
  ungroup() %>%
  pivot_wider(names_from = Microbiome:Nitrogen, values_from = AG_Biomass:Nod_Density) %>%
  drop_na()
```

Correlations

Fixing Nodule Density

Table 1: Fitness correlations between local and nonlocal-rural for fixing nodule density.

	Nonlocal_R	Local
Nonlocal_R	1.000	0.251
Local	0.251	1.000

Table 2: Fitness correlations between local and nonlocal-urban for fixing nodule density.

	Nonlocal_U	Local
Nonlocal_U	1.000	0.305
Local	0.305	1.000

Table 3: Fitness correlations between nonlocal-rural and nonlocal-urban for fixing nodule density.

	Nonlocal_R	Nonlocal_U
Nonlocal_R	1.000	-0.015
Nonlocal_U	-0.015	1.000

Aboveground Biomass & Nodule Density

Table 4: Fitness correlations between local and nonlocal-rural by nitrogen treatment for aboveground biomass and nodule density.

	AG_Biomass_Nonlocal_R_Ambient_N	AG_Biomass_Nonlocal_R_N_Addition	AG_Biomass_Local_Ambient_N	AG_Biomass_Local_N_Addition	Nod_Density_Nonlocal_R_Ambient_N	Nod_Density_Nonlocal_R_N_Addition	Nod_Density_Local_Ambient_N	Nod_Density_Local_N_Addition
AG_Biomass_Nonlocal_R_Ambient_N	1.000	0.384	0.558	0.206	-0.155	-0.192	-0.164	0.179
AG_Biomass_Nonlocal_R_N_Addition	0.384	1.000	0.615	0.447	-0.056	0.266	0.034	0.313
AG_Biomass_Local_Ambient_N	0.558	0.615	1.000	0.597	0.048	0.126	-0.091	0.331
AG_Biomass_Local_N_Addition	0.206	0.447	0.597	1.000	-0.044	0.061	-0.176	0.293
Nod_Density_Nonlocal_R_Ambient_N	-0.155	-0.056	0.048	-0.044	1.000	0.046	0.053	0.344
Nod_Density_Nonlocal_R_N_Addition	-0.192	0.266	0.126	0.061	0.046	1.000	0.044	0.311
Nod_Density_Local_Ambient_N	-0.164	0.034	-0.091	-0.176	0.053	0.044	1.000	0.127
Nod_Density_Local_N_Addition	0.179	0.313	0.331	0.293	0.344	0.311	0.127	1.000

Table 5: Fitness correlations between local and nonlocal-urban by nitrogen treatment for aboveground biomass and nodule density.

	AG_Biomass_Nonlocal_U_Ambient_N	AG_Biomass_Nonlocal_U_N_Addition	AG_Biomass_Local_Ambient_N	AG_Biomass_Local_N_Addition	Nod_Density_Nonlocal_U_Ambient_N	Nod_Density_Nonlocal_U_N_Addition	Nod_Density_Local_Ambient_N	Nod_Density_Local_N_Addition
AG_Biomass_Nonlocal_U_Ambient_N	1.000	0.379	0.301	0.220	0.134	0.394	0.231	0.513
AG_Biomass_Nonlocal_U_N_Addition	0.379	1.000	0.526	0.639	-0.010	0.424	-0.222	0.196
AG_Biomass_Local_Ambient_N	0.301	0.526	1.000	0.617	0.020	-0.009	-0.084	0.437
AG_Biomass_Local_N_Addition	0.220	0.639	0.617	1.000	-0.026	0.168	-0.178	0.298
Nod_Density_Nonlocal_U_Ambient_N	0.134	-0.010	0.020	-0.026	1.000	0.362	0.153	0.394
Nod_Density_Nonlocal_U_N_Addition	0.394	0.424	-0.009	0.168	0.362	1.000	0.011	0.254
Nod_Density_Local_Ambient_N	0.231	-0.222	-0.084	-0.178	0.153	0.011	1.000	0.120
Nod_Density_Local_N_Addition	0.513	0.196	0.437	0.298	0.394	0.254	0.120	1.000

Table 6: Fitness correlations between nonlocal-rural and nonlocal-urban by nitrogen treatment for aboveground biomass and nodule density.

	AG_Biomass_Nonlocal_R_Ambient_N	AG_Biomass_Nonlocal_R_N_Addition	AG_Biomass_Nonlocal_U_Ambient_N	AG_Biomass_Nonlocal_U_N_Addition	Nod_Density_Nonlocal_R_Ambient_N	Nod_Density_Nonlocal_R_N_Addition	Nod_Density_Nonlocal_U_Ambient_N	Nod_Density_Nonlocal_U_N_Addition
AG_Biomass_Nonlocal_R_Ambient_N	1.000	0.384	0.194	0.471	-0.108	-0.202	0.089	0.138
AG_Biomass_Nonlocal_R_N_Addition	0.384	1.000	0.416	0.591	-0.048	0.265	0.147	0.369
AG_Biomass_Nonlocal_U_Ambient_N	0.194	0.416	1.000	0.379	-0.124	0.145	0.134	0.394
AG_Biomass_Nonlocal_U_N_Addition	0.471	0.591	0.379	1.000	-0.218	0.069	-0.010	0.424
Nod_Density_Nonlocal_R_Ambient_N	-0.108	-0.048	-0.124	-0.218	1.000	0.084	-0.282	-0.189
Nod_Density_Nonlocal_R_N_Addition	-0.202	0.265	0.145	0.069	0.084	1.000	0.320	-0.050
Nod_Density_Nonlocal_U_Ambient_N	0.089	0.147	0.134	-0.010	-0.282	0.320	1.000	0.362
Nod_Density_Nonlocal_U_N_Addition	0.138	0.369	0.394	0.424	-0.189	-0.050	0.362	1.000

Cockerham's Test

