How many tree species in French Guiana Tropical Moist Forest?

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Abstract

Abstract of the article.

1 Introduction

2 Methods

Self-similarity (Harte, Kinzig, and Green, Harte et al.; Harte, Mccarthy, Taylor, Kinzig, and Fischer, Harte et al.).

Estimation of the richness of an Indian forest (Krishnamani, Kumar, and Harte, Krishnamani et al.).

2.1 Data

3 Results

3.1 Plots

3.2 Random plot

One plot per location

```
# One plot per location...
Plots %>%
    mutate(Random = runif(n())) -> RandomizedPlots
RandomizedPlots %>%
   group_by(Location) %>%
    summarize(MaxRandom = max(Random)) %>%
    rename(Random = MaxRandom) %>%
    inner_join(RandomizedPlots) %>%
 select(Plot) -> SelectedPlots
## Joining, by = c("Location", "Random")
# ...or all plots SelectedPlots <- Plots['Plot']
# Distances
library("dbmss") %>%
   suppressMessages()
Plots %>%
   inner_join(SelectedPlots) %>%
   rename(PointName = Plot, X = X_UTM, Y = Y_UTM,
    PointType = Location) %>%
    mutate(PointWeight = 1) %>%
    wmppp(unitname = c("meter", "meters")) %>%
    pairdist() %>%
    as.dist -> Distances
```

3.3 Sorensen

Joining, by = "Plot"

```
library("ade4") %>%
    suppressMessages()
Abundances %>%
    inner_join(SelectedPlots) %>%
    select(-Plot) %>%
    dist.binary(method = 5) -> Sorensen

## Joining, by = "Plot"
Sorensen <- 1 - Sorensen</pre>
```

3.4 Relation

```
tibble(Sorensen = as.numeric(log10(Sorensen)), Distance = as.numeric(log10(Distances))) %>%
    filter(Distance > 3) -> dist_plots
lm(Sorensen ~ Distance, data = dist_plots) -> regression
regression %>%
    summary()

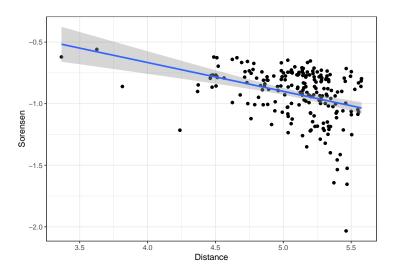
##

## Call:
## lm(formula = Sorensen ~ Distance, data = dist_plots)
##

## Residuals:
## Min 1Q Median 3Q Max
## -1.02518 -0.09879 0.02880 0.15867 0.29373
##

## Coefficients:
## Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.27000 0.20849 1.295 0.197
```

`geom_smooth()` using formula 'y ~ x'



Bootstrap

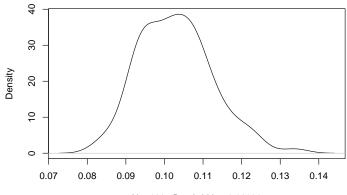
```
library("broom")
estimate_z <- function() {
    # Select one plot per location...
Plots %>%
        mutate(Random = runif(n())) -> RandomizedPlots
RandomizedPlots %>%
        group_by(Location) %>%
        summarize(MaxRandom = max(Random)) %>%
        rename(Random = MaxRandom) %>%
        inner_join(RandomizedPlots) %>%
        suppressMessages %>%
        select(Plot) -> SelectedPlots
# Calculate distances
Plots %>%
```

```
inner_join(SelectedPlots) %>%
          suppressMessages %>%
          rename(PointName = Plot, X = X_UTM, Y = Y_UTM,
               PointType = Location) %>%
          mutate(PointWeight = 1) %>%
wmppp(unitname = c("meter", "meters")) %>%
          suppressWarnings %>%
          pairdist() %>%
          as.dist -> Distances
     # Calculate Sorensen divergence
     Abundances %>%
          inner_join(SelectedPlots) %>%
    suppressMessages %>%
select(-Plot) %>%
dist.binary(method = 5) -> Sorensen
Sorensen <- 1 - Sorensen
     # Regress
     tibble(Sorensen = as.numeric(log10(Sorensen)),
          Distance = as.numeric(log10(Distances))) %>%
          dplyr::filter(Distance > 3) %>%
lm(Sorensen ~ Distance, data = .) %>%
          tidy %>%
          dplyr::filter(term == "Distance") %>%
select(estimate) %>%
    pull -> z
z <- -z/2
    return(z)
}
n_simulations \leftarrow 100
pgb <- txtProgressBar(min = 0, max = n_simulations)
sim_z <- rep(0, n_simulations)</pre>
for (i in 1:n_simulations) {
    sim_z[i] <- estimate_z()</pre>
     setTxtProgressBar(pgb, i)
}
```

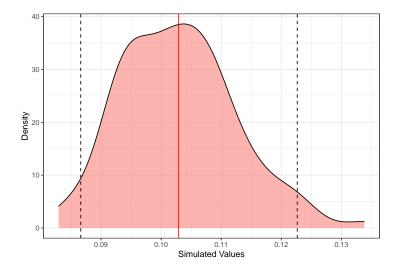
===========

```
sim_z %>%
density %>%
plot
```





```
entropart::as.SimTest(mean(sim_z), sim_z) %>%
   autoplot
```



