
A new individual-based model

Zdenko Heyvaert

February 2017

1 SIMULATION RULES

We start from the interaction matrix $\mathbf{\Omega} \in \mathbb{R}^{(S+1) \times (S+1)}$

$$\mathbf{\Omega} = \begin{pmatrix} 0 & 0 & 0 & \cdots & 0 \\ r_1 & \Omega_{11} & \Omega_{12} & \cdots & \Omega_{1S} \\ r_2 & \Omega_{21} & \Omega_{22} & \cdots & \Omega_{2S} \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ r_S & \Omega_{S1} & \Omega_{S2} & \cdots & \Omega_{SS} \end{pmatrix} \quad (1.1)$$

with the $r_i \equiv \Omega_{i0} \sim \mathcal{U}(0, 1)$ the growth rates and $\Omega_{ij} \sim \mathcal{U}(-1, 1)$ the interaction probabilities. We took $\Omega_{ii} = -1, \forall i$ (like Gibson), because if we took it 0 like in Solé, in most cases all but one or two species got extinct and the remaining one took over the entire lattice. The negative diagonal ensures that species cannot keep growing indefinitely.

Every species also has an immigration rate μ_i and an extinction rate e_i , contained in the vectors $\boldsymbol{\mu}$ and \mathbf{e} .

Before summarizing the interaction rules, we discuss how we implemented the strongly interacting species in this model. A SIS has the ability to let another species grow with e.g. 700%, cfr. the interaction matrix \mathbf{A} on page 13 of Gibson. Because we are dealing with probabilities which cannot exceed the 100% by construction, we'll have to be creative and solve this in another way.

I was thinking of the most efficient way to implement this and came up with this model. It is based on the fact that we consider the spatially implicit Solé model: because the position of a certain individual on the lattice is irrelevant, only the total number of individuals of each species needs to be taken into account and all information is contained in the state vectors.

The idea is that you have an $S + 1$ -dimensional statevector

$$\mathbf{x}(t) = \begin{pmatrix} x_0(t) \\ x_1(t) \\ \vdots \\ x_S(t) \end{pmatrix} \quad (1.2)$$

containing the abundances of all species and the number of empty sites x_0 . For all t , $\sum_{i=0}^S x_i(t) = N$, the number of sites. This rule is implicit because it will be automatically satisfied by the rules of interaction. This vector plays two roles:

1. Obviously it is the quantity we are interested in and which we will evolve in time to let it reach a steady state value \mathbf{x}^* ;
2. The first step in every interaction will be to draw a random species $A \in [0, S]$, with the probability of species A to be chosen at time step t being $x_A(t)/N$. Note that we also allow for empty sites to be drawn, in this case immigration can take place, analogous to the lattice model.

The question is how many interactions q there will be in every time step. This number will depend on the number of strongly interacting species (SISs) and their strengths. Generally we can say that $q \geq N$, with the equality in the absence of SISs. This is how it works: we create an additional $S + 1$ -dimensional vector \mathbf{y} , which is not a real state vector but the so-called *interaction vector*. This is how we construct \mathbf{y} : we start from \mathbf{x} but multiply every SIS by a certain SISfactor.

To give an example, imagine we have 5 species on a lattice with 110 sites. If species nr. 5 is the SIS, with SISfactor = 100, we derive the y_i from the x_i like this:

$$\begin{pmatrix} x_0 \\ x_1 \\ x_2 \\ x_3 \\ x_4 \\ x_5 \end{pmatrix} = \begin{pmatrix} 10 \\ 20 \\ 20 \\ 20 \\ 20 \\ 20 \end{pmatrix} \rightarrow \begin{pmatrix} y_0 \\ y_1 \\ y_2 \\ y_3 \\ y_4 \\ y_5 \end{pmatrix} = \begin{pmatrix} 10 \\ 20 \\ 20 \\ 20 \\ 20 \\ 2000 \end{pmatrix} \quad (1.3)$$

This vector plays two roles:

1. It determines the number of interactions in a given time step, via $q(t) = \sum_{i=0}^S y_i(t)$;
2. After choosing species A with probability determined by the state vector \mathbf{x}/N , we choose a random species B with probability determined by the interaction vector $\mathbf{y}/$.

After the q interactions, the time step is complete and we update the state vector \mathbf{x} . The interaction vector is NOT updated: we calculate a new \mathbf{y} using \mathbf{x} at the beginning of each time step.

We will now discuss the interaction rules, which have the advantage of being very simple.

The interaction possibilities are the following:

1. $\Omega_{AB} = 0$ (this means B has no influence on A)
 \rightarrow nothing happens
2. $\Omega_{AB} < 0$ (this means B has a negative influence on A)
 - $x_0 \mapsto x_0 + 1$
 - $x_A \mapsto x_A - 1$
with probability $|\Omega_{AB}|$
3. $\Omega_{AB} > 0$ (this means B has a positive influence on A)
 - $x_0 \mapsto x_0 - 1$
 - $x_A \mapsto x_A + 1$
with probability Ω_{AB}

Finally, notice that this model is still 100% individual based, although we do not explicitly make use of lattice sites which are occupied/empty. With every step we take, we always keep this lattice in mind. For every interaction, we choose two random individuals A and B with probabilities proportional to their occurrences on the (virtual) lattice. When an individual A disappears, it is always replaced by an empty site (and vice versa), so the total number of sites is always conserved.

