How many tree species in French Guiana Tropical Moist Forest?

Eric Marcon

Ariane Mirabel

Jean-François Molino

Grégoire Vincent

Daniel Sabatier

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Abstract

The biodiversity of tropical rainforest is difficult to assess. Yet, its estimation is necessary for conservation purposes, to evaluate our level of knowledge and the risks faced by the forest in relation to global change. Our contribution is to estimate the regional richness of tree species from local but widely spread inventories. Guyadiv is a network of forest plots installed over the whole territory of French Guiana, where trees over 10 cm DBH are identified. We use its information (1180 species censused in 76 one-hectare plots) to estimate the exponent of the species-area relationship, assuming Arrhenius's power law. We can then extrapolate the number of species from a local, wide inventory (62.5 ha in Paracou research station). We evaluate the number of tree species around 2000 over the territory.

1 Introduction

Biodiversity assessment in tropical moist forests is a practical challenge but a major goal considering they are the most diverse terrestrial ecosystems. Estimating the number of tree species is made possible by the long-term effort of sampling resulting in thousands of forest plots organized in various networks. In French Guiana, the Guyadiv network consists of xxx plots accross the whole forest. Based on similar datasets, the diversity of tree species has been estimated in Amazonia (ter Steege, Pitman, Sabatier, Baraloto, Salomão, Guevara, Phillips, Castilho, Magnusson, Molino, Monteagudo, Núñez Vargas,

Montero, Feldpausch, Coronado, Killeen, Mostacedo, Vasquez, Assis, Terborgh, Wittmann, Andrade, Laurance, Laurance, Marimon, Marimon, Guimarães Vieira, Amaral, Brienen, Castellanos, Cárdenas López, Duivenvoorden, Mogollón, Matos, Dávila, García-Villacorta, Stevenson Diaz, Costa, Emilio, Levis, Schietti, Souza, Alonso, Dallmeier, Montoya, Fernandez Piedade, Araujo-Murakami, Arroyo, Gribel, Fine, Peres, Toledo, Aymard, Baker, Cerón, Engel, Henkel, Maas, Petronelli, Stropp, Zartman, Daly, Neill, Silveira, Paredes, Chave, Lima Filho, Jørgensen, Fuentes, Schöngart, Cornejo Valverde, Di Fiore, Jimenez, Peñuela-Mora, Phillips, Rivas, van Andel, von Hildebrand, Hoffman, Zent, Malhi, Prieto, Rudas, Ruschell, Silva, Vos, Zent, Oliveira, Schutz, Gonzales, Trindade Nascimento, Ramirez-Angulo, Sierra, Tirado, Umaña Medina, van der Heijden, Vela, Vilanova Torre, Vriesendorp, Wang, Young, Baider, Balslev, Ferreira, Mesones, Torres-Lezama, Urrego Giraldo, Zagt, Alexiades, Hernandez, Huamantupa-Chuquimaco, Milliken, Palacios Cuenca, Pauletto, Valderrama Sandoval, Valenzuela Gamarra, Dexter, Feeley, Lopez-Gonzalez, and Silman, ter Steege et al.; ter Steege, Prado, de Lima, Pos, de Souza Coelho, de Andrade Lima Filho, Salomão, Amaral, de Almeida Matos, Castilho, Phillips, Guevara, de Jesus Veiga Carim, Cárdenas López, Magnusson, Wittmann, Martins, Sabatier, Irume, da Silva Guimarães, Molino, Bánki, Piedade, Pitman, Ramos, Monteagudo Mendoza, Venticinque, Luize, Núñez Vargas, Silva, de Leão Novo, Reis, Terborgh, Manzatto, Casula, Honorio Coronado, Montero, Duque, Costa, Castaño Arboleda, Schöngart, Zartman, Killeen, Marimon, Marimon-Junior, Vasquez, Mostacedo, Demarchi, Feldpausch, Engel, Petronelli, Baraloto, Assis, Castellanos, Simon, de Medeiros, Quaresma, Laurance, Rincón, Andrade, Sousa, Camargo, Schietti, Laurance, de Queiroz, Nascimento, Lopes, de Sousa Farias, Magalhães, Brienen, Aymard C., Revilla, Vieira, Cintra, Stevenson, Feitosa, Duivenvoorden, Mogollón, Araujo-Murakami, Ferreira, Lozada, Comiskey, de Toledo, Damasco, Dávila, Lopes, García-Villacorta, Draper, Vicentini, Cornejo Valverde, Lloyd, Gomes, Neill, Alonso, Dallmeier, de Souza, Gribel, Arroyo, Carvalho, de Aguiar, do Amaral, Pansonato, Feeley, Berenguer, Fine, Guedes, Barlow, Ferreira, Villa, Peñuela Mora, Jimenez, Licona, Cerón, Thomas, Maas, Silveira, Henkel, Stropp, Paredes, Dexter, Daly, Baker, Huamantupa-Chuquimaco, Milliken, Pennington, Tello, Pena, Peres, Klitgaard, Fuentes, Silman, Di Fiore, von Hildebrand, Chave, van Andel, Hilário, Phillips, Rivas-Torres, Noronha, Prieto, Gonzales, de Sá Carpanedo, Gonzales, Gómez, de Jesus Rodrigues, Zent, Ruschel, Vos, Fonty, Junqueira, Doza, Hoffman, Zent, Barbosa, Malhi, de Matos Bonates, de Andrade Miranda, Silva, Barbosa, Vela, Pinto, Rudas, Albuquerque, Umaña, Carrero Márquez, van der Heijden, Young, Tirado, Correa, Sierra, Costa, Rocha, Vilanova Torre, Wang, Oliveira, Kalamandeen, Vriesendorp, Ramirez-Angulo, Holmgren, Nascimento, Galbraith, Flores, Scudeller, Cano, Ahuite Reategui, Mesones, Baider, Mendoza, Zagt, Urrego Giraldo, Ferreira, Villarroel, Linares-Palomino, Farfan-Rios, Farfan-Rios, Casas, Cárdenas, Balslev, Torres-Lezama, Alexiades, Garcia-Cabrera, Valenzuela Gamarra, Valderrama Sandoval, Ramirez Arevalo, Hernandez, Sampaio, Pansini, Palacios Cuenca, de Oliveira, Pauletto, Levesley, Melgaço, and Pickavance, ter Steege et al.) and at the world scale (Slik, Arroyo-Rodríguez, Aiba, Alvarez-Loayza, Alves,

