

Evaluating Changes in Morphophysiological Traits of Plant Communities Over Time Post

Abandonment of mining in the coal region of Brazil

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```

# Tabelas de contagem das características para o tempo 1 (3-10 anos)

#Origin
origem_1 <- c(266, 31)
o_categorias_1 <- c("Native", "Exotic")
o_tabela_1 <- data.frame(o_categorias_1, origem_1)

#Root
root_1 <- c(193, 115)
r_categorias_1 <- c("Pivot", "Fasciculated")
r_tabela_1 <- data.frame(r_categorias_1, root_1)

#Life form
Life_form_1 <- c(189, 55, 22, 20, 17)
LF_categorias_1 <- c("Herb", "Shrub", "Tree", "Sub-shrub", "Liana")
LF_tabela_1 <- data.frame(LF_categorias_1, Life_form_1)

#Photosynthetc mechanism
Photosynthetc_mechanism_1 <- c(222, 39)
PM_categorias_1 <- c("C3", "C4")
PM_tabela_1 <- data.frame(PM_categorias_1, Photosynthetc_mechanism_1)

#Life cycle
Life_cycle_1 <- c(203, 67)
LC_categorias_1 <- c("Perennial", "Annual")
LC_tabela_1 <- data.frame(LC_categorias_1, Life_cycle_1)

#Pollination
Pollination_1 <- c(108, 87, 58, 17, 1)
P_categorias_1 <- c("Entomophilia", "Anemophily", "Various", "Zoophilya",
  "Autophilya")
P_tabela_1 <- data.frame(P_categorias_1, Pollination_1)

#Seed dispersal
Seed_1 <- c(81, 75, 72)
S_categorias_1 <- c("Anemochory", "Zoochory", "Autochory")
S_tabela_1 <- data.frame(S_categorias_1, Seed_1)

```

```

# Chi-square test tempo 1 usando Pearson
chisq.test(origem_1)
chisq.test(root_1)
chisq.test(Life_form_1)
chisq.test(Photosynthetc_mechanism_1)
chisq.test(Life_cycle_1)
chisq.test(Pollination_1)
chisq.test(Seed_1)

###

# Tabela de contagem das carateristicas para o tempo 2 (11-25 anos)

#Origin
origem_2 <- c(171, 13)
o_categorias_2 <- c("Native", "Exotic")
o_tabela_2 <- data.frame(o_categorias_2, origem_2)

#Root
root_2 <- c(132, 51)
r_categorias_2 <- c("Pivot", "Fasciculated")
r_tabela_2 <- data.frame(r_categorias_2, root_2)

#Life form
Life_form_2 <- c(60, 66, 40, 8, 9)
LF_categorias_2 <- c("Herb", "Shrub", "Tree", "Sub-shrub", "Liana")
LF_tabela_2 <- data.frame(LF_categorias_2, Life_form_2)

#Photosynthetc mechanism
Photosynthetc_mechanism_2 <- c(138, 11, 5)
PM_categorias_2 <- c("C3", "C4", "CAM")
PM_tabela_2 <- data.frame(PM_categorias_2, Photosynthetc_mechanism_2)

#Life cycle
Life_cycle_2 <- c(147, 15)
LC_categorias_2 <- c("Perennial", "Annual")
LC_tabela_2 <- data.frame(LC_categorias_2, Life_cycle_2)

#Pollination

```

```

Pollination_2 <- c(61, 24, 38, 25, 4)
P_categorias_2 <- c("Entomophilia", "Anemophily", "Various", "Zoophilya",
                    "Autophilya")
P_tabela_2 <- data.frame(P_categorias_2, Pollination_2)
#Seed dispersal
Seed_2 <- c(52, 68, 11, 5)
S_categorias_2 <- c("Anemochory", "Zoochory", "Autochory", "Various")
S_tabela_2 <- data.frame(S_categorias_2, Seed_2)

# Chi-square test tempo 2 usando Pearson
chisq.test(origem_2)
chisq.test(root_2)
chisq.test(Life_form_2)
chisq.test(Photosynthetc_mechanism_2)
chisq.test(Life_cycle_2)
chisq.test(Pollination_2)
chisq.test(Seed_2)

#Tabela de contagem das carateristicas para o tempo 3 (26-40 anos)
#Origin
origem_3 <- c(101, 6)
o_categorias_3 <- c("Native", "Exotic")
o_tabela_3 <- data.frame(o_categorias_3, origem_3)
#Root
root_3 <- c(82, 25)
r_categorias_3 <- c("Pivot", "Fasciculated")
r_tabela_3 <- data.frame(r_categorias_3, root_3)
#Life form
Life_form_3 <- c(23, 38, 43, 4, 2)
LF_categorias_3 <- c("Herb", "Shrub", "Tree", "Sub-shrub", "Liana")
LF_tabela_3 <- data.frame(LF_categorias_3, Life_form_3)

```