2 SOME OBSERVATIONS

We investigate if our new model obeys to the same laws as the model introduced by Solé in his paper. For example, the scaling relation (figure 2.1).

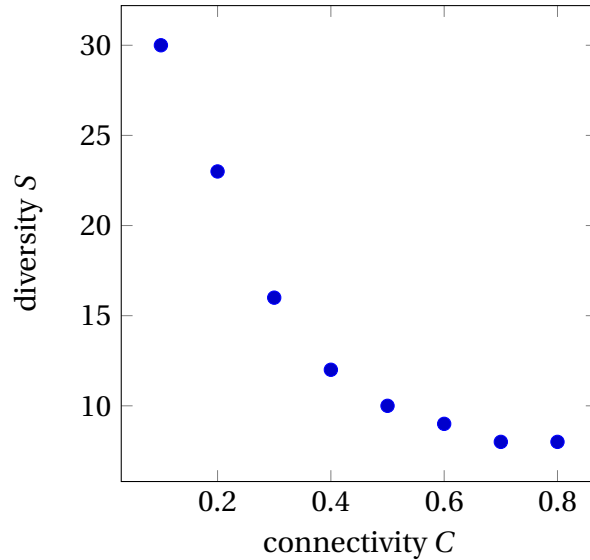


Figure 2.1: Diversity-connectivity relation for $\mu = 0.01$ and $e = 0$ in the absence of a SIS. We considered a pool of 400 species.

The diversity appears to decrease with the connectivity in a (sort of) hyperbolic fashion, in agreement with the Solé model. I didn't make a fit (yet) because the data aren't really statistically justified; I should take averages and include error bars for the fluctuations which are certainly there. The figure was created with just one simulation for each datapoint.

Let us now consider the rank-frequency plots (see fig. 4 in Solé):

