**Journal of Tropical Ecology - Supplementary material**

Higher fire frequency impaired woody species regeneration in a southeastern Amazonian forest

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**Content of this file: Scripts used in R environment for statistical Analysis**

**#Individual-based species accumulation curves**

raref<-read.table(file.choose(),header=T,dec=".")

raref

str(raref)

names(raref)

library(vegan)

source("http://www.jennajacobs.org/R/rarefaction.txt")

curva <- rarefaction(raref, subsample=1, plot=TRUE, color=TRUE, error=TRUE, legend=TRUE, symbol)

write.csv(curva$richness, file="curva.csv")

write.csv(curva$SE, file="curvaSE.csv")

fig<-read.table(file.choose(),header=T,dec=",")

head(fig)

str(fig)

attach(fig)

plot(B0,type="l",bty="l",xlab="Individuals",ylab="Species")

lines(X95upper,lty=1,col="grey")

lines(X95lower,lty=1,col="grey")

lines(B3,lty=2)

lines(B6,lty=3)

legend("bottomright",legend=c("B0","B3","B6"),lty=c(1,2,3),bty="n")

**Nonmetric multidimensional scaling (NMDS) ordination, generated from a Bray-Curtis dissimilarity matrix; Analysis of Similarity (ANOSIM test)**

library(vegan)

BC.esp<-read.table(file.choose(),header=T)

BC.esp

str(BC.esp)

names(BC.esp)

BC.trat<-read.table(file.choose(),header=T)

BC.trat

str(BC.trat)

names(BC.trat)

tab.similaridade<-vegdist(BC.esp)

NMDS←metaMDS(tab.similaridade)

ordiplot(NMDS, type ="text")

fig<-ordiplot(NMDS, type ="points", bty="l")

attach(BC.trat)

ordiellipse(NMDS,trat,label=T)

points(fig,"sites",c("B00","B010","B0100","B015","B0250","B030","B050","B0500","B0750"),pch=1)

points(fig,"sites",c("B30","B310","B3100","B315","B3250","B330","B350","B3500","B3750"), pch=21, bg="grey")

points(fig,"sites",c("B60","B6100","B615","B6250","B650","B6500","B6750"),pch=21,col="black", bg="black")

anosim<-anosim(tab.similaridade, trat)

summary(anosim)

**IndVal test**

indval<-read.table(file.choose(),header=T)

indval

str(indval)

names(indval)

groups<-c(1,1,1,1,1,1,1,1,1,2,2,2,2,2,2,2,2,2,3,3,3,3,3,3,3,3)

library(indicspecies)

indval.test<-multipatt(indval,groups,control=how(nperm=999))

summary(indval.test)

summary(indval.test,alpha=0.1)

**Spearman’s correlations from a Bioenv matrix**

library(vegan)

ES<-read.table(file.choose(),header=T)

ES

str(ES)

AM<-read.table(file.choose(),header=T, dec=",")

AM

str(AM)

bio<-bioenv(ES,AM)

summary(bio)

bio

**Generalized Linear Model (GLM) for tree species regenerating individuals using soil humidity, microclimate, LAI, grass cover and treatments as fixed factors.**

ab<-read.table(file.choose(),header=T,dec=",")

ab

str(ab)

names(ab)

m1<-glm(abund~SU12+SU20+ST+AT+RH+LAI+trat+capim+moitas,data=ab,family=poisson)

m1

summary(m1)

3.3226/2

m2<-glm(abund~SU20+ST+AT+RH+LAI+trat+capim+moitas,data=ab,family=quasipoisson)

m2

summary(m2)

m3<-glm(abund~SU20+ST+AT+RH+LAI+trat+capim,data=ab,family=quasipoisson)

m3

summary(m3)

m4<-glm(abund~SU20+AT+RH+LAI+trat+capim,data=ab,family=quasipoisson)

m4

summary(m4)

m5<-glm(abund~SU20+AT+RH+LAI+capim,data=ab,family=quasipoisson)

m5

summary(m5)

m6<-glm(abund~AT+RH+LAI+capim,data=ab,family=quasipoisson)

m6

summary(m6)

**GLM analysis for grass cover and tree species regenerating individuals (plots as sampling units) using treatment (B0, B3, B6) and edge distance as fixed factors. (prop.cob = grass cover in %, , trat = treatments, disT = edge distance)**

## grass cover with treatment and edge distance

> capim\_texto<-glm(prop.cob~trat\*distT, family=quasibinomial, data=dados)

> anova(capim\_texto, test = "F")

Analysis of Deviance Table

Model: quasibinomial, link: logit

Response: prop.cob

Terms added sequentially (first to last)

Df Deviance Resid. Df Resid. Dev F Pr(>F)

NULL 269 201.614

trat 2 47.255 267 154.359 66.8515 < 2.2e-16 \*\*\*

distT 8 49.426 259 104.933 17.4810 < 2.2e-16 \*\*\*

trat:distT 16 22.112 243 82.821 3.9103 1.519e-06 \*\*\*

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

>

> summary(capim\_texto)

Call:

glm(formula = prop.cob ~ trat \* distT, family = quasibinomial,

data = dados)

Deviance Residuals:

Min 1Q Median 3Q Max

-1.57345 -0.28065 -0.10013 -0.00008 2.14597

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) -1.8575 0.5501 -3.376 0.000855 \*\*\*

tratB3 -1.8061 1.3239 -1.364 0.173746

tratB6 1.6770 0.6672 2.513 0.012607 \*

distTAA -17.7086 2021.7257 -0.009 0.993018

distTAAA -17.7086 2021.7257 -0.009 0.993018

distTAB -17.7086 2021.7257 -0.009 0.993018

distTB -2.0344 1.4512 -1.402 0.162225

distTC -2.3271 1.6416 -1.418 0.157579

distTF -17.7086 2021.7257 -0.009 0.993018

distTK -2.0344 1.4512 -1.402 0.162225

distTP -2.7377 1.9679 -1.391 0.165451

tratB3:distTAA 18.8599 2021.7262 0.009 0.992565

tratB6:distTAA 20.4014 2021.7259 0.010 0.991957

tratB3:distTAAA 20.5953 2021.7261 0.010 0.991880

tratB6:distTAAA 19.0974 2021.7258 0.009 0.992471

tratB3:distTAB 20.4524 2021.7261 0.010 0.991937

tratB6:distTAB 18.7845 2021.7258 0.009 0.992594

tratB3:distTB 3.3843 1.9968 1.695 0.091390 .

tratB6:distTB 2.1949 1.5459 1.420 0.156949

tratB3:distTC 4.8104 2.0836 2.309 0.021799 \*

tratB6:distTC -0.3362 1.8754 -0.179 0.857868

tratB3:distTF 17.4804 2021.7265 0.009 0.993108

tratB6:distTF 15.6919 2021.7259 0.008 0.993814

tratB3:distTK -13.8681 2021.7265 -0.007 0.994533

tratB6:distTK -17.3512 2021.7262 -0.009 0.993159

tratB3:distTP -13.1648 2021.7270 -0.007 0.994810

tratB6:distTP -2.3752 3.3346 -0.712 0.476973

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasibinomial family taken to be 0.3534299)

Null deviance: 201.614 on 269 degrees of freedom

Residual deviance: 82.821 on 243 degrees of freedom

AIC: NA

Number of Fisher Scoring iterations: 18

>

**regenerating tree species individuals (number of individuals = abun, trat = treatments, disT = edge distance)**

> regn\_tex<-glm(abun~trat\*distT, family=quasipoisson, data=dados)

> anova(regn\_tex, test = "F")

Analysis of Deviance Table

Model: quasipoisson, link: log

Response: abun

Terms added sequentially (first to last)

Df Deviance Resid. Df Resid. Dev F Pr(>F)

NULL 269 861.51

trat 2 122.49 267 739.02 26.3174 4.512e-11 \*\*\*

distT 8 133.86 259 605.16 7.1903 1.505e-08 \*\*\*

trat:distT 16 120.87 243 484.29 3.2463 4.111e-05 \*\*\*

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

>

> summary(regn\_tex)

Call:

glm(formula = abun ~ trat \* distT, family = quasipoisson, data = dados)

Deviance Residuals:

Min 1Q Median 3Q Max

-3.2199 -1.1832 -0.4472 0.3882 7.4981

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) 5.878e-01 3.596e-01 1.635 0.103400

tratB3 6.061e-01 4.470e-01 1.356 0.176349

tratB6 -1.099e+00 7.191e-01 -1.528 0.127885

distTAA -9.445e-01 6.795e-01 -1.390 0.165825

distTAAA -9.445e-01 6.795e-01 -1.390 0.165825

distTAB -1.099e+00 7.191e-01 -1.528 0.127885

distTB -9.445e-01 6.795e-01 -1.390 0.165825

distTC -4.925e-01 5.838e-01 -0.844 0.399751

distTF 2.007e-01 4.848e-01 0.414 0.679315

distTK 1.528e+00 3.966e-01 3.854 0.000149 \*\*\*

distTP 6.931e-01 4.404e-01 1.574 0.116787

tratB3:distTAA 2.812e-01 8.180e-01 0.344 0.731353

tratB6:distTAA -1.585e+01 1.673e+03 -0.009 0.992450

tratB3:distTAAA -1.542e-01 8.624e-01 -0.179 0.858293

tratB6:distTAAA 5.390e-01 1.196e+00 0.451 0.652739

tratB3:distTAB 3.102e-01 8.619e-01 0.360 0.719258

tratB6:distTAB -1.569e+01 1.673e+03 -0.009 0.992523

tratB3:distTB -2.552e+00 1.691e+00 -1.509 0.132541

tratB6:distTB 1.099e+00 1.087e+00 1.010 0.313267

tratB3:distTC -7.014e-01 8.025e-01 -0.874 0.382964

tratB6:distTC 8.701e-02 1.145e+00 0.076 0.939475

tratB3:distTF -2.088e+00 8.781e-01 -2.378 0.018198 \*

tratB6:distTF -1.299e+00 1.337e+00 -0.972 0.331974

tratB3:distTK -2.460e+00 6.378e-01 -3.857 0.000147 \*\*\*

tratB6:distTK -3.320e+00 1.695e+00 -1.959 0.051246 .

tratB3:distTP -1.482e+00 6.478e-01 -2.287 0.023039 \*

tratB6:distTP -1.526e-14 8.807e-01 0.000 1.000000

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasipoisson family taken to be 2.327117)

Null deviance: 861.51 on 269 degrees of freedom

Residual deviance: 484.29 on 243 degrees of freedom

AIC: NA

Number of Fisher Scoring iterations: 15

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