3.5 Extrapolation

```
# Extrapolation de Paracou : .625km², 604 sp >
# c=631
(c <- 600/0.625^z)

## Distance
## 633.9184

# Nombre d'espèces total
(spsim <- c * 80000^z)

## Distance
## 2375.18
```

3.6 Fisher

```
# Nombre d'arbres

Ntrees <- 8 * 10^6 * mean(colSums(Abundances[, -1]))

# Taux de couverture par placette

library("entropart") %>% suppressMessages()

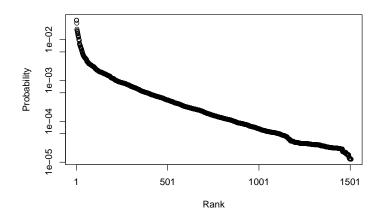
C <- apply(Abundances[, -1], 1, function(X) Coverage(X))

# Distribution de probabilités, corrigée par les

# taux de couverture

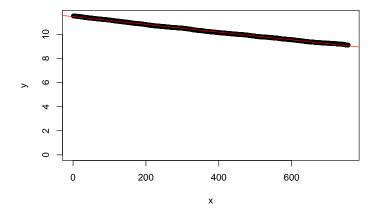
(DbsProba <- C %*% as.matrix(Abundances[, -1]/rowSums(Abundances[, -1]))/nrow(Abundances)

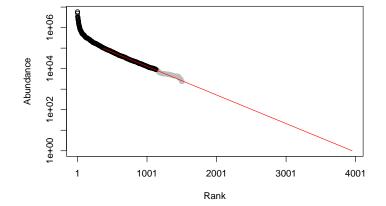
plot(as.ProbaVector(ObsProba))
```

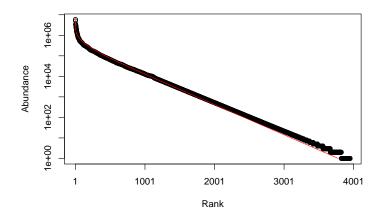


```
# Abondances
EstimatedAbd <- as.AbdVector(round(ObsProba * Ntrees,</pre>
   0))
# 50% centraux
EA50 <- as.AbdVector(sort(EstimatedAbd, decreasing = T)[round(length(EstimatedAbd)/4):round(length(EstimatedAbd) *
   3/4)])
x <- 1:length(EA50)
y <- as.numeric(log(EA50))
# Régression rang-abondance sur la partie
# rectiligne de la courbe
EA50lm \leftarrow lm(y \sim x)
# Nombre d'espèces extrapolé
NbSpecies <- round(-EA50lm$coefficients[1]/EA50lm$coefficients[2]) +
   round(length(EstimatedAbd)/4) - 1
# Régression de la partie rectiligne
plot(y \sim x, ylim = c(0, max(y)))
summary(EA50lm)
##
## Call:
## lm(formula = y \sim x)
##
## Residuals:
##
         Min
                     1Q
                           Median
                                          ЗQ
## -0.050607 -0.026011 -0.004327 0.017631 0.084264
##
## Coefficients:
##
                  Estimate Std. Error t value
## (Intercept) 1.147e+01 2.303e-03 4981.6
## x
                -3.208e-03 5.278e-06 -607.8
##
               Pr(>|t|)
## (Intercept)
                 <2e-16 ***
## x
                  <2e-16 ***
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 0.03161 on 753 degrees of freedom
## Multiple R-squared: 0.998, Adjusted R-squared: 0.998
## F-statistic: 3.694e+05 on 1 and 753 DF, p-value: < 2.2e-16
```

```
abline(a = EA50lm$coefficients[1], b = EA50lm$coefficients[2],
    col = "red")
```







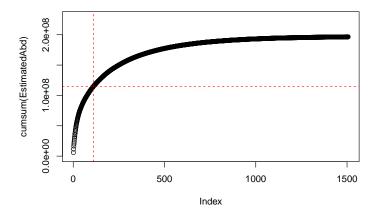
```
## $alpha
## [1] 294.5374

# Nombre d'espèces estimées
NbSpecies

## (Intercept)
```

3.7 Hyperdominance

```
# Hyperdominance
EstimatedAbd <- sort(round(ObsProba * Ntrees, 0), decreasing = TRUE)
plot(cumsum(EstimatedAbd), ylim = c(0, Ntrees))
abline(h = Ntrees/2, lty = 2, col = "red")
hdSpecies <- min(which(cumsum(EstimatedAbd) > Ntrees/2))
abline(v = hdSpecies, lty = 2, col = "red")
```



References

Harte, J., A. Kinzig, and J. Green. Self-similarity in the distribution and abundance of species. 284(5412), 334–336.

Harte, J., S. Mccarthy, K. Taylor, A. Kinzig, and M. L. Fischer. Estimating species-area relationships from scale plot to landscape data using species spatial-turnover. 86(1), 45–54.

Krishnamani, R., A. Kumar, and J. Harte. Estimating species richness at large spatial scales using data from small discrete plots. 27(5), 637–642.