DAY 4: Meta-community modeling

German Centre for Integrative Biodiversity Research (iDiv)
Halle-Jena-Leipzig

Meta-community modeling

Course: Modeling species distribution and biodiversity patterns

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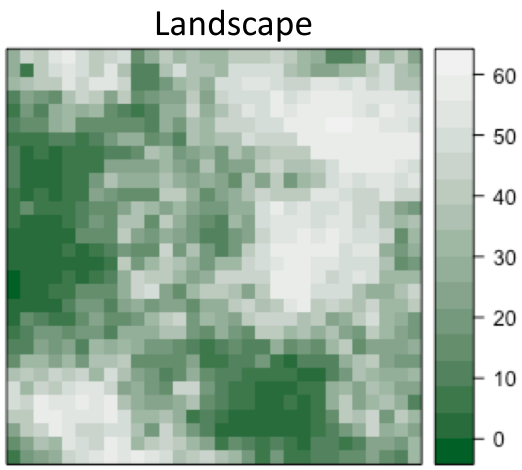
iDiv is a research centre of the
DFG Deutsche Forschungsgemeinschaft

A mechanistic meta-community model

Model SPATCOM by Duarte Viana & Jon Chase

- Goal: model the **spatial distribution** of species
- The virtual landscape is a grid
- It is an individual-based model
- Each cell occupied by maximum 1 individual
- Landscape is characterized by an environmental variable (pH, soil water, temperature, …)



Viana DS & Chase JM (2019): „Spatial scale modulates the inference of metacommunity assembly processes". *Ecology*, **100**:1–9.

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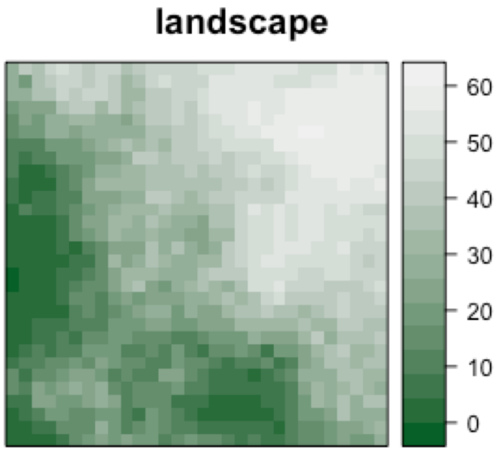
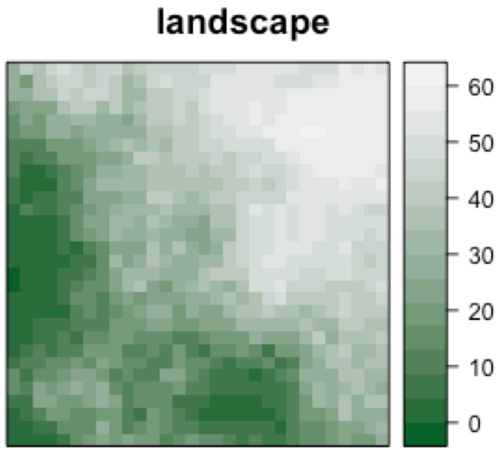
First step: Initialization

- Randomly generate the virtual landscape



First step: Initialization

- Randomly generate the virtual landscape
- Then, a fixed number of cells (80%) are filled with individuals



meta-community

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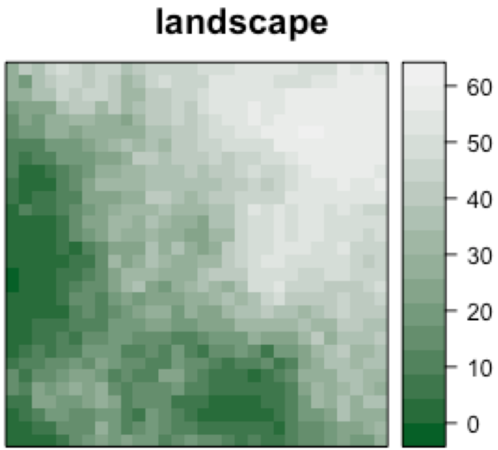
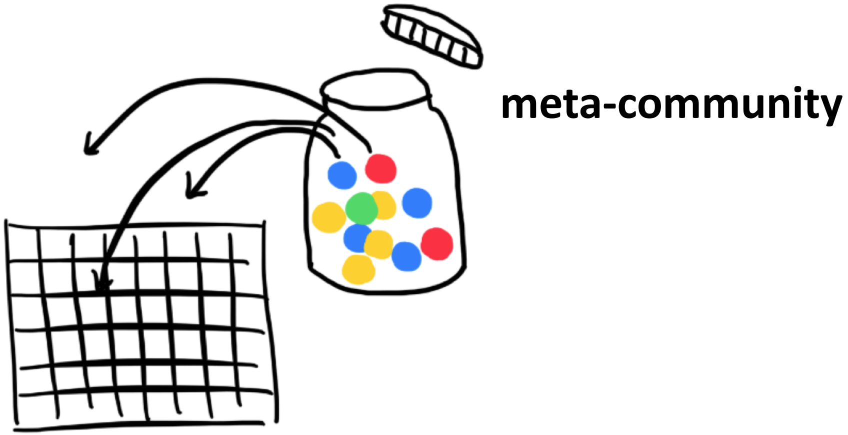
First step: Initialization

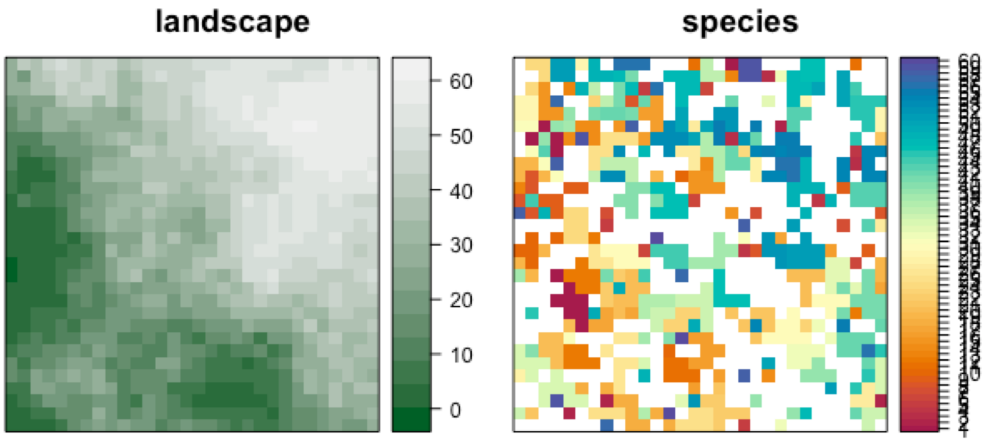
- Randomly generate the virtual landscape
- Then, a fixed number of cells (here 80%) are filled with individuals
- These individuals are drawn randomly from the metacommunity