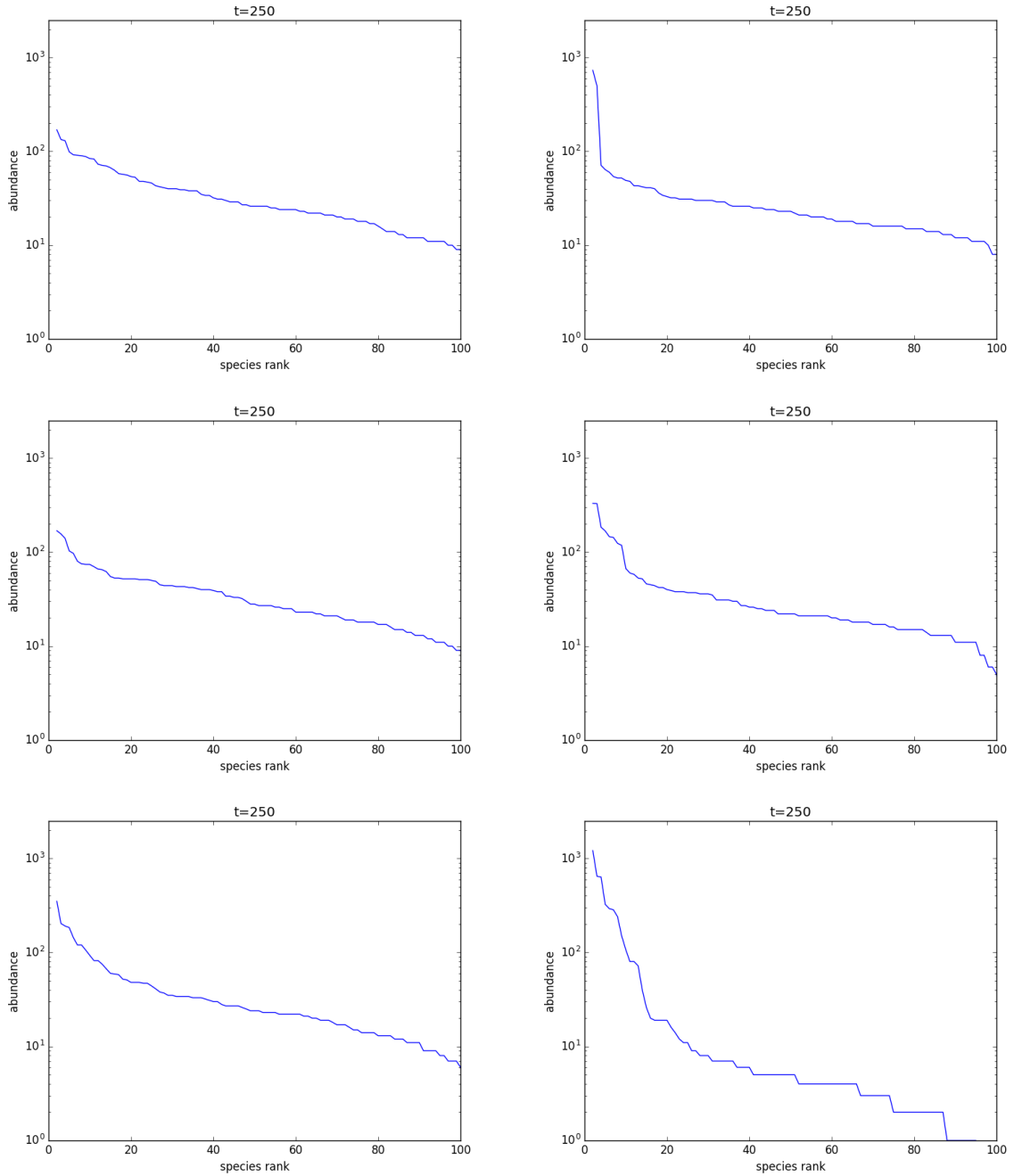


Figure 2.2: Left: distribution for $C = 0.1, 0.5, 0.9$ without presence of a SIS. Right: same connectivities but with 1 SIS present (SISfactor=200). Parameters: $\mu = e = 0.3, S = 100$.

Both increasing C and adding a SIS to the system yields more species with very high abundances and fewer species with very low abundances. So from fig. 2.2 we already expect there should be clustering when adding a SIS to the system, as the state vectors are qualitatively (and quantitatively) different. This is also visualized in figure 2.3.

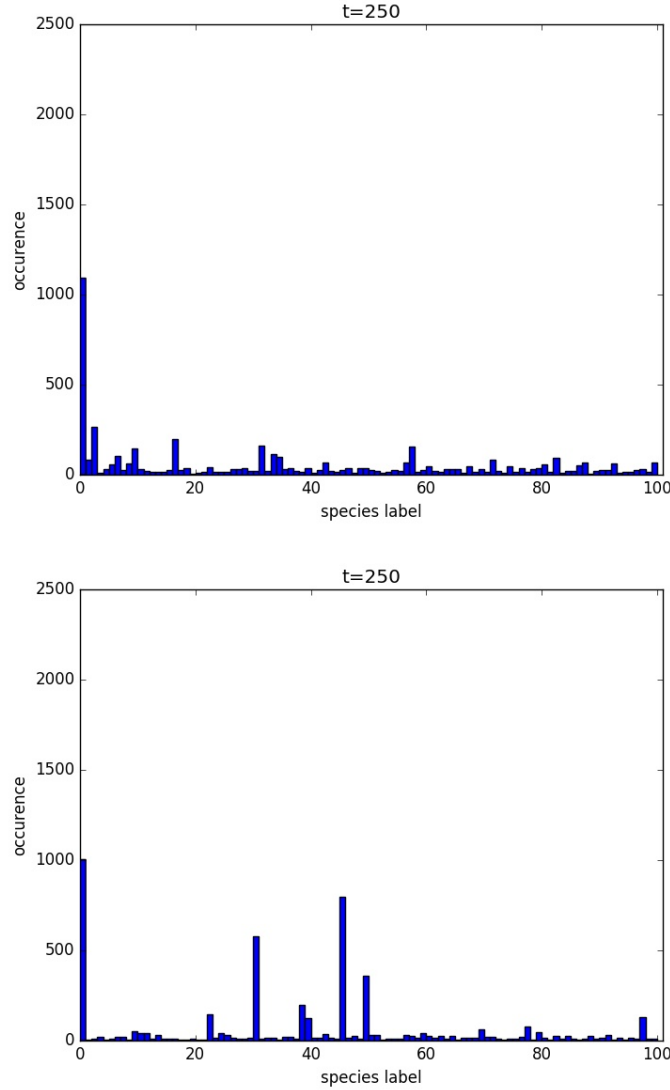


Figure 2.3: System in the absence (top) and presence (bottom) of a SIS (nr. 20). The SIS itself is negligible (occupies less than 1% of the lattice sites), but has a huge effect on the other species. The bar at the left represents the number of empty sites. Parameters: $C = 0.5$, $e = 0.3$, $\mu = 0.4$, $S = 100$, $SISfactor=200$.

So basically, what this shows is that in order for one or more dominant species to be present in a system with a small number of connections, we need at least one strongly interacting species (although this SIS is never the dominant species itself).

3 CLUSTERING ANALYSIS

We always used the following parameters:

number of species in metacommunity	S	100
number of species in local communities	s	80
number of local communities	LCs	500
number of lattice sites	sites	5000
connectance of the interaction matrix	connectance	0.5
the relative strength of the SISs	SISfactor	200
$\Omega_{AB} \sim \mathcal{U}(-\text{maxinteraction}, \text{maxinteraction})$	maxinteraction	0.9
migration rate	mu	0.4
extinction rate	e	0.3

3.1 ONE SINGLE SIS

The clustering analysis is shown in figure 3.1. Comparing with figure 1.1 from my report on GLV, the clustering is less strong but still clearly present. The reason for this is simply because the immigration rate in the GLV model was 0, where it is 0.4 here. Gibson mentioned that increasing the immigration rate would decrease the clustering strength. Figures 3.2 and 3.3 show that the criterium whether a local community belongs to a certain cluster or not, is the presence or absence of species nr. 20 (the SIS).

