Growth, Survival, Diversity and Concentration

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Abstract

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

1 Purpose

This exploratory study is a proof of concept for modeling plant growth and survival with respect to relative concentration and diversity.

A set of plants is simulated in a square area with R (R Core Team, 2023). Each plant belongs to an economic sector and has a size. Each sector is drawn separately. Location is generated according to a classical point process, and plant sizes according to a random distribution.

The growth model follows Audretsch and Dohse (2007). Exogenous variables are the plant environment, summarized here by its X coordinate: a positive gradient of growth conditions exists from west to east. The local geographic concentration of the sector around each plant (Lang et al., 2020) and the local diversity (Marcon et al., 2014) of sectors in the neighborhood of each plant are the variables of interest.

The survival model is similar. Exogenous variables are summarized by the Y coordinate.

2 Data generation

2.1 Point set

Plants are simulated in a square window by the *Spatdiv* package.

```
library("SpatDiv")
# Geometry of the window
window_size <- 2000  # Small during development
unit_name <- c("meter", "meters")
# Density
plants_n_per_area <- 100/1e+06
# Number of sectors
sectors_n <- 5
# Spatial concentration of plants
thomas_scale <- window_size/3
thomas_mu <- 100
```

The community is simulated:

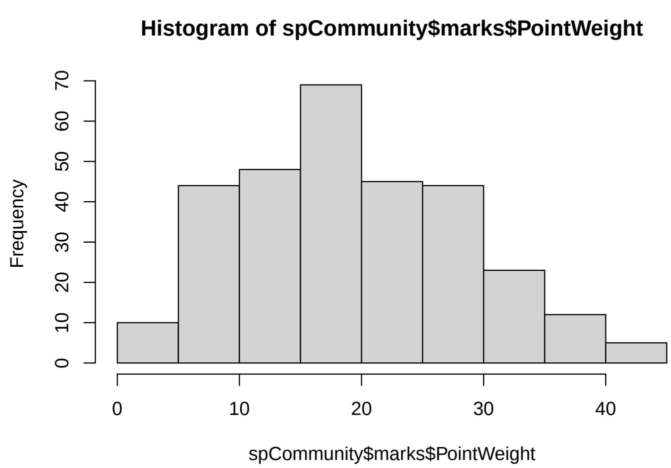
```
library("spatstat")
rSpCommunity(n = 1, size = window_size^2 * plants_n_per_area,
    S = sectors_n, Spatial = "Thomas", scale = thomas_scale,
    mu = thomas_mu, Sizes = "Weibull", win = square(r = window_size,
        unitname = unit_name)) -> spCommunity
# Number of plants
spCommunity$n
```

```
## [1] 300
```

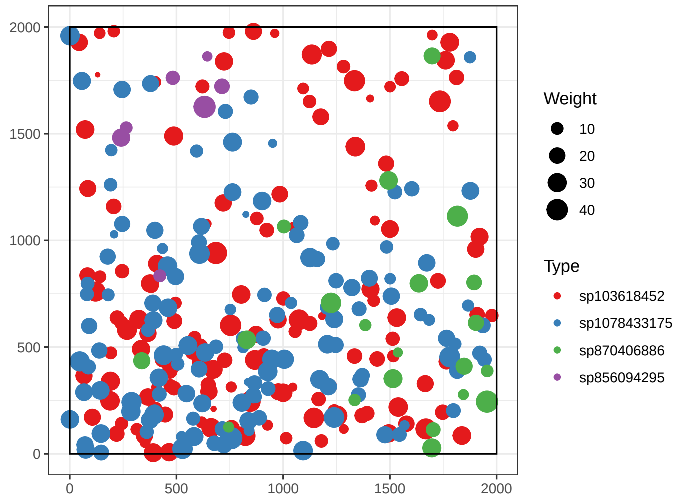
```
# Per sector
summary(spCommunity$marks$PointType)
```

```
##  sp103618452 sp1078433175  sp870406886
##          143          129           21
##  sp856094295
##            7
```