```
## Cockerham data
cockerham.data <- read_csv(
  "data/cockerham_data_cleaned-alternate.csv",
  col_types = c("ffnnn"),
  show_col_types = FALSE
)
```

Set Functions

```
## Function for imperfect correlation (page 88, Cockerham 1963)
imperfect_correlation <- function(Vg1, Vg2, Rg) {
  out <- 2 * sqrt(Vg1) * sqrt(Vg2) * (1 - Rg)

  return(out)
}


## Function for heterogeneous variances (page 88, Cockerham 1963)
heterogeneous_variances <- function(Vg1, Vg2) {
  out <- ((sqrt(Vg1) - sqrt(Vg2))^2)

  return(out)
}


## Calculate imperfect correlation values for each row
cockerham.data$Crossing <- sapply(1:nrow(cockerham.data), FUN = function(r) {
  Vg1 <- cockerham.data$Vg1[r]
  Vg2 <- cockerham.data$Vg2[r]
  Rg <- cockerham.data$Rg[r]

  crossing.value <- imperfect_correlation(Vg1, Vg2, Rg)

  return(crossing.value)
})

## Calculate heterogeneous variance values for each row
cockerham.data$Heterogeneous_Variances <- sapply(1:nrow(cockerham.data), FUN = function(r) {
  Vg1 <- cockerham.data$Vg1[r]
  Vg2 <- cockerham.data$Vg2[r]

  heterogeneous.variance.value <- heterogeneous_variances(Vg1, Vg2)

  return(heterogeneous.variance.value)
})
```

Calculations for Cockerham's Test

Aboveground Biomass

```r
## Group by trait and calculate sum of imperfect correlation values
# Divide by number of environments*(number of environments - 1) as per Cockerham 1963
aboveground.biomass.crossing <- cockerham.data %>%
  filter(Trait == "Aboveground_Biomass") %>%
  summarise(Crossing_Sum = sum(Crossing) / (6 * (6 - 1)))

## Group by trait and calculate sum of heterogeneous variances values
# Divide by number of environments*(number of environments - 1) as per Cockerham 1963
aboveground.biomass.heterogeneous.variance <- cockerham.data %>%
  filter(Trait == "Aboveground_Biomass") %>%
  summarise(Hetero_Variance_Sum = sum(Heterogeneous_Variances) / (6 * (6 - 1)))

## Make tibble for aboveground biomass calculation
aboveground.biomass.cockerham.data <- tibble(
  Trait = "Aboveground_Biomass",
  aboveground.biomass.crossing,
  aboveground.biomass.heterogeneous.variance
) %>%
  mutate(Total_Variance = Crossing_Sum + Hetero_Variance_Sum) %>%
  mutate(Percent_Crossing = 100 * Crossing_Sum / Total_Variance)
```

Nodule Density

```r
## Group by trait and calculate sum of imperfect correlation values
# Divide by number of environments*(number of environments - 1) as per Cockerham 1963
nodule.density.crossing <- cockerham.data %>%
  filter(Trait == "Nodule_Density") %>%
  summarise(Crossing_Sum = sum(Crossing) / (6 * (6 - 1)))

## Group by trait and calculate sum of heterogeneous variances values
# Divide by number of environments*(number of environments - 1) as per Cockerham 1963
nodule.density.heterogeneous.variance <- cockerham.data %>%
  filter(Trait == "Nodule_Density") %>%
  summarise(Hetero_Variance_Sum = sum(Heterogeneous_Variances) / (6 * (6 - 1)))

## Make tibble for Nodule Density calculation
nodule.density.cockerham.data <- tibble(
  Trait = "Nodule_Density",
  nodule.density.crossing,
  nodule.density.heterogeneous.variance
) %>%
  mutate(Total_Variance = Crossing_Sum + Hetero_Variance_Sum) %>%
  mutate(Percent_Crossing = 100 * Crossing_Sum / Total_Variance)
```

Fixing Nodule Density

```r
## Group by trait and calculate sum of imperfect correlation values
# Divide by number of environments*(number of environments - 1) as per Cockerham 1963
fixing.nodule.density.crossing <- cockerham.data %>%
  filter(Trait == "Fixing_Nodule_Density") %>%
  summarise(Crossing_Sum = sum(Crossing) / (3 * (3 - 1)))

## Group by trait and calculate sum of heterogeneous variances values
# Divide by number of environments*(number of environments - 1) as per Cockerham 1963
fixing.nodule.density.heterogeneous.variance <- cockerham.data %>%
  filter(Trait == "Fixing_Nodule_Density") %>%
  summarise(Hetero_Variance_Sum = sum(Heterogeneous_Variances) / (3 * (3 - 1)))

## Make tibble for Nodule Density calculation
fixing.nodule.density.cockerham.data <- tibble(
  Trait = "Fixing_Nodule_Density",
  fixing.nodule.density.crossing,
  fixing.nodule.density.heterogeneous.variance
) %>%
  mutate(Total_Variance = Crossing_Sum + Hetero_Variance_Sum) %>%
  mutate(Percent_Crossing = 100 * Crossing_Sum / Total_Variance)
```

Results of Cockerham's Tests

Table 7: Results of Cockerham's test for aboveground biomass, nodule density, and fixing nodule density.

Trait	Crossing_Sum	Hetero_Variance_Sum	Total_Variance	Percent_Crossing
Aboveground_Biomass	0.00123	0.00013	0.00136	90.64643
Nodule_Density	0.00375	0.00057	0.00432	86.90567
Fixing_Nodule_Density	0.00190	0.00004	0.00194	97.87555

R Session Information

Table 8: 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