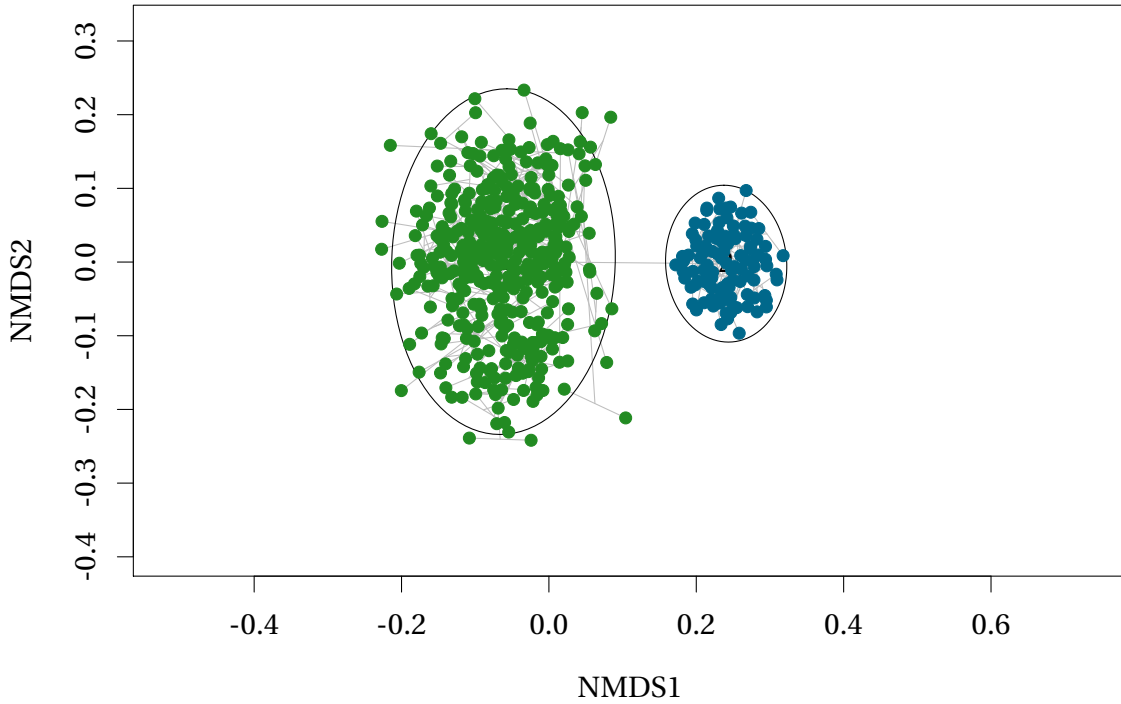


Figure 3.1: Two clusters are visible when performing principle coordinate analysis in the case of 1 strongly interacting species.