```

#Photosynthetc mechanism
Photosynthetc_mechanism_3 <- c(93, 4)
PM_categorias_3 <- c("C3", "C4")
PM_tabela_3 <- data.frame(PM_categorias_3, Photosynthetc_mechanism_3)

#Life cycle
Life_cycle_3 <- c(82, 10)
LC_categorias_3 <- c("Perennial", "Annual")
LC_tabela_3 <- data.frame(LC_categorias_3, Life_cycle_3)

#Pollination
Pollination_3 <- c(41, 10, 15, 26)
P_categorias_3 <- c("Entomophilia", "Anemophily", "Various", "Zoophilya")
P_tabela_3 <- data.frame(P_categorias_3, Pollination_3)

#Seed dispersal
Seed_3 <- c(18, 57, 5, 2)
S_categorias_3 <- c("Anemochory", "Zoochory", "Autochory", "Various")
S_tabela_3 <- data.frame(S_categorias_3, Seed_3)


# Chi-square test tempo 1 usando Pearson
chisq.test(origem_3)
chisq.test(root_3)
chisq.test(Life_form_3)
chisq.test(Photosynthetc_mechanism_3)
chisq.test(Life_cycle_3)
chisq.test(Pollination_3)
chisq.test(Seed_3)


#Para os dados com mais de dois valores#####
# Todas as combinações par a par
combos <- combn(length(Seed_1), 2)

# Vetor para armazenar p-values

```

```

p_values <- numeric(ncol(combos))
comparacoes <- character(ncol(combos))

# Loop para testes par a par
for(i in 1:ncol(combos)){
  idx <- combos[,i]

  # Matriz 2x2 para teste de Fisher
  tabela <- matrix(c(
    Seed_1[idx[1]], Seed_1[idx[2]],      # contagens dos dois grupos
    sum(Seed_1) - Seed_1[idx[1]], sum(Seed_1) - Seed_1[idx[2]] # resto das espécies
  ), nrow = 2, byrow = TRUE)

  teste <- fisher.test(tabela)

  # Salvar resultados
  p_values[i] <- teste$p.value
  comparacoes[i] <- paste(S_categorias_1[idx[1]], "vs", S_categorias_1[idx[2]])
}

# Ajuste de p-valores (Bonferroni)
p_adj <- p.adjust(p_values, method = "bonferroni")

# Mostrar resultados
resultados <- data.frame(
  Comparacao = comparacoes,
  p_value = p_values,
  p_ajustado = p_adj
)

print(resultados)

```

```

# Função para comparações par a par usando Fisher e ajuste Bonferroni
comparacoes_par_a_par <- function(contagens, categorias) {
  combos <- combn(length(contagens), 2)
  p_values <- numeric(ncol(combos))
  comparacoes <- character(ncol(combos))

  for(i in 1:ncol(combos)){
    idx <- combos[,i]

    # Criar matriz 2x2 para Fisher
    tabela <- matrix(c(
      contagens[idx[1]], contagens[idx[2]],
      sum(contagens) - contagens[idx[1]], sum(contagens) - contagens[idx[2]]
    ), nrow = 2, byrow = TRUE)

    teste <- fisher.test(tabela)

    p_values[i] <- teste$p.value
    comparacoes[i] <- paste(categorias[idx[1]], "vs", categorias[idx[2]])
  }

  # Ajustar p-values Bonferroni
  p_adj <- p.adjust(p_values, method = "bonferroni")

  # Retornar resultados
  resultados <- data.frame(
    Comparacao = comparacoes,
    p_value = p_values,
    p_ajustado = p_adj
  )
}

```

```

return(resultados)
}

# -----
# Seed dispersal - tempo 1
Seed_1 <- c(81, 75, 72, 8)
S_categorias_1 <- c("Anemochory", "Zoochory", "Autochory", "Various")
comparacoes_par_a_par(Seed_1, S_categorias_1)

# Pollination - tempo 1
Pollination_1 <- c(108, 87, 58, 17, 1)
P_categorias_1 <- c("Entomophilia", "Anemophily", "Various", "Zoophilya", "Autophilya")
comparacoes_par_a_par(Pollination_1, P_categorias_1)

# Life form - tempo 1
Life_form_1 <- c(189, 55, 22, 20, 17)
LF_categorias_1 <- c("Herb", "Shrub", "Tree", "Sub-shrub", "Liana")
comparacoes_par_a_par(Life_form_1, LF_categorias_1)

# -----
# Seed dispersal - tempo 2
Seed_2 <- c(52, 68, 11, 5)
S_categorias_2 <- c("Anemochory", "Zoochory", "Autochory", "Various")
comparacoes_par_a_par(Seed_2, S_categorias_2)