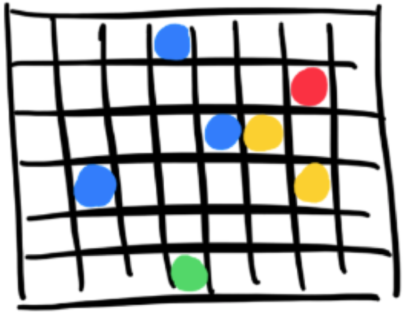
First step: Initialization

- Randomly generate the virtual landscape
- Then, a fixed number of cells (here 80%) are filled with individuals
- These individuals are drawn randomly from the metacommunity
- From there, the simulation is started



Model processes

In each time step, the following happens:



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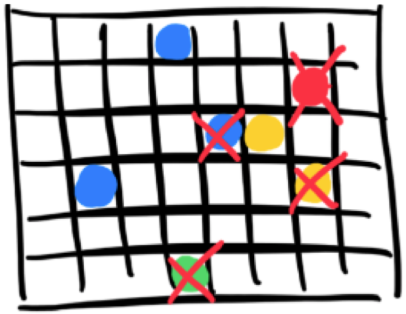
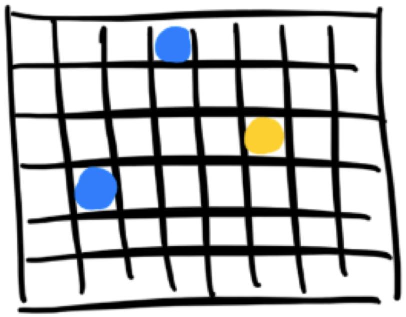
Model processes

In each time step, the following happens:

1. Mortality (fraction of *D* individuals dies)



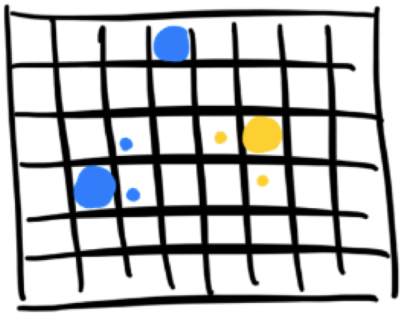
Model processes



In each time step, the following happens:

1. Mortality (fraction of *D* individuals dies)
2. Colonization:

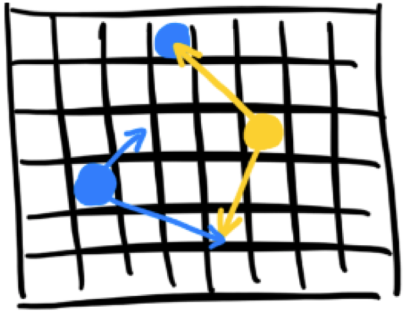
Model processes



In each time step, the following happens:

1. Mortality (fraction of *D* individuals dies)
2. Colonization:
   a) Reproduction (fraction of *M* individuals reproduces by producing *Z* propagules each)

Model processes



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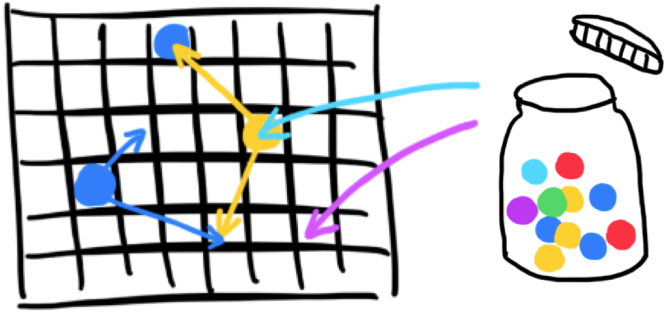
Model processes



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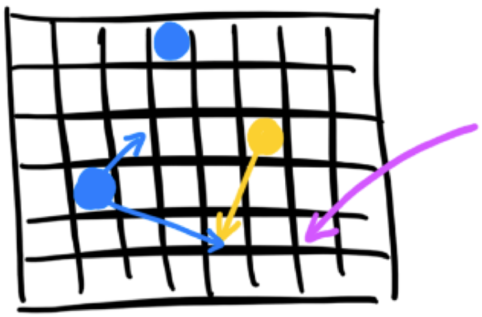
Model processes



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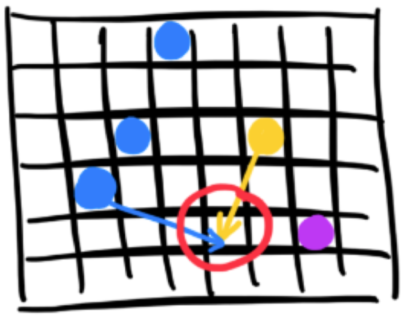
   d) Competition: Only a few propagules actually survive. Propagules arriving at occupied cells die (priority effect). Propagules arriving at empty cells compete for colonization. Competition takes place among all arriving propagules (incl. immigrants).

Model processes



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   d) Competition: Only a few propagules actually survive. Propagules arriving at occupied cells die (priority effect). Propagules arriving at empty cells compete for colonization. Competition takes place among all arriving propagules (incl. immigrants).
   e) The winner colonizes the cell.

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Who colonises, dies, reproduces?

- This is defined by the type of meta-community mechanism
- As a first standard, we use a “species-sorting” mechanism (Leibold et al. 2004)
- Vital processes of individuals are influenced by how well adapted they are to their environment

→ **Niche** concept

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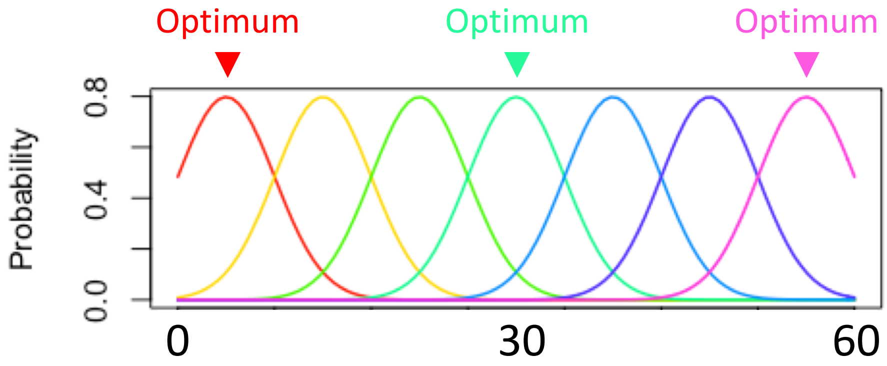
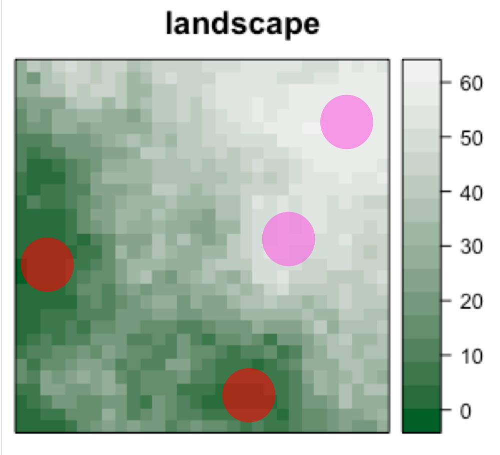
Who dies, reproduces, and colonises?