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




```
# Map
autoplot(spCommunity)
```



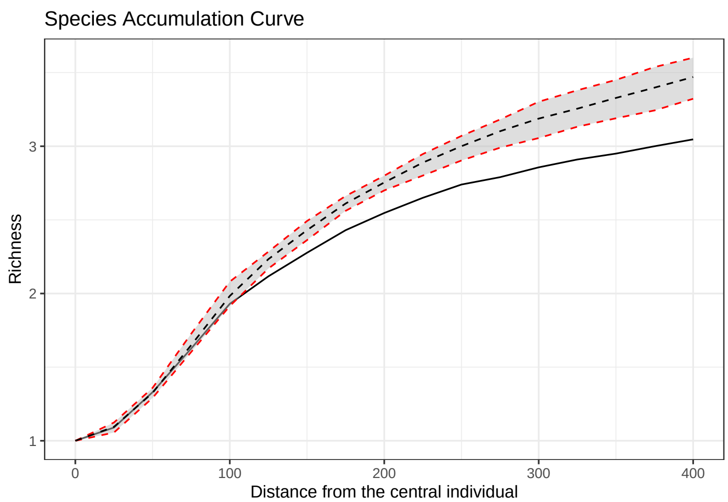
2.2 Parameters

```
# Number of simulations to compute confindence
# envelopes
n_simulations <- 10  # Small during development
```

3 Diversity

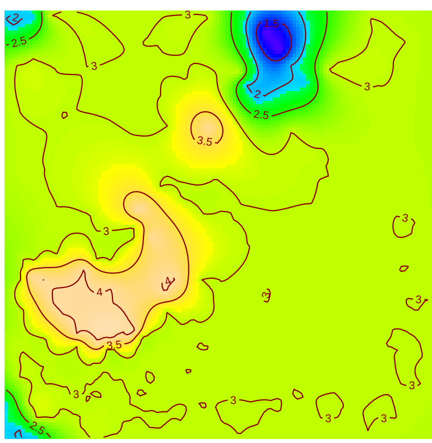
Accumulation.

```
# 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)
autoplot(accum)
```

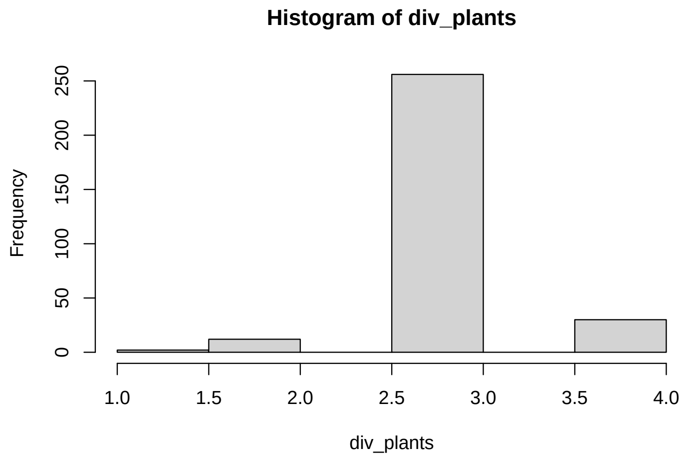



```
# Map the local diversity (richness at 4 x dist
# to neighbor)
MapPlot(accum, Order = 0, NeighborHood = dist_neighbor *
    4)
```

```
## [using ordinary kriging]
```