# Pollination - tempo 2
Pollination_2 <- c(61, 24, 38, 25, 4)
P_categorias_2 <- c("Entomophilia", "Anemophily", "Various", "Zoophilya", "Autophilya")
comparacoes_par_a_par(Pollination_2, P_categorias_2)

```



```
# Life form - tempo 2
```

```
Life_form_2 <- c(60, 66, 40, 8, 9)
```

```
LF_categorias_2 <- c("Herb", "Shrub", "Tree", "Sub-shrub", "Liana")
```

```
comparacoes_par_a_par(Life_form_2, LF_categorias_2)
```

```
# -----
```

```
# Seed dispersal - tempo 3
```

```
Seed_3 <- c(18, 57, 5, 2)
```

```
S_categorias_3 <- c("Anemochory", "Zoochory", "Autochory", "Various")
```

```
comparacoes_par_a_par(Seed_3, S_categorias_3)
```

```
# Pollination - tempo 3
```

```
Pollination_3 <- c(41, 10, 15, 26)
```

```
P_categorias_3 <- c("Entomophilia", "Anemophily", "Various", "Zoophilya")
```

```
comparacoes_par_a_par(Pollination_3, P_categorias_3)
```

```
# Life form - tempo 3
```

```
Life_form_3 <- c(23, 38, 43, 4, 2)
```

```
LF_categorias_3 <- c("Herb", "Shrub", "Tree", "Sub-shrub", "Liana")
```

```
comparacoes_par_a_par(Life_form_3, LF_categorias_3)
```

```
##### Analise das características ao longo dos tempos
```

```
library(ggplot2)
```

```
library(tidyr)
```

```
library(dplyr)
```

```
library(multcompView)
```

```
# =====
```

```
# Função para Chi-quadrado (para contagens altas)
```

```
plot_categoria_chi <- function(mat, nome_categoria){
```

```
  test_global <- chisq.test(mat, correct = FALSE)
```

```
cat("\nCategoria:", nome_categoria, "\n")
print(test_global)
```

```
df <- as.data.frame(mat)
df[[nome_categoria]] <- rownames(mat)
df_tidy <- pivot_longer(df, cols = starts_with("tempo"),
                        names_to = "Tempo", values_to = "Contagem")
df_tidy$Grupo <- ""
```

```
# Letras de significância pairwise
```

```
for(i in 1:nrow(mat)){
  tempos <- colnames(mat)
  conts <- as.numeric(mat[i,])
  n_total <- colSums(mat)
```

```
pvals_pairwise <- matrix(1, ncol = length(conts), nrow = length(conts))
rownames(pvals_pairwise) <- colnames(pvals_pairwise) <- tempos
```

```
for(a in 1:(length(conts)-1)){
  for(b in (a+1):length(conts)){
    test <- prop.test(x = c(conts[a], conts[b]), n = n_total[c(a,b)])
    pvals_pairwise[a,b] <- test$p.value
    pvals_pairwise[b,a] <- test$p.value
  }
}
```

```
letters <- multcompLetters(pvals_pairwise < 0.05)$Letters
df_tidy$Grupo[df_tidy[[nome_categoria]] == rownames(mat)[i]] <- letters
}
```

```
gg <- ggplot(df_tidy, aes(x = Tempo, y = Contagem, fill = !!sym(nome_categoria))) +
```

```

geom_bar(stat = "identity", position = position_dodge()) +
geom_text(aes(label = Grupo), position = position_dodge(width = 0.9), vjust = -0.5, size = 5) +
labs(title = paste(nome_categoria, "ao longo do tempo"), y = "Número de espécies") +
theme_minimal()

return(gg)
}

# =====
# Função para Fisher (para contagens baixas)
plot_categoria_fisher <- function(mat, nome_categoria){

  cat("\nCategoria:", nome_categoria, "\n")

  df <- as.data.frame(mat)
  df[[nome_categoria]] <- rownames(mat)
  df_tidy <- pivot_longer(df, cols = starts_with("tempo"),
                        names_to = "Tempo", values_to = "Contagem")

  df_tidy$Grupo <- ""

  for(i in 1:nrow(mat)){
    tempos <- colnames(mat)
    conts <- as.numeric(mat[i,])

    pvals_pairwise <- matrix(1, ncol = length(conts), nrow = length(conts))
    rownames(pvals_pairwise) <- colnames(pvals_pairwise) <- tempos

    for(a in 1:(length(conts)-1)){
      for(b in (a+1):length(conts)){
        test_mat <- matrix(c(conts[a], sum(mat[,a])-conts[a],

```