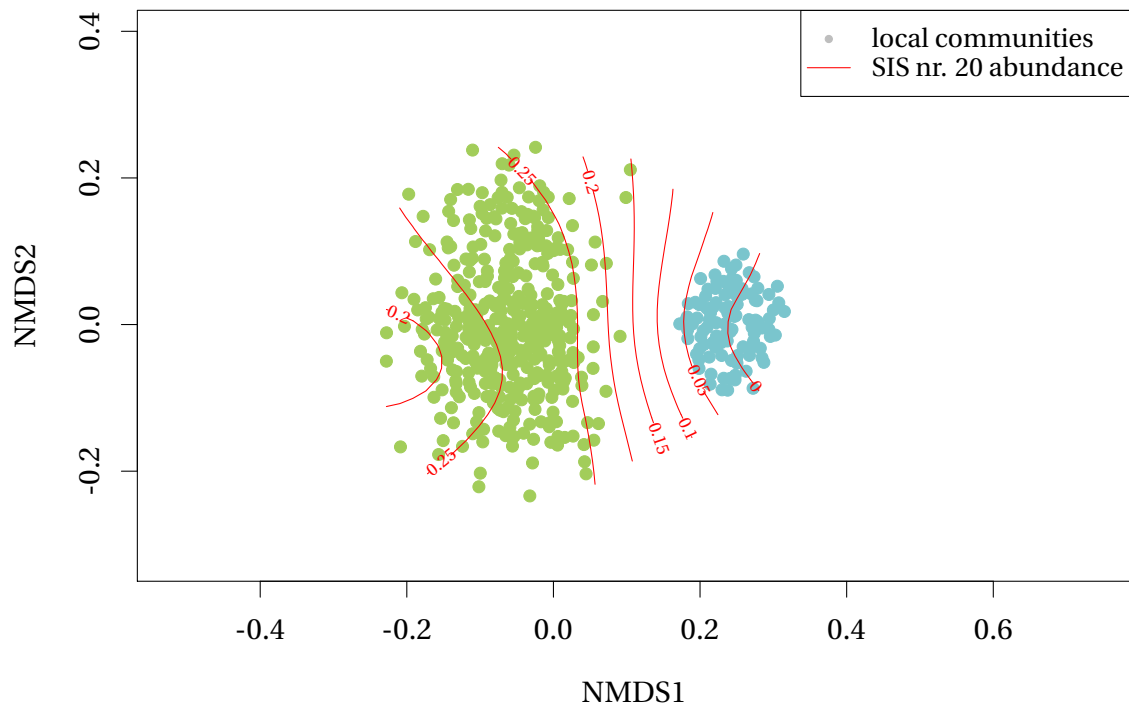


Figure 3.2: The red lines show the gradient of the relative abundance of the strongly interacting species (nr. 20) in the PCA plane. They are just indicative to show the global trend and local deviations are possible.

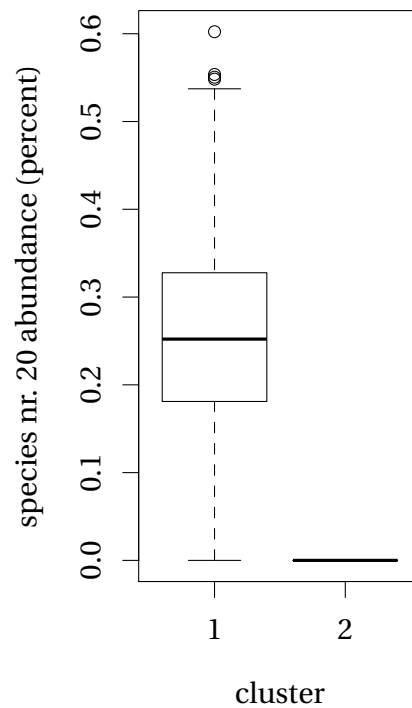


Figure 3.3: SIS abundance in the green (1) and blue (2) clusters.

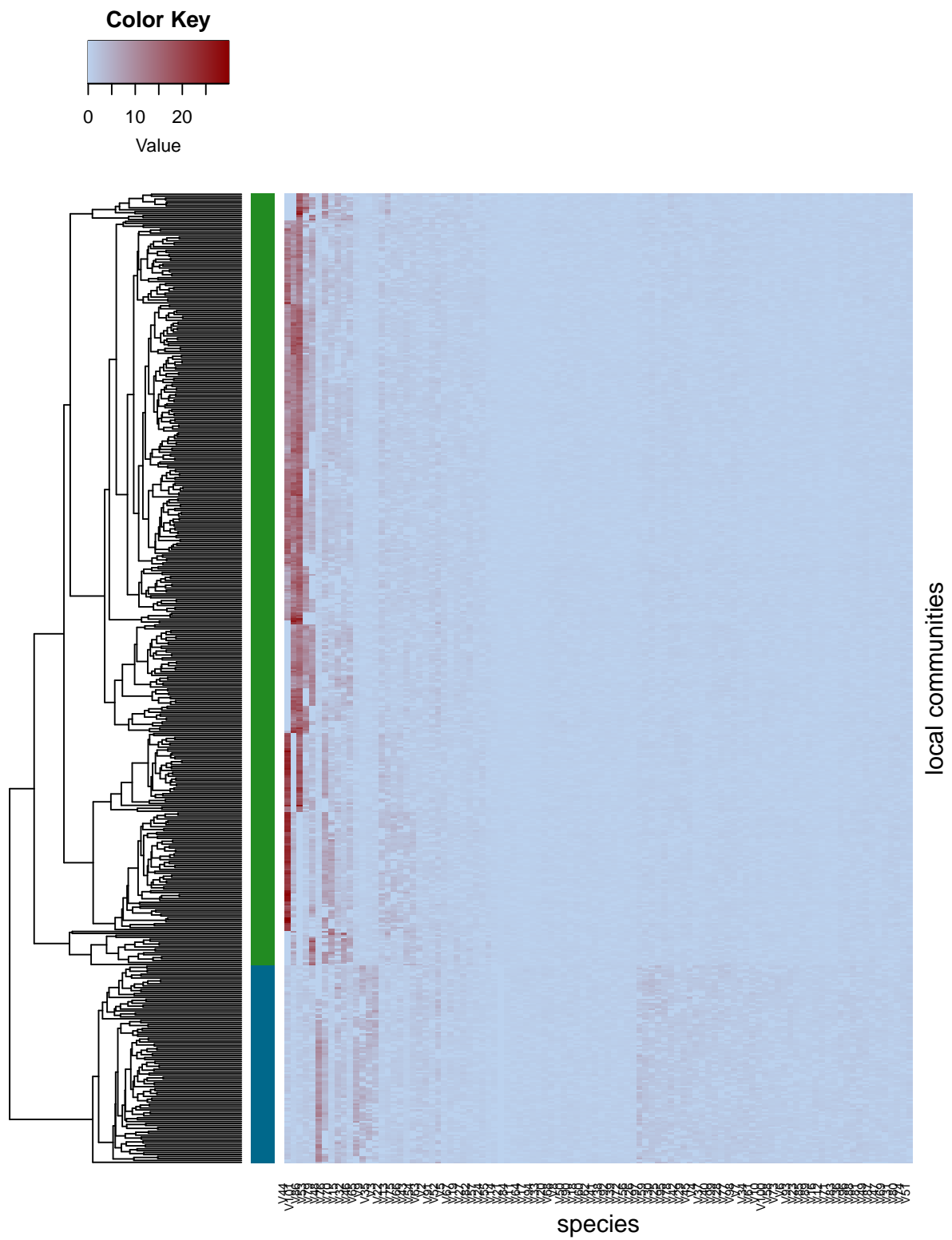


Figure 3.4: Heat map in the case of 1 strongly interacting species.