Ashton, Balvanera, Bastian, Bellingham, van den Berg, Bernacci, da Conceição Bispo, Blanc, Böhning-Gaese, Boeckx, Bongers, Boyle, Bradford, Brearley, Breuer-Ndoundou Hockemba, Bunyavejchewin, Calderado Leal Matos, Castillo-Santiago, Catharino, Chai, Chen, Colwell, Robin, Clark, Clark, Clark, Culmsee, Damas, Dattaraja, Dauby, Davidar, DeWalt, Doucet, Duque, Durigan, Eichhorn, Eisenlohr, Eler, Ewango, Farwig, Feeley, Ferreira, Field, de Oliveira Filho, Fletcher, Forshed, Franco, Fredriksson, Gillespie, Gillet, Amarnath, Griffith, Grogan, Gunatilleke, Harris, Harrison, Hector, Homeier, Imai, Itoh, Jansen, Joly, de Jong, Kartawinata, Kearsley, Kelly, Kenfack, Kessler, Kitayama, Kooyman, Larney, Laumonier, Laurance, Laurance, Lawes, Amaral, Letcher, Lindsell, Lu, Mansor, Marjokorpi, Martin, Meilby, Melo, Metcalfe, Medjibe, Metzger, Millet, Mohandass, Montero, de Morisson Valeriano, Mugerwa, Nagamasu, Nilus, Ochoa-Gaona, Onrizal, Page, Parolin, Parren, Parthasarathy, Paudel, Permana, Piedade, Pitman, Poorter, Poulsen, Poulsen, Powers, Prasad, Puyravaud, Razafimahaimodison, Reitsma, dos Santos, Roberto Spironello, Romero-Saltos, Rovero, Rozak, Ruokolainen, Rutishauser, Saiter, Saner, Santos, Santos, Sarker, Satdichanh, Schmitt, Schöngart, Schulze, Suganuma, Sheil, da Silva Pinheiro, Sist, Stevart, Sukumar, Sun, Sunderland, Suresh, Suzuki, Tabarelli, Tang, Targhetta, Theilade, Thomas, Tchouto, Hurtado, Valencia, van Valkenburg, Van Do, Vasquez, Verbeeck, Adekunle, Vieira, Webb, Whitfeld, Wich, Williams, Wittmann, Wöll, Yang, Adou Yao, Yap, Yoneda, Zahawi, Zakaria, Zang, de Assis, Garcia Luize, and Venticinque, Slik et al.). The methods used in these studies are not appropriate to estimate regional diversity, i.e. at a smaller scale where dispersal limitation is critical. The contibution of this paper is to estimate the number of tree species at the regional scale, in French Guiana (8 million hectares of tropical moist forest with no ecological boundary to distinguish them from the rest of Amazonia) and demonstrate which method is valid to do so. We build on Harte's self similarity model (Harte, Kinzig, and Green, Harte et al.) that implies the power-law relatioship of Arrhenius (Arrhenius) and provides a technique to evaluate its parameters (Harte, Mccarthy, Taylor, Kinzig, and Fischer, Harte et al.), previously applied by Krishnamani, Kumar, and Harte (Krishnamani et al.) in the Western Ghats, India. We show that the log-series model underlying the work of ter Steege, Pitman, Sabatier, Baraloto, Salomão, Guevara, Phillips, Castilho, Magnusson, Molino, Monteagudo, Núñez Vargas, Montero, Feldpausch, Coronado, Killeen, Mostacedo, Vasquez, Assis, Terborgh, Wittmann, Andrade, Laurance, Laurance, Marimon, Marimon, Guimarães Vieira, Amaral, Brienen, Castellanos, Cárdenas López, Duivenvoorden, Mogollón, Matos, Dávila, García-Villacorta, Stevenson Diaz, Costa, Emilio, Levis, Schietti, Souza, Alonso, Dallmeier, Montoya, Fernandez Piedade, Araujo-Murakami, Arroyo, Gribel, Fine, Peres, Toledo, Aymard, Baker, Cerón, Engel, Henkel, Maas, Petronelli, Stropp, Zartman, Daly, Neill, Silveira, Paredes, Chave, Lima Filho, Jørgensen, Fuentes, Schöngart, Cornejo Valverde, Di Fiore, Jimenez, Peñuela-Mora, Phillips, Rivas, van Andel, von Hildebrand, Hoffman, Zent, Malhi, Prieto, Rudas, Ruschell, Silva, Vos, Zent, Oliveira, Schutz, Gonzales, Trindade Nascimento, Ramirez-Angulo, Sierra, Tirado, Umaña Medina, van der Heijden, Vela, Vilanova Torre, Vriesendorp, Wang, Young, Baider, Balslev, Ferreira, Mesones, Torres-Lezama,