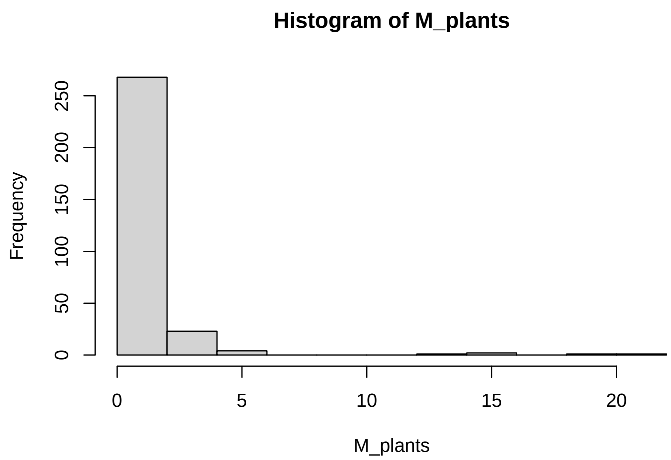
```
# Diversity at 4 times the average distance to
# neighbor
accum_5 <- DivAccum(spCommunity, r.seq = c(0, dist_neighbor *
    4), q.seq = 0:2, Individual = TRUE)
# Extract the data [order, distance, points]
div_plants <- accum_5$Neighborhoods[1, 2, ]
# Distribution of richness
hist(div_plants)
```



4 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

Higher concentration implies lower diversity, which may be an issue to disentangle their effects. Yet, it appears that the correlation remains very low at realistic levels of concentration.

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

```
## [1] -0.05844276
```

5 Growth model

The model defines growth as

$$\ln(Size_{i,t+1}) = \ln(Size_{i,t}) + \alpha_g x + \beta_g Conc_{i,t} + \gamma_g Div_{i,t} + \epsilon^g_{i,t}.$$

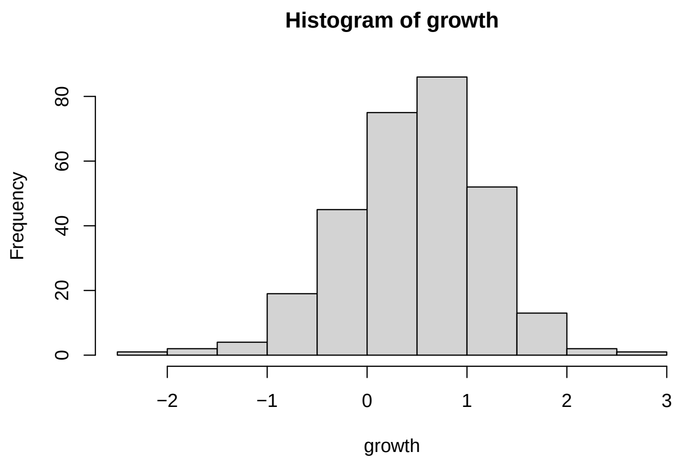
5.1 Parameters

```
alpha_g <- 1/max(spCommunity$x)
conc <- scale(log(M_plants + 1))
beta_g <- 1/max(conc)
div <- scale(div_plants)
gamma_g <- 1/max(div)
epsilon_g <- rnorm(spCommunity$n, 0, 0.5)
```

5.2 Simulation

Simulate growth.

```
growth <- alpha_g * spCommunity$x + beta_g * conc +
    gamma_g * div + epsilon_g
hist(growth)
```




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

5.3 Inference

Check that parameters can be inferered from the data.

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

```
##
## Call:
## lm(formula = growth_obs ~ spCommunity$x + conc + div)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.24251 -0.28582  0.00468  0.31011  1.33206
##
## Coefficients:
##                Estimate Std. Error t value
## (Intercept)   2.289e-02  5.507e-02   0.416
## spCommunity$x 4.904e-04  5.258e-05   9.327
## conc          1.692e-01  2.866e-02   5.903
## div           4.452e-01  2.898e-02  15.362
##               Pr(>|t|)
## (Intercept)      0.678
## spCommunity$x  < 2e-16 ***
## conc          9.75e-09 ***
## div            < 2e-16 ***
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.493 on 296 degrees of freedom
## Multiple R-squared:  0.5063, Adjusted R-squared:  0.5013
## F-statistic: 101.2 on 3 and 296 DF,  p-value: < 2.2e-16
```

6 Survival model

A model similar to that of growth makes the log-odds of survival

$$\mathrm{logit}(p_{i,t+1}) = \alpha_s y + \beta_s Conc_{i,t} + \gamma_s Div_{i,t} + \epsilon^s_{i,t}.$$