3.2 Two SISs

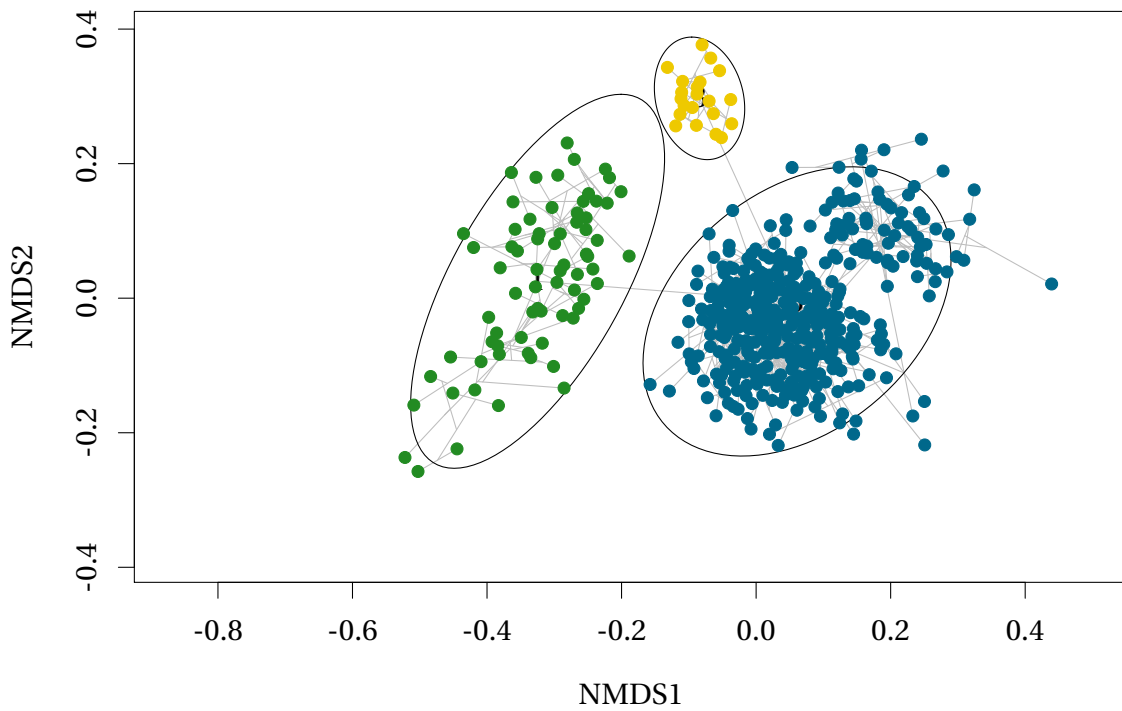


Figure 3.5

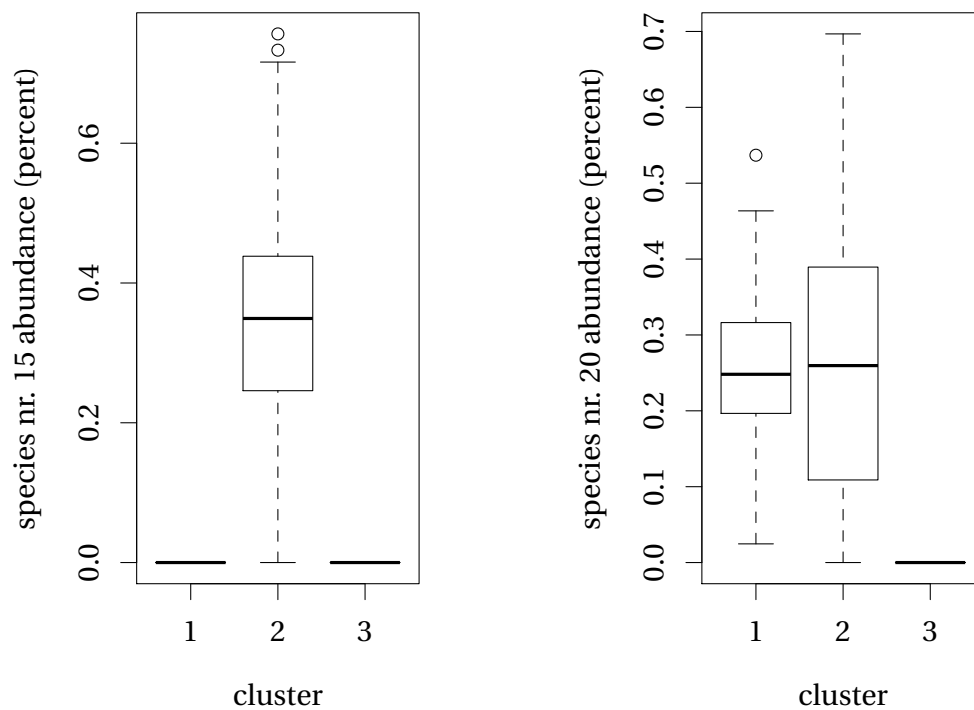


Figure 3.6: SISs nr. 15 and nr. 20 abundance in the green (1), blue (2) and yellow (3) clusters.