Urrego Giraldo, Zagt, Alexiades, Hernandez, Huamantupa-Chuquimaco, Milliken, Palacios Cuenca, Pauletto, Valderrama Sandoval, Valenzuela Gamarra, Dexter, Feeley, Lopez-Gonzalez, and Silman (ter Steege et al.) does not apply at the regional scale.

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

```
# Decrypt the vault
library("secret") %>%
    suppressMessages()
name_project <- "GF-Richness"
vault <- "vault"
Sys.setenv(USER_KEY = usethis::proj_path(paste0(name_project,
    ".rsa")))
Plots <- get_secret("Plots", vault = vault)
Abundances <- get_secret("Abundances", vault = vault)
```

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
```

```
## Joining, by = "Plot"
```

3.3   Sorensen

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

```
## Joining, by = "Plot"
```

```
Sorensen <- 1 - Sorensen
```

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
## Distance    -0.23400    0.04088  -5.723 3.63e-08
##
## (Intercept)
## Distance    ***
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1985 on 207 degrees of freedom
## Multiple R-squared:  0.1366, Adjusted R-squared:  0.1325
## F-statistic: 32.76 on 1 and 207 DF,  p-value: 3.63e-08
```

```
(-regression$coefficients[2]/2 -> z)
```
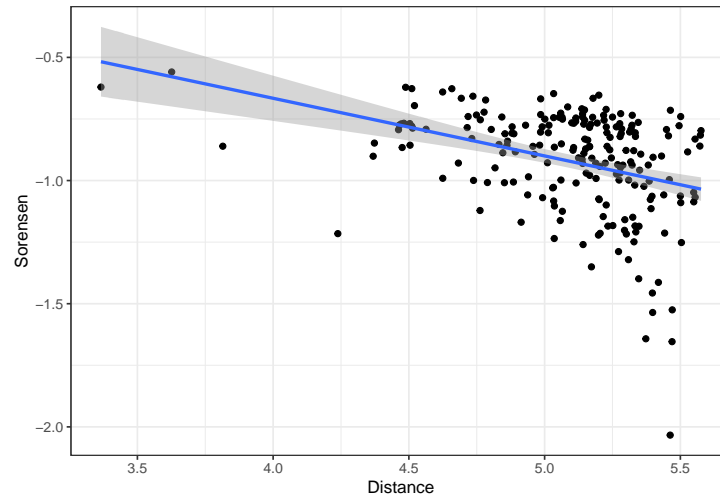
```
##  Distance
## 0.1170003
```

```
dist_plots %>%
    ggplot(aes(x = Distance, y = Sorensen)) + geom_point() +
    geom_smooth(method = lm)
```

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


Bootstrap

```r
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 <- 100
pgb <- txtProgressBar(min = 0, max = n_simulations)
sim_z <- rep(0, n_simulations)
for (i in 1:n_simulations) {
    sim_z[i] <- estimate_z()
    setTxtProgressBar(pgb, i)
}
```
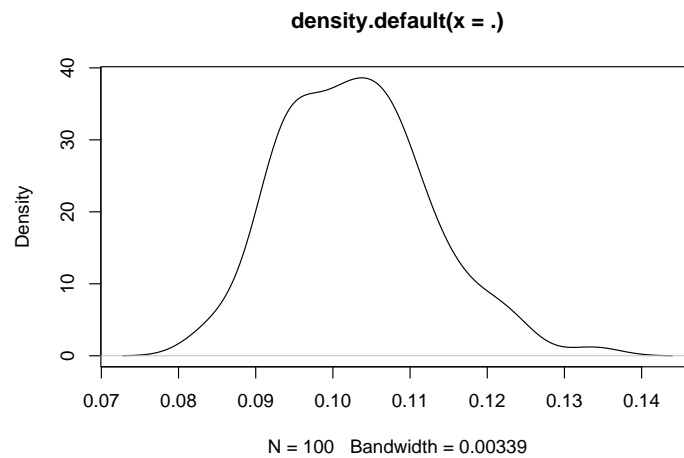
```
## =================================================
```

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

density.default(x = .)