```

        conts[b], sum(mat[,b])-conts[b]),
        nrow = 2, byrow = TRUE)

test <- fisher.test(test_mat)
pvals_pairwise[a,b] <- test$p.value
pvals_pairwise[b,a] <- test$p.value
}
}

letters <- multcompLetters(pvals_pairwise < 0.05)$Letters
df_tidy$Grupo[df_tidy[[nome_categoria]] == rownames(mat)[i]] <- letters
}

gg <- ggplot(df_tidy, aes(x = Tempo, y = Contagem, fill = !!sym(nome_categoria))) +
  geom_bar(stat = "identity", position = position_dodge()) +
  geom_text(aes(label = Grupo), position = position_dodge(width = 0.9), vjust = -0.5, size = 5) +
  labs(title = paste(nome_categoria, "ao longo do tempo"), y = "Número de espécies") +
  theme_minimal()

return(gg)
}

# =====
# Origin (Chi-quadrado)
Origen_temp <- matrix(c(
  266, 171, 101, # Native
  31, 13, 6 # Exotic
), nrow = 2, byrow = TRUE)
rownames(Origen_temp) <- c("Native", "Exotic")
colnames(Origen_temp) <- c("tempo1", "tempo2", "tempo3")

# Root (Chi-quadrado)

```

```

Root_temp <- matrix(c(
  193, 132, 82,
  115, 51, 25
), nrow = 2, byrow = TRUE)
rownames(Root_temp) <- c("Pivot", "Fasciculated")
colnames(Root_temp) <- c("tempo1", "tempo2", "tempo3")

```

Life form (Fisher)

```

Life_form_temp <- matrix(c(
  189, 60, 23,
  55, 66, 38,
  22, 40, 43,
  20, 8, 4,
  17, 9, 2
), nrow = 5, byrow = TRUE)
rownames(Life_form_temp) <- c("Herb", "Shrub", "Tree", "Sub-shrub", "Liana")
colnames(Life_form_temp) <- c("tempo1", "tempo2", "tempo3")

```

Pollination (Fisher)

```

Pollination_temp <- matrix(c(
  108, 61, 41,
  87, 24, 10,
  58, 38, 15,
  17, 25, 26,
  1, 4, 0
), nrow = 5, byrow = TRUE)
rownames(Pollination_temp) <- c("Entomophilia", "Anemophily", "Various", "Zoophilya",
"Autophilya")
colnames(Pollination_temp) <- c("tempo1", "tempo2", "tempo3")

```

Photosynthetic (Fisher)

```

Photosynthetc_mechanism_temp <- matrix(c(

```

```

222, 138, 93,
39, 11, 4,
0, 5, 0
), nrow = 3, byrow = TRUE)
rownames(Photosynthetc_mechanism_temp) <- c("C3", "C4", "CAM")
colnames(Photosynthetc_mechanism_temp) <- c("tempo1", "tempo2", "tempo3")

```

```

# Seed dispersal (Chi-quadrado)

```

```

Seed_temp <- matrix(c(
81, 52, 18,
75, 68, 57,
72, 11, 5,
8, 5, 2
), nrow = 4, byrow = TRUE)
rownames(Seed_temp) <- c("Anemochory", "Zoochory", "Autochory", "Various")
colnames(Seed_temp) <- c("tempo1", "tempo2", "tempo3")

```

```

# Life cycle (Chi-quadrado)

```

```

Life_cycle_temp <- matrix(c(
203, 147, 82,
67, 15, 10
), nrow = 2, byrow = TRUE)
rownames(Life_cycle_temp) <- c("Perennial", "Annual")
colnames(Life_cycle_temp) <- c("tempo1", "tempo2", "tempo3")

```

```

# =====

```

```

# Gerar gráficos

```

```

g1 <- plot_categoria_chi(Origen_temp, "Origin")
g2 <- plot_categoria_chi(Root_temp, "Root")
g3 <- plot_categoria_fisher(Life_form_temp, "Life_form")
g4 <- plot_categoria_fisher(Pollination_temp, "Pollination")

```

```
g5 <- plot_categoria_fisher(Photosynthetc_mechanism_temp, "Photosynthetic")
g6 <- plot_categoria_fisher(Seed_temp, "Seed")
g7 <- plot_categoria_chi(Life_cycle_temp, "Life_cycle")
```

Mostrar gráficos

g1

g2

g3

```
chisq.test(Life_form_temp, simulate.p.value = TRUE, B = 1e5)
```

g4

```
chisq.test(Pollination_temp, simulate.p.value = TRUE, B = 1e5)
```

g5

```
chisq.test(Photosynthetc_mechanism_temp, simulate.p.value = TRUE, B = 1e5)
```

g6

```
chisq.test(Seed_temp, simulate.p.value = TRUE, B = 1e5)
```

g7