- Each species has an optimum along the environmental gradient
- It will do better at its optimum:
  - it has a higher probability to reproduce
  - it has a lower probability to die
  - It has a higher probability to win competition





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Getting started

1. Download the GitHub repository and unzip

   `github.com/chase-lab/biodiv-patterns-course`

2. Open the folder: `week1 / 4_thursday / SPATCOM_for_students`

3. Open script “`main_script.R`” in RStudio

4. Insert path to the folder in line 22

   ```
   setwd(“xxx/SPATCOM_for_students”)
   ```

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[R studio]

→ Install and load packages

→ General structure of the code

→ Output generated by SPATCOM

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Exercise I:

Get to know SPATCOM

and interpret its results

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Exercise 1: Changing model parameters

Run code section 1 to install and load packages.

Then, experiment with decreasing and increasing:

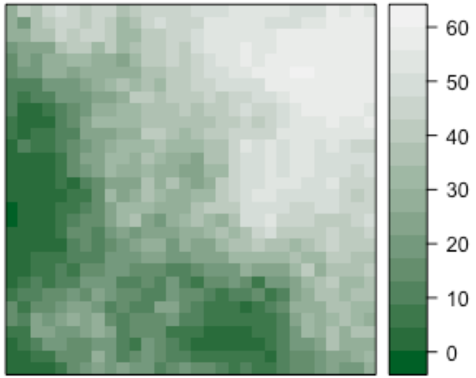
- the strength of autocorrelation in the landscape (`cor.env`)
- the sampling duration (`G`)
- the mortality rate (`D`)

→ Run code sections 2-5 to test their effect on the model results.

What happens?

Exercise 1: Autocorrelation of the landscape

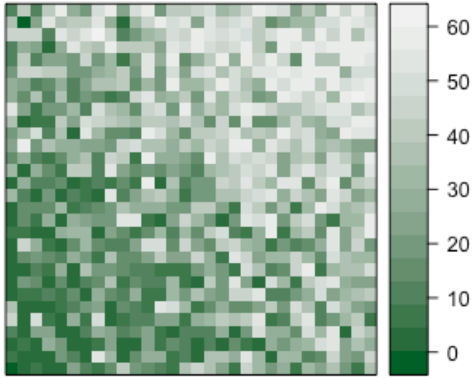
`cor.env = 30 (default)`



Exercise 1: Autocorrelation of the landscape

- For low autocorrelation, the virtual landscape is nearly random

`cor.env = 0.1`



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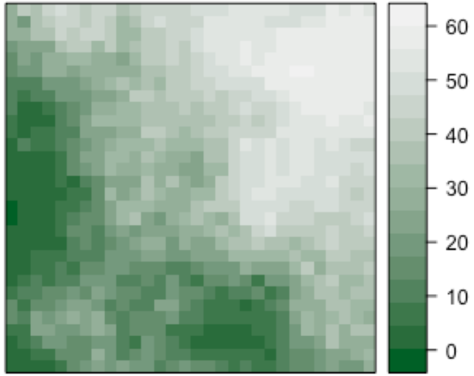

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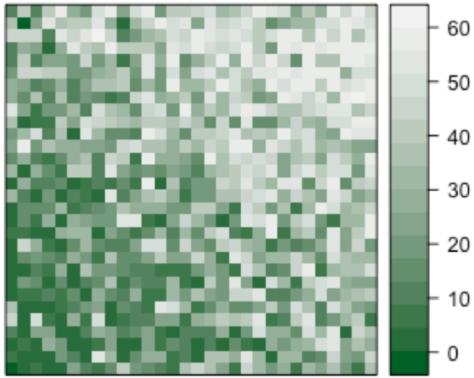
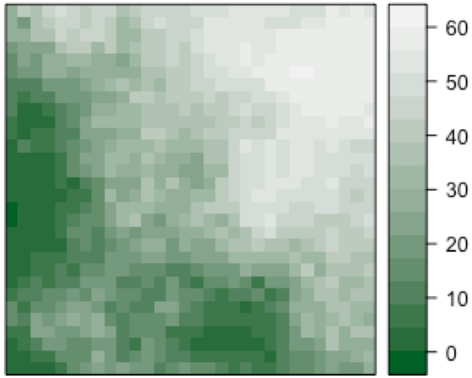
Exercise 1: Autocorrelation of the landscape

- For low autocorrelation, the virtual landscape is nearly random
- For high autocorrelation, the landscape shows a smooth environmental gradient
- The species distribution follows the environmental pattern

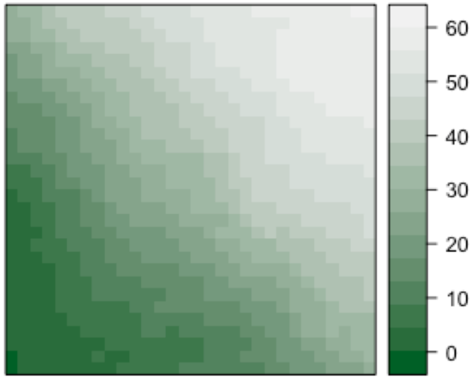
`cor.env = 0.1`



`cor.env = 30 (default)`

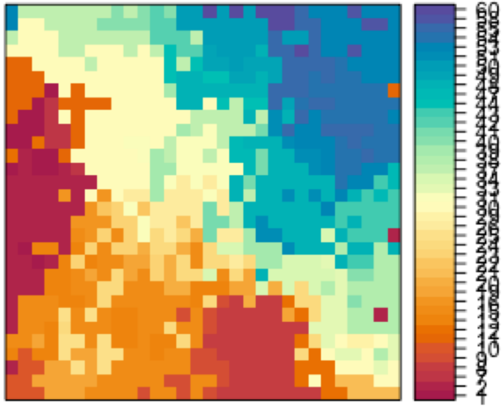


`cor.env = 1000`



Exercise 1: Sampling duration (number of generations)

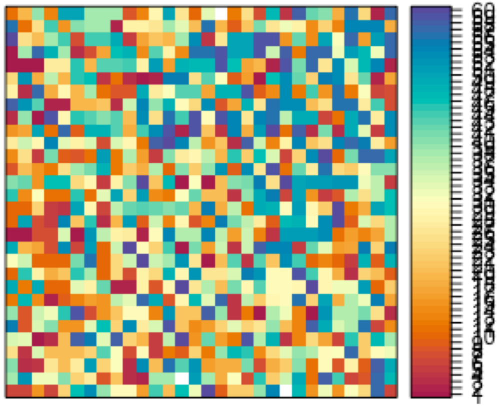
G = 1000 (default)



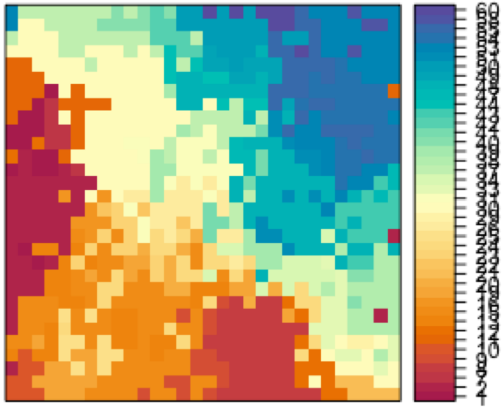
Exercise 1: Sampling duration (number of generations)