N = 100   Bandwidth = 0.00339

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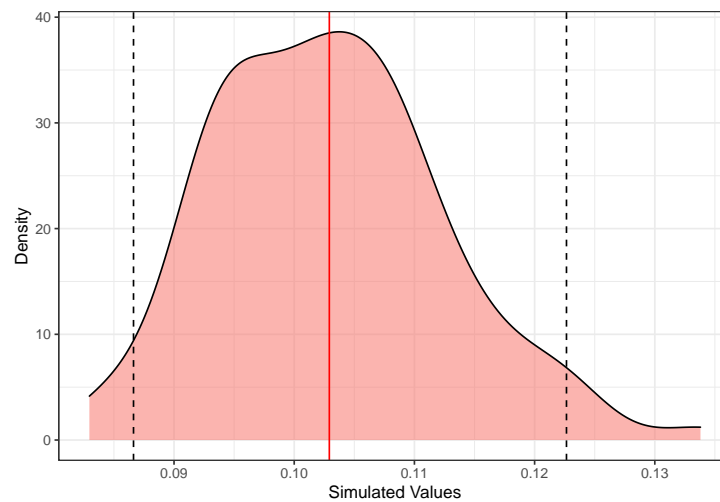
3.5 Extrapolation

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

```
## Distance
## 633.9184
```

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

```
## Distance
##  2375.18
```