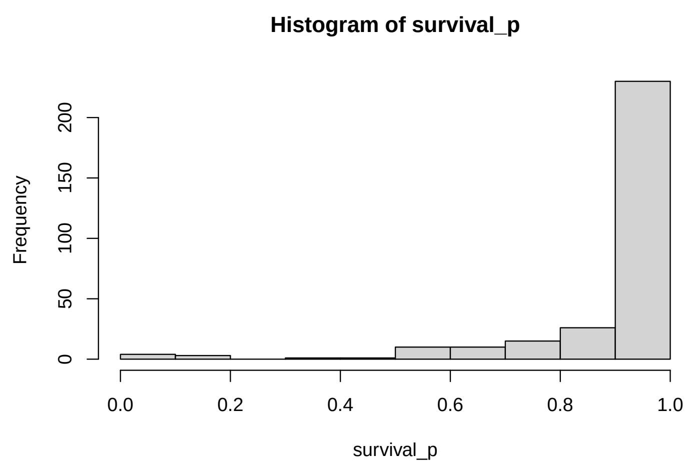
6.1 Parameters

```
alpha_s <- 10/max(spCommunity$y)
beta_s <- 0
gamma_s <- 1
epsilon_s <- rnorm(spCommunity$n, 0, 0.5)
```

6.2 Simulation

Simulate survival

```
survival_logit <- alpha_s * spCommunity$x + beta_s *
    conc + gamma_s * div + epsilon_s
# Inv-logit function
survival_p <- 1/(1 + exp(-survival_logit))
hist(survival_p)
```




```
# Draw survival
survival_obs <- rbinom(spCommunity$n, 1, survival_p)
# Mortality
1 - sum(survival_obs)/spCommunity$n
```

```
## [1] 0.09
```

6.3 Inference

Check that parameters can be inferred from the data.

```
survival_obs <- log(size_t1/spCommunity$marks$PointWeight)
glm_survival <- glm(survival_obs ~ spCommunity$y +
    conc + div)
summary(glm_survival, family = "binomial")
```

```
##
## Call:
## glm(formula = survival_obs ~ spCommunity$y + conc + div)
##
## Coefficients:
##                Estimate Std. Error t value
## (Intercept)   4.512e-01  5.380e-02   8.386
## spCommunity$y 1.631e-05  6.138e-05   0.266
## conc          1.565e-01  3.314e-02   4.722
## div           4.050e-01  3.298e-02  12.280
##               Pr(>|t|)
## (Intercept)   2.07e-15 ***
## spCommunity$y    0.791
## conc          3.61e-06 ***
## div            < 2e-16 ***
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 0.3144298)
##
##     Null deviance: 145.742  on 299  degrees of freedom
## Residual deviance:  93.071  on 296  degrees of freedom
## AIC: 510.24
##
## Number of Fisher Scoring iterations: 2
```

7 Conclusion

These simulations show that both local concentration and diversity may influence plant growth and survival. We provide methods to compute their values and estimate their effect.

The application of this proof of concept to the real world requires characterizing pertinent exogenous variables (here summarized by the X and Y coordinates) and neighborhood sizes (here arbitrarily set to 1/10 of the window's size).

References

Audretsch, D. B. and D. Dohse (2007, April). Location: A Neglected Determinant of Firm Growth. *Review of World Economics 143*(1), 79–107.

Lang, G., E. Marcon, and F. Puech (2020). Distance-based measures of spatial concentration: Introducing a relative density function. *The Annals of Regional Science 64*, 243–265.

Marcon, E., I. Scotti, B. Hérault, V. Rossi, and G. Lang (2014). Generalization of the partitioning of Shannon diversity. *Plos One 9*(3), e90289.

R Core Team (2023). *R: A Language and Environment for Statistical Computing.* Vienna, Austria: R Foundation for Statistical Computing.