Growth, Survival, Diversity and Concentration

Eric Marcon

Florence Puech

June 1, 2023

Abstract

Exploratory model of growth and survival depending on Diversity and concentration.

1 Data generation

1.1 Point set

Plants are simulated in a square window

```
library("SpatDiv")
# Geometry of the window
window_size <- 20000
unit_name <- c("meter", "meters")
# Density
plants_n_per_area <- 100/1e+06
# Number of sectors
sectors_n <- 20
# Spatial concentration of plants
thomas_scale <- window_size/10
thomas_mu <- 100
```

The community is simulated:

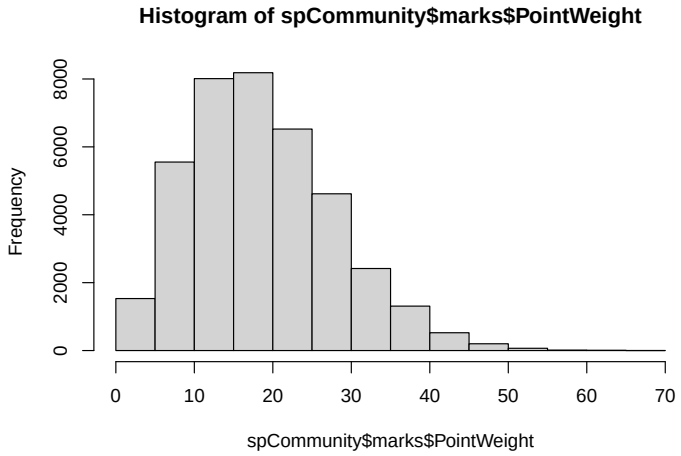
```
library("spatstat")
rSpCommunity(n = 1, size = window_size^2 * plants_n_per_area,
    S = sectors_n, Spatial = "Thomas", scale = thomas_scale,
    mu = thomas_mu, Sizes = "Weibull", win = square(r = window_size,
        unitname = unit_name)) -> spCommunity
# Number of plants
spCommunity$n
```

```
## [1] 38964
```

```
# Per sector
summary(spCommunity$marks$PointType)
```

```
##  sp103618452  sp469590019 sp1078433175
##         1118         1690         2396
##  sp870406886  sp856094295 sp2034800618
##          122         3086          205
##  sp221053885   sp48280303 sp1967995229
##         2699          641         1802
## sp1953462239  sp294352985  sp729553207
##         1825          756         1753
##  sp215954973 sp1002782691  sp920513358
##         3820          755         5248
## sp1142810744  sp197128656   sp45219221
##          112         3652          827
## sp1231666643  sp353783310
##         2464         3993
```

```
# Sizes
hist(spCommunity$marks$PointWeight)
```



1.2 Parameters

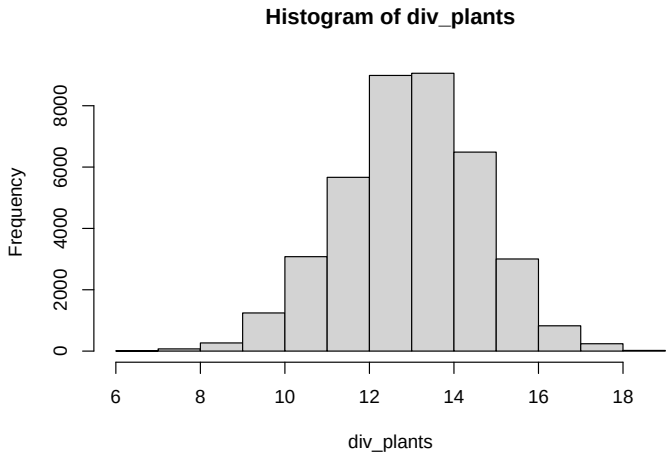
```
n_simulations <- 10
```

2 Diversity

Accumulation.

```
# Average distance between plants
dist_neighbor <- 1/sqrt(plants_n_per_area)
# Accumulation of diversity with confidence
# interval (not run) accum <- DivAccum(
# spCommunity, r.seq = c( 0, seq( from =
# dist_neighbor / 4, to = dist_neighbor * 4, by =
# dist_neighbor / 4 ) ), q.seq = 0:2, H0 =
# 'RandomLocation', NumberOfSimulations =
# n_simulations, Individual = TRUE ) Diversity at
# 4 times the average distance to neighbor
```