3.6 Fisher

```r
# 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
ObsProba <- C %*% as.matrix(Abundances[, -1]/rowSums(Abundances[,
    -1]))/nrow(Abundances)
plot(as.ProbaVector(ObsProba))
```
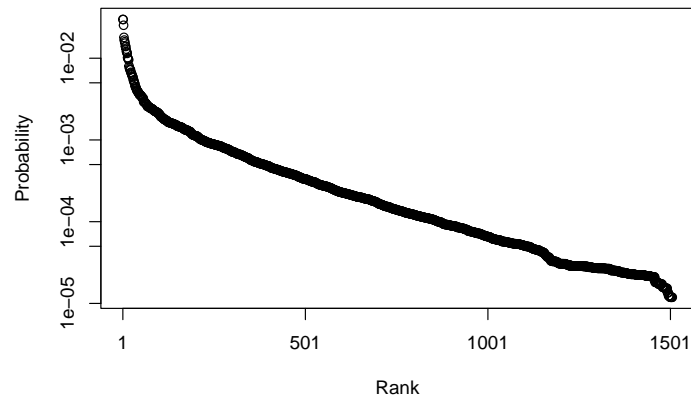
```r
# Abondances
EstimatedAbd <- as.AbdVector(round(ObsProba * Ntrees,
    0))
# 50% centraux
EA50 <- as.AbdVector(sort(EstimatedAbd, decreasing = T)[round(length(EstimatedAbd)/4):round(length(EstimatedAbd) *
    3/4)])
x <- 1:length(EA50)
y <- as.numeric(log(EA50))
# Régression rang-abondance sur la partie
# rectiligne de la courbe
EA50lm <- lm(y ~ 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 ~ x, ylim = c(0, max(y)))
summary(EA50lm)
```

```
##
## Call:
## lm(formula = y ~ x)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -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 '**' 0.01 '*' 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")
```
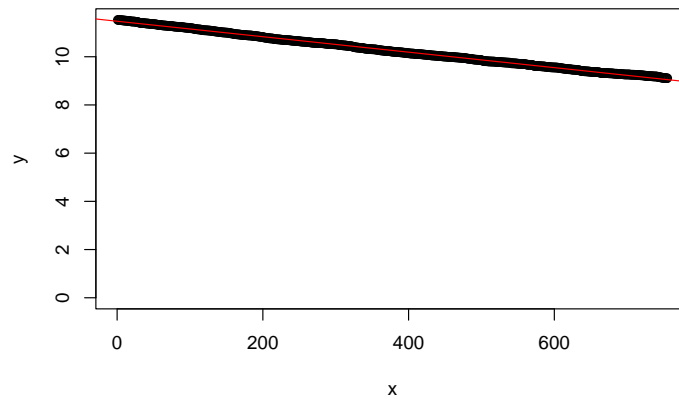


```
# Metacommunauté complète: partie observée
EA75 <- sort(EstimatedAbd, decreasing = T)[1:round(length(EstimatedAbd) *
    3/4)]
plot(EstimatedAbd, ylim = c(1, max(EA75)), xlim = c(0,