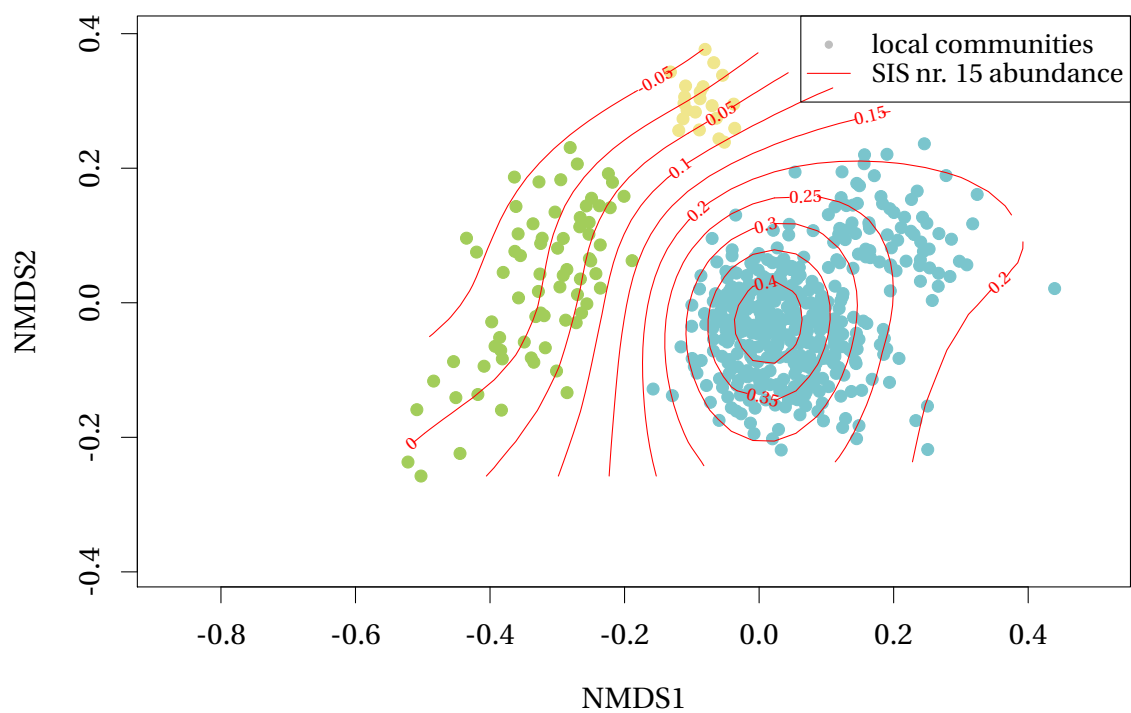


Figure 3.7

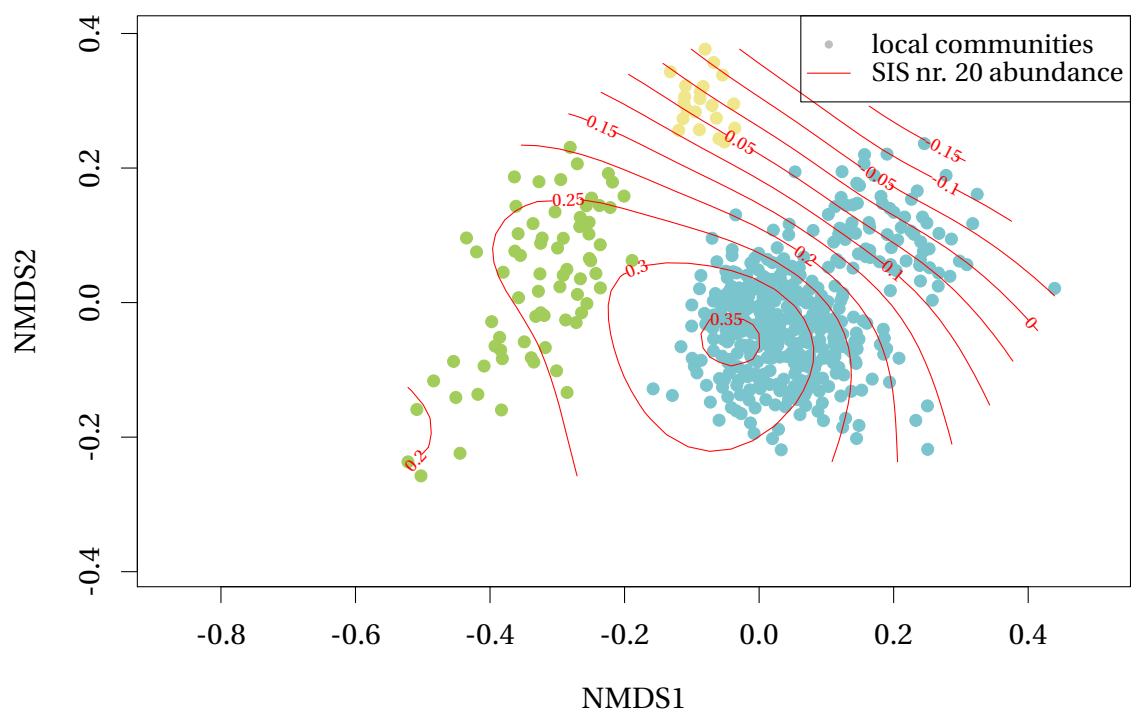


Figure 3.8