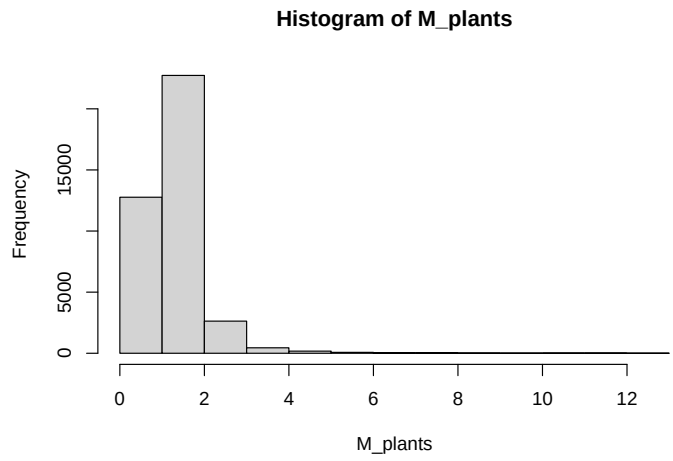
```
accum_5 <- DivAccum(spCommunity, r.seq = c(0, dist_neighbor *
    4), q.seq = 0:2, Individual = TRUE)
div_plants <- accum_5$Neighborhoods[1, 2, ]
# Distribution of richness
hist(div_plants)
```



3 Concentration

Spatial concentration of sectors

```
# Compute individual M
library("dbmss")
# Compute concentration of each sector
M_plants <- numeric(spCommunity$n)
for (sector in levels(spCommunity$marks$PointType)) {
    M_sector <- Mhat(spCommunity, r = c(0, window_size/10),
        ReferenceType = sector, Individual = TRUE)
    point_numbers <- as.integer(substring(names(M_sector)[-(1:3)],
        3))
    M_plants[point_numbers] <- as.numeric(as.data.frame(M_sector)[2,
        -(1:3)])
}
hist(M_plants)
```



Correlation

```
cor(M_plants, div_plants)
```

```
## [1] -0.009871965
```

4 Growth model

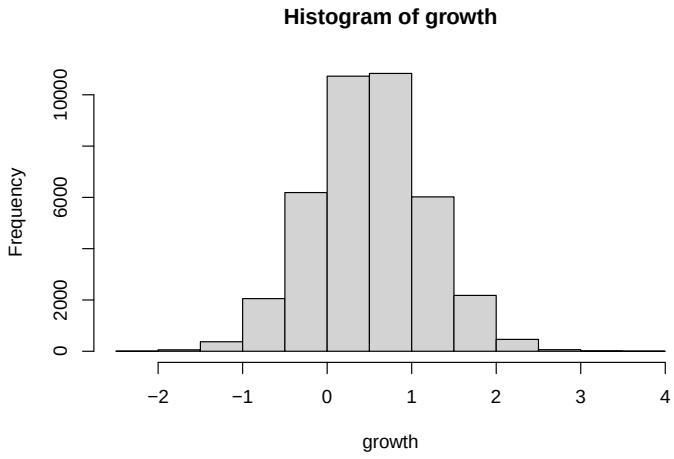
The model defines growth as $\ln(Size_{i,t+1}) = \ln(Size_{i,t}) + \alpha x + \beta Conc_{i,t} + \gamma Div_{i,t} + \epsilon_{i,t}$.

4.1 Parameters

```
alpha <- 1/max(spCommunity$x)
conc <- scale(log(M_plants + 1))
beta <- 1/max(conc)
div <- scale(div_plants)
gamma <- 1/max(div)
epsilon <- rnorm(spCommunity$n, 0, 0.5)
```

4.2 Simulation

```
growth <- alpha * spCommunity$x + beta * conc + gamma *
    div + epsilon
hist(growth)
```




```
size_t1 <- spCommunity$marks$PointWeight * exp(growth)
```

4.3 Inference

```
growth_obs <- log(size_t1/spCommunity$marks$PointWeight)
lm_plants <- lm(growth_obs ~ spCommunity$x + conc +
    div)
summary(lm_plants)
```

```
##
## Call:
## lm(formula = growth_obs ~ spCommunity$x + conc + div)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.92864 -0.33907 -0.00108  0.34013  2.09676
##
## Coefficients:
##                  Estimate Std. Error t value
## (Intercept)   -2.395e-03  5.185e-03  -0.462
## spCommunity$x  5.028e-05  4.451e-07 112.970
## conc           1.353e-01  2.542e-03  53.233
## div            3.000e-01  2.542e-03 118.020
##               Pr(>|t|)
## (Intercept)      0.644
## spCommunity$x   <2e-16 ***
## conc            <2e-16 ***
## div             <2e-16 ***
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5015 on 38960 degrees of freedom
## Multiple R-squared:  0.4328, Adjusted R-squared:  0.4328
## F-statistic:  9910 on 3 and 38960 DF,  p-value: < 2.2e-16
```