For very short simulation, the result still resembles the initial random distribution

`G = 2`



`G = 1000 (default)`

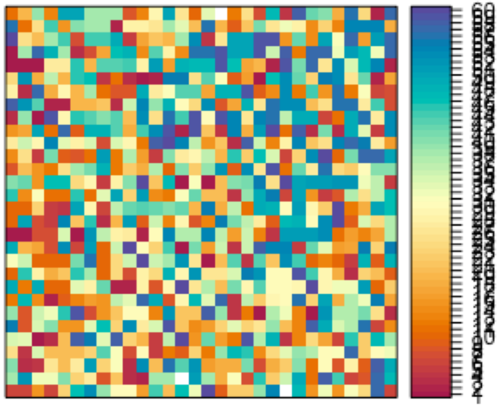


Exercise 1: Sampling duration (number of generations)

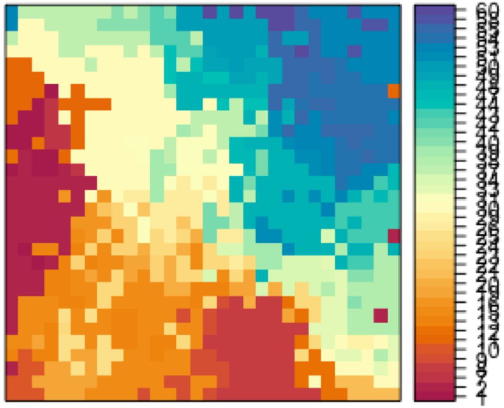
For very short simulation, the result still resembles the initial random distribution

For our default generation time, the “long term state” of the system has been reached

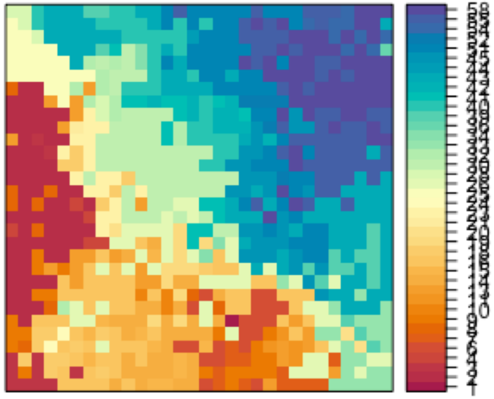
G = 2



G = 1000 (default)



G = 2000



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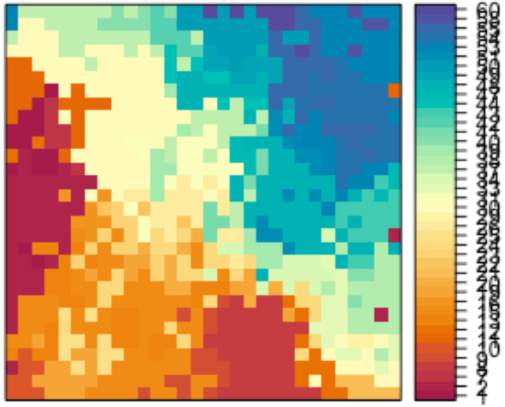
Exercise 1: Mortality rate

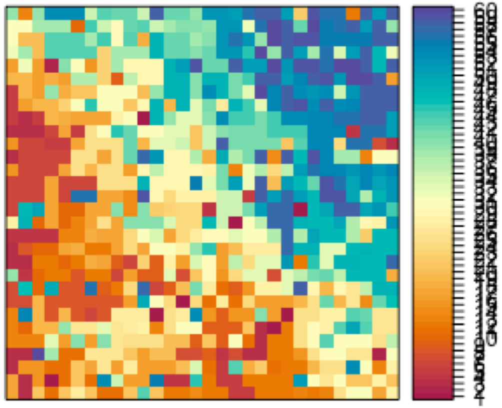
D = 0.01 (default)



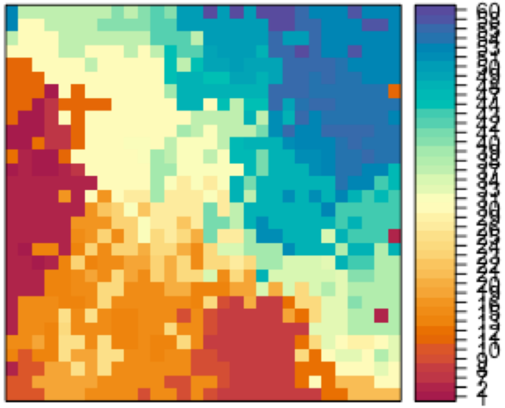
Exercise 1: Mortality rate

For very low mortality, some of the initial “random” species persist until the end

D = 0.001



D = 0.01 (default)

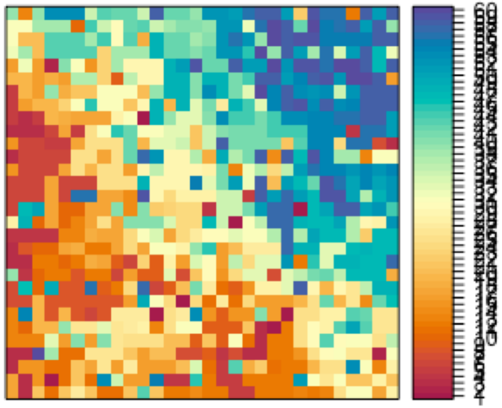


Exercise 1: Mortality rate

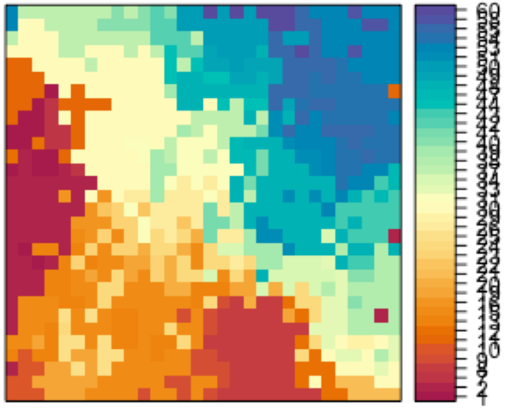
For very low mortality, some of the initial “random” species persist until the end

For very high mortality, reproduction is not high enough to fill all cells

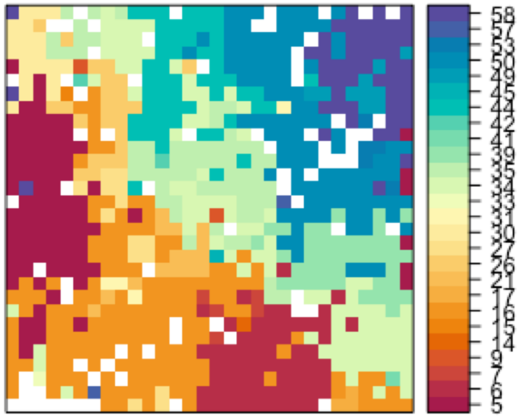
D = 0.001



D = 0.01 (default)



D = 0.9



Exercise II:

Regional species richness

Exercise 2: Regional richness

- Regional richness = number of species in the landscape
- Try to increase the regional species richness
- Experiment with the model parameters. Which options do you have?

Exercise 2: Regional richness

Examples to increase regional richness:

1. Increase the regional species pool (R = 120, increases probability for immigration of new species, but this saturates at some point)
2. Increase size of the grid (grid.side = 100, more species get a chance to establish)
3. Reduce the number of propagules (Z = 1, this makes immigration more likely, as less offspring from local reproduction compared to fixed number of immigrated)
4. Increase dispersal length (sd.disp = 30, makes it more likely that other species than the neighbors arrive at a given cell)
5. Decrease mortality rate (D = 0.001, this makes it more likely for “exotics” to persist)

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Exercise 2: Regional richness

Examples to increase regional richness:

1. Increase the regional species pool (R = 120, increases probability for immigration of new species, but this saturates at some point)
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4. Increase dispersal length (sd.disp = 30, makes it more likely that other species than the neighbors arrive at a given cell)
5. Decrease mortality rate (D = 0.001, this makes it more likely for "exotics" to persist)

→ **Restore to default parameters** to save simulation time!

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Exercise III:

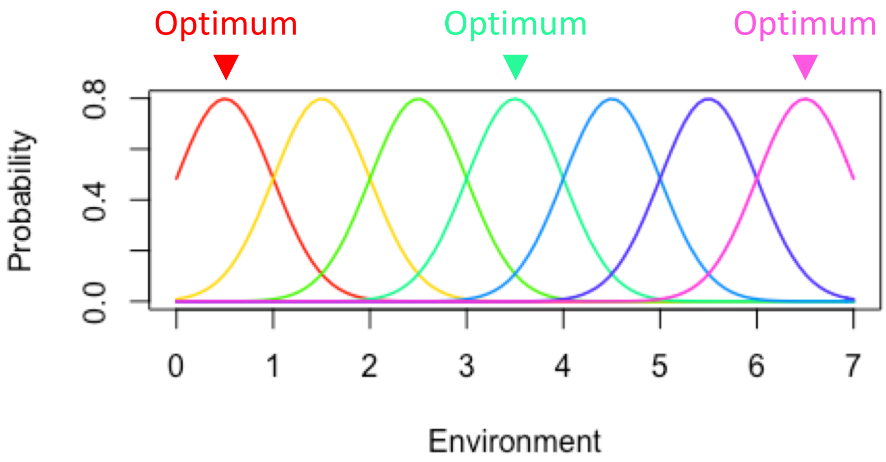
From niche-based

towards neutral

Who dies, reproduces, and colonises?

Until now:

The **better adapted** species!



Who dies, reproduces, and colonises?

Now we change the type of meta-community mechanism.

Instead of niche-based (”species-sorting”), we are going to apply **neutral mechanisms.**

This means, community dynamics are stochastic.

Thus:

- **Random** individuals dies
- **Random** individuals reproduce
- **Random** individuals win the competition and colonise

Exercise 3a

- Change the meta-community to neutral mechanism

  `meta.type = "NM"`

- Do several simulation runs for a variable landscape (<u>comment</u> the seed)

```
# Initialize environment / landscape
# set.seed(79)
```

- How does the species distribution change?
- How does it relate to the landscape?

Exercise 3a

- Change the meta-community to neutral mechanism

  `meta.type = “NM”`

- Do several simulation runs for a variable landscape (<u>comment</u> the seed)

  # Initialize environment / landscape

  # set.seed(79)

- How does the species distribution change?
- How does it relate to the landscape?
- Answer: it is random and not at all determined by the landscape!

Transition from niche-based to neutral

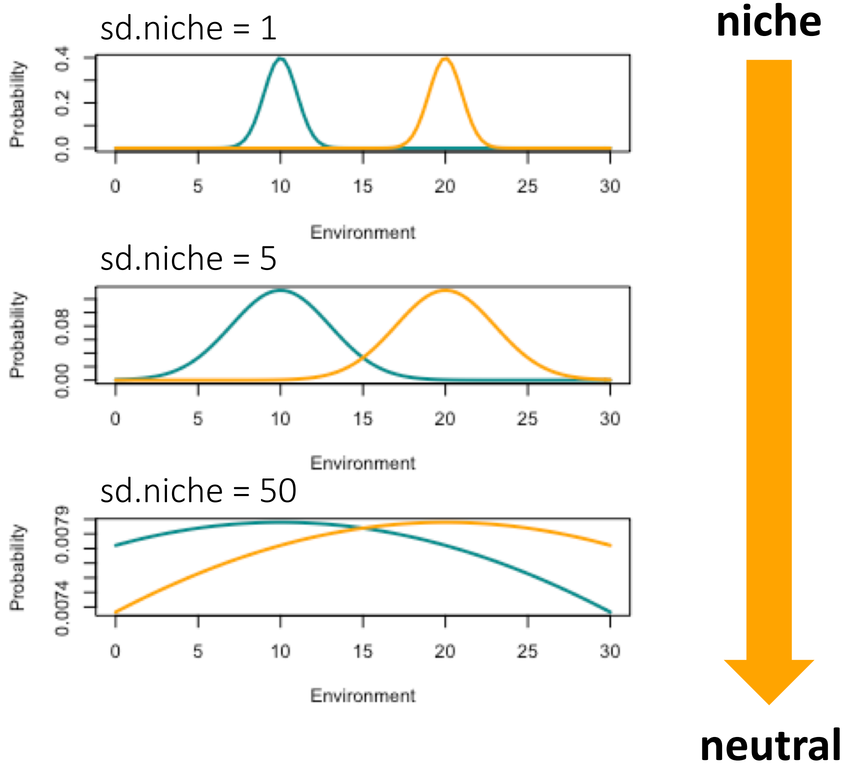
We can **change gradually** between pure niche-based and neutral dynamics

We do this by modifying the niche width:

Small niche = niche-based

Large niche = more neutral

Competition happens where multiple lines are above zero



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Exercise 3b

- Change the meta-community mechanism back to niche-based ("species-sorting")
  `meta.type = "SS"`

- Now increase the niche gradually! For example:
  ```
  sd.niche = 20
  sd.niche = 30
  sd.niche = 40
  ```

- What effect does this have on the species distribution?

Exercise 3b

- Change the meta-community mechanism back to niche-based ("species-sorting")

  `meta.type = "SS"`

- Now increase the niche gradually! For example:

  ```
  sd.niche = 20
  sd.niche = 30
  sd.niche = 40
  ```

- What effect does this have on the species distribution?

Answer: For higher niche-width (as neutrality increases), the species distribution becomes increasingly independent from the landscape.

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Exercise IV:

Impact of dispersal on

local richness

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Exercise 4

- Local richness = number of species in a **small part** of the landscape (e.g. 5x5 cells)
- Restore the niche width to the default

```
sd.niche = 10
```

- Do this for fixed landscape (uncomment the seed)

  # Initialize environment / landscape

  set.seed(79)

- Experiment with changing the dispersal length (`sd.disp`) of individuals
- For both metacommunity types (i.e. meta.type = ”SS” and meta.type = “NM”)
- What is the effect on local species richness?

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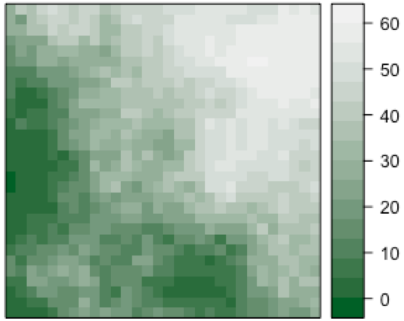
Impact of dispersal on local richness

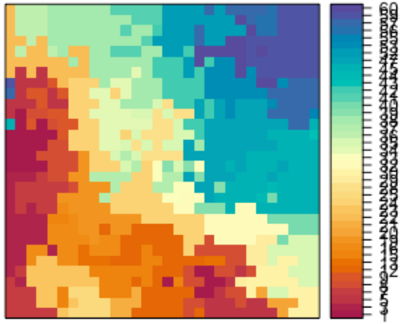
Landscape

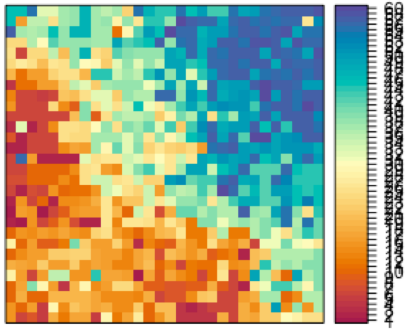


Dispersal low
(sd.disp = 0.05)

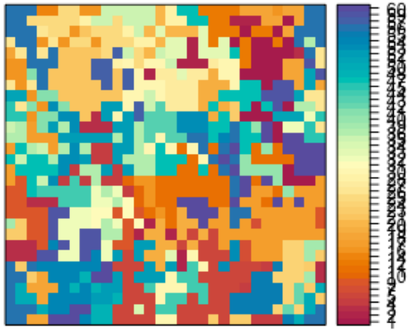
Dispersal high
(sd.disp = 50)

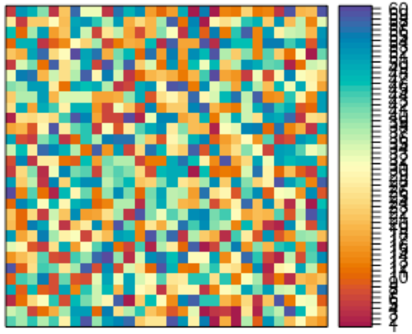
Niche-based





Neutral





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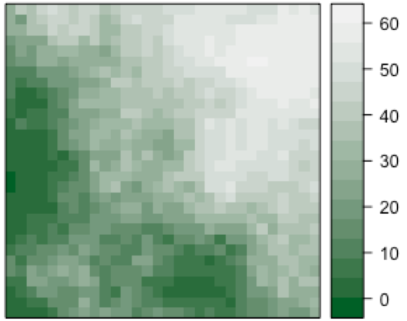
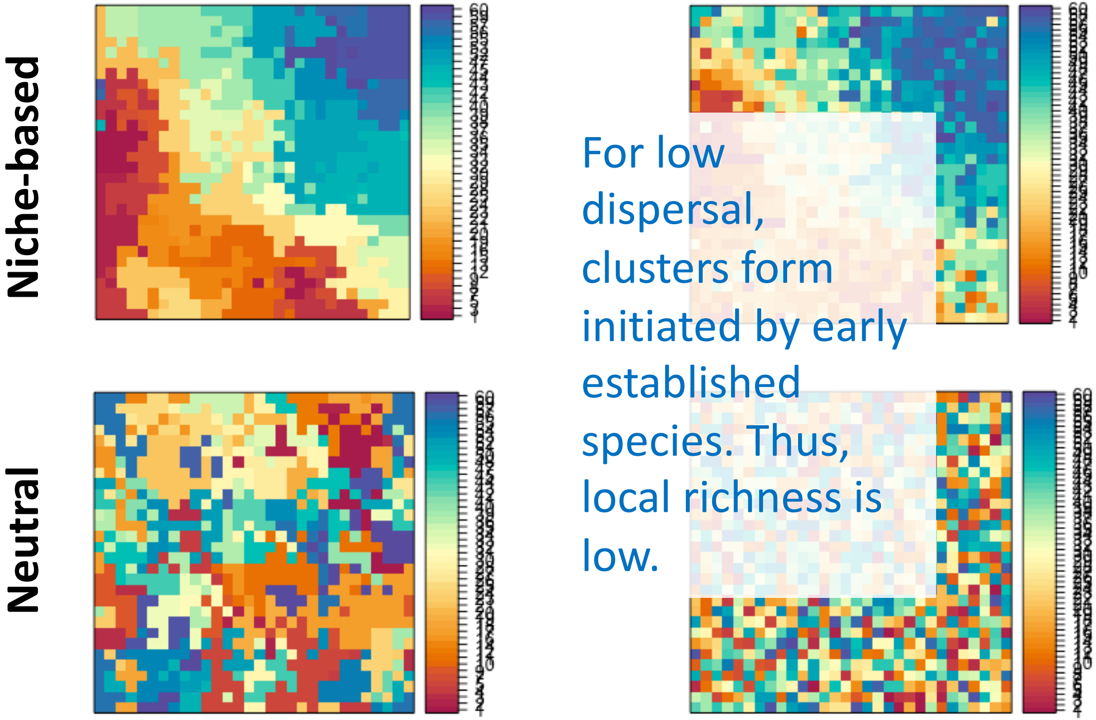
Impact of dispersal on local richness

Landscape



Dispersal low
(sd.disp = 0.05)

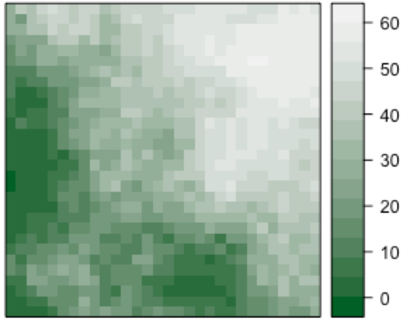
Dispersal high
(sd.disp = 50)



For low dispersal, clusters form initiated by early established species. Thus, local richness is low.

Impact of dispersal on local richness

Landscape



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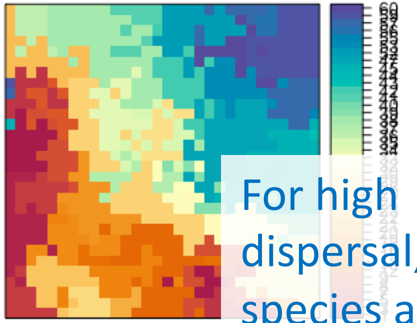
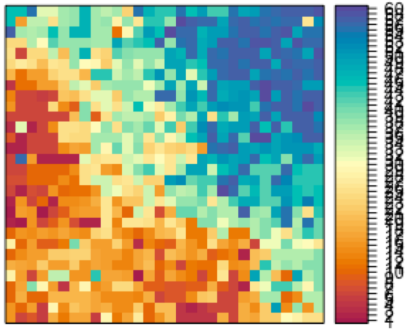
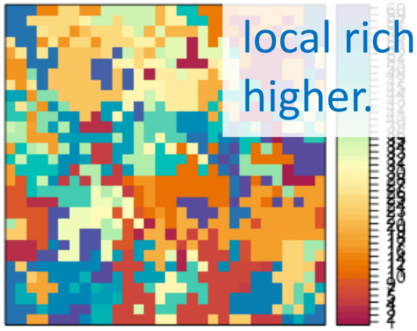
Dispersal high
(sd.disp = 50)

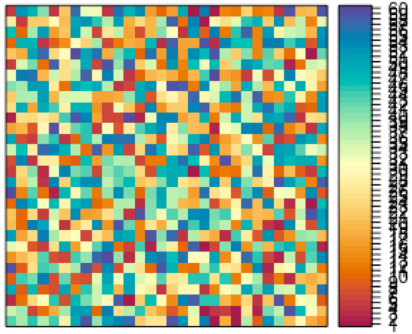
Niche-based





Neutral





For high dispersal, species are less clustered, so local richness is higher.

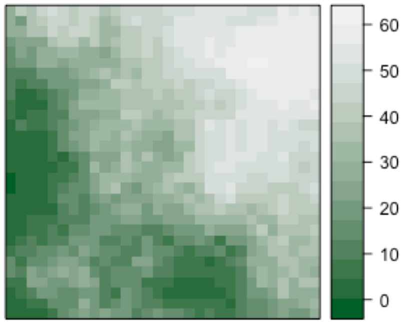
Impact of dispersal on local richness

Dispersal low
(sd.disp = 0.05)

Dispersal high
(sd.disp = 50)

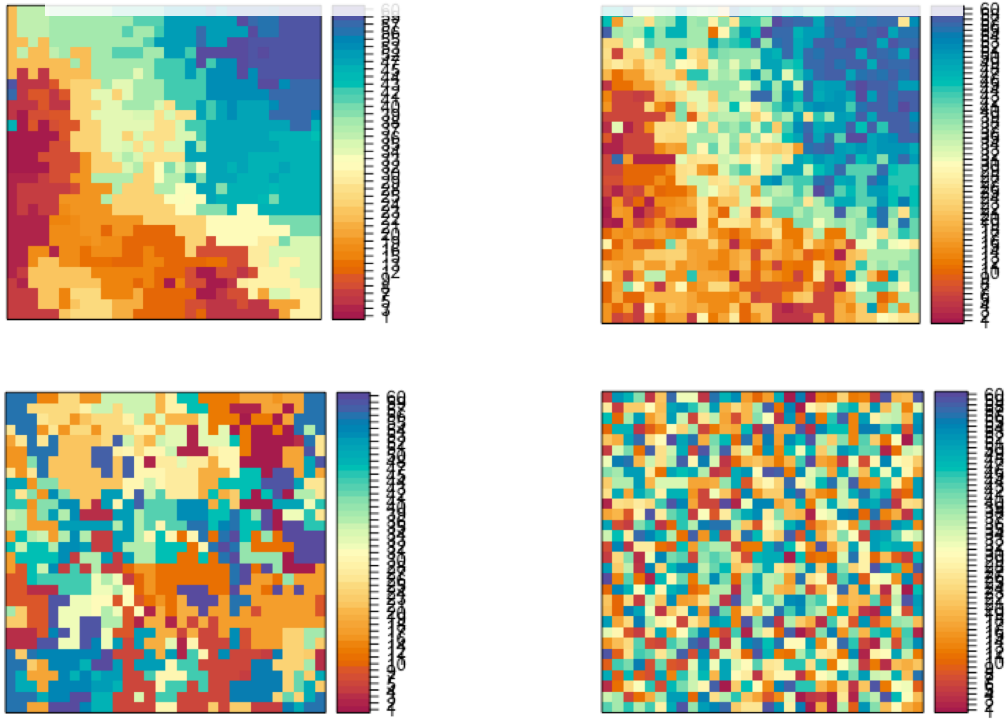
Niche-based outcomes are dependent on the landscape.

Landscape



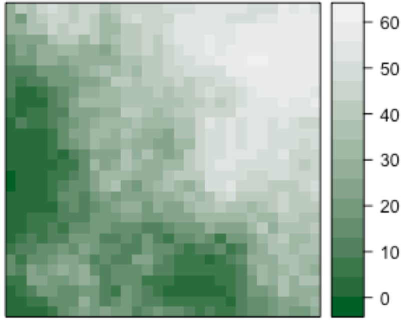
Niche-based

Neutral



Impact of dispersal on local richness

Landscape



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Niche-based

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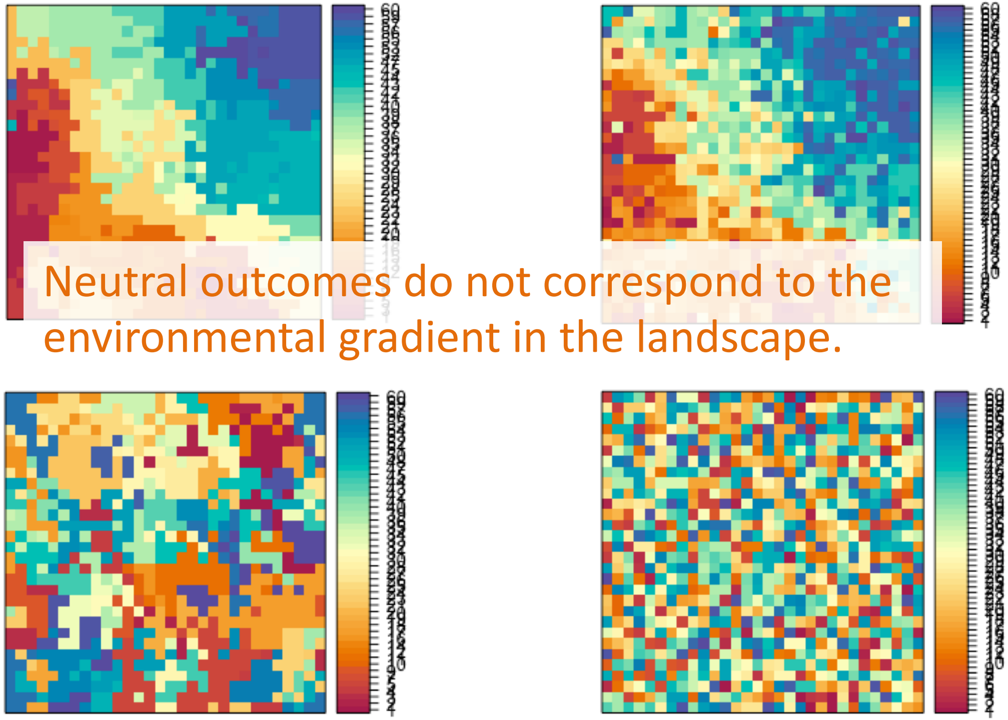


Neutral outcomes do not correspond to the environmental gradient in the landscape.

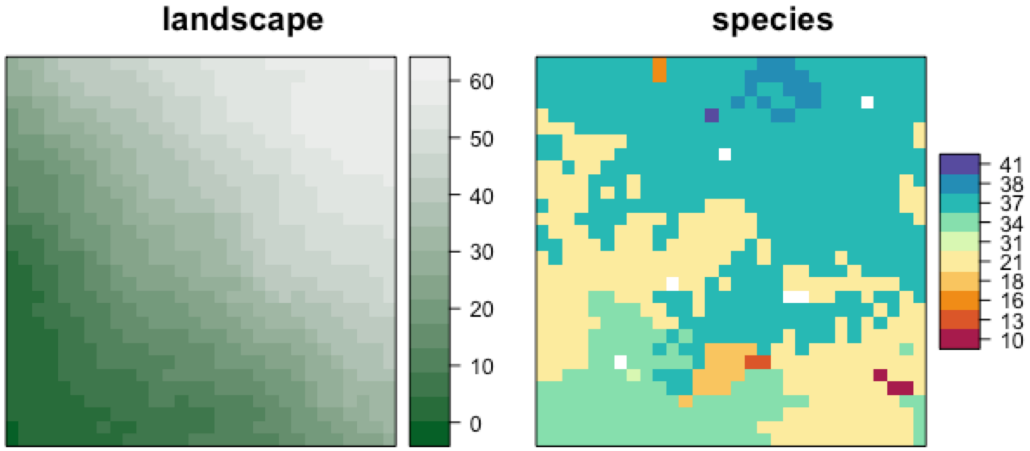
Exercise: What’s the lowest regional richness you can get?

- Prerequisites:
  - More than half of cells must be occupied at the end
  - Without changing:
    - grid size (grid.side)
    - regional species pool (R)
    - or generation time! (G)

Exercise: What's the lowest regional richness you can get?

Mine is about 7-13 with the following parameters:

```
grid.side = 30
R = 60
J = 0.05
cor.env = 1000
D = 0.9
M = 0.7
Z = 100
meta.type = "SS"
sd.disp = 0.01
sd.niche = 100
G = 1000
```



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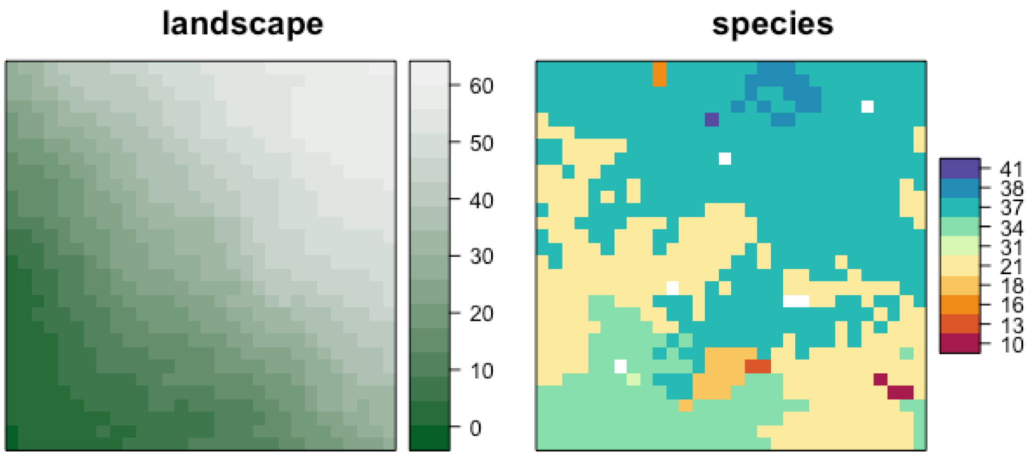


Why does this configuration produce such low richness?

→ This maximizes local reproduction,
minimizes immigration and stochasticity

What is this model used for?

What explains spatial distribution:
- the environment (niche selection)?
- or dispersal (neutral)?

→ This depends on the <u>sampling scale</u>, e.g. the spatial extent of sampling
- For small spatial extent (i.e. all the samples are from relatively similar environment), dispersal is more important

CONCEPTS & SYNTHESIS

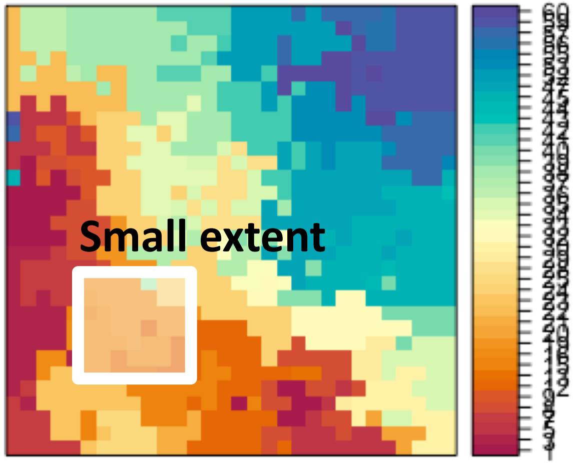
EMPHASIZING NEW IDEAS TO STIMULATE RESEARCH IN ECOLOGY

Ecology, 100(2), 2019, e02576

Spatial scale modulates the inference of metacommunity assembly processes

Duarte S. Viana[1,3] and Jonathan M. Chase[1,2]

[1]*German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Leipzig, Germany*
[2]*Institute for Computer Science, Martin Luther University Halle-Wittenberg, Halle (Saale), Germany*



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What is this model used for?

What explains spatial distribution:

- the environment (niche selection)?
- or dispersal (neutral)?

→ This depends on the sampling scale, e.g. the spatial extent of sampling

- For small spatial extent (i.e. all the samples are from relatively similar environment), dispersal is more important
- For large spatial extent (i.e. high heterogeneity within the samples), environment is more important

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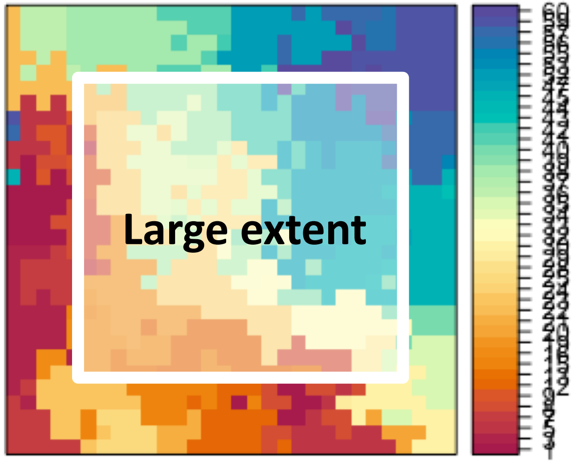

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