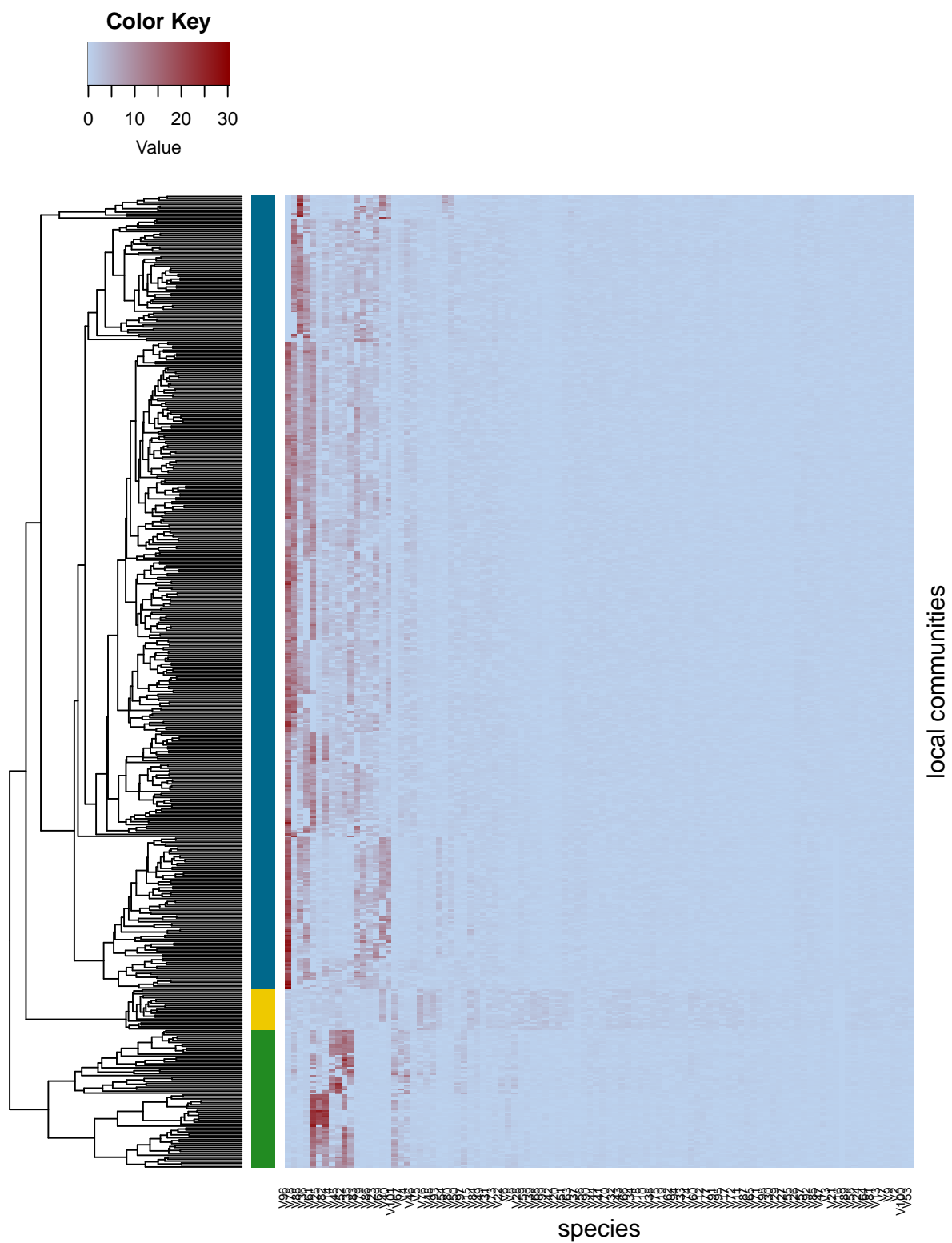


Figure 3.9: Heat map in the case of 1 strongly interacting species.