    NbSpecies), col = "grey")
points(EA75, ylim = c(1, max(EA75)), xlim = c(0, -EA50lm$coefficients[1]/EA50lm$coefficients[2]))
Extra <- exp(EA50lm$coefficients[1]) * cumprod(rep(exp(EA50lm$coefficients[2]),
    NbSpecies - round(length(EstimatedAbd)/4) + 1))
lines(x = round(length(EstimatedAbd)/4):NbSpecies,
    y = Extra, col = "red")
```
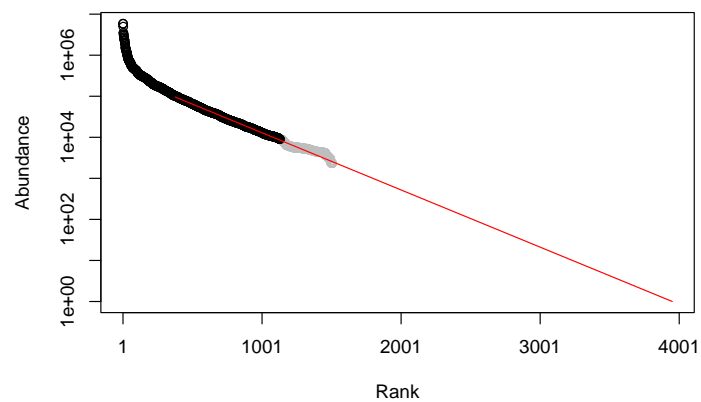
```
# Vérification : effectif total
(Ntotal <- sum(EA75) + sum(Extra[(length(EA75) - NbSpecies +
    length(Extra) + 1):length(Extra)]))
```

```
## [1] 197186462
```

```
# Ajustement d'une log-série
plot(as.AbdVector(round(c(EA75, Extra[(length(EA75) -
    NbSpecies + length(Extra) + 1):length(Extra)]))),
    Distribution = "lseries")
```
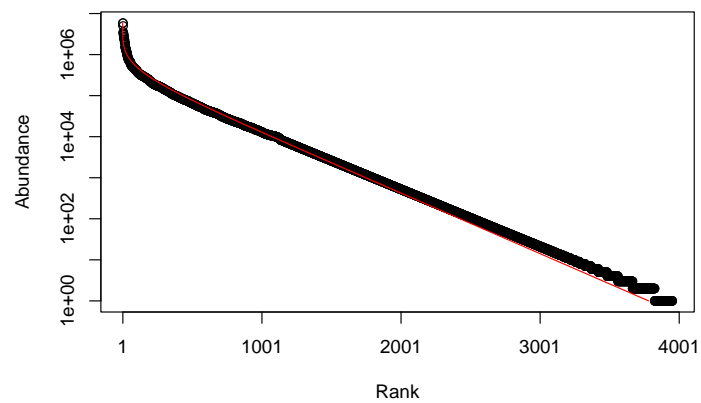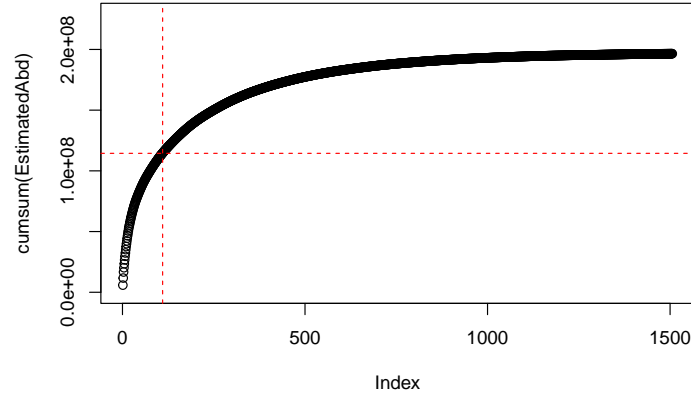


```
## $alpha
## [1] 294.5374
```

```
# Nombre d'espèces estimées
NbSpecies
```

```
## (Intercept)
##        3951
```

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

Arrhenius, O. Species and area. *9*(1), 95–99